


# GAMMA Dental Software

*A Dental  
Documentation and  
Planning Tool*

**Instructions for Use** 

**MD**  0483

 **GAMMA**  
Medizinisch-wissenschaftliche  
Fortbildungs-GmbH





# GAMMA Dental Software

## Instructions for Use

for  
GAMMA Dental Software,  
version 8.9

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# 1 Introduction

Thank you for showing your confidence in us by purchasing GAMMA Dental Software. You have purchased an innovative medical software based on our experience of more than 25 years in the dental industry. On the following pages, we would like to help you get acquainted with the software and its modules.

## 1.1 Explanation of used symbols

The following symbols are used on the product and/or within the operating instructions:



Follow operating instructions



Medical device



Unique Device Identifier (UDI)



Manufacturer



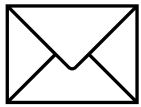
Manufacturing date



Phone number



Fax number



E-Mail address



Internet address

## 1.2 Intended purpose

GAMMA Dental Software is a standalone modular software package for the ascertainment, display, and documentation of various dental patient information. The CADIAX modules are intended for the recording of hinge axis movements of the human mandible obtained using CADIAX devices, the display of such movements, and the calculation of adjustment settings for different articulators. The CADIAS modules are intended for the identification of anatomical landmarks on radiological images of the human skull and the creation of cephalometric tracings and analyses thereof. The CADIAS 3D module is intended for the visualization and analysis of static and dynamic occlusion of 3D dental models in a virtual articulator. All other modules support the presentation and documentation of the acquired information.

## 1.3 Intended users

GAMMA Dental Software is intended for professional use by dental practitioners and dental technicians.

Using the CADIAX and CADIAS modules of GAMMA Dental Software requires the user to be acquainted with the basic methods of acquisition and interpretation of condylographic and cephalometric data, respectively. Optionally, the user may enroll in postgraduate education courses, where the advanced theoretical and practical aspects of said tasks are taught by experienced practitioners. Such education programs are common practice in this field of dental medicine.

Successful operation of GAMMA Dental Software requires the user to have basic knowledge regarding the user interface conventions of the Microsoft Windows operating system. The installation, activation, and operation of the software is described in the instructions for use and can be performed by the qualified end user. Additional training focusing on the tools and workflows of GAMMA Dental Software is not required, but can be individually arranged with GAMMA or one of its international distributors.

## 1.4 About this manual

The authors of this user manual assume that the reader has a basic knowledge in the fields of condylography, working with a face-bow, and transferring the cranial relation into an articulator.




In addition, basic knowledge of the Microsoft Windows operating system is required. You should be familiar with the user interface and other operational elements of Windows programs. This handbook is not a substitute for a basic education in using the Windows operating system. If you have only little or no knowledge of Windows, we recommend that you first become acquainted with the system. This will make it much easier to work with GAMMA Dental Software.

Within the descriptions of this manual, it is assumed that the reader has activated his software with a license that allows the usage of all modules of GAMMA Dental Software ("AM" edition). Hence, it might

happen that this manual describes functions that are not available with your license (refer to section "Compare editions" <sup>16</sup>).

## 1.5 Symbols and notations

Special attention will be brought to important aspects using the following symbols:

	<b>Warning</b>	Possible sources of error, or the danger of a possible operational error.
	<b>Attention</b>	Especially important information regarding the topic being described.
	<b>Information</b>	Useful tips and tricks.

The following symbols and notations will be used in this user manual to describe certain commands and instructions for operating the software:

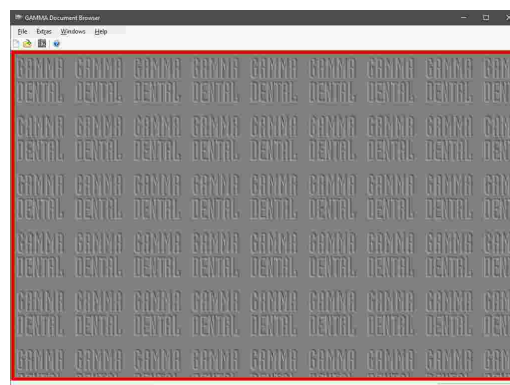
- Designations of keys will be written in italic font style. For combinations of keys, the individual key specifiers will be concatenated with plus signs (+). For example, *Ctrl+D* means: Hold down the *Ctrl* key on your keyboard and simultaneously press the *D* key.
- Names of menu items in the software will be written in italic font style. If several menu items need to be selected in succession, they will be concatenated with arrows. For example, *File → Close* means: First, click on the *File* menu item in the menu bar, then click on the menu item *Close* in the opened menu.

The first occurrence of ***Special Terms*** that may be used in subsequent descriptions are highlighted in bold and italic font style.

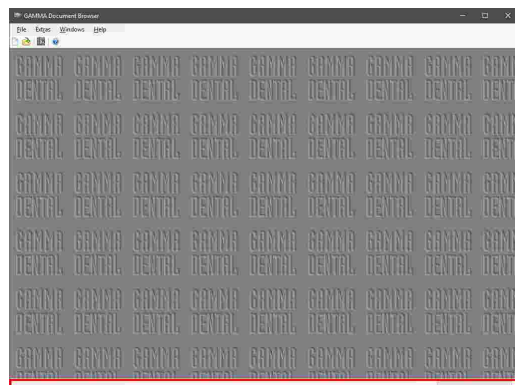
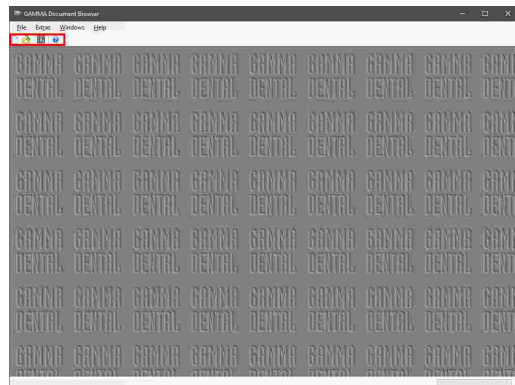
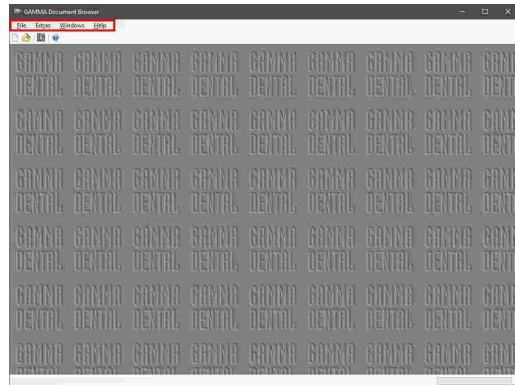
## 1.6 User interface terminology

All GAMMA software applications use a user interface layout consisting of the following parts:

- The ***Working Area*** is the area of the application that displays the actual patient data and will therefore receive the highest amount of attention and interaction.



- The hierarchical menu structure of the **Menu Bar** at the upper border of the window provides access to many of the application's functionalities. Most general application settings that are independent of the actual patient data can be configured here.
- The **Tool Bar** that is located below the menu bar provides icons to quickly access commonly used functionalities. The availability of these icons can depend on the actual state and working context of the application.
- The **Status Bar** at the lower border of the window displays contextual information regarding the actual state of the application as well as progress information in the case of long-running tasks.



## 1.7 Compare editions

GAMMA Dental Software is available in several editions with varying sets of features. Depending on your license code, some of the features described in this manual might not be accessible in your software. Please contact GAMMA or your local dealer in case of any questions regarding the pricing of the individual editions and upgrade possibilities.

The following table shows which software modules are included in which edition of GAMMA Dental Software. Please also find a brief description of the individual modules below.

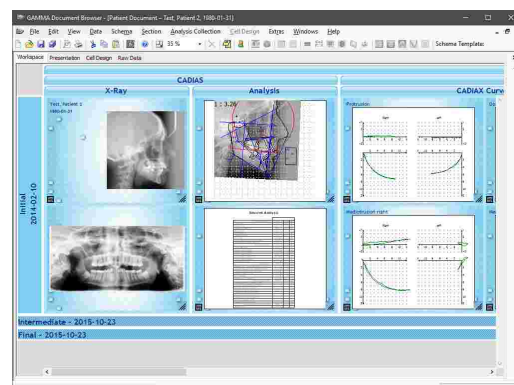
Software module	Edition				
	Viewer	C	C3D	C3D+	AM
GAMMA Document Browser	✓	✓	✓	✓	✓
GDSW classic	✓	✓	✗	✓	✓
<b>CADIAX (Condylology)</b>					
Condylology recording with CADIAX compact 2	✗	✓	✗	✓	✓
Condylology recording with CADIAX 4	✗	✗	✗	✗	✓
Digitization of analog condylology recordings	✗	✓	✗	✓	✓
Input of cusp tips coordinates for wax-up	✗	✗	✗	✓	✓
Analysis of condylographic recordings	✓	✓	✗	✓	✓
<b>CADIAS (Cephalometry)</b>					
Creation of cephalometric tracings	✗	✗	✗	✓	✓
Cephalometric analysis and treatment visualization	✓	✗	✗	✓	✓
<b>CADIAS 3D (Occlusion analysis in 3D)</b>					
Import of 3D dental models	✗	✗	✓	✓	✓
Occlusion analysis based on 3D dental models	✓	✗	✓	✓	✓

The icons used in the table above are to be interpreted as follows:

- ✓ Module is included.
- ✗ Module is not included.

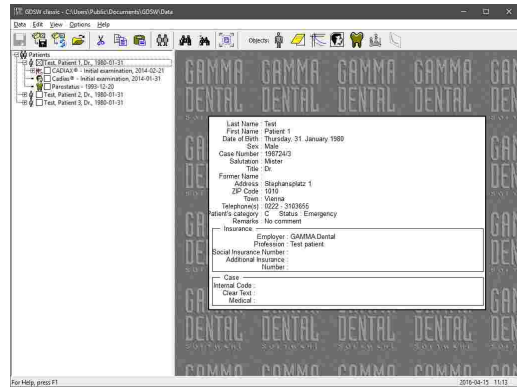
### GAMMA Document Browser

GAMMA Document Browser enables the aggregation and management of all kinds of patient data while keeping it in a structured and presentation-ready form.. It also provides convenient access to the applications of the CADIAX, CADIAS, and CADIAS 3D software modules. For more information, please refer to chapter "GAMMA Document Browser" <sup>34</sup>.



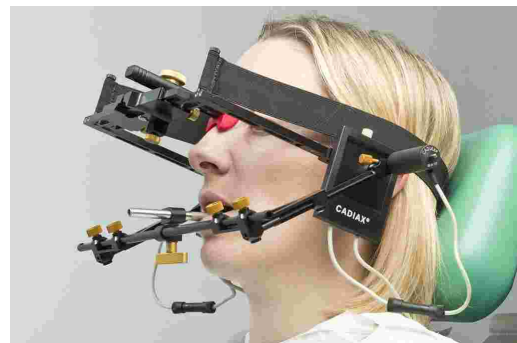
**GDSW classic**

GDSW classic is the legacy patient data management application of GAMMA Dental Software that is included for backwards compatibility. It provides access to the CADIAX and CADIAS modules, but not CADIAS 3D. For new data, we recommend using GAMMA Document Browser instead. Existing data can be converted to the new format. For more information, please refer to chapter "GDSW classic<sup>91</sup>".



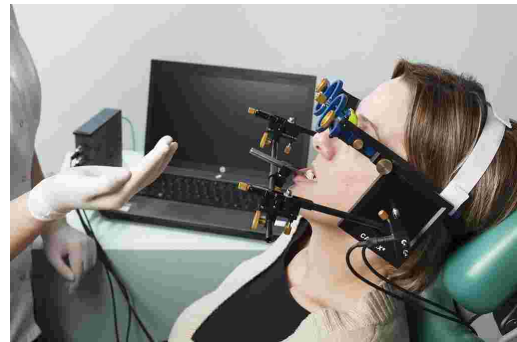
**Condylography recording with CADIAX compact devices**

Allows the recording of movements of the temporomandibular joint using the devices CADIAX compact 2 or CADIAX 4 with the "compact" sensor set. The recorded movements can then be transferred to the condylographic analysis module for detailed analysis and the calculation of articulator settings. Please refer to chapter "CADIAX compact 2 Recorder<sup>116</sup>" for more information.



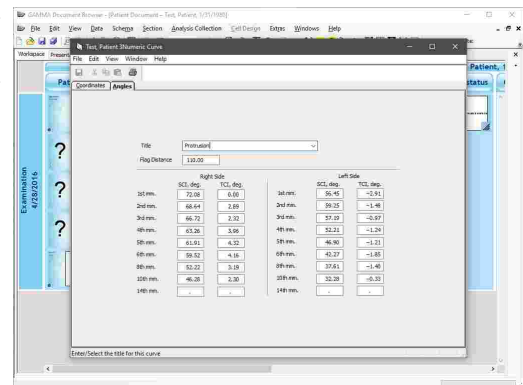
**Condylography recording with CADIAX 4 and CADIAX diagnostic**

Allows the recording of movements of the temporomandibular joint using the devices CADIAX 4 with the "diagnostic" sensor set or CADIAX diagnostic. The recorded movements can then be transferred to the condylographic analysis module for detailed analysis and the calculation of articulator settings. Please refer to chapter "CADIAX Recorder<sup>118</sup>" for more information.



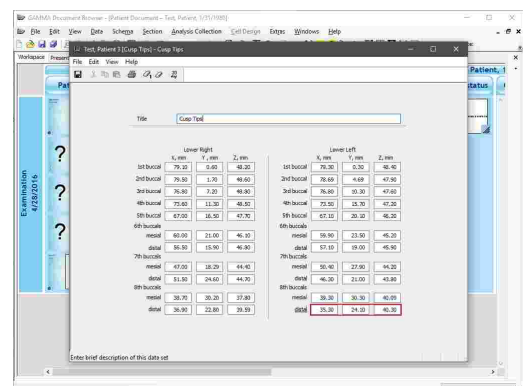
## Digitization of analog condylography recordings

Provides an input mask for entering the coordinates or angles that were measured during analog condylography tracings. The digitized movements can then be used for calculating articulator settings in the condylographic analysis module. Please refer to chapter "Numeric Curve Editor<sup>119</sup>" for more information.



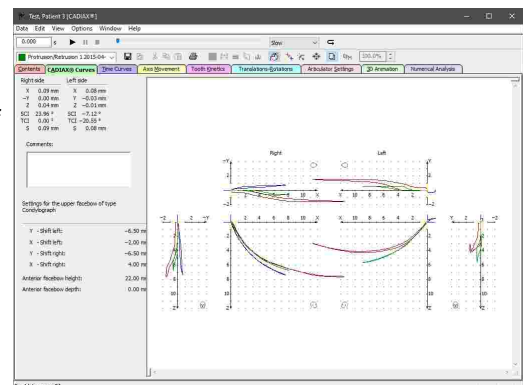
## Input of cusp tips coordinates for wax-up

Provides an input mask for entering the X/Y/Z coordinates measured on the cusp tips on dental models. These coordinates can then be transferred to the condylographic analysis module for calculating functional guidance angles and other values required for a wax-up procedure. Please refer to chapter "Cusp Tips Editor<sup>121</sup>" for more information.



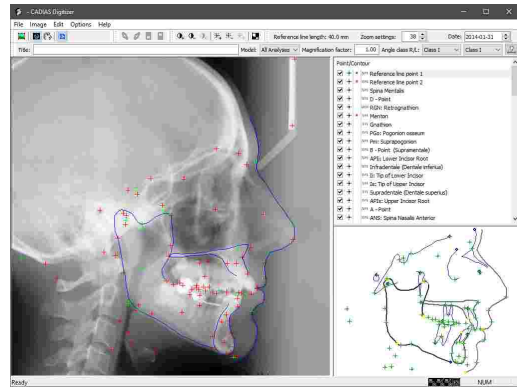
## Analysis of condylographic recordings

Aggregates the condylographic recordings made in the other modules and provides various modes of visualization for analyzing the movement patterns of the temporomandibular joint. Also allows the calculation of articulator settings based on the recorded movements and the printing of reports for documentation. Please refer to chapter "CADIAX Analyzer<sup>124</sup>" for more information.



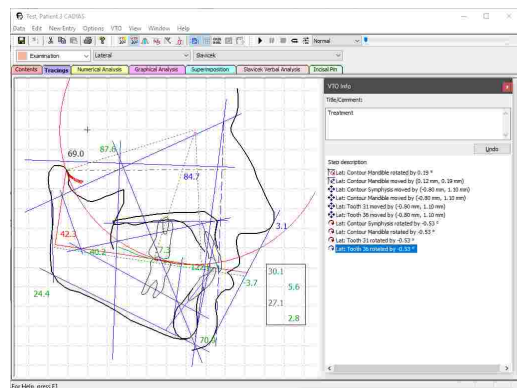
### Creation of cephalometric tracings

Allows the creation of cephalometric tracings by digitizing anatomical points and contours on various types of x-ray images. These tracings can then be transferred to the cephalometric analysis module. Please refer to chapter "CADIAS Digitizer<sup>176</sup>" for more information.



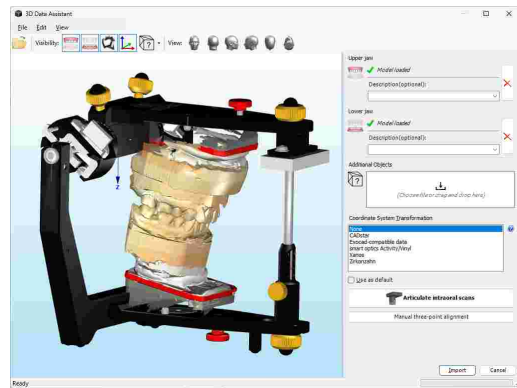
### Cephalometric analysis and treatment visualization

Allows the detailed analysis of x-ray tracings, consisting of anatomical measurements, assessment of cephalometric relations, and visualization of treatment objectives. Please refer to chapter "CADIAS Analyzer<sup>196</sup>" for more information.



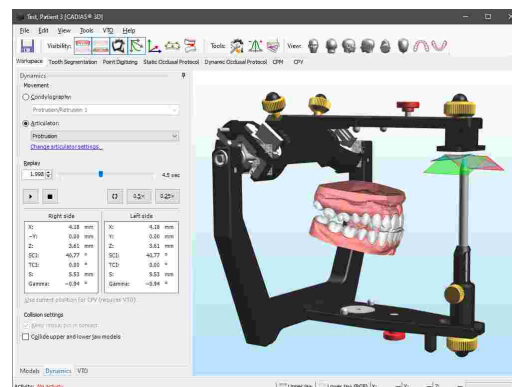
### Import of 3D dental models

Extends GAMMA Document Browser with a utility for importing and preprocessing 3D dental models, generated using 3D dental scanners or third-party dental CAD/CAM software. These models can be stored together with other data in the patient file and be analyzed in the CADIAS 3D analysis module. Please refer to chapter "Importing CADIAS 3D data<sup>82</sup>" for more information.



## Occlusion analysis based on 3D dental models

Allows the sophisticated occlusal analysis of 3D dental models in a virtual articulator or in combination with the CADIAX condylographic movements recorded on the patient. Please refer to chapter "CADIAX 3D<sup>239</sup>" for more information.



## 2 First use

### 2.1 System requirements

A computer is required in order to use GAMMA Dental Software. The following minimum requirements apply for all software modules including CADIAX and CADIAS:

<i>Operating system</i>	Windows 10 Version 22H2 (64-bit) or Windows 11 Version 24H2 (64-bit)
<i>Processor</i>	x64-based mid-range multi-core processor (Intel Core i5, AMD Ryzen 5 or comparable)
<i>Main memory</i>	4 GB RAM
<i>Screen</i>	720p resolution with 8-bit color depth

The following additional minimum requirements apply for the CADIAS 3D software module:

<i>Main memory</i>	8 GB RAM
<i>Graphics</i>	Mid-range graphics card with DirectX 11.1 support and 2 GB graphics memory (Nvidia GeForce RTX 4060, AMD Radeon RX 7600 or comparable)
<i>Screen</i>	1080p resolution with 8-bit color depth

### 2.2 Installing the software

The most recent version of GAMMA Dental Software is available for download from the *Downloads* section of our website at [www.gammadental.com](http://www.gammadental.com). There, you can also find the current Instructions for Use for all our products and additional information material for free and without registration.

Follow the steps below in order to install GAMMA Dental Software. If an older version of GAMMA Dental Software exists on your computer, the installation routine will carry out an update, which will preserve the existing personal settings.

Do not switch off your computer while installing or updating. If you are using a notebook, please ensure that the computer will not run out of power during the update or installation procedure. Moreover, please ensure that you have your license code available when launching the installation routine. You can find this code on your license letter that you received from GAMMA.

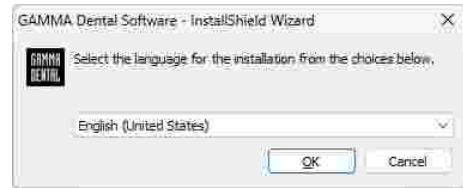


The update procedure will in no way touch your existing patient files. **Nevertheless, we recommend backing up your patient data before performing an update.** You can easily identify the patient files to back up by their \*.fgw (GDSW classic) and \*.gdb (GAMMA Document Browser) file extensions. The database directory where these files are located is indicated in the respective application.

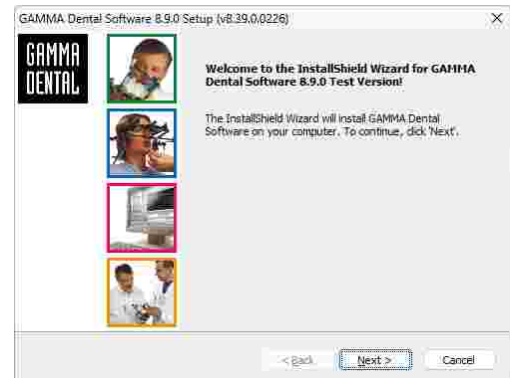
After having downloaded the installation package as a setup file, simply execute that file to start the installation.

To start the installation from the USB flash drive, simply insert it into a free USB port of your computer. The logo printed on the flash drive should typically be located on the top side. If the installation routine does not start automatically, you can launch it by executing the file *setup.exe* that you can find in the folder *Setup* on the *GDSW* drive. The Instructions for Use are located in the subfolder *Manuals*. A suitable PDF viewer application is included with every Windows installation.

After starting the installation, you will be asked to specify your preferred language of the software. You can change this setting at any time after the installation (refer to chapter "Changing the language" <sup>293</sup>).



In the following dialog, click on *Next* to continue the installation procedure.

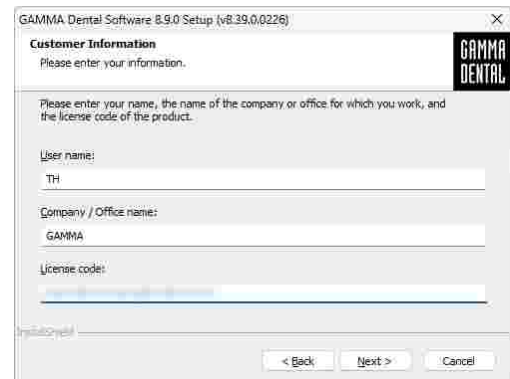


Please read through the conditions in the license agreement carefully. If you accept its terms, select the appropriate option and continue by clicking *Next*.

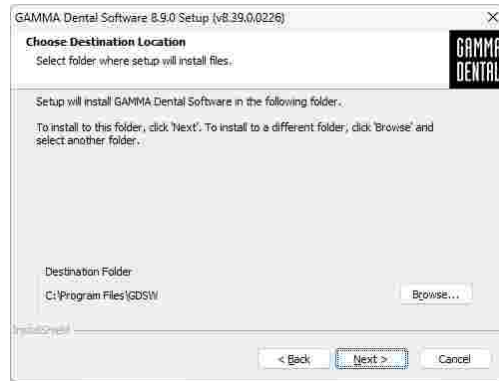


Enter your user information and your license code in the corresponding fields and click *Next* to continue. You find the license code in the accompanying license letter or on your delivery note.

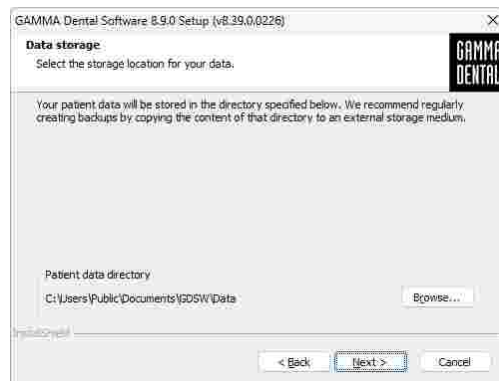
The user information entered here will be used on the printouts created by the software and can be changed at a later time (refer to chapter "Changing user information" <sup>294</sup>).



In the next step, you will be asked to which directory the program files shall be copied. We recommend using the default setting. Again, click *Next* to continue.



Lastly, specify the directory in which the software should store the patient files. This directory can be on a network drive if you want your data to be accessible from multiple workstations.

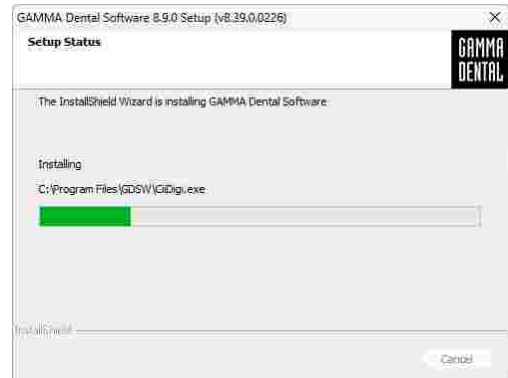


**i** If you are installing GAMMA Dental Software in a network environment with multiple workstations accessing the same file sharing server, you can configure the software to use a directory on that server for storing the patient files. It is not necessary to install the software on the server itself.

Preparations of the software installation are now completed. To start copying the program files, click *Install*.



The installation routine will now copy the necessary data onto your computer. This can take several minutes.



Installation of the software is now completed. By selecting the respective option, you can start GAMMA Document Browser or GDSW classic in order to continue with the activation procedure.



## 2.3 Starting and activating the software

You can start GAMMA Document Browser or GDSW classic via the Windows start menu (*All Programs* → *GAMMA Dental Software* → *Document Browser* or *GDSW classic*) or via the respective link on the desktop:



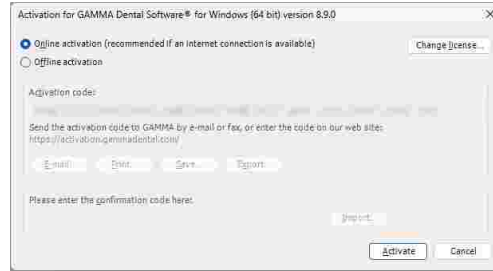
If you plan using the software on a virtual environment (e.g. Parallels Desktop), we strongly recommend to update both your operating system and your virtualization software to the latest version before activating. Otherwise, software activation might not be possible.

Please also note that an update of your virtualization software, once GAMMA Dental Software is installed, can cause hardware information used to activate the software to be changed, which will render your activation invalid. GAMMA does not take any responsibility for validity of license codes being lost this way. Furthermore, using the software on a virtual environment may cause poor performance or even the loss of certain functionalities.

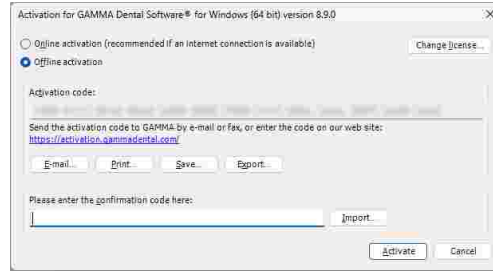
For these reasons, please deactivate all automatic update functionalities of your virtualization software and strongly consider using a native environment (Boot Camp on Apple Mac systems) instead.


When starting the software for the first time, the activation dialog will be shown.

If you are installing GAMMA Dental Software on a computer with internet connection, simply leave *Online activation* selected and click the button *Activate*. No further step is required in this case and you can immediately start using the software.



If the computer does not have an internet connection, select *Offline activation*. Send the displayed activation code to GAMMA either via mail, fax, or visit the activation website on another computer to activate your software.

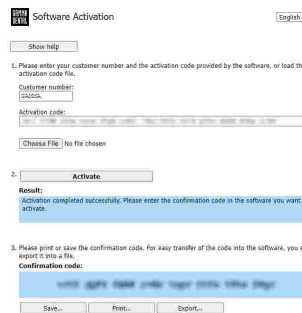


 To avoid mistakes caused by typing the codes by hand, the system provides export and import functionalities.

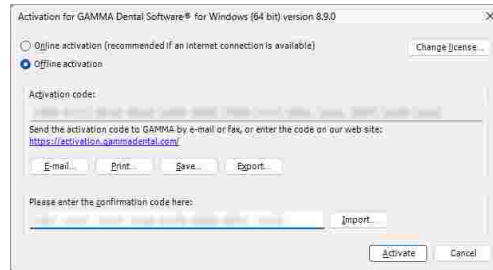
If you prefer to transmit your activation code via GAMMA's homepage, start your web browser and visit:

<http://activation.gammadental.com/>

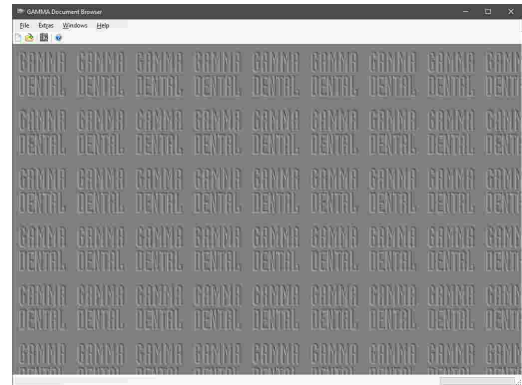
Enter your customer number and the activation code and click on *Activate*. You can find your customer number on the license letter.



Enter the resulting confirmation code that you will see on the website in the activation dialog. By clicking on *Activate*, the activation is now also completed on a system without internet connection.



Upon successful activation, the software is ready for operation.



For instructions on how to display the active licensing information and for changing the license code, please refer to chapters "Viewing the licensing information<sup>295</sup>" and "Changing the license code<sup>296</sup>", respectively.

### 3 Quickstart

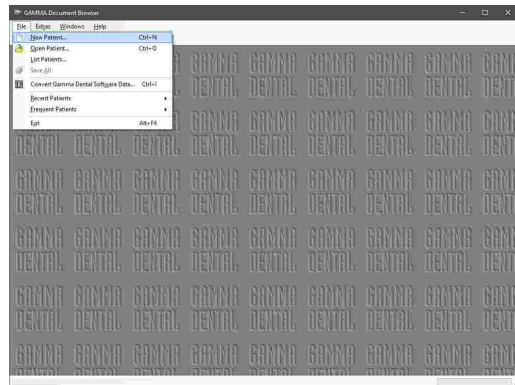
#### 3.1 Jaw movement registration with CADIAX compact 2

Follow the steps below to record condylography curves with your CADIAX compact 2 device and display a CADIAX analysis.

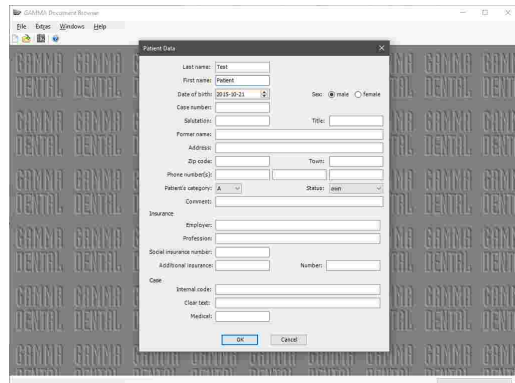
1. Connect the CADIAX device to your computer.




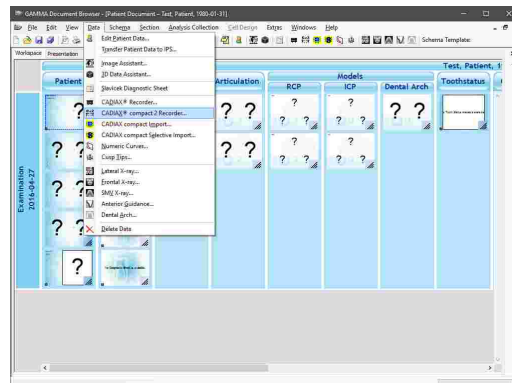
2. Start GAMMA Document Browser and create a new patient file via the menu *File* → *New Patient*.



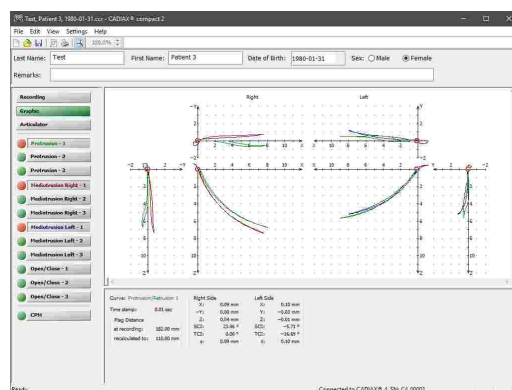
3. Enter the patient's personal information and click *OK*.



4. Start the recorder software via the menu *Data* →  *CADIAX compact 2 Recorder*.



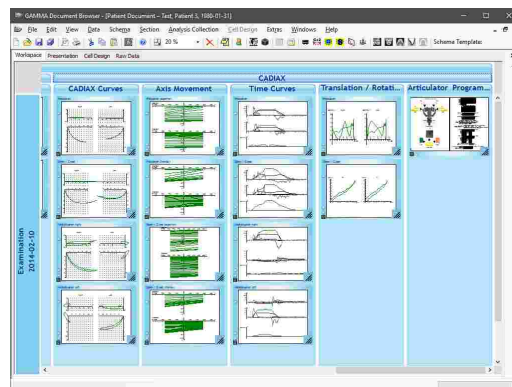
5. Perform the recordings, save the data, and close the software.



Please consult the instruction manual of your CADIAX device for detailed instructions on how to perform condylography recordings.

6. GAMMA Document Browser will automatically display several preview graphics of the recorded curves.

You can double-click any of the data areas to start CADIAX Analyzer and analyze the curves in detail.



For further information regarding the analysis of condylography recordings with CADIAX Analyzer, please refer to chapter "CADIAX Analyzer [124]".

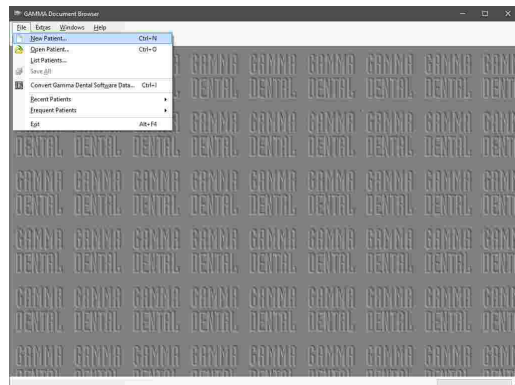
### 3.2 Jaw movement registration with CADIAX 4 or CADIAX diagnostic

Follow the steps below to record condylography curves with your CADIAX 4 or CADIAX diagnostic device and display a CADIAX analysis.

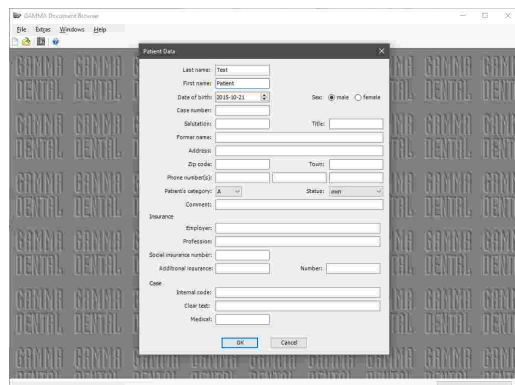
1. Connect the CADIAX device to your computer.



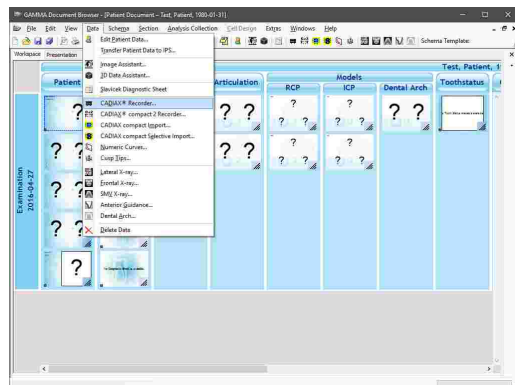
2. Start GAMMA Document Browser and create a new patient file via the menu *File* → *New Patient*.



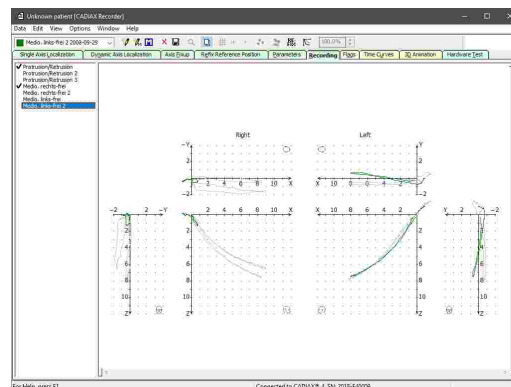
3. Enter the patient's personal information and click **OK**.



4. Start the recorder software via the menu *Data* → *CADIAX Recorder*.



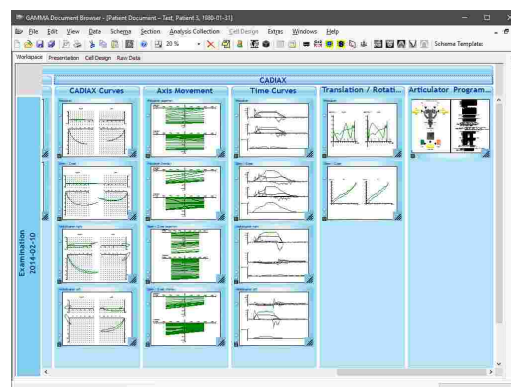
5. Perform the recordings, save the data, and close the recording application.



**i** Please consult the instruction manual of your CADIAX device for detailed instructions on how to perform condylography recordings.

6. GAMMA Document Browser will automatically display several preview graphics of the recorded curves.

You can double-click any of the data areas to start CADIAX Analyzer and analyze the curves in detail.

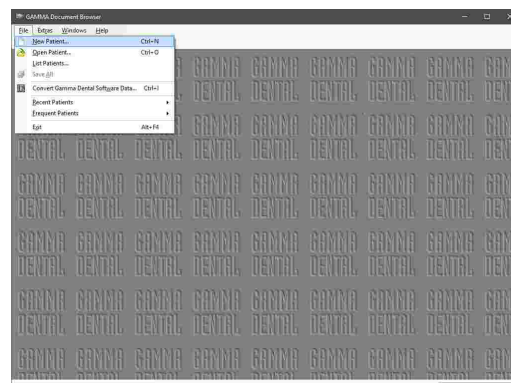


**i** For further information regarding the analysis of condylography recordings with CADIAX Analyzer, please refer to chapter "CADIAX Analyzer<sup>124</sup>".

### 3.3 Creating a lateral x-ray tracing

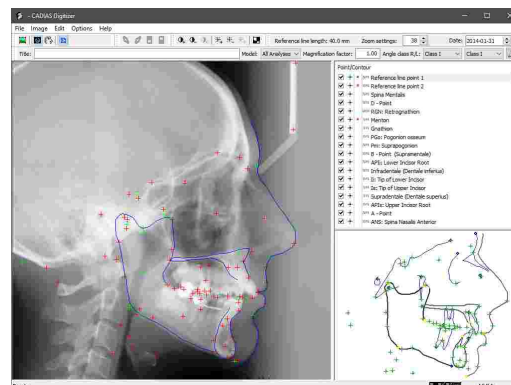
Follow the steps below to digitize a lateral x-ray image and display a CADIAS analysis.

1. Start GAMMA Document Browser and create a new patient file via the menu *File* → *New Patient*.



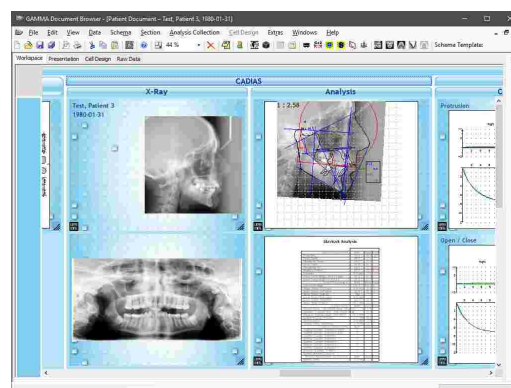


6. Digitize the required points and contours, save the data and close the software.



7. GAMMA Document Browser will automatically display a preview of the tracing and of the numerical analysis.

You can double-click any of the data areas to start CADIAS Analyzer and analyze the tracing in detail.



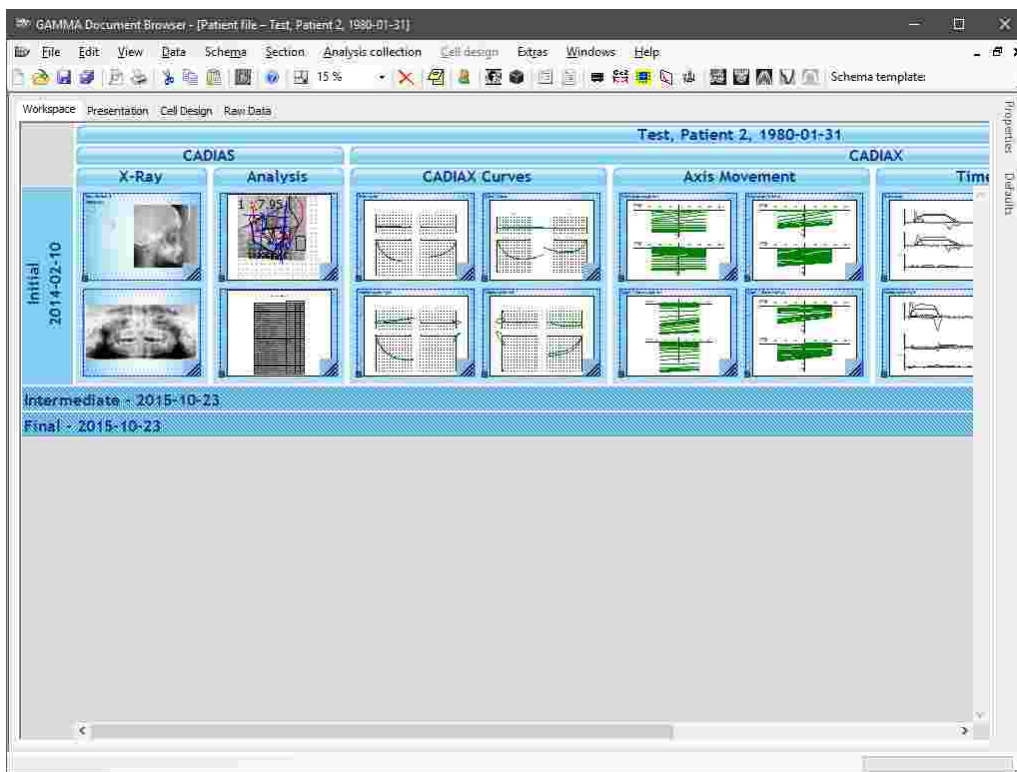
For further information regarding the analysis of x-ray tracings with CADIAS Analyzer, please refer to chapter "CADIAS Analyzer<sup>196</sup>".

## 4 GAMMA Document Browser

The **GAMMA Document Browser** is a cutting-edge dental case documentation and planning tool. It supports the user-friendly acquisition, analysis and administration of all kinds of functional diagnostic data and related documents that accumulate in a modern dental practice or laboratory.

GAMMA Document Browser provides an extensive set of tools for the visualization and presentation of various types of information. Even such heterogeneous data as e.g. images, condylographic records, Microsoft Office documents, articulator settings or diagnostic sheets can be created, organized, and integrated into patient case files.

The software itself represents a valuable tool which can even be run as a standalone patient management system for dental offices. Besides all novel features, GAMMA Document Browser of course provides the full CADIAX condylography and CADIAS cephalometry functionality known from GDSW classic (see chapters "CADIAX<sup>114</sup>" and "CADIAS<sup>175</sup>", respectively).



GAMMA Document Browser is the successor of the GDSW classic module when it comes to patient management in GAMMA Dental Software. GAMMA Document Browser provides features that far exceed the capabilities of GDSW classic while keeping your data in a form that is clearly structured and presentation-ready at any time.

When installing GAMMA Dental Software, both GDSW classic and GAMMA Document Browser are installed simultaneously. The two applications are completely independent and use different patient databases. To transition from GDSW classic to GAMMA Document Browser, the latter application provides a conversion feature that allows you to convert patient files into the new format while leaving the existing patient files unchanged (refer to chapter "Converting data of GDSW classic<sup>39</sup>").

## 4.1 Starting the application

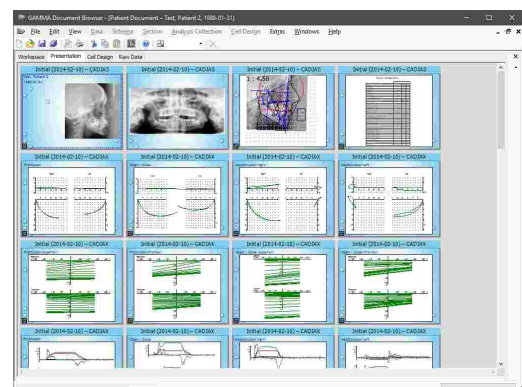
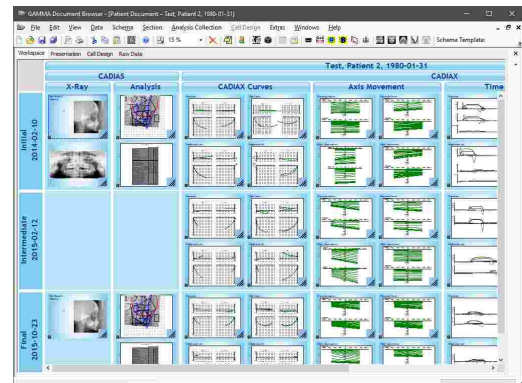
You can start GAMMA Document Browser via the Windows start menu (*All Programs* → *GAMMA Dental Software* → *Document Browser*) or via the shortcut on the desktop:



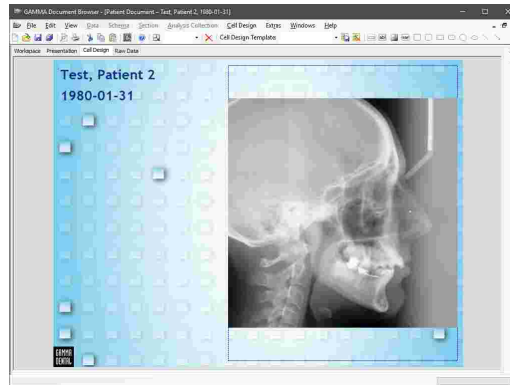
## 4.2 User interface

The user interface of GAMMA Document Browser consists of the following four views:

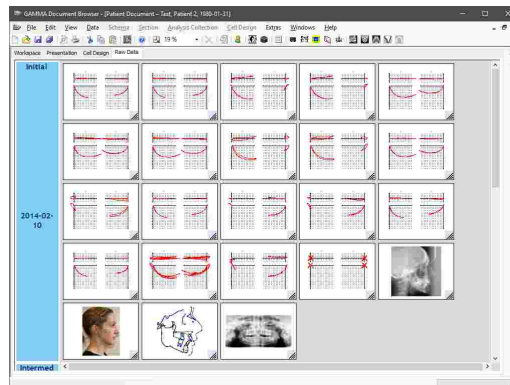
- The **Workspace** view that displays patient data structurally ordered by examination and data type. See chapter "The Workspace<sup>40</sup>".
- The **Presentation** view that displays cells sequentially and allows the information to be prepared for presentations. See chapter "The Presentation view<sup>51</sup>".



- The **Cell Design** view that enables you to customize the layout and the appearance of individual cells. See chapter "The Cell Design view<sup>54</sup>".



- The **Raw Data** view that lists all data contained in the patient database independently of the layout defined in the other views. See chapter "The Raw Data view<sup>57</sup>".




### 4.3 Managing patient files

GAMMA Document Browser stores the information of each patient in an individual \*.gdb-file on your computer. The default directory where these files can be found is as follows:

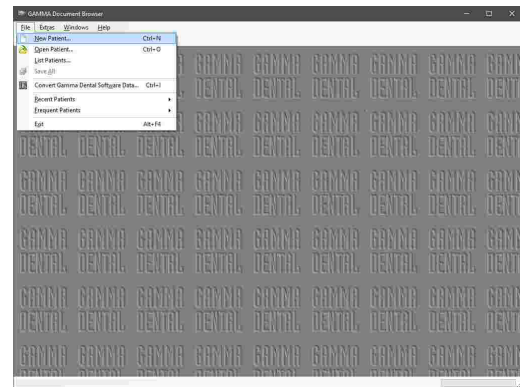
C:\Users\Public\Documents\GDSW\Data\

You can change this directory either while installing the software or at a later time (refer to chapter "Changing the database path<sup>39</sup>").

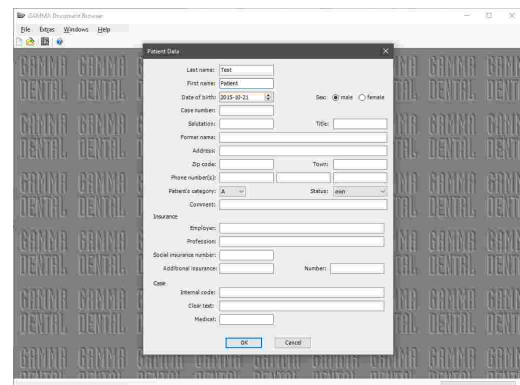
 GAMMA Document Browser comes with several ready-made patient files that you can use to get to know and experiment with the software. These "Test Patient" files are automatically copied to the database directory during installation and can safely be deleted if necessary.

### 4.3.1 Creating a new patient file

You can create a new patient file at any time via the menu *File* → *New patient*.



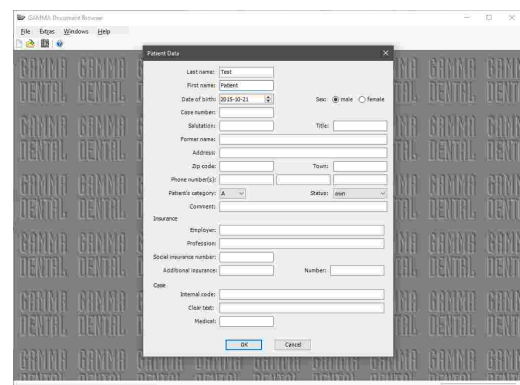
An input form will be displayed, in which you can enter the basic data of the patient (refer to chapter "Entering patient information" <sup>37</sup>).



### 4.3.2 Entering patient information

When creating a new patient file, you can enter the personal information of the patient as well as practice-specific information for identifying and categorizing the patient case.

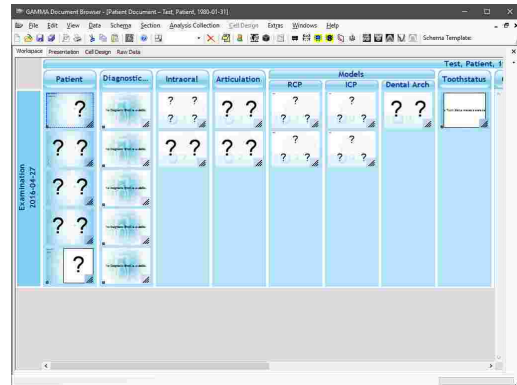
Press the button *OK* to continue.



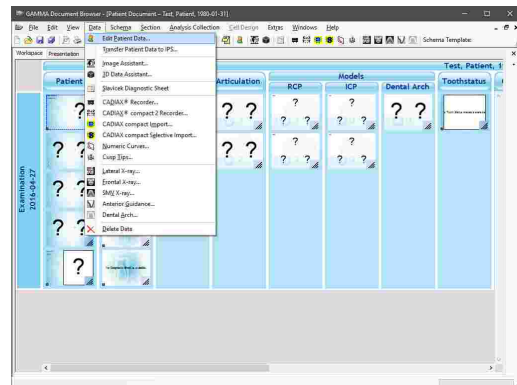
All patient information inputs are optional. However, it is recommended to enter at least the patient's first name, last name, and date of birth. This information is used for identifying the patient in the database and the date of birth is additionally used for determining age-dependent norm values for cephalometric analyses in the CADIAS module.

After confirming your inputs, you will be presented the Workspace without any data. For information on how to import images, create CADIAX condylography recordings and digitize anatomical points on an x-ray image, please refer to chapter "Inserting data" <sup>60</sup>.

Once you save the patient file for the first time, the application will create a respective \*.gdb file in your database directory.

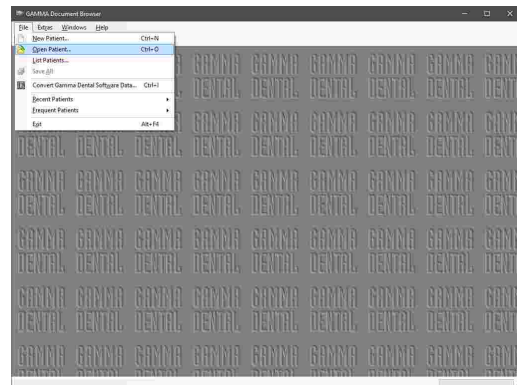


To modify the initially specified patient data later on, you can reopen the patient data input via the menu *Data* → *Edit patient data*.

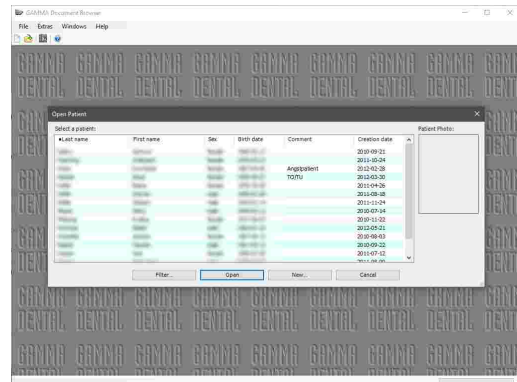


### 4.3.3 Opening patient files

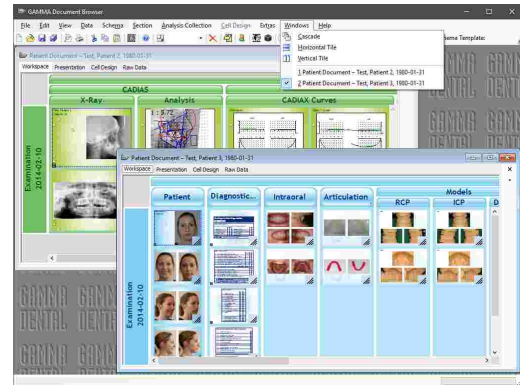
You can open existing patient files at any time via the menu *File* → *Open patient*.



Alternatively, you can select the patient file to open from a comprehensive, filterable list that you can display menu *File* → *List patients*. By default, the list displays all patient files in the database.



When multiple patient files are opened, you can switch between them via the *Windows* menu.

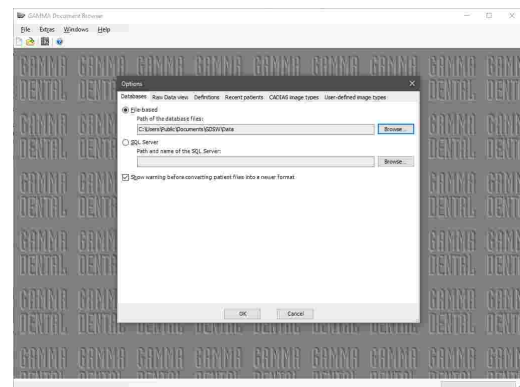


**i** GAMMA Document Browser remembers the patient files that were used most recently and most often. You can quickly open those files again via the menu *File* → *Recent Patients* or *File* → *Frequent Patients*, respectively.

#### 4.3.4 Changing the database path

You can change this directory via the menu *Extras* → *Options*, on the register *Databases*. This can be useful if you want to put the files onto a network storage that is accessible from multiple workstations.

For copying files into or out of your database directory, you can quickly open that folder via the menu *File* → *Open Database Directory*.




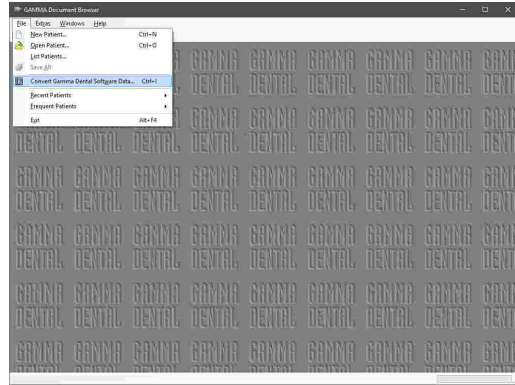
**i** Rather than working file-based, GAMMA Document Browser can also be configured to store patient data in an SQL Server database. Due to the increased complexity, this is only recommended for extremely large patient databases consisting of several hundreds to thousands of patient files, where the maximum performance is required. Please contact GAMMA to get the instructions for correctly setting up the SQL Server instance.

**!** Please note that, when patient files are accessed via a network, it is vital for the connection to remain established for as long as the software is running. Unexpected network interruptions may lead to loss or corruption of stored patient data.

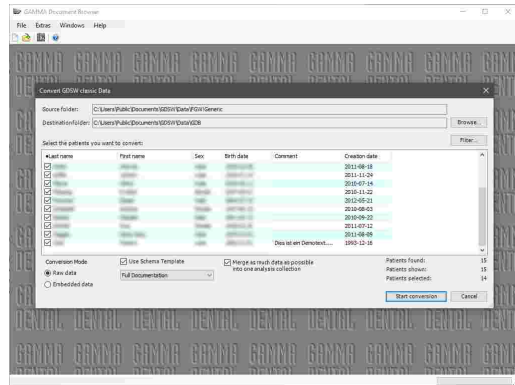
#### 4.3.5 Converting data of GDSW classic


To ease the transition from GDSW classic to GAMMA Document Browser, the latter provides a feature for converting your existing patient database. This conversion transfers all recorded data into the new file format. It does however not affect the original files, which you will still be able to edit in GDSW classic.

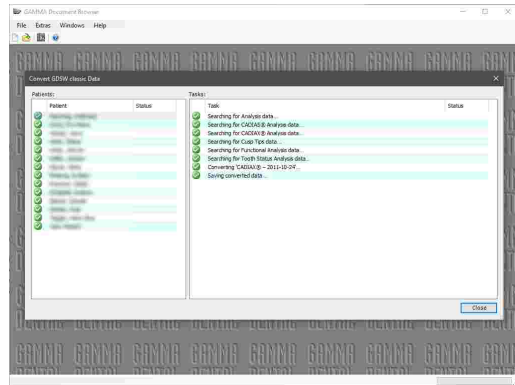
Start GAMMA Document Browser and open the conversion dialog via the menu *File* →  *Convert GDSW classic data*.



Select the patient files to convert and specify the desired conversion options. Then press the button *Start conversion*.



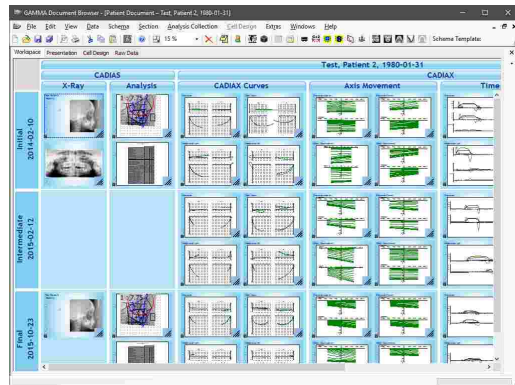
A dialog will appear that shows the progress of conversion. You can close the window once all patients have been converted. The converted patient files can now be opened via the menu *File* →  *Open patient*.



### 4.4 The Workspace

Most activity in GAMMA Document Browser takes place in the **Workspace** view. The layout ("schema") of this view can be customized to display all the data you need for the specific patient case. The software comes with several templates for this layout (refer to chapter "Schema Design Templates" <sup>43</sup>).

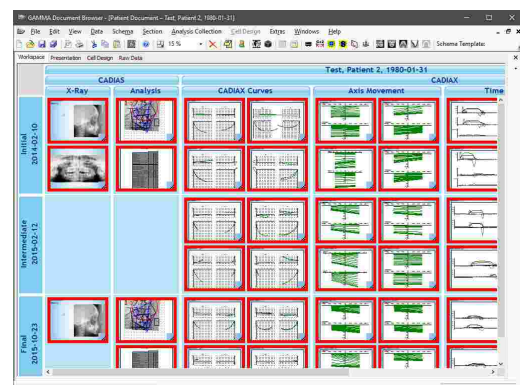
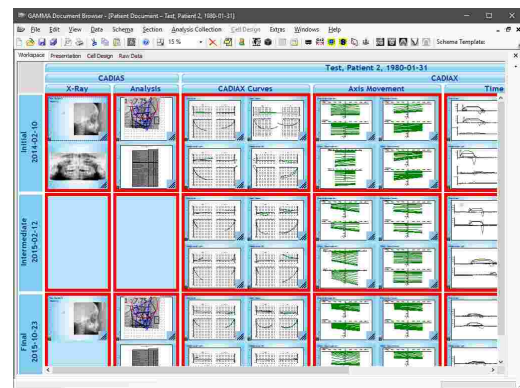
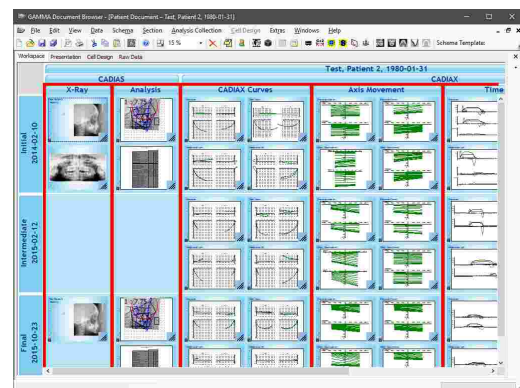
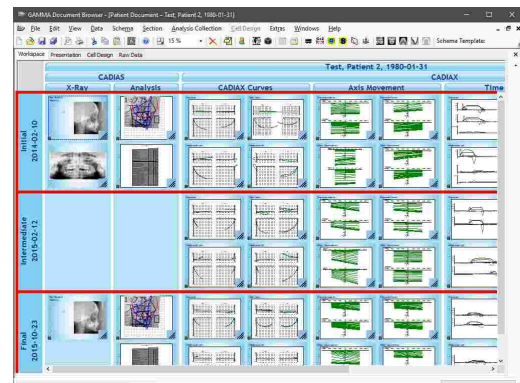
Please note that the Workspace does not necessarily display all the data that is contained in the database. To view all the contents like images, condylography curves, x-ray tracings, etc., switch to the Raw Data <sup>57</sup> view.



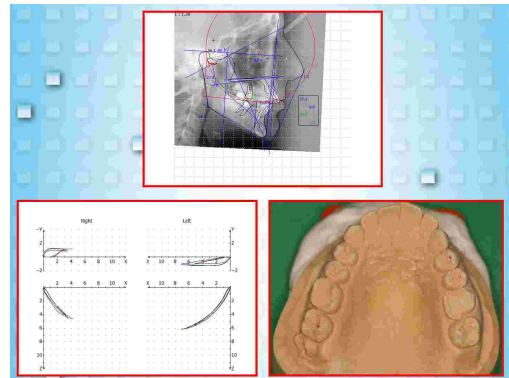
#### 4.4.1 Elements in the Workspace

The Workspace layout is constructed from the following elements:

- The "rows" in the Workspace are referred to as **Analysis Collections**. Each Analysis Collection represents one patient session or examination, which are sorted by their creation date in chronological order.
- The "columns" in the Workspace are called **Sections**. These Sections are used to logically separate different types of data and can have a hierarchical structure. For example, you can have a section "CADIAX" with sub-sections for the actual condyle movement curves, joint axis movement, and articulator settings.
- The areas created by the grid of horizontal analysis collections and vertical sections are called **Section Workspaces**.
- Each section workspace can contain an arbitrary number of **Cells**, which are analogous to the slides of a presentation. The number of cells is not required to be equal across Analysis Collections. For example, you can create a layout that shows CADIAX x-ray tracings only in the initial and the final examinations.



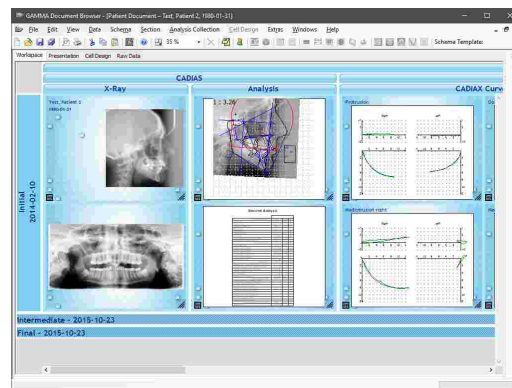
- Finally, cells themselves have an individual layout that may contain **Data Areas**, which are linked to data in the database and display it in a certain way, as well as static design elements like rectangle shapes, text, or images (refer to chapter "The Cell Design view" [54]).



### 4.4.2 Changing the zoom value

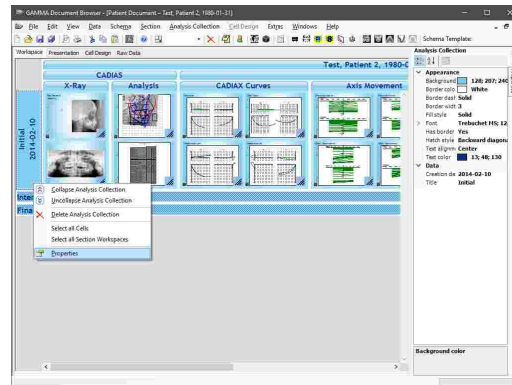
To change the size with which cells are displayed, use the resize-handle at their bottom right corner or adjust the zoom value via the menu *View* → *Zoom*.

You can quickly fit a single cell into the available space by double-clicking it. Here, make sure to perform the double-click on the background of the cell rather than a region covered by a data area, since doing the latter will open the associated data item instead.



### 4.4.3 Formatting Workspace elements

The appearance of all elements in the Workspace can be customized via a side panel that you can display by right-clicking an item and choosing the menu entry *Properties*. This panel always shows the properties of the currently selected element, which is highlighted by a blue dashed outline in the Workspace.



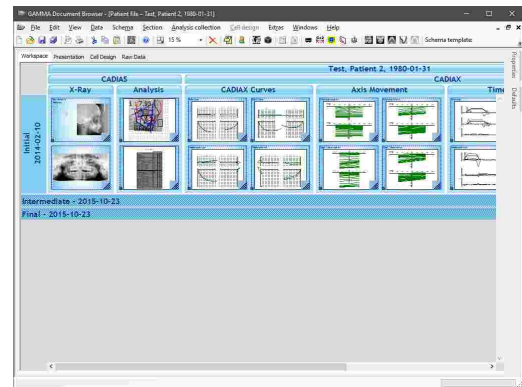
**i** In addition to the *Properties* side panel, GAMMA Document Browser offers a *Defaults* side panel on the right border, which allows specifying the default appearance of newly inserted Workspace elements. The adjustments made in this panel are applied to the current schema design template and saved with it.

### 4.4.4 Selecting multiple Workspace elements

You can select multiple elements at a time by holding down the *Ctrl* or *Shift* key on your keyboard while selecting.

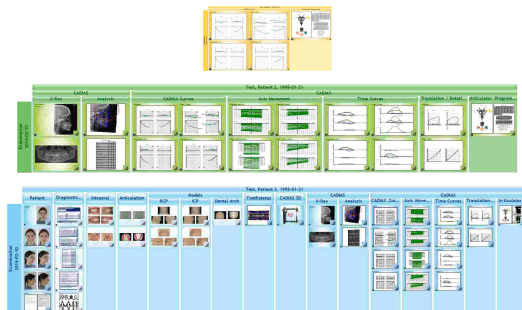
If you keep the *Alt* key pressed while clicking on a data area, the application will automatically select the underlying cell. This is useful especially in combination with the *Ctrl* or *Shift* keys for selecting multiple cells.

In the context menus of analysis collections and sections you can furthermore find features for quickly selecting all contained cells or section workspaces.

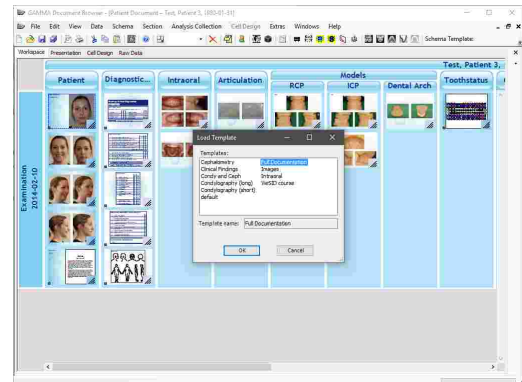


### 4.4.5 Schema Design Templates

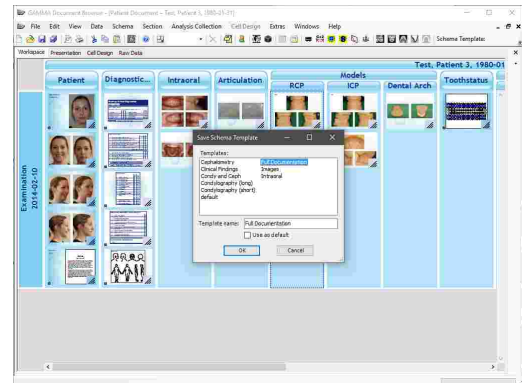
GAMMA Document Browser comes with templates for various Workspace layouts, referred to as **Schema Design Templates**.



You can apply a schema design template via the menu *Schema* → *Load template*. Then, select the template to apply from the dialog and press *OK*.




If you modified an existing Schema Design Template or created your own Workspace layout, you can save it as a new template via the menu *Schema* → *Save template*. Then, enter the name to use and choose whether the new template shall be used as the default layout for all new patient files.

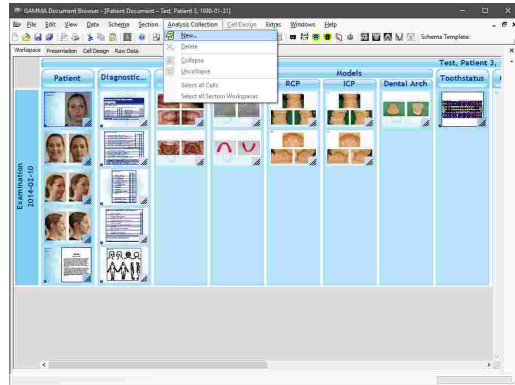


**i** Schema design templates are part of the definition files of GAMMA Dental Software and can therefore easily be copied to other computers or be made accessible to multiple computers via a network. Please refer to chapter "Definition files" <sup>297</sup> for more information.

## 4.4.6 Analysis Collections


### 4.4.6.1 Creating a new analysis collection

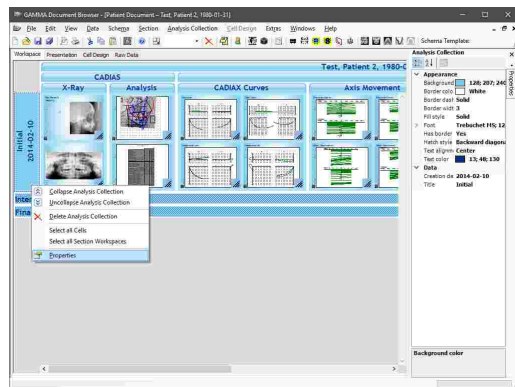
You can create new, empty analysis collections via the menu *Analysis Collection* →  *New*.



**i** Each section provides a property named *Create duplicate cells*, which, when enabled, will cause the respective cells of the latest analysis collection to be replicated in the newly created analysis collection. This makes it easy to keep a consistent layout across multiple examinations.

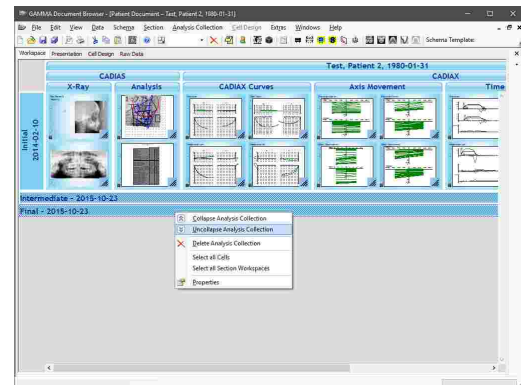
### 4.4.6.2 Changing title or date of an analysis collection

To change the title or date of an analysis collection, you can right-click it and choose  *Properties* for adjusting this information.



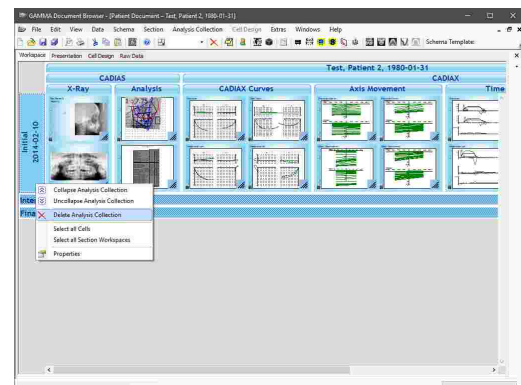
### 4.4.6.3 Collapsing an analysis collection

In addition, you can collapse and uncollapse analysis collections via the context menu or by double-clicking them with the left mouse button.



### 4.4.6.4 Deleting an analysis collection

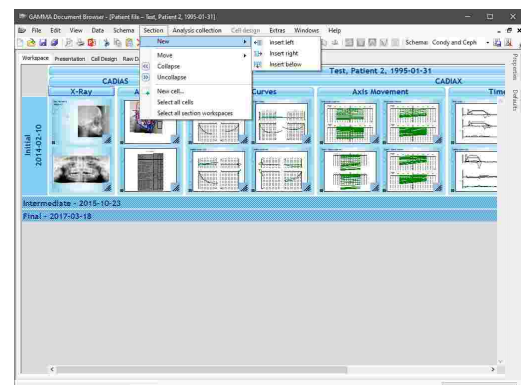
You can delete an entire analysis collection by clicking it with the right mouse button and choosing **Delete analysis collection** from the context menu. Please note that this will also cause all contained cells and data items to be removed permanently.



## 4.4.7 Sections

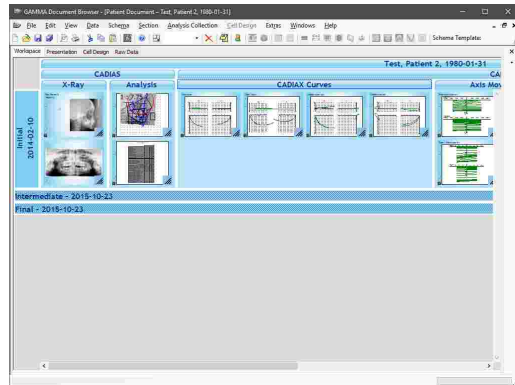
### 4.4.7.1 Creating a new section

In every patient file, the topmost section will always display the patient's name and date of birth. For inserting a new section, select the existing section next to where you want to insert the new one and continue via the menu **Section** → **New**. Here, you will have the possibility to insert the new section on the same level or as a child of the selected one.




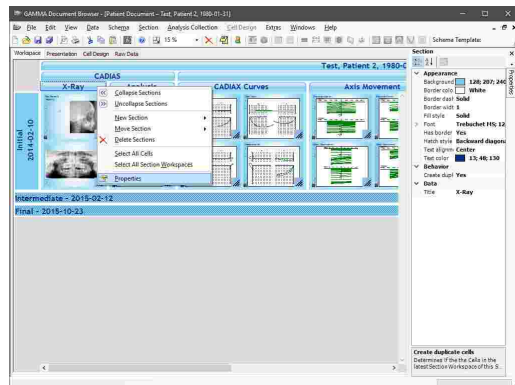
### 4.4.7.2 Resizing a section

To adjust the width of a section, e.g. for adding another column of cells, you can move your mouse cursor onto the border between two sections (the cursor will change its appearance), hold the left mouse button down, and move the border as needed.



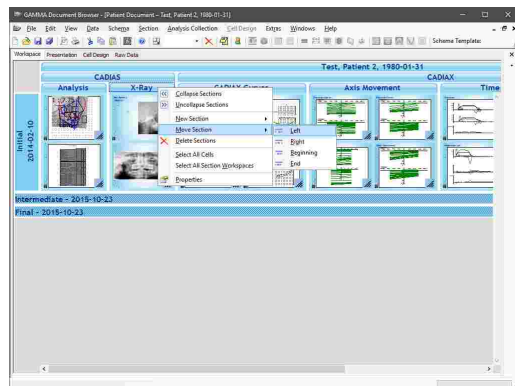
### 4.4.7.3 Changing the title of a section

Similar to analysis collections, you can right-click a section and choose  *Properties* to adjust its title as well as appearance settings like color, font, and border.



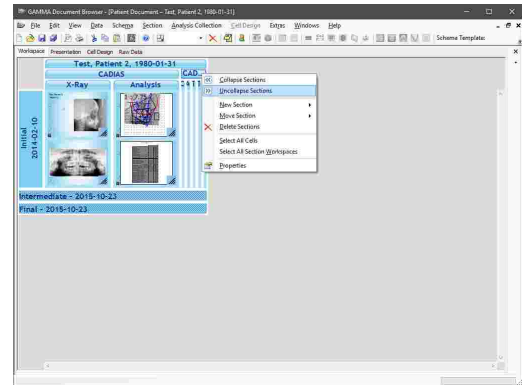
### 4.4.7.4 Changing the order of sections

You can change the order of the Sections in the Workspace by clicking them with the right mouse button and choosing *Move section*.



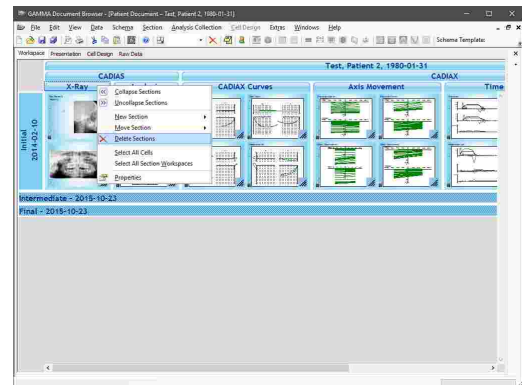
#### 4.4.7.5 Collapsing a section

It is also possible to collapse and uncollapse Sections via the context menu or by double-clicking them with the left mouse button.



#### 4.4.7.6 Deleting a section

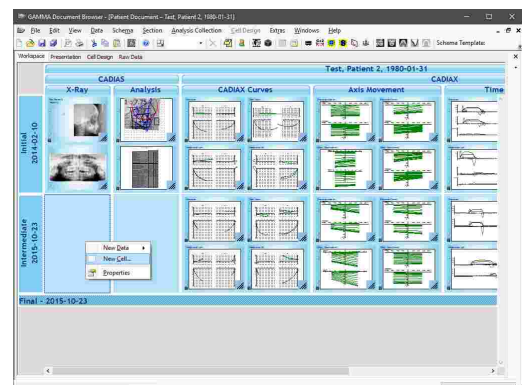
To delete a section, simply right-click it to open the context menu and choose **Delete section**. When deleting a section that contains child sections, you have the possibility to either delete just the selected section, which will move the child sections one level up, or to delete it together with all child sections.



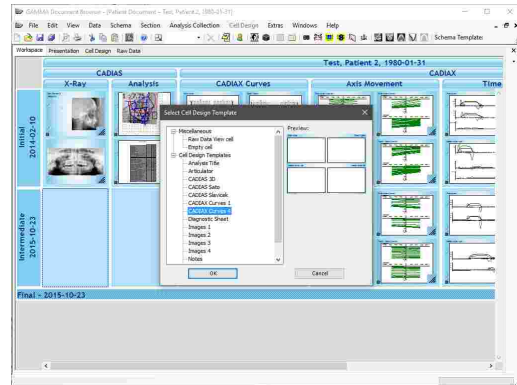
### 4.4.8 Cells

#### 4.4.8.1 Inserting a new cell

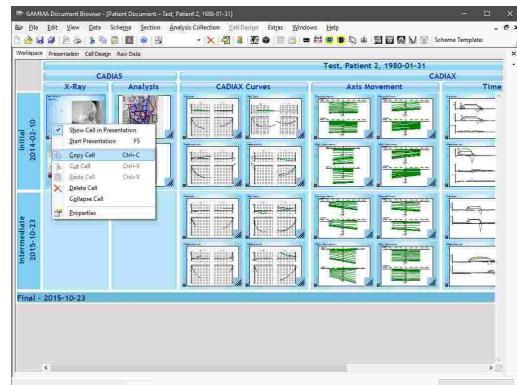
To create a new cell, right-click onto the section workspace where you want to insert it and choose **New cell**.



A dialog will appear that shows the available cell layouts, called **Cell Design Templates**. Just like schema design templates, you can create new cell design templates or modify existing ones (refer to chapter "The Cell Design view<sup>54</sup>" for more information). Select the one you want to insert and press **OK**.

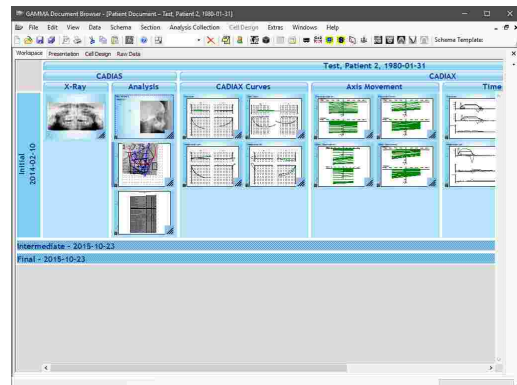


You can also create cells by copying existing ones and pasting them in the selected section workspace via the menu **Edit** → **Paste cell**. This even works if the copied cell is located in a different patient file.



#### 4.4.8.2 Changing the order of cells

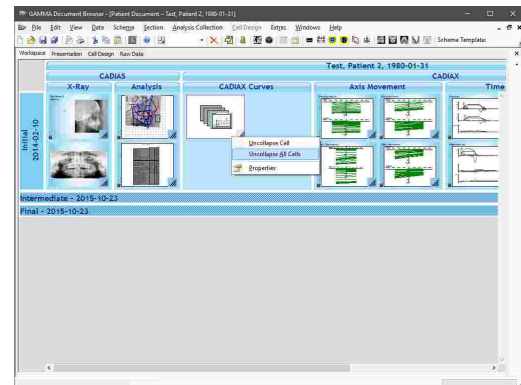
You can freely change the order of cells in the Workspace by grabbing them with the left mouse button and dragging them to the new location while keeping the mouse button pressed.



### 4.4.8.3 Collapsing cells

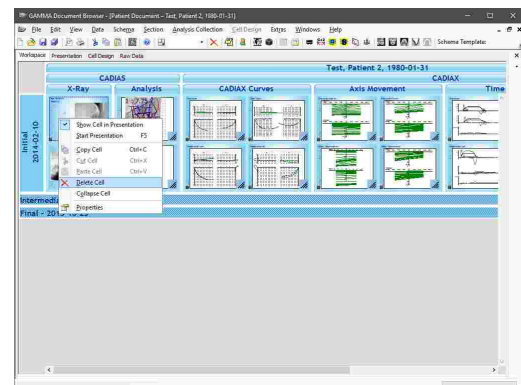
Cells contained in a section workspace can be collapsed into a single stack via their context menu entry *Collapse cell*. Scrolling the mouse wheel while the cursor is over the topmost cell will cycle through the underlying cells, letting you choose the one to be displayed on top.

To uncollapse the stack and restore the cells, click it with the right mouse button and choose *Uncollapse all cells*.



### 4.4.8.4 Deleting cells

To delete a selected cell, open its context menu and choose ~~X~~ *Delete cell*. This also works when multiple cells are selected.

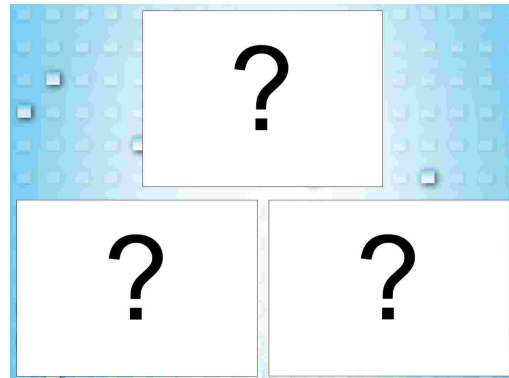


### 4.4.9 Data Areas

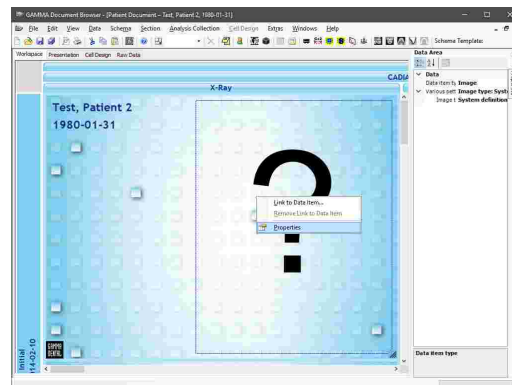
Data areas are used to take data from the database and display it in the Workspace and other views. Each data area can be linked either directly to a single primary **Data Item** (e.g. image, condylography curve, cusp tips coordinates), or contain a so called **Analysis** that is created based on such data. For example, CADIAS analyses are created based on an x-ray image and a collection of digitized anatomical points and contours, which appear as two separate data items in the Raw Data view.


The type of data displayed by a data area is defined by the applied schema design template. Whenever a data item is added to the database, the corresponding data areas will be updated to display that item. For example, if a data area is configured to display a lateral x-ray image, an image of that type will be displayed immediately in the corresponding data area after it is imported.

If the type of data expected by a data area is not present in the database, the data area will indicate this by displaying a question mark. If needed, you can hide these question marks via the menu *Extras* → *Options*, on the register *Definitions*.



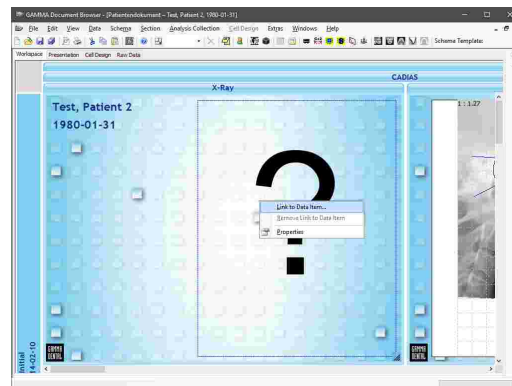
You can determine what type of data a data area expects by right-clicking it, choosing *Properties*, and checking the property *Data item type*.



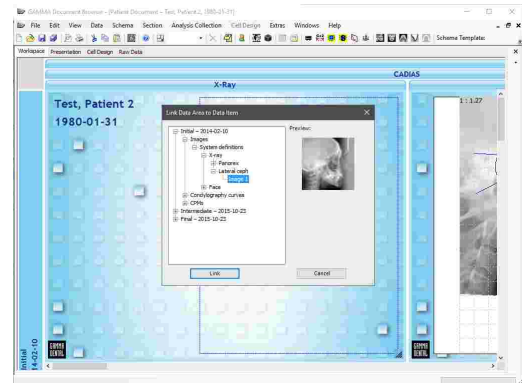
 For instructions on how to import data or create analyses, please refer to chapter "Inserting data".

#### 4.4.9.1 Linking data areas to data items

To manually link an empty data area to a data item and therefore override the link specified by the schema design template, you can simply double-click the data area or choose *Link to data item* from the context menu.

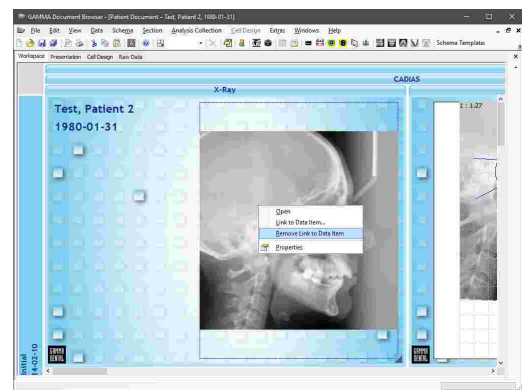


In the following dialog, you can select the data item that should be displayed by the data area. The items in the dialog are grouped by analysis collection and then by their type. Press *Link* or double-click an item to confirm your selection.



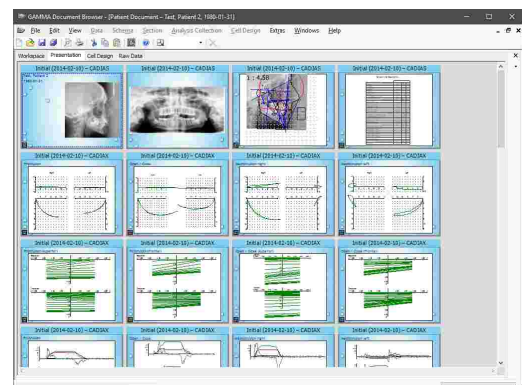
#### 4.4.9.2 Unlinking data areas from data items

If you want to remove the current link of a data area, you can right-click it and choose *Remove link* from the context menu. This will cause the displayed data to be replaced by a question mark. However, the data item itself will remain in the database and still be visible in the Raw Data view.



### 4.5 The Presentation view

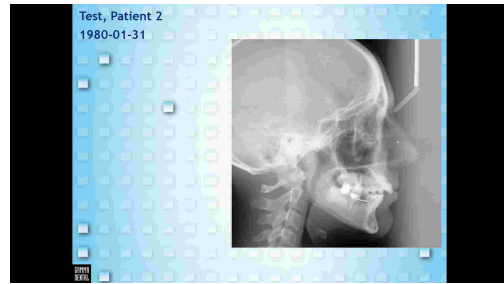
The **Presentation** view is useful for the discussion, documentation, and presentation of patient cases. It mirrors the cells also displayed in the Workspace view, but presents them in sequential order. Whenever you add or remove a cell in the Workspace, it will also be added or removed in the Presentation view. The order of cells in the two views can however be changed independently.



### 4.5.1 Starting an on-screen presentation

You can start a full-screen presentation via the menu *View* → *Start presentation* or by pressing the *F5* key on your keyboard. The presentation will start at the selected cell, or at the beginning if no cell is selected.

During presentation, you can switch to the next slide by pressing the left mouse button, the *Space* bar, or the arrow keys. To exit the presentation, press *Escape*.

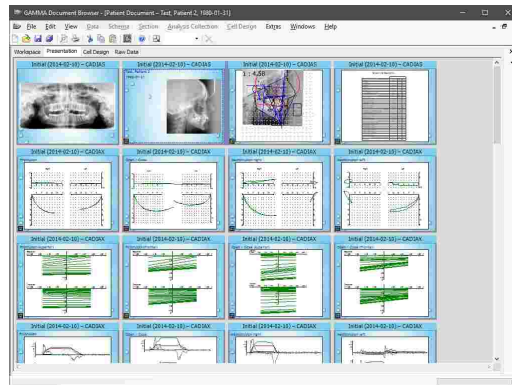


**i** You can change the aspect ratio of all cells via the properties in the Cell Design view. This allows for a full-screen presentation without black bars on wide-screen formats like 16:9 or 16:10.

### 4.5.2 Changing the presentation sequence

The order with which the cells are displayed during presentation is defined by their order in the Presentation view. There, you can reorder cells by simply dragging them with the left mouse button.

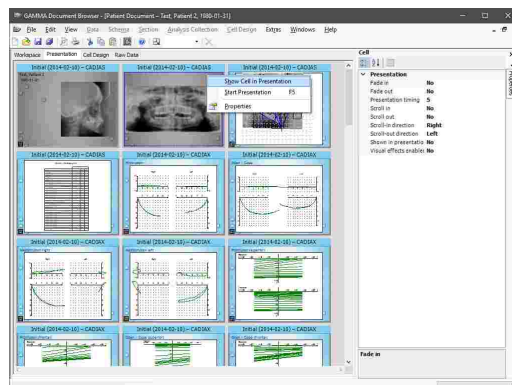
Please note that reordering cells in the Presentation view does not have any effect on their position in the Workspace.



### 4.5.3 Hiding cells from presentation

You can exclude certain cells from presentation via their context menu option *Show cell in presentation* or via their Properties side panel. Hidden cells will appear grayed out.

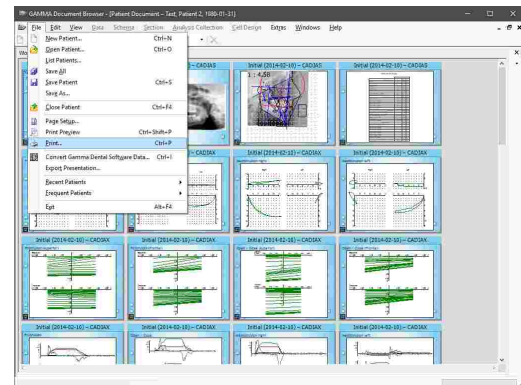
In addition, the properties of each cell contain settings for simple transition animations during presentation. It is also possible to configure an automatic presentation, where each slide will be displayed for a certain amount of time before the application will automatically switch to the next one.



**i** The Presentation view provides a property *Hide cells without data in presentation*, which will cause cells with only unlinked data areas (indicated by question marks) to be hidden automatically. To access this property, make sure that no cell is selected, e.g. by clicking on the gray background of the view.

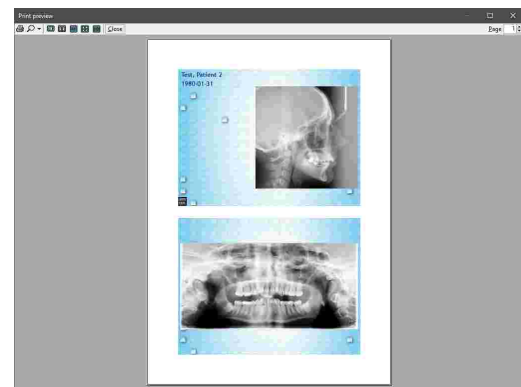
#### 4.5.4 Printing

To print cells, to show a print preview, or to change the page format of the printout, use the respective entries in the *File* menu.




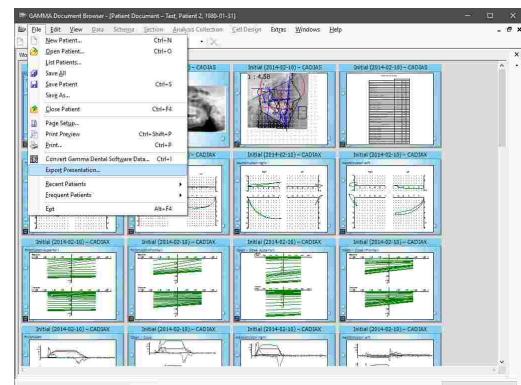
You can adjust the number of cells to be printed on one page via the property *Cells per page* of the Presentation view.

The printout will include all cells that are also included in a presentation. To exclude certain cells, simply hide them from presentation via their context menu.

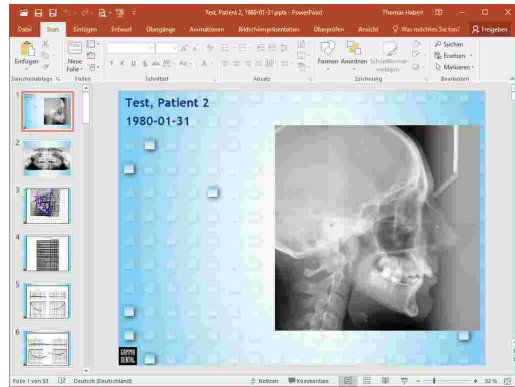


#### 4.5.5 PowerPoint export

To create more sophisticated presentations, you can export the cells in the format of Microsoft PowerPoint via the menu *File* →  *Export presentation*.

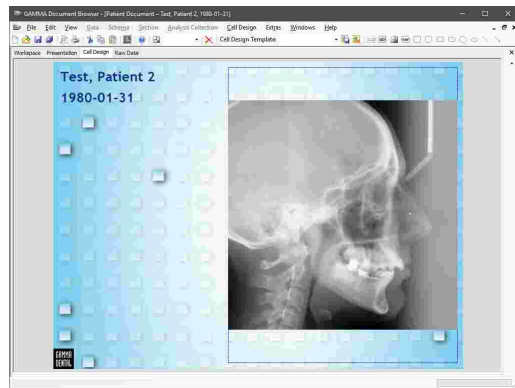


The slides in the exported \*.pptx file will equal the ones shown in the presentation of GAMMA Document Browser. Therefore, if you want to exclude certain cells, simply hide them via their context menu in the Presentation view.



## 4.6 The Cell Design view

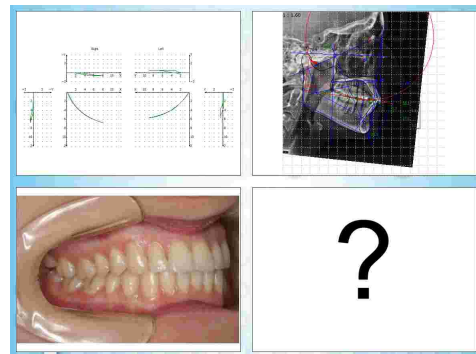
Using the *Cell Design* view, you can change the layout of a single cell in the Workspace or Presentation view. To edit a cell, select it in either of those two views and switch to the Cell Design view.



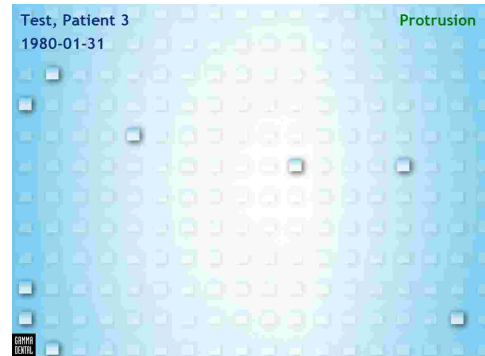
### 4.6.1 Elements in Cell Design

The layout of a cell can incorporate any number of the following:

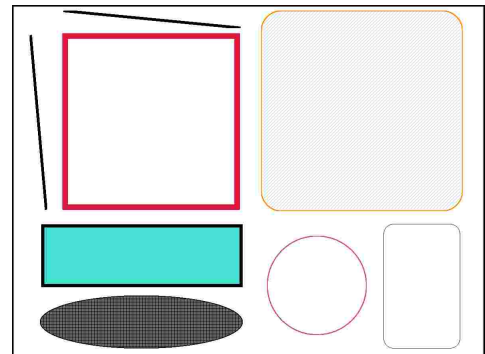
- **Data Areas** are used to display data contained in the database. This includes patient photos, condylography curves, x-ray tracings, or anything else. Data areas that have not yet been linked to data are displayed with a question mark.



- **Design Elements** are not related to data directly. These elements do not take their data from the database, but display static text and images. Variables can be used to display general information related to the patient or analysis collection, such as name, date of birth, or examination date.

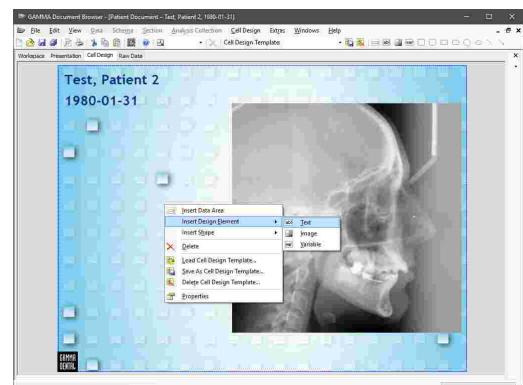


- **Shapes** are simple graphical elements that can be used to add visual hints or structure to a cell's layout. For example, these can be rectangles, circles, or lines.




#### 4.6.2 Adding Cell Design elements

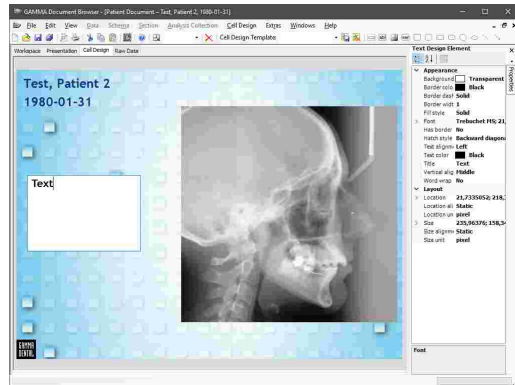
To add an element to a cell, right-click its background, select the type of element to insert from the context menu, and draw it at the desired location by pressing and holding the left mouse button while moving the mouse.



### 4.6.3 Formatting Cell Design elements

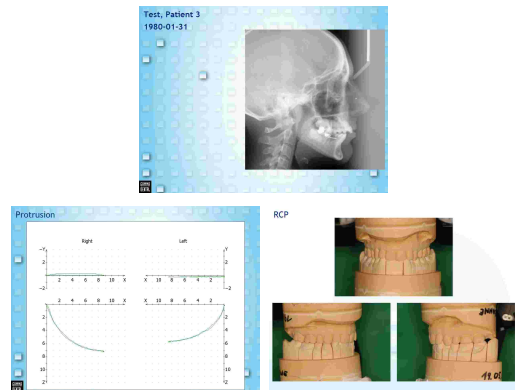
Similar to the Workspace view, you can change various appearance properties of the layout elements as well as of the cell itself. To do so, right-click the element and choose  *Properties* from the context menu.


To edit the text displayed by a text element, you can simply double-click it. Pressing the *Enter* key will confirm the input while pressing *Shift+Enter* will insert a line break.

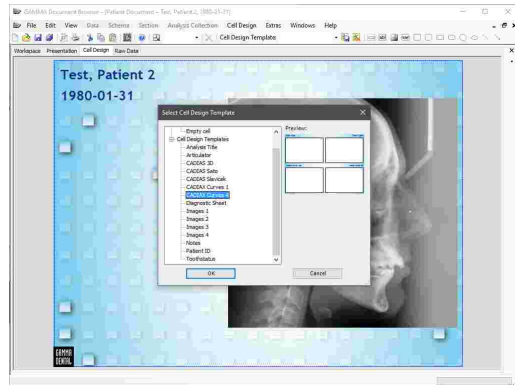



### 4.6.4 Cell Design Templates

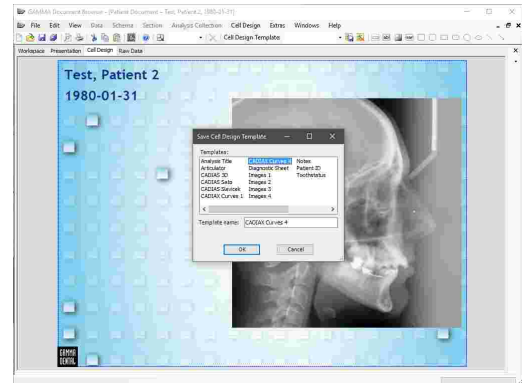
GAMMA Document Browser comes with templates for various cell layouts, referred to as **Cell Design Templates**.




You can apply a cell design template via the menu *Cell Design* →  *Select template*. Then, select the template to apply from the dialog and press *OK*.



If you modified an existing cell design template or created your own cell layout, you can save it as a new template via the menu *Cell Design* →  *Save template*. Then, enter the name to use and press *OK*.

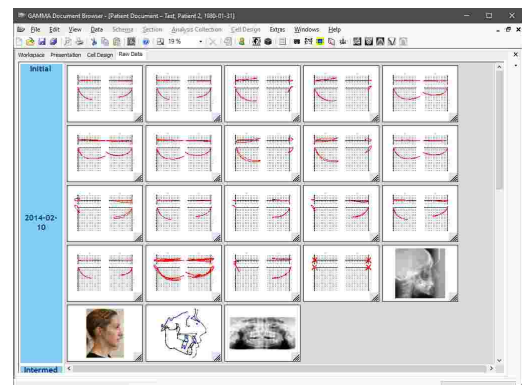



 Cell design templates are part of the definition files of GAMMA Dental Software and can therefore easily be copied to other computers or be made accessible to multiple computers via a network. Please refer to chapter "Definition files [\[297\]](#)" for more information.

## 4.7 The Raw Data view


The **Raw Data** view displays all primary data items contained in the patient file's database. Here, you find all patient photos, condylography curves, x-ray digitizings, among other data that was created for the patient, grouped by analysis collection.

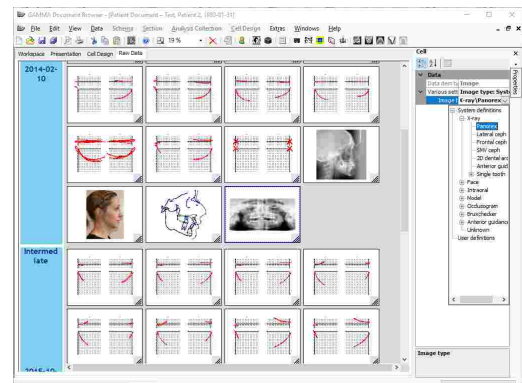
Analysis information that was created based on this raw data, such as CADIAX or CADIAS analyses, do not appear in this view.



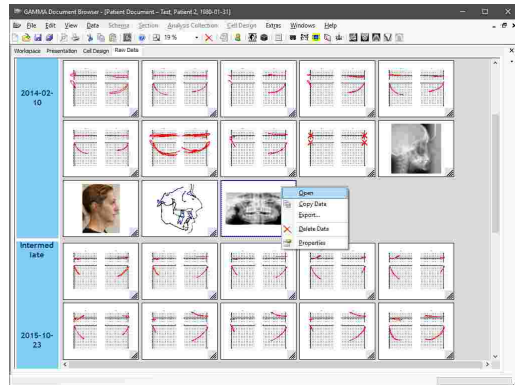
 Information like the name of a condylography curve, the title of a CADIAS digitizing, or the type of an image will appear as a tool tip if you keep the mouse cursor over the item for a brief period of time.

### 4.7.1 Editing raw data

Some types of data items provide properties that can be modified, for example if you want to correct the type of a previously imported image. To do so, right-click the item to modify and choose  *Properties* from the context menu.



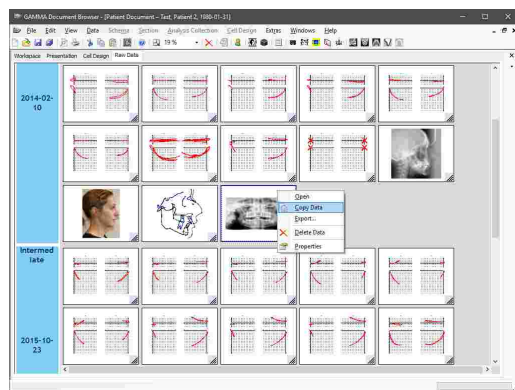
In addition, some data items, like images and CADIAS digitizings, can be edited further via their context menu entry *Open* or via a double-click. This can be useful for example to change the brightness or contrast levels of an image after the import or the correct the location of digitized points.



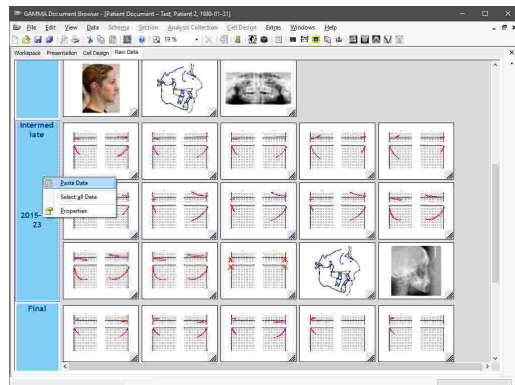
### 4.7.2 Copying and pasting raw data

You can easily duplicate data items by clicking them with the right mouse button and choosing *Copy data* in the context menu or press the key combination *Ctrl+C* on your keyboard.


To copy multiple data items, you can select them while holding down the *Ctrl* or *Shift* key or use the *Select all data* entry in the context menu of the analysis collection.



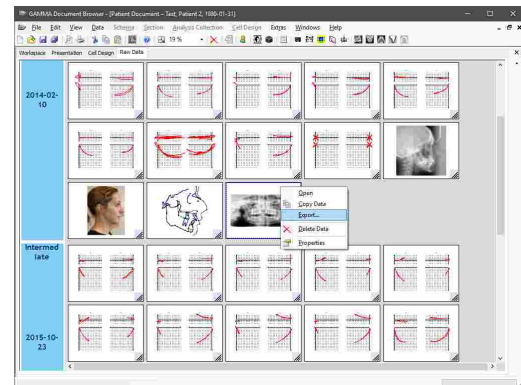
Then, right-click the analysis collection where you would like to insert the data and choose *Paste data* or press the key combination *Ctrl+V*. The target analysis collection can even be in a different patient file.




### 4.7.3 Exporting raw data

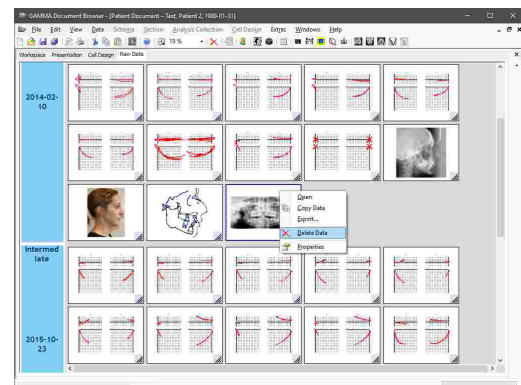
In the Raw Data view, you can export images that were loaded into the patient database via the entry  **Export** in their context menu. This is also possible when multiple images were selected.

Alternatively, you can export images by simply dragging the items from the Raw Data view and dropping them in a file explorer window or another third-party application such as Microsoft Word.



### 4.7.4 Deleting raw data

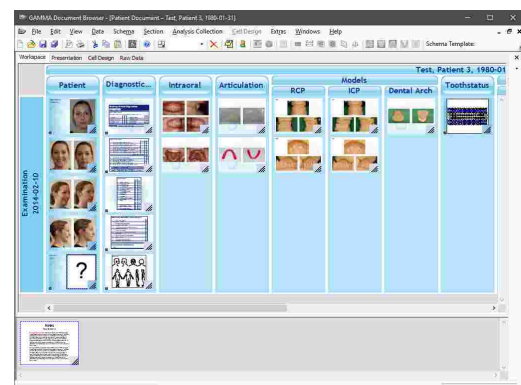
To permanently remove data from the database, select all the data items that you want to remove and choose  **Delete data** in the context menu.




## 4.8 The Orphan view

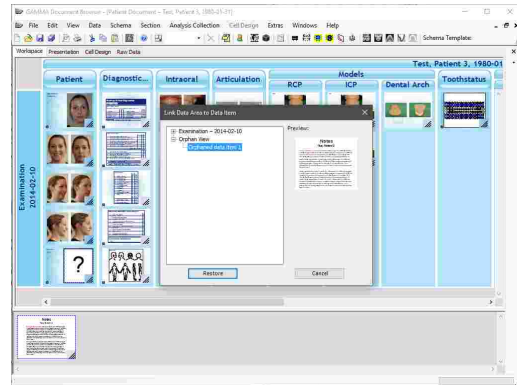
Most data stored in a patient file of GAMMA Document Browser is represented in the Raw Data view. However, when you create a manual preview of a CADIAX or CADIAS analysis, or embed a foreign OLE object, that data will only reside in the data area itself and have no representation in the Raw Data view. Now, when the data area becomes unlinked, e.g. because the parent cell is deleted or another schema design template is selected, the embedded data becomes "orphaned". For this reason, GAMMA Document Browser provides the **Orphan View** that stores the orphaned data items so that they may be restored at a later occasion.

You can show the Orphan View via the menu *View* → *Show orphan view*, which will make it appear at the bottom border of the window.



To restore an orphaned data item, right-click the data area that should display the item and choose *Link to data item*. You can then select the item under the *Orphan view* sub-section of the opened dialog.

If you want to permanently delete an orphaned data item, right-click it and choose  *Delete data* from the context menu.




## 4.9 Inserting data

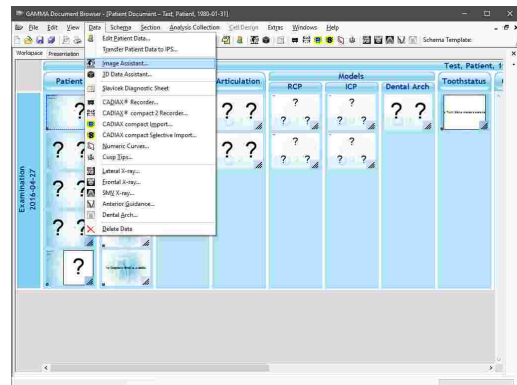
Hitherto we have focused our attention mainly on GAMMA Document Browser's organizational structure. The following subchapters will describe how all kinds of data are imported into a patient file and how you can use this data to create sophisticated CADIX and CADIAS analyses.

### 4.9.1 Importing images

During the course of a treatment, an arbitrarily large number of photographs may be taken. These can include intraoral photos, photos of the patient's face, of plaster models, x-ray images in digital form, and so on. GAMMA Document Browser can load all kinds of images and store them centralized in a single patient file right next to other diagnostic records, while always keeping the data in a presentable form.

The import of images into GAMMA Document Browser is carried out via the **Image Assistant** that not only categorizes them, but also provides basic image editing capabilities to prepare the images as needed.

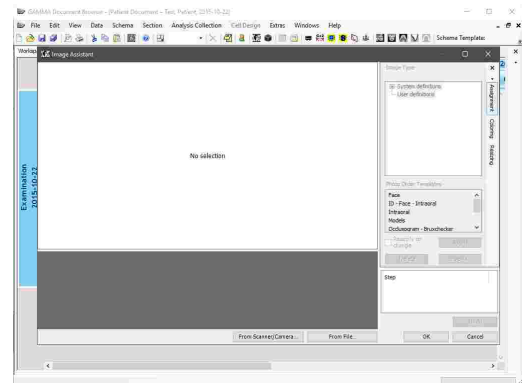
You can start the Image Assistant via the toolbar button  *Image Assistant* or the associated entry in the *Data* menu. If there are multiple analysis collections present, you will have to select one of them to specify where the data should be inserted.



The Image Assistant consists of a large display area for the currently edited image, a horizontal preview bar below that area from which you can select the image to edit, and a panel on the right side that provides the controls for assigning image types and manipulating the current image.

To load images from files, use the button *From file* or simply drag and drop the image files from your file explorer onto the Image Assistant window. Alternatively, you can paste images from the clipboard or load them directly from a connected camera or scanner.

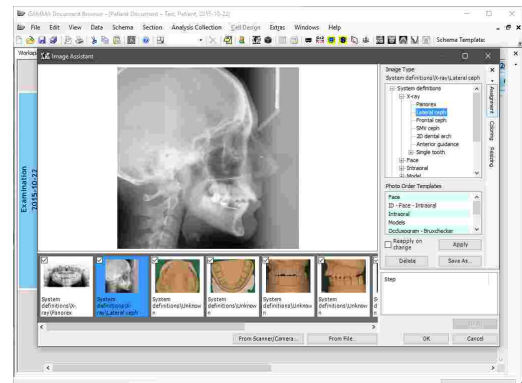
To copy the currently displayed image to the clipboard, press the keyboard shortcut *Ctrl+C*.



#### 4.9.1.1 Assigning image types

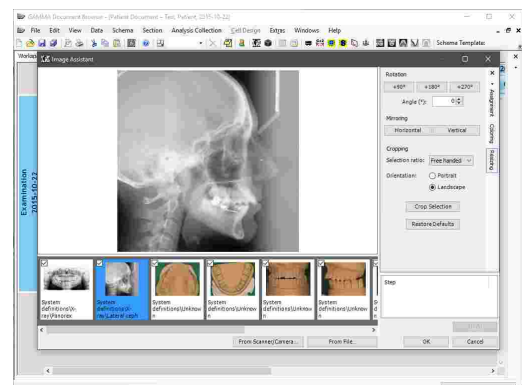
To categorize the images you have loaded into the assistant, it is required to assign an image type to all of them. You can do so via the *Assignment* panel or by clicking the images with the right mouse button in the preview bar and using the *Image Type* submenu. The current type of an image is shown below its preview. By default, it is *Unknown*.

If you find yourself assigning the same sequence of image types for every patient, please refer to chapter "Photo Order Templates<sup>63</sup>" for a way to conveniently assign all types at once.

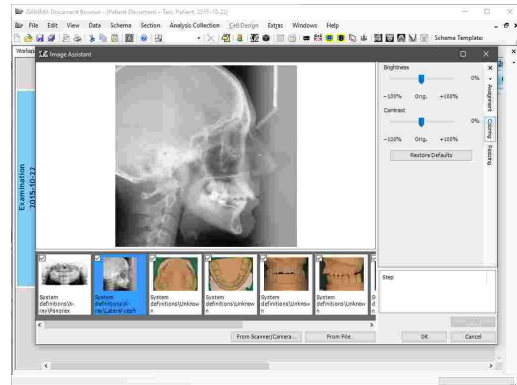


#### 4.9.1.2 Editing images

On the panel *Resizing* you will find the tools to rotate, mirror, and crop the current image. All of these modification steps can be undone via the list below the panel.



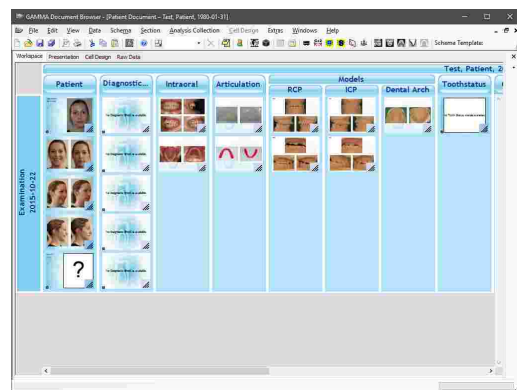
If needed, you can adjust the brightness and contrast of the current image via the *Coloring* panel.



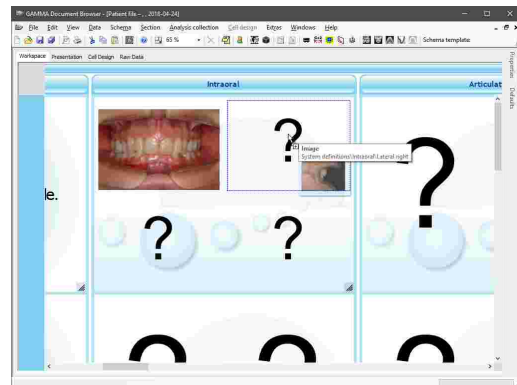
### 4.9.1.3 Importing images

After all loaded images have been assigned an image type, you can click *OK* to import them. If you want to exclude certain images from the import, simply uncheck their check box in the preview bar.

If the image types have been assigned correctly, the Workspace will display the images in the appropriate data areas immediately after the import.

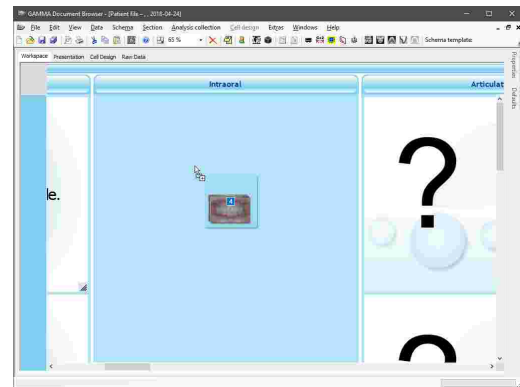


To quickly fill individual data areas with images, you can simply drag image files from a file explorer window over the Workspace of GAMMA Document Browser. Whenever you move the mouse cursor over a data area that expects an image, a tooltip will show the associated image type. Drop the image file to have it imported into the database, be assigned the image type, and be linked to the data area automatically.

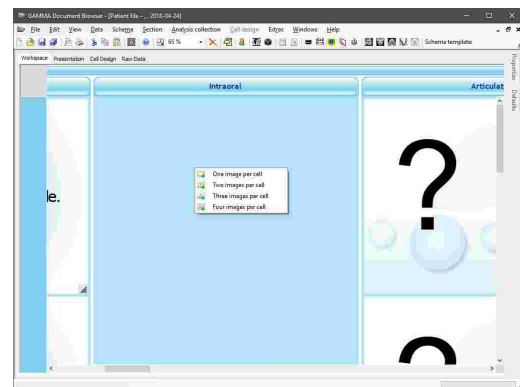


#### 4.9.1.4 Creating image cells

If you want to add additional image cells to the schema layout of a particular patient case, you can quickly do so by dragging the image files from a file explorer window into GAMMA Document Browser.

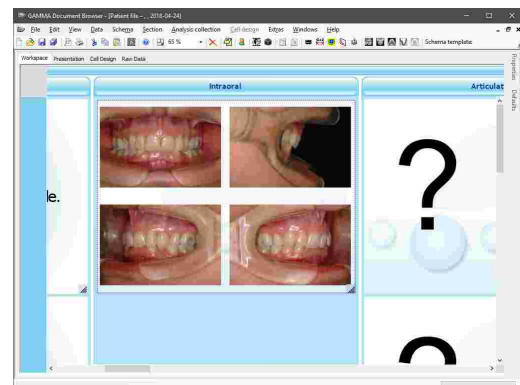


When dropping the files onto a section workspace, a pop-up menu will appear, letting you choose the number of images to be displayed on each of the cells that will be inserted.



The application will then automatically create the required number of cells, import the image files into the database, and link them to the appropriate data areas.

Please note that the images will be assigned the image type *Unknown*, which you can change by right-clicking the respective image, choosing *Properties*, and adjusting the *Image type* property as needed.



#### 4.9.1.5 Photo Order Templates

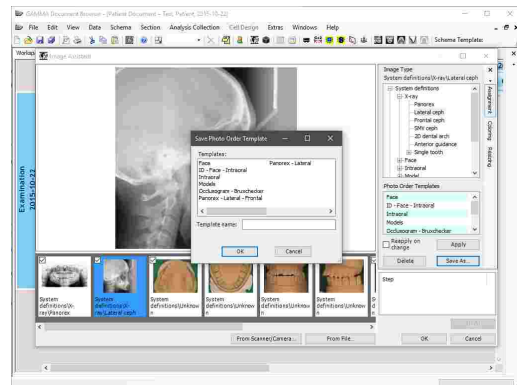
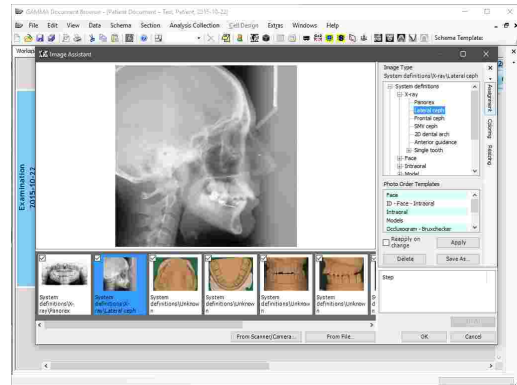
If you find that you are assigning the same sequence of image types during the image import of every patient, you can speed up this process by creating **Photo Order Templates** that can be applied with the press of a button.


GAMMA Document Browser comes with templates for various image type sequences that you can select on the *Assignment* panel of the Image Assistant. To apply such a photo order template, select it from the list and press *Apply*. The assignment will start at the first image and disregards the images that are not going to be imported into the database, as indicated by their check box in the preview bar.

If you want to automatically re-apply the template when certain images are excluded or included for the import, check the option *Reapply on change*.

You can save the image type sequence of the currently loaded images via the button *Save as*. The sequence will then appear as another photo order template that you reuse for all upcoming patients.

Should you want to permanently delete a specific template, simply select it in the list and press *Delete*.

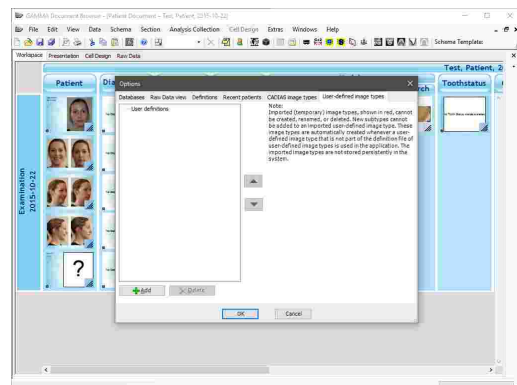


 Photo order templates are part of the definition files of GAMMA Dental Software and can therefore easily be copied to other computers or be made accessible to multiple computers via a network. Please refer to chapter "Definition files [297]" for more information.

#### 4.9.1.6 User-defined image types

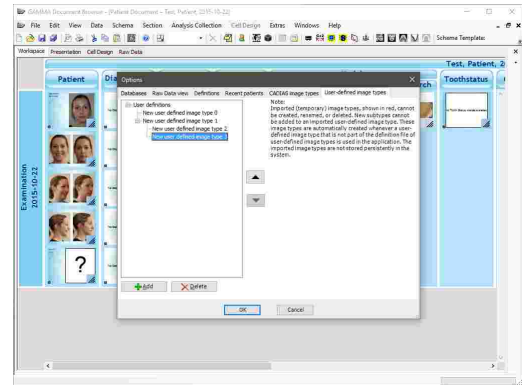
If the predefined image types are not sufficient for your needs, you can create your own, user-defined image types via the menu *Extras* → *Options*, on the register *User-defined image types*.

If the opened patient file contains images with user-defined types that were not created on your system, these types will be shown in red and cannot be modified.




Use the provided buttons to create new image types or modify existing ones. Press **OK** to confirm.

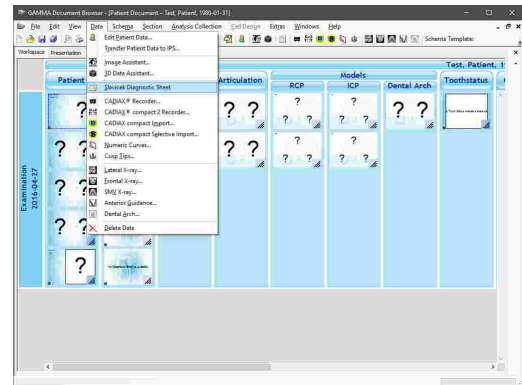
During the next image import, you will be able to assign the user-defined image types just like you can assign the system-defined ones.



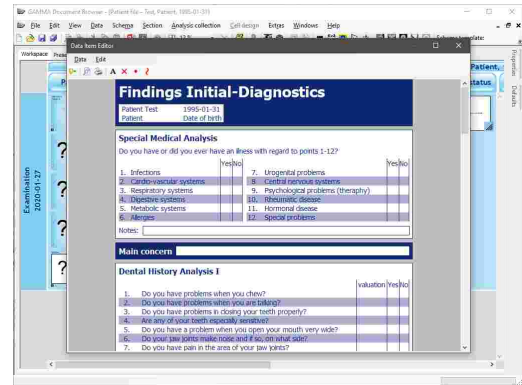
### 4.9.2 Entering a diagnostic sheet


The **Diagnostic Sheet** is a digital form that you can use to document the patient's psychic and physical condition during the initial anamnesis.

You can add a diagnostic sheet to the current analysis collection via the toolbar button  *Slavicek Diagnostic Sheet* or the associated entry in the *Data* menu. There can only be a single diagnostic sheet in each analysis collection. If there are multiple analysis collections present, you will have to select one of them to specify where the data should be inserted.




In the opened form editor, you can fill out the form by clicking the Yes/No options, entering text information, or marking potential pain spots in the displayed graphics. You can close the editor when you are finished.

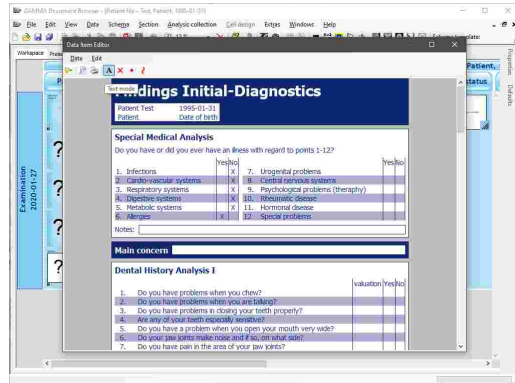


 To easily transfer the values entered in the diagnostic sheet to external applications, you can copy them to the clipboard using the context menu.

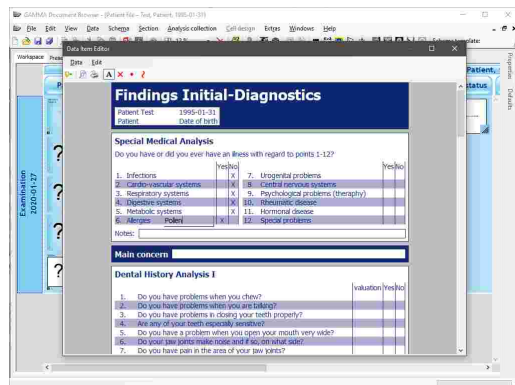
### 4.9.2.1 Text mode in the diagnostic sheet

The diagnostic sheet provides input boxes for entering notes below certain sections. For instance, these can be useful to clarify what types of allergies the patient has. Alternatively, you can use text mode to add notes anywhere on the form.

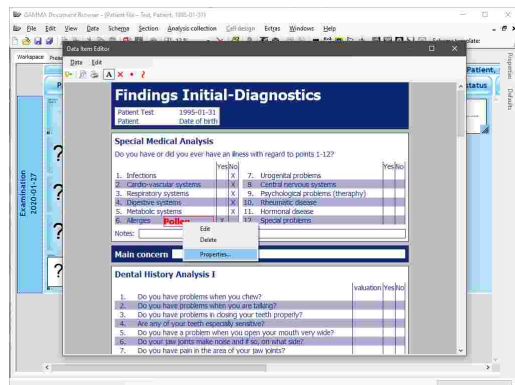
To activate text mode, simply press the toolbar button  *Text mode*.




While text mode is activated, you can draw a rectangular text box on the form by pressing and holding the left mouse button. After you entered the text, press the *Esc* key to stop editing.



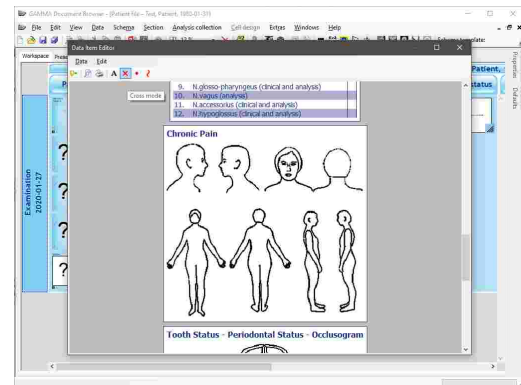
By right-clicking the text box, you can edit the text, delete it, or change properties like font size or color.



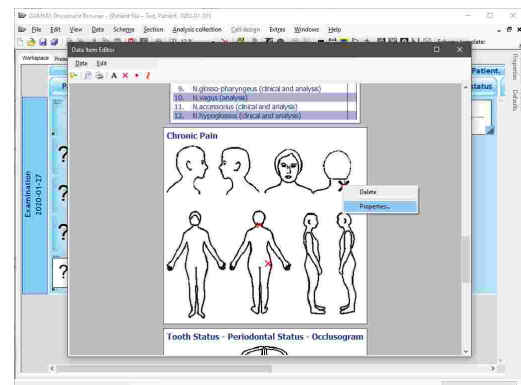
 Make sure to exit text mode via the context menu once you finished your text input and want to continue filling out the form.

### 4.9.2.2 Drawing mode in the diagnostic sheet

Just like text mode, you can activate drawing mode for drawing crosses, points, or lines using the respective button in the toolbar. In the graphical sections, this mode is permanently active.



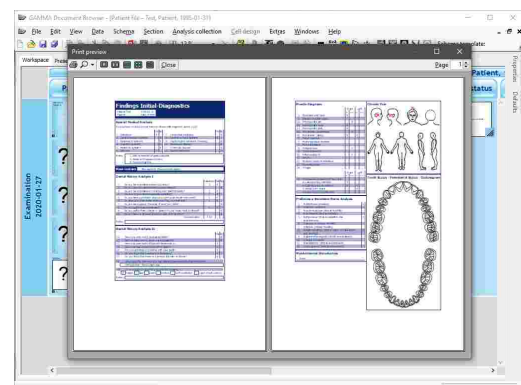
To change the appearance properties of a drawing, like color or thickness, right-click it and choose *Properties*. You can also delete it by choosing *Delete* in the context menu.



Make sure to exit drawing mode via the context menu once you finished your drawings and want to continue filling out the form.

### 4.9.2.3 Printing a diagnostic sheet

To print the Diagnostic Sheet, to show a print preview, or to change the page format of the printout, use the respective buttons in the toolbar.




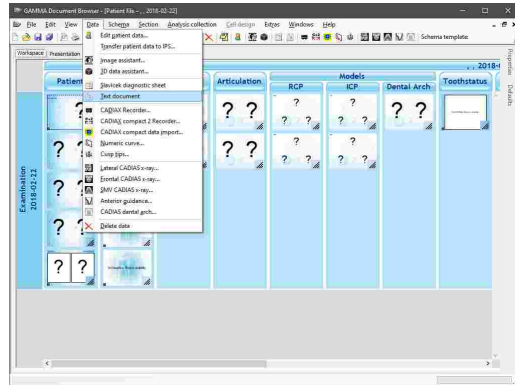
### 4.9.3 Inserting text documents

GAMMA Document Browser can aggregate diagnostic protocols, treatment plans, and other text-based documentation that might arise in daily practice in the form of **Text Documents**. These documents are based on the Rich Text Format (RTF), which supports the usual text formatting options such as color, font style, and paragraphing, as well as indentation, enumeration, and even in-text images. Text

documents can be viewed and edited using the WordPad application that is part of the Windows operating system and are therefore compatible across practices without the requirement for any third-party software.

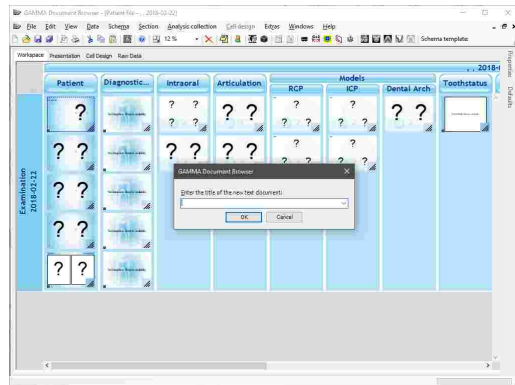
Text documents are primary data items and are therefore displayed in the Raw Data view. The automatic correlation between text documents and data areas in the Workspace is carried out based on the document's title, for instance "Diagnosis" or "Treatment Plan".

You can insert a new text document via the toolbar button  *Text document* or the associated entry in the *Data* menu. If there are multiple analysis collections present, you will have to select one of them to specify where the data should be inserted.

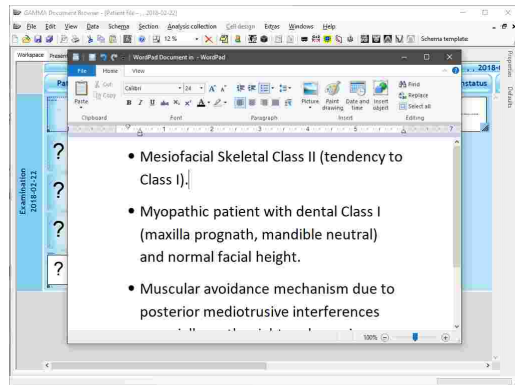


Subsequently, enter the title of the new text document. If the Workspace already contains a data area that expects a document with the exact same title, it will be linked to the document automatically.

Alternatively, you can just double-click the empty data area to create the text document with the corresponding title.



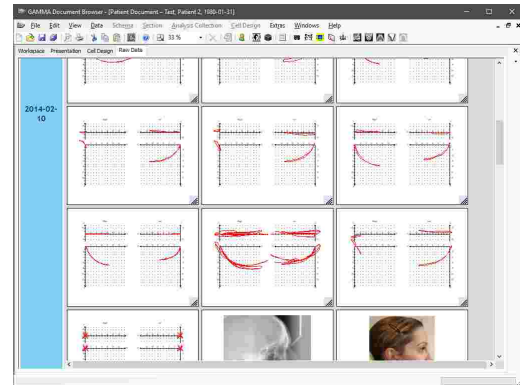
In both cases, the WordPad application will open and allow you to enter the desired information. Simply close the application when you have finished editing the document. This will save the data automatically and display a preview in the linked data area.



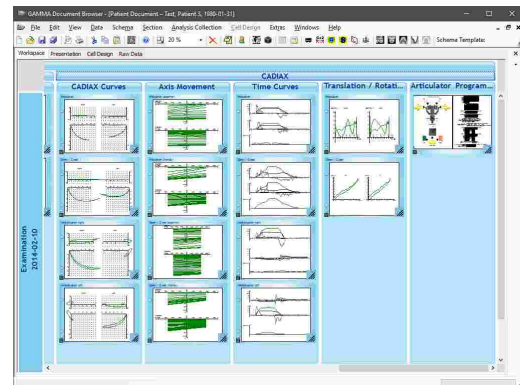
#### 4.9.4 Recording CADIAX condylography data

The **CADIAX** module processes movement recordings of the temporomandibular joint as well as condyle position measurements (CPMs) and the coordinates of cusp tips on dental plaster models. Based on this information, the included applications allow the analysis of joint-related dysfunctions and the calculation of articulator settings necessary for reproducing the movements in an articulator.

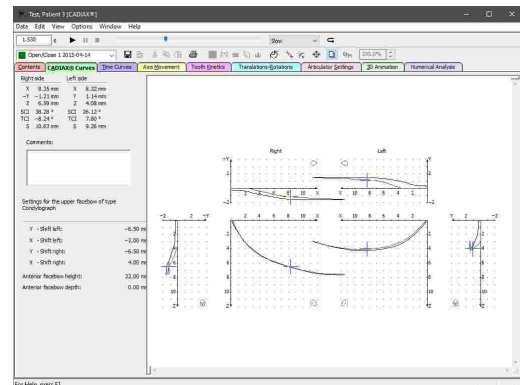
In GAMMA Document Browser, each condylography curve, CPM, and cusp tips recording is treated as a primary data item that appears in the Raw Data view (see chapter "The Raw Data view<sup>[57]</sup>"). Here, you will find them displayed alongside other data items such as images and CADIAX x-ray data.




Based on these digitizings, you can add cells in the Workspace view that automatically display miscellaneous analyses, such as axis movement graphs, time curves, or articulator settings (see chapter "Creating CADIAX analyses<sup>[75]</sup>").



To analyze the recordings in detail, you can start the **CADIAX Analyzer** application by double-clicking any of the CADIAX previews displayed in the Workspace.



 Please refer to chapter "CADIAX<sup>[114]</sup>" for more information regarding the CADIAX module as a whole and to subchapter "CADIAX Analyzer<sup>[124]</sup>" for more information regarding the CADIAX Analyzer application in particular.

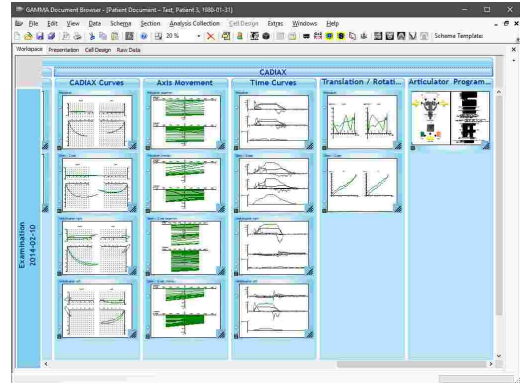
#### 4.9.4.1 Recording data with CADIAX compact 2

GAMMA Dental Software supports the recording of condylography data with the devices CADIAX 4 and CADIAX compact 2, using the **CADIAX compact 2 Recorder** application. Since CADIAX 4 can operate with two types of sensors, make sure that the "compact" sensor set is mounted when using the device in the CADIAX compact 2 Recorder application. This sensor set consists of 40x40 mm flags and single-pin styli.



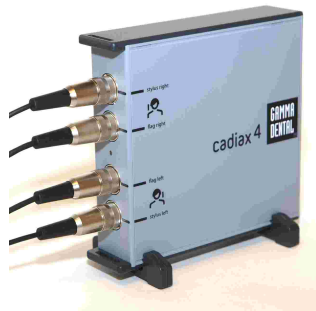
If the Workspace of GAMMA Document Browser already contains Data Areas for CADIAX analyses, these will be updated to automatically display a preview of the recorded curves.

Double-click any of the previews to start the CADIAX Analyzer application, which provides the tools to analyze the recordings in detail.



#### 4.9.4.2 Recording data with CADIAX 4 or CADIAX diagnostic


GAMMA Dental Software supports the recording of condylography data with the devices CADIAX 4 and CADIAX diagnostic, using the **CADIAX Recorder** application. Since CADIAX 4 can operate with two types of sensors, make sure that the "diagnostic" sensor set is mounted when using the device in the CADIAX Recorder application. This sensor set consists of 60x60 mm flags and double-pin styli.

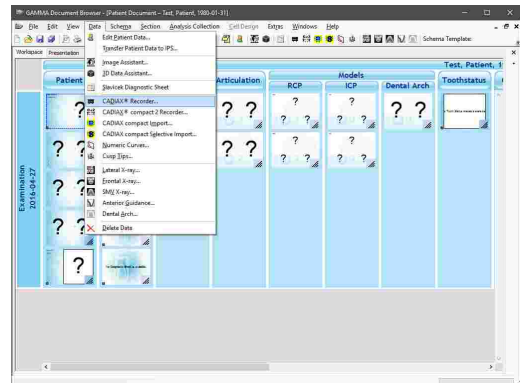


The CADIAX 4 device with the "diagnostic" sensor set connected, which occupies all four of the device's connectors.



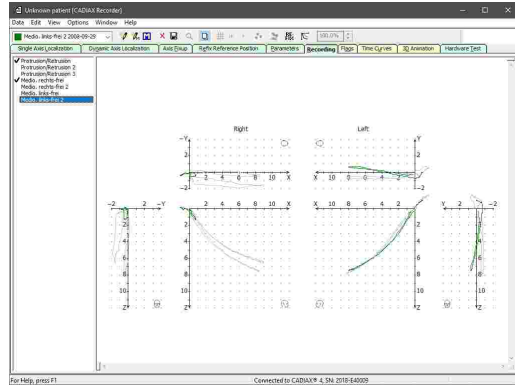
The CADIAX diagnostic device.

You can start the CADIAX Recorder application via the button  **CADIAX Recorder** in the toolbar or the associated entry in the *Data* menu. If there are multiple analysis collections present, you will have to select one of them to specify where the data should be inserted.



Once CADIAX Recorder has been opened, perform the condylography and CPM recordings, save the data, and then close the application.

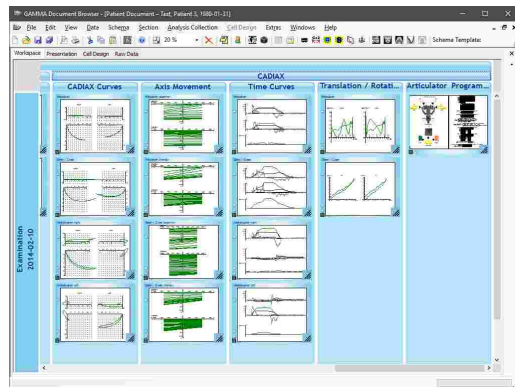
Subsequently, the recordings will appear in the Raw Data view of GAMMA Document Browser and can be used in a CADIAX analysis.



**i** Please consult the instruction manual of your CADIAX device for detailed instructions on how to perform condylography recordings.

If the Workspace of GAMMA Document Browser already contains data areas for CADIAX analyses, these will be updated to automatically display a preview of the recorded curves.

Double-click any of the previews to start the CADIAX Analyzer application, which provides the tools to analyze the recordings in detail.




#### 4.9.4.3 Importing data from CADIAX compact

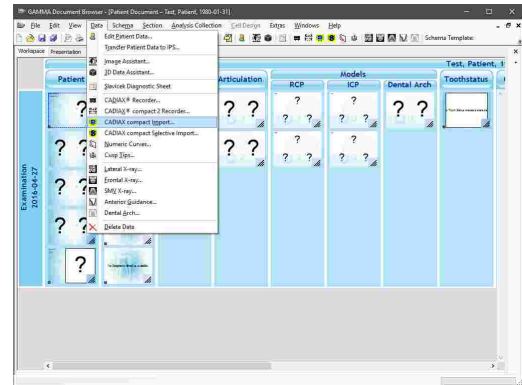
The discontinued CADIAX compact device was a stand-alone recording unit that does not require a connection to a PC for carrying out a condylography recording or for calculating articulator settings.

GAMMA Dental Software can import the recordings stored in the internal memory of the device via the **CADIAX compact Import** functionality. This import procedure does not remove the recordings from the device.



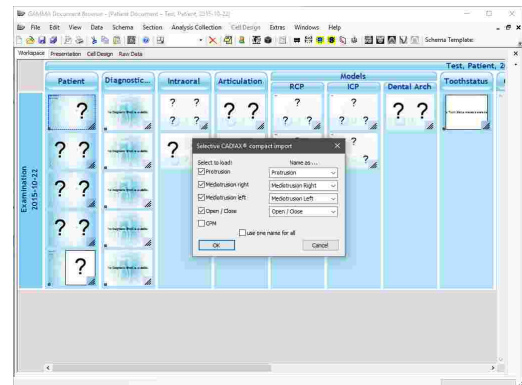
**i** Please consult the instruction manual of your CADIAX device for detailed instructions on how to perform condylography recordings.

You can start the data import from CADIAX compact via the button  *CADIAX compact import* in the toolbar or the associated entry in the *Data* menu. If there are multiple analysis collections present, you will have to select one of them to specify where the data should be inserted.



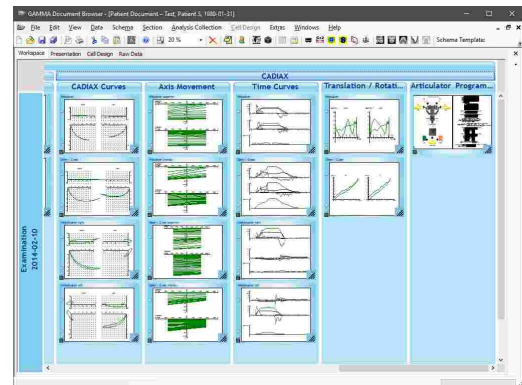
A dialog will appear that allows you to select the recordings you would like to import and to change their name as needed. Start the import by pressing OK.

Subsequently, the recordings will appear in the Raw Data view of GAMMA Document Browser and can be used in a CADIAX analysis.




If the Workspace of GAMMA Document Browser already contains Data Areas for CADIAX analyses, these will be updated to automatically display a preview of the imported curves.

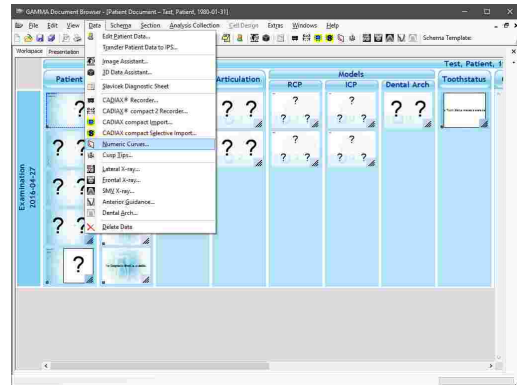
Double-click any of the previews to start the CADIAX Analyzer application, which provides the tools to analyze the recordings in detail.



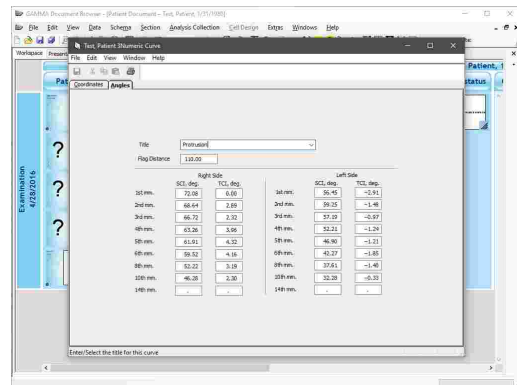
#### 4.9.4.4 Entering numeric curves


Using the **Numeric Curve Editor**, you can create condylography movements by entering X/Y/Z coordinate points or SCI and TCI angle values for given millimeters of excursion. This functionality is useful for digitizing mandibular movement curves that were created with an analog recording system on writing paper or similar and measured manually. The numeric curves created hereby can be used in the other software modules just like electronically recorded curves for analysis and calculation of articulator settings.


You can start the Numeric Curve Editor application via the button  *Numeric Curves* in the toolbar or the associated entry in the *Data* menu. If there are multiple Analysis Collections present, you will have to select one of them to specify where the data should be inserted.

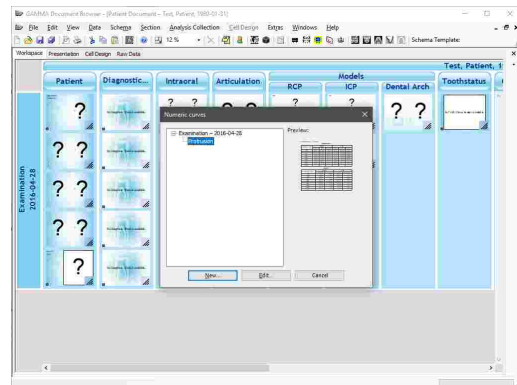


In the now opened Numeric Curve Editor application, you can enter a name for the numeric curve and the coordinates or angles themselves. Save your changes and close the window to continue.




 Please refer to chapter "Numeric Curve Editor<sup>119</sup>" for more information regarding the Numeric Curve Editor application.

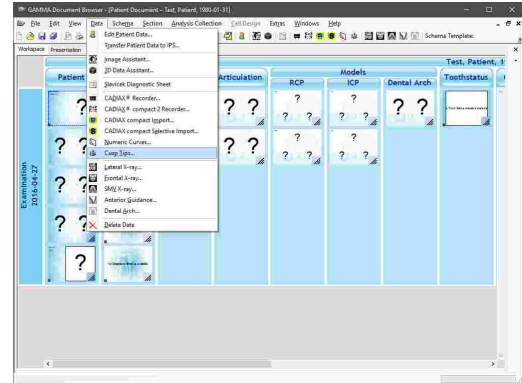
To modify a numeric curve later on, press the toolbar button  *Numeric Curves* again, select the item that you want to modify and press the button *Edit*.



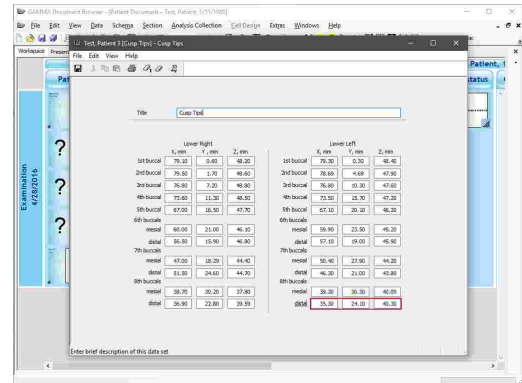
#### 4.9.4.5 Entering cusp tips coordinates


Using the *Cusp Tips Editor*, you can introduce the X/Y/Z coordinates of the lower jaw's cusp tips into the articulator calculation of CADIAX Analyzer. The application will then be able to calculate the ideal incisal table settings to be used for designing occlusal surfaces during a wax-up procedure (refer to chapter "Articulator settings<sup>148</sup>").


You can start the Cusp Tips Editor application via the button  *Cusp Tips* in the toolbar or the associated entry in the *Data* menu. If there are multiple Analysis Collections present, you will have to select one of them to specify where the data should be inserted.

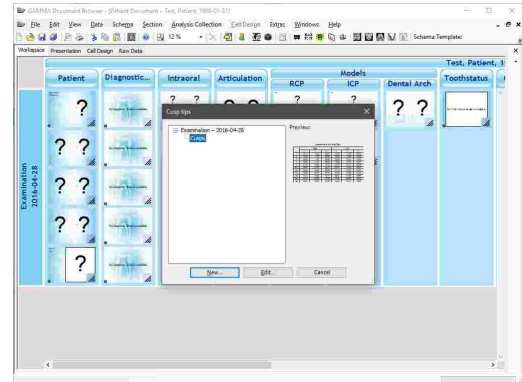


In the now opened Cusp Tips Editor application, you can enter a name for the cusp tips data and the coordinates themselves. Save your changes and close the window to continue.



 Please refer to chapter "Cusp Tips Editor<sup>121</sup>" for more information regarding the Cusp Tips Editor application.

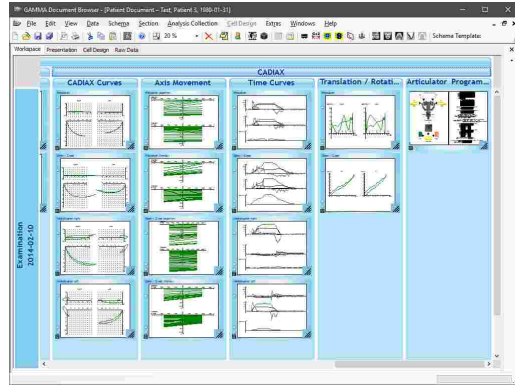
To modify a numeric curve later on, press the toolbar button  *Cusp Tips* again, select the item that you want to modify and press the button *Edit*.



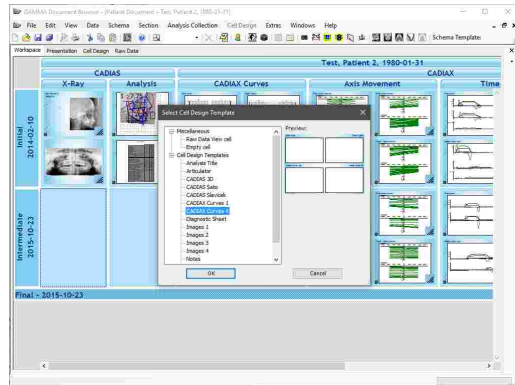
#### 4.9.4.6 Creating a CADIAX analysis

CADIAX analyses allow GAMMA Document Browser to create various previews of recorded condylography data and present them in the Workspace. Naturally, this requires the appropriate data to be present in the database.

The easiest way to display a CADIAX analysis is to apply a schema design template that includes the appropriate cells, for example the template "Full Documentation" (see chapter "Schema Design Templates" [43](#)).

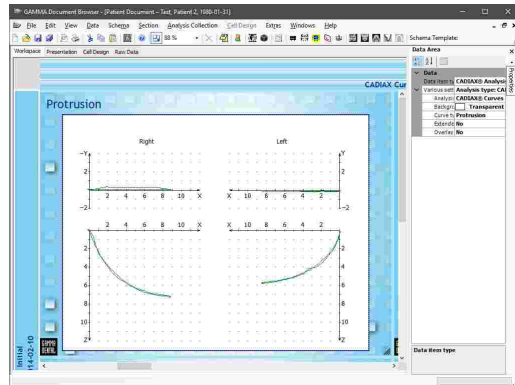


If you want to insert an additional cell that displays CADIAX information, you can do so by creating a new cell based on a predefined template (see chapter "Cells" [47](#)).

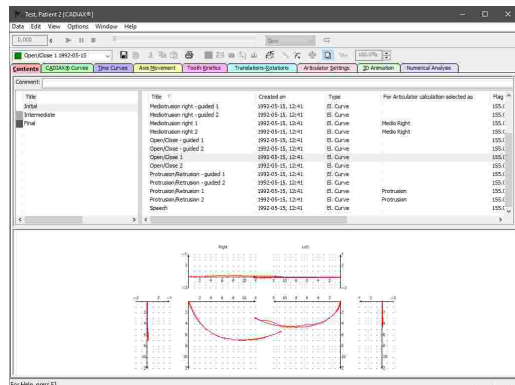



In principle, you could also modify any of the existing data areas to display the desired type of analysis by adjusting its property *Data item type*.

To change the way in which a CADIAX analysis presents the underlying condylography recordings, right-click the data area and choose *Properties* from the context menu. Here, you can adjust various appearance settings of the analysis as well as select the type of graphics to be displayed, such as time curves, translation-rotation graphs, or articulator settings.

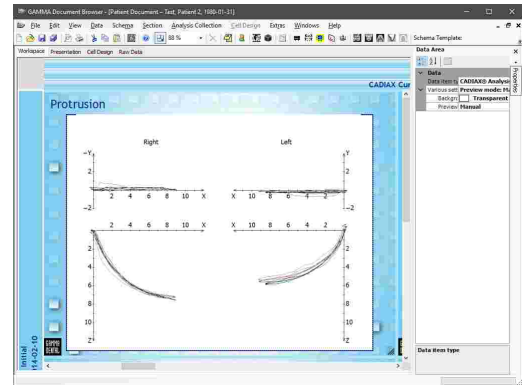


To analyze recordings in detail, you can start the CADIAX Analyzer application by double-clicking any of the CADIAX analyses.



 Please refer to chapter "CADIAX Analyzer" [124](#) for more information regarding the CADIAX Analyzer application.

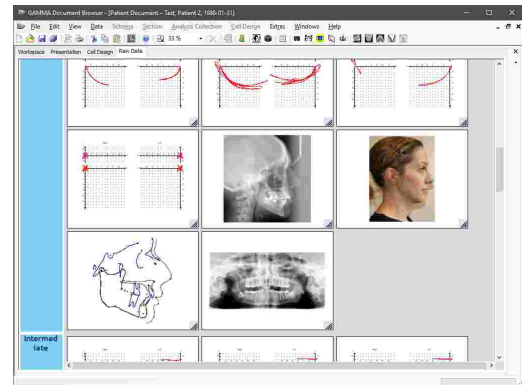
You can create a custom CADIAX preview in the Workspace by opening the analysis, activating the desired view, and then closing and saving the analysis. Contrary to **automatically created** analyses, these custom previews are referred to as **manually created** analyses.



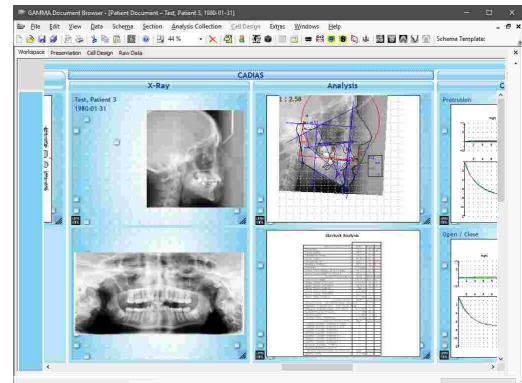
### 4.9.5 Inserting CADIAX x-ray data

The **CADIAX** module allows the analysis of anatomical relations in the patient's skull and the documentation of planned treatments thereof. Its data is created by digitizing anatomical points on x-ray images and can be combined with condylography data stored in CADIAX analyses.

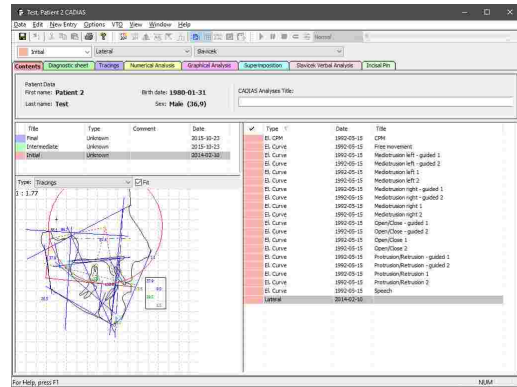
In GAMMA Document Browser, each digitizing of an x-ray image is treated as a primary data item that appears in the Raw Data view (see chapter "The Raw Data view<sup>[57]</sup>"). Here, you will find them displayed alongside other data items such as images and CADIAX condylography curves.



Based on these digitizings, you can add cells in the Workspace view that automatically display miscellaneous analyses, such as cephalometric tracings or numerical tables (see chapter "Creating CADIAX analyses<sup>[80]</sup>").



To analyze the digitizings in detail, you can start the **CADIAS Analyzer** application by double-clicking the Data Area that displays the CADIAS analysis.



**i** Please refer to chapter "CADIAS<sup>175</sup>" for more information regarding the CADIAS module as a whole and to subchapter "CADIAS Analyzer<sup>196</sup>" for more information regarding the CADIAS Analyzer application in particular.

#### 4.9.5.1 Creating a new digitizing

**i** Before starting CADIAS Digitizer, we recommended to import the x-ray images into the database of GAMMA Document Browser. This import is carried out via the Image Assistant, where you can identify the images by assigning them the appropriate image type (see chapter "Importing images<sup>60</sup>"). This way, CADIAS Digitizer will automatically display the relevant image once opened. By default, it expects the images to be of the following types:

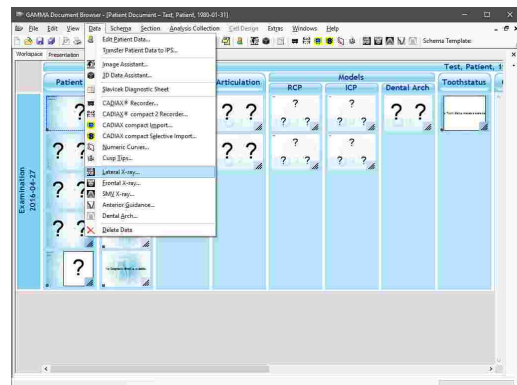
- **Lateral x-ray:** *System definitions\X-ray\Lateral ceph*
- **Lateral patient photo:** *System definitions\Face\Non smiling\Lateral*
- **Frontal x-ray:** *System definitions\X-ray\Frontal ceph*
- **Frontal patient photo:** *System definitions\Face\Non smiling\Frontal*
- **SMV x-ray:** *System definitions\X-ray\SMV ceph*
- **Anterior guidance:** *System definitions\X-ray\Anterior guidance*
- **Dental arch:** *System definitions\X-ray\2D dental arch*

You can modify these expected image types in GAMMA Document Browser via the menu *Extras → Options*, on the register *CADIAS Image Types*.

In GAMMA Document Browser, you can open the CADIAS Digitizer application via one of the following entries in the *Data* menu, depending on which type of data you want to enter:

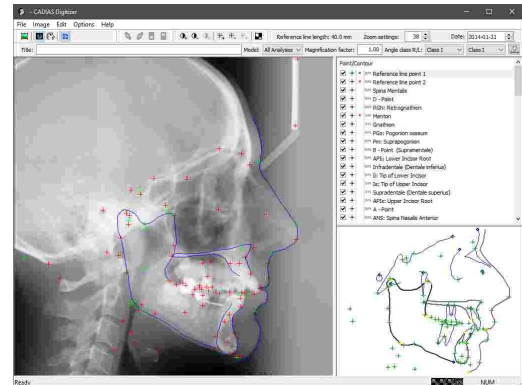
- *Lateral x-ray*
- *Frontal x-ray*
- *SMV x-ray*
- *Anterior guidance*
- *Dental arch*

If there are multiple analysis collections present, you will have to select one of them beforehand to specify where the data should be inserted.



Once CADIAS Digitizer has been opened, it will automatically load the appropriate image if such is present in the database. You can then digitize the points and contours on the image, save the data, and finally close the application.

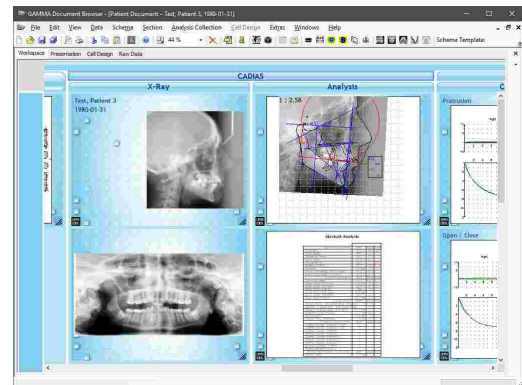
Subsequently, the digitizing will appear in the Raw Data view of GAMMA Document Browser and can be used in a CADIAS analysis.



**i** Please refer to chapter "CADIAS Digitizer<sup>176</sup>" for more information regarding the CADIAS Digitizer application.

**i** If you load the images to be digitized within the CADIAS Digitizer application, they will be automatically transferred to the patient database of GAMMA Document Browser upon saving.

If the Workspace of GAMMA Document Browser already contains data areas for CADIAS analyses, these will be updated to automatically display a preview of the digitized data.

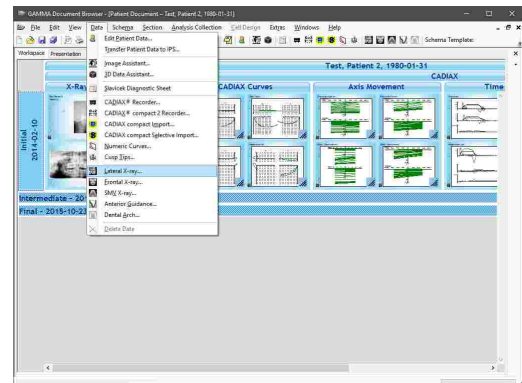


**!** If you want to create multiple digitizings of the same type for a particular patient, for example to compare cephalometric relations before and after a treatment, it is recommended to store each of them in a separate analysis collection of GAMMA Document Browser. Please refer to section "Analysis Collections<sup>44</sup>" for instructions on how to create analysis collections.

#### 4.9.5.2 Editing an existing digitizing

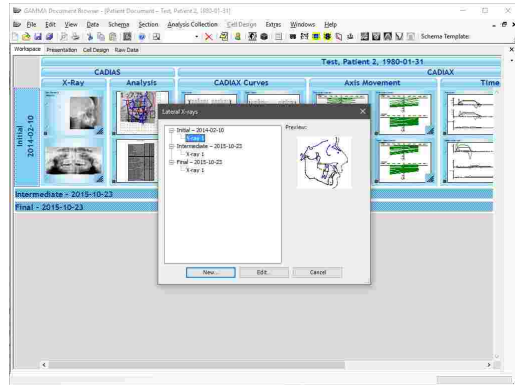
To edit an existing x-ray digitizing in GAMMA Document Browser, you can open the CADIAS Digitizer application via one of the following entries in the *Data* menu, depending on which type of data you want to edit:

- Lateral x-ray
- Frontal x-ray
- SMV x-ray
- Anterior guidance
- Dental arch

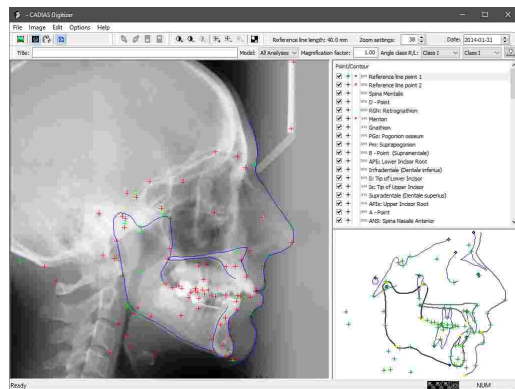


If there are multiple analysis collections present, you will have to select one of them beforehand.

Subsequently, a dialog will appear in which you can select the digitizing to edit. Select the desired entry and press the button *Edit*.



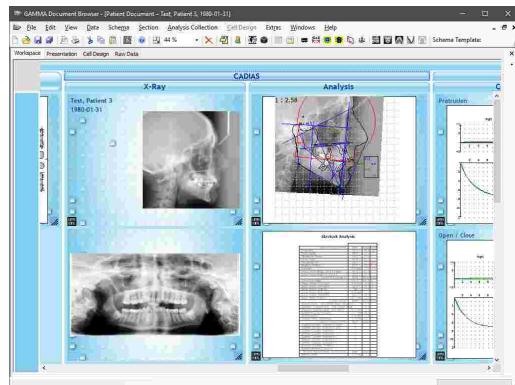
Once CADIAS Digitizer has been opened, you can make the necessary changes and save the digitizing. CADIAS analyses in the Workspace of GAMMA Document Browser will be recalculated automatically.



### 4.9.5.3 Creating a CADIAS analysis

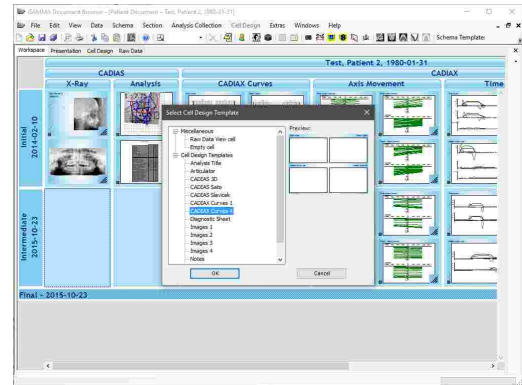
CADIAS analyses allow GAMMA Document Browser to create various previews of digitized x-ray images and present them in the Workspace. Naturally, this requires the appropriate data to be present in the database.

The easiest way to create a CADIAS analysis is to apply a schema design template that includes the appropriate cells, for example the template "Full Documentation" (see chapter "Schema Design Templates" <sup>43</sup>).

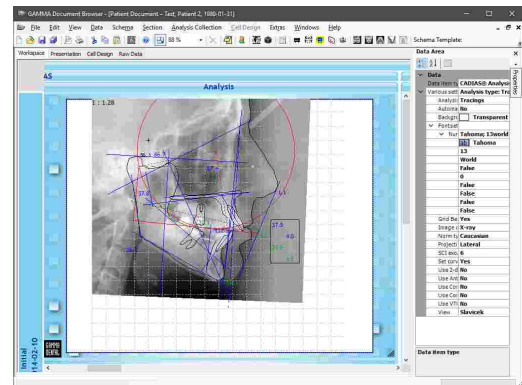


If you want to insert an additional cell that displays CADIAS information, you can do so by creating a new Cell based on a predefined template (see chapter "Cells" [47]).

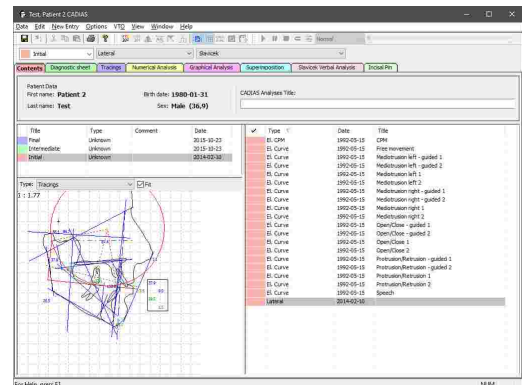
In principle, you could also modify any of the existing data areas to display the desired type of analysis by adjusting its property *Data item type*.




To change the way in which a CADIAS analysis presents the underlying digitizings, right-click the data area and choose *Properties* from the context menu. Here, you can adjust various appearance settings of the analysis as well as select the type of graphics to be displayed, such as tracings, numerical analysis tables, or verbal analysis statements.

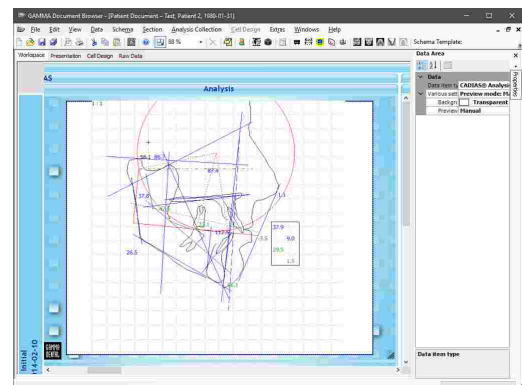


To analyze the digitizings in detail, you can start the CADIAS Analyzer application by double-clicking any of the CADIAS analyses.



 Please refer to chapter "CADIAS Analyzer" [96] for more information regarding the CADIAS Analyzer application.

You can create a custom CADIAS preview in the Workspace by opening the analysis, activating the desired view, and then closing and saving the analysis. Contrary to *automatically created* analyses, which are based on the properties of the Data Area, these custom previews are referred to as *manually created* analyses.

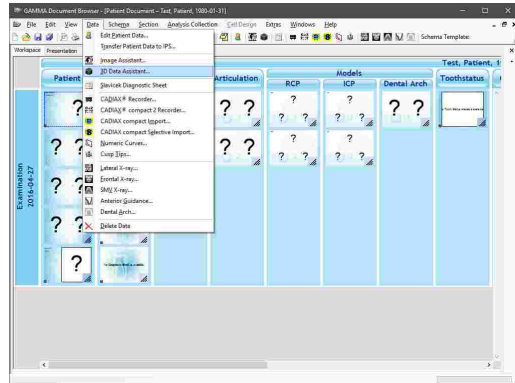


### 4.9.6 Importing CADIAS 3D data

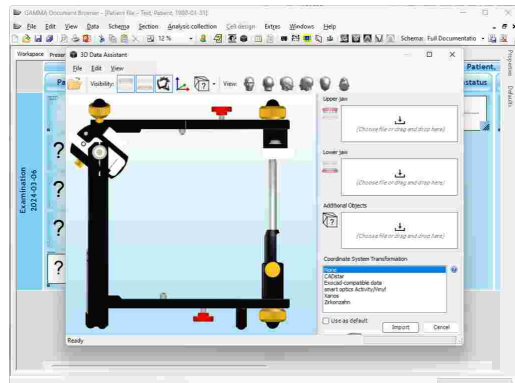
GAMMA Document Browser supports the import of 3D models of the patient's dentition, which can subsequently be used for virtual occlusion analysis and design in the **CADIAS 3D** module. These models can be captured either directly on the patient using an intraoral scanner or from plaster models using a laboratory scanner.

The import of 3D models into GAMMA Document Browser is carried out via the **3D Data Assistant**, which also provides basic 3D editing capabilities to prepare the models as needed.

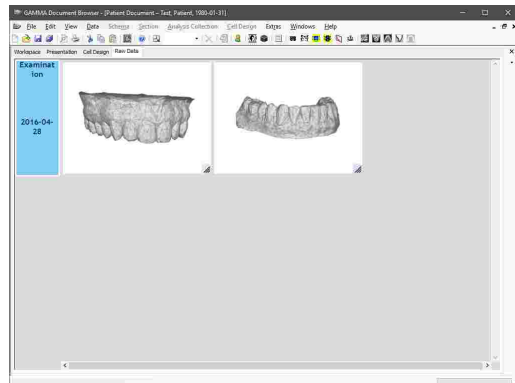
You can start the 3D Data Assistant via the toolbar button **3D Data Assistant** or the associated entry in the **Data** menu. If there are multiple analysis collections present, you will have to select one of them to specify where the data should be inserted.



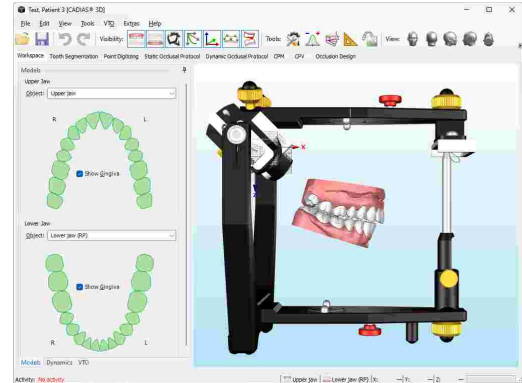
The 3D Data Assistant consists of a large display area for the currently loaded 3D data and a panel on the right side, which provides the controls for loading models and articulating them in the virtual articulator. Please refer to chapter "Importing 3D data<sup>242</sup>" for more information about using the 3D Data Assistant.




After articulating the models in the 3D Data Assistant and finishing the import, they will be stored in the patient database and appear as individual data items in the Raw Data view.



To analyze the imported models in detail, you can start the **CADIAS 3D** application by double-clicking any data area that displays a CADIAS 3D analysis (refer to chapter "Creating CADIAS 3D analyses<sup>83</sup>").

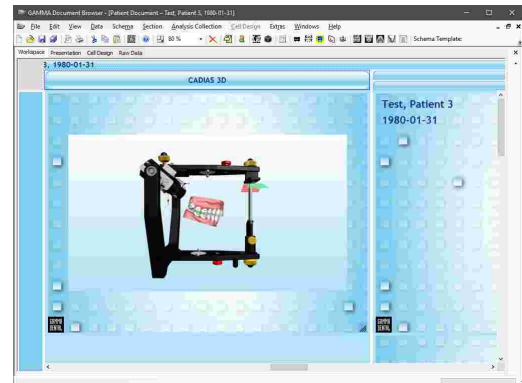


 Please refer to chapter "CADIAS 3D<sup>239</sup>" for more information regarding the CADIAS 3D module.

#### 4.9.6.1 Creating CADIAS 3D analyses

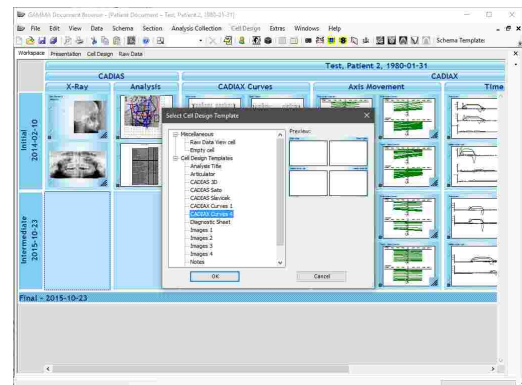
CADIAS 3D analyses allow GAMMA Document Browser to process 3D models of the patient's dentition and enables you to carry out diagnostic evaluations and anatomical measurements based on this information. Naturally, this requires the appropriate data to have been imported in the database.

The easiest way to create a CADIAS 3D analysis is to apply a schema design template that includes the appropriate cells, for example the template "Full Documentation" (see chapter "Schema Design Templates<sup>43</sup>").

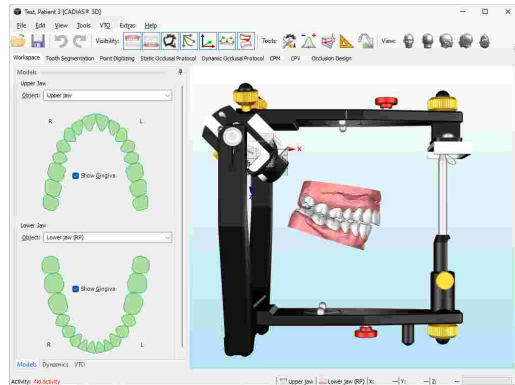


If you want to insert an additional cell that displays CADIAS 3D information, you can do so by creating a new Cell based on a predefined template (see chapter "Cells<sup>47</sup>").

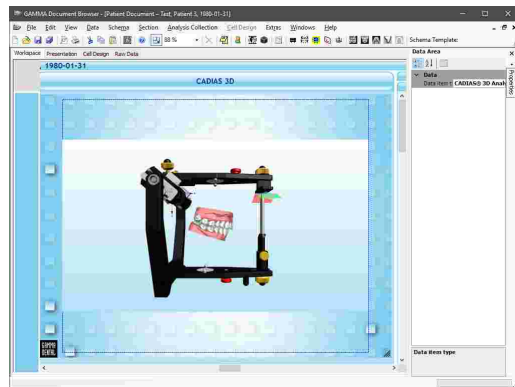
In principle, you could also modify any of the existing data areas to display the desired type of analysis by adjusting its property *Data item type*.



To analyze the 3D models in detail, you can start the **CADIAS 3D** application by double-clicking any of the CADIAS 3D analyses.



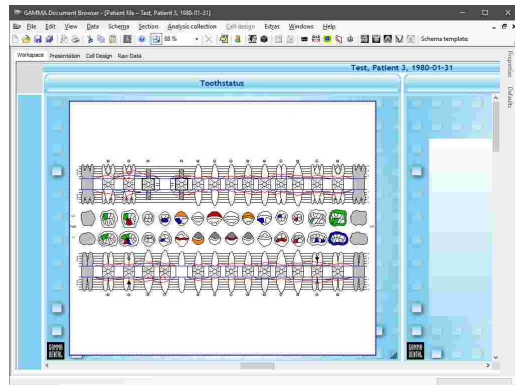
A CADIAS 3D analysis will always display a preview of the 3D scene that was displayed when the application was closed the last time.



#### 4.9.7 Entering tooth status information

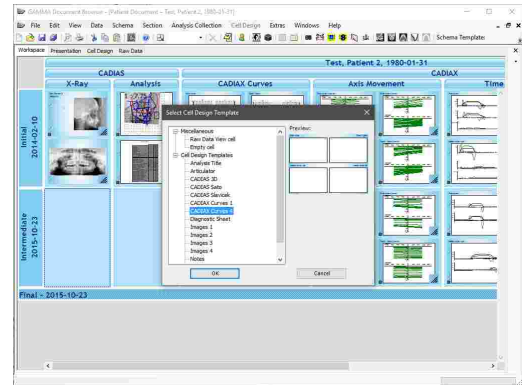
Tooth status analyses allow GAMMA Document Browser to store information regarding the patient's parodontal, functional, and overall dental situation. For the display and editing of this information, the **Tooth Status** application is used.

The easiest way to create a tooth status analysis is to apply a schema design template that includes the appropriate cells, for example the template "Full Documentation" (see chapter "Schema Design Templates" <sup>43</sup>).

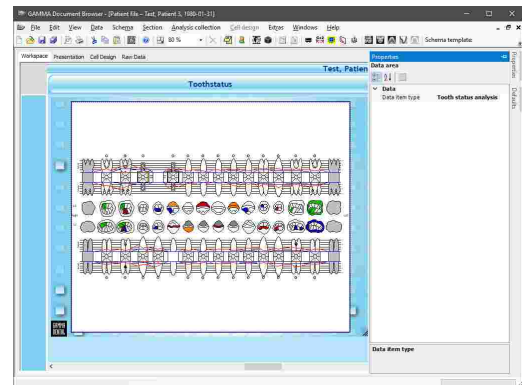


If you want to insert an additional cell that displays tooth status information, you can do so by creating a new cell based on a predefined template (see chapter "Cells <sup>47</sup>").

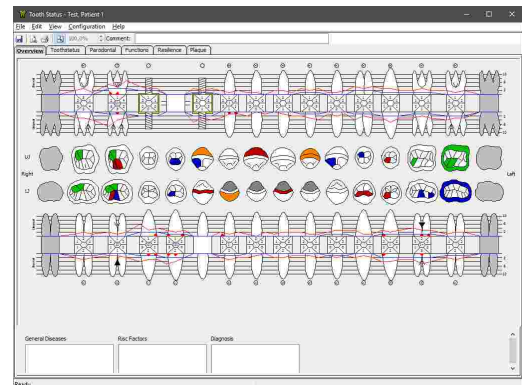
In principle, you can modify any data area to display a tooth status analysis by changing its property *Data item type*.




Tooth status analyses always display the overview graphic, which combines the entered tooth status information in a clear and comprehensive form.



To view or edit the displayed information, you can start the tooth status application by double-clicking the tooth status analysis.



 Please refer to chapter "Tooth status <sup>282</sup>" for more information regarding the tooth status application.

### 4.9.8 Inserting foreign OLE objects

GAMMA Document Browser supports the embedding of arbitrary file types by means of the OLE (Object Linking and Embedding) technology. This allows you to store all sorts of data, such as Microsoft Office documents, PDF files, or even audio or video files right next to the patient data obtained with GAMMA Document Browser. External files that are embedded into the patient file in this way are referred to as **Foreign OLE Objects**.

The easiest way to add a foreign OLE object is to apply a schema design template that includes the appropriate cells, for example the template "Full Documentation" (see chapter "Schema Design Templates" <sup>43</sup>).

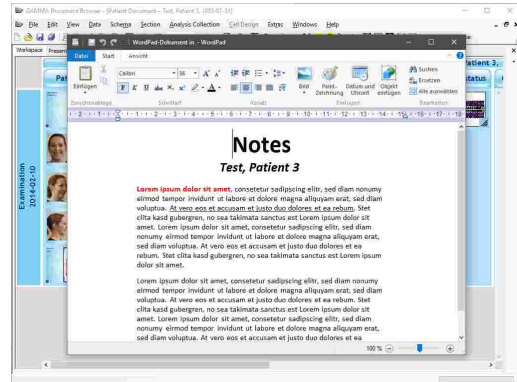
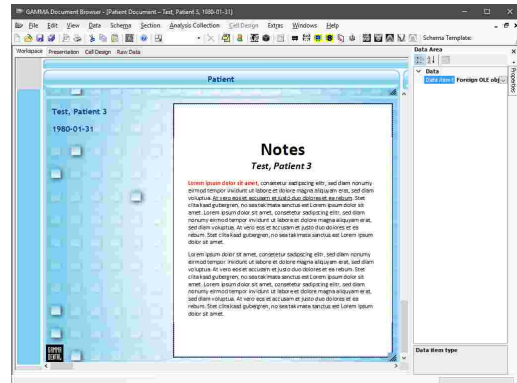
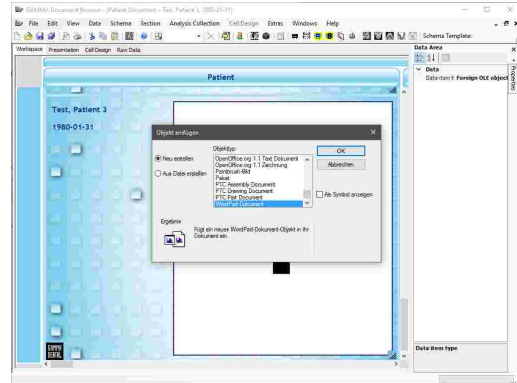
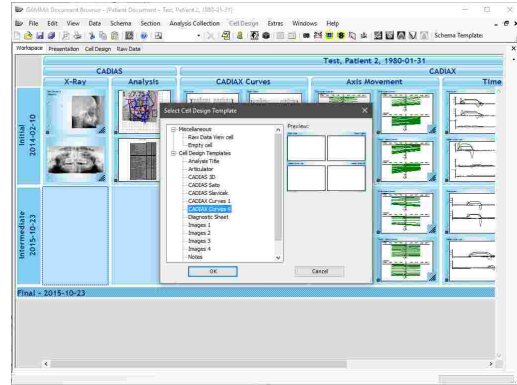
If you want to insert an additional cell that displays OLE objects, you can do so by creating a new cell based on a predefined template (see chapter "Cells" <sup>47</sup>).

In principle, you can modify any data area to display a foreign OLE object by changing its property *Data item type*.

By double-clicking the data area, you can show the object insertion dialog, where you can either create a new document or select an existing file to be embedded.

GAMMA Document Browser will automatically create a preview of the embedded file or document and display it in the data area.

To open the embedded file or document, simply double-click the data area or choose *Open* in its context menu.





If you want to open or edit an OLE object of a format not natively provided by GAMMA Dental Software or the Windows operating system, you need to have the corresponding application installed. For example, Microsoft Office is required for Word, Excel, or PowerPoint documents. This also applies when you want to share your data with other users.

#### 4.10 Configuring the VDDS-media interface

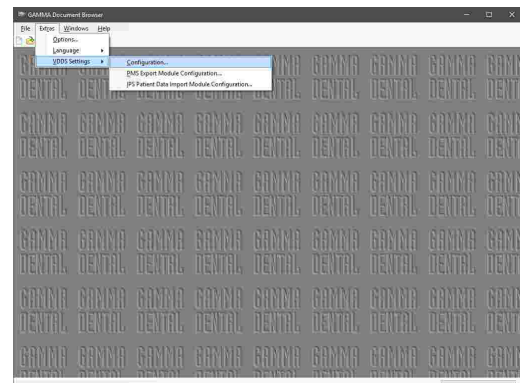
The VDDS-media interface serves the exchange of basic patient information (e.g. name, date of birth) between the software products used in dental practices. It allows for a centralized acquisition of patient data, so that this information does not have to be entered multiple times, for each used software product. Applications that support this interface can transfer the patient information to other applications by the press of a button.

In most cases, a dental practice will use a single practice management software, where patient information is kept in a database and that is also used for scheduling appointments and so forth. Using the VDDS-media interface, other software for x-ray imaging or condylography recording can be started directly from the practice management software when needed. In this example, the practice management software takes the role of the PMS (Practice Management System) while the recording software takes the role of the IPS (Image Processing System). GAMMA Dental Software supports the VDDS-media interface in version 1.4 and can operate either as PMS or IPS.

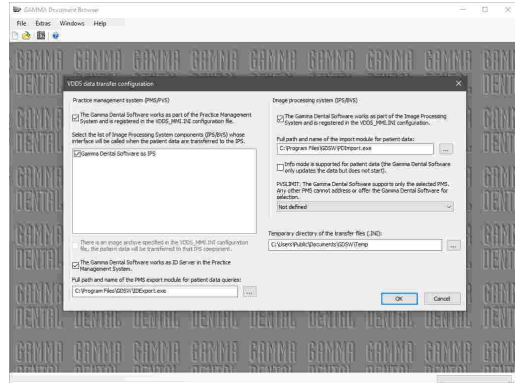
Technically, the transfer of patient information is carried out via a temporary text-based \*.ini-file that is created by the exporting application and passed to the importing one. All applications on a system that use the VDDS-media interface register themselves in the *VDDS\_MMI.ini* configuration file that is located in the Windows system directory.

Further information regarding the VDDS-media interface as well as the full technical specification can be found on the website of the Association of German Dental Software Companies (German: "Verband deutscher Dental-Software Unternehmen") at [www.vdds.de](http://www.vdds.de).

In GAMMA Document Browser, you can open the general VDDS configuration dialog via the menu *Extras* → *VDDS interface* → *Configuration*.



In this dialog, you can first of all specify whether GAMMA Dental Software should register itself as PMS or IPS.

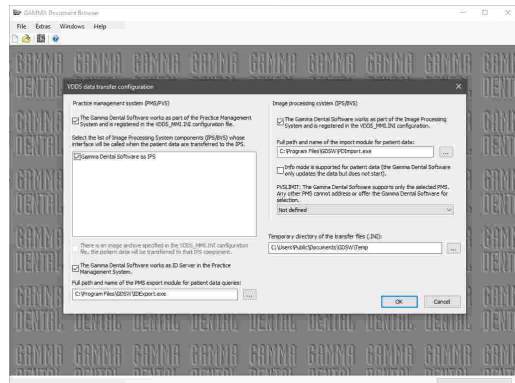


**i** Please note that for changing the general VDDS-media configuration, the software has to be started with administrative privileges.

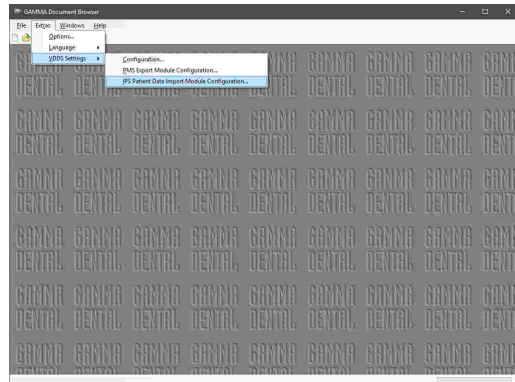
### 4.10.1 Importing patient data using the VDDS-media interface

This chapter describes how you can configure GAMMA Document Browser to receive patient information from third-party practice management software over the VDDS-media interface.

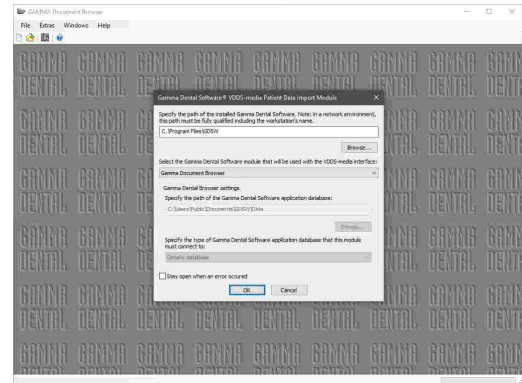
In the general VDDS-media configuration dialog, ensure that GAMMA Dental Software is registered as IPS and that the path of the import module refers to the file *PDImport.exe* in the software's installation directory. Apply the settings by pressing **OK**.



Open the configuration dialog for the import module via the menu *Extras* → *VDDS interface* → *Configure patient data import module*.

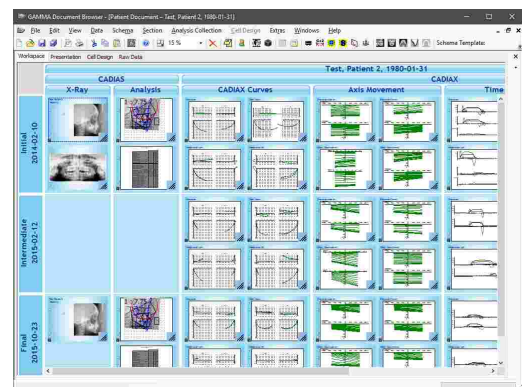


In this dialog, specify the installation directory of GAMMA Dental Software and select *GAMMA Document Browser* as the module to be started. Confirm by pressing **OK**.



GAMMA Dental Software should now appear as a VDDS-media client (IPS) in your practice management software. Please consult the instruction manual of that software for further information.

Now, when opening GAMMA Dental Software from the practice management software for a specific patient, the appropriate patient file should automatically be opened in GAMMA Document Browser or be created if it does not yet exist.



**i** If the transfer of patient information into GAMMA Dental Software does not work as expected, you can configure the import module to stay open when an error occurred. To do so, simply check the check box in the bottom area of the dialog. The displayed error messages can be helpful in diagnosing the cause of the issue.

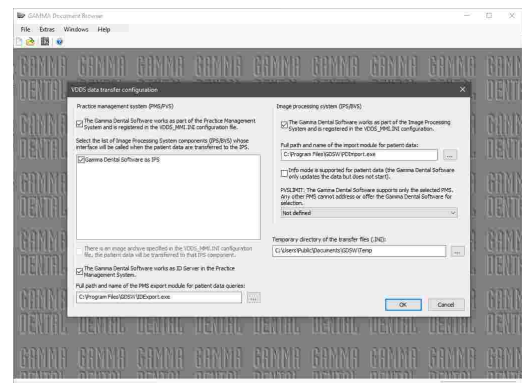
#### 4.10.2 Exporting patient data using the VDDS-media interface

This chapter describes how you can configure GAMMA Document Browser to provide patient information to third-party software over the VDDS-media interface.

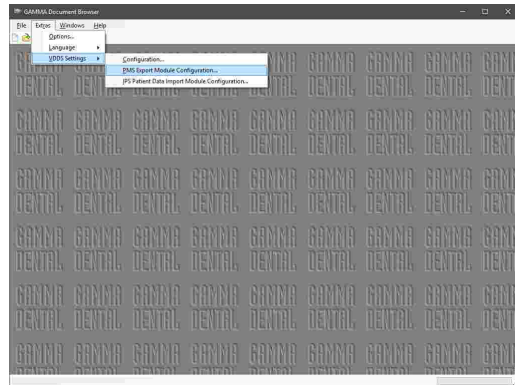
In the general VDDS-media configuration dialog, ensure that GAMMA Dental Software is registered as PMS and that the path of the export module refers to the file *IDExport.exe* in the software's installation directory. Furthermore, select the IPS applications to which the patient information shall be transferred.

Here you can also set the ID Server option, which declares GAMMA Dental Software as the provider of global VDDS-media patient IDs for other applications using the interface.

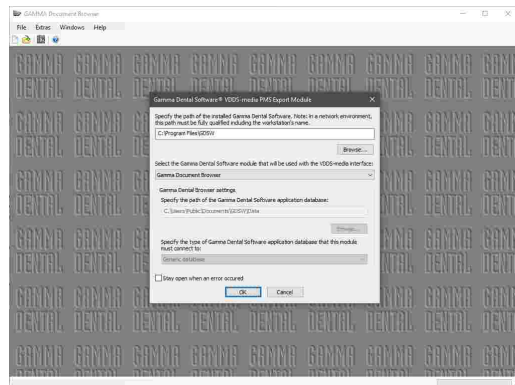
Apply the settings by pressing **OK**.



Subsequently, open the configuration dialog for the export module via the menu *Extras* → *VDDS interface* → *Configure patient data export module*.

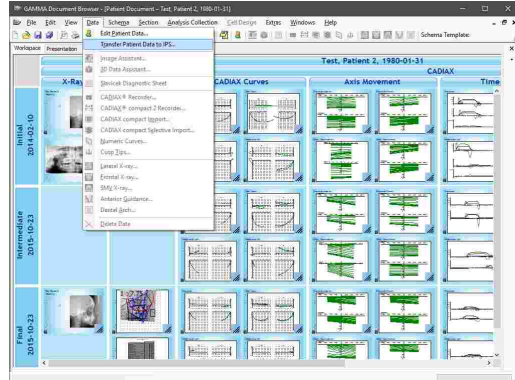


In this dialog, specify the installation directory of GAMMA Dental Software and select *GAMMA Document Browser* as the module to be used. Confirm by pressing *OK*.



GAMMA Dental Software should now appear as a VDDS-media sender (PMS) in your third-party software. Please consult the instruction manual of that software for further information.

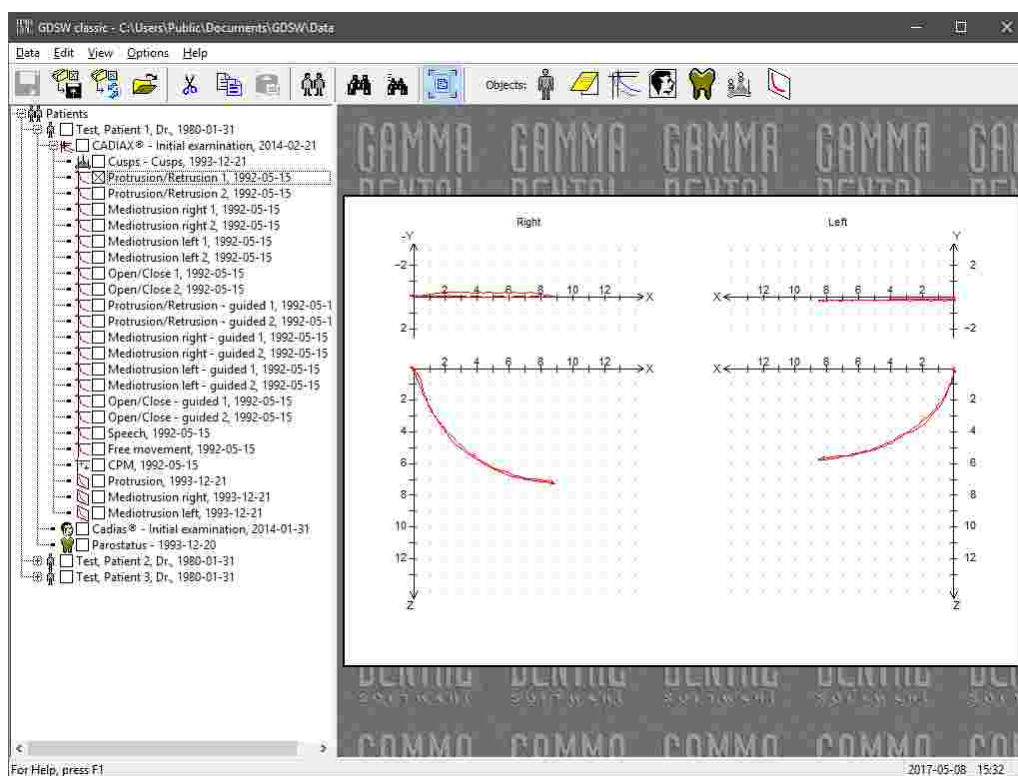
Now, whenever a patient file is opened in GAMMA Document Browser, you can transfer the information of that patient to the third-party software via the menu *Data* → *Transfer patient data to IPS*.



**i** If the transfer of patient information to third-party software does not work as expected, you can configure the export module to stay open when an error occurred. To do so, simply check the check box in the bottom area of the dialog. The displayed error messages can be helpful in diagnosing the cause of the issue.

## 5 GDSW classic

**GDSW classic** is the classical patient data management module of GAMMA Dental Software. It provides basic features for managing patient information and is tightly integrated with the CADIAX condylography and CADIAS cephalometry modules (see chapters "CADIAX<sup>114</sup>" and "CADIAS<sup>175</sup>", respectively).

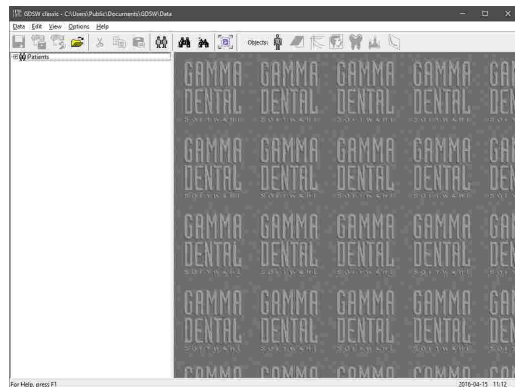


The GDSW classic module has been superseded by GAMMA Document Browser as the new patient management application of GAMMA Dental Software (see chapter "GAMMA Document Browser<sup>34</sup>"). GAMMA Document Browser provides features that far exceed the capabilities of GDSW classic while keeping your data in a form that is clearly structured and presentation-ready at any time.

When installing GAMMA Dental Software, both GDSW classic and GAMMA Document Browser are installed simultaneously. The two applications are completely independent and use different patient databases. To transition from GDSW classic to GAMMA Document Browser, the latter application provides a conversion feature that allows you to convert patient files into the new format while leaving the existing patient files unchanged (refer to chapter "Converting data of GDSW classic<sup>39</sup>").

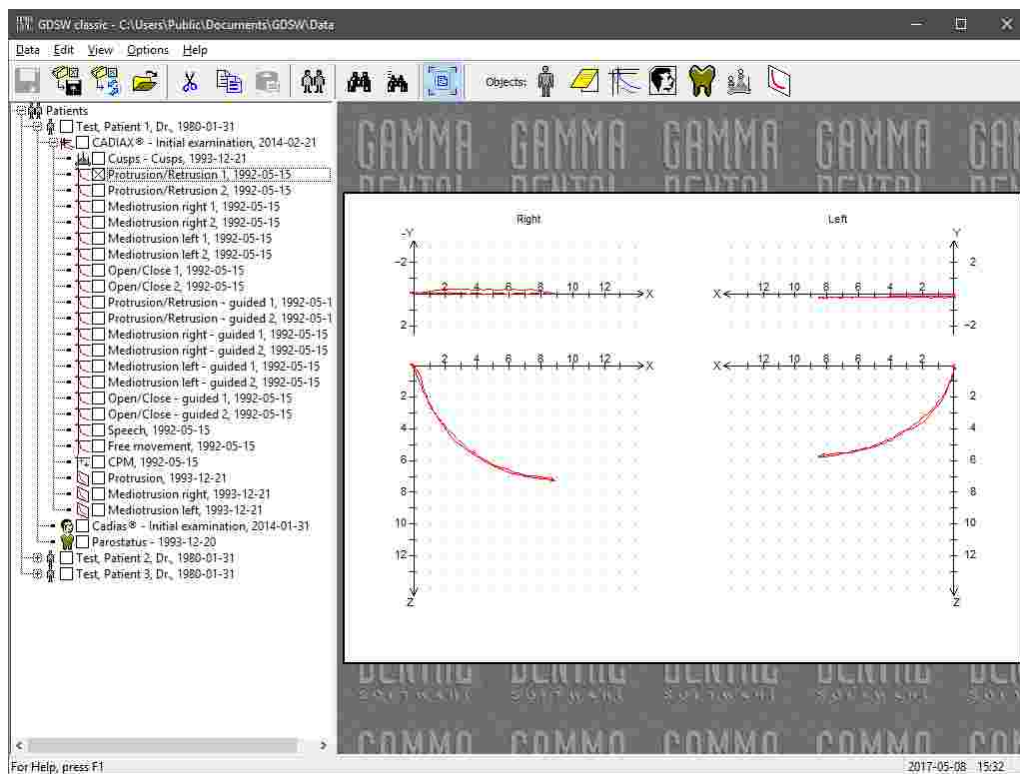
## 5.1 Starting the application

You can start GDSW classic via the Windows start menu (*All Programs* → *GAMMA Dental Software* → *GDSW classic*) or via the shortcut on your desktop:

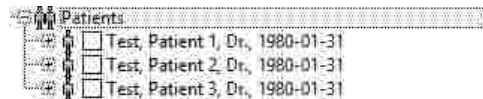


## 5.2 User interface

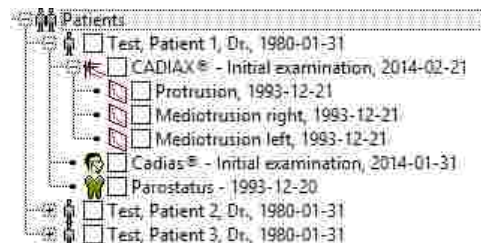
The user interface of GDSW classic is separated into the so-called **Patient Tree** on the left side and the **Preview Area** on the right side.




The patient tree displays all patient files that are contained in the specified database directory. The individual patient entries can be expanded and collapsed via a double-click or by clicking the adjacent plus/minus symbols.



Each patient entry can contain an arbitrary number of sub-objects, such as CADIAX analyses, CADIAS analyses, or tooth status analyses. These can be grouped together in analysis collections and may further be divided into their own sub-items. For example, CADIAX analyses can be expanded to provide direct access to the individual condylography recordings.



By selecting an entry in the patient tree, you can have the application display the corresponding preview in the preview area. To modify the displayed information or to analyze it in detail, double-click the preview to open the editing application. You can fit the preview into the display area using the toolbar button  *Fit Contents to Window*.




You can select multiple items in the patient tree by holding down the *Ctrl* key or the *Shift* key while clicking the items. This can be useful if you want to copy, delete, or export multiple sets of data at once. In addition, you can move or copy data between patients or analyses by simply dragging the items with the mouse and dropping them where needed.

### 5.3 Managing patient files

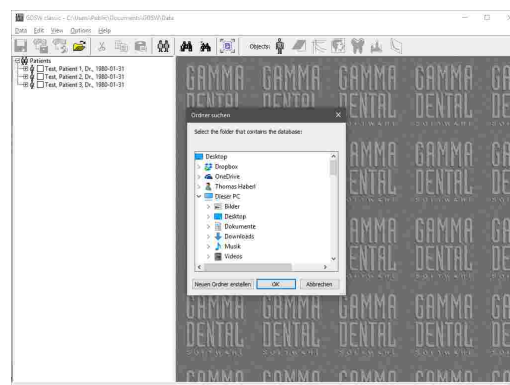
GDSW classic stores the data of each patient in an individual \*.fgw-file on your computer's hard disk. The default directory where these files can be found is as follows:

*C:\Users\Public\Documents\GDSW\Data\*

You can change this directory either when installing the software or at a later time.

GDSW classic does not open your patient files one by one, but lists all files of a specific directory. The currently selected directory is displayed in the title of the application's main window. To show the patient files of a different directory, use the toolbar button  *Open Database*.

If you want to access your database directory from multiple workstations, you can put your data on a network storage and configure the software on all workstations to use that path.




When you double-click a patient file in Windows Explorer, GDSW classic will open with the appropriate directory selected. The most recently used database directories will be offered for quick selection in the *Data* menu. The last one will be restored automatically when you restart the software.

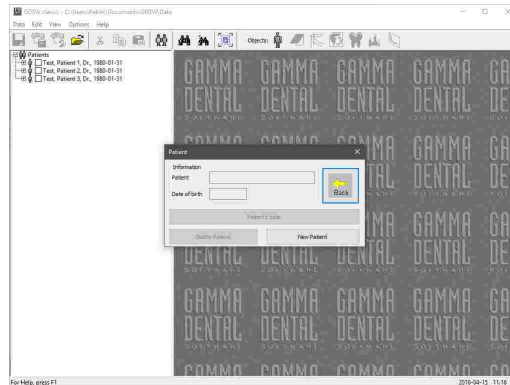
For copying files into or out of your database directory, you can quickly open that folder via the menu *Data* → *Open Database Directory*.



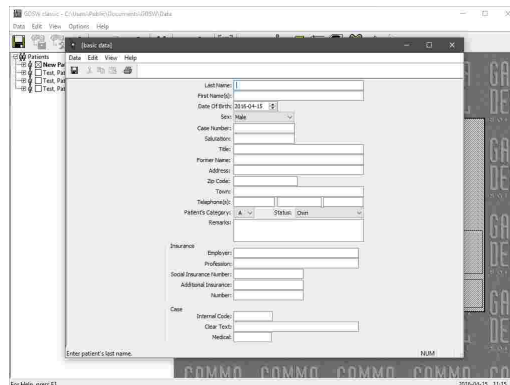
GDSW classic comes with a ready-made patient file that you can use to get to know and experiment with the software. This "Test Patient" file is automatically copied to the database directory during installation and can safely be deleted.

### 5.3.1 Creating a new patient file

You can create a new patient file at any time via the toolbar button  *Patient Data*. Press *New Patient* in the appearing dialog.



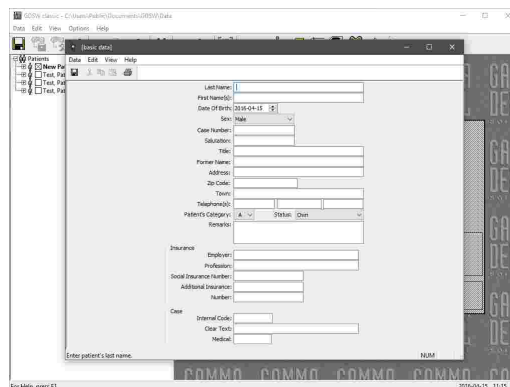
An input form will be displayed, in which you can enter the basic data of the patient (refer to chapter "Entering patient information" <sup>94</sup>).




### 5.3.2 Entering patient information


When creating a new patient file, you can enter the personal information of the patient as well as practice-specific information for identifying and categorizing the patient case.


Save your changes and close the window to continue.

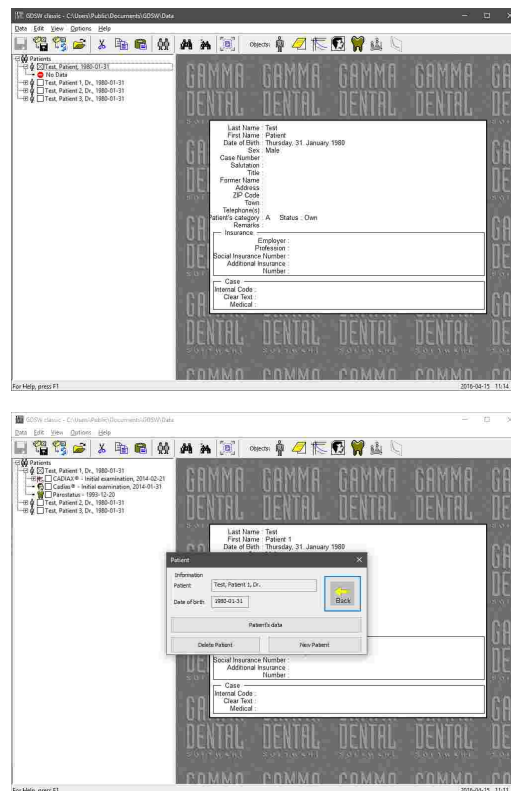


 All patient information inputs are optional. However, it is recommended to enter at least the patient's first name, last name, and date of birth. This information is used for identifying the patient in the database and the date of birth is additionally used for determining age-dependent norm values for cephalometric analyses in the CADIAS module.

Subsequently, you will find that a new, empty patient entry has been created. For information on how to create CADIAX condylography recordings, digitize anatomical points on an x-ray image, or enter tooth status information, please refer to chapter "Inserting data" <sup>98</sup>.

When you save the database via the toolbar button , the application will create a respective \*.fgw file in your database directory.


To modify the initially specified patient data later on, select the patient entry and simply double-click the preview that is displayed on the right half of the window. Alternatively, you can press the toolbar button  *Patient Data* again, and choose *Patient's Data*.

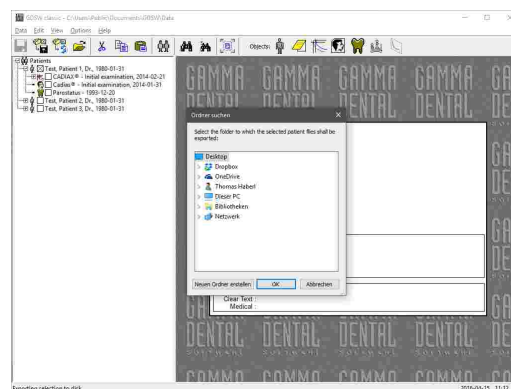



You can print the entered patient information via the menu *File* → *Print*. That menu also provides options for showing a print preview and for configuring the format of the printout.

### 5.3.3 Exporting patient files

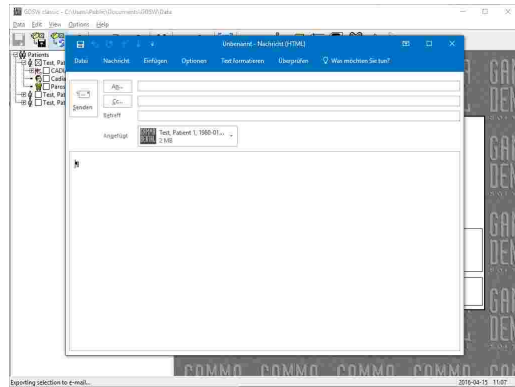
Since each patient in GDSW classic is represented in its own \*.fgw file, you can easily copy and backup your data by copying the content of your database directory. However, GDSW classic also provides two convenient **Export** features to export them from within the application. During this procedure, the original data will remain in your database.


To export a number of patient files from your database to a different directory, for example onto a removable USB drive, proceed as follows. Select the corresponding entries in the patient tree and press the toolbar button  *Export Patient Selection to Medium*. In the appearing dialog, you can select the directory to which the files should be exported and confirm by pressing *OK*.



For sharing data with your colleagues, you can export patient files directly to your e-mail application via the toolbar button  *Export Patient Selection via E-Mail*. This will create a new e-mail message and add the selected patient files as an attachment.


Please note that this requires an e-mail client software to be installed on your system, for example Windows Live Mail, Mozilla Thunderbird, or Microsoft Outlook.




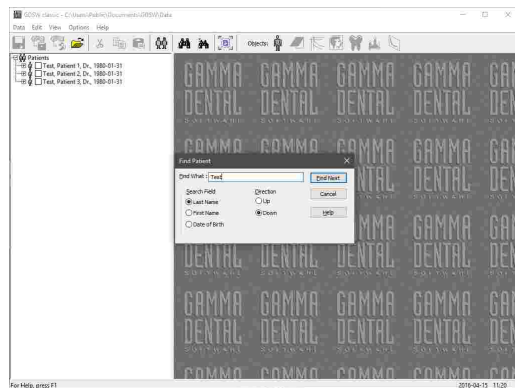
 To export multiple patient files at once, simply select them in the patient tree before initiating the export. You can do so by holding down the *Ctrl* key or the *Shift* key while clicking the entries.


### 5.3.4 Searching patients

If you have many patients in your database and want to locate a particular patient quickly, you can use the **Search** functionality. It allows finding the patient by entering a part of the patient's information.

To open the search dialog, use the toolbar button  *Find Patient*. Here, you can specify if you want to search for the patient's last name, first name, or date of birth. Press *OK* to start the search. If a patient that matches the search criteria is found, its entry will become selected in the patient tree.

In case you were looking for a different patient, you can continue the search by pressing the toolbar button  *Find Next* or the *F3* key on your keyboard.



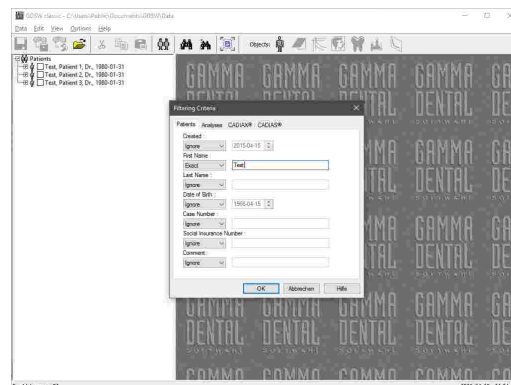
 An even easier way to search for a patient with a specific last name is to type the name on your keyboard while the patient tree is in focus.


### 5.3.5 Filtering patients

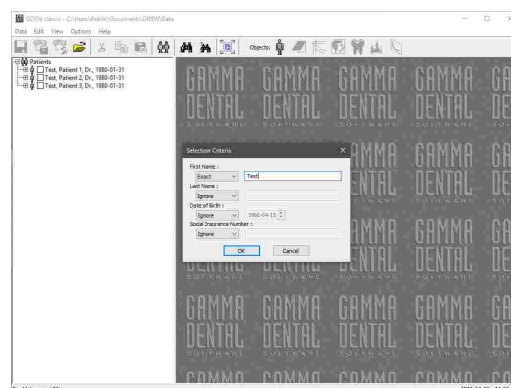
Instead of showing all patients in the selected database directory, GDSW classic can only display the entries that meet certain filter criteria. You can specify these criteria as described below.

Use the menu entry *View* → *Filters* to open the **Filter** dialog. This dialog provides numerous options for filtering patients, analysis collections, and CADIAX or CADIAS analyses. When a filter is applied, only the items that meet those criteria will remain listed in the patient tree. To deactivate filtering and display all items, simply set all the inputs to *Ignore*.

After confirming your inputs by pressing *OK*, collapse and open the patient tree one more time to apply the new filter. Please note that the filter will be reset when you restart the application.



A similar feature is the **Patient Selection** functionality, which you can invoke via the toolbar button  *Patient Selection* or the menu entry *View* → *Patient selection*. Here, you can filter the displayed patients by last name, first name, date of birth, or social security number. Unlike the filter dialog however, this information is stored persistently and will be re-applied when you open the application the next time.



Besides *Ignore*, each type of filter criteria has multiple filter options that can be selected using the combo box before the input field. For example, when filtering for a patient with a specific last name, the option *Prefix* will return the patients who's name starts with the given characters, while *Exact* will only return patients that exactly match the specified string. Furthermore, date inputs (patient's date of birth, analysis creation date, etc.) provide options for filtering data within an arbitrary time span, and CADIAX analyses can even be filtered for specific curve names.



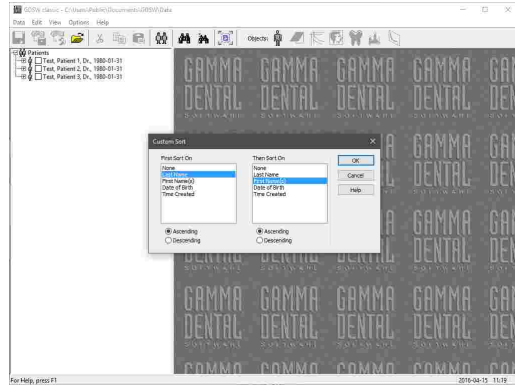
If you notice that some entries are missing from your patient tree, but you are sure that the corresponding patient files are present in your database folder, please verify that all inputs in the patient selection dialog are set to *Ignore*.

### 5.3.6 Changing the patient sort order

By default, the entries in the patient tree of GDSW classic are sorted alphabetically by last name and then by first name. You can customize this sort order via the menu entry *View* → *Sort*.

In the sort order dialog, you have the possibility to configure the information by which the patient entries are sorted first. This can be either first name, last name, date of birth, or creation time. If this information is equal for two patients, they will be sorted according to the second type of information. For both sort iterations, you can specify whether the sorting should be carried out in ascending or descending order.

Press OK to confirm your selection. The application will apply the new sort order immediately and remember it for when you start the software the next time.



## 5.4 Inserting data

The application provides the following toolbar buttons for adding or editing the data of a patient file:



### Analysis collection

Opens the dialog for adding, editing, or deleting analysis collections. (See chapter "Creating analysis collections" [\[99\]](#).)



### CADIAX

Opens the dialog for adding, editing, or deleting CADIAX analyses. (See chapter "Recording CADIAX condylography data" [\[100\]](#).)



### CADIAS

Opens the dialog for adding, editing, or deleting CADIAS analyses. (See chapter "Inserting CADIAS x-ray data" [\[104\]](#).)



### Tooth status

Opens the dialog for adding, editing, or deleting tooth status analyses. (See chapter "Entering tooth status information" [\[107\]](#).)



### Cusp tips

Opens the dialog for adding, editing, or deleting cusp tips data items. (See chapter "Entering cusp tips coordinates" [\[103\]](#).)




### Numeric curve

Opens the dialog for adding, editing, or deleting numeric curves. (See chapter "Entering numeric curves" [\[102\]](#).)




Alternatively, you can reach all of these operations via the entry *New GAMMA Object* in the context menu of the patient tree.

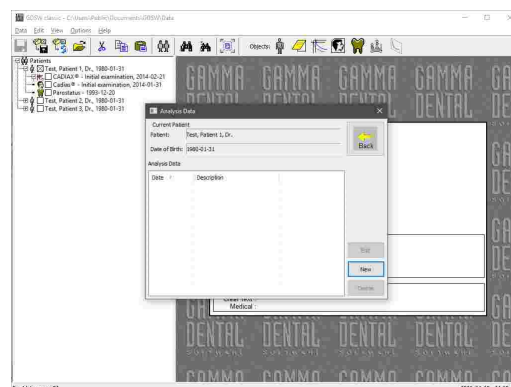


Please note that when saving data in the sub-modules of GDSW classic, the changed data will not automatically be written to the patient file. The changes will be kept in main memory until you press the toolbar button  Save or close the sub-module. Should this lead to complications, you can disable the automatic saving when exiting a module via the menu *Options* → *Storage handling*.

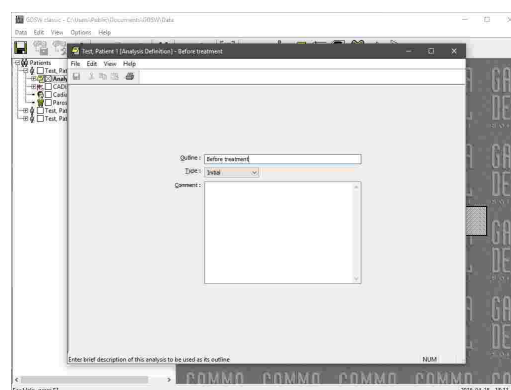
### 5.4.1 Creating analysis collections

**Analysis collections** in GDSW classic provide a convenient way of segregating data below the patient level. Each analysis collection represents an examination or patient visit and can contain any number of sub-objects, such as CADIAX or CADIAS analyses, tooth status items, OLE objects, etc. This means that you can easily separate the recordings made before, during, and after a treatment.

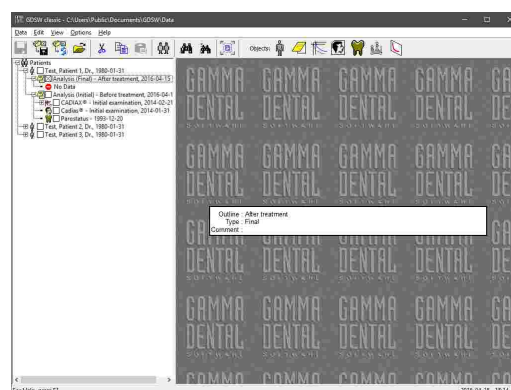
To create a new analysis collection, select the patient entry where it should be inserted, and press the toolbar button  *Analysis Collections*. The appearing dialog lists all analysis collections that have been created for the patient. Press the *New* button to continue.




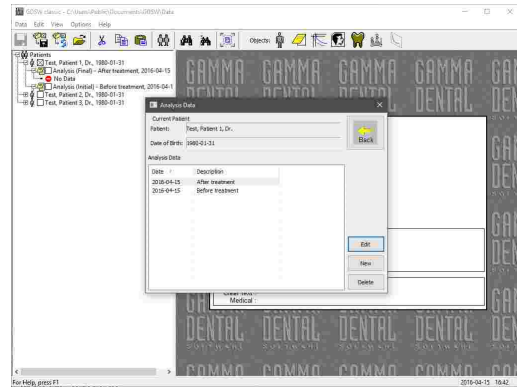
Now you can enter a name for the analysis collection, specify its type, and write down arbitrary remarks as needed. All inputs are optional. Save your changes and close the window to continue.




Subsequently, you will find that a new, empty analysis collection has been created. You can add recorded data into this collection just like you would add it directly below the patient level.



To modify the information of an analysis collection later on, select it and simply double-click the preview that is displayed on the right half of the window. Alternatively, you can press the toolbar button  *Analysis Collections* again and choose *Edit*.

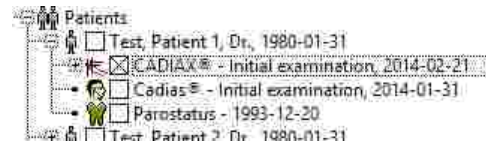


 Like patient information, you can print analysis collection information via the menu *File* → *Print*. The menu also provides options for showing a print preview and for configuring the format of the printout.

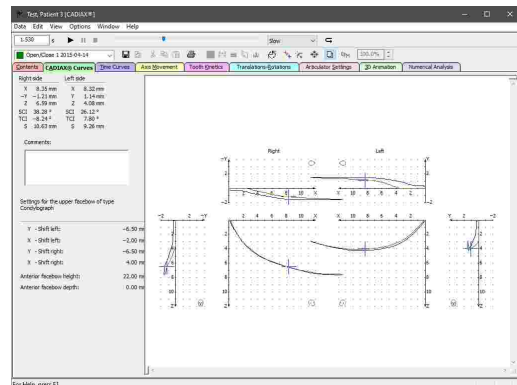
### 5.4.2 Recording CADIAX condylography data


The **CADIAX** module processes movement recordings of the temporomandibular joint as well as condyle position measurements (CPMs) and the coordinates of cusp tips on dental plaster models. Based on this data, the included applications allow the analysis of joint-related dysfunctions and the calculation of articulator settings necessary for reproducing the movements in an articulator.

CADIAX data is stored within so-called CADIAX analysis objects. In the patient tree, these objects appear below the patient level and can be expanded/collapsed themselves to list all contained data items.




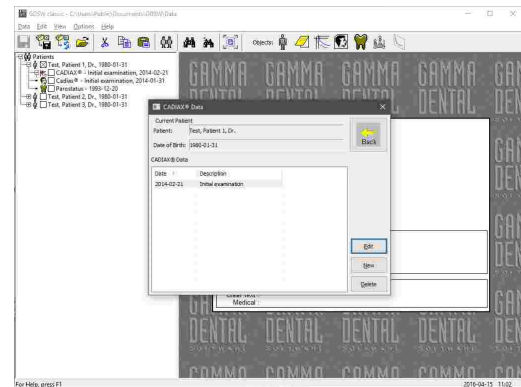
To analyze the recordings in detail, you can start the **CADIAX Analyzer** application by selecting a CADIAX analysis and double-clicking its preview in the preview area.



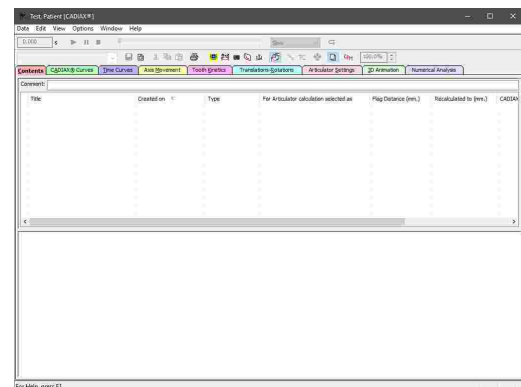
 Please refer to chapter "CADIAX<sup>114</sup>" for more information regarding the CADIAX module as a whole and to subchapter "CADIAX Analyzer<sup>124</sup>" for more information regarding the CADIAX Analyzer application in particular.

### 5.4.2.1 Creating a CADIAX analysis


To create a new CADIAX analysis, select the patient entry where it should be inserted and press the toolbar button  *CADIAX Analyses*. The appearing dialog lists all CADIAX analyses that have been created for the patient. Press the *New* button to continue.

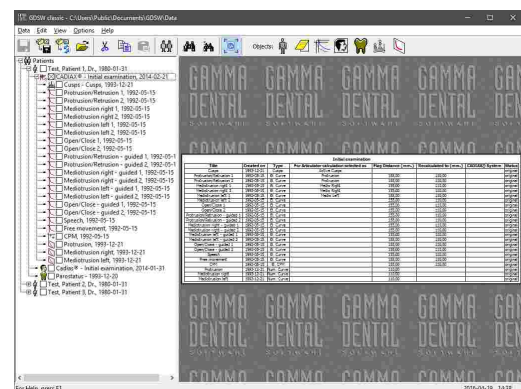


Subsequently, the new entry will be created in the patient tree and the CADIAX Analyzer application will be opened. From here, you can start recording or importing condylography curves or enter cusp tips coordinates via the *Data* menu.

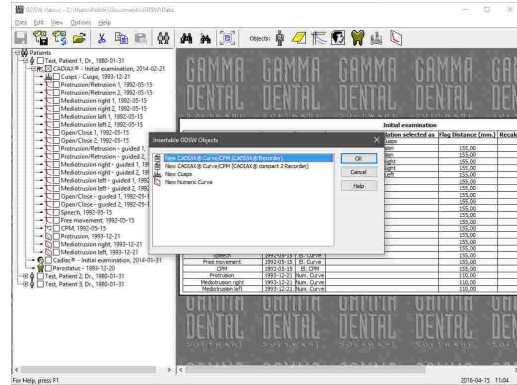


### 5.4.2.2 Editing a CADIAX analysis

To edit an existing CADIAX analysis, you can open it by double-clicking the preview on the right half of the window. Alternatively, you can press the toolbar button  *CADIAX Analyses* again and choose *Open*.



To start the recording software directly from GDSW classic, you can right-click the analysis entry in the patient tree and choose *New GAMMA Object* from the context menu.

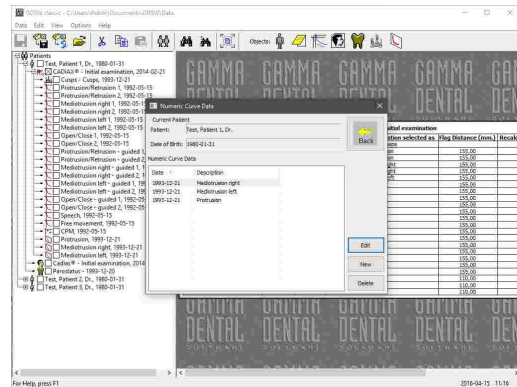


**i** It is also possible to view the contents of multiple CADIAX analyses combined, as if they were part of the same analysis. This can be useful to compare condylography recordings across different analyses or even across patients. To do so, select the desired analyses in the patient tree while holding down the *Ctrl* key on your keyboard. Subsequently, you can start the CADIAX Analyzer application via the menu entry *Edit → Open multiple CADIAX Objects*.

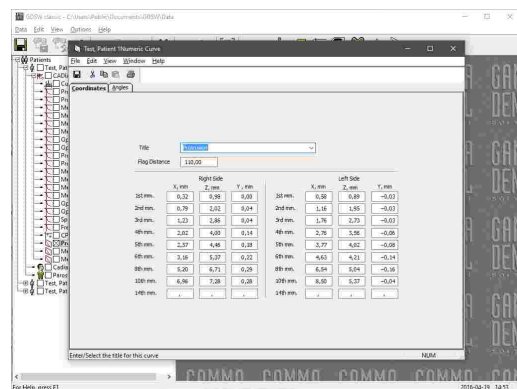
### 5.4.2.3 Entering numeric curves

Using the *Numeric Curve Editor*, you can create condylography movements by entering X/Y/Z coordinate points or SCI and TCI angle values for given millimeters of excursion. This functionality is useful for digitizing mandibular movement curves that were created with an analog recording system on writing paper or similar and measured manually. The numeric curves created hereby can be used in the other software modules just like electronically recorded curves for analysis and calculation of articulator settings.

To create a new numeric curve, select the CADIAX analysis where it should be inserted, and press the toolbar button *Numeric Curves*. The appearing dialog lists all numeric curve data items that have been created for the patient. Press the *New* button to continue.




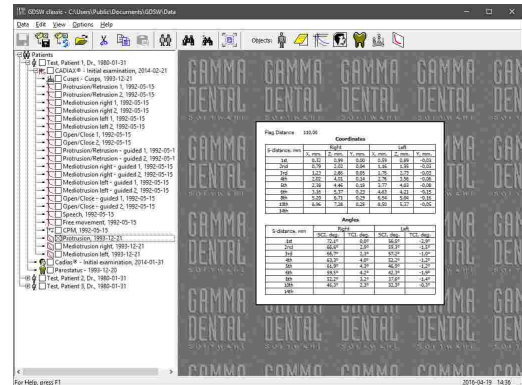
In the now opened *Numeric Curve Editor* application, you can enter a name for the numeric curve and the coordinates or angles themselves. Save your changes and close the window to continue.



 Please refer to chapter "Numeric Curve Editor<sup>119</sup>" for more information regarding the Numeric Curve Editor application.


Subsequently, you will find that an entry for the new numeric curve has been created.

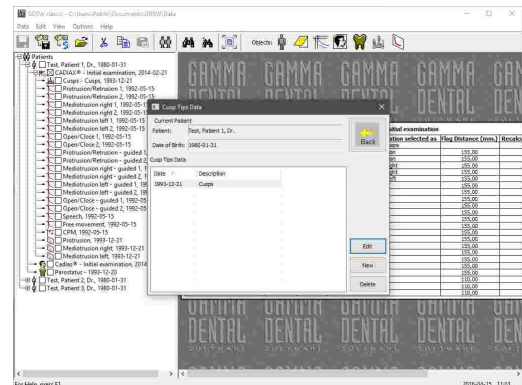
To modify the coordinates later on, select the item in the patient tree and simply double-click the preview that is displayed on the right half of the window. Alternatively, you can press the toolbar button  *Numeric Curves* again and choose *Open*.



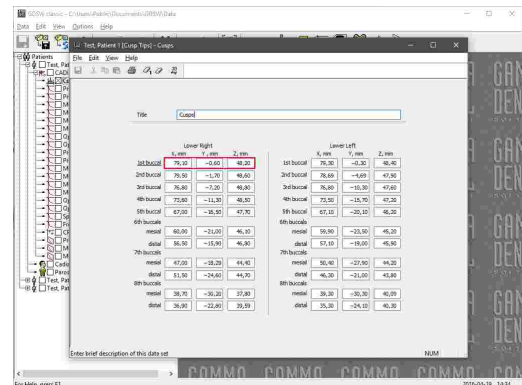
### 5.4.2.4 Entering cusp tips coordinates


Using the *Cusp Tips Editor*, you can introduce the X/Y/Z coordinates of the lower jaw's cusp tips into the articulator calculation of CADIAX Analyzer. The application will then be able to calculate the ideal incisal table settings to be used for designing occlusal surfaces during a wax-up procedure (refer to chapter "Articulator settings<sup>148</sup>").

To create a new cusp tips data item, select the patient entry or CADIAX analysis where it should be inserted, and press the toolbar button  *Cusp Tips*. The appearing dialog lists all cusp tips data items that have been created for the patient. Press the *New* button to continue.




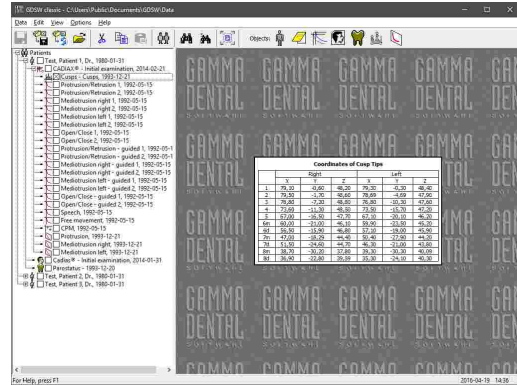
In the now opened Cusp Tips Editor application, you can enter a name for the cusp tips data and the coordinates themselves. Save your changes and close the window to continue.




 Please refer to chapter "Cusp Tips Editor<sup>121</sup>" for more information regarding the Cusp Tips Editor application.

Subsequently, you will find that an entry for the new cusp tips coordinates has been created.

To modify the coordinates later on, select the item in the patient tree and simply double-click the preview that is displayed on the right half of the window. Alternatively, you can press the toolbar button  *Cusp tips operations* again and choose *Open*.

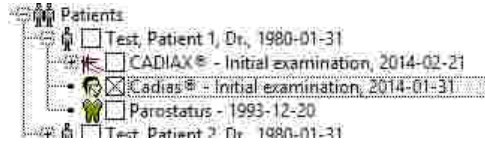


 Unlike other CADIAX data, cusp tips coordinates can also be inserted on the same patient tree level as CADIAX analyses, not necessarily below them. However, if they should be included in articulator calculation, they need to be contained in a CADIAX analysis.

### 5.4.3 Inserting CADIAS x-ray data

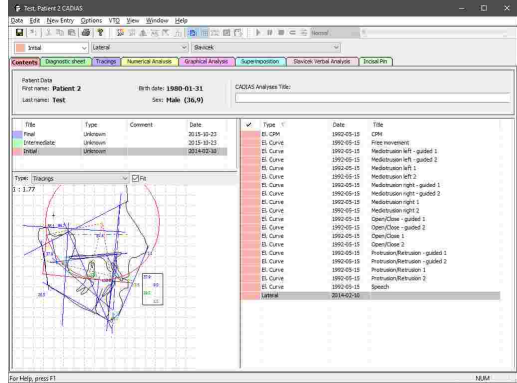
The **CADIAS** module allows the analysis of anatomical relations in the patient's skull and the documentation of planned treatments thereof. Its data is created by digitizing anatomical points on x-ray images and can be combined with condylography data stored in CADIAX analyses.


CADIAS data is stored in so-called CADIAS analysis objects that appear in the patient tree below the patient level.




Please note that each CADIAS analysis object in the patient tree can itself contain the data of multiple examinations. This means that it is not necessary to create one analysis for every examination.

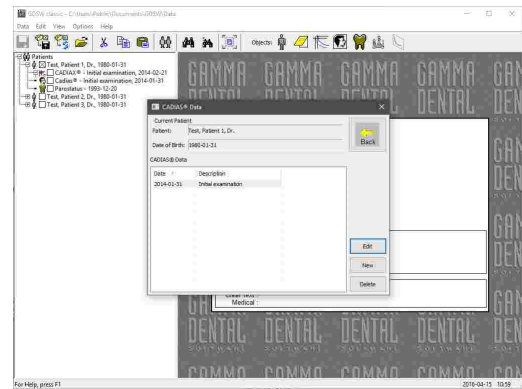
To analyze the digitizings in detail, you can start the **CADIAS Analyzer** application by selecting a CADIAS analysis object and double-clicking its preview in the preview area.



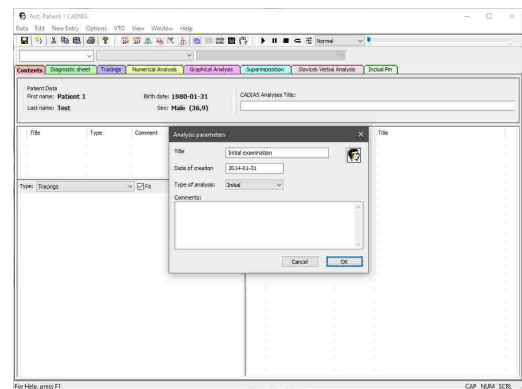
 Please refer to chapter "CADIAS <sup>175</sup>" for more information regarding the CADIAS module as a whole and to subchapter "CADIAS Analyzer <sup>196</sup>" for more information regarding the CADIAS Analyzer application in particular.

### 5.4.3.1 Creating a CADIAS analysis

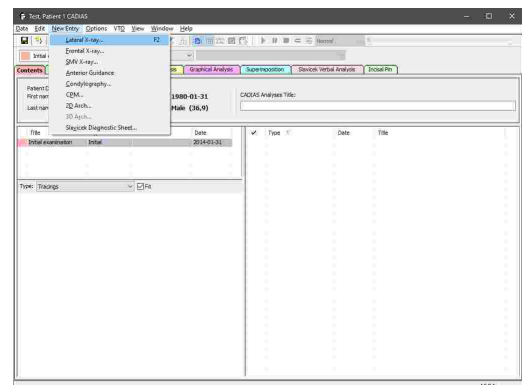
To create a new CADIAS analysis object, select the patient entry where it should be inserted, and press the toolbar button  *CADIAS Analyses operations*. The appearing dialog lists all CADIAS analyses objects that have been created for the patient. Press the *New* button to continue.



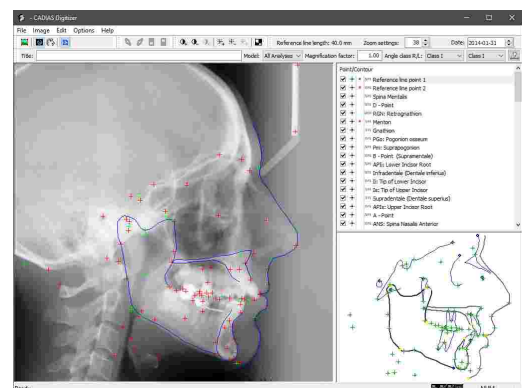
Subsequently, the new entry will be created in the patient tree and the CADIAS Analyzer application will be opened with a dialog in which you can specify the details of the current examination. Press *OK* to confirm your input.




Now, you can start the *CADIAS Digitizer* application for digitizing x-ray images or enter other information via the *New Entry* menu.

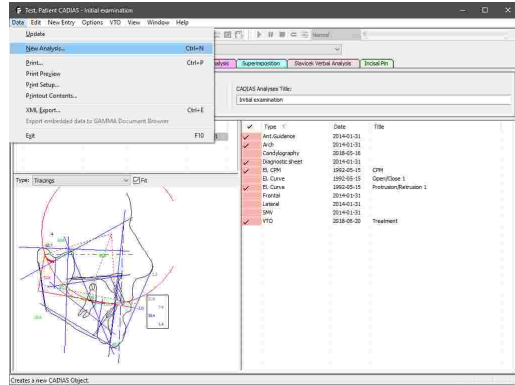


In CADIAS Digitizer, you can load the image to digitize via the menu *Image*.




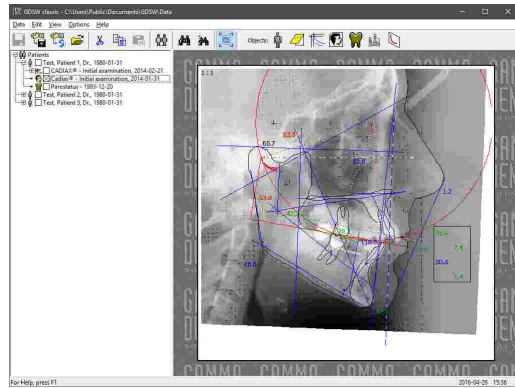
 Please refer to chapter "CADIAS Digitizer<sup>176</sup>" for more information regarding the CADIAS Digitizer application.

Please note that while each CADIAS analysis object can contain multiple analyses, each analysis can contain only one digitizing of a specific type. This means that if you want to enter two x-ray digitizings of lateral projection, you will have to create a second analysis via the menu *Data* → *New Analysis* beforehand.

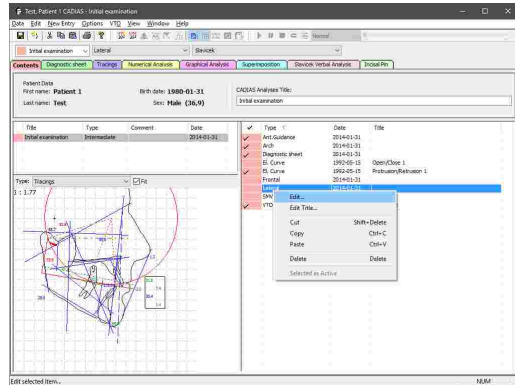


### 5.4.3.2 Editing a CADIAS analysis

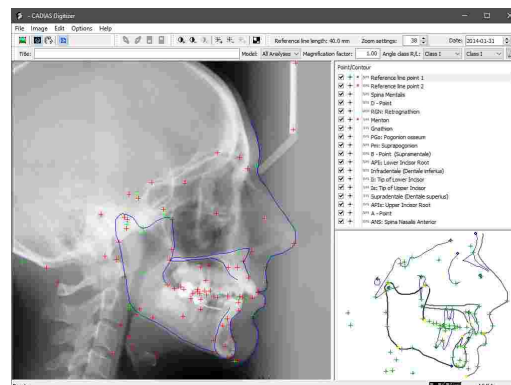
To edit an existing CADIAS analysis object, you can open it by double-clicking the preview on the right half of the window. Alternatively, you can press the toolbar button  *CADIAS Analyses* again and choose *Open*.



In the *Contents* pane of the CADIAS Analyzer window, you can now right-click the entry that you want to change and choose *Edit*. This applies to digitizings as well as other types of data that were entered manually, such as Condyle Position Measurements (CPMs).



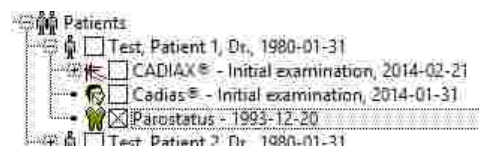
Once CADIAS Digitizer has been opened, you can make the necessary changes and save the digitizing. The evaluations in CADIAS Analyzer will be updated automatically.




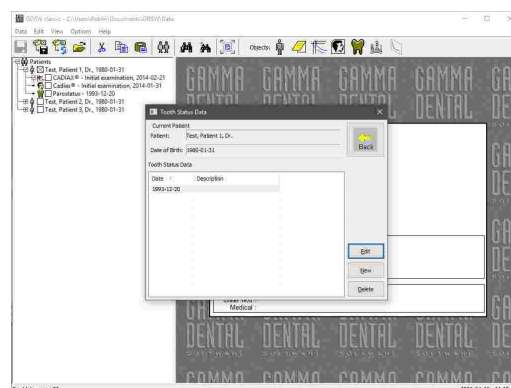
### 5.4.4 Entering tooth status information

Using the **Tooth Status** application, you can document the patient's parodontal, functional, and overall dental situation.

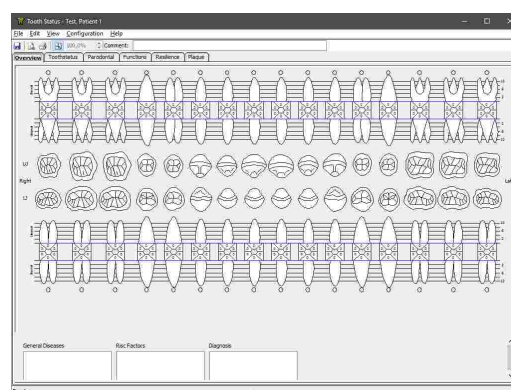
Tooth status analyses appear in the patient tree below the patient level.





To create a new tooth status analysis, select the patient entry where it should be inserted, and press the toolbar button  **Tooth Status**. The appearing dialog lists all tooth status analyses that have been created for the patient. Press the **New** button to continue.

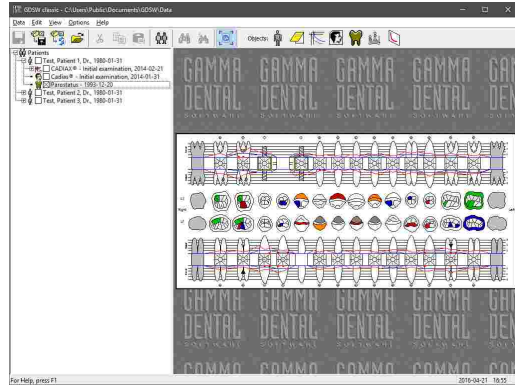


Subsequently, the new entry will be created in the patient tree and the tooth status application will be opened. From here, you can switch to the individual panes to enter the respective information.



 Please refer to chapter "Tooth Status <sup>282</sup>" for more information regarding the Tooth Status application.

To edit an existing tooth status analysis, you can open it by double-clicking the preview on the right half of the window. Alternatively, you can press the toolbar button  *Tooth Status* again and choose *Open*.

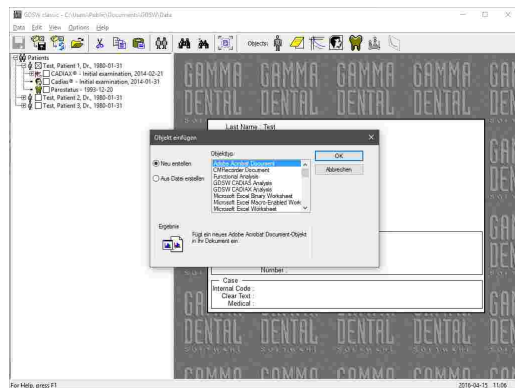


### 5.4.5 Inserting foreign OLE objects

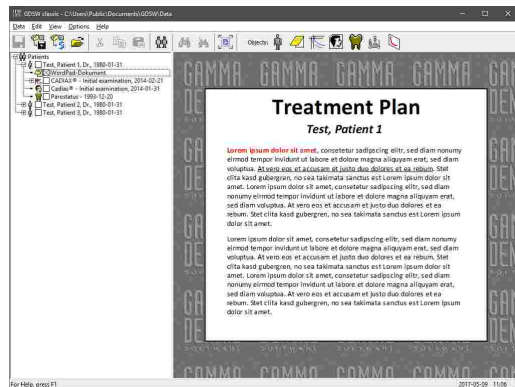
GDSW classic supports the embedding of arbitrary file types by means of the OLE (Object Linking and Embedding) technology. This allows you to store all sorts of data, such as pictures, Microsoft Office documents, PDF files, or even audio or video files right next to the patient data obtained with GDSW classic. External files that are embedded into the patient file in this way are referred to as **Foreign OLE Objects**.


To insert a new OLE object, select and right-click the patient entry where it should be inserted, and choose *Insert OLE Object* from the context menu. In the appearing dialog, you can choose whether you want to create a new file of a specific format, or embed an existing one. Press the *OK* button to continue.

Subsequently, the new entry will be created in the patient tree and the application associated with that file type will be opened.



To edit an embedded OLE object, you can open it by double-clicking the preview on the right half of the window.



 If you want to open or edit an OLE object of a format not natively provided by GAMMA Dental Software or the Windows operating system, you need to have the corresponding application installed. For example, Microsoft Office is required for Word, Excel, or PowerPoint documents. This also applies when you want to share your data with other users.

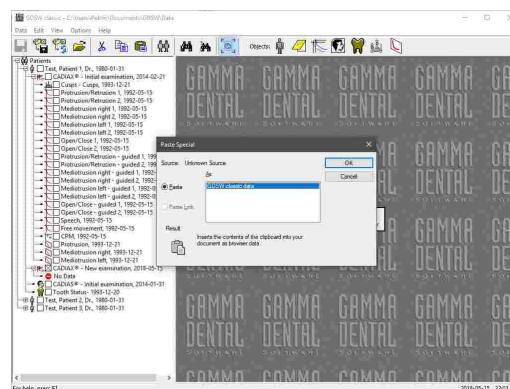
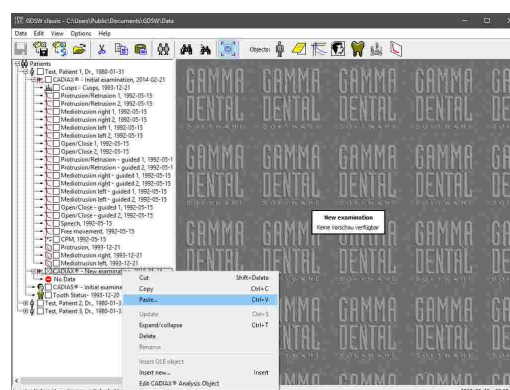
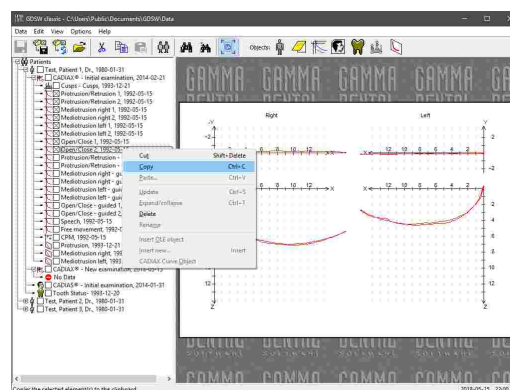
## 5.5 Copying and pasting data

You can easily duplicate entries in the patient tree by clicking them with the right mouse button and choosing *Copy* in the context menu. Alternatively, you can select the entries and press the key combination *Ctrl+C* on your keyboard. By choosing *Cut* in the context menu, the entries will be removed from their original location once pasted.

To copy or cut multiple entries, you can select them while holding down the *Ctrl* or *Shift* key.

Then, right-click the patient entry, the analysis collection, or the analysis where you would like to insert the data and choose *Paste*. Alternatively, you can select the target entry and press the key combination *Ctrl+V*. The target entry can be located in a different patient file or even in a second instance of GDSW classic with another database directory.

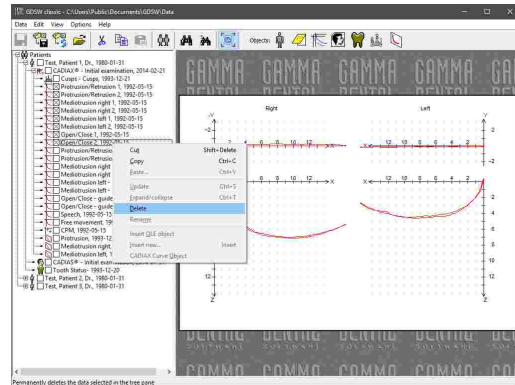
Finally, confirm the paste operation by pressing *OK* in the dialog that appears.



It is also possible to move or copy data by dragging the entries to another location in the patient tree while keeping the left or right mouse button pressed.

## 5.6 Deleting data

To permanently remove data from the database, select all entries in the patient tree that you would like to remove and choose *Delete* in the context menu.



## 5.7 Configuring the VDDS-media interface

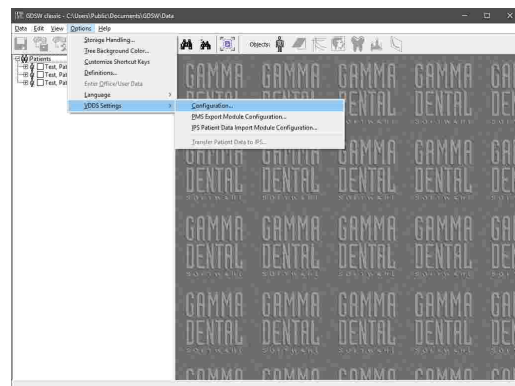
The VDDS-media interface serves the exchange of basic patient information (e.g. name, date of birth) between the software products used in dental practices. It allows for a centralized acquisition of patient data, so that this information does not have to be entered multiple times, for each used software product. Applications that support this interface can transfer the patient information to other applications by the press of a button.

In most cases, a dental practice will use a single practice management software, where patient information is kept in a database and that is also used for scheduling appointments and so forth. Using the VDDS-media interface, other software for x-ray imaging or condylography recording can be started directly from the practice management software when needed. In this example, the practice management software takes the role of the PMS (Practice Management System) while the recording software takes the role of the IPS (Image Processing System). GAMMA Dental Software supports the VDDS-media interface in version 1.4 and can operate either as PMS or IPS.

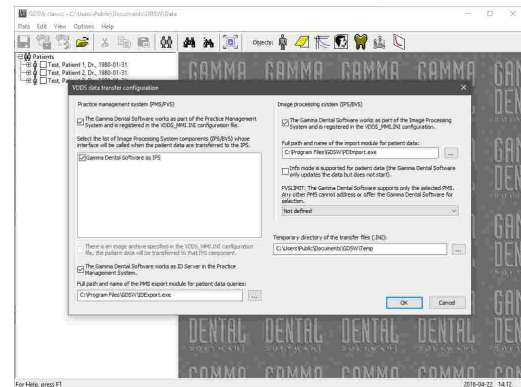
Technically, the transfer of patient information is carried out via a temporary text-based *\*.ini*-file that is created by the exporting application and passed to the importing one. All applications on a system that use the VDDS-media interface register themselves in the *VDDS\_MMI.ini* configuration file that is located in the Windows system directory.

Further information regarding the VDDS-media interface as well as the full technical specification can be found on the website of the Association of German Dental Software Companies (German: "Verband deutscher Dental-Software Unternehmen") at [www.vdds.de](http://www.vdds.de).

In GDSW classic, you can open the general configuration dialog via the menu *Options* → *VDDS-media Interface* → *Configure Interface*.



In this dialog, you can first of all specify whether GAMMA Dental Software should register itself as PMS or IPS.

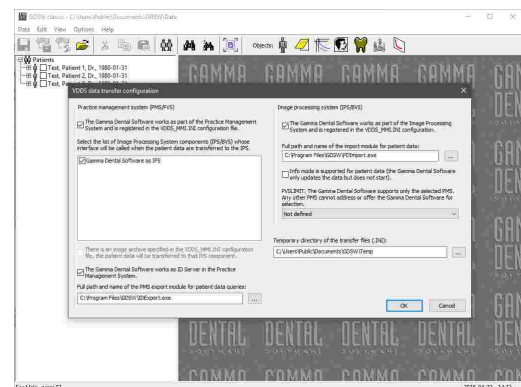


Please note that for changing the general VDDS-media configuration, the software has to be started with administrative privileges.

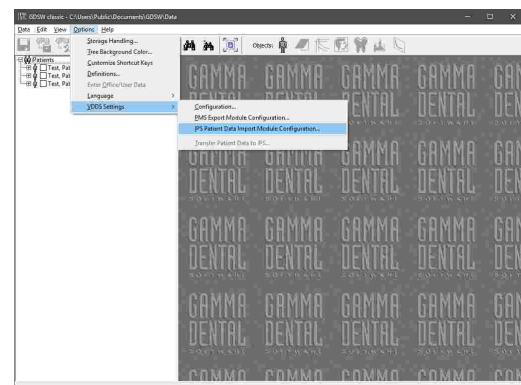
### 5.7.1 Importing patient data using the VDDS-media interface

This chapter describes how you can configure GDSW classic to receive patient information from third-party practice management software over the VDDS-media interface.

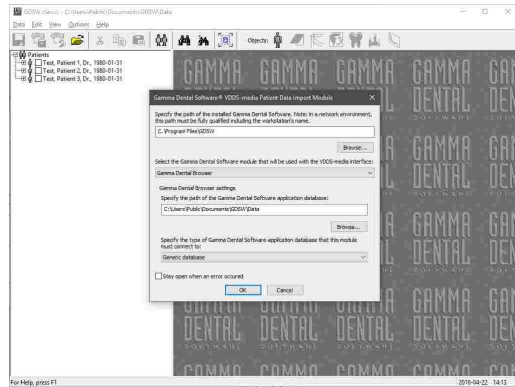
In the general VDDS-media configuration dialog, ensure that GAMMA Dental Software is registered as IPS and that the path of the import module refers to the file *PDImport.exe* in the software's installation directory. Apply the settings by pressing **OK**.



Open the configuration dialog for the import module via the menu *Options* → *VDDS-media Interface* → *Configure Patient Data Import Module*.

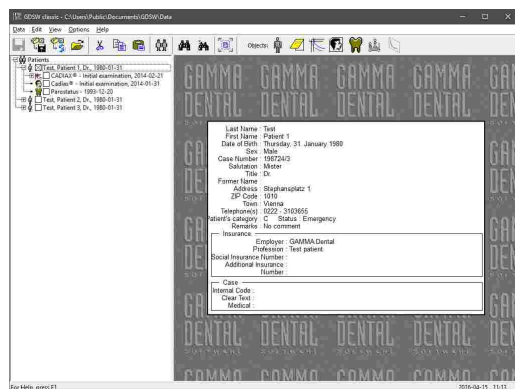


In this dialog, specify the installation directory of GAMMA Dental Software and select *GDSW classic* as the module to be used. Also, specify the directory where your patient files are stored. Confirm by pressing **OK**.



GAMMA Dental Software should now appear as a VDDS-media client (IPS) in your practice management software. Please consult the instruction manual of that software for further information.

Now, when opening GAMMA Dental Software from the practice management software for a specific patient, the appropriate patient file should automatically be opened in GDSW classic or be created if it does not yet exist.



**i** If the transfer of patient information into GAMMA Dental Software does not work as expected, you can configure the import module to stay open when an error occurred. To do so, simply check the check box in the bottom area of the dialog. The displayed error messages can be helpful in diagnosing the cause of the issue.

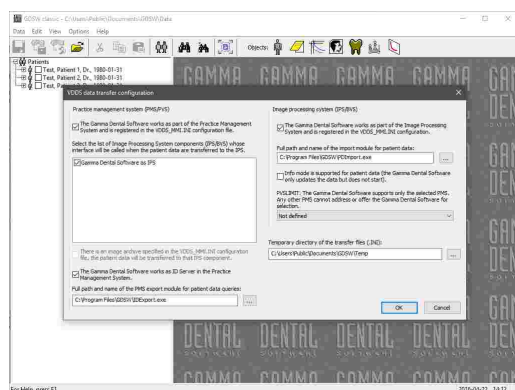
### 5.7.2 Exporting patient data using the VDDS-media interface

This chapter describes how you can configure GDSW classic to provide patient information to third-party software over the VDDS-media interface.

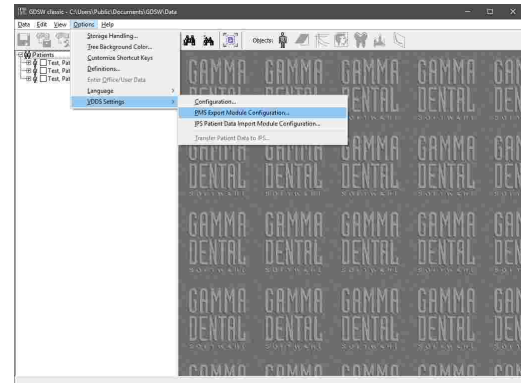
In the general VDDS-media configuration dialog, ensure that GAMMA Dental Software is registered as PMS and that the path of the export module refers to the file *IDExport.exe* in the software's installation directory. Furthermore, select the IPS applications to which the patient information shall be transferred.

Here you can also set the ID Server option, which declares GAMMA Dental Software as the provider of global VDDS-media patient IDs for other applications using the interface.

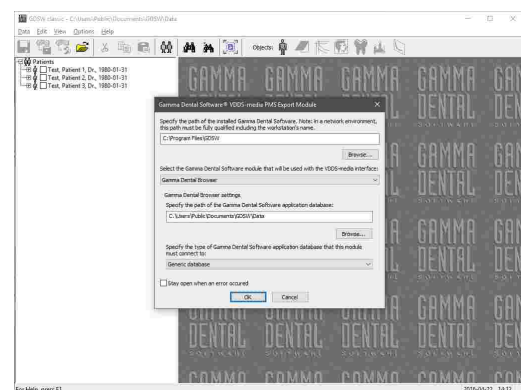
Apply the settings by pressing **OK**.



Open the configuration dialog for the export module via the menu *Options* → *VDDS-media Interface* → *Configure Patient Data Export Module*.

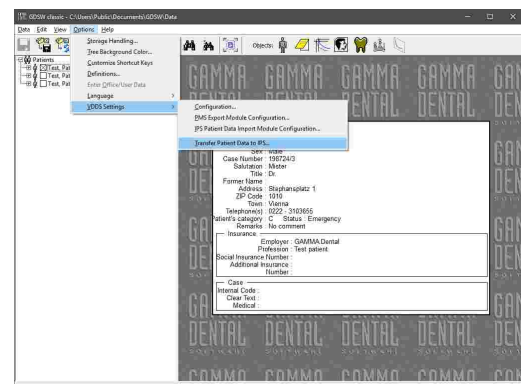


In this dialog, specify the installation directory of GAMMA Dental Software and select *GDSW classic* as the module to be used. Also, specify the directory where your patient files are stored. Confirm by pressing *OK*.



GAMMA Dental Software should now appear as a VDDS-media sender (PMS) in your third-party software. Please consult the instruction manual of that software for further information.

Now, whenever a patient file is selected in GDSW classic, you can transfer the information of that patient to the third-party software via the menu *Options* → *VDDS-media Interface* → *Transfer Patient Data*.



If the transfer of patient information to third-party software does not work as expected, you can configure the export module to stay open when an error occurred. To do so, simply check the check box in the bottom area of the dialog. The displayed error messages can be helpful in diagnosing the cause of the issue.

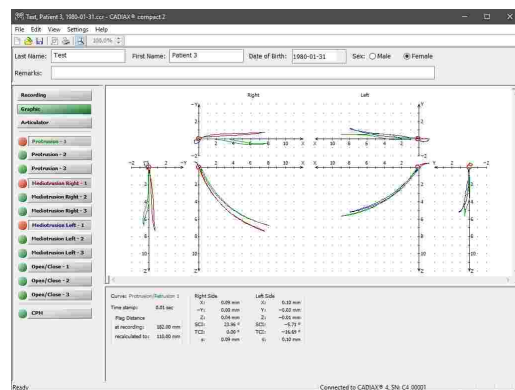
## 6 CADIAX

**CADIAX** stands for the computer-aided analysis of axiographic/condylographic data. This software module is integrated into the patient data management applications GAMMA Document Browser and GDSW classic and automatically installed during the installation of GAMMA Dental Software. The CADIAX module processes the following types of data:

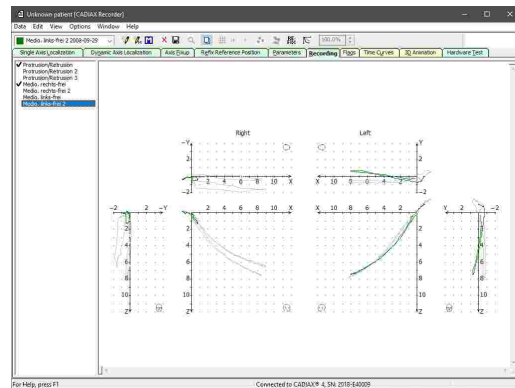
- Electronically or mechanically recorded movement tracks of the lower jaw.
- Condylographic position measurements (CPM).
- X/Y/Z-coordinates of the dental cusp tips of the lower jaw.

This data can furthermore be included in the cephalometric evaluations of the CADIAS module (refer to chapter "CADIAS Analyzer<sup>[196]</sup>") or in analyzing the occlusal function in the CADIAS 3D module (refer to chapter "CADIAS 3D<sup>[239]</sup>"). The CADIAX module consists of the following applications:

- **CADIAS compact 2 Recorder** for recording condylographic movements with the "compact" sensor set (refer to chapter "CADIAX compact 2 Recorder<sup>[116]</sup>").



- **CADIAX Recorder** for recording condylographic movements with the "diagnostic" sensor set (refer to chapter "CADIAX Recorder<sup>[118]</sup>").



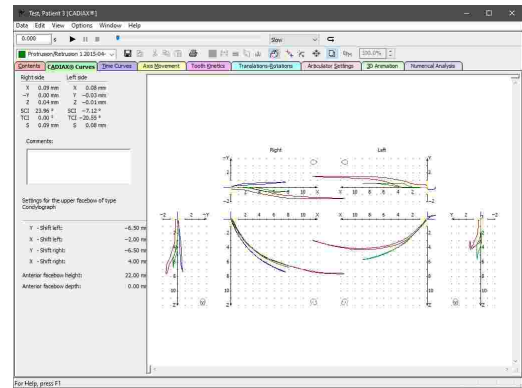
- **Numeric Curve Editor** for digitizing analog condylography recordings (refer to chapter "Numeric Curve Editor<sup>[119]</sup>").

	Right Side			Left Side		
	X, mm	Z, mm	Y, mm	X, mm	Z, mm	Y, mm
1st min.	0.32	0.99	0.00	0.92	0.89	-0.03
2nd min.	0.79	2.02	0.04	1.18	1.95	-0.03
3rd min.	1.13	3.08	0.04	1.78	2.73	-0.03
4th min.	1.62	4.00	0.14	2.76	3.36	-0.06
5th min.	2.17	4.46	0.18	3.77	4.02	-0.08
6th min.	2.56	5.17	0.22	4.63	4.51	-0.14
7th min.	3.20	6.71	0.28	6.01	5.94	-0.16
8th min.	4.06	7.38	0.28	8.00	5.37	-0.04
9th min.	-	-	-	-	-	-
10th min.	-	-	-	-	-	-

- **Cusp Tips Editor** for entering cusp tips coordinates, which can be used to calculate individual incisal pin table settings (refer to chapter "Cusp Tips Editor" <sup>121</sup>).

Lower Right			Lower Left				
X, mm	Y, mm	Z, mm	X, mm	Y, mm	Z, mm		
3rd buccal	75.32	0.82	48.22	3rd buccal	75.20	0.20	48.40
2nd buccal	76.50	1.50	48.20	2nd buccal	76.60	4.00	47.50
1st buccal	76.80	2.20	48.20	1st buccal	76.90	10.30	47.60
4th buccal	73.62	11.30	48.30	4th buccal	73.50	13.70	47.30
5th buccal	67.02	16.50	47.70	5th buccal	67.10	20.10	48.20
6th buccal	60.00	21.00	46.30	6th buccal	59.90	23.50	45.30
mesial	56.50	15.50	48.20	mesial	57.10	19.00	45.90
distal	47.00	18.20	44.40	distal	50.40	27.00	44.20
1st buccal	51.50	24.02	44.70	1st buccal	46.30	21.00	43.80
mesial	38.70	30.30	37.80	mesial	39.30	30.30	40.00
distal	36.90	22.80	29.80	distal	35.20	24.10	40.70

- **CADIAX Analyzer** for evaluating condylography recordings and calculating articulator settings (refer to chapter "CADIAX Analyzer" <sup>124</sup>).

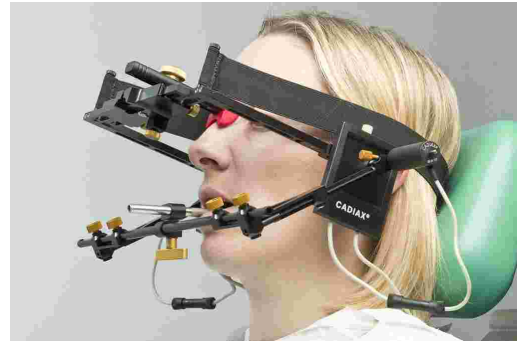


In this chapter, you will find a comprehensive description of these applications.

Depending on your software license, some or all of the features provided by the CADIAS module may not be available. Please refer to chapter "Compare editions" <sup>16</sup>.

## 6.1 CADIAX compact 2 Recorder


The **CADIAX compact 2 Recorder** application is used for the recording of condylography data with the devices CADIAX compact 2 and CADIAX 4, using the "compact" sensor set (40x40 mm flags and single-pin styli). Recordings made with this application are usually carried out on the anatomical, i.e. statistically averaged hinge axis, and are primarily used for calculating articulator settings.

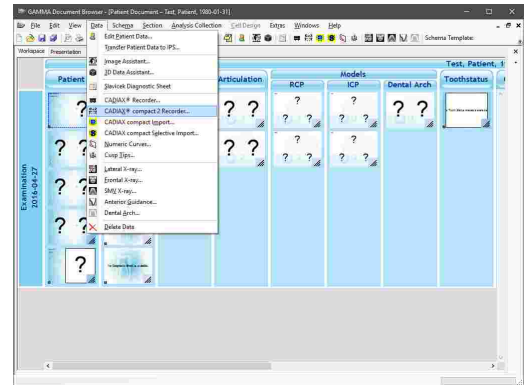



**!** Please note that the compact sensor set does not capture the rotational component of the mandibular movement and hence does not allow for some types of analyses such as rotation/translation graphs or tooth kinetics.

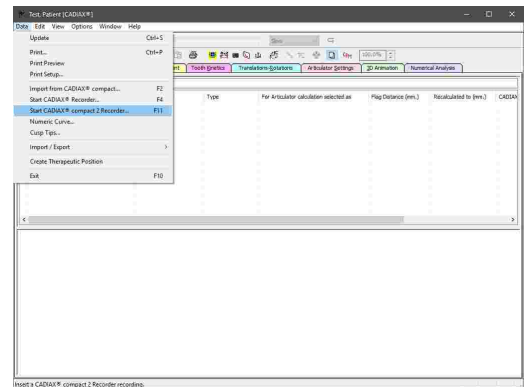
### 6.1.1 Starting the application

CADIAX compact 2 Recorder is an integral part of GAMMA Dental Software and can be started from GAMMA Document Browser as well as from GDSW classic:

- To start CADIAX compact 2 Recorder from GAMMA Document Browser, use the button  CADIAX compact 2 Recorder in the toolbar or the associated entry in the *Data* menu. Please refer to chapter "Recording CADIAX condylography data<sup>68</sup>" for more information.



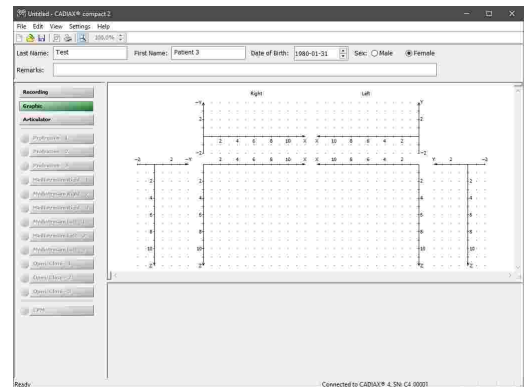
- To start CADIAX compact 2 Recorder from GDSW classic, you first have to create a new CADIAX analysis. In the now opened CADIAX Analyzer, you can start the recording application via the button  CADIAX compact 2 Recorder in the toolbar. Please refer to chapter "Recording CADIAX condylography data<sup>100</sup>" for more information.




Alternatively, you can start CADIAX compact 2 Recorder in standalone mode to be independent of those applications by using the shortcut in the start menu (*All Programs* → *GAMMA Dental Software* → *CADIAX compact 2 Recorder*):



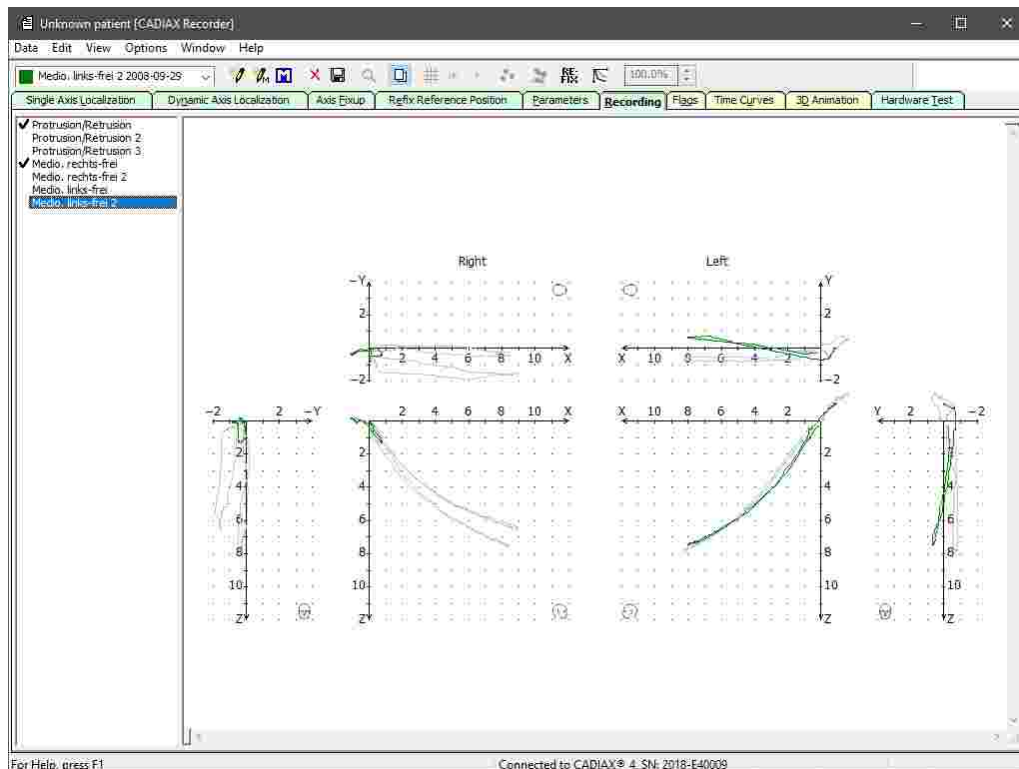
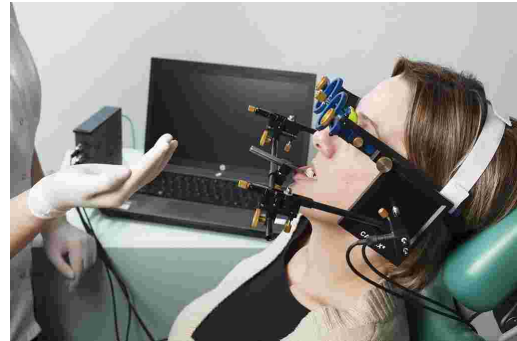
In this mode, the application additionally allows you to enter basic patient data and calculate articulator settings. For analyzing the recordings in detail, you will however have to transfer them to one of the patient management applications.



 Please consult the instruction manual of your CADIAX device for detailed instructions on how to perform condylography recordings.


## 6.2 CADIAX Recorder

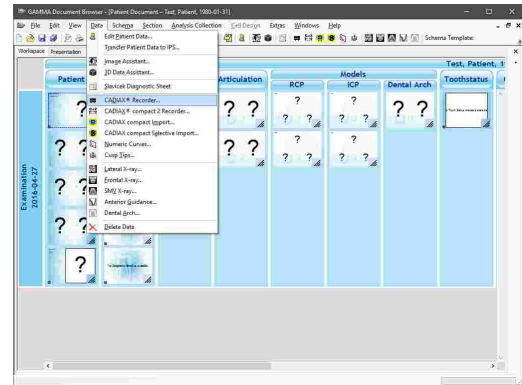
The **CADIAX Recorder** application is used for the recording of condylography data with the devices CADIAX diagnostic and CADIAX 4, using the "diagnostic" sensor set (60x60 mm flags and double-pin styli). The software supports an electronic localization of the actual hinge axis and allows an unlimited number of recordings to be made for every patient. As the measurement electronics are capable of determining the rotatory component of jaw movements, it is possible to record functional movements such as bruxing, chewing, or swallowing and to analyze them for diagnostic purposes.




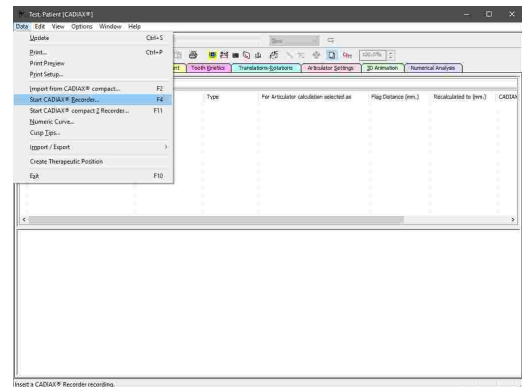
### 6.2.1 Starting the application


CADIAX Recorder is an integral part of GAMMA Dental Software and can be started from GAMMA Document Browser as well as from GDSW classic:

- To start CADIAX Recorder from GAMMA Document Browser, use the button  *CADIAX Recorder* in the toolbar or the associated entry in the *Data* menu. Please refer to chapter "Recording CADIAX condylography data<sup>68</sup>" for more information.



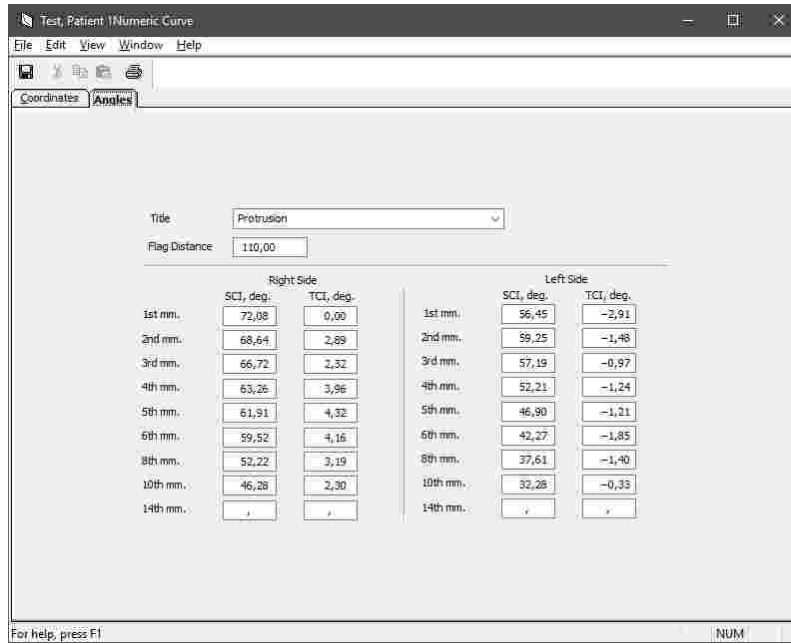
- To start CADIAX Recorder from GDSW classic, you first have to create a new CADIAX analysis. In the now opened CADIAX Analyzer, you can start the recording application via the button  *CADIAX Recorder* in the toolbar. Please refer to chapter "Recording CADIAX condylography data<sup>100</sup>" for more information.



 Please consult the instruction manual of your CADIAX device for detailed instructions on how to perform condylography recordings.



### 6.3 Numeric Curve Editor

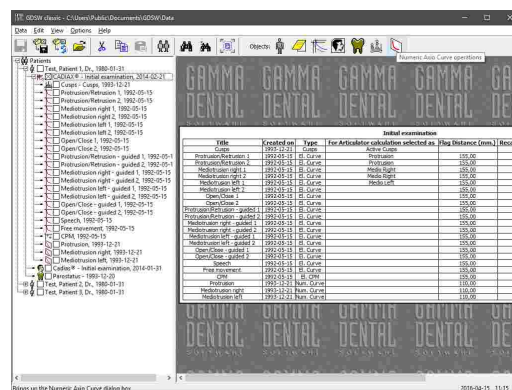
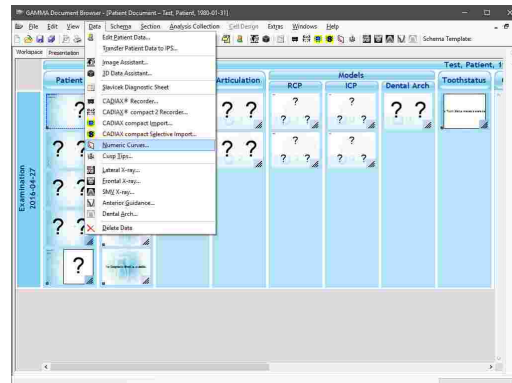
Using the **Numeric Curve Editor**, you can create condylography movements by entering X/Y/Z coordinate points or SCI and TCI angle values for given millimeters of excursion. This functionality is useful for digitizing mandibular movement curves that were created with an analog recording system on writing paper or similar and measured manually. The numeric curves created hereby can be used in the other software modules just like electronically recorded curves for analysis and calculation of articulator settings.



### 6.3.1 Starting the application

The Numeric Curve Editor is an integral part of GAMMA Dental Software and can be started from GAMMA Document Browser as well as from GDSW classic:

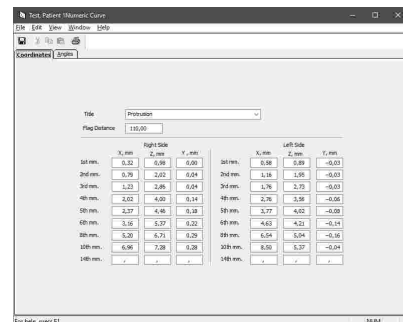
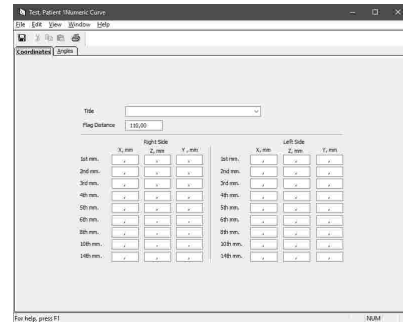
- To enter a new numeric curve in GAMMA Document Browser, use the button  *Numeric Curves* in the toolbar or the associated entry in the *Data* menu. Please refer to chapter "Entering numeric curves" <sup>[73]</sup> for more information.
- To enter a new numeric curve in GDSW classic, select the CADIAX analysis where it should be inserted and press the button  *Numeric Curves* in the toolbar. Please refer to chapter "Entering numeric curves" <sup>[102]</sup> for more information.



### 6.3.2 Entering numeric curves

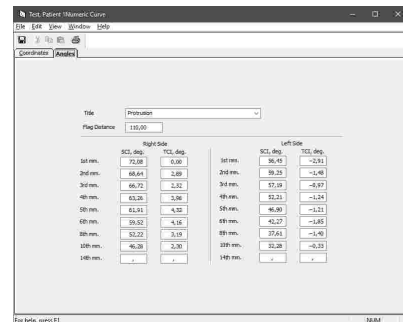
Using the combo box on the top, you can enter the name of the curve or select one of the predefined names. Below that, you will find an input box for the flag distance used during recording, in millimeters. This value specifies the distance between the writing surface of the right and left flag.

By default, a condylography movement is entered as a sequence of three-dimensional X/Y/Z point coordinates. You can determine these coordinates by manually measuring the recorded tracing on the writing paper. The excursion distances denote the linear distance between the points of measurement and the reference point. The latter usually coincides with the starting point of the curve. You may omit the fields for which no corresponding value is available.



**i** Refer to chapter "The reference coordinate system <sup>299</sup>" for a detailed description of the coordinate system used by the software.

Alternatively you can enter the curve as a sequence of angle values for the sagittal (SCI) and transversal (TCI) condylar inclination. To do so, you can switch between the *Coordinates* and *Angles* panes at any time. Already entered values will automatically recalculated into the respectively other format.



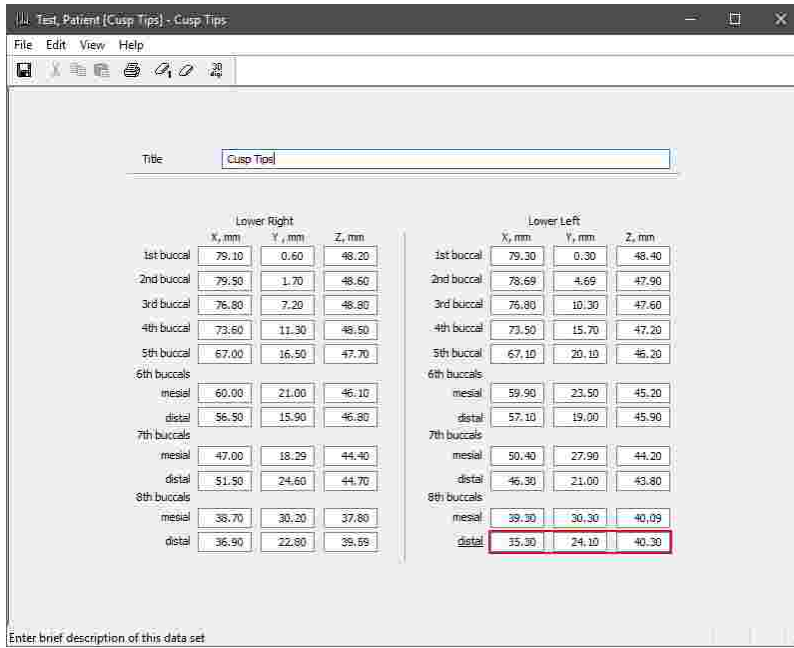
Finally, save your data and close the window to return to the invoking application.

**i** You can print the entered coordinate values and angles via the menu *File* → *Print*. That menu also provides options for showing a print preview and for configuring the format of the printout.

**i** Using the menu entry *File* → *Export to File*, you can save the numeric curve as a file for transferring it to another computer or for restoring it later. You can import the file using the entry *Import from File* in the same menu.

### 6.4 Cusp Tips Editor

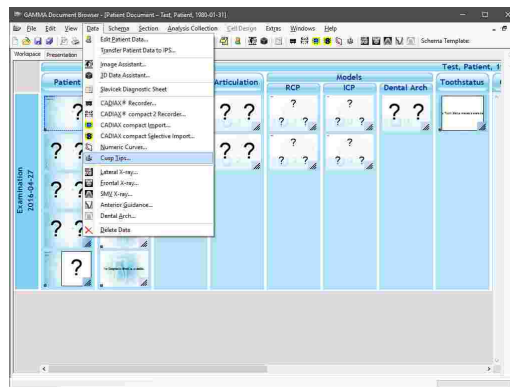
Using the *Cusp Tips Editor*, you can introduce the X/Y/Z coordinates of the lower jaw's cusp tips into the articulator calculation of CADIAX Analyzer. The application will then be able to calculate the ideal incisal table settings to be used for designing occlusal surfaces during a wax-up procedure (refer to chapter "Articulator settings <sup>148</sup>").



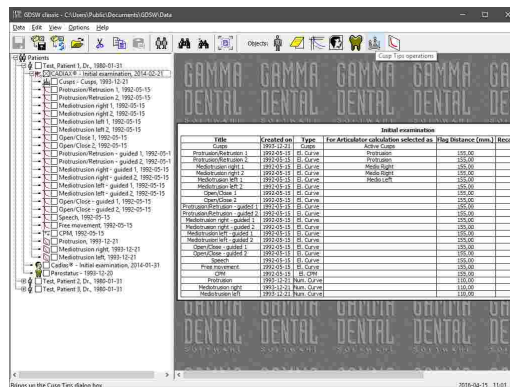
### 6.4.1 Starting the application

The Cusp Tips Editor is an integral part of GAMMA Dental Software and can be started from GAMMA Document Browser as well as from GDSW classic:

- To enter a new set of cusp tips coordinates in GAMMA Document Browser, use the button *Cusp Tips* in the toolbar or the associated entry in the *Data* menu. Please refer to chapter "Entering cusp tips coordinates" <sup>74</sup> for more information.



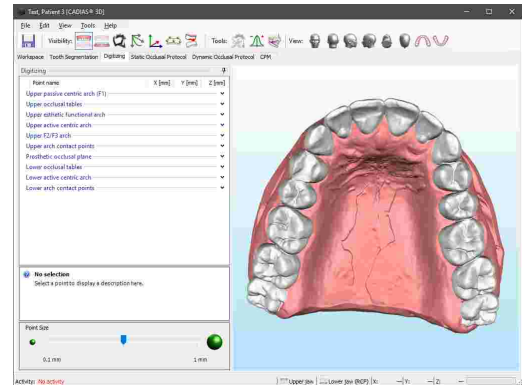
- To enter a new set of cusp tips coordinates in GDSW classic, select the CADIAX analysis where it should be inserted and press the button *Cusp Tips* in the toolbar. Please refer to chapter "Entering cusp tips coordinates" <sup>103</sup> for more information.



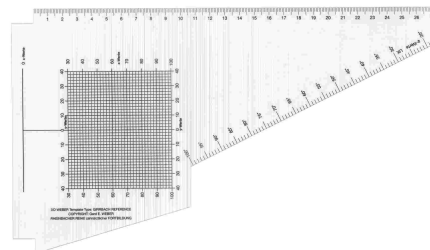
### 6.4.2 Measuring cusp tips coordinates

Measurement of the cusp tips coordinates can be carried out in the following ways:

- By digitizing a 3D dental model in CADIAS 3D (refer to chapter "Point digitizing<sup>260</sup>"). To do so, digitize the points of the lower active centric, right-click the list of points and choose the menu entry *Copy cusp tips*. Subsequently, you can paste the copied coordinates in the cusp tips editor using the menu *Edit* → *Paste Data from CADIAS 3D*.



- By directly measuring on a plaster model mounted in the articulator. For the Reference SL articulator, a 3D measurement template according to Weber is available (order number 04-000004).

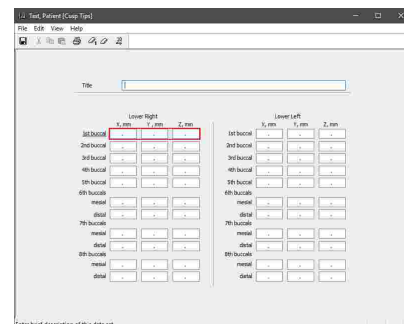


- Using an electronic 3D coordinate measurement device with a mounting interface for articulated dental casts, provided such is at your disposal.





### 6.4.3 Entering cusp tips coordinates

In the cusp tips editor, you can enter a title for the data set of cusp tips coordinates at the very top of the input form. This title allows for differentiation when you intend to create multiple data sets. You can then continue with entering the measured coordinate values.

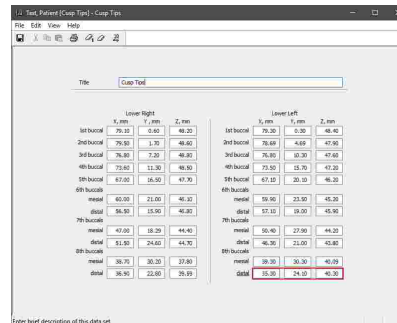


**!** The input of coordinate values for the Y axis in the cusp tips editor uses a different method than the other software modules. The Y values of cusp tips are entered as their distance from the median-sagittal plane, wherefore the values should in most cases be positive. They can however be negative if the measured cusp tip is situated on the respectively opposite side of the median-sagittal plane. For example, the Y coordinate of the lower right incisor cusp would be entered as a negative value if the cusp lies on the left side of the median-sagittal plane, and vice versa.

**i** Refer to chapter "The reference coordinate system<sup>[299]</sup>" for a detailed description of the coordinate system used by the software.

The three input boxes of the currently focused cusp are outlined in red. To delete the currently selected data or the entire data set, use the toolbar buttons  *Clear Selected Coordinates* and  *Clear All Coordinates*, respectively.

Finally, save your data and close the window to return to the invoking application.

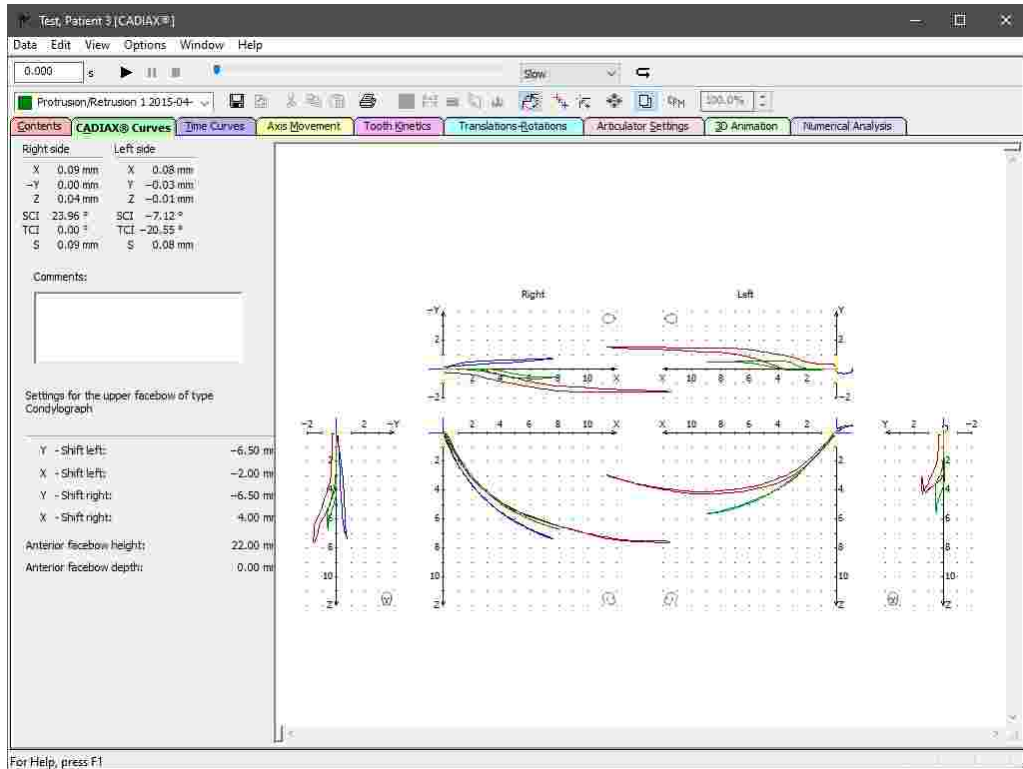


**i** You can print the entered coordinate values via the menu *File* → *Print*. That menu also provides options for showing a print preview and for configuring the format of the printout.

**i** Using the menu entry *File* → *Export to File*, you can save the numeric curve as a file for transferring it to another computer or for restoring it later. You can import the file using the entry *Import from File* in the same menu.

## 6.5 CADIAX Analyzer

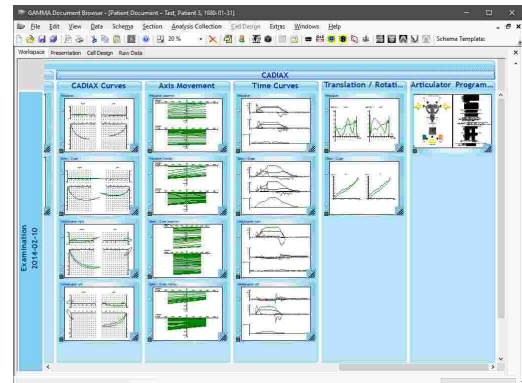
CADIAX Analyzer is the application for analyzing the dynamic movements of the temporomandibular joint as recorded during condylography (refer to chapter "CADIAX compact 2 Recorder<sup>[116]</sup>" or "CADIAX Recorder<sup>[118]</sup>"). It allows those recordings to be replayed and visualized in various forms as well as the calculation of ideal articulator settings for reproducing the movements in an articulator.




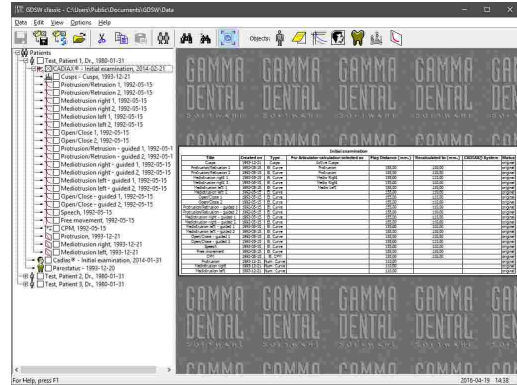
### 6.5.1 Starting the application

CADIAX Analyzer is an integral part of GAMMA Dental Software and can be started from GAMMA Document Browser as well as from GDSW classic:

- You can start CADIAX Analyzer from GAMMA Document Browser by double-clicking one of the CADIAX data areas. Please refer to chapter "Recording CADIAX condylography data" for more information.



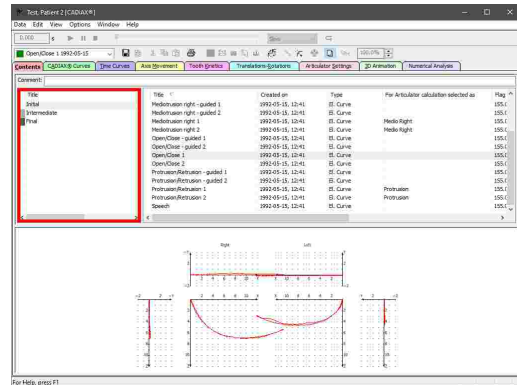
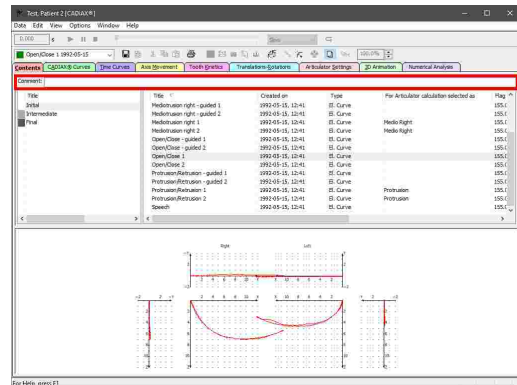
- In GDSW classic, you can create a new CADIAX analysis via the button  CADIAX in the toolbar. Please refer to chapter "Recording CADIAX condylography data" <sup>100</sup> for more information.



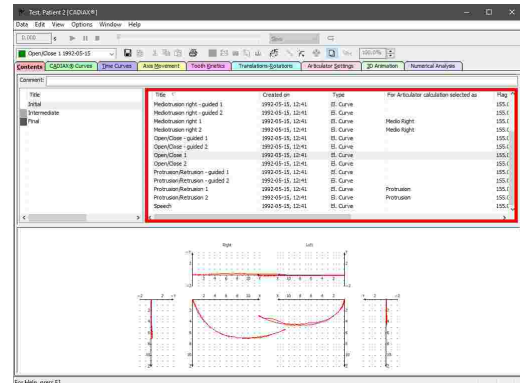
### 6.5.2 Contents

The *Contents* pane is the default view in CADIAX Analyzer and gives you an overview of the data available for the current patient. The user interface consists of the following parts:

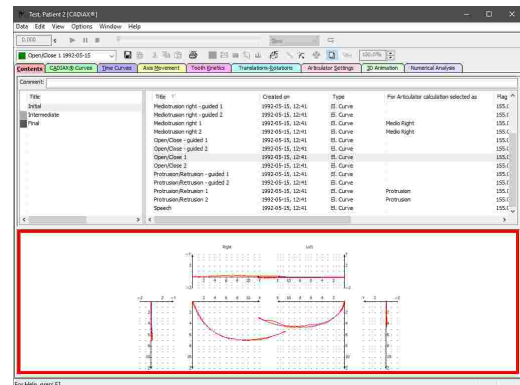
- On the top of the pane, you can find a **comment box** for entering an arbitrary comment or the title of the current analysis. The information entered here will only be saved persistently when the application has been started from GDSW classic.
- On the left side, the application shows a list of **analyses** created for the patient. Each analysis usually corresponds to a single patient visit.



- The right side shows a list of **data items** contained in the currently selected analysis. This includes condylography curves, condyle position measurements (CPMs) as well as cusp tips coordinates. You can find a summary of the information displayed in this list in chapter "The list of data items<sup>127</sup>".



- Below the list of analyses, you can see a **preview** of the currently selected data items. Using the menu *View* → *Preview*, you can choose whether this area should be displayed on the bottom, on the right, or not at all.



**i** The list of analysis will only be displayed if the application has been started from GAMMA Document Browser. If it has been started from GDSW classic, it will only list the data of the opened analysis.

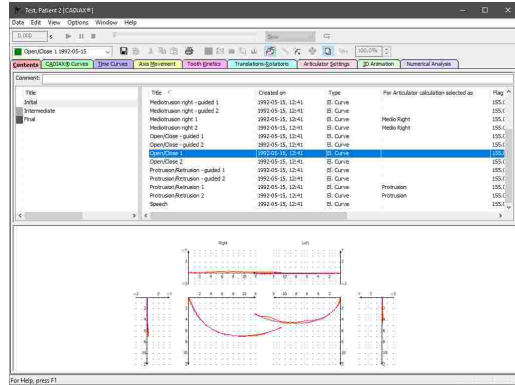
**i** You can select multiple examinations by clicking them while keeping the *Ctrl* or *Shift* key pressed. The data items of all selected examinations will then be displayed simultaneously. This can be useful, for example, if you want to combine an actual x-ray tracing with the condylography recording of a previous examination. This method of multiple selection is also provided in the list of data items, whereby you can easily copy or delete multiple data items at once.

**!** Please note that by default, the displayed condylography movements do not directly correspond to the movement of the patient's condyles, but are recalculated to the intercondylar distance of the articulator. Please refer to chapter "Changing the intercondylar distance<sup>161</sup>" for more information.

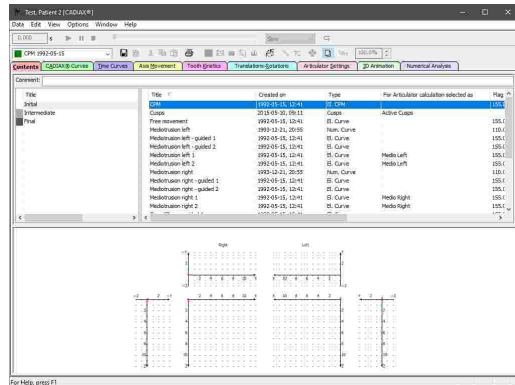
**6.5.2.1 The list of data items**

The *Contents* pane lists all CADIAX data items in the current analysis. These data items can be of the following types:

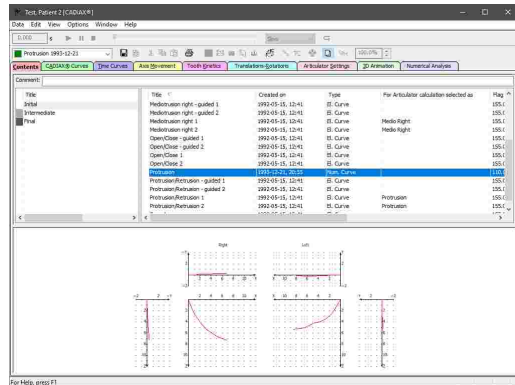
- **El. Curve:** A condylography movement recorded electronically with a CADIAX device.



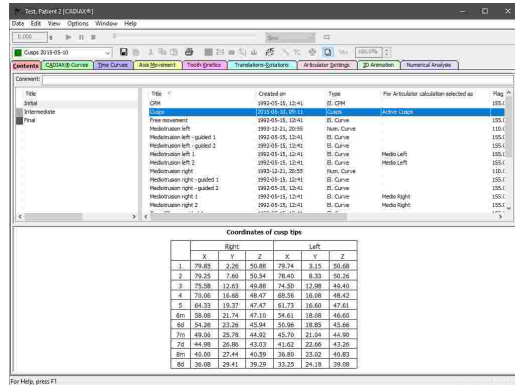
- **El. CPM:** A condyle position measurement (CPM) recorded electronically with a CADIAX device. Each CPM describes the positional difference between two or more mandibular positions.



- **Num. Curve:** A condylography movement that has been entered with the Numeric Curve Editor (refer to chapter "Numeric Curve Editor<sup>[119]</sup>"). That application allows the digitizing of condylography movements that were recorded mechanically on writing paper.



- **Cusps:** The X/Y/Z coordinates of the lower jaw's cusp tips, which have been entered using the Cusp Tips Editor (refer to chapter "Cusp Tips Editor<sup>[121]</sup>"). These coordinates allow the application to calculate individual settings for waxing up in the articulator.



The list of data items in the *Contents* pane has the following columns:

- **Title:** The title of the data object, such as the name of a condylography curve.

- **Created on:** The date and time of when the data item has been created. In case of a condylography curve, this is the date and time of the recording.
- **Type:** One of the data item types stated above.
- **For Articulator calculation selected as:** Indicates whether and how the object is used in the calculation of articulator settings (refer to chapter "Selecting data for articulator calculation" [\[136\]](#)).
- **Flag distance:** The distance between the measuring flags during recording, in millimeters.
- **Recalculated to:** The intercondylar distance to which the displayed recordings are recalculated (refer to chapter "Changing the intercondylar distance" [\[161\]](#)), in millimeters.
- **CADIAX system:** The model name of the CADIAX device with which the data item has been recorded.
- **Status:** Indicates whether the data item has been corrected or modified within the application (refer to chapters "Zero point adjustment" [\[141\]](#) and "Hinge axis correction" [\[142\]](#)).



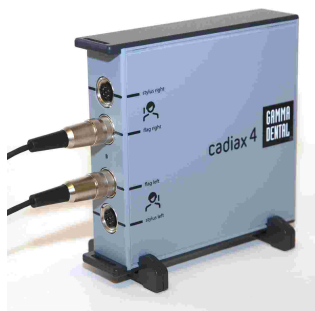
You can specify a column by which to sort the list of data items by clicking the respective column header. Clicking it again will toggle between ascending and descending sort order.



By holding down the *Ctrl* or *Shift* key, you can select multiple data items at once. This is useful, for instance, if you want to superimpose multiple curves (refer to chapter "Overlay mode" [\[163\]](#)). To select all data items of the currently selected type, you can simply press *Ctrl+A*.

### 6.5.2.2 Recording data with CADIAX compact 2

GAMMA Dental Software supports the recording of condylography data with the devices CADIAX 4 and CADIAX compact 2, using the **CADIAX compact 2 Recorder** application. Since CADIAX 4 can operate with two types of sensors, make sure that the "compact" sensor set is mounted when using the device in the CADIAX compact 2 Recorder application. This sensor set consists of 40x40 mm flags and single-pin styli.



The CADIAX 4 device with the "compact" sensor set connected, which occupies only the central two of the device's connectors.




The CADIAX compact 2 device.

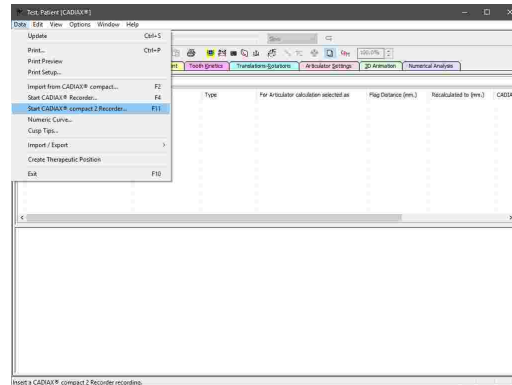


Please note that the compact sensor set does not capture the rotational component of the mandibular movement and hence does not allow for some types of analyses such as rotation/translation graphs or tooth kinetics.

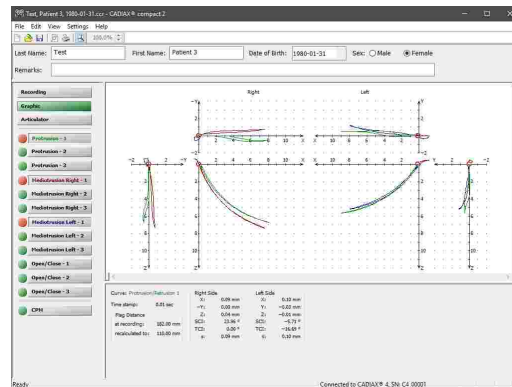



Starting CADIAX compact 2 Recorder in CADIAX Analyzer is only possible when the latter application has itself been started from GDSW classic. If the application has been started from GAMMA Document Browser, the recording application can be started from the patient database therein (refer to chapter "Recording data with CADIAX compact 2" [\[69\]](#)).

You can start the CADIAX compact 2 Recorder application via the button  **CADIAX compact 2 Recorder** in the toolbar or the associated entry in the **Data** menu.

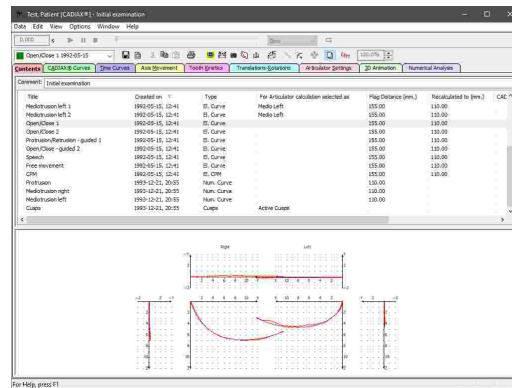


Once CADIAX compact 2 Recorder has been opened, perform the condylography and CPM recordings, save the data, and then close the application.



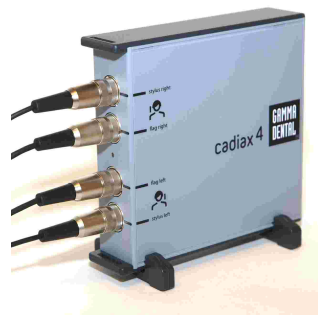
 Please consult the instruction manual of your CADIAX device for detailed instructions on how to perform condylography recordings.

Subsequently, the recordings will appear in the list of data items and can be used for detailed analyses or for calculating the articulator settings.



### 6.5.2.3 Recording data with CADIAX 4 or CADIAX diagnostic

GAMMA Dental Software supports the recording of condylography data with the devices CADIAX 4 and CADIAX diagnostic, using the **CADIAX Recorder** application. Since CADIAX 4 can operate with two types of sensors, make sure that the "diagnostic" sensor set is mounted when using the device in the CADIAX Recorder application. This sensor set consists of 60x60 mm flags and double-pin styli.




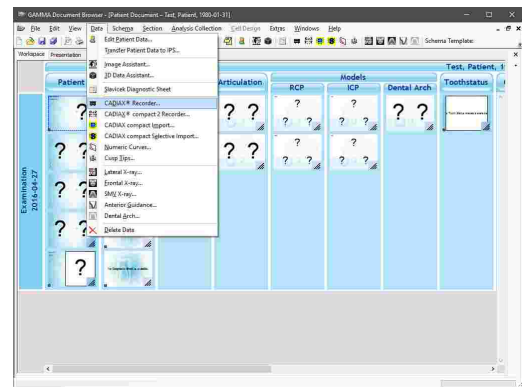
The CADIAX 4 device with the "diagnostic" sensor set connected, which occupies all four of the device's connectors.



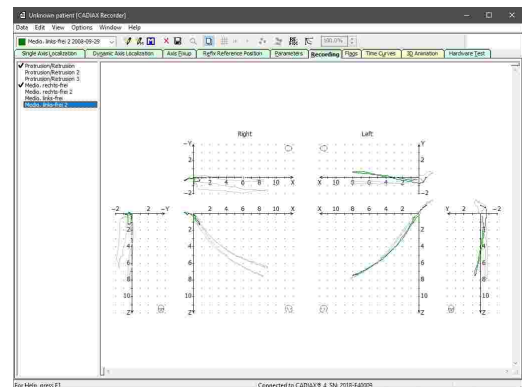
The CADIAX diagnostic device.

**i** Starting CADIAX Recorder in CADIAX Analyzer is only possible when the latter application has itself been started from GDSW classic. If the application has been started from GAMMA Document Browser, the recording application can be started from the patient database therein (refer to chapter "Recording data with CADIAX 4 or CADIAX diagnostic [71]").

You can start the CADIAX Recorder application via the button  *CADIAX Recorder* in the toolbar or the associated entry in the *Data* menu.

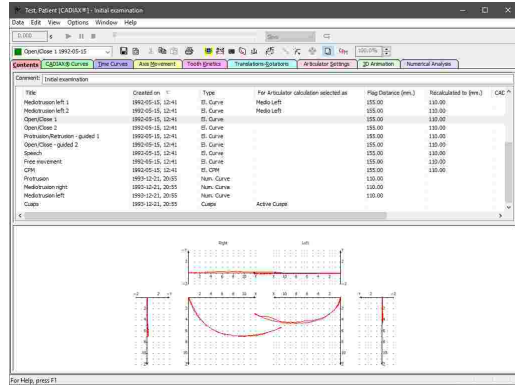


Once CADIAX Recorder has been opened, perform the condylography and CPM recordings, save the data, and then close the application.



**i** Please consult the instruction manual of your CADIAX device for detailed instructions on how to perform condylography recordings.

Subsequently, the recordings will appear in the list of data items and can be used for detailed analyses or for calculating the articulator settings.



### 6.5.2.4 Importing data from CADIAX compact

The discontinued CADIAX compact device was a stand-alone recording unit that does not require a connection to a PC for carrying out a condylography recording or for calculating articulator settings.

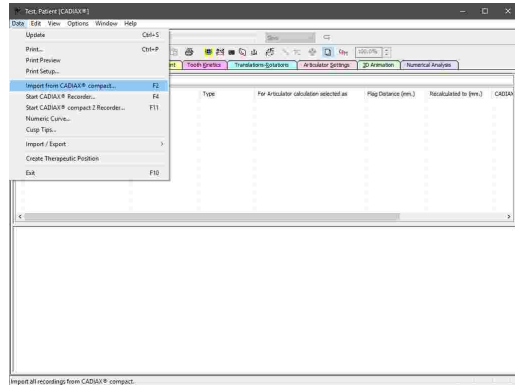
GAMMA Dental Software can import the recordings stored in the internal memory of the device via the **CADIAX compact import** functionality. This import procedure does not remove the recordings from the device.



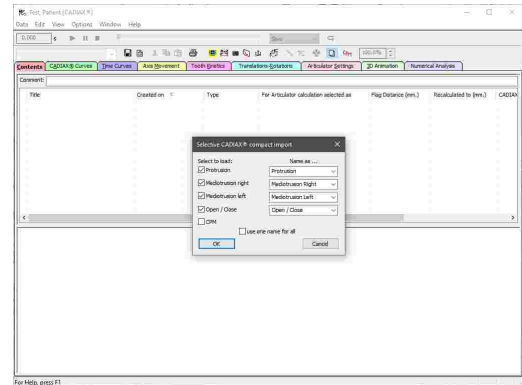
**i** Please consult the instruction manual of your CADIAX device for detailed instructions on how to perform condylography recordings.

**i** Importing data from CADIAX compact in CADIAX Analyzer is only possible when the application has been started from GDSW classic. If the application has been started from GAMMA Document Browser, the data management is carried out in the patient database therein (refer to chapter "Importing data from CADIAX compact").

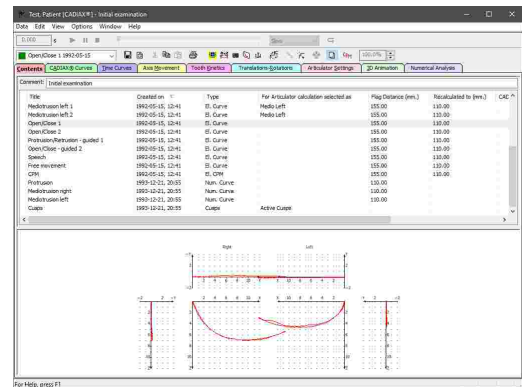
You can start the data import from CADIAX compact via the button **CADIAX compact import** in the toolbar or the associated entry in the *Data* menu.



A dialog will appear that allows you to select the recordings you would like to import and to change their name as needed. Start the import by pressing **OK**.



Subsequently, the recordings will appear in the list of data items and can be used for detailed analyses or for calculating the articulator settings.

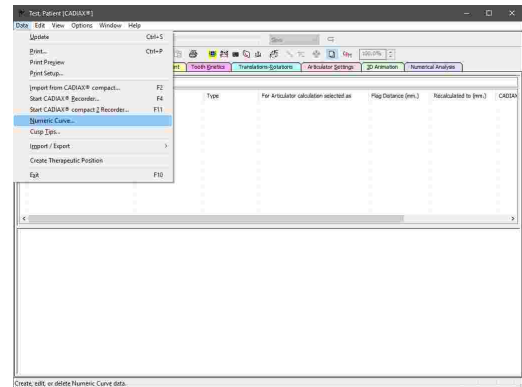


### 6.5.2.5 Entering numeric curves

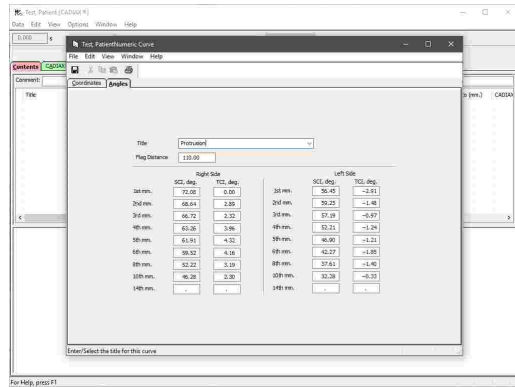
Using the **Numeric Curve Editor**, you can create condylography movements by entering X/Y/Z coordinate points or SCI and TCI angle values for given millimeters of excursion. This functionality is useful for digitizing mandibular movement curves that were created with an analog recording system on writing paper or similar and measured manually. The numeric curves created hereby can be used in the other software modules just like electronically recorded curves for analysis and calculation of articulator settings.

Entering numeric curves in CADIAX Analyzer is only possible when the application has been started from GDSW classic. If the application has been started from GAMMA Document Browser, the data management is carried out in the patient database therein (refer to chapter "Entering numeric curves" <sup>73</sup>).

You can start the Numeric Curve Editor application via the button **Numeric Curves** in the toolbar or the associated entry in the **Data** menu.

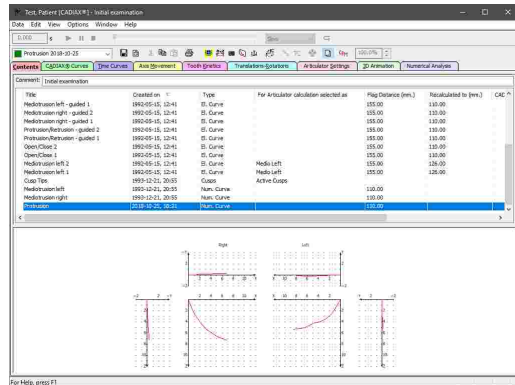



In the now opened Numeric Curve Editor application, you can enter a name for the numeric curve and the coordinates or angles themselves. Save your changes and close the window to continue.

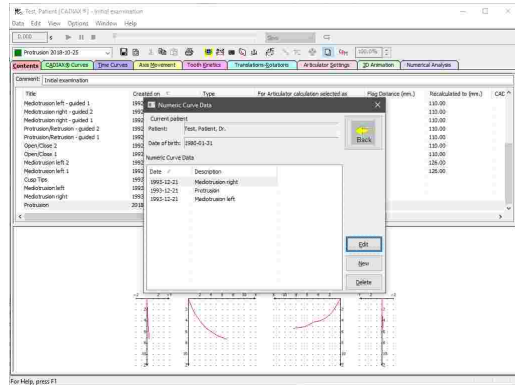


 Please refer to chapter "Numeric Curve Editor<sup>119</sup>" for more information regarding the Numeric Curve Editor application.

Subsequently, the numeric curve will appear in the list of data items and can be used for detailed analyses or for calculating the articulator settings.




To modify a numeric curve later on, press the toolbar button  *Numeric Curves* again, select the item that you want to modify and press the button *Edit*.

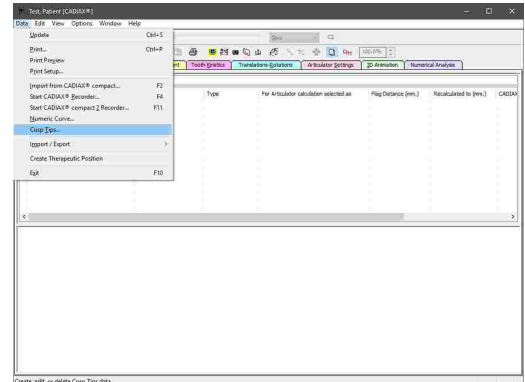


### 6.5.2.6 Entering cusp tips coordinates

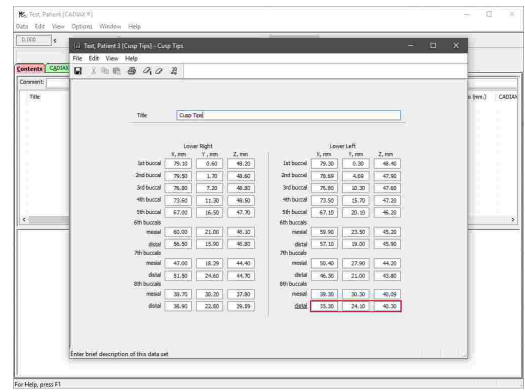
Using the *Cusp Tips Editor*, you can introduce the X/Y/Z coordinates of the lower jaw's cusp tips into the articulator calculation of CADIAX Analyzer. The application will then be able to calculate the ideal incisal table settings to be used for designing occlusal surfaces during a wax-up procedure (refer to chapter "Articulator settings<sup>148</sup>").

**i** Entering cusp tips coordinates in CADIAX Analyzer is only possible when the application has been started from GDSW classic. If the application has been started from GAMMA Document Browser, the data management is carried out in the patient database therein (refer to chapter "Entering cusp tips coordinates" <sup>74</sup>).

You can start the Cusp Tips Editor application via the button  *Cusp Tips* in the toolbar or the associated entry in the *Data* menu.

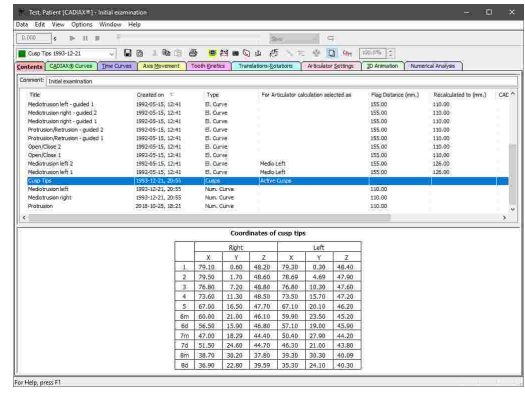


In the now opened Cusp Tips Editor application, you can enter a name for the cusp tips data and the coordinates themselves. Save your changes and close the window to continue.

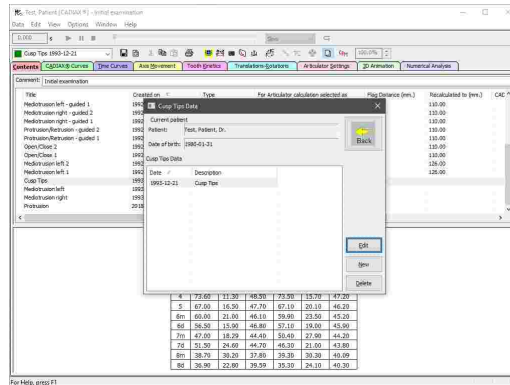


**i** Please refer to chapter "Cusp Tips Editor" <sup>121</sup> for more information regarding the Cusp Tips Editor application.

Subsequently, the cusp tips will appear in the list of data items and can be used for detailed analyses or for calculating the articulator settings.



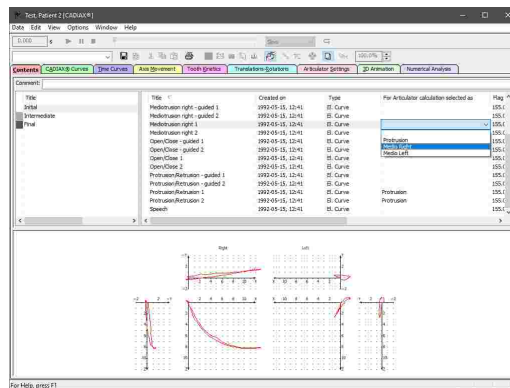
To modify cusp tips data later on, press the toolbar button *Cusp Tips* again, select the item that you want to modify and press the button *Edit*.



### 6.5.2.7 Selecting curves for articulator calculation

In the list of data items you can furthermore select the protrusion and mediotrusion curves that are to be used for calculating the ideal articulator settings (refer to chapter "Articulator settings" ).

To do so, move your mouse cursor over the column *For articulator selection selected as* in the list of data items. For each curve, you will see a combo box that allows you to specify whether the curve should be used as protrusion, mediotrusion right/left, or not at all. Alternatively, you can select one or more curves, right-click them, and change the selection via the context menu item *Select as*.

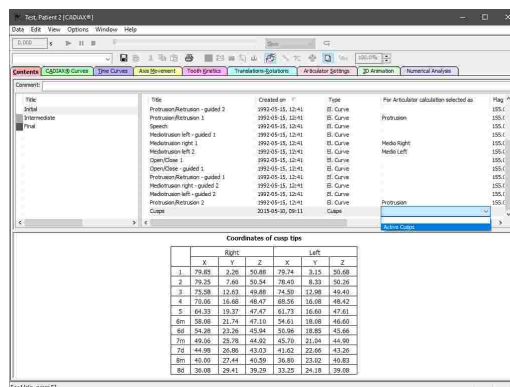


For the calculation of articulator settings, it is sufficient if just a single curve is selected for each curve type. However, it is recommended to select at least three curves per type, from which the application will form an average that is a better representation of the actual patient movements.

### 6.5.2.8 Selecting cusp tips for articulator calculation

If you have entered the cusp tips coordinates of the lower jaw, you can have the software calculate ideal incisal table settings (refer to chapters "Entering cusp tips coordinates" and "Cusp tips positions" , respectively).

Like condylography curves, you can change this selection via the column *For articulator selection selected as* in the list of data items or via the context menu of the respective data item.

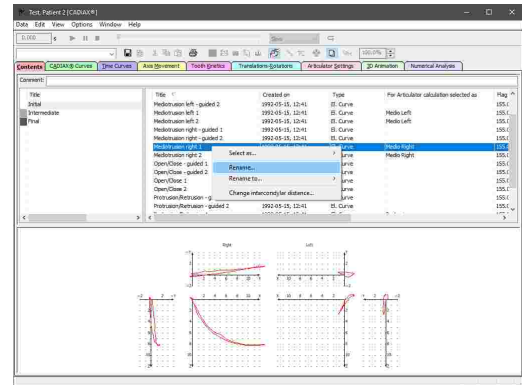


Only one set of cusp tips coordinates can be selected for articulator calculation at once. If multiple sets of data are present, selecting one of them will automatically deselect the other ones.

### 6.5.2.9 Renaming data items

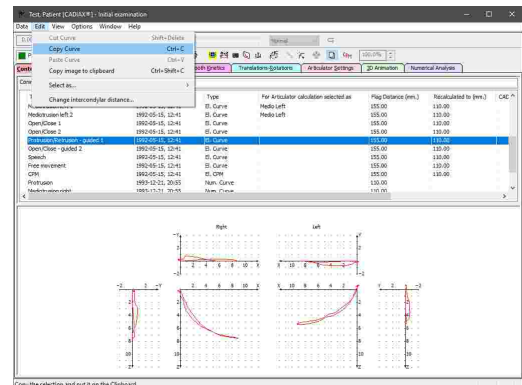
To rename a CADIAX recording, right-click in the list of data items and choose *Rename*. Subsequently, enter the new name and confirm by pressing the enter key.

In this context menu, you can also find dedicated entries to quickly rename a condylography curve to the common designations "Protrusion", "Mediotrusion right", or "Mediotrusion left".

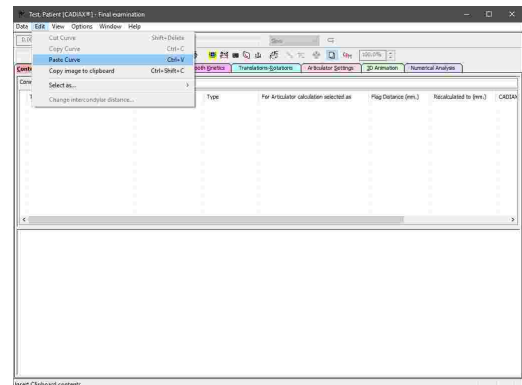


### 6.5.2.10 Copying and pasting data items

To copy one or more data items from one analysis object to another, select them in the list and choose *Copy Curve* in the *Edit* menu.



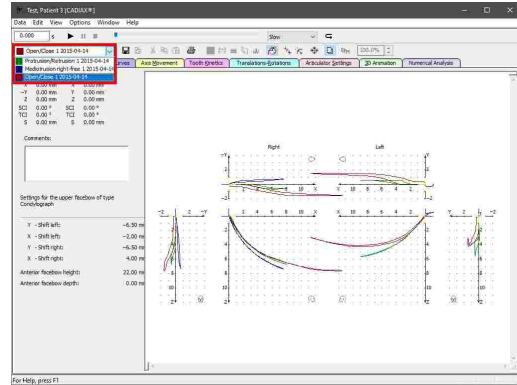
Subsequently, you can paste the copied data using the menu entry *Paste Curve* in the data list of the second analysis. Using this method, you can also duplicate data items within the same analysis.



**i** Copying and pasting data items in CADIAX Analyzer is only possible when the application has been started from GDSW classic. If the application has been started from GAMMA Document Browser, the data management is carried out in the patient database therein (refer to chapter "Copying and pasting raw data" 584).

### 6.5.3 Selecting the active recording

If you have selected multiple recordings in the *Contents* pane, you can switch between them using the combo box in the toolbar also in every other pane. Alternatively, you can have the curves superimposed by activating the overlay mode (refer to chapter "Overlay mode [163]").

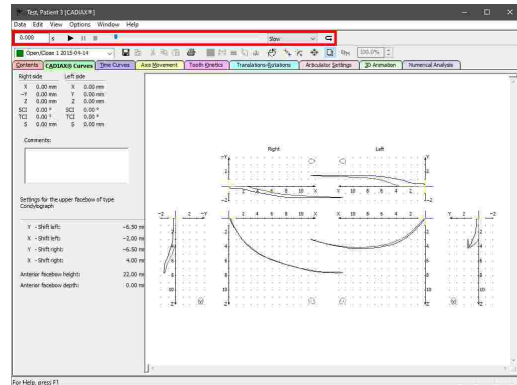


**!** Please note that some editing operations, such as the zero point adjustment (refer to chapter "Zero point adjustment [141]"), are only applied to the curve that is selected as active, even if overlay mode is activated.

### 6.5.4 Replaying a condylography recording

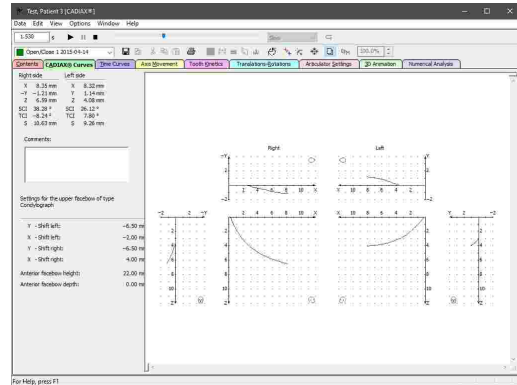
CADIAAX Analyzer allows the realistic replay of mandibular movements that have been recorded with the CADIAAX condylography systems. This replay functionality is provided in all panes except *Contents* and *Numerical Analysis*. Only the curve that is currently selected as active will be replayed, even if overlay mode is enabled (refer to chapters "Overlay mode [163]" and "Selecting the active recording [138]", respectively).

You can control the replay of the active curve via the **replay toolbar** on the upper border of the window.

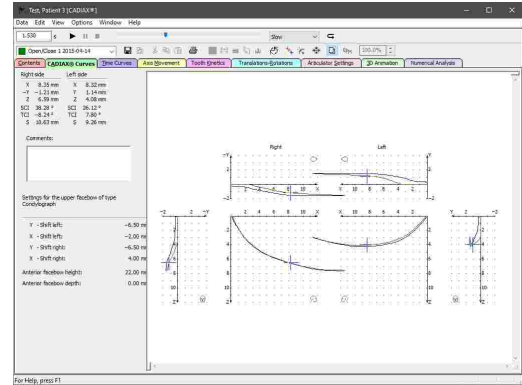


Start the replay by pressing the button **▶ Start replay**. To pause a replay at the current time position or to stop it entirely, use the buttons **⏸ Pause replay** and **■ Stop replay**, respectively. By activating the button **🔄 Loop**, you can enable an infinite replay loop.

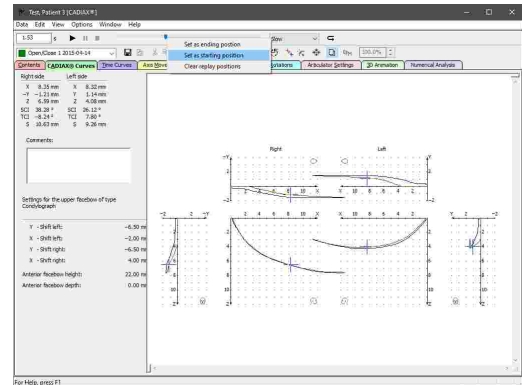
Use the slider to manually jump to a particular time position. You can skip through the time positions step-by-step using the arrow keys or the page-up and page-down keys on your keyboard.



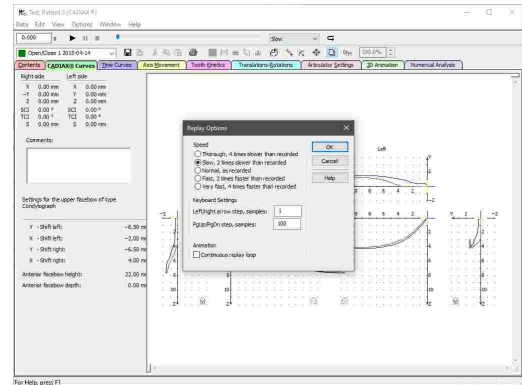
A cursor indicates the selected time position in the curve display. By clicking on the curve with the left mouse button, you can immediately jump to a specific time position.



The context menu of the slider allows you to set the current time position as start or end position of the automatic replay. You can reset those positions in the same way or by simply selecting another curve as active.

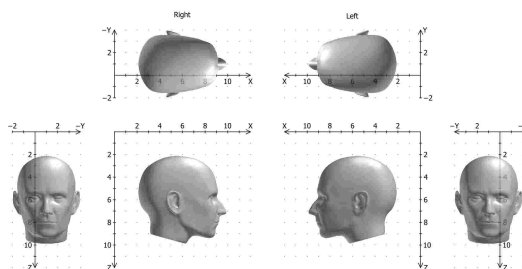



You can select the speed of the automatic replay using the combo box in the replay toolbar. The menu item *Options* → *Replay* provides access to more detailed configuration settings.



### 6.5.5 CADIAX curves

The *CADIAX Curves* pane provides the default display style of condylography curves, which is also employed by other CADIAX applications. The sagittal views (X/Z-plane) are displayed centrally, with the transversal views (X/Y-plane) above. The frontal views (Y/Z-plane) are shown on the right and left side and can be hidden as needed (refer to chapter "Coordinate system display<sup>164</sup>").



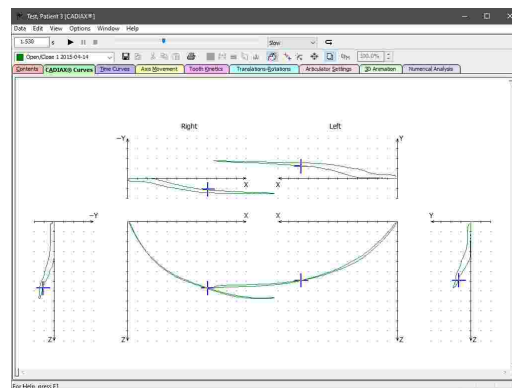
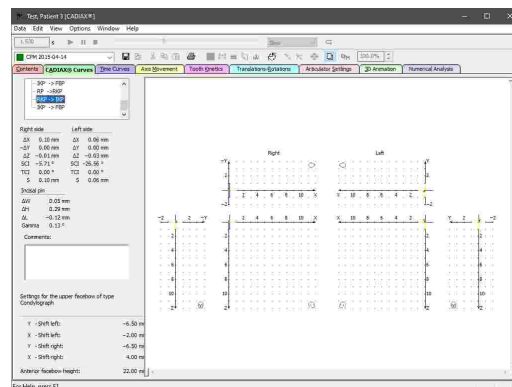
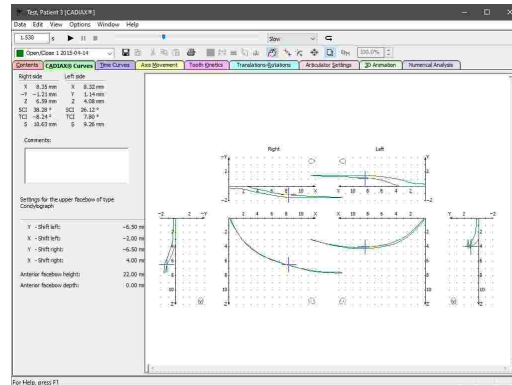
 Refer to chapter "The reference coordinate system<sup>299</sup>" for a detailed description of the coordinate system used by the software.

If a condylography curve is selected as active, the side bar on the left border of the window displays the following information:

- The numerical **measurement values** of the currently selected time position. By selecting a point on the curve, you can immediately jump to the respective time position.
- A text box for entering an arbitrary **comment** for the recording being displayed (refer to chapter "Entering Comments" [144]).
- The **face bow parameters** used during the recording.

Condyle position measurements (CPM) may contain multiple individual measurement positions. When a CPM is selected as active, you can choose the position to be displayed via the list on the top of the side bar or by simply clicking the position in the coordinate system.

While overlay mode is disabled, you can choose to display the excursion and incursion parts of the curve in different colors (refer to chapter "Overlay mode" [163]). You can find this and further settings regarding the display of the coordinate system in the **View** menu (refer to chapter "Coordinate system display" [164]).




**i** The abbreviations and acronyms used for the numerical values are explained in chapter "Abbreviations of numerical values" [171].

**i** The replay bar allows you to animate the movement of a displayed condylography curve in real-time (refer to chapter "Replaying a condylography recording" [138]).


### 6.5.5.1 Zero-point adjustment

In some recordings, for example on patients with an unstable reference position, the starting point of the condylography curve might not coincide with the origin of the coordinate system.


You can move those curves into the origin of the coordinate system manually or automatically using the zero-point adjustment.

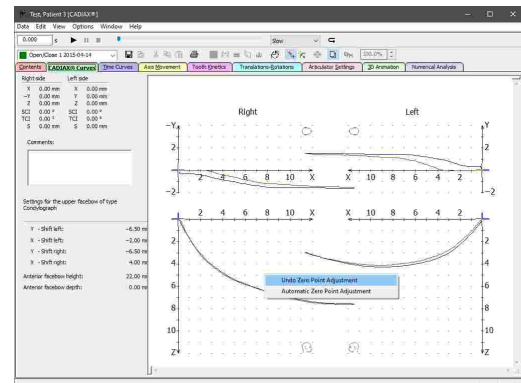
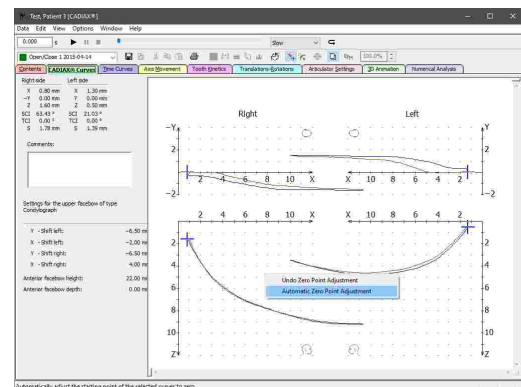
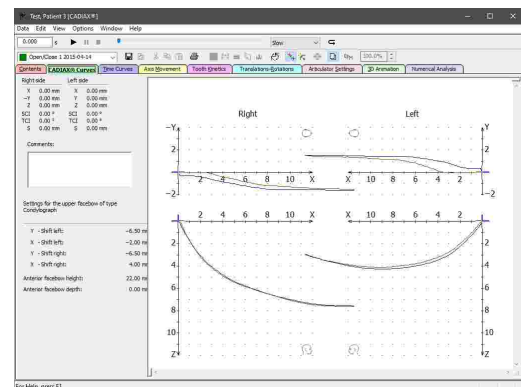
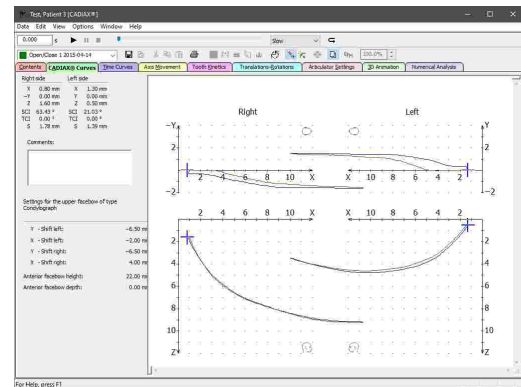
To activate this feature, use the icon  *Manual Zero-Point Adjustment* in the toolbar. Subsequently, you can move the curve to the desired position in the coordinate system by dragging it while keeping the left mouse button pressed. To deactivate the adjustment mode and apply your changes, use the same toolbar icon another time.


The modified recording will then be marked with the status "Zero-point adjusted" in the *Contents* pane (refer to chapter "The list of data items" [127](#)).

Using the icon  *Automatic Zero-Point Adjustment* or the corresponding entry in the context menu of the coordinate system, you can have the starting point of the curve moved into the coordinate system origin automatically. This functionality is also available in the *Contents* pane and can even be applied to multiple curves at once.

By selecting a specific time position on the curve before applying an automatic zero-point adjustment, you can choose to use the selected position as the new zero-point. This can for example be useful to compensate for the mandibular shift to a therapeutic position during splint therapy.


To undo a zero-point adjustment at a later point in time, activate the functionality again, using the icon  *Manual Zero-Point Adjustment*. Click the coordinate system with the right mouse button and select the entry *Undo Zero-Point Adjustment* in the appearing context menu.




 Please note that the zero point adjustment is only applied to the curve that is currently selected as active, even if overlay mode is activated and multiple curves are displayed at once (refer to chapters "Selecting the active curve<sup>[138]</sup>" and "Overlay mode<sup>[163]</sup>", respectively).

### 6.5.5.2 Hinge axis correction

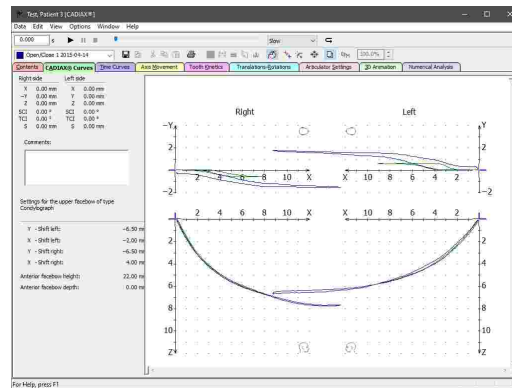
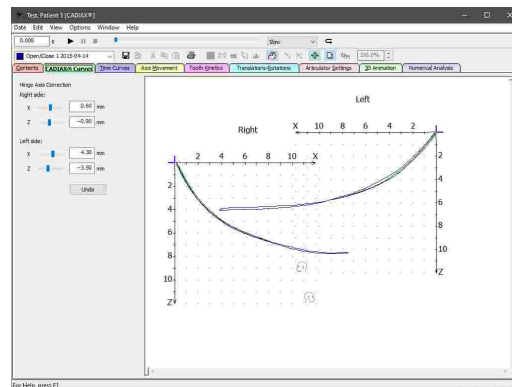
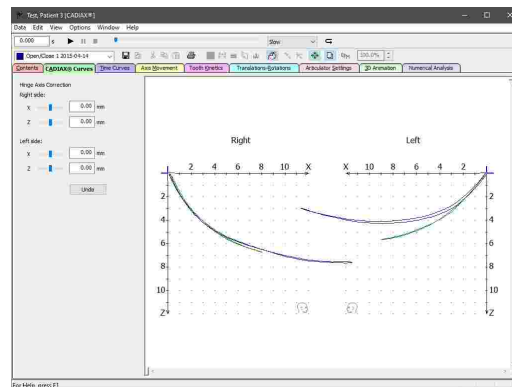
If the hinge axis of the temporomandibular joint has been incorrectly determined during the CADIAX recording, it will result in a distortion of the recorded movements, since the rotation center no longer coincides with the coordinate system, i.e. the reference position. Such an error becomes especially apparent when superimposing protrusion curves with open/close movements, which, provided that the hinge axis has been located correctly, should show a strong correspondence in the initial movement phase. For information on superimposing curves using the overlay mode, please refer to chapter "Overlay mode<sup>[163]</sup>".

To correct an incorrectly located hinge axis, activate the icon  *Hinge axis correction* in the toolbar on the *CADIAX curves* pane. This will reduce the coordinate system to just the right and left view of the sagittal plane and the side bar will provide controls for specifying the desired correction offset.

You can then move the coordinate system by dragging it with the left mouse button or by entering numerical offset values until the initial sections of the protrusion and open/close movements coincide. This method for recalculating curves to the new, corrected position is also used for calculating the movements of individual positions on the teeth (refer to chapters "Tooth kinetics<sup>[146]</sup>" and "Tooth kinetics<sup>[159]</sup>").

Using the button *Undo*, you can undo your last modifications. Press the icon  *Hinge axis correction* in the toolbar again to apply your changes and exit hinge axis correction.

The modified recording will then be marked with the status "Hinge axis corrected" in the *Contents* pane (refer to chapter "The list of data items<sup>[127]</sup>").



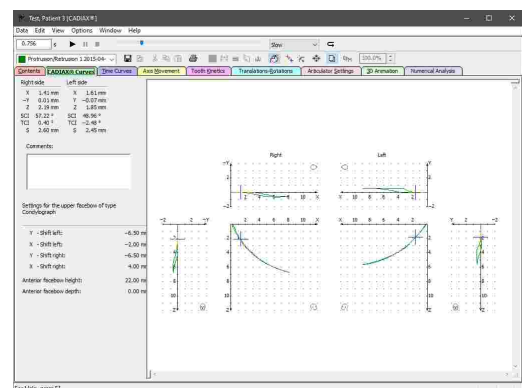
**!** The hinge axis correction can only be applied to curves that contain the rotational component in addition to the condylar offsets along the X, Y, and Z-axes. Such recordings can only be made with the devices CADIAX 4 or CADIAX diagnostic and are carried out with CADIAX Recorder as the recording application (refer to chapter "CADIAX Recorder<sup>[118]</sup>").


**!** Please note that the hinge axis correction will always be applied to all curves selected on the Contents pane, even if overlay mode is deactivated (refer to chapter "Overlay mode<sup>[163]</sup>").

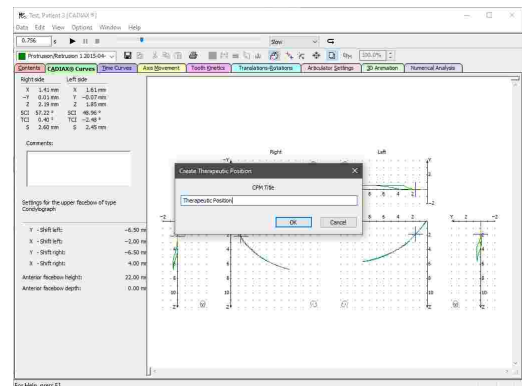
### 6.5.5.3 Creating a therapeutic position

When visualizing a treatment objective in the CADIAS module, the mandible can be repositioned to a particular CPM position (refer to chapter "Movement to CPM position<sup>[229]</sup>"). CADIAX Analyzer provides a functionality for creating such a therapeutic CPM position from any condylography movement.

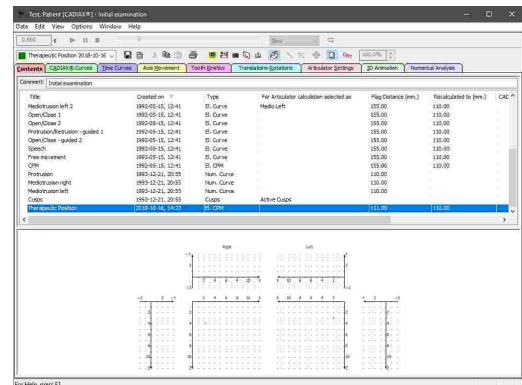
To do so, select the movement and the time position, which you would like to use as therapeutic position, in the CADIAX curves pane.



Subsequently, press the icon  *Create therapeutic position* in the toolbar. A dialog will appear, in which you can specify the title of the CPM data item that is to be created.

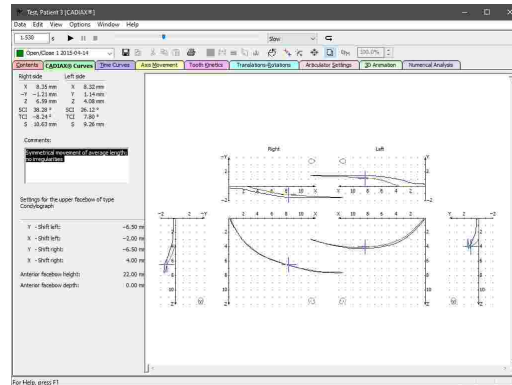


Confirm by pressing *OK*, upon which the new CPM data item will appear in the list of data items in the *Contents* pane. When using GAMMA Document Browser, the CPM item will automatically be displayed the next time you start CADIAX Analyzer. With GDSW classic, you will have to copy and paste the data item manually (refer to chapter "Inserting CADIAX condylography data<sup>[204]</sup>").



### 6.5.5.4 Entering comments

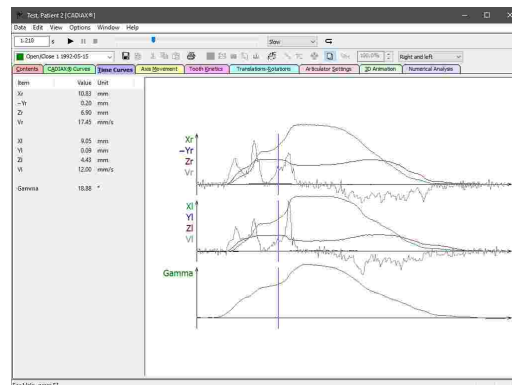
In the *CADIAX curves* pane, you can enter an arbitrary comment for the currently displayed recording, for example to annotate the data with your diagnostic findings.



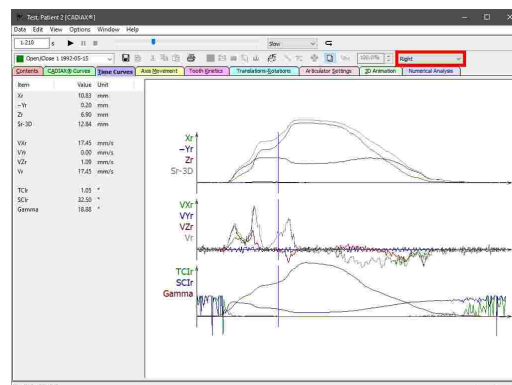
### 6.5.6 Time curves


The *Time curves* view illustrates the progression of a condylography recording over time. With that intent, it allows the recorded X/Y/Z-coordinates as well as the derived values for velocity, acceleration, and angle measurements to be superimposed or displayed side-by-side. This view gives you the possibility to evaluate the uniformity of a movement and potentially identify dysgnathic misbehaviors such as a clicking joint, which would manifest as a significant peak in the velocity curve.

The side bar displays the numerical measurement values of the currently selected time position, which is indicated by a vertical line in the curve display. By selecting a point on one of the curves, you can immediately jump to the respective time position.



Using the combo box in the toolbar or the corresponding entries in the *View* menu, you can choose between the predefined views for right, left, or for comparing right and left patient side.



 The abbreviations and acronyms used for the numerical values are explained in chapter "Abbreviations of numerical values" <sup>171</sup>.



The replay bar allows you to animate the movement of a displayed condylography curve in real-time (refer to chapter "Replaying a condylography recording" [1381](#)).

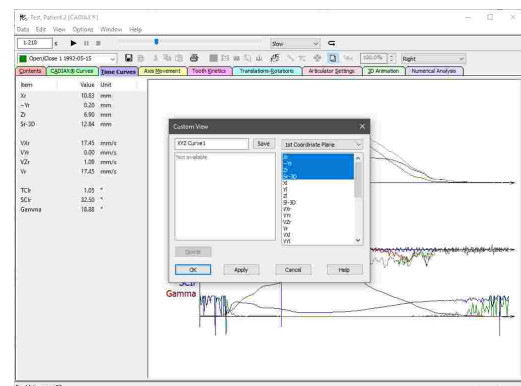
### 6.5.6.1 Defining a custom view

Using the menu *View* → *Custom*, you can define a custom time curves view as a supplement to the predefined views.

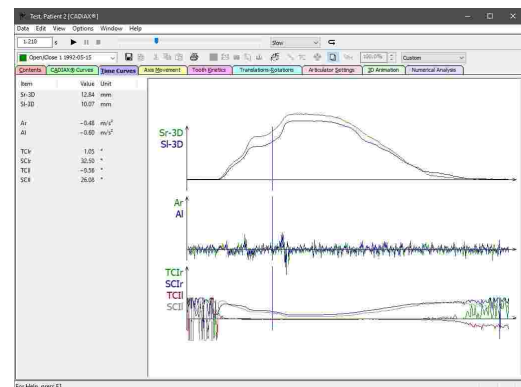
In the dialog that appears, you can switch between the three available coordinate planes. Specify the numerical values that you would like to have displayed in the respective coordinate plane by selecting them in the list. If no values are selected, the respective coordinate plane will be hidden.

On the left side, you can save the custom view under an arbitrary name. Here, you can also load and delete existing views.

Press *OK* or *Apply* to use the specified custom view.



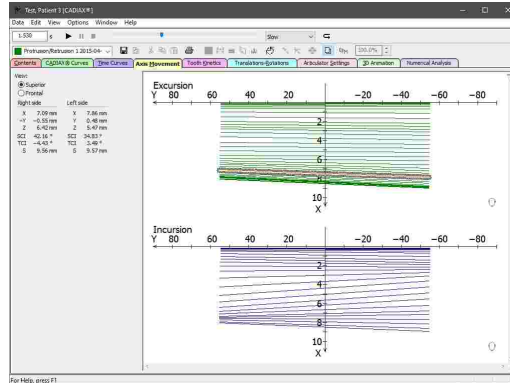
The time curve display will be updated accordingly and the side bar will display the appropriate numerical values. If you have saved your custom view, you will also be able to select it in the combo box in the toolbar.



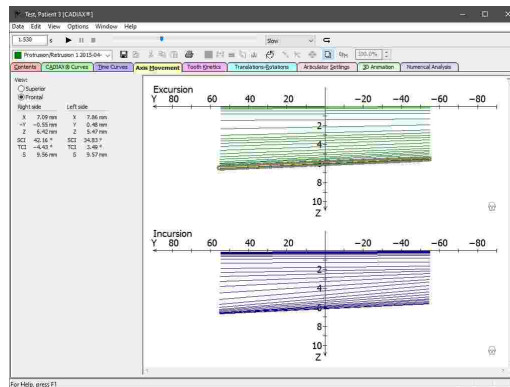
### 6.5.7 Axis movement

On the *Axis movement* pane, you can find the illustrated movement of the temporomandibular joint axis. The axis is displayed as a line between right and left axis points, which are ascertained during a CADIAX recording on the patient. This view allows you to evaluate the symmetry of the lower jaw movement, meaning how evenly the right and left condyle are moving.

For reasons of comprehensibility, the excursion and incursion movements are visualized in separate coordinate systems. Please note that only every fifth time position is illustrated by a line connecting the right and left condyle position. By selecting one of those lines, you can immediately jump to the respective time position. The side bar always provides the numerical measurement values of the current time position.



By default, axis movements are displayed from superior, i.e. in the transversal plane (X/Y). Using the radio buttons in the side bar or the entries in the View menu, you can switch to a view in the frontal plane (Y/Z).



**i** The abbreviations and acronyms used for the numerical values are explained in chapter "Abbreviations of numerical values [171]".

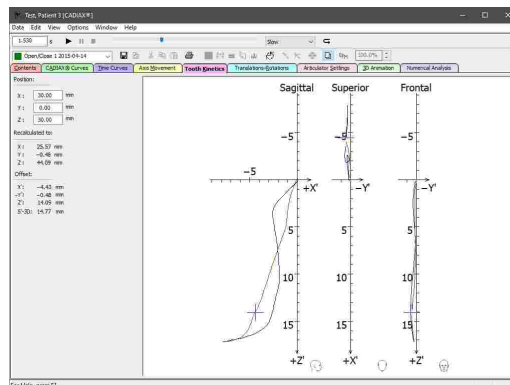
**i** The replay bar allows you to animate the movement of a displayed condylography curve in real-time (refer to chapter "Replaying a condylography recording [138]").

### 6.5.8 Tooth kinetics

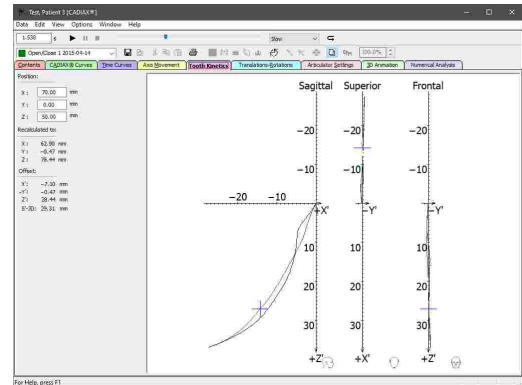
In the *Tooth kinetics* view, you can recalculate a condylography movement to a particular position in the coordinate system. For example, this can be used to trace the movement paths of a lower tooth's cusp tip.

In the side bar, you can enter the X/Y/Z-coordinates of the position to which the condylography movement shall be recalculated. You can measure these coordinates on a dental model articulated in either the mechanical or virtual articulator (refer to chapter "Cusp Tips Editor [121]").

Tooth kinetics curves are displayed in three coordinate systems, one for the sagittal (X/Z), transversal (superior; X/Y) and frontal plane (Y/Z), respectively. The origin of each coordinate systems corresponds to the position to which the condylography movement is recalculated.



The side bar displays the absolute coordinates of the selected time position as well as their relative offset from the position of recalculation. By selecting a point on the curve, you can immediately jump to the respective time position.



**!** Tooth kinetics can only be calculated for curves that contain the rotational component in addition to the condylar offsets along the X, Y, and Z-axes. Such recordings can only be made with the devices CADIAX 4 or CADIAX diagnostic and are carried out with CADIAX Recorder as the recording application (refer to chapter "CADIAX Recorder" <sup>118</sup>).

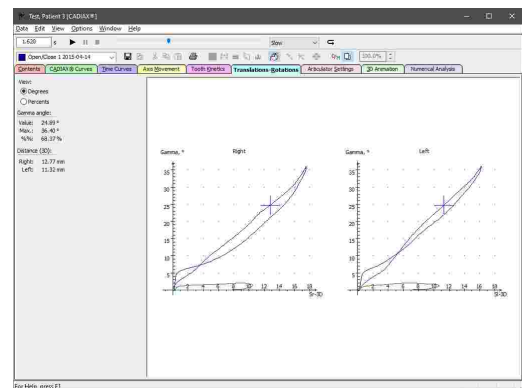
**i** The abbreviations and acronyms used for the numerical values are explained in chapter "Abbreviations of numerical values" <sup>171</sup>.

**i** The replay bar allows you to animate the movement of a displayed condylography curve in real-time (refer to chapter "Replaying a condylography recording" <sup>138</sup>).

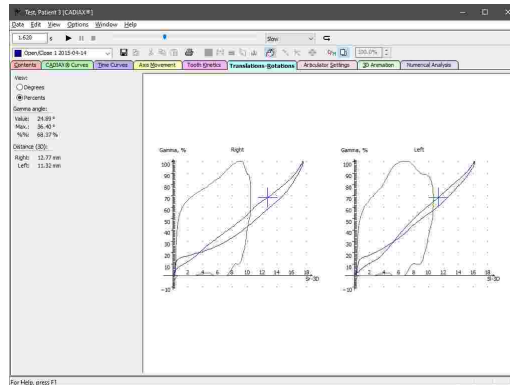
### 6.5.9 Translations-Rotations

In the *Translations-Rotations* view, the application illustrates the progression of the mandibular opening rotation relative to the excursion distance. This allows you to evaluate the uniformity of the joint rotation as well as the maximum mouth opening achieved during the individual movements. This rotation angle is referred to as "Gamma".

The side bar displays the Gamma angle and the bilateral excursion distance of the selected time position. By selecting a point on the curve, you can immediately jump to the respective time position.



Using the entries provided in the *View* menu, you can toggle the coordinate system display between showing absolute angle values and relative percent values. The latter is especially well-suited for superimposing multiple curves with different maximum rotation values.



**!** The translations-rotations graphs can only be calculated for curves that contain the rotational component in addition to the condylar offsets along the X, Y, and Z-axes. Such recordings can only be made with the devices CADIAX 4 or CADIAX diagnostic and are carried out with CADIAX Recorder as the recording application (refer to chapter "CADIAX Recorder" <sup>118</sup>).

**i** The abbreviations and acronyms used for the numerical values are explained in chapter "Abbreviations of numerical values" <sup>171</sup>.

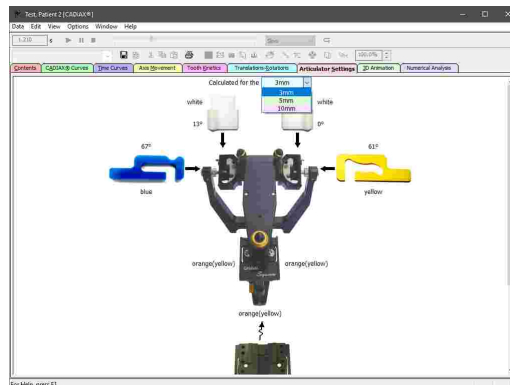
**i** The replay bar allows you to animate the movement of a displayed condylography curve in real-time (refer to chapter "Replaying a condylography recording" <sup>138</sup>).

### 6.5.10 Articulator settings

A fully adjustable articulator is capable of mechanically reproducing virtually all naturally-occurring mandibular movements. On the *Articulator settings* pane, CADIAX Analyzer displays the settings that allow the best possible reproduction of the condylography curves selected on the *Contents* pane (refer to chapter "Selecting curves for articulator calculation" <sup>136</sup>). Whenever you change that selection, the application will recalculate the articulator settings automatically.

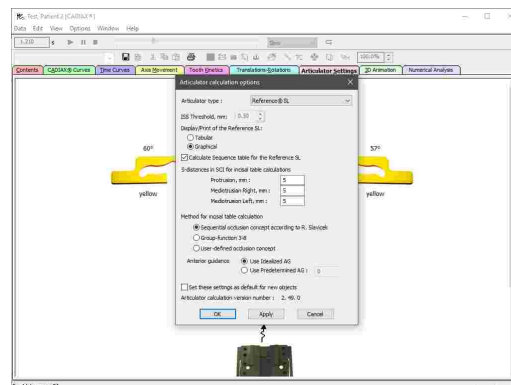
By default, the software calculates the settings for the Reference SL articulator and displays them in a convenient graphical format. Using the combo box above the graphic, you can specify whether the settings should be calculated for the 3rd, 5th, or 10th millimeter of condylar excursion.

To change the type of articulator or other calculation options, use the corresponding options dialog (refer to chapter "Configuring the articulator calculation" <sup>149</sup>).



### 6.5.10.1 Configuring the articulator calculation

For configuring the calculation of articulator settings, open the corresponding options dialog using the menu *Options* → *Articulator settings*.

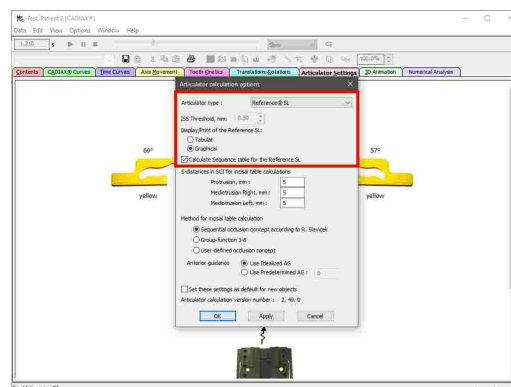


By activating the check box on the bottom of the dialog, you can specify that the current settings should be used by default for all new CADIAX analyses.

#### 6.5.10.1.1 Selecting an articulator type

In the upper section of the dialog, you can select the type of articulator for which the settings should be calculated. For some articulators, the possibility to specify the ISS threshold is provided, at which the transversal Bennett movement will be separated into an immediate and a progressive part (refer to chapter "Immediate side shift (ISS)"<sup>[307]</sup>).

For the Reference SL articulator, you can furthermore toggle between graphical and tabular display of the calculated values as well as whether the Sequence incisal table should be calculated (refer to chapter "Sequence incisal table settings"<sup>[155]</sup>).



The following types of articulators are available for selection (in alphabetical order):

#### Amann Girrbach

- Artex Arcon AP
- Artex Arcon AR
- Artex CP
- Artex CN
- Artex CR
- Artex CT
- Artex Nonarcon TK
- Artex Nonarcon TR
- Artex SL

#### Denar

- Denar Anamark
- Denar D5A (Calculation in retrusive mode "R" or in intercondylar mode "I")
- Denar Mark 320
- Denar Mark 330

Denar Mark II

**Hanau**

- Hanau 96H2
- Hanau Modular
- Hanau Wide-Vue

**Ivoclar Vivadent**

- Ivoclar Stratos 200
- Ivoclar Stratos 300

**KaVo**

- KaVo Protar

**Panadent**

**GAMMA**

- Reference A
- Reference I
- Reference LF
- Reference SL

**SAM**

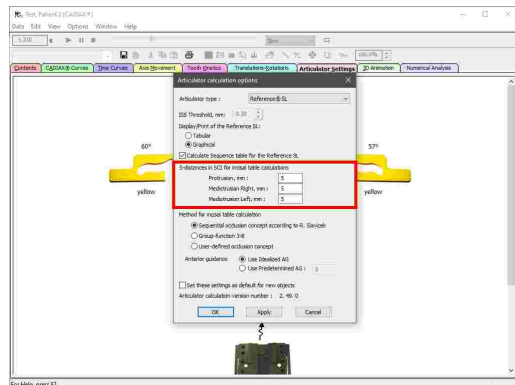
**Whip Mix**

- Model 2240
- Model 2340
- Model 3040
- Model 3140
- Model 8500

**6.5.10.1.2 Configuring the incisal table calculation**

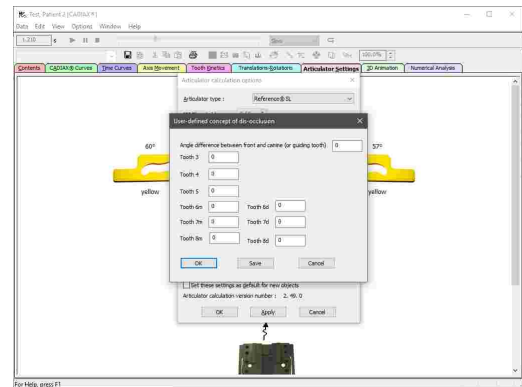
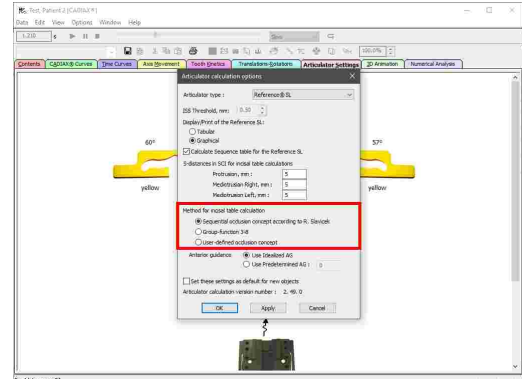
Using the input boxes in the options dialog, you can specify the excursion distances on the condylography curves at which the sagittal and transversal condylar inclination will be measured for the purpose of incisal table calculation. These values should generally match the distances with which you program the condylar elements of the articulator (refer to chapter "Condylar settings [153]").

Please note that changing the value for the right mediotrusion curve affects the left guidance angle of the incisal table and vice versa.

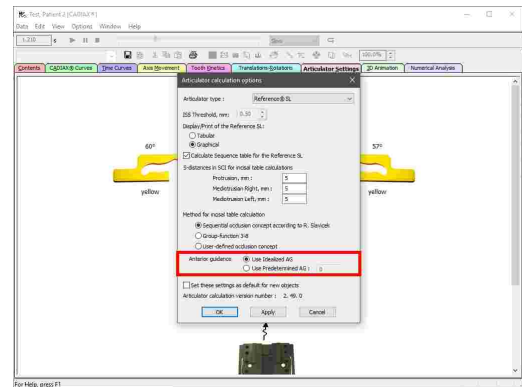


The method of incisal table calculation defines the occlusion concept, according to which the mediotrusive tooth guidances should be calculated. The following methods are available for selection:

- The concept of sequential occlusion according to Slavicek (refer to chapter "The concept of sequential occlusion<sup>1521</sup>").
- A group function concept, in which the teeth from canine to third molar are equally involved in lateral guidance. In this concept, all disocclusion angles are set to zero.
- A user-defined occlusion concept, in which you can specify your own desired disocclusion angles for the individual teeth. The values entered here will be subtracted from the anterior guidance.



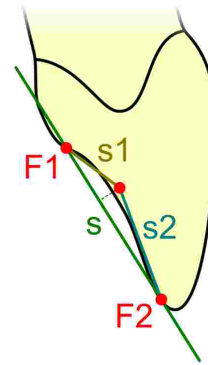
The last option in this dialog allows you to specify whether an ideal or a user-defined anterior guidance should be used as a basis for calculating the incisal table settings. The ideal anterior guidance is calculated based on an empirically determined relation to the sagittal condylar inclination.



### 6.5.10.1.3 Occlusion concepts

A so-called occlusion concept (also referred to as "disocclusion concept") dictates the functional interplay of the maxillary and mandibular teeth in laterotrusion movement on the laterotrusive side.

Generally speaking, each buccal cusp tip of a mandibular lateral tooth follows the guidance path that is provided by the antagonist tooth in the maxilla during a laterotrusion movement. The initial maxillary contact point in this movement is defined as functional point 1 (**F1**). The final point of the guidance path is consequently referred to as functional point 2 (**F2**). The line **s** is defined by these two functional points.



For better differentiation between the flatter and the steeper part of the incisors' lingual surfaces, the additional chords **s1** and **s2** are defined between the functional points and the point of maximum altitude on the tooth surface.

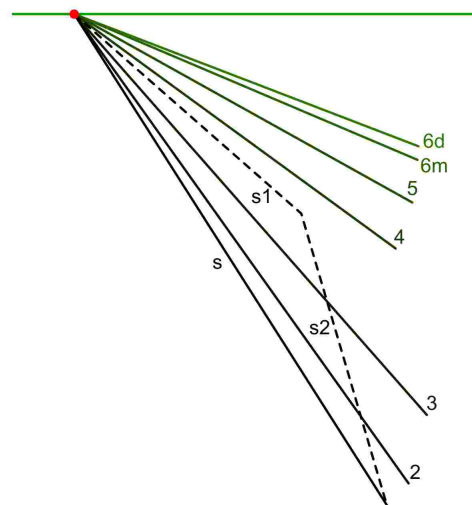
An occlusion concept describes how each mandibular cusp moves relative to the guidance track of the respective maxillary antagonist tooth: whether it remains in contact throughout or whether it progressively lifts off with a specific angle of disocclusion. Teeth that remain in contact with the antagonist's guiding surface during a laterotrusion movement are referred to as **guiding** teeth. It lies in the geometric nature of every occlusion concept that at least one tooth must be guiding at any time. Teeth that depart from their intended guiding track are referred to as **disoccluding**, whereby the relative angle of departure is considered to range from slightly to strongly disoccluding.

**i** In the articulator calculation options of CADIAX Analyzer, it is possible to select between the concept of sequential occlusion according to Slavicek (refer to chapter "The concept of sequential occlusion<sup>[152]</sup>"), group function with all disocclusion angles set to zero, as well as a user-defined concept with custom disocclusion angles (refer to chapter "Configuring the incisal table calculation<sup>[150]</sup>").

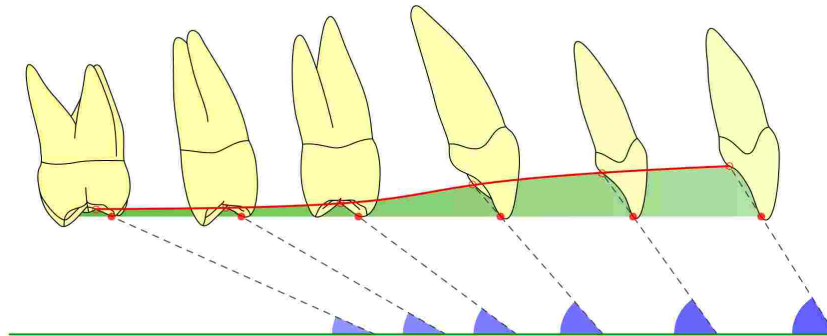
**6.5.10.1.4 The concept of sequential occlusion**

In his professorial dissertation published in 1984, Professor Rudolf Slavicek measured and statistically evaluated the morphological-functional inclinations of the maxillary buccal cusps for the front and lateral tooth regions, relative to the axis-orbital reference plane. Result of this analysis are the following average inclinations for the maxillary guiding surfaces:

- Tooth 1: 57.57° (s)
- 41.36° (s1)
- 73.41° (s2)
- Tooth 2: 54.59°
- Tooth 3: 48.72°
- Tooth 4: 36.16°
- Tooth 5: 29.18°
- Tooth 6: 23.05° (mesial)
- 21.50° (distal)



Illustrating the functional chords relative to the reference plane clearly shows a dominance of the front-canine group when compared to the lateral teeth, as well as a sequentially decreasing slope of cusp inclination:



Here, it shall be noted that the sequential occlusion concept according to Slavicek disregards the second and third molar, hence no corresponding values are calculated. The dominant principle of this concept is to entrust the first molar with the responsibility of guidance during laterotrusion and mediotrusion movements. The more posterior teeth are supposed to disocclude without any ex-centric or in-centric contact. Therefore, the second and third molars only have supporting function and must not be used in the guidance concept of natural dentition. It is an important task of the first molar to ensure strict disocclusion of the posterior two molars. If the guidance of the first molar is too flat, the principle of a lingualized occlusion should be employed. When aiming for balanced occlusion, entirely different rules apply.

### 6.5.10.2 Condylar settings

The tabular view of articulator settings is usually comprised of the following tables, all of which concern the settings of the condylar elements of the articulator:

- The **average angle values** of the curves that have been selected for articulator calculation. The retrusive angles are measured on the rotating working side of the mediotrusion curves. The suffix character denotes the quadrant of the coordinate system in which the retrusion movement takes place (refer to chapter "Retrusion direction<sup>[154]</sup>").

	Protrusion		Mediotrusion right		Mediotrusion left	
	SCI right	SCI left	S C I	T C I	S C I	T C I
1st	67.0°	72.2°	71.9°	19.6°	57.1°	-9.2°
2nd	67.2°	68.0°	69.8°	19.7°	59.3°	-4.7°
3rd	65.9°	62.8°	69.5°	17.4°	57.7°	-4.1°
4th	63.4°	59.4°	65.8°	15.9°	55.8°	-3.2°
5th	61.1°	53.6°	63.7°	14.5°	52.9°	-2.7°
6th	58.6°	49.7°	61.0°	10.7°	49.9°	-2.3°
8th	51.9°	42.1°	54.8°	8.8°	42.8°	-1.7°
10th	44.8°	35.2°	48.1°	7.2°	36.4°	-1.2°
14th			35.4°	6.5°		
	Retrusion					
-1.	46.4°r	46.3°r				
-2.	41.9°r	32.9°r				

- The recommended settings for programming the **sagittal condylar inclination** (SCI) on the articulator.

Inlay	Right			Left		
	3rd mm	5th mm	10th mm	3rd mm	5th mm	10th mm
Straight	●67°	64°	53°	67°	60°	45°
Convex	61°	●60°	●56°	●61°	●57°	●47°
Retrusive	Blue	Yellow	Yellow	Yellow	Yellow	Yellow

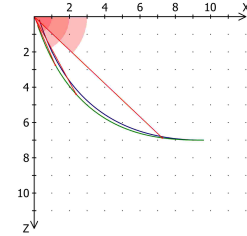
- The recommended settings for programming the **transversal condylar inclination** (TCI, also referred to as "Bennett") on the articulator.

	Right			Left		
	3rd mm	5th mm	10th mm	3rd mm	5th mm	10th mm
WHITE	●13°	●11°	●8°	●0°	●0°	●0°
YELLOW	0°	0°	0°	0°	0°	0°
RED	0°	0°	0°	0°	0°	0°
BLUE	0°	0°	0°	0°	0°	0°

Please note that the different types of articulators provide a varying degree of adjustability, meaning that the number of tables as well as their content is dependent on the selected type of articulator. Most articulators are adjustable at least in regards to the inclination of the sagittal and transversal condylar guidance. Some fully-adjustable articulators, such as the Reference SL, additionally provide multiple

inserts for adapting the shape of the condylar guidance path to the patient's actual movement. Further, some articulators allow programming the immediate side shift of the Bennett movement (ISS; refer to chapter "Immediate side shift (ISS)"<sup>[301]</sup>). The ISS threshold used for this purpose can be configured in the calculation options.

All settings are calculated starting at the origin of the coordinate system and up to the **3rd**, **5th**, and **10th** millimeter of condylography excursion. Depending on which part of the movement is to be reproduced in the articulator, the condylar elements have to be programmed with the appropriate values. This is especially important for the wax-up procedure, as a condylography curve's initial curvature can differ significantly from its entire curvature and an incorrect setting can therefore lead to entirely different movement paths of the dental cusps.

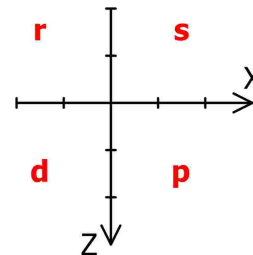


If multiple inserts for altering the shape of the condylar path are available for selection, the application will calculate the settings for each of them and indicate the best-fitting insert using bold font and a prefixed dot, for example: **•67°**. All displayed angle values are generally limited to the mechanical adjustment range of the selected articulator.


### 6.5.10.2.1 Retrusion direction

Depending on the quadrant of the coordinate system in which a retrusion movement takes place, the following designations are used:

- **r** A **retrusive** movement in the posterior, upper quadrant (- X/- Z).
- **s** A **surtrusive** movement in the anterior, upper quadrant (+X/- Z).
- **d** A **detrusive** movement in the posterior, lower quadrant (- X/+Z).
- **p** A **protrusive** movement in the anterior, lower quadrant (+X/+Z).



The designations for the four quadrants of the coordinate system in a retrusion movement, illustrated for the right patient side.

 Refer to chapter "The reference coordinate system"<sup>[299]</sup> for a detailed description of the coordinate system used by the software.

### 6.5.10.3 Incisal table settings

The intended purpose of setting the incisal table is to provide a guiding surface that forces the movement path of a mandibular dental cusp into a specific inclination relative to the axis-orbital plane. Subsequently, the appropriate guiding surface can be waxed-up on the maxillary antagonist tooth in order to realize the occlusion concept specified in the calculation options (refer to chapter "Configuring the incisal table calculation"<sup>[150]</sup>).

By selecting a data set of mandibular cusp tips coordinates on the *Contents* pane, these coordinates can be incorporated in the calculation of incisal table settings (refer to chapter "Selecting cusp tips for articulator calculation<sup>[136]</sup>"). When selected, the coordinates will appear in the tabular view of the articulator settings.

**Coordinates of cusp tips**

	Right			Left		
	X	Y	Z	X	Y	Z
1	79.85	2.26	50.88	79.74	3.15	50.68
2	79.25	7.60	50.54	78.40	8.33	50.26
3	75.58	12.63	49.88	74.50	12.98	49.40
4	70.06	16.68	48.47	68.56	16.08	48.42
5	64.33	19.37	47.47	61.73	16.60	47.61
6m	58.08	21.74	47.10	54.61	18.08	46.60
6d	54.28	23.26	45.94	50.96	18.85	45.66
7m	49.06	25.78	44.92	45.70	21.04	44.90
7d	44.98	26.86	43.03	41.62	22.66	43.26
8m	40.00	27.44	40.59	36.80	23.02	40.83
8d	36.08	29.41	39.29	33.25	24.18	39.08

Calculation of incisal table settings furthermore considers the patient's individual sagittal and transversal condylar inclination. The excursion distance, at which these angles are measured on the condylography curve can be configured in the calculation options (refer to chapter "Configuring the incisal table calculation<sup>[150]</sup>").

**6.5.10.3.1 Sequence incisal table settings**

The Sequence incisal table (order number 04-000013) is an accessory part for the Reference SL articulator, which allows for a convenient adjustment of the protrusive and mediotrusive guidance inclinations. The flexible concept of exchangeable inserts makes it easy to wax-up the desired occlusion concept while taking into consideration the patient's individual condylar inclination. The basis is always the natural morphological sequence in the human masticatory organ.

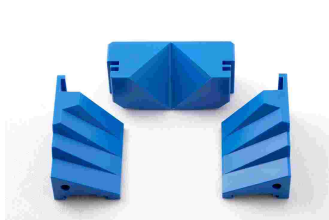


**Gamma Sequence Incisal Table**  
 Condylography values used for calculations  
 Protrusion at 5 mm: SCI 57.4°  
 Mediotrusion right at 5 mm: SCI 63.7° TCI 14.5°  
 Mediotrusion left at 5 mm: SCI 52.9° TCI -2.7°  
 Suggested sequence table setting  
 Protrusion element: ORANGE(YELLOW)  
 Right lateral element: ORANGE(YELLOW)  
 Left lateral element: ORANGE(YELLOW)

The articulator settings view displays the recommended settings for the Sequence incisal table as well as the condylar inclinations used for their calculation below the condylar settings. The Sequence incisal table settings are provided in both the graphical and in the tabular view.

The differently-colored guidance elements can be combined as needed and possess the following inclinations to the axis-orbital plane:

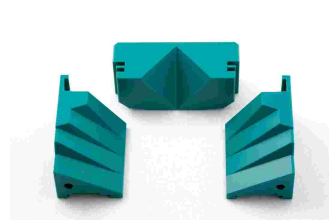
**Blue guidance elements**



- Protrusive: 46°
- Tooth 3: 51°
- Tooth 4: 41°
- Tooth 5: 33°
- Tooth 6: 25°

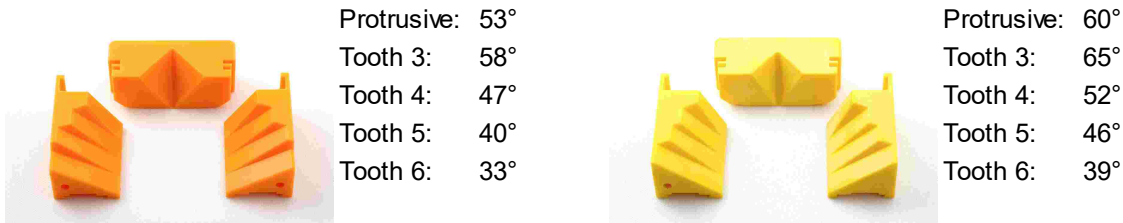
**Orange guidance elements**

**Green guidance elements**



- Protrusive: 49°
- Tooth 3: 55°
- Tooth 4: 44°
- Tooth 5: 37°
- Tooth 6: 29°

**Yellow guidance elements**



**i** The yellow guidance elements are not part of the standard set and can be purchased separately (order number 04-000013Y). If this color allows for the best possible reproduction of the calculated guidance track, it will be denoted in brackets.

The recommended protrusive guidance inclination of the Sequence incisal table is calculated from the cusp tips coordinates of the two central mandibular incisors. The mediotrusive guidance sequence is calculated based on the canine coordinates of the respective patient side.

If no data set of measured cusp tips coordinates has been selected, the following empirically determined coordinates will be used for the incisors:

- X: 70.5 mm
- Y: 0.0 mm
- Z: 48.0 mm

The default coordinates used for the canines are as follows:

- X: 66.0 mm
- Y: 13.5 mm
- Z: 50.0 mm

### 6.5.10.3.2 Individual incisal table settings

Rather than using the predefined sequence of lateral guidance inclinations provided by the Sequence incisal table, it is also possible to have these inclinations calculated for each tooth individually. This enables you to realize your occlusion concept of choice by waxing-up the appropriate guiding surfaces in the articulator.

**i** Please note that the tables depicted below are only shown when the articulator settings are displayed in tabular form (refer to "Selecting an articulator type<sub>149</sub>"). and cusp tips coordinates have been selected for articulator calculation (refer to "Selecting cusp tips for articulator calculation<sub>136</sub>").

For freely adjusting the inclination angles in the Reference SL articulator, you will need the anterior guidance unit with double-pin (order number 06-231750), which provides individually adjustable inserts for the protrusive and mediotrusive right and left guidance angles.



The condylar inclination values as well as the occlusion concept and anterior guidance angle used for the calculation of the incisal table settings are part of the articulator settings for documentation purposes.

The following table shows the guidance angles calculated for the cusp tips of the lower jaw as well as the incisal table setting that allow reproduction of those angles in the articulator.

#### Condylography values used for calculations

Protrusion at 5 mm: SCI 57.4°  
 Mediotrusion right at 5 mm: SCI 63.7° TCI 14.5°  
 Mediotrusion left at 5 mm: SCI 52.9° TCI -2.7°  
 Calculation for incisal table settings: Sequential disocclusion according to R. Slavicek  
 Computed using ideal anterior guidance

	Calculated vertical cusp tip positions							
	Right				Left			
	TA	I-Table	T-S1	T-S2	TA	I-Table	T-S1	T-S2
1	57.0°	57°	45°	65°	57.0°	57°	45°	65°
2	57.0°	57°	45°	65°	57.0°	57°	45°	65°
3	47.0°	65°			47.0°	64°		
4	34.6°	52°			34.6°	52°		
5	27.6°	44°			27.6°	44°		
6m	21.5°	35°			21.5°	35°		
6d	19.9°	33°			19.9°	33°		
7m								
7d								
8m								
8d								

The same values are calculated for the "ideal" cusp tips coordinates, which result from vertically projecting the cusp tips onto the curve of Spee. Following the definition by Orthlieb J.D., this curve is calculated based on the perpendicular distance between occlusal plane and hinge axis ("DPO").

	Ideal cusp tip positions (curve of Spee)							
	Right				Left			
	TA	I-Table	T-S1	T-S2	TA	I-Table	T-S1	T-S2
1	57.0°	57°	45°	65°	57.0°	57°	45°	66°
2	57.0°	57°	45°	65°	57.0°	57°	45°	66°
3	47.0°	65°			47.0°	64°		
4	34.6°	52°			34.6°	52°		
5	27.6°	44°			27.6°	44°		
6m	21.5°	35°			21.5°	35°		
6d	19.9°	33°			19.9°	33°		
7m								
7d								
8m								
8d								

The following column titles are used in both tables:

- Tooth** The nominal tooth angle calculated for the respective mandibular cusp tip, relative to the axis-orbital plane. For measuring the inclination of incisors 1 and 2, the movement track is projected onto the median-sagittal plane. For all other teeth, the inclination is measured directly on the appropriate plane in three-dimensional space. The angles specified here can be realized by waxing-up the corresponding guiding surface on the maxillary antagonist tooth.
- Table** The angle to which to set the incisal table in order to guide the mandibular cusp with the inclination given as "Tooth", relative to the axis-orbital plane. Thus, by setting this angle, the cusp will move along the line "s" between functional points 1 and 2 (refer to chapter "Occlusion concepts" <sup>151</sup>).
- T - S1 and T - S2** The angle to which to set the incisal table in order to guide the mandibular cusp along the flatter section "s1" or the steeper section "s2" of the incisors' lingual surfaces, respectively. These values are not provided for the other teeth.

### 6.5.10.4 Occlusal plane analysis

Lastly, the articulator settings also include analysis values for the lower occlusal plane.

**i** Please note that the tables depicted below are only shown when the articulator settings are displayed in tabular form (refer to "Selecting an articulator type<sup>[149]</sup>") and cusp tips coordinates have been selected for articulator calculation (refer to "Selecting cusp tips for articulator calculation<sup>[136]</sup>").

This includes the perpendicular distance between occlusal plane and right or left hinge axis point, respectively ("DPO"), as well as the radius of the curve of Spee according to the definition by Orthlieb J.D. That curve is also used for calculating the ideal cusp tip coordinates (refer to chapter "Individual incisal table settings<sup>[156]</sup>").

**Occlusal Plane Value**

DPO ( hinge axis to plane of occlusion )	Right	35	mm
	Left	37	mm
Radius of the curve of Spee ( Orthlieb )	Right	84	mm
	Left	82	mm

The second table shows the calculated angle differences between the patient's average sagittal condylar inclination and the cusp inclinations 20°, 25°, and 30°, for several predefined occlusion concepts.

**Occlusal plane adjustment for average SCI value: 57° (5 mm)**

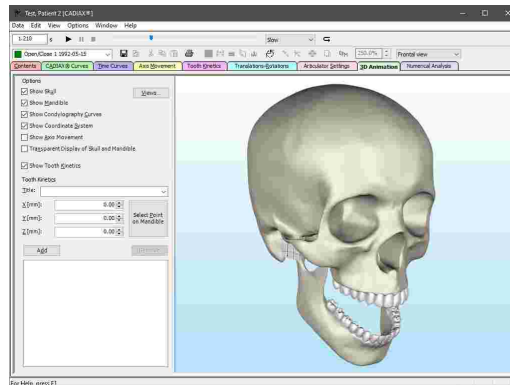
	Cuspal Angle	20°	25°	30°
Balanced Occlusion 1/6		37°	32°	27°
Balanced Occlusion 1/7		46°	41°	36°
Canine protected Occlusion 1/6		28°	23°	18°
Canine protected Occlusion 1/7		37°	32°	27°

### 6.5.11 3D animation

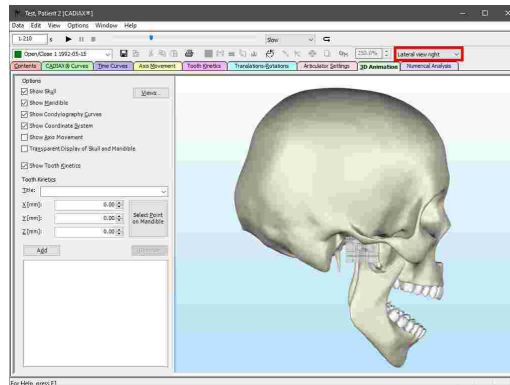
The *3D animation* view allows the visualization of a condylography movement using a virtual patient skull. This view is especially useful for comprehending a movement in its anatomical context and for presenting those interactions to the patient.

Use the left and right mouse buttons and the mouse wheel to navigate within the 3D environment. You can move the view by pressing and holding the left mouse button, rotate it with the right mouse button, and zoom in and out by scrolling with the mouse wheel.

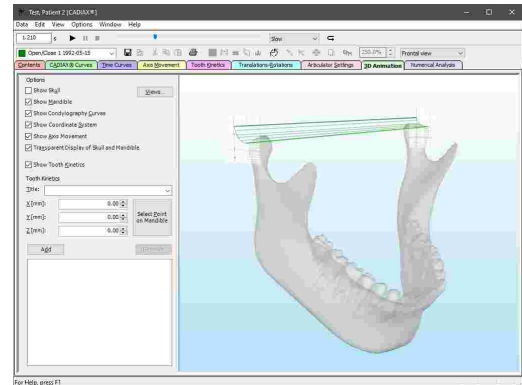
The side bar on the left window border provides further possibilities of interaction with the 3D environment.



To switch to a predefined view from the front, right, left, or top, use the combo box in the toolbar. This combo box will also provide the custom views defined as described in chapter "Defining a custom view<sup>[160]</sup>".



Using the side bar, you can toggle the visibility of the individual elements in the 3D environment, such as the model of the cranium or the display of axis movements.



**i** The replay bar allows you to animate the movement of a displayed condylography curve in real-time (refer to chapter "Replaying a condylography recording" <sup>138</sup>).

**!** The patient skull visualized in this view is only representative for the anatomy of the actual patient and may differ from it significantly. If you intend to analyze the patient-individual occlusion, consider using the CADIAS 3D module instead (refer to chapter "CADIAS 3D" <sup>235</sup>).

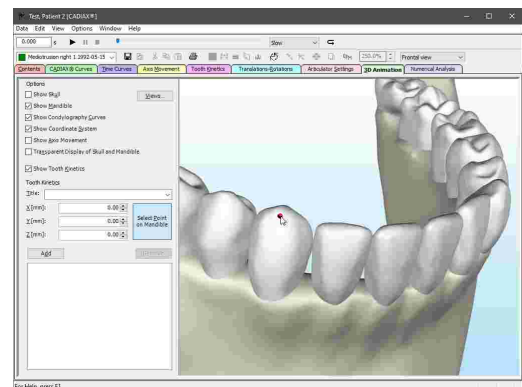
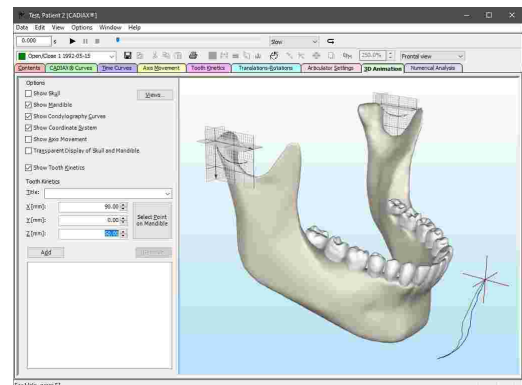
### 6.5.11.1 Displaying tooth kinetics

By specifying tooth kinetics, you can have a condylography movement be recalculated to a particular point in the coordinate system. For example, this can be used to trace the movement paths of a lower tooth's cusp tip.

The side provides the possibility to enter a title and the coordinates of a tooth position for this purpose. While you enter the coordinates, the corresponding tooth kinetics curve will be displayed in the 3D environment.

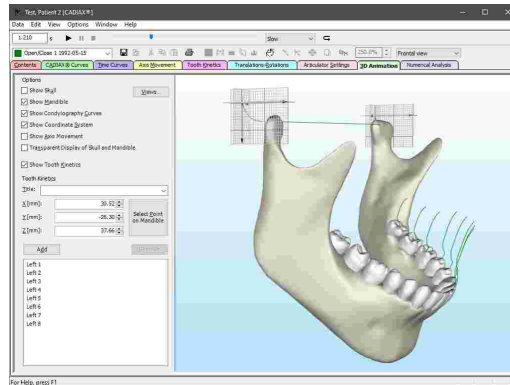
By selecting a predefined title, you can apply the default coordinates of a particular tooth position. If you have entered patient-individual cusp tips coordinates and selected them as active (refer to chapters "Entering cusp tips coordinates" <sup>134</sup> and "Selecting data for articulator calculation" <sup>136</sup>, respectively), those coordinates will be used instead.

Using the button next to the coordinate input, you can select any point on the 3D model of the mandible, of which the coordinates will be filled in automatically.



To have the tooth kinetics curve of the specified position be displayed permanently, press the button *Add*. The position will be added to the list and will persist even after you restart the application.

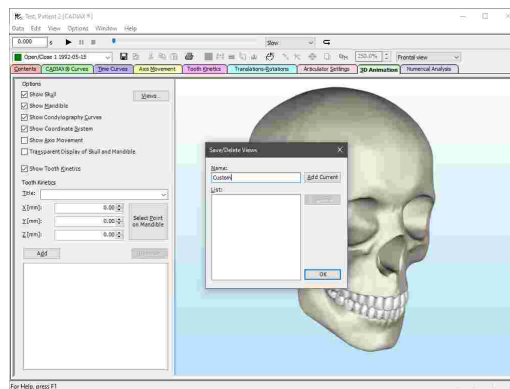
To rename a tooth position, select the entry in the list and click it a second time with the left mouse button. You can remove a saved tooth position using the button *Remove*.



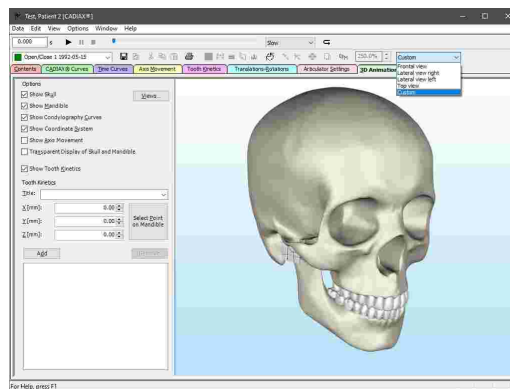
**!** Tooth kinetics can only be calculated for curves that contain the rotational component in addition to the condylar offsets along the X, Y, and Z-axes. Such recordings can only be made with the devices CADIAX 4 or CADIAX diagnostic and are carried out with CADIAX Recorder as the recording application (refer to chapter "CADIAX Recorder<sup>118</sup>").

### 6.5.11.2 Defining a custom view

Using the button *Views* in the side bar, you can save the current view of the 3D environment for later use. Enter the name under which to save the view in the dialog that appears and press *Add current*.



Subsequently, you will be able to select the custom view via the combo box in the toolbar that also allows you to switch to one of the system-defined views.

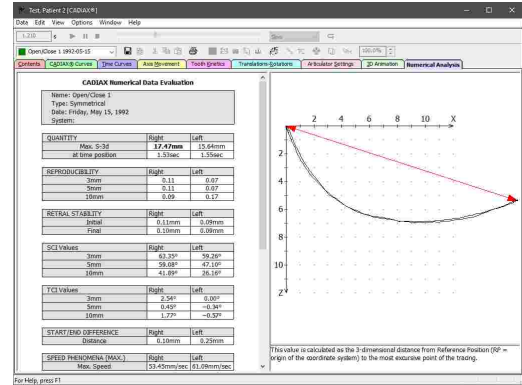


### 6.5.12 Numerical analysis

The *Numerical Analysis* pane you can find various numerical parameters calculated from the active condylography curve. This includes the maximum excursion distance, the stability of the joint position in the initial and final phase of the movement, symmetry values for comparing right and left patient side, and many more.

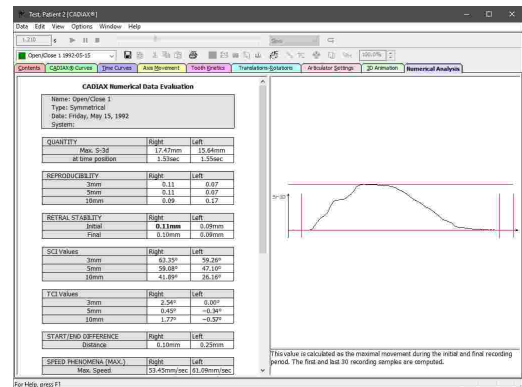
On its left half, this pane displays the numerical analysis parameters for right and left patient side in tabular form. If you selected multiple curves on the *Contents* pane and have overlay mode activated, the tables of the individual curves will be displayed below one another (refer to chapter "Overlay mode" <sup>163</sup>).

Please note that some values are only displayed for specific types of curves. For example, assessing the relation between translational and rotational component is only useful for open/close movements.



By selecting a value in the table, you can have the application display a graphical illustration and an explanatory description of the selected value on the right side of the window.

By default, the value currently selected is highlighted using a bold font. You can change the fonts used in this pane via the menu *Options* → *Numerical Analysis Fonts*.



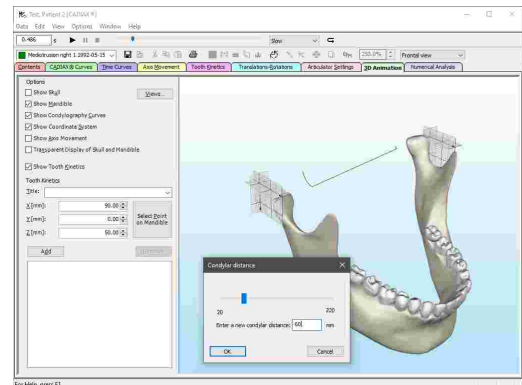
## 6.5.13 Calculation options

### 6.5.13.1 Changing the intercondylar distance

When recording mandibular movements as part of a CADIAX condylography, electronic measuring flags are mounted on the upper face bow's right and left patient side, in close proximity to the hinge axis. The distance between these two flags is referred to as **flag distance** and is obtained from the face bow parameters that are entered before the recording.

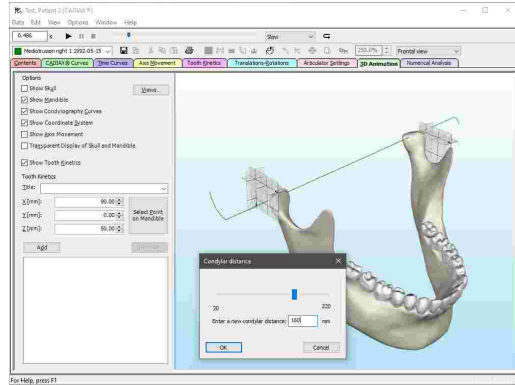
It must be noted that the stylus movements on the measuring flags do not exactly correspond to the movements of the anatomical condyles, but rather to their outward projection. The differences between the two are most obvious with unilateral mediotrusion movements. For this reason, it is not possible to transfer the recorded movements into the mechanical articulator without recalculating them to the distance of the condylar joints therein (**intercondylar distance**).

By default, all condylography recordings are recalculated to an articulator intercondylar distance of 110 mm. You can adjust this distance by selecting one or more recordings on the *Contents* pane and then activating the menu item *Edit* → *Change intercondylar distance* in any view.



The displayed condylography curves are automatically updated with each change to the intercondylar distance. Press *OK* to apply the entered distance and recalculate the articulator settings.

The actual intercondylar distance of a recording is given in the list of data objects in the *Contents* pane (refer to chapter "Columns in the list of data items" [127]).



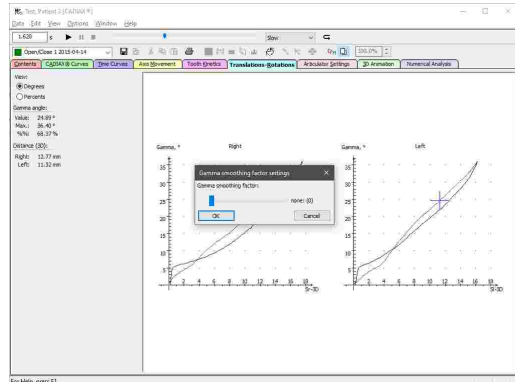
### 6.5.13.2 Gamma smoothing factor

When recording condylography using the devices CADIAX 4 or CADIAX diagnostic, the system is able to measure the rotational component of the mandible, referred to as "Gamma". This value is obtained based on the positions of the two styli on the conductive flag surface, which can only be measured with a certain resolution. This in combination with external influences onto the measurement system can induce minor positional variations in the realm of few hundredths of a millimeter. Small as they are, these variations become obvious in the rotational component, where they manifest as steps or peaks. For example, a positional variation of 0.1 mm over a distance of 10 mm can already result in an angular deviation of 0.5°.

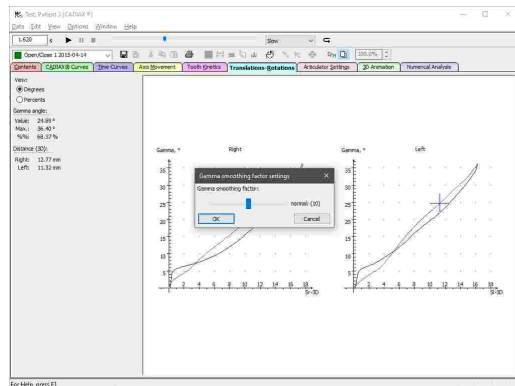
For this reason, CADIAX Analyzer provides the possibility to specify a smoothing factor that is applied to all Gamma rotation values displayed in the application. Its influence is especially prominent in the *Translations-Rotations* view, *Tooth kinetics* as well as in the *3D animation*.

Using the menu *Options* → *Gamma smoothing factor*, you can open the dialog for specifying the factor to be used by the application.

The smoothing is implemented as a moving average with the number of iterations specified in this dialog. More iterations mean a stronger smoothing of the rotation values. By default, this value is set to 10.



Specify the desired factor using the slider and confirm by pressing *OK*. You should see the rotation values adapt accordingly.



**i** Setting the Gamma smoothing factor only serves the display of the condylography curves and does not alter the persistently stored recording data.

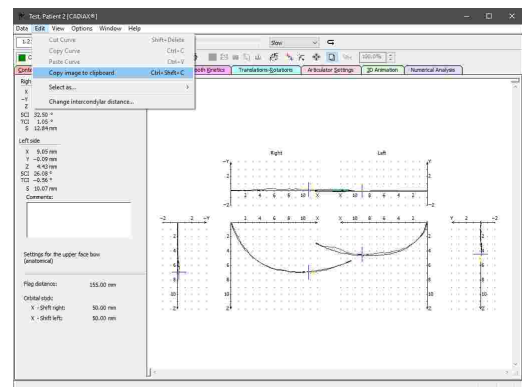
**!** The Gamma smoothing factor only has an effect on curves that contain the rotational component in addition to the condylar offsets along the X, Y, and Z-axes. Such recordings can only be made with the devices CADIAX 4 or CADIAX diagnostic and are carried out with CADIAX Recorder as the recording application (refer to chapter "CADIAX Recorder" <sup>118</sup>).

## 6.5.14 Display options

### 6.5.14.1 Copying the view to the clipboard

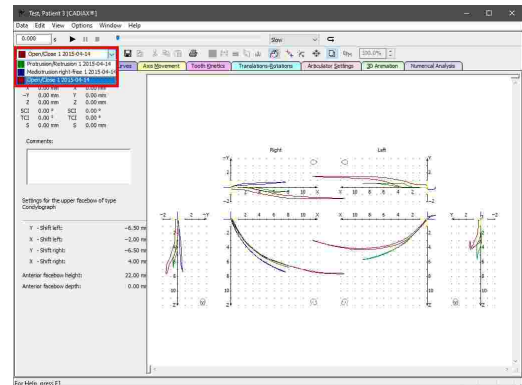
To copy the current view as an image to the clipboard, use the menu entry *Edit* → *Copy Image to Clipboard*.


You can then paste the copied image for further editing or for creating presentations into external applications such as Microsoft Paint or Microsoft PowerPoint.

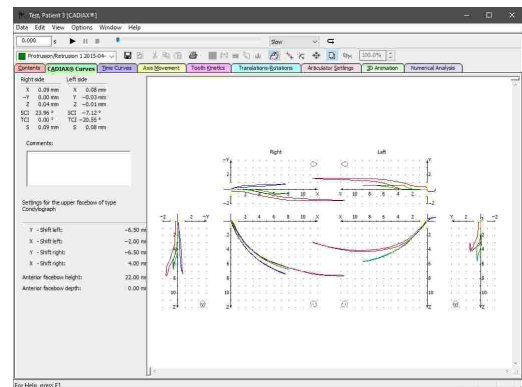



### 6.5.14.2 Overlay mode

By default, when multiple recordings are selected on the *Contents* pane, only one of them will be displayed at a time and you will have to switch between the curves using the combo box in the toolbar (refer to chapter "Selecting the active recording" <sup>138</sup>).




As an alternative, you can enable the overlay mode via the toolbar button  *Overlay mode*, which will cause all selected curves to be superimposed. When enabled, each curve will use its own distinct color to provide differentiation.

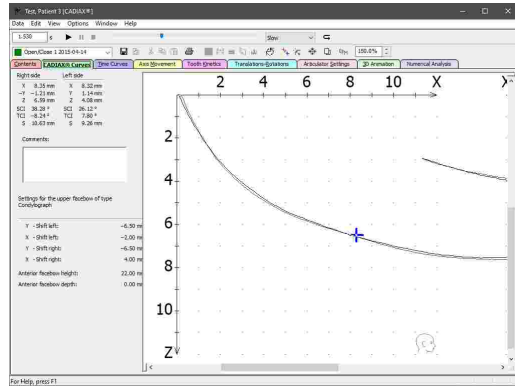


 Please note that some editing operations, such as the zero point adjustment (refer to chapter "Zero point adjustment<sup>[141]</sup>"), are only applied to the curve that is selected as active, even if overlay mode is activated.

### 6.5.14.3 Changing the zoom value

By default, the curves displayed by the application are fitted into the available display area. To display them in a fixed size instead, deactivate the option  **Zoom to fit** in the tool bar. In the now available input field, you can enter a percentage value between 10% and 250% that will subsequently be used in all views.

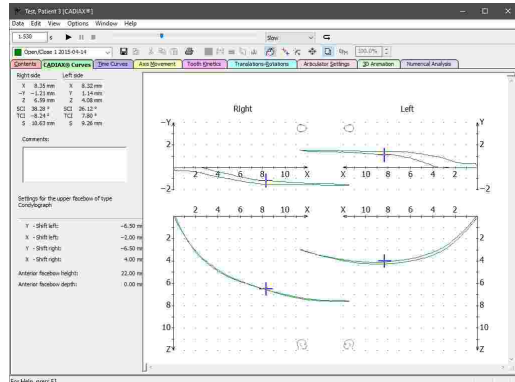
You can also access this option via the menu *View* → *Zoom settings*.



### 6.5.14.4 Coordinate system display

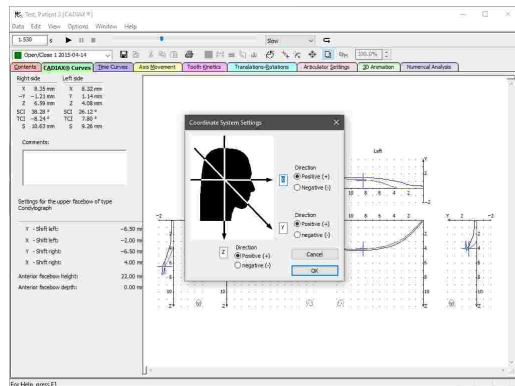
CADIAX Analyzer provides a variety of options for the display of the coordinate system. Partially, these are shared with the recording applications CADIAX Recorder and CADIAX compact 2 Recorder (refer to chapters "CADIAX Recorder<sup>[118]</sup>" and "CADIAX compact 2 Recorder<sup>[116]</sup>", respectively).

Using the menu *View* → *Extended View*, you can show or hide the complementary coordinate systems that display the frontal projection of the recorded movements.

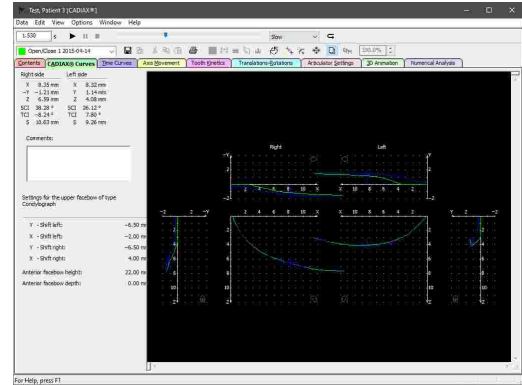


The application provides a dialog via the menu *Options* → *Coordinate System* that allows you to customize the labels (X, Y, and Z) and directions (positive or negative) of the individual coordinate system axes.

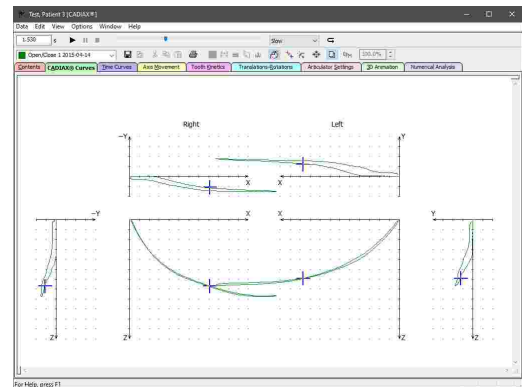
The settings specified here are also used for the display of numerical values in the left side panel.




In case of nostalgia, you can activate the darker color scheme of the DOS application via the menu *View* → *GDS/DOS Color Scheme*.



The *View* menu furthermore provides various options for showing or hiding certain elements of the user interface, such as the left side panel, the axis labels of the coordinate system, or the head pictograms illustrating the viewing direction of the individual graphs. Here, you can also find settings for changing the fonts and the pen widths used by the application.

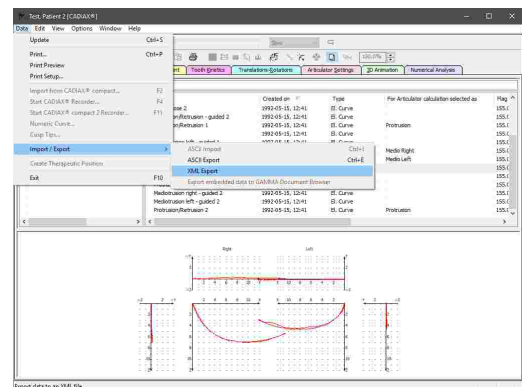


 Refer to chapter "The reference coordinate system <sup>299</sup>" for a detailed description of the coordinate system used by the software.

## 6.5.15 Export and import of data

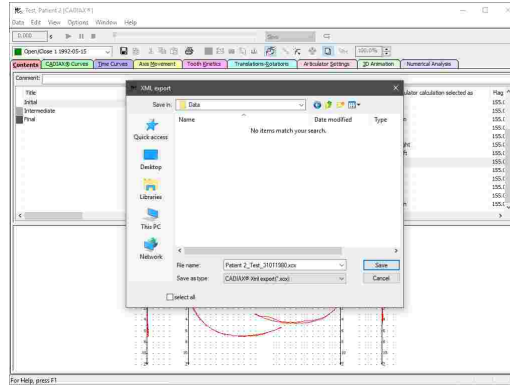
### 6.5.15.1 XML export

To export the condylographic data of the CADIAX module for custom evaluations or for processing it in third-party applications, CADIAX Analyzer provides a feature for exporting this data in the human- and machine-readable XML format. To do so, use the menu item *Data* → *Import / Export* → *XML Export*.



In the subsequent dialog, you can choose between two formats:

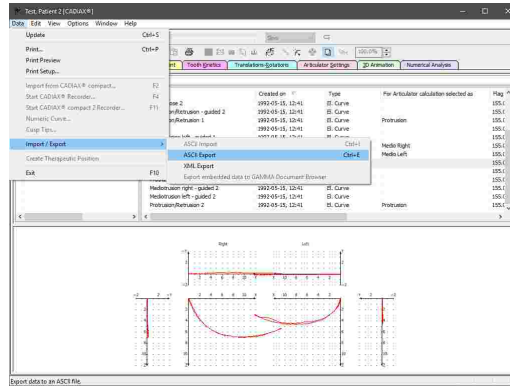
- One compatible with the Jaw Motion Import module of the popular 3D-CAD/CAM application Exocad (file extension *.jawmotion*).
- A generic XML format that supports all types of CADIAX recordings (file extension *.xcx*).



**!** The XML export for Exocad only supports protrusion, mediotrusion, and open/close movements. Exocad version 2.4 (Plowdiv) or higher as well as a license granting the use of the Jaw Motion Import module is required.

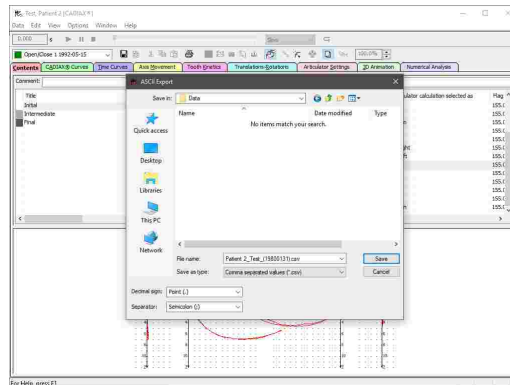
### 6.5.15.2 ASCII export

To export the condylographic data of the CADIAX module for custom evaluations, CADIAX Analyzer provides a feature for exporting this data in the human- and machine-readable CSV format ("Comma-Separated Values"). To do so, select the condylography curves to be exported in the list of data items and use the menu item *Data* → *Import / Export* → *ASCII Export*.



In the subsequent dialog, you can choose the characters to use as decimal separator and value separator. These characters must not be the same as this would lead to misinterpretation of the data during the ASCII import (refer to chapter "ASCII import" <sup>167</sup>).

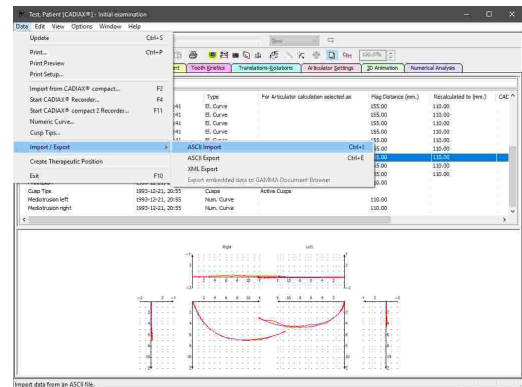
Files exported using this functionality can have the file extension *csv*, *txt*, *asc*, or *dat*.



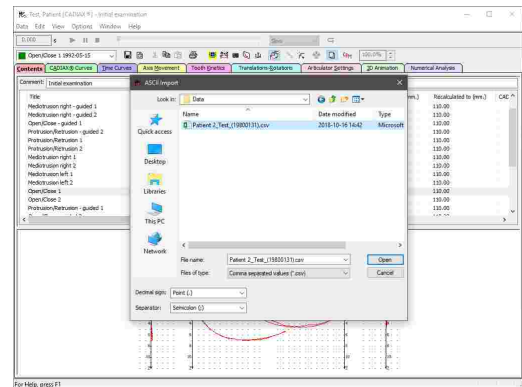
**!** The ASCII export is only possible for electronically recorded condylography curves. For exporting condyle position measurements (CPM), numeric curves, or cusp tips, you can use the XML export instead (refer to chapter "XML export" <sup>165</sup>).

### 6.5.15.3 ASCII import

To import the curves that were exported during the ASCII export (refer to chapter "ASCII export"<sup>[168]</sup>), use the menu item *Data* → *Import / Export* → *ASCII Import*.

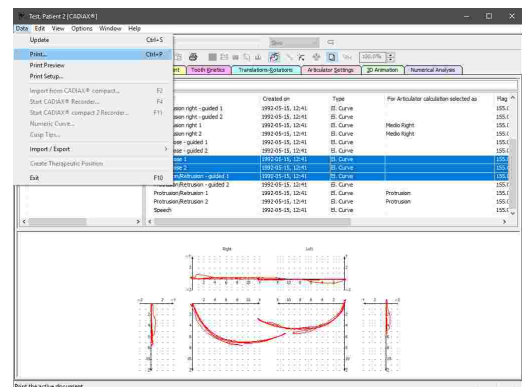


In the subsequent dialog, you can choose the characters to use as decimal separator and value separator. These characters must match those that were used during the export.

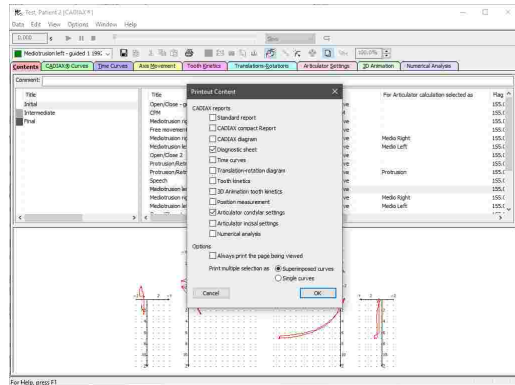


### 6.5.16 Printing

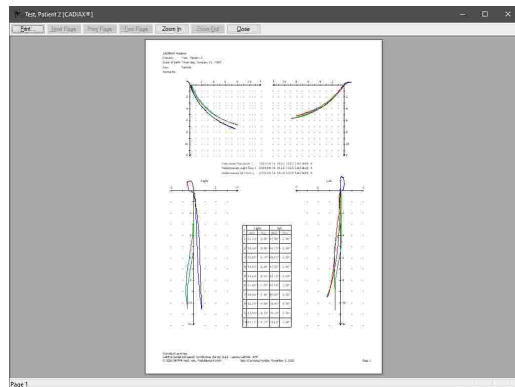
To print the selected CADIAX recordings, show a print preview, or change the page format of the printout, use the respective entries in the *Data* menu.



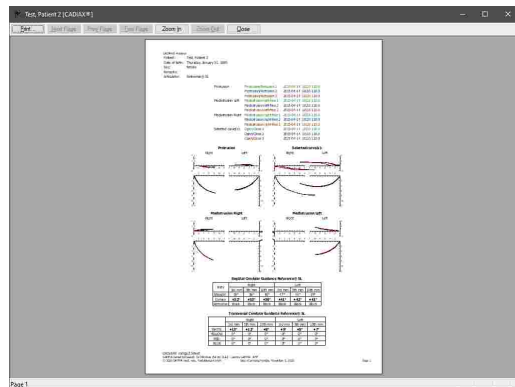
Prior to printing, you will be shown a dialog in which you can select the reports to be printed and specify other printing-related settings. The following reports are available for selection:



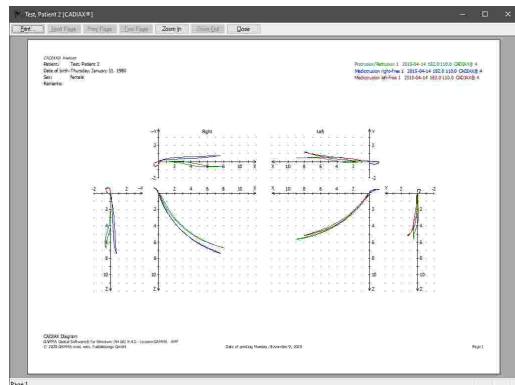
- Standard report



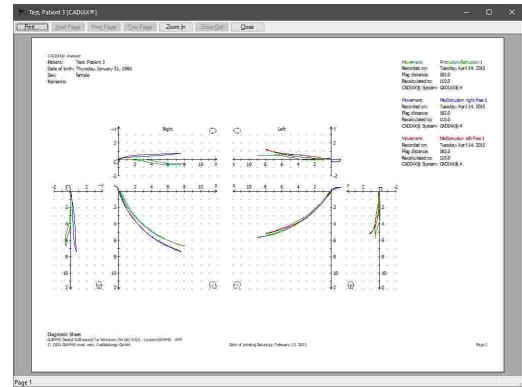
- CADIAX compact report



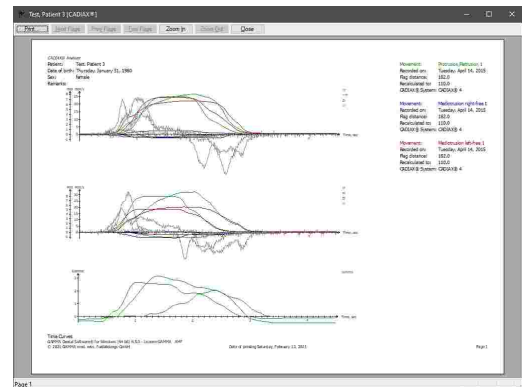
- CADIAX diagram



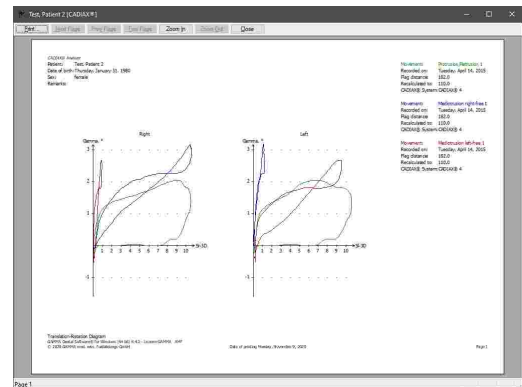
- Diagnostic sheet



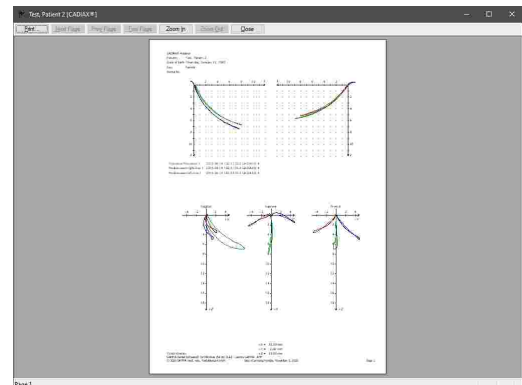
- Time curves



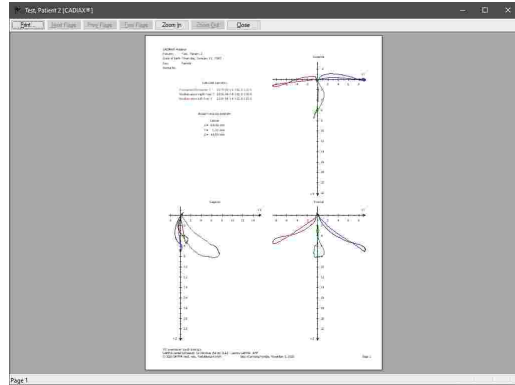
- Translation-rotation diagram



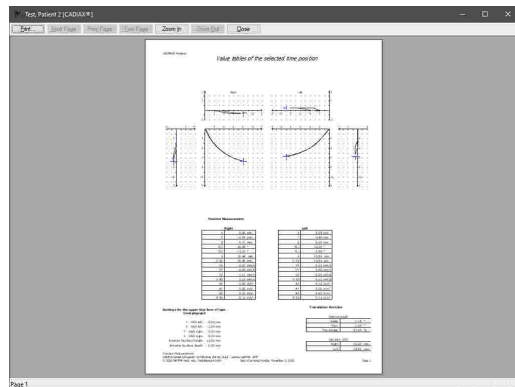
- Tooth kinetics



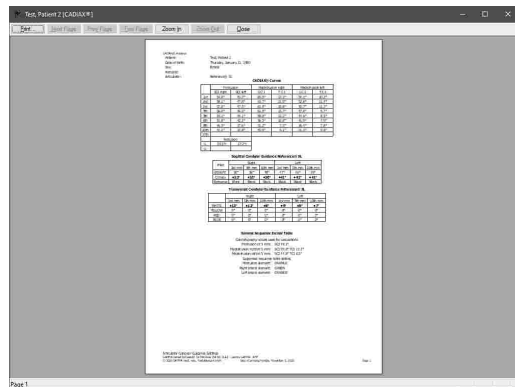
- Tooth kinetics of 3D animation



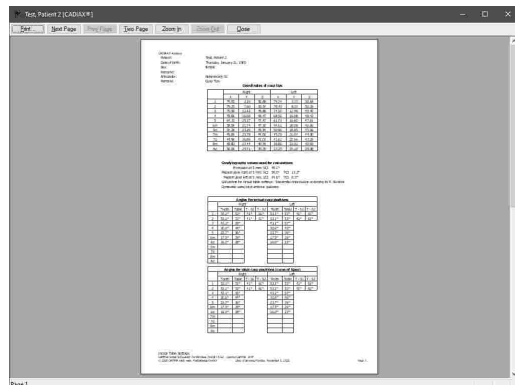
- Position measurement (measurement values for the currently selected time position)



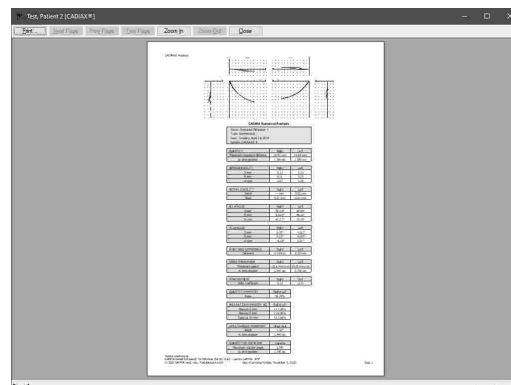
- Articulator condylar settings



- Articulator incisal settings



- Numerical analysis



## 6.6 Abbreviations of numerical values

Based on the condylography recordings, the CADIAX applications compute a multitude of numerical values, which can be useful for the detailed analysis. The abbreviations used for those values are explained below.



Refer to chapter "The reference coordinate system" <sup>299</sup> for a detailed description of the coordinate system used by the software.

The condylar shift along the **X**-, **Y**-, and **Z**-axes are given in millimeters and are relative to the origin of the coordinate system. The latter corresponds to the reference position that has been set during the condylography recording.

- **Xr** The displacement of the right condyle, measured along the X-axis (anterior/posterior). Positive values indicate an anterior movement.
- **Yr** The displacement of the right condyle, measured along the Y-axis (right/left). Positive values indicate a movement to the right.
- **Zr** The displacement of the right condyle, measured along the Z-axis (up/down). Positive values indicate a downwards movement.
- **Xl** The displacement of the left condyle, measured along the X-axis (anterior/posterior). Positive values indicate an anterior movement.
- **Yl** The displacement of the left condyle, measured along the Y-axis (right/left). Positive values indicate a movement to the right.
- **Zl** The displacement of the left condyle, measured along the Z-axis (up/down). Positive values indicate a downwards movement.



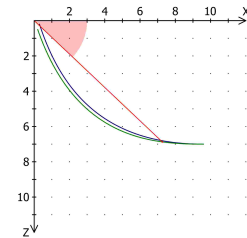
If the axis label is preceded by a minus sign, the respective coordinate value has to be interpreted as a movement opposing the direction of the axis. Furthermore, please note that the axis labels and directions can be customized (refer to chapter "Coordinate system display" <sup>164</sup>) and might therefore differ from the designations used in this chapter.

- **Gamma** The rotation angle of the mandible around the hinge axis, in degrees. Positive values indicate an opening rotation.

The distance **S** generally denotes the distance of the condyle from the reference position, in millimeter.

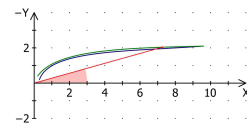
- **Sr** The excursion distance of the right condyle, measured in the X/Z-plane.
- **Sl** The excursion distance of the left condyle, measured in the X/Z-plane.
- **Sr-3D** The excursion distance of the right condyle, measured in three-dimensional space.
- **Sl-3D** The excursion distance of the left condyle, measured in three-dimensional space.

The sagittal condylar inclination (**SCI**) is measured in the sagittal plane (X/Z) and describes the angle that the condyle position encloses with the X-axis, in degrees.



- **SClr** The sagittal condylar inclination of the right condyle position.
- **SCIl** The sagittal condylar inclination of the left condyle position.

The transversal condylar inclination (**TCI**) is measured in the transversal plane (X/Y) and describes the angle that the condyle position encloses with the Y-axis, in degrees.



- **TClr** The transversal condylar inclination of the right condyle position.
- **TCIl** The transversal condylar inclination of the left condyle position.

The velocity of a condyle is denoted as **V** and has the unit millimeter per second (mm/s). This value is calculated from the distance between the current and the previous condyle position and the amount of time that has passed between the two.

- **Vr** The velocity of the right condyle at the current time position, measured in three-dimensional space.
- **Vl** The velocity of the left condyle at the current time position, measured in three-dimensional space.
- **VXr** The velocity of the right condyle at the current time position, measured along the X-axis.
- **VYr** The velocity of the right condyle at the current time position, measured along the Y-axis.
- **VZr** The velocity of the right condyle at the current time position, measured along the Z-axis.
- **VXI** The velocity of the left condyle at the current time position, measured along the X-axis.
- **VYI** The velocity of the left condyle at the current time position, measured along the Y-axis.
- **VZI** The velocity of the left condyle at the current time position, measured along the Z-axis.

The acceleration of a condyle is denoted as **A** and has the unit millimeter per second squared (mm/s<sup>2</sup>). This value describes the change in velocity between the current and the previous condyle position, taking into account the time that has passed between the two.

- **Ar** The acceleration of the right condyle at the current time position, measured in three-dimensional space.
- **Al** The acceleration of the left condyle at the current time position, measured in three-dimensional space.
- **AXr** The acceleration of the right condyle at the current time position, measured along the X-axis.

- **AYr** The acceleration of the right condyle at the current time position, measured along the Y-axis.
- **AZr** The acceleration of the right condyle at the current time position, measured along the Z-axis.
- **AXl** The acceleration of the left condyle at the current time position, measured along the X-axis.
- **AYl** The acceleration of the left condyle at the current time position, measured along the Y-axis.
- **AZl** The acceleration of the left condyle at the current time position, measured along the Z-axis.

### 6.6.1 Condyle position measurements (CPM)

A condyle position measurement (CPM) describes the positional difference between two mandibular positions. The title of a CPM measurement is usually composed of the designators of start and end position, connected by an illustrative arrow. For example, a CPM titled "RCP -> ICP" describes the lower jaw movement from retral contact position to intercuspation. The following acronyms are commonly used, although their definition can vary depending on region and methodology:

- **RP** Reference position
- **RCP** Retral contact position
- **ICP** Intercuspal position
- **RES** Resilience of the temporomandibular joint
- **ETP** Expected therapeutic position
- **IVP** Ideal vertical position
- **FBP** Forced bite position

The measurements between the two mandibular positions are differential, as indicated by the prefix  $\Delta$  (Delta). All distance measurements are given in millimeters:

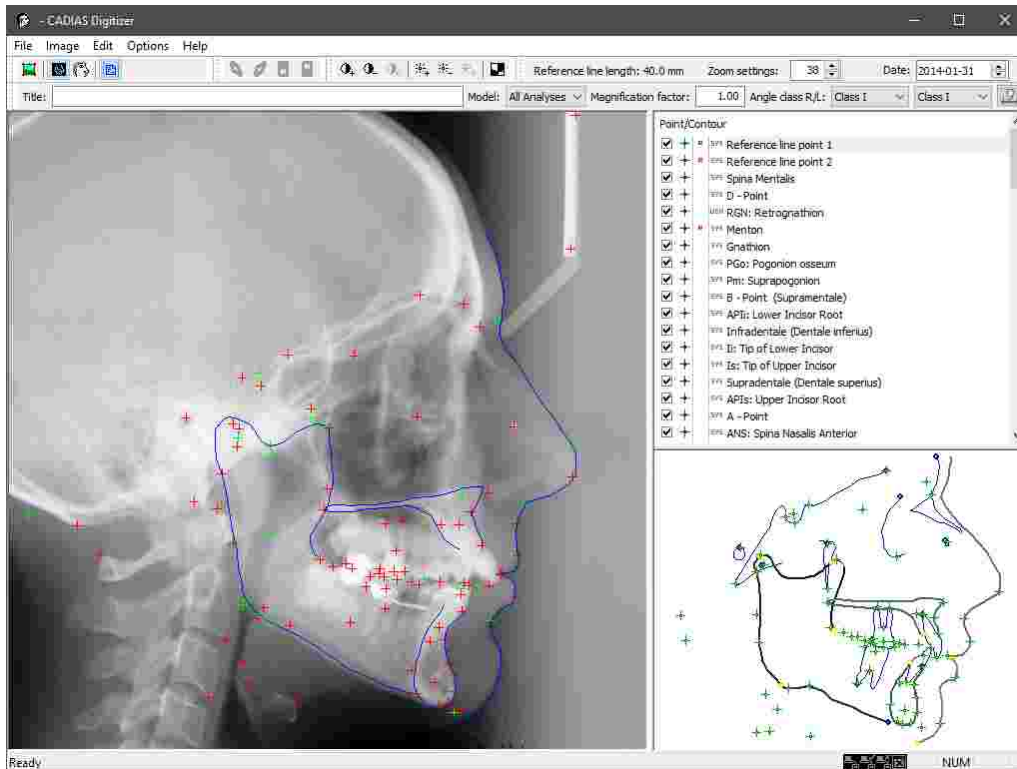
- **$\Delta Xr$**  The displacement of the right condyle, measured along the X-axis (anterior/posterior). Positive values indicate an anterior movement.
- **$\Delta Zr$**  The displacement of the right condyle, measured along the Z-axis (up/down). Positive values indicate a downwards movement.
- **$\Delta Y$**  The displacement of the right and left condyle, measured along the Y-axis (right/left). Positive values indicate a movement to the right. Due to the rigidity of the mandible, lateral shift is given by a single value rather than separate values for right and left side.
- **$\Delta Xl$**  The displacement of the left condyle, measured along the X-axis (anterior/posterior). Positive values indicate an anterior movement.
- **$\Delta Zl$**  The displacement of the left condyle, measured along the Z-axis (up/down). Positive values indicate a downwards movement.
- **$\Delta H$**  The change to the height of the articulator's incisal pin that results from the movement from first to second position. Positive values indicate a raise of the incisal pin.
- **$\Delta W$**  The side shift of the articulator's incisal pin. Positive values indicate a movement to the left patient side.

- **$\Delta L$**  The anterior or posterior shift of the articulator's incisal pin. Positive values indicate an anterior movement.
- ***Gamma*** The amount of hinge axis rotation between the two positions, in degrees. Positive values indicate an opening rotation.



## 7.1 CADIAS Digitizer

CADIAS Digitizer is the application for digitizing anatomical points and contours on x-ray images and other photographs. These digitizings can then be analyzed and evaluated in the CADIAS Analyzer application (see chapter "CADIAS Analyzer [196]").

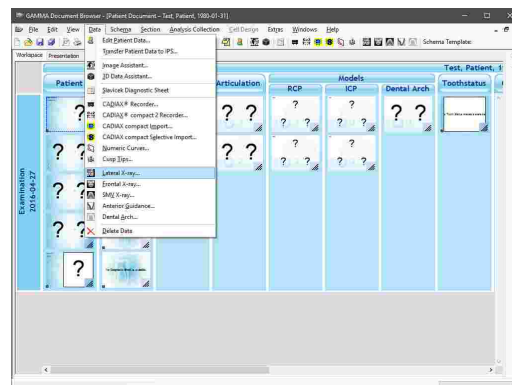



### 7.1.1 Starting the application

CADIAS Digitizer is an integral part of GAMMA Dental Software and can be started from GAMMA Document Browser as well as from GDSW classic:

- To create a new CADIAS digitizing in GAMMA Document Browser, use one of the following entries in the *Data* menu:
  - Lateral x-ray
  - Frontal x-ray
  - SMV x-ray
  - Anterior guidance
  - Dental arch

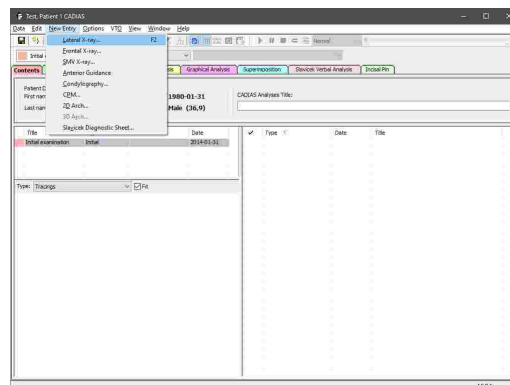
Please refer to chapter "Inserting CADIAS x-ray data [77]" for more information.



- In GDSW classic, you will first have to start CADIAS Analyzer via the button  CADIAS operations in the toolbar. Subsequently, you can create a new digitizing via one of the following entries in the *New Entry* menu:

- Lateral X-ray
- Frontal X-ray
- SMV X-ray
- Anterior guidance
- Condylography
- Dental arch

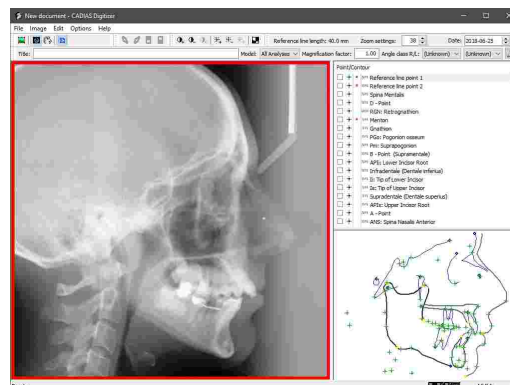
Please refer to chapter "Inserting CADIAS x-ray data<sup>104</sup>" for more information.



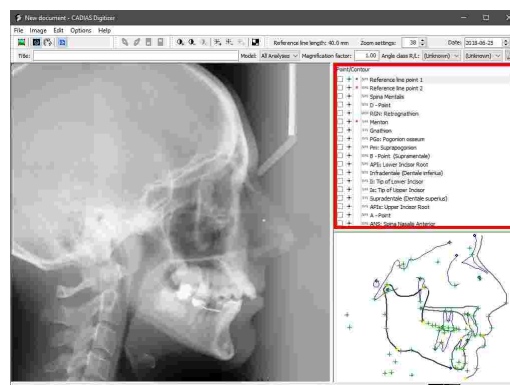
### 7.1.2 User interface

The user interface of CADIAS Digitizer can be separated into the following three areas:

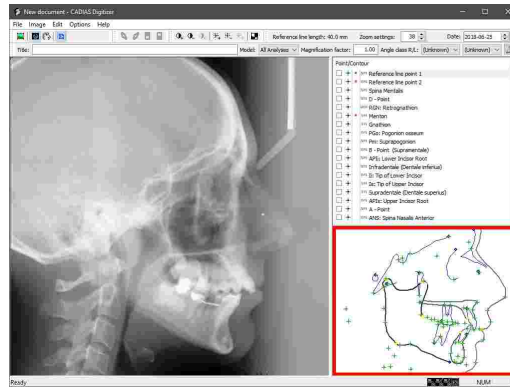
- The **working area** with the image to be digitized and the already marked points and contours.



- The list of anatomical point and contour **landmarks** to be marked on the image.




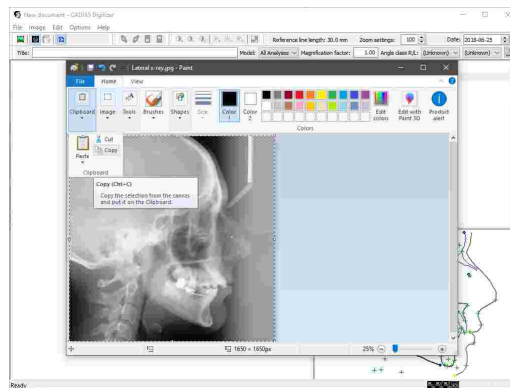
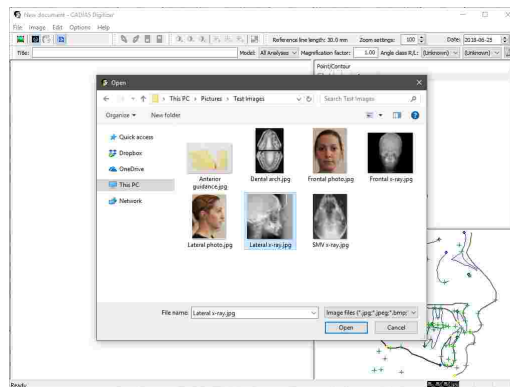
- The **preview area** that highlights the approximate location of the currently selected point or contour.



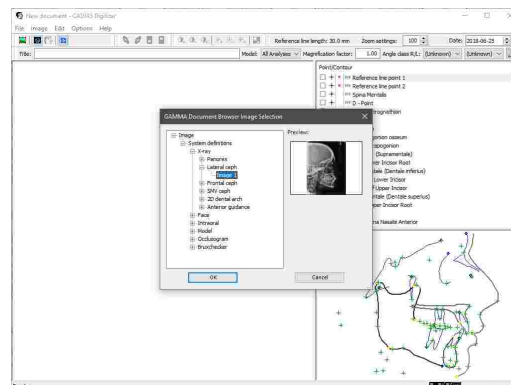
### 7.1.3 Loading an image

To load the image to be digitized into CADIAS Digitizer, the application provides the following options in the menu *Image*:

- From an image file on your PC or a network location. Alternatively, you can use the button  *Load a picture* in the toolbar or simply drag and drop the file from your file explorer onto the application window.
- From the clipboard, after you have copied the image data in a graphics application.



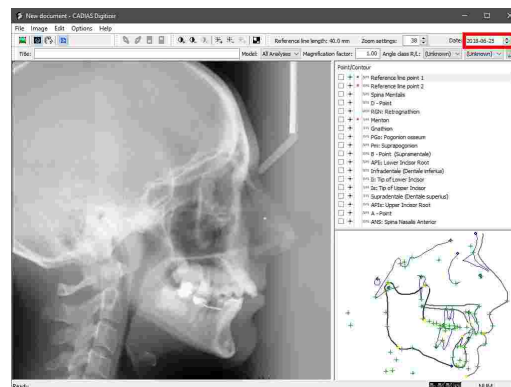
- If CADIAS Digitizer has been started from GAMMA Document Browser, from the patient database therein. If the correct image type has been assigned during the image import in the database, the appropriate image will appear automatically as soon as CADIAS Digitizer is started (refer to chapter "Importing images").



**!** To allow for accurate identification of anatomical landmarks, images imported in CADIAS Digitizer are required to have a pixel density of at least 150 pixel per inch (equates to roughly 59 pixel per centimeter).

### 7.1.4 Entering a date

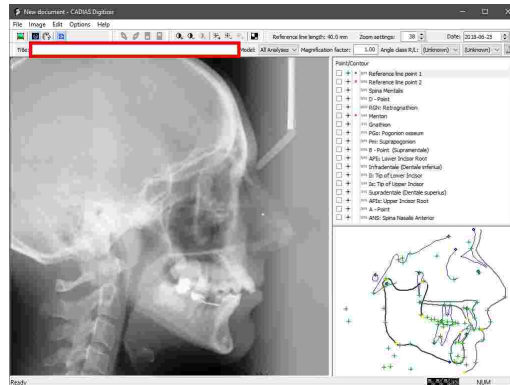
You can enter the date of the digitizing via the input box in the toolbar. For x-ray images of the patient, this should be the date when the image was taken. For images of the dental model, which are used for digitizing the anterior guidance or the dental arch, it should be the date of the impression.



**!** Based on the date of the digitizing and the patient's date of birth, the application calculates the patient's age at the time of the examination. The age is then used to calculate age-dependent norm values for the cephalometric analyses of CADIAS Analyzer. For this reason, it is especially important to enter the correct x-ray date for adolescent patients (between 5 and 18 years).

### 7.1.5 Entering a title

To differentiate between digitizings of the same patient, you can enter a short textual description in the tool bar of CADIAS Digitizer. This title will then be displayed in the list of data items in CADIAS Analyzer (refer to section "Contents" [197](#)).

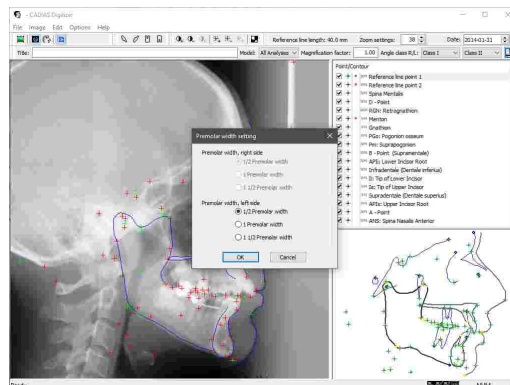
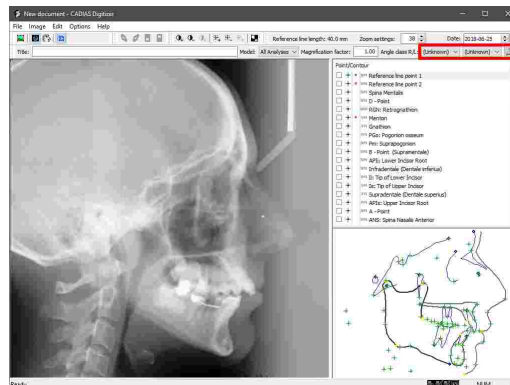


### 7.1.6 Entering the Angle class

When digitizing a lateral x-ray image, the toolbar provides additional selection boxes for the occlusal relation of upper and lower jaw. For both right and left patient side, you can select one of the following Angle classes:

- Class I (Neuroocclusion): The mesial cusp of the upper first molar occludes between the great cusps of the lower first molar.
- Class II (Distal occlusion; Overbite): The mesial cusp of the upper first molar occludes anterior of the mesial cusp of the lower first molar.
- Class III (Mesial occlusion; Underbite): The mesial cusp of the upper first molar occludes posterior to the distal cusp of the lower first molar.

If the occlusion of the right or left patient side has been identified as class II or class III, you can enter a premolar width of 1/2, 1, or 1 1/2 for the respective side by pressing the button *Premolar width* in the toolbar.




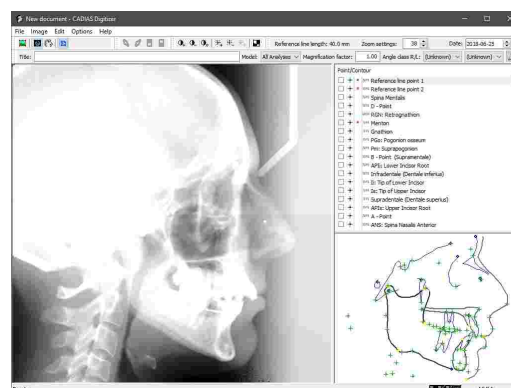
**i** The information entered here is used to calculate the dental class in CADIAS Analyzer (refer to chapter "Slavicek verbal analysis" [221](#)).


## 7.1.7 Image display settings

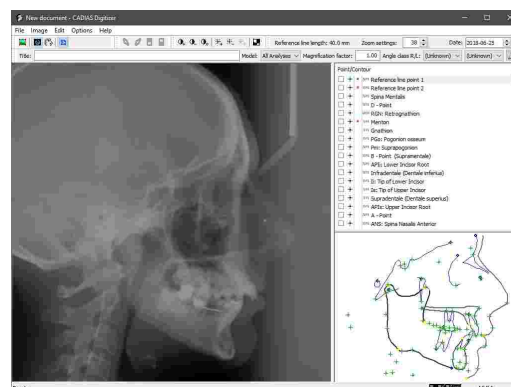
CADIAS Digitizer provides various display settings to simplify the digitizing procedure. This can be especially useful for improving the visibility of anatomical structures when digitizing x-ray images. All changes made to the appearance of the image are purely visual and do not affect the original data of the loaded image in any way.


### 7.1.7.1 Adjusting the contrast

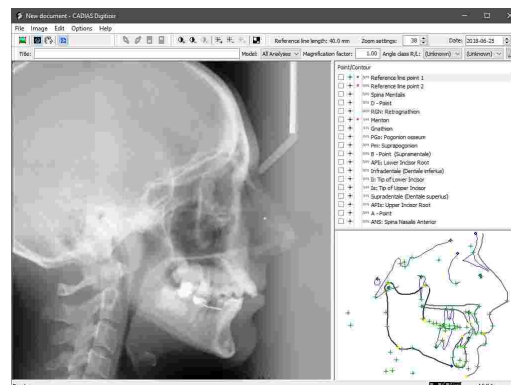
To increase the contrast, i.e. the difference in brightness between dark and light areas of the image, use the button  *Higher contrast* in the toolbar.



Using the button  *Lower contrast*, you can reduce the contrast by the same amount.




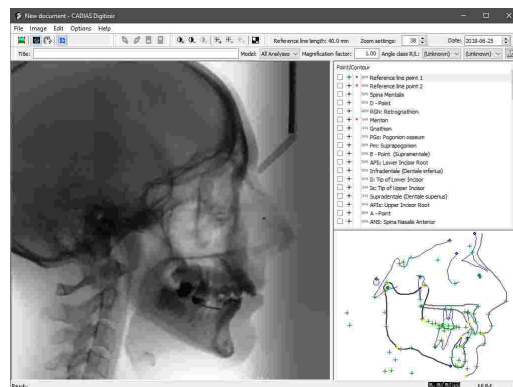
To reset the contrast to the original value, use the button  *Reset contrast to default*.



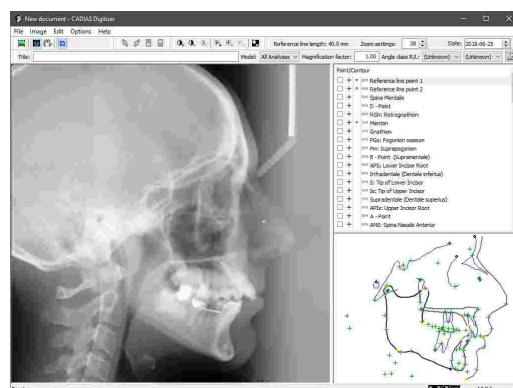


### 7.1.7.3 Inverting the image

In some cases, anatomical structures are more clearly visible when the colors of the image have been inverted. To invert the displayed image, use the button  *Invert picture* in the toolbar.

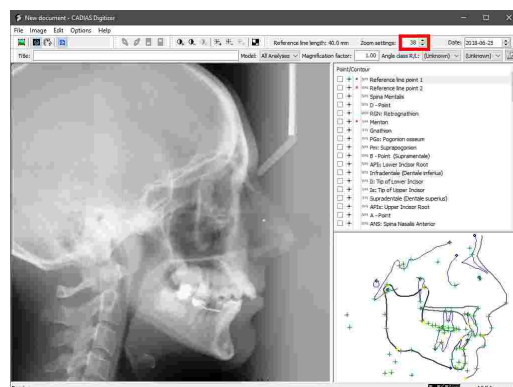


By pressing the button another time, the original colors will be restored.

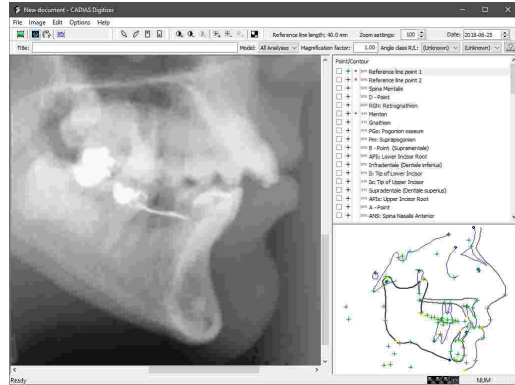



### 7.1.7.4 Adjusting the zoom value

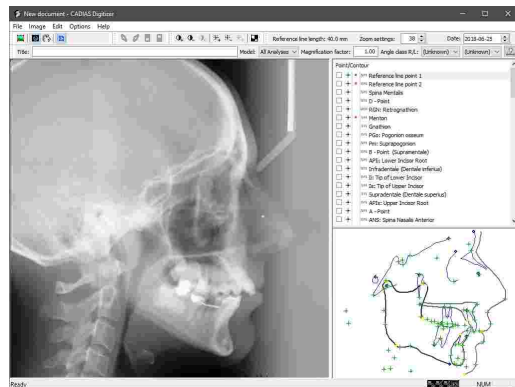
By entering a zoom value in the toolbar, you can enlarge or reduce the part of the image that is being displayed.



You can pan the display area across the image by using the scroll bars on the right and bottom border or by holding down the mouse wheel.

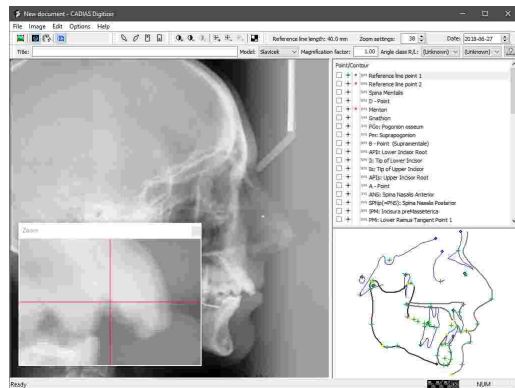


To restore the original view and fit the whole image into the available display area, use the button  *Fit/Unfit picture* in the toolbar.



### 7.1.7.5 Using the zoom window

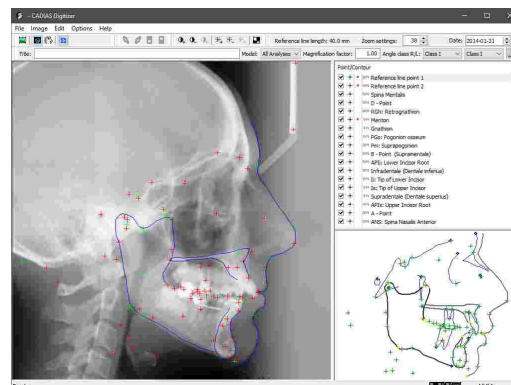
Via the menu *Options* → *Show Zoom Window* you can show a window with an enlarged view of the actual mouse cursor position.



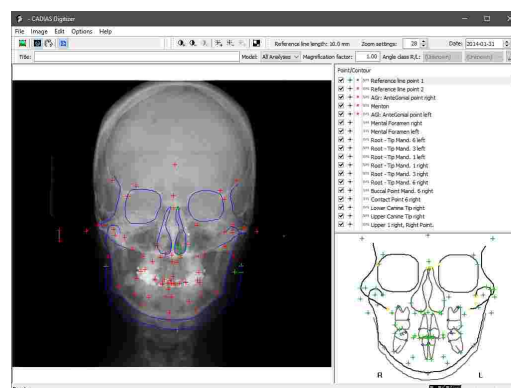
### 7.1.8 Lateral, frontal, and SMV x-ray images

CADIAS Digitizer allows digitizing x-ray images in the following projections, which will serve as the basis for subsequently creating cephalometric analyses with CADIAS Analyzer.

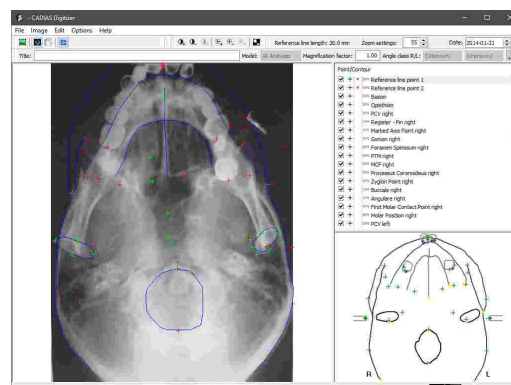
- Lateral x-rays




- Frontal x-rays



- Submentovortex x-rays (SMV, also referred to as "basal")



After having loaded the image to be digitized, you can start with digitizing the anatomical points and contours on the image. While the following chapter demonstrates the procedure based on a lateral x-ray image, the procedure for frontal and SMV x-ray images is similar. Notable differences will be described where necessary.

 For more information regarding the usage and evaluation of the digitized data, please refer to chapter "CADIAS Analyzer<sup>196</sup>".

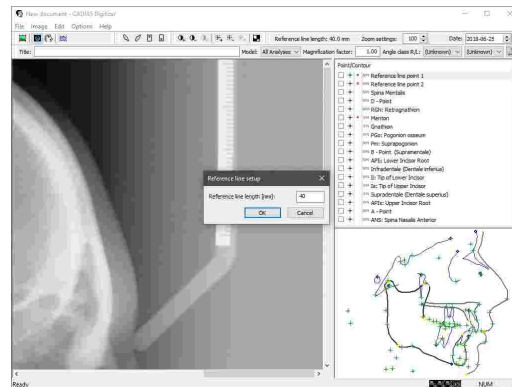
### 7.1.8.1 Entering the reference line

To carry out true-to-life distance measurements on a digital image, the points digitized on the computer screen have to be recalculated to their real distance in millimeters. This is done by digitizing the end points of a millimeter scale included in the image, here referred to as "reference line".

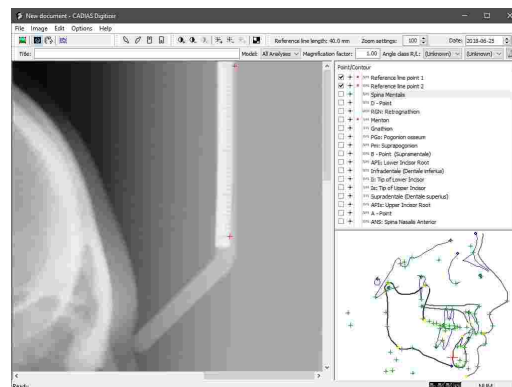
**!** For processing x-ray images in CADIAS Digitizer, it is required that the x-ray machine used for image acquisition provides a calibrated millimeter scale that is visible in the x-ray image. For digitizing photographs of an anterior guidance impression or of the dental arch, it is sufficient to include any commercially available millimeter ruler in the frame.

**!** For maximum accuracy, the reference distance should be as large as possible. The closer the reference points are on the screen, the more the pixel-to-millimeter recalculation factor will be influenced by the imprecision with which the points are digitized, which can eventually result in deviations in the cephalometric evaluations. For this reason, it is not possible to enter reference distances shorter than 10 mm.

You can enter the length of the millimeter scale in the x-ray image via the menu *Options* → *Reference Line Length*. This setting only has to be entered for the first digitizing of each type and will be saved for future inputs. The currently specified reference line length is displayed in the tool bar.



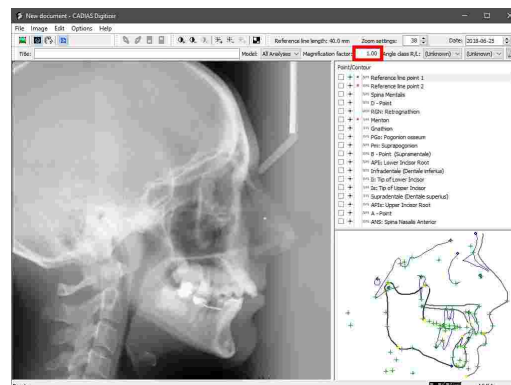
Subsequently, digitize the two reference line points at the ends of the millimeter scale.



### 7.1.8.2 Setting the magnification factor

Besides entering a reference line length, the software also allows entering an independent magnification factor. For x-ray images, this factor will cause a recalculation of proportions in the tracing to the true proportions on the patient. For example, with a magnification factor of 1.1, a distance of 10 mm on the patient corresponds to a distance of 11 mm on the x-ray image.

To enter a magnification factor, use the appropriate input box in the tool bar.



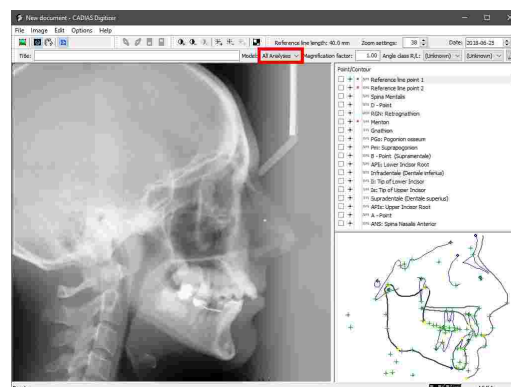
**!** When using a modern x-ray machine with integrated millimeter scale at the same distance from the image plane as the patient's median-sagittal plane, the magnification factor must always be set to 1.00. In case of doubt, please contact the manufacturer of your x-ray machine. Entering an incorrect magnification factor can compromise the correctness of the cephalometric evaluations.

**i** To determine the magnification factor for non-x-ray images, you can take a picture of an object of a known size. The result of the division of imaged size by true size is the magnification factor that has to be entered in the software. For example, if the true length of the object is 10 cm and on the image it is 11.7 cm, the magnification factor equals  $11.7 \div 10 = 1.17$ .

### 7.1.8.3 Selecting an input model


The digitizing of anatomical point and contour landmarks is always carried out in a predefined input sequence. For this purpose, the software provides multiple input models with varying amounts of data to be digitized. Depending on what analysis you would like to create from the digitizing (e.g. "Slavicek" or "Sato"), you can limit your inputs to the points and contours that are required for that particular analysis. By selecting the input model "All analyses", the software will provide all available landmarks for digitization, which will enable you to freely choose the analysis to create later on.

In CADIAS Digitizer, you can choose the input model to use via the combo box in the toolbar.

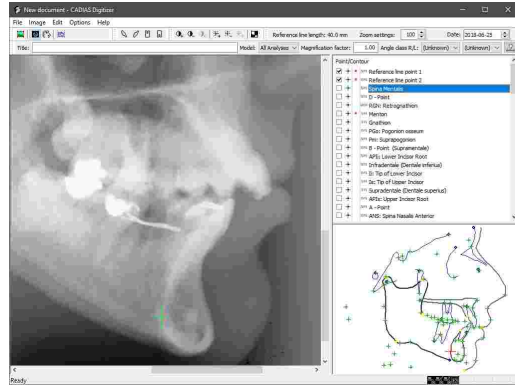



**i** Many anatomical points and contours are used in multiple analyses and are therefore included in multiple input models. It must be noted that changing the selected input model only affects which points and contours are displayed in the list. Unused entries are hidden without causing a loss of already digitized data.


### 7.1.8.4 Digitizing points on the image

Points are indicated with the icon  in the list of items to be digitized. After you select a point, the approximate location of the anatomical landmark will be highlighted in the preview area in the bottom right corner. To digitize the point in the displayed image, move the mouse cursor to the respective location and press the left mouse button. The selection will automatically advance to the next item to be digitized.

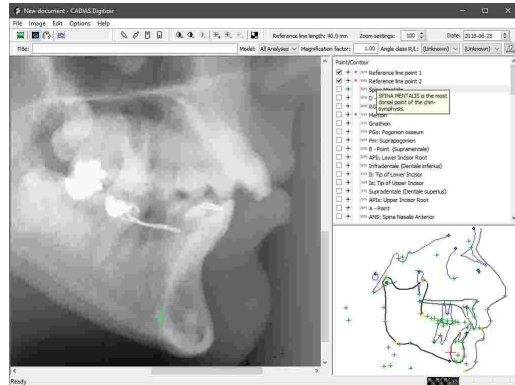
To correct the location of an already digitized point, simply select the list entry again and place the point at the correct location.



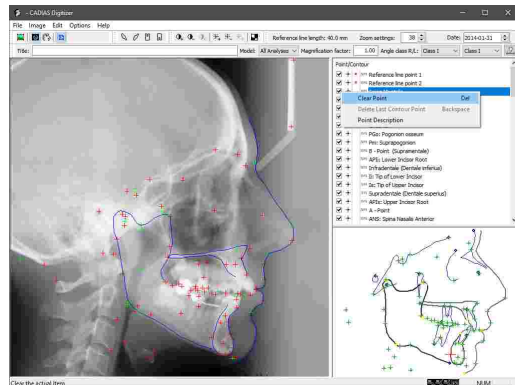
 You can skip arbitrary points or contours by manually selecting the subsequent list entries. However, before you can save the digitizing, you will have to digitize all entries marked with a **R** ("Required").

 You can customize the display settings of the mouse cursor or the highlighted elements in the preview area via the menu *Options* → *Marker Color And Size*.


By right-clicking a list entry, you can display a brief description of the respective point's anatomical location.



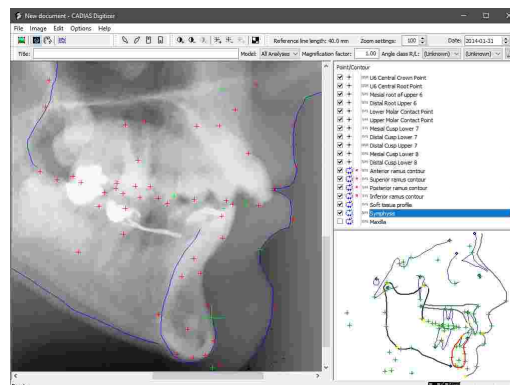
To delete an already digitized point, use the context menu of the list entry or simply press the *Del* key on your keyboard.





### 7.1.8.5 Digitizing contours on the image

Contours are indicated with the icon  in the list of items to be digitized. After you select a contour, the approximate location of the anatomical landmark will be highlighted in the preview area in the bottom right corner. To digitize the contour in the displayed image, move the mouse cursor in small steps from the start to the end of the contour while repeatedly pressing the left mouse button. Alternatively, you can keep the left mouse button pressed throughout. By pressing the right mouse button, the contour input will be finished and the selection will advance to the next item to be digitized.

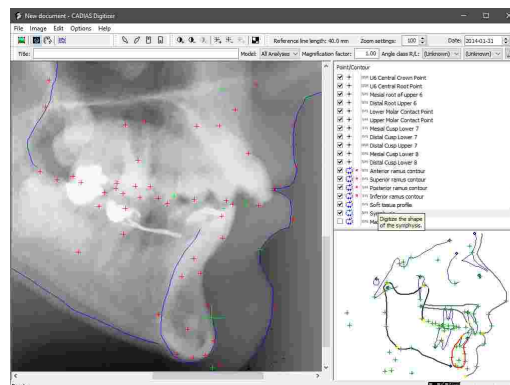
To correct an already digitized contour, simply select the list entry and digitize it again. If you only need to undo the last points of the contour, press the *Backspace* key on your keyboard.



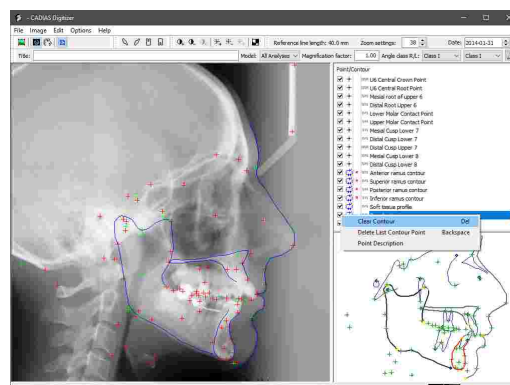
 You can skip arbitrary points or contours by manually selecting the subsequent list entries. However, before you can save the digitizing, you will have to digitize all entries marked with a **R** ("Required").

 You can customize the display settings of the mouse cursor or the highlighted elements in the preview area via the menu *Options* → *Marker Color And Size*.

By right-clicking a list entry, you can display a brief description of the respective contour's anatomical location.







To delete an already digitized contour, use the context menu of the list entry or simply press the *Del* key on your keyboard.



### 7.1.8.6 Using tooth templates

Tooth templates allow you to simultaneously digitize all anatomical points belonging to a particular tooth, such as crown, root, and contact points. This functionality is only available for lateral x-ray images.

Press one of the following toolbar buttons to insert the template for the corresponding tooth:

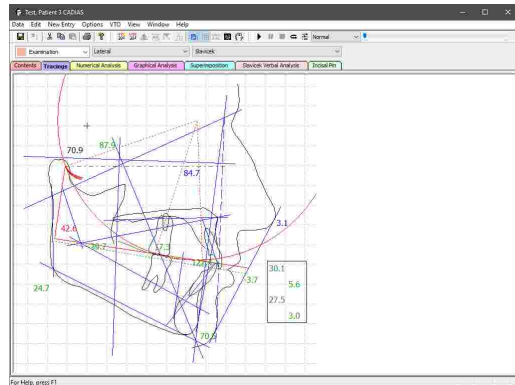
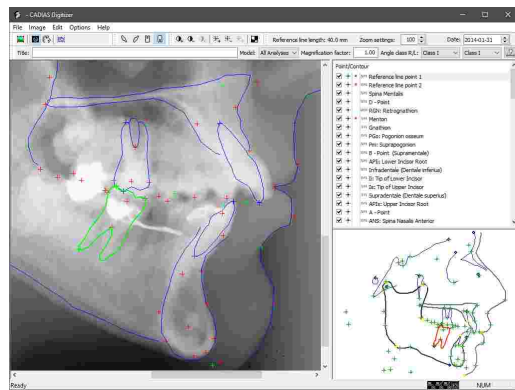
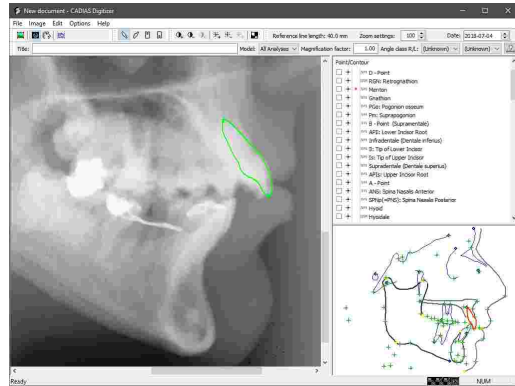
-  Insert upper 1 tooth shape template
-  Insert upper 6 tooth shape template
-  Insert lower 1 tooth shape template
-  Insert lower 6 tooth shape template

Subsequently, the tooth template will appear in the upper left corner of the image area. You can move it to the appropriate location by dragging it with the left mouse button held down.

By dragging the root or cusp tip point, you can adjust the shape of the tooth to the anatomical situation. You can furthermore rotate the tooth template around the root point by dragging it with the right mouse button or resize it by scrolling with the mouse wheel.


Finally, press the *Enter* key or simply select the next point to be digitized in order to confirm the placement of the tooth template and have the points defined thereon digitized.

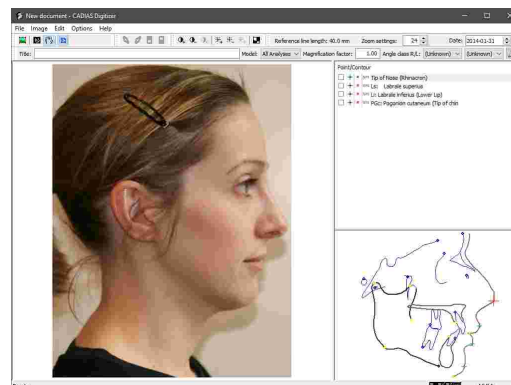
For positioning the tooth shapes in the tracings, CADIAS Analyzer uses the root and crown points of the respective teeth. If these points have been digitized via tooth templates, the teeth in the tracing will be displayed as they were during digitizing.




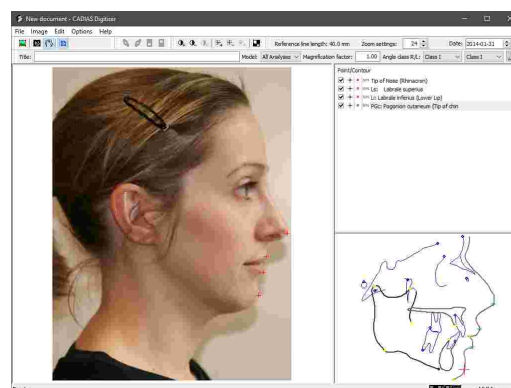
### 7.1.8.7 Superimposing x-ray and patient photo

To superimpose the tracing of an x-ray image with the patient photo in CADIAS Analyzer later on, you will have to digitize a number of points on both images during the digitizing procedure. The software is then able to align the two images together.

To digitize points on the patient photo, press the button  **Show Photo** in the toolbar. If no patient photo has been loaded yet, you can now load the image from file, from the clipboard, or from the database of GAMMA Document Browser. Please refer to chapter "Loading an image<sup>178</sup>" for further information.



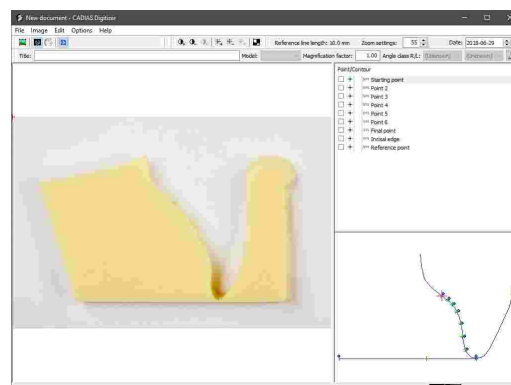
Then, digitize the points displayed in the list just like you did for the x-ray image. You can return to the digitizing of the x-ray image by pressing the button  **Show X-Ray** in the toolbar.



### 7.1.9 Anterior guidance

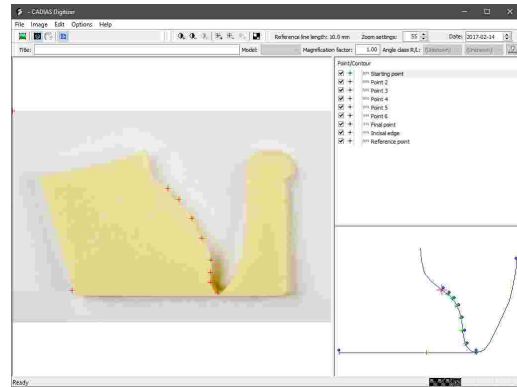
CADIAS Digitizer can also be used for digitizing the patient-individual anterior guidance, which can subsequently be combined with lateral x-ray tracings. For this purpose, usually the cross-section of a silicone impression of the incisal region is used.

Load the image of the anterior guidance and digitize the guiding surface from starting point to end point with evenly distributed intermediate points.



Finally, digitize the incisal tip and the reference point. The line between these two points must be parallel to the axis orbital plane and exactly 10 mm long. Only then can the anterior guidance be correctly combined with the lateral tracing.

You can now save the entered data and close the application.



**i** The digitizing procedure in itself is similar to the digitizing of an x-ray image. You can find more information regarding this topic in chapter "Lateral, frontal, and SMV x-ray images" <sup>184</sup>.

**i** For more information regarding the usage and evaluation of the digitized data, please refer to chapter "CADIAS Analyzer" <sup>196</sup>.

### 7.1.10 Dental arch

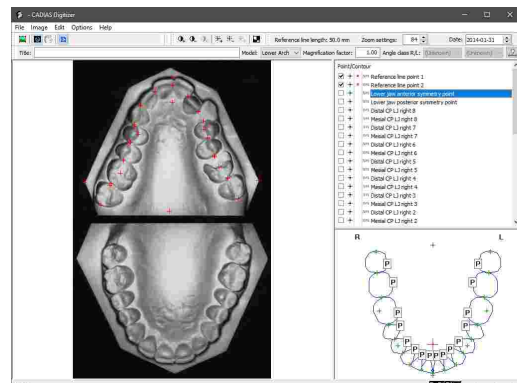
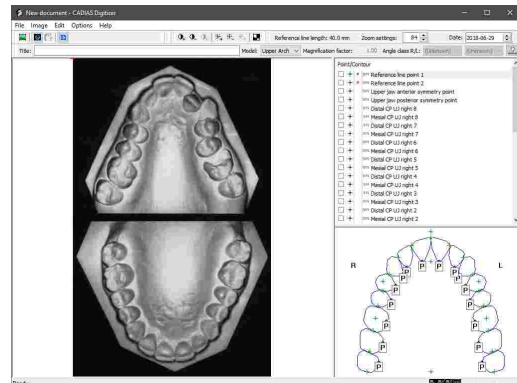
In CADIAS Digitizer you can also digitize the occlusal view of the upper and lower dental arch for evaluating this data in CADIAS Analyzer.

Load the image of the dental arch and start the digitizing by entering the points of the upper arch.

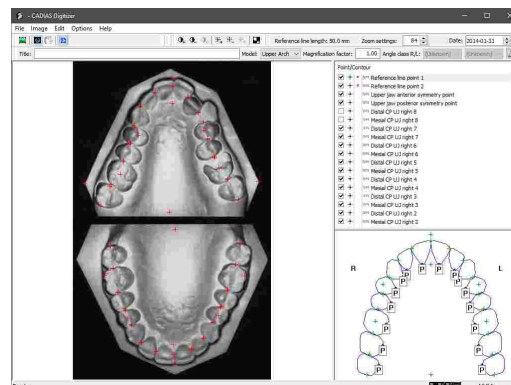
In the preview area, you furthermore have the possibility to enter information regarding the status of the individual teeth. The text boxes therein accept the following inputs:

- **P**: The tooth is part of the permanent dentition.
- **M**: The tooth did not form or has been extracted.
- **N**: The tooth did not erupt.
- **D**: The tooth is part of the deciduous dentition.

Subsequently, change the input model to digitize the points of the lower arch.



If some teeth are missing, you can skip the associated points. Finally, you can save the entered data and close the application.



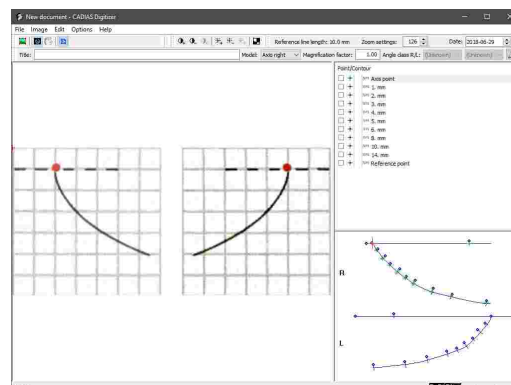
**i** The digitizing procedure in itself is similar to the digitizing of an x-ray image. You can find more information regarding this topic in chapter "Lateral, frontal, and SMV x-ray images" [184](#).

**i** For more information regarding the usage and evaluation of the digitized data, please refer to chapter "CADIAS Analyzer" [196](#).

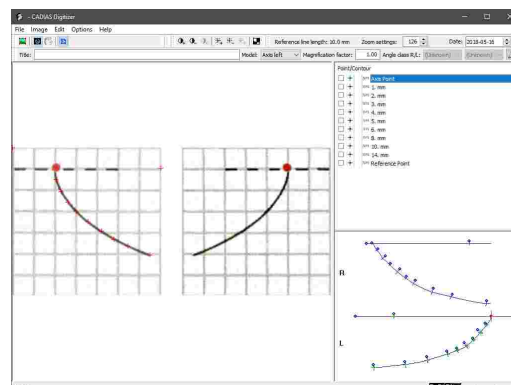
### 7.1.11 Analog condylography curves

If CADIAS Digitizer has been started from GDSW classic, you can digitize analog condylography curves that were recorded on writing paper.

To do so, load the image of the condylography curve and digitize the recording of the right patient side. Start at the axis point and digitize up to the maximum possible length.

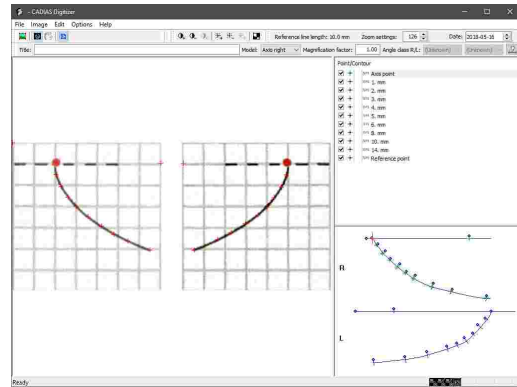


Subsequently, change the input model to digitize the points of the left patient side.



Finally, digitize the reference point at a distance of 10 mm from the axis point. The line between these two points must be parallel to the axis orbital plane. Only then can the condylography curve be correctly combined with the lateral tracing.

You can now save the entered data and close the application.



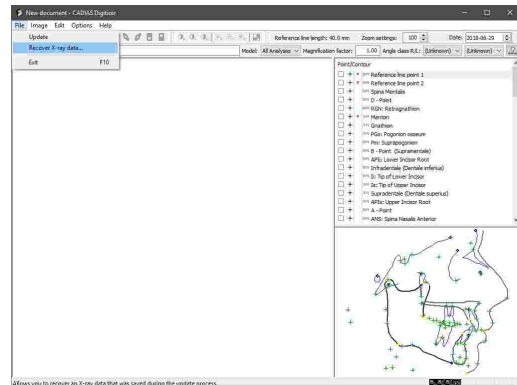
**i** The digitizing procedure in itself is similar to the digitizing of an x-ray image. You can find more information regarding this topic in chapter "Lateral, frontal, and SMV x-ray images" <sup>184</sup>.

**i** For more information regarding the usage and evaluation of the digitized data, please refer to chapter "CADIAS Analyzer" <sup>196</sup>.

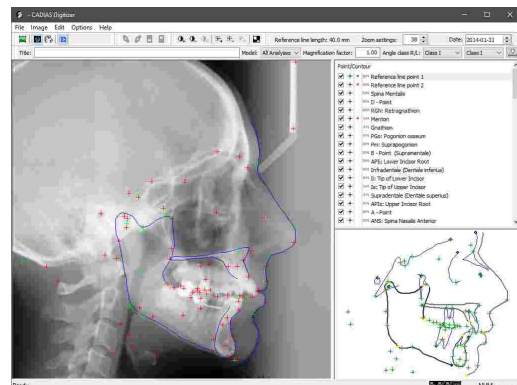
### 7.1.12 Recovering digitized data

When saving a digitizing in CADIAS Digitizer, the application will automatically create backup files that can be used to recover the data in case of an unexpected computer or software crash.

To recover a backup file, create a new digitizing of the same type and choose the menu entry *Data* → *Recover X-ray data* in CADIAS Digitizer.



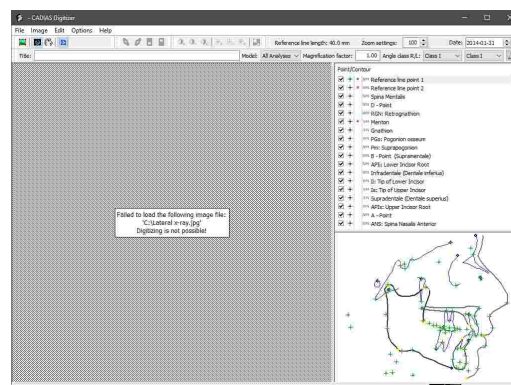
The application will then load the associated image and recover the digitized points and contours. You can now save the data normally.



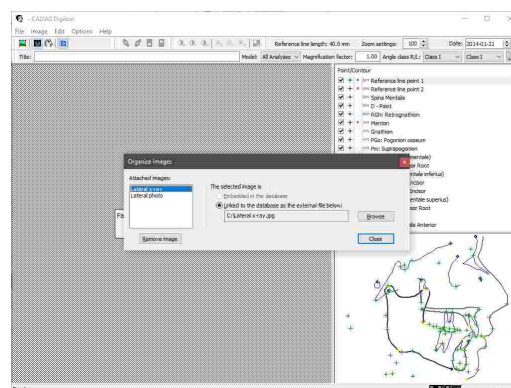
### 7.1.13 Changing image linkage

Digitizings that were created in GDSW classic do not store the digitized image itself, but rather the file path from which the image has been loaded.

If this file path changes, e.g. because the image file is renamed or moved to another folder, CADIAS Digitizer will be unable to display the image.



In this case you can use the menu *Image* → *Organize Images* to adjust the file path and restore the lost image file.



In GAMMA Document Browser, digitized images are imported directly into the patient database and therefore remain available even if the original image file is removed.

### 7.1.14 Measurement accuracy

The maximum error with which the coordinates of anatomical landmarks can be measured using CADIAS Digitizer constitutes 0.005 mm. The additional error incurred by each pixel of deviation from the correct landmark location corresponds to the physical pixel size, which is dependent on the resolution (pixel density) of the image being digitized. For example, pixel sizes for typical image resolutions are:

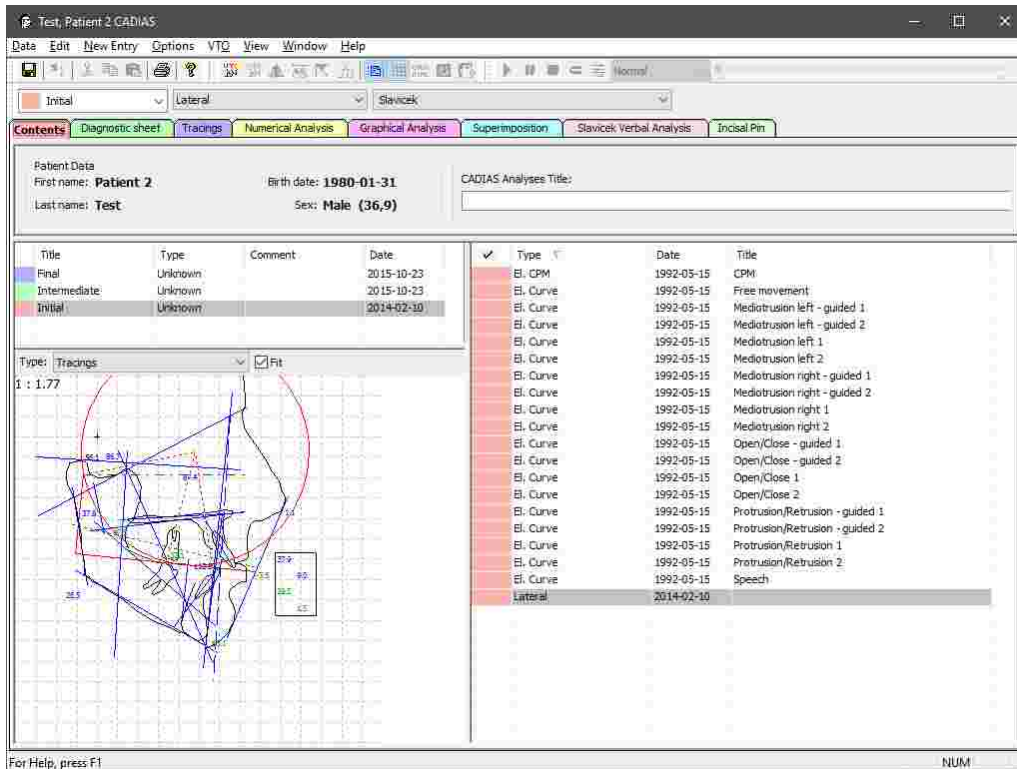
Image resolution	Pixel size
75 dpi	0.34 mm
150 dpi	0.17 mm
300 dpi	0.08 mm
600 dpi	0.04 mm



Accurate measurements can only be obtained when both the reference line and the magnification factor have been entered correctly (refer to chapters "Entering the reference line" and "Setting the magnification factor"). Make sure to verify these inputs before finishing the digitizing procedure as failure to do so can compromise the correctness of the cephalometric evaluations.

## 7.2 CADIAS Analyzer

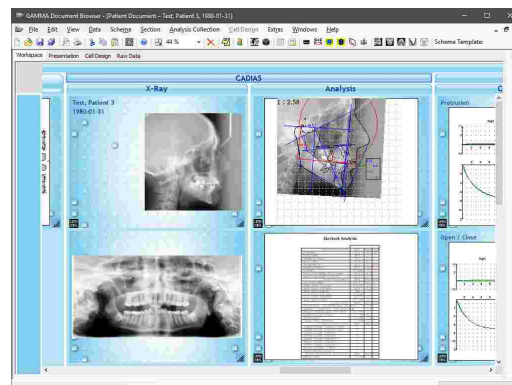
CADIAS Analyzer is the application for analyzing cephalometric properties and cranial relations. This information is created based on the anatomical points and contours that were digitized on x-ray and other images in the CADIAS Digitizer application (see chapter "CADIAS Digitizer" (176)).



### 7.2.1 Starting the application

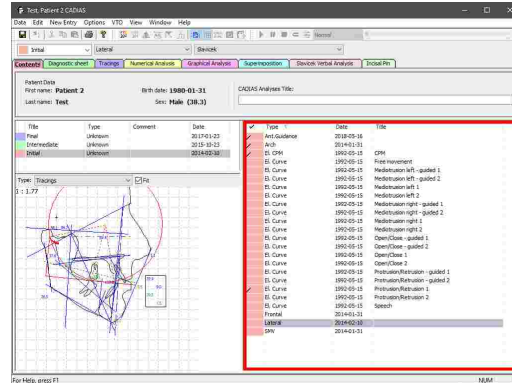
CADIAS Analyzer is an integral part of GAMMA Dental Software and can be started from GAMMA Document Browser as well as from GDSW classic:

- You can start CADIAS Analyzer from GAMMA Document Browser by double-clicking one of the CADIAS data areas. Please refer to chapter "Inserting CADIAS x-ray data" (77) for more information.

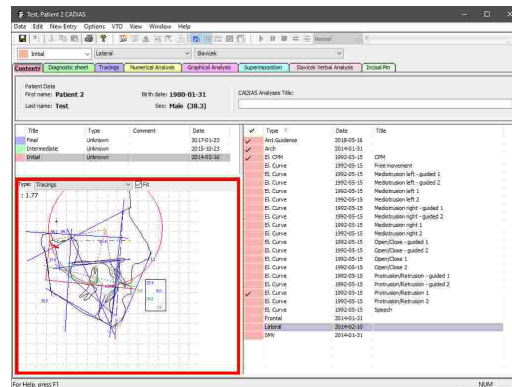




- The right side shows a list of **data items** contained in the currently selected analysis. This can include not only x-ray digitizings, but also condylographic movements recorded in the CADIAX module. The currently active data items are indicated by check marks (refer to chapter "Selecting data items as active [206]").



- Below the list of analyses, you can see a **preview** of a tracing, a numerical analysis, or a Slavicek verbal analysis for the currently selected analysis.



**i** You can select multiple examinations by clicking them while keeping the *Ctrl* or *Shift* key pressed. The data items of all selected examinations will then be displayed simultaneously. This can be useful, for example, if you want to combine an actual x-ray tracing with the condylography recording of a previous examination.

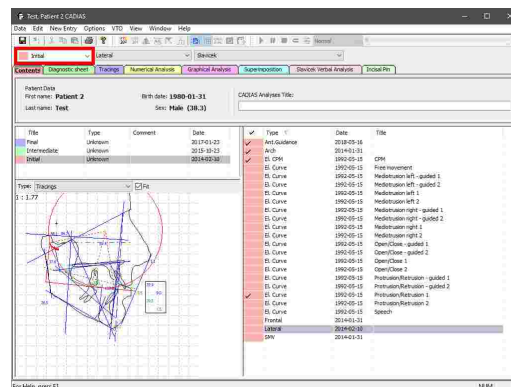
This method of multiple selection is also provided in the list of data items, whereby you can easily copy or delete multiple data items at once.

**i** You can specify a column by which to sort the list of data items by clicking the respective column header. Clicking it again will toggle between ascending and descending sort order.

### 7.2.2.1 CADIAX analyses

To keep the patient data that has been collected over multiple examinations separated, CADIAX Analyzer allows you to create dedicated analyses for each individual patient visit.

You can select the analysis, of which the data is being displayed, via the **analysis toolbar** in all views. This combo box is synchronized with the analysis selection in the *Contents* pane.

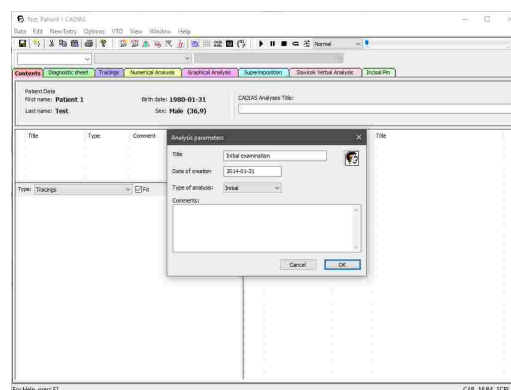


**i** Manually managing CADIAS analyses is only possible when the application has been started from GDSW classic. If the application has been started from GAMMA Document Browser, it will automatically retrieve the analysis collections from the patient database therein (refer to chapter "Analysis collections" <sup>44</sup>T).

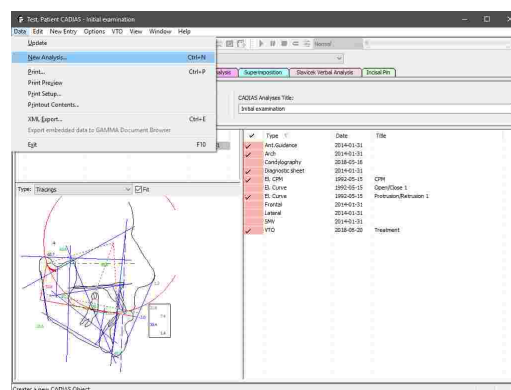
### 7.2.2.1.1 Creating a new CADIAS analysis

When opening a CADIAS analysis object that was just created in GDSW classic for the first time, a dialog for entering basic information of the analysis will appear automatically. Here, you can enter the title, date, type (initial, intermediate, or final) as well as an arbitrary description. All inputs are optional.

Press **OK** to confirm your inputs and create the new analysis.



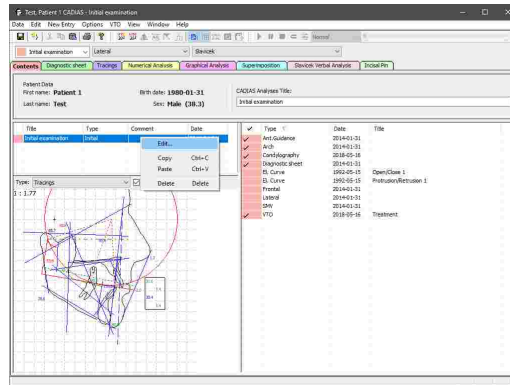
To create additional analyses at a later time, you can open the dialog again via the menu *Data* → *New analysis*.



### 7.2.2.1.2 Editing a CADIAS analysis

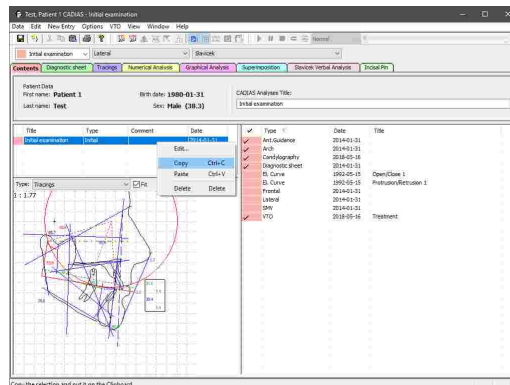
To edit the information specified during the creation of a CADIAS analysis, such as title, date, or description, right-click the respective entry in the list of analyses and choose *Edit*.

This will open the dialog for editing the actual information. Confirm your changes by pressing *OK*.



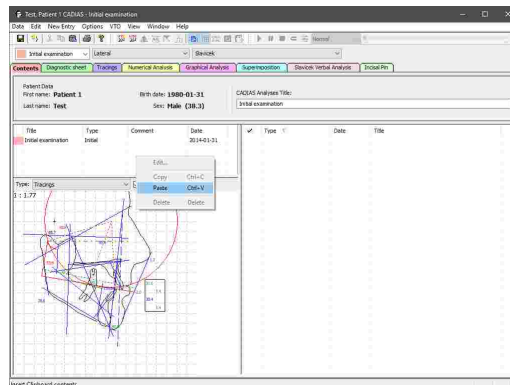
### 7.2.2.1.3 Copying a CADIAS analysis

To copy individual CADIAS analyses from one analysis object to another, right-click the analysis and choose *Copy*.



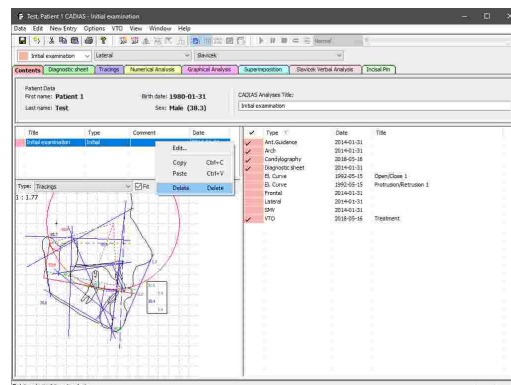
Subsequently, you can paste the copied analysis using the context menu entry *Paste* in the analysis list of the second analysis object. Using this method, you can also duplicate analyses within the same analysis object.

It is also possible to move an analysis between two opened CADIAS analysis objects via drag-and-drop.



### 7.2.2.1.4 Deleting a CADIAS analysis

To permanently delete a CADIAS analysis, right-click the respective entry in the list of analyses and choose **Delete**.

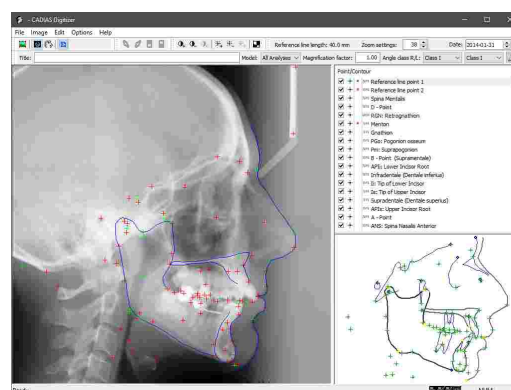


### 7.2.2.2 Digitizings

With CADIAS Analyzer, you can manage and create evaluations based on the following digitized data. These digitizings are created using the CADIAS Digitizer application (refer to section "CADIAS Digitizer<sup>176</sup>"):

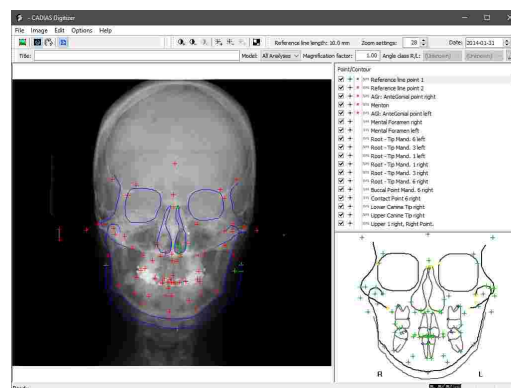
- **X-ray images in lateral projection:**

Digitizing is carried out in the median-sagittal plane. From the digitized images, the CADIAS Analyzer application allows the creation of cephalometric analyses, such as tracings or numerical analyses.



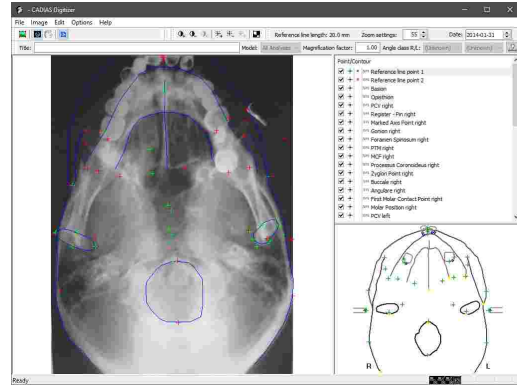
- **X-ray images in frontal projection:**

Digitizings are carried out in the frontal plane. Similar to lateral x-ray images, CADIAS Analyzer allows the creation of cephalometric analyses for frontal x-rays.

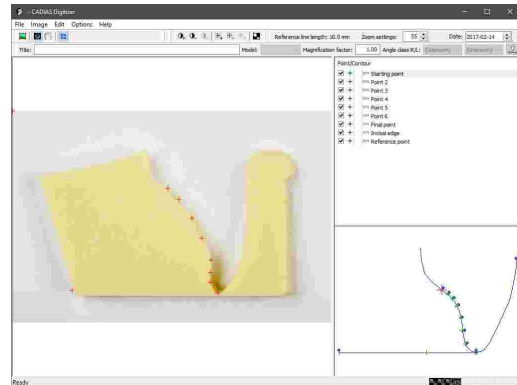


- **X-ray images in submentovertebral projection (SMV, also referred to as "basal"):**

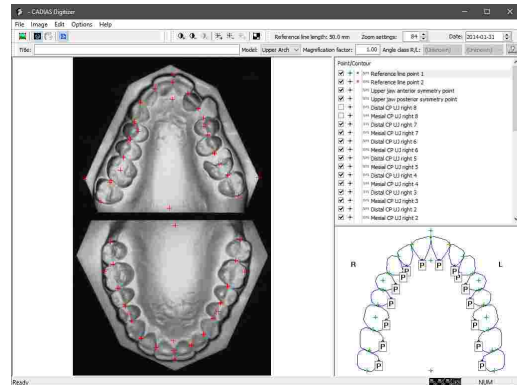
Digitizings are carried out in the transversal plane. Similar to lateral x-ray images, CADIAS Analyzer allows the creation of cephalometric analyses for SMV x-rays.



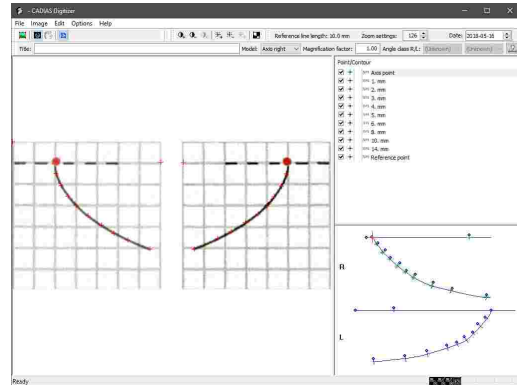
- The patient-individual **anterior guidance**, which can subsequently be combined with lateral x-ray tracings for evaluation and movement simulation. These images are usually taken from the cross-section of a silicone impression of the incisal region.



- The occlusal view of the upper and lower **dental arch**. Just like other tracings, multiple dental arch tracings can be superimposed in the CADIAS Analyzer application, for example to compare the dental situation before and after a treatment.



- In addition, if the application has been started from GDSW classic, it is possible to digitize **analog condylography curves** that were recorded on writing paper. In GAMMA Document Browser, you can use the functionality for entering numeric curves instead (refer to chapter "Entering numeric curves" <sup>73</sup>).

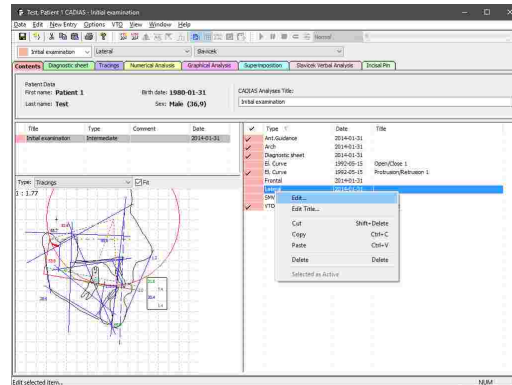




### 7.2.2.2 Editing an existing digitizing


To edit an existing digitizing at a later time, right-click the associated entry in the list of data items and choose *Edit*.

CADIAS Digitizer will open, in which you can make the necessary changes and save the digitizing. Already calculated analyses in CADIAS Analyzer will be updated automatically.

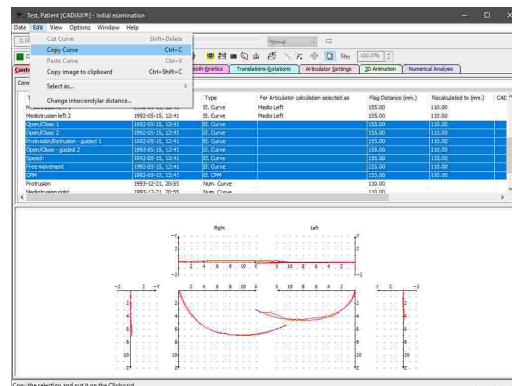


### 7.2.2.3 Inserting CADIAX condylography data

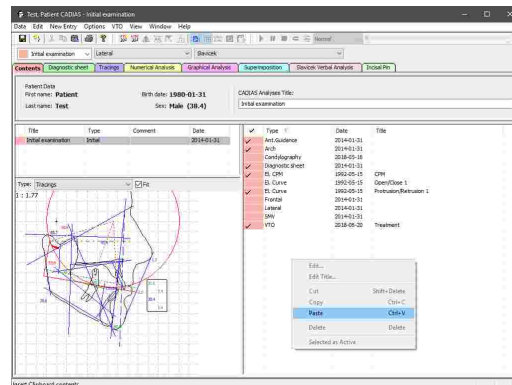
CADIAS Analyzer allows the incorporation of condylography data recorded with the CADIAX module, which can subsequently be used in cephalometric analyses and the visualization of treatment objectives (refer to chapters "Tracings<sup>[215]</sup>", "Numerical analysis<sup>[219]</sup>", and "Visualized Treatment Objectives (VTOs)<sup>[223]</sup>").

 Inserting CADIAX condylography data in CADIAS Analyzer is only possible when the application has been started from GDSW classic. If the application has been started from GAMMA Document Browser, it will automatically retrieve all the condylography recordings stored in the patient database (refer to chapter "Recording CADIAX condylography data<sup>[68]</sup>").

To transfer any CADIAX recordings from a CADIAX analysis to a CADIAS analysis, open the CADIAX Analyzer application, select the recordings on the Contents pane, and copy them using the menu *Edit* → *Copy Curves*.



The copied data can then be inserted in the *Contents* pane of CADIAS Analyzer. To do so, right-click in the list of data items and choose *Paste*.



### 7.2.2.4 Condyle Position Measurements (CPM)

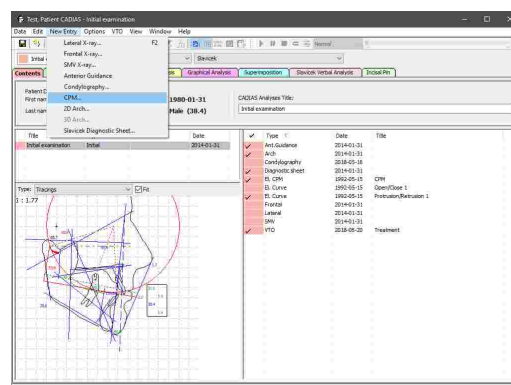
A condyle position measurement (CPM) describes the movement of the condyles from one temporomandibular joint position to another. CADIAS Analyzer allows you to manually enter such measurement values in order to use them for the visualization of treatment objectives (refer to chapter "Visualized Treatment Objectives (VTOs)"<sup>[223]</sup>).



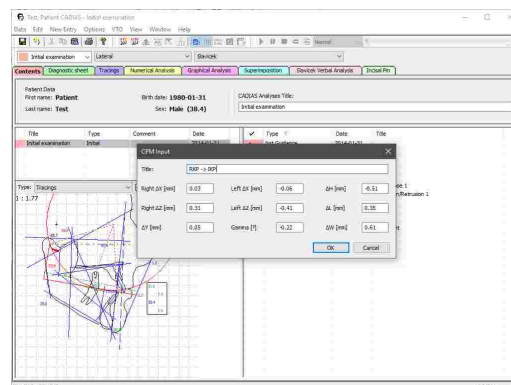
Inserting CPMs in CADIAS Analyzer is only possible when the application has been started from GDSW classic. If the application has been started from GAMMA Document Browser, the data management is carried out in the patient database therein (refer to chapter "Recording CADIAX condylography data"<sup>[68]</sup>).

#### 7.2.2.4.1 Entering a new CPM

To insert new CPM data, use the menu entry *New Entry* → *CPM*.




This will open a dialog in which you can enter the below described values.



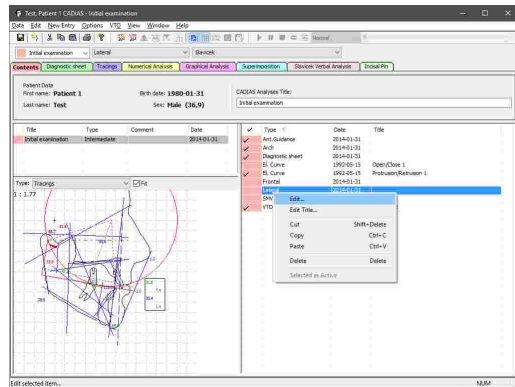
- **ΔX, ΔY, ΔZ** The condylar shift from the first to the second TMJ position, along the respective coordinate system axis. Due to the rigidity of the mandible, lateral shift along the Y-axis is given by a single value rather than separate values for right and left side.
- **Gamma** The amount of hinge axis rotation between the two positions. Positive values indicate an opening rotation.
- **ΔH** The change to the height of the articulator's incisal pin that results from the movement from first to second position. Positive values indicate a raise of the incisal pin.
- **ΔW** The side shift of the articulator's incisal pin. Positive values indicate a movement to the left patient side.

- **ΔL** The anterior or posterior shift of the articulator's incisal pin. Positive values indicate an anterior movement.

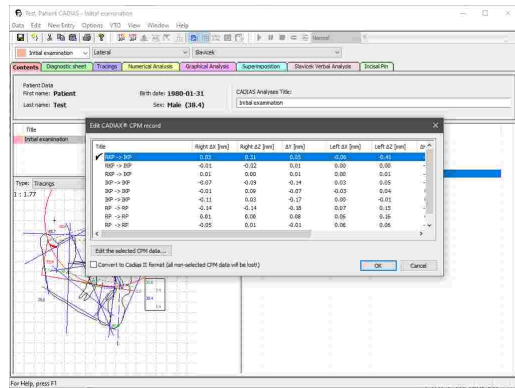
 Refer to chapter "The reference coordinate system [299]" for a detailed description of the coordinate system used by the software.

### 7.2.2.4.2 Editing an existing CPM

To edit an existing CPM item at a later time, right-click the associated entry in the list of data items and choose *Edit*. This will open the above-shown dialog again and allow you to make the desired changes.



If the CPM item opened for editing has been inserted from CADIAX and contains itself multiple measurements, a dialog listing the individual measurements will be displayed. By selecting a measurement and pressing the button below the list, you can edit the values of that particular measurement.

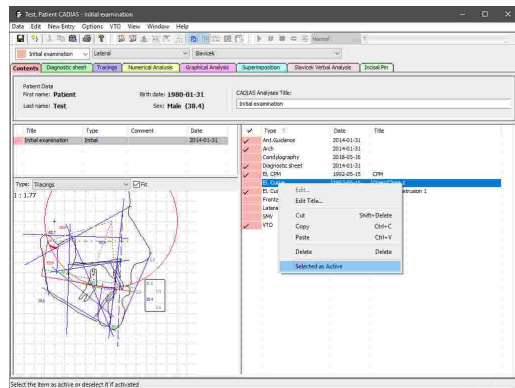


In this dialog, you can also reduce a multi-measurement CPM to just the measurement that is currently selected as active. To do so, check the corresponding check box before pressing OK. This will permanently delete the unused measurements.

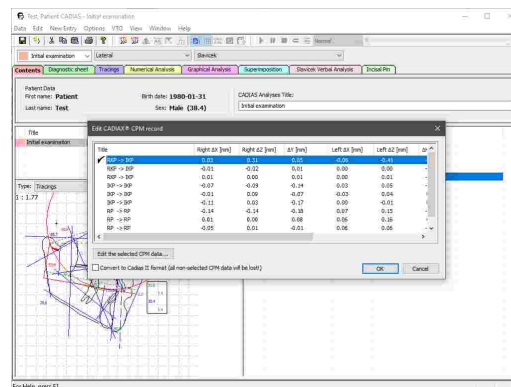
### 7.2.2.5 Selecting data items as active

If there are several data items of a specific type available, for example multiple condylography curves, you will have to specify which of them should be used in the calculation of the various analyses.

To do so, simply double-click the data item to use in the list on the *Contents* pane. The currently active item will be marked with a check mark  in the list. Alternatively, you can right-click the item and choose *Select As Active*. For each type of data item, only one can be selected as active at a time.

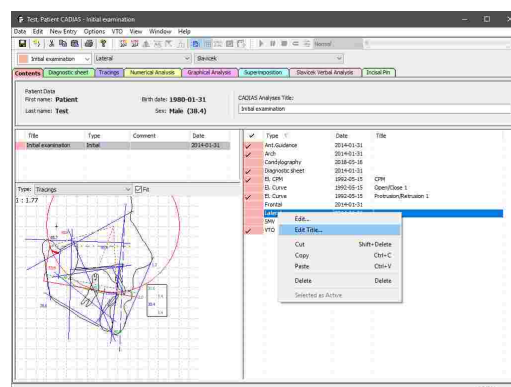


CPM data items can contain multiple individual measurements. To select the measurement to use, open the selection dialog by right-clicking the item and choosing *Edit*. You can then select a measurement as active by double-clicking it in the list, which will highlight it with a check mark.



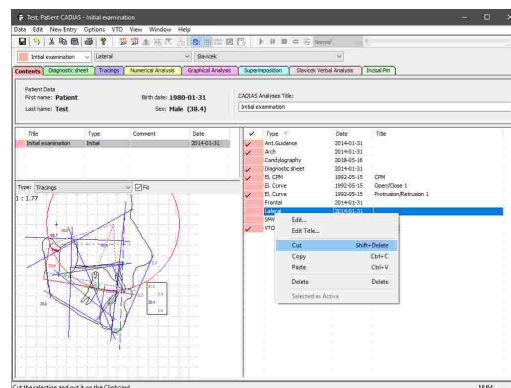
### 7.2.2.6 Renaming data items

When an analysis contains multiple data items of the same type, you should consider assigning each item a unique name to be able to differentiate between them. You can rename existing items by right-clicking them in the list on the *Contents* pane and choosing *Edit Title*.

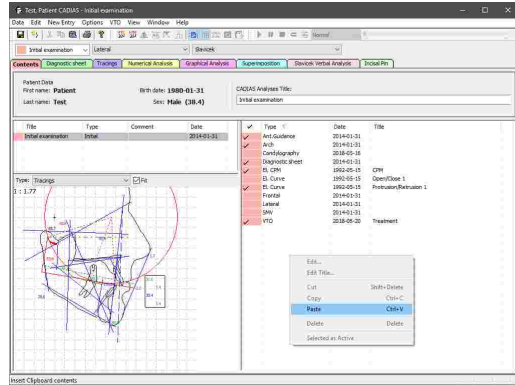


### 7.2.2.7 Copying and pasting data items

To copy one or more data items from one analysis object to another, select them in the list, right-click them, and choose *Copy*.

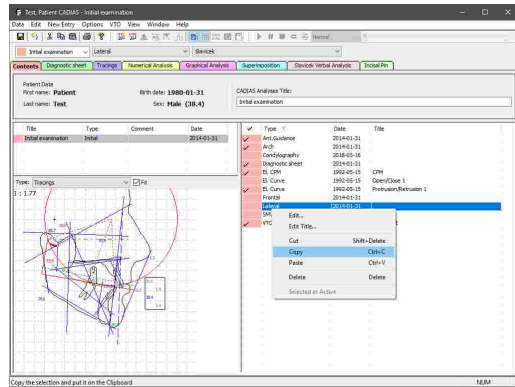


Subsequently, you can paste the copied data using the context menu entry *Paste* in the data list of the second analysis. Using this method, you can also duplicate data items within the same analysis.



To move the data from one analysis to another, use the context menu entry *Cut*.

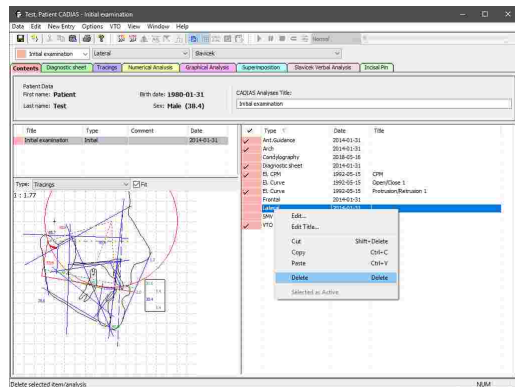
It is also possible to move the selected data items between two opened CADIAS analysis objects via drag-and-drop.



**i** Copying and pasting data items within CADIAS Analyzer is only possible if the application has been started from GDSW classic. If the application has been started from GAMMA Document Browser, you can access the data items via the raw data view therein (refer to chapter "Copying and pasting raw data<sup>58 1)</sup>").

### 7.2.2.8 Deleting data items

To permanently delete data items from an analysis, select them in the list, right-click them, and choose *Delete*.



**i** Deleting data items within CADIAS Analyzer is only possible if the application has been started from GDSW classic. If the application has been started from GAMMA Document Browser, you can access the data items via the raw data view therein (refer to chapter "Copying and pasting raw data<sup>58 1)</sup>").

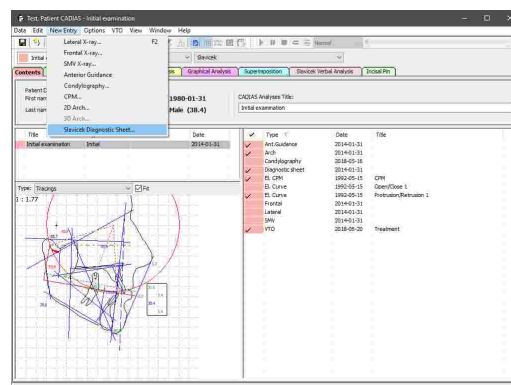
### 7.2.3 Diagnostic sheet

The diagnostic sheet is a digital form that you can use to document the patient's psychic and physical condition during the initial anamnesis.

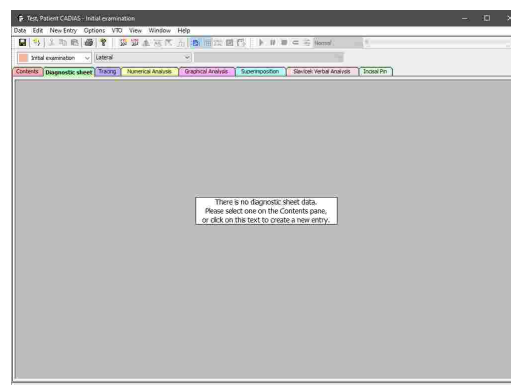
**i** Inserting a diagnostic sheet in CADIAS Analyzer is only possible when the application has been started from GDSW classic. In GAMMA Document Browser, diagnostic sheets are managed as stand-alone data items without a connection to the CADIAS module (refer to chapter "Entering a diagnostic sheet").

#### 7.2.3.1 Creating or editing a diagnostic sheet

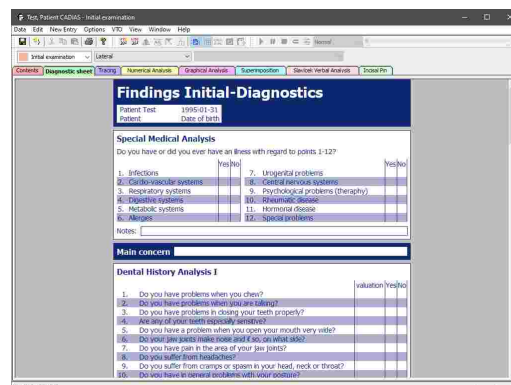
To insert a new diagnostic sheet, use the menu entry *New Entry* → *Diagnostic sheet*.




Alternatively, if no diagnostic sheet has been created yet, you can also switch to the *Diagnostic Sheet* pane and simply click on the displayed information text.



Subsequently, the form will appear in the *Diagnostic Sheet* pane. Here, you can fill it out by clicking the Yes/No options, entering text information, or marking potential pain spots in the displayed graphics.

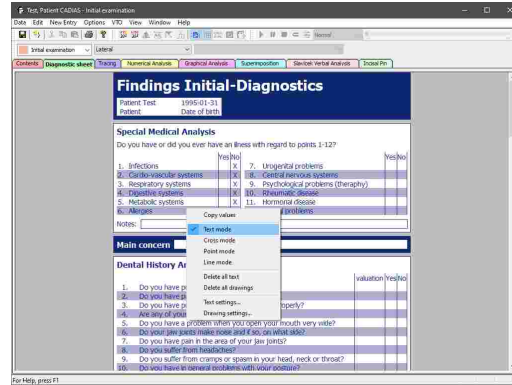


 If you inserted multiple diagnostic sheets into the same analysis, the *Diagnostic Sheet* view will always display the sheet that has been selected as active on the *Contents* pane (refer to chapter "Selecting data items as active" <sup>206</sup>).

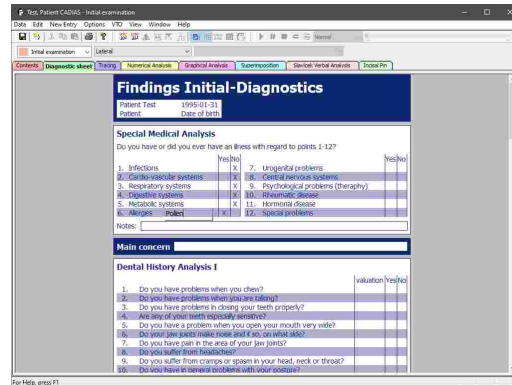
### 7.2.3.2 Text mode in the diagnostic sheet

The diagnostic sheet provides input boxes for entering notes below certain sections. For instance, these can be useful to clarify what types of allergies the patient has. Alternatively, you can use text mode to add notes anywhere on the form.

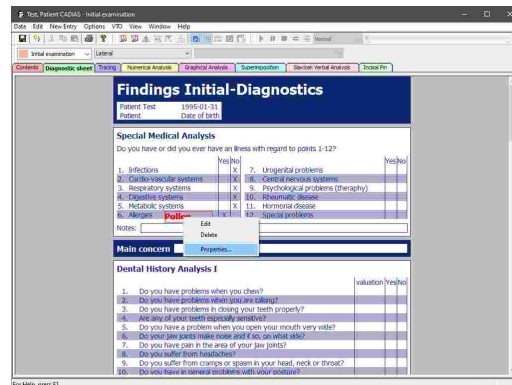
To do so, right-click on the section of the form where you would like to write text and choose *Text mode*.




While text mode is enabled, you can draw a rectangular text box by pressing and holding the left mouse button. After you entered the text, press the *Esc* key to confirm.



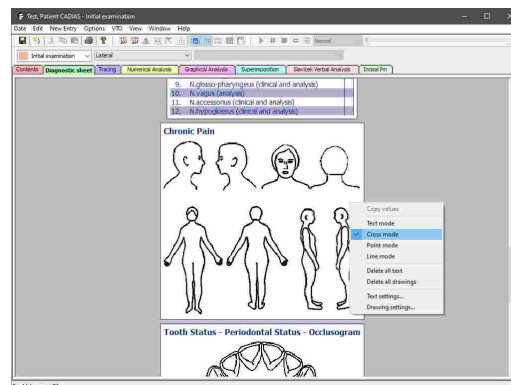
By right-clicking the text box, you can edit the text, delete it, or change properties like font size or color.



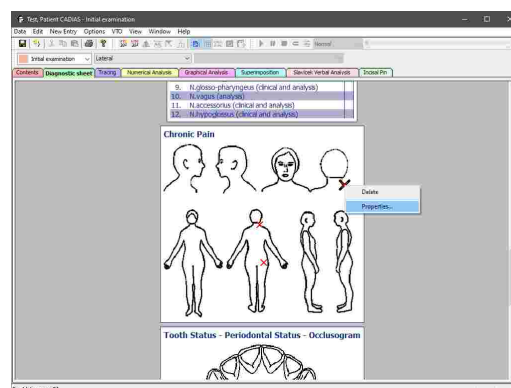
 Make sure to exit text mode via the context menu once you finished your text input and want to continue filling out the form.

### 7.2.3.3 Drawing mode in the diagnostic sheet

Just like text mode, you can activate drawing mode for drawing crosses, points, or lines by right-clicking any section of the form. In the graphical sections, this mode is permanently active.



To change the appearance properties of a drawing, like color or thickness, right-click it and choose *Properties*. You can also delete it by choosing *Delete* in the context menu.

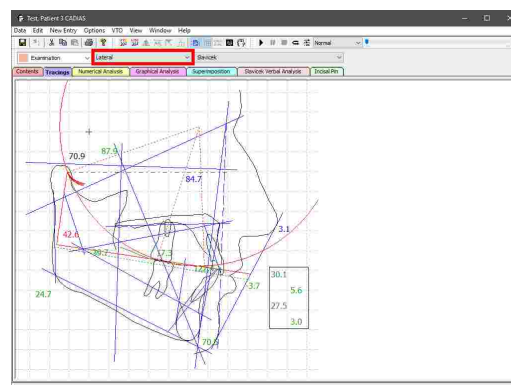


Make sure to exit drawing mode via the context menu once you finished your drawings and want to continue filling out the form.

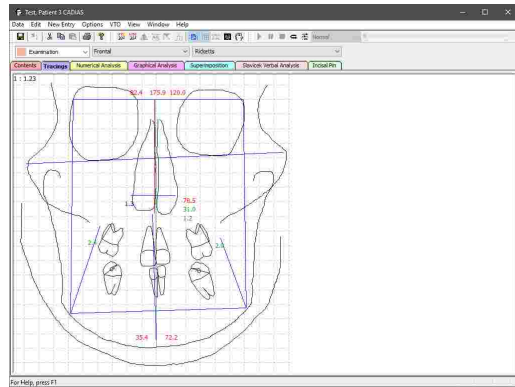
### 7.2.4 Selecting the projection

CADIAS Analyzer processes x-ray images in lateral, frontal and SMV projection (refer to chapter "Digitizings [2011]"). To switch between the projections in any of the analysis views, use the second combo box in the analysis toolbar. Naturally, it will only offer those projections for selection, of which the corresponding x-ray images have been digitized. For example, in the *Tracings* view:

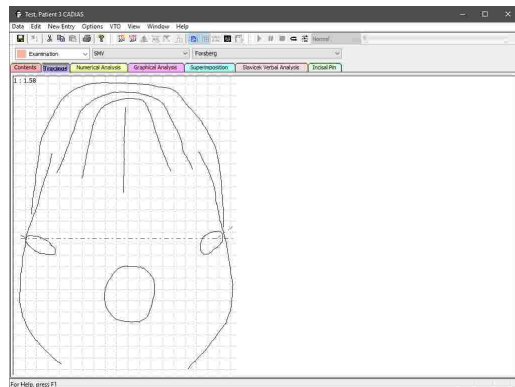
- Tracing of an x-ray image in **lateral projection** according to Slavicek



- Tracing of an x-ray image in **frontal projection** according to Ricketts



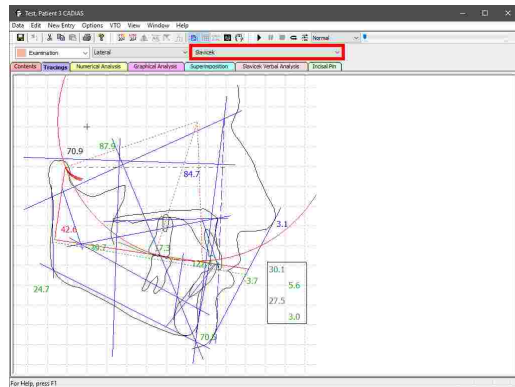
- Tracing of an x-ray image in **SMV projection** according to Forsberg



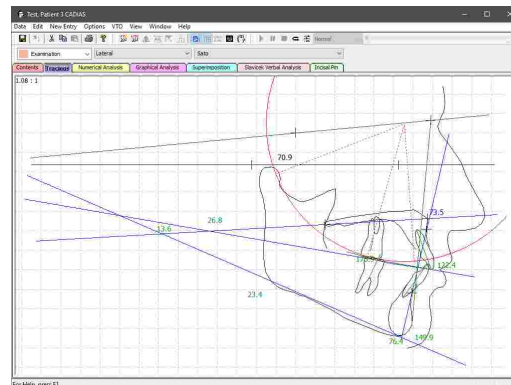
## 7.2.5 Selecting an analysis definition

Most analysis types are provided in several variants according to the definition of the respective author. You can switch between these definitions using the third combo box in the analysis toolbar. Taking the *Tracings* view for example:

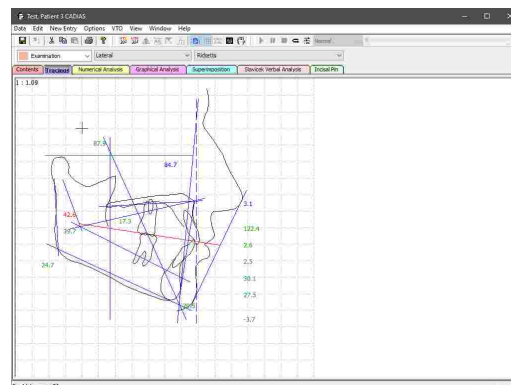
- Lateral tracing according to **Slavicek**



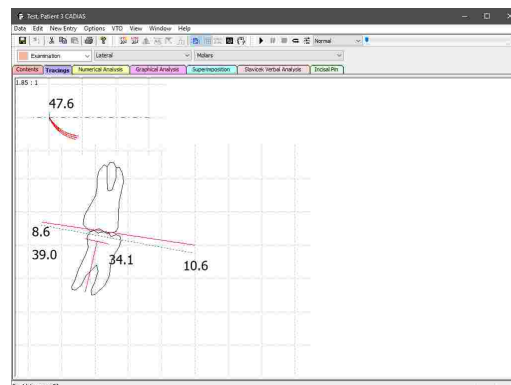
- Lateral tracing according to **Sato**



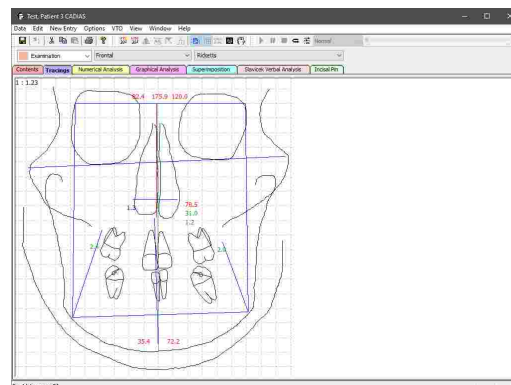
- Lateral tracing according to **Ricketts**




- Interrelation of the upper and lower first **Molars**





- Frontal tracing according to **Ricketts**

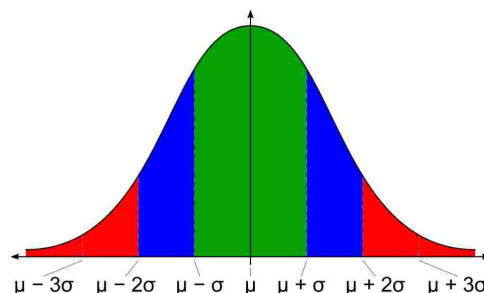




 The calculated value lies within one standard deviation of the norm value.

 The calculated value lies between one and two standard deviations of the norm value.

 The calculated value lies more than two standard deviations away from the norm value.



In a normal distribution, the mean is usually denoted with  $\mu$  ("My") and the standard deviation with  $s$  ("Sigma"). For a normally distributed variable, about 68% of the measured values lie within one standard deviation around the mean and 95% lie within two standard deviations.

The deviation of the measured value from the norm value is furthermore used to calculate a **trend**, which indicates by how many standard deviations the measured value deviates from the norm value. If the measured values lies within one standard deviation, no trend will be calculated.

For some anatomical values, a deviation in a particular direction correlates to a specific type of facial shape. The trend indicates this circumstance via a label appended to the number of standard deviations:

- + or -      The deviation is positive (+) or negative (-).
- **X** or **V**      The deviation indicates a convex (**X**) or concave (**V**) facial shape.
- **B** or **D**      The deviation indicates a brachyfacial (**B**) or dolichofacial (**D**) facial shape.

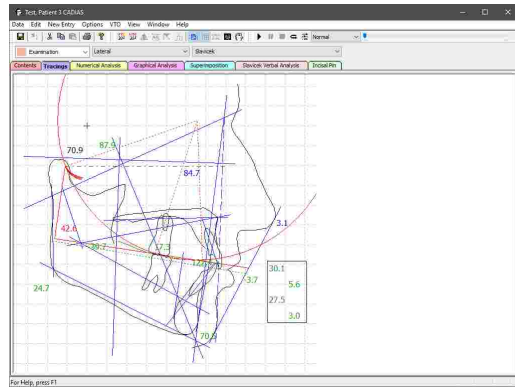
Lastly, the number of standard deviations that the measured value deviates from the norm is additionally indicated with the corresponding number of asterisks appended to the trend value:

- \*              The deviation lies between one and two standard deviations.
- \*\*             The deviation lies between two and three standard deviations.
- \*\*\*            The deviation lies between three and four standard deviations.
- \*\*\*>         The deviation exceeds four standard deviations.


### 7.2.7 Tracing

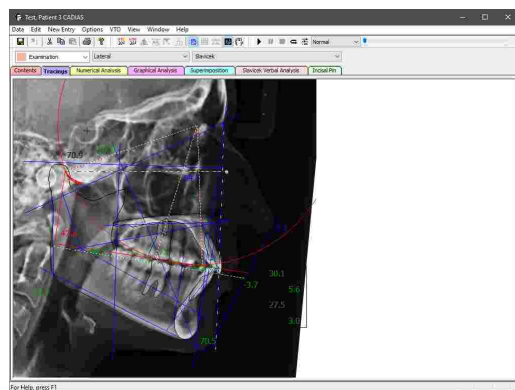
Tracings are used for the graphical visualization of anatomical points and contours that have been digitized on the x-ray image. This graphic is supplemented with colored lines, in most cases used for the illustration of anatomical planes. In addition, they include numerical values that are essential for the analysis according to the respective author.


To view a tracing in CADIAS Analyzer, switch to the *Tracing* pane. You can select the projection and analysis definition to be displayed via the analysis toolbar (refer to chapters "Selecting the projection<sup>211</sup>" and "Selecting an analysis definition<sup>212</sup>", respectively).

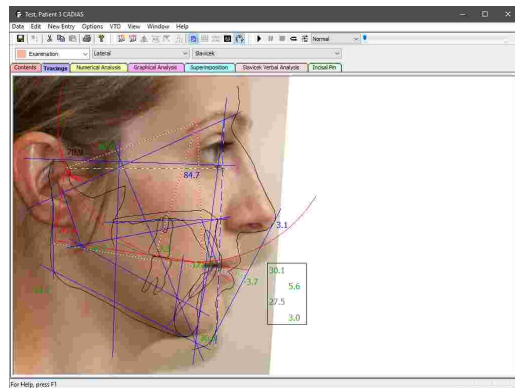


### 7.2.7.1 Overlaying a patient image


To display the digitized x-ray image behind the tracing, activate the button  *Show x-ray* in the toolbar.

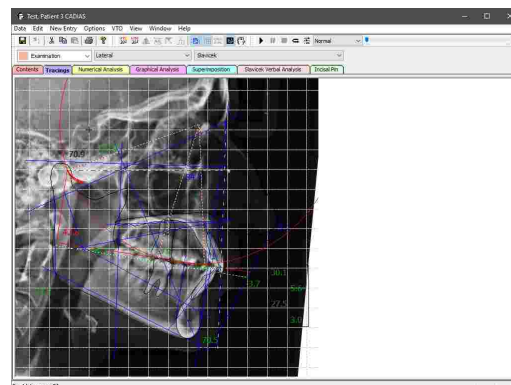


If you have digitized the required landmarks on the patient photo (refer to chapter "Superimposing x-ray and patient photo<sup>190</sup>"), you can activate the toolbar button  *Show photo* to display this photo behind the tracing.



### 7.2.7.2 Showing the background grid

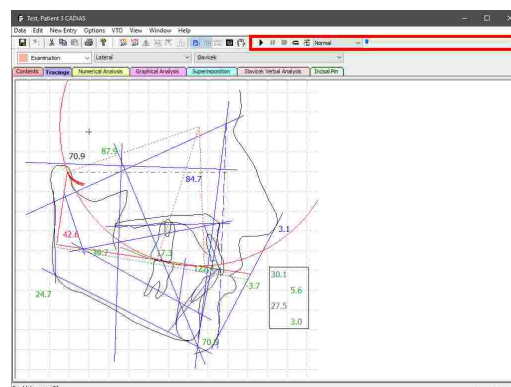
To bring the dimensions of the anatomical structures into perspective, you can use the toolbar button  **Show grid** to show a 10 mm grid in the background.







### 7.2.7.3 Replaying a condylography recording

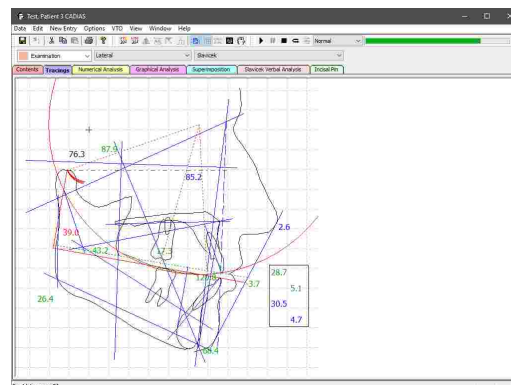
CADIAS Analyzer allows the realistic animation of the mandible in the tracing based on a condylography curve that has been recorded on the patient. To do so, the curve has to be inserted in the CADIAS analysis and selected as active on the Contents pane (refer to chapters "Inserting CADIAX condylography data<sup>[204]</sup>" and "Selecting data items as active<sup>[206]</sup>", respectively).


Subsequently, the condylography curve will be displayed in the tracing and you can control its replay via the **Animation Toolbar**.



Start the replay by pressing the button  **Start replay**. To pause a replay at the current time position or to stop it entirely, use the buttons  **Pause replay** and  **Stop replay**, respectively. By activating the button  **Loop**, you can enable an infinite replay loop.

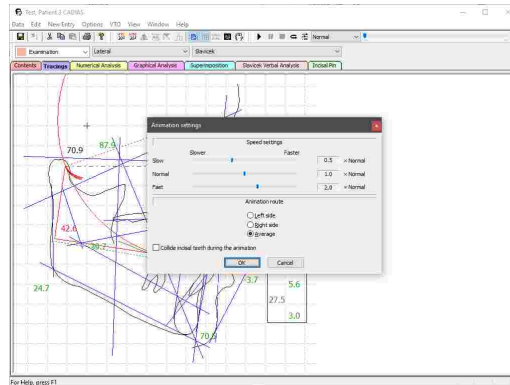
Use the slider to manually jump to a particular time position. You can skip through the time positions step-by-step using the arrow keys or the page-up and page-down keys on your keyboard.



You can select the speed of the automatic replay using the combo box in the animation toolbar. The button  *Animation settings* provides access to more detailed configuration settings.

In this dialog you can also select whether the animation should use the recording track of the right patient side, the left patient side, or an average of both.

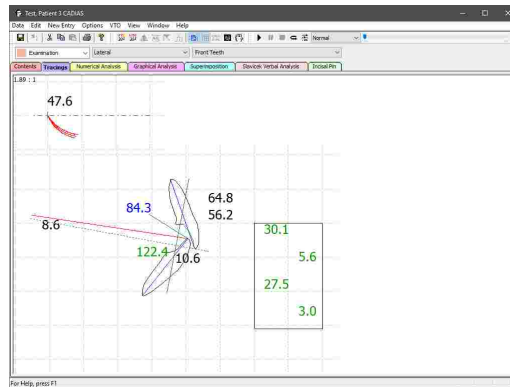
Furthermore, you can activate that the incisors collide during animation. If this option is activated, the lower incisor will slide along the guiding surface of the upper incisor, avoiding intersections.



### 7.2.7.4 Incorporating an anterior guidance

To incorporate a digitized, patient-individual anterior guidance in the tracing, you first have to select it as active on the *Contents* pane (refer to chapters "Anterior guidance<sup>[191]</sup>" and "Selecting data items as active<sup>[206]</sup>", respectively).

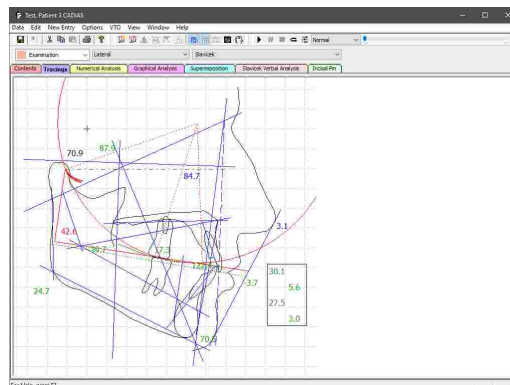
The shape of the upper incisor will thus be adapted according to the individual anterior guidance, which will be visualized in green color.



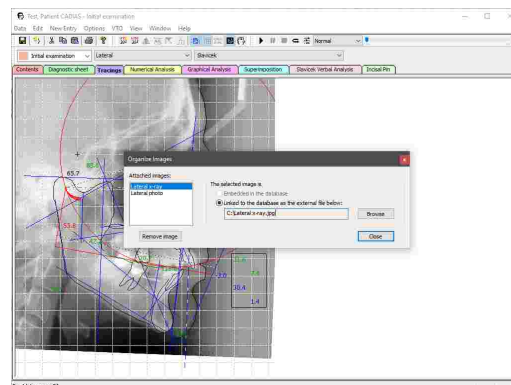
### 7.2.7.5 Changing image linkage

Digitizings that were created in GDSW classic do not store the digitized image itself, but rather the file path from which the image has been loaded.

If this file path changes, e.g. because the image file is renamed or moved to another folder, CADIAS Analyzer will be unable to display the image even if the corresponding option has been activated.



In this case you can use the menu *Image* → *Organize Images* to adjust the file path and restore the lost image file.

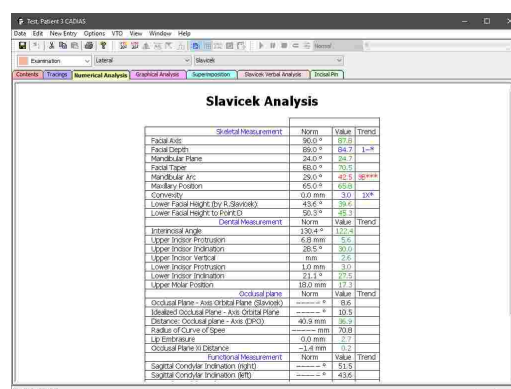


In GAMMA Document Browser, digitized images are imported directly into the patient database and therefore remain available even if the original image file is removed.

### 7.2.8 Numerical analysis

Numerical analyses provide a compact summary of the anatomical values calculated from the digitized x-ray image. These values are enlisted in tabular form and allow the easy comparison of measurements at various points in time.

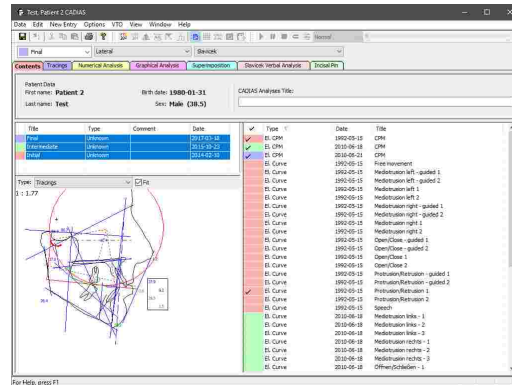
To view a numerical analysis in CADIAS Analyzer, switch to the *Numerical Analysis* pane. You can select the projection and analysis definition to be displayed via the analysis toolbar (refer to chapters "Selecting the projection<sup>[211]</sup>" and "Selecting an analysis definition<sup>[212]</sup>", respectively).



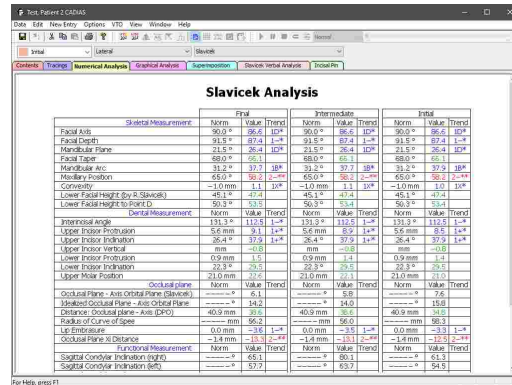
**i** The numerical analysis will only display those values for which all required anatomical points and contours have been digitized. Values that cannot be calculated will remain blank. Furthermore, please note that some values can only be calculated after a condylography curve or anterior guidance has been selected as active on the *Contents* pane (refer to chapter "Selecting data items as active<sup>[206]</sup>").

### 7.2.8.1 Comparing multiple analyses

To compare the numerical analysis of multiple patient visits, select the corresponding examinations on the *Contents* pane.



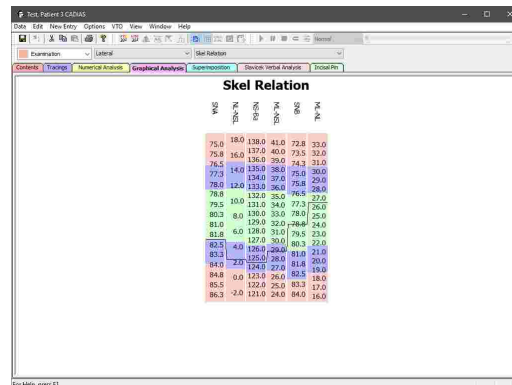
The *Numerical Analysis* pane will thus show the available measurements side-by-side.



### 7.2.9 Graphical analysis

Graphical analyses conveniently aggregate the values that determine certain anatomical properties. Centrally in each column, you can find the norm value with color-coded areas of first, second, and third standard deviation (refer to chapter "Display of numerical values[214]"). The actually measured value is illustrated by a line therein.

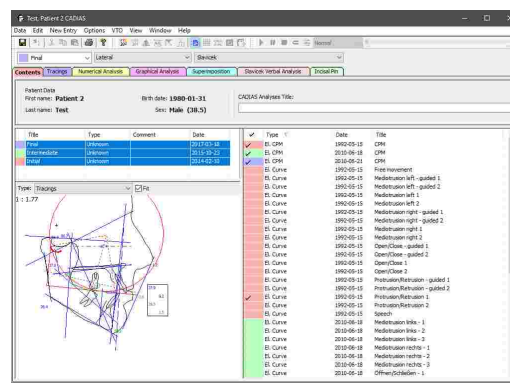
To view a graphical analysis in CADIAS Analyzer, switch to the *Graphical Analysis* pane. Graphical analyses are only available for x-ray images in lateral projection. You can select the analysis definition to be displayed via the analysis toolbar (refer to chapter "Selecting an analysis definition[212]").



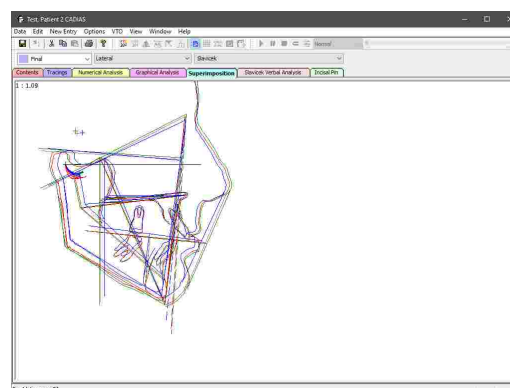
## 7.2.10 Superimposition

Superimpositions can be used to overlay the tracings of the patient that were created at different points in time or over the course of a treatment.

First, select the examinations on the *Contents* pane.



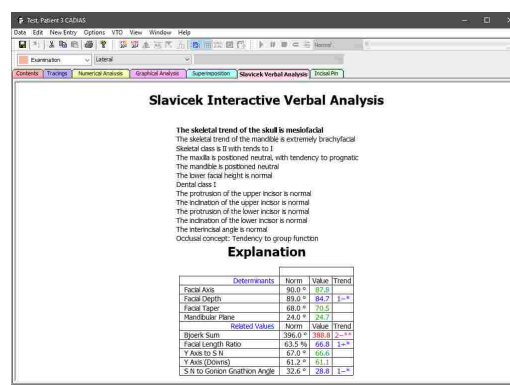
Then, switch to the *Superimposition* pane. The digitizings of the previously selected examinations will be displayed superimposed, using unique colors. You can select the projection and analysis definition to be displayed via the analysis toolbar (refer to chapters "Selecting the projection<sup>[211]</sup>" and "Selecting an analysis definition<sup>[212]</sup>", respectively).



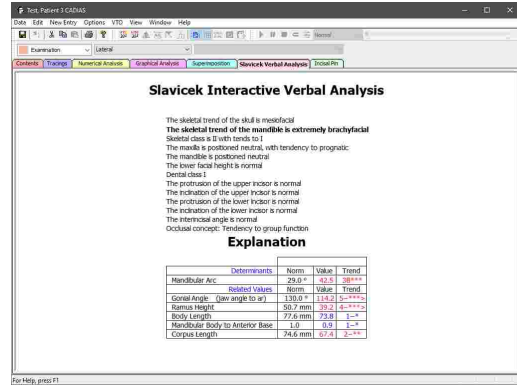
## 7.2.11 Slavicek verbal analysis

The Slavicek verbal analysis describes the patient situation in text form and, complemented by the measured determinant values.

To view the verbal analysis in CADIAS Analyzer, switch to the *Slavicek Verbal Analysis* pane. The verbal analysis is only available for x-ray images in lateral projection.

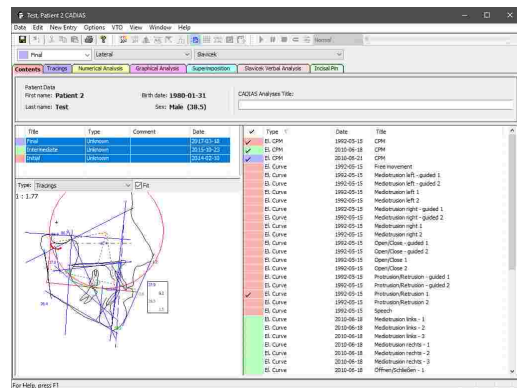


In the upper section of the analysis, you can select one of the statements, which will cause the table below to display the associated measurement values. These are separated into the values that determined the respective statement and other, thematically related values.

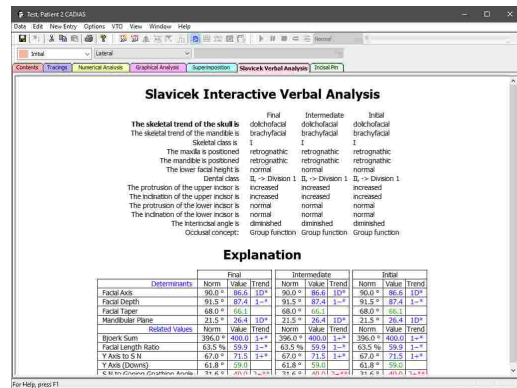


### 7.2.11.1 Comparing multiple analyses

To compare the verbal analysis of multiple patient visits, select the corresponding examinations on the *Contents* pane.



The *Slavicek Verbal Analysis* pane will thus show the available measurements side-by-side.



### 7.2.12 Incisal pin table

The incisal pin table can be used to correlate adjustments of the incisal pin height with the resulting changes to particular anatomical measurement values. An incisal pin height of zero represents the initial reference value, i.e. the actually measured patient situation. In order to calculate the table, the incisal pin is virtually raised (positive value) and lowered (negative value) by the respective value in millimeters and the effects on the anatomical values are documented.

To view the incisal table in CADIAS Analyzer, switch to the *Slavicek Verbal Analysis* pane. The verbal analysis is only available for x-ray images in lateral projection.

	0.0	1.0	2.0	3.0	4.0	5.0	6.0	8.0	10.0	12.0	14.0	16.0	20.0
Incisal pin height	0.0	1.0	2.0	3.0	4.0	5.0	6.0	8.0	10.0	12.0	14.0	16.0	20.0
Lower face height	39.6	40.0	40.4	40.8	41.2	41.6	42.0	42.7	43.3	44.1	44.8	45.3	46.7
LFH norm	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6	43.6
LFH variation	0.0	0.4	0.8	1.2	1.6	2.0	2.4	3.1	3.9	4.5	5.2	5.9	7.1
Menton vertical	0.0	0.4	0.8	1.3	1.7	2.1	2.4	3.2	3.9	4.5	5.2	5.9	7.1
Popinion sagittal	0.0	-0.8	-1.6	-2.4	-3.2	-4.0	-4.8	-6.4	-8.1	-9.7	-11.4	-13.0	-16.3
Incisal inf. vertical	0.0	0.5	1.1	1.7	2.2	2.7	3.2	4.2	5.2	6.2	7.1	8.0	9.6
Incisal inf. sagittal	0.0	-0.6	-1.1	-1.7	-2.3	-2.9	-3.5	-4.7	-5.9	-7.1	-8.3	-9.5	-11.5
Canaline inf. vertical	0.0	0.5	1.0	1.5	2.0	2.5	2.9	3.9	4.7	5.6	6.4	7.3	8.9
Canaline inf. sagittal	0.0	-0.6	-1.1	-1.7	-2.3	-2.8	-3.4	-4.6	-5.8	-7.0	-8.3	-9.5	-11.5

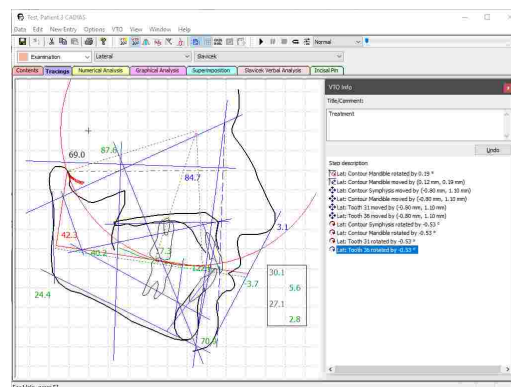
  


	0.0	-1.0	-2.0	-3.0	-4.0	-5.0	-6.0	-8.0	-10.0	-12.0	-14.0	-16.0	-20.0
Incisal pin height	0.0	-1.0	-2.0	-3.0	-4.0	-5.0	-6.0	-8.0	-10.0	-12.0	-14.0	-16.0	-20.0
Lower face height	39.6	39.2	38.8	38.3	37.9	37.4	36.9	36.0	35.0	33.9	32.8	31.7	29.2
LFH norm	43.6	43.4	43.2	43.0	42.8	42.6	42.4	41.9	41.4	40.9	40.4	39.9	38.4
LFH variation	0.0	-0.4	-0.8	-1.3	-1.7	-2.2	-2.7	-3.6	-4.6	-5.7	-6.8	-7.9	-10.4
Menton vertical	0.0	-0.4	-0.9	-1.4	-1.8	-2.3	-2.8	-3.8	-4.9	-6.0	-7.2	-8.5	-11.2
Popinion sagittal	0.0	0.8	1.6	2.4	3.1	3.9	4.8	6.4	8.1	9.7	11.5	13.4	16.4
Incisal inf. vertical	0.0	-0.6	-1.2	-1.7	-2.3	-2.8	-3.4	-4.6	-5.8	-7.1	-8.3	-9.5	-11.5
Incisal inf. sagittal	0.0	0.6	1.1	1.6	2.1	2.7	3.2	4.2	5.2	6.1	6.9	7.7	9.1
Canaline inf. vertical	0.0	-0.5	-1.1	-1.6	-2.1	-2.7	-3.2	-4.4	-5.4	-6.5	-7.6	-8.6	-10.4
Canaline inf. sagittal	0.0	0.5	1.1	1.6	2.1	2.6	3.1	4.1	5.1	6.0	6.8	7.6	8.9

### 7.2.13 Visualized Treatment Objectives (VTOs)


The documentation and visualization of orthodontic treatments in the CADIAS module revolves around the concept of so-called **VTO** items (Visualized Treatment Objective). These items provide the means to define and visualize individual phases of a treatment, such as a controlled repositioning of the anatomical structures that have been digitized on the x-ray image. Subsequently, the analyses described in the previous chapters can be calculated based on the altered craniomandibular situation and compared with the initial situation.


The creation and manipulation of VTOs takes place in the *Tracings* pane with activated VTO mode.

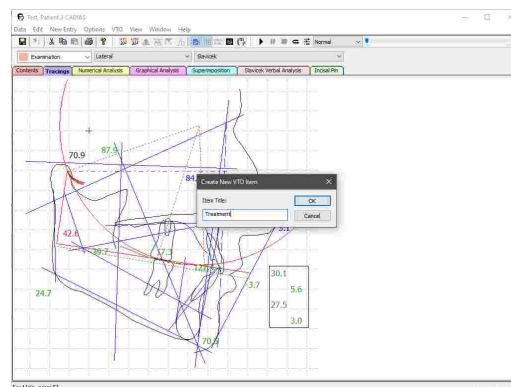


 The definition of a VTO is only possible based on a lateral tracing. Frontal and SMV tracings cannot be used for this purpose.

#### 7.2.13.1 Creating a VTO

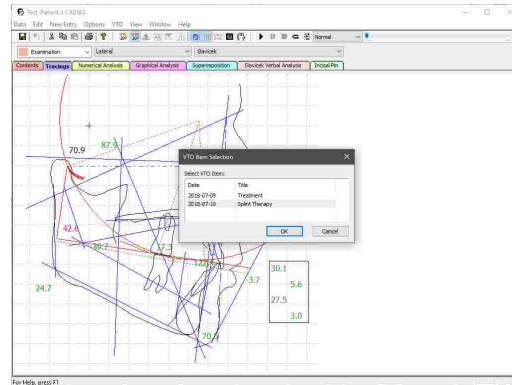
To activate the VTO mode, switch to the *Tracings* pane and press the button  *Activate VTO Mode* in the toolbar. If no VTO has been created yet, a dialog will appear that allows you to enter the title of the new VTO.

To create a new VTO while the VTO mode is already active, use the button  *New VTO* in the toolbar.



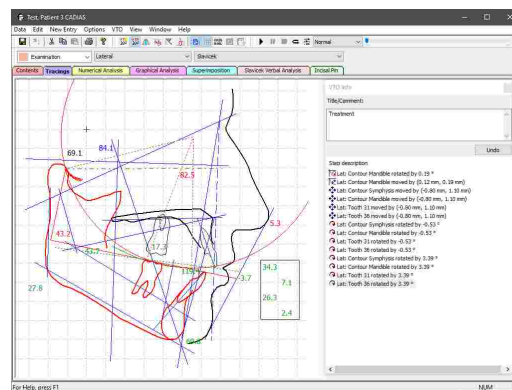
Should you activate the VTO mode while a VTO is already present, that VTO will be activated automatically. If multiple VTOs are present, another dialog will appear that allows you to select the VTO to be activated.

VTOs appear as data items on the *Contents* pane and can be selected as active, just like other data items (refer to chapter "Selecting data items as active" [206]). By manually selecting the active VTO, you can switch between multiple treatment objectives.



### 7.2.13.2 Manual movements

With VTO mode activated, you can manipulate the location of anatomical structures in the tracing. When you move the mouse cursor over a structure that can be manipulated, it will be highlighted in red color. You can then translate it on the sagittal plane by dragging it with the left mouse button pressed. With the right mouse button, you can rotate it around its associated pivot point.

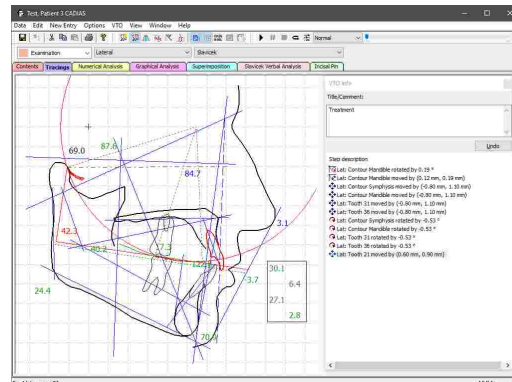


**i** Translational movements of the anatomical structures in sagittal (X) or vertical (Z) direction are specified in to the axis-orbital coordinate system (refer to chapter "The reference coordinate system" [299]). However, please note that some tracings do not use the axis-orbital plane as reference and are therefore displayed with an orientation that does not coincide with those directions.

### 7.2.13.3 VTO info dialog


After each manipulation of the VTO, an entry will be added to the list of modifications in the VTO info dialog and the numerical values displayed in the tracing will be updated to reflect the new situation. By pressing the *Undo* button in this dialog, you can undo the last modification.

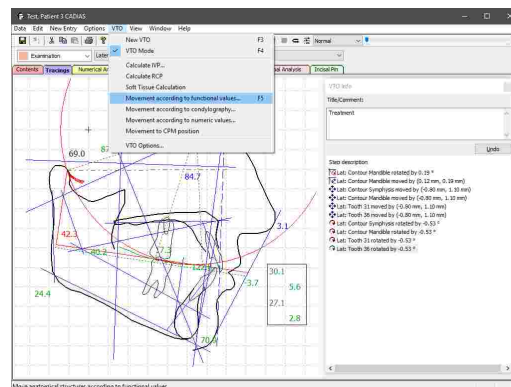
All of this also applies to the VTO manipulations described in the following chapters.



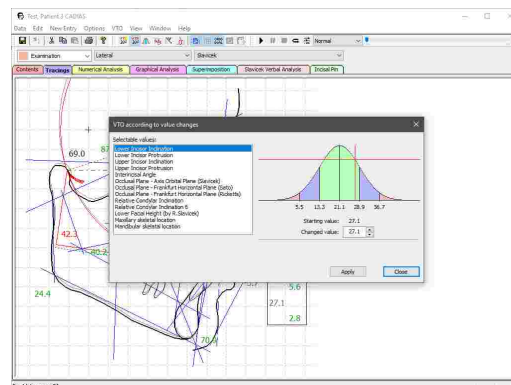
**i** If the VTO info dialog is not visible even though the VTO mode is activated, you can restore its visibility via the corresponding option in the menu *VTO* → *VTO Options*.

### 7.2.13.4 Movement according to functional values

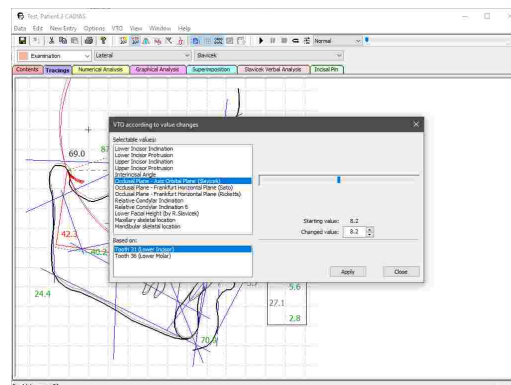
To apply changes based on functional parameters, press the button  *Movement according to functional values* in the toolbar or the corresponding entry in the VTO menu while VTO mode is active.




A dialog will appear, in which you can select the functional value to be adjusted on the left side. On the right side, the normal distribution of the selected value with colors indicating the first and second standard deviation (refer to section "Display of numerical values<sup>[214]</sup>"). The actual value is indicated by a vertical dashed line. By clicking the desired value in the graphical display or by entering a numerical value in the input box below you can set the functional parameter as appropriate. Press the button *Apply* to have the anatomical structures adapted accordingly.




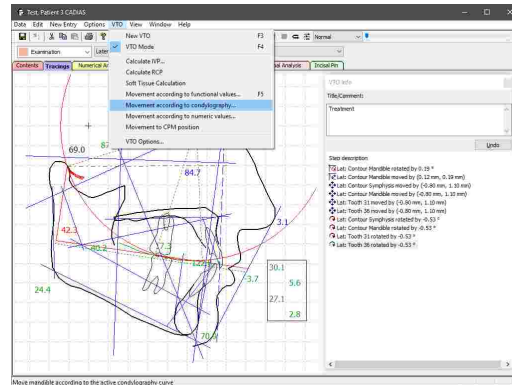
If the selected functional parameter is dependent on multiple anatomical structures, an additional selection box will appear, in which you can select the structure to which to apply the adjustment. For example, the interincisal angle can be adjusted by altering the inclination of either the upper or the lower incisor.



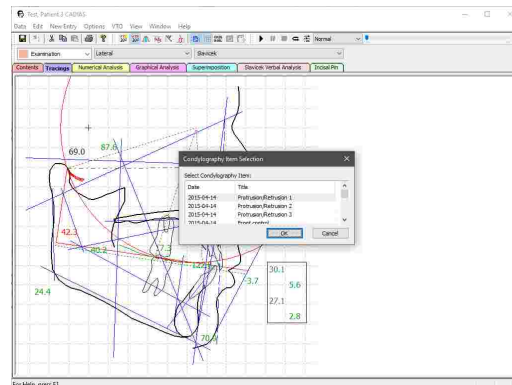
 Movements according to a functional value are only possible when the points and contours required for calculating the value have been digitized. Furthermore, please note that some values can only be calculated after a condylography curve has been selected as active on the *Contents* pane (refer to chapter "Selecting data items as active<sup>[206]</sup>").

### 7.2.13.5 Movement according to condylography

To move the mandible along a condylography recording, press the button  *Movement according to condylography* in the toolbar or the corresponding entry in the VTO menu while VTO mode is active.

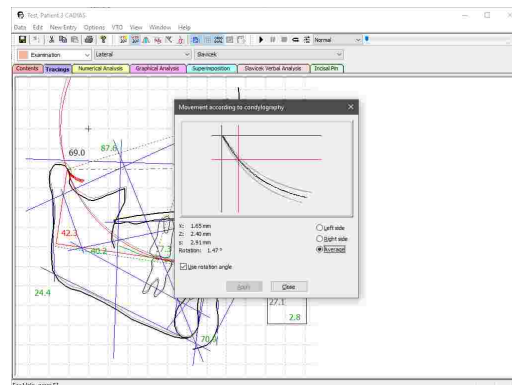


If multiple condylography curves are available, a dialog will appear, in which you can select the movement to be used. This dialog provides not only electronically recorded movements for selection, but also those that have been entered numerically or digitized from analog tracings (refer to chapters "Inserting CADIAX condylography data<sub>204</sub>" and "Digitizings<sub>201</sub>", respectively).




The condylography curve that is currently selected as active in the *Contents* pane will be selected by default in this dialog (refer to chapter "Selecting data items as active<sub>206</sub>").

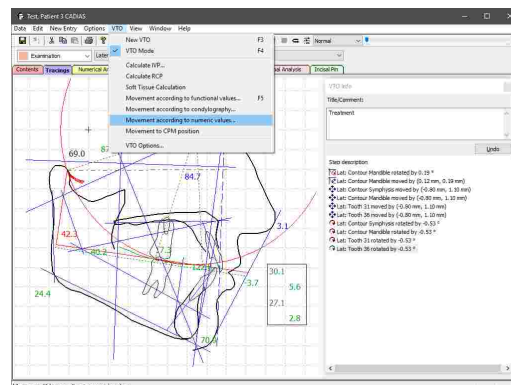
Afterwards you will be shown a dialog with a graphical representation of the condylography curve, in which you can select the desired mandibular position. The X and Z coordinate of the current mouse cursor position as well as the corresponding distance from the zero point, *s*, and the rotation angle will be displayed on the left side below the graphic. The latter can be taken into consideration for the repositioning by checking the check box below. Furthermore, you can choose whether the movement of the left or right patient side or an average of both should be used.



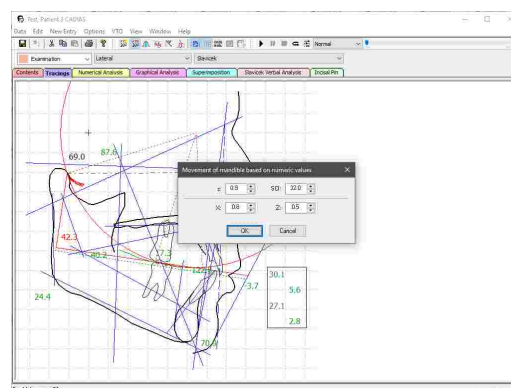
Finally, press *Apply* to move the mandible to the selected position.

### 7.2.13.6 Movement according to numeric values

In order to set the position of the mandible to a numerically defined value, press the button  *Movement according to numeric values* in the toolbar or the corresponding entry in the VTO menu while VTO mode is active.

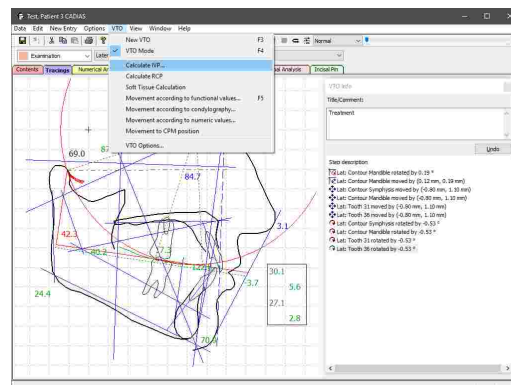


In the appearing dialog, you can specify the movement either as a combination of distance from zero point and SCI angle (Sagittal Condylar Inclination) or by setting the translation in X (sagittal) and Z (vertical) direction. The software will automatically calculate the values for the respectively other input method. Press OK to move the mandible to the specified position.

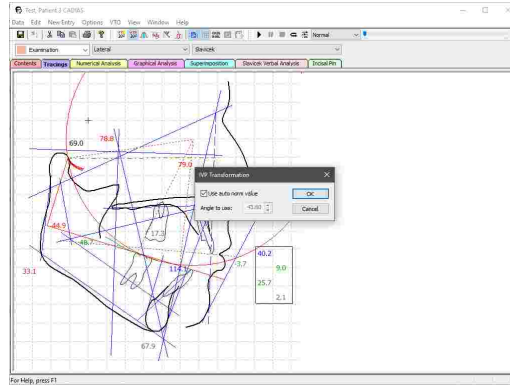


### 7.2.13.7 Recalculation to IVP

To automatically adjust the lower facial height to the ideal vertical position (IVP), use the menu VTO → *Calculate IVP* while VTO mode is active.

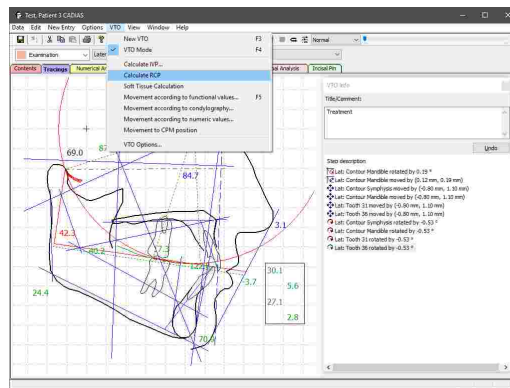


In the appearing dialog, you can specify the angle to which to set the lower facial height. By default, this angle will be the clinically evaluated norm value. You can uncheck the check box in order to enter a custom value.

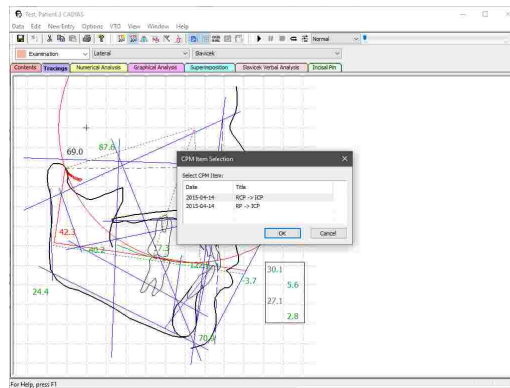


### 7.2.13.8 Recalculation to RCP

To recalculate the position of the mandible to RCP (Retral Contact Position), use the menu **VTO** → *Calculate RCP* while VTO mode is active.

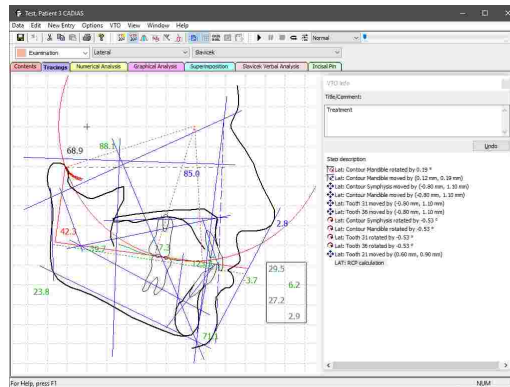


If multiple CPM items are available, a dialog will appear, in which you can select the movement to be used. This dialog provides not only electronically recorded movements for selection, but also those that have been entered numerically (refer to chapters "Inserting CADIAX condylography data<sup>[204]</sup>" and "Condyle Position Measurements (CPM)<sup>[205]</sup>", respectively).



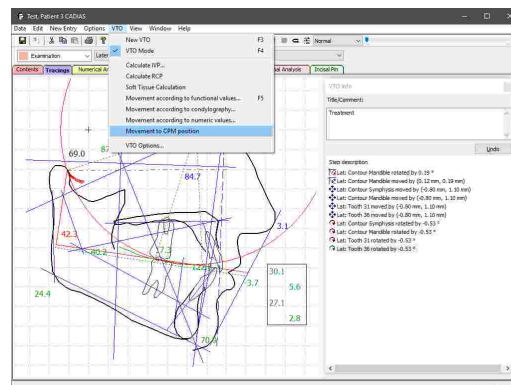
The CPM item that is currently selected as active in the *Contents* pane will be selected by default in this dialog (refer to chapter "Selecting data items as active<sup>[206]</sup>").

The application will then calculate the RCP based on the active CPM recording and subsequently adjust the location and opening rotation of the mandible accordingly.



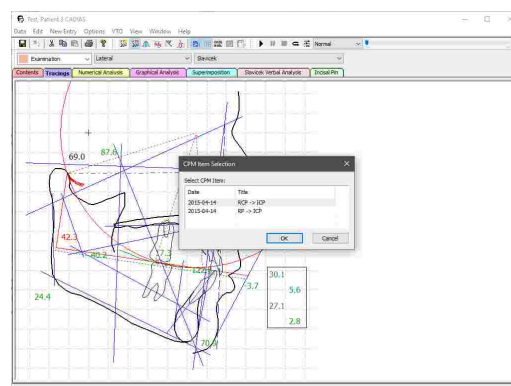
### 7.2.13.9 Movement to CPM position

To apply the movement described by a CPM recording to the mandible, use the menu *VTO* → *Movement to CPM position* while VTO mode is active.

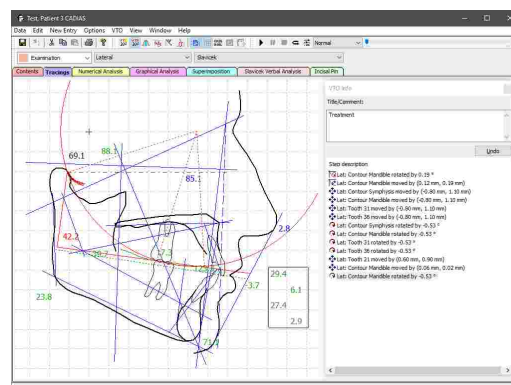


If multiple CPM items are available, a dialog will appear, in which you can select the movement to be used. This dialog provides not only electronically recorded movements for selection, but also those that have been entered numerically (refer to chapters "Inserting CADIAX condylography data<sup>[204]</sup>" and "Condyle Position Measurements (CPM)<sup>[205]</sup>", respectively).


The CPM item that is currently selected as active in the *Contents* pane will be selected by default in this dialog (refer to chapter "Selecting data items as active<sup>[206]</sup>").

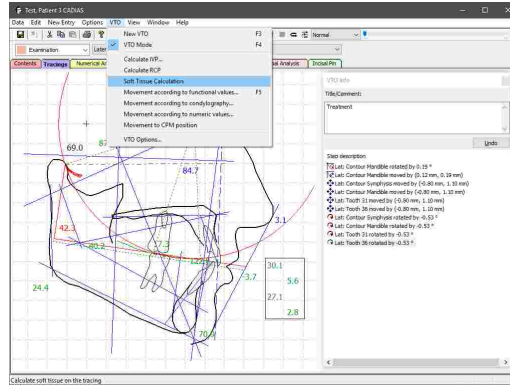


Subsequently, the location and opening rotation of the mandible will be adjusted according to the values described by the CPM recording.

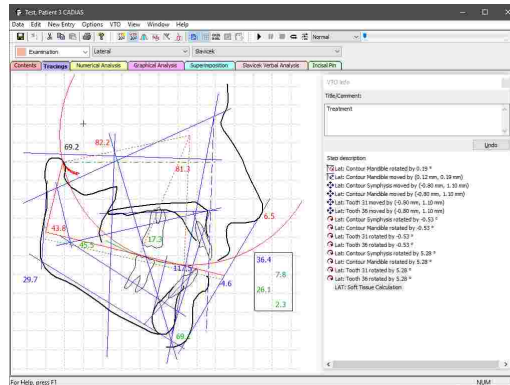



### 7.2.13.10 Soft tissue calculation

To recalculate the soft tissue contour following a manipulation of the bony structures, press the button  *Soft tissue calculation* in the toolbar or the corresponding entry in the *VTO* menu while *VTO* mode is active.




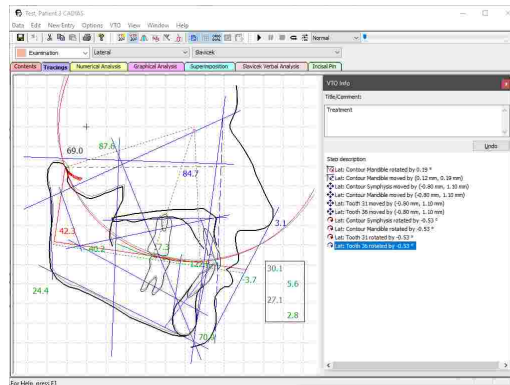
The soft tissue contour will subsequently be recalculated according to the new location of maxilla and mandible.



 To have the soft tissue contour be recalculated after each *VTO* manipulation, you can activate the corresponding option in the menu *VTO* → *VTO Options*. Please note that the soft tissue will only be recalculated automatically after you have performed a manual calculation.

### 7.2.13.11 Superimposing the initial situation

To illustrate the differences resulting from the manipulations made as part of the active *VTO*, you can keep the initial situation displayed in the background using the button  *Original tracing* in the toolbar.

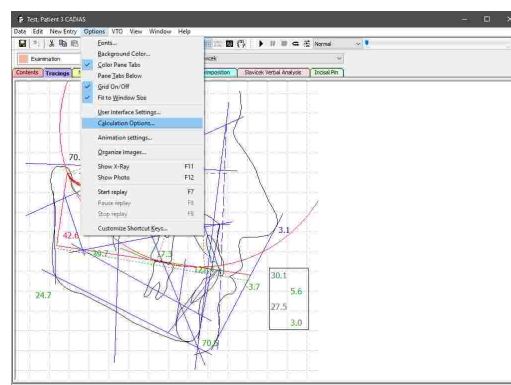


This also applies to the panes *Numerical Analysis* and *Slavicek Verbal Analysis.*, which will display the values for the initial and the VTO situation side-by-side if superimposition is activated.

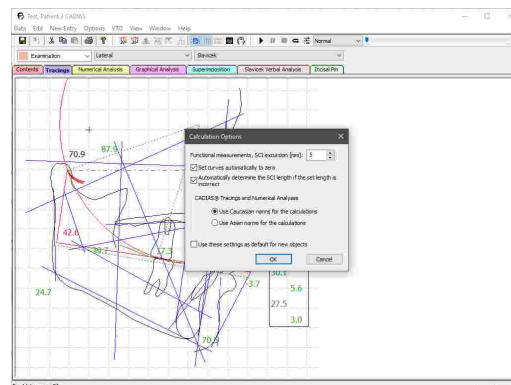
Skeletal Measurement	Initial			Intermediate			Final		
	Norm	Value	Trend	Norm	Value	Trend	Norm	Value	Trend
Facial Axis	90.0°	86.2	10°	90.0°	86.2	10°	90.0°	86.2	10°
Facial Depth	31.5 mm	37.4	1+*	31.5 mm	37.4	1+*	31.5 mm	37.4	1+*
Mandibular Plane	21.5°	26.4	10°	21.5°	26.4	10°	21.5°	26.4	10°
Facial Taper	60.0°	65.0	10°	60.0°	65.0	10°	60.0°	65.0	10°
Mandibular ang.	31.2°	37.2	10°	31.2°	37.2	10°	31.2°	37.2	10°
Mandibular Position	45.0°	50.2	2+**	45.0°	50.2	2+**	45.0°	50.2	2+**
Convergency	-1.0 mm	1.1	10°	-1.0 mm	1.1	10°	-1.0 mm	1.1	10°
Lower Facial Height (by R. Slavicek)	45.1 mm	47.4	1+*	45.1 mm	47.4	1+*	45.1 mm	47.4	1+*
Lower Facial Height to Point G	50.2 mm	53.2	1+*	50.2 mm	53.2	1+*	50.2 mm	53.2	1+*
Dental Measurement									
Intermaxillary angle	133.3°	133.4	1+*	133.3°	133.4	1+*	133.3°	133.4	1+*
Upper Incisor Protrusion	5.4 mm	9.1	1+*	5.4 mm	9.9	1+*	5.4 mm	11.5	1+*
Upper Incisor Tilt	36.4°	37.2	1+*	36.4°	37.9	1+*	36.4°	37.9	1+*
Upper Incisor Vertical	mm	-0.9	mm	-0.9	mm	-0.9	mm	-0.9	mm
Lower Incisor Protrusion	0.9 mm	1.5	0.9 mm	1.1	0.9 mm	1.1	0.9 mm	1.1	
Lower Incisor Inclination	29.2°	29.5	29.2°	29.5	29.2°	29.5	29.2°	29.5	
Upper Molar Position	21.0 mm	22.2	21.0 mm	22.1	21.0 mm	22.1	21.0 mm	21.0	
Occlusal plane									
Occlusal Plane - Axis Orbital Plane (Slavicek)	mm	6.1	mm	5.8	mm	5.8	mm	7.6	
Distance Occlusal Plane - Axis Orbital Plane	mm	14.2	mm	14.0	mm	14.0	mm	15.8	
Distance Occlusal Plane - Axis (SPQ)	mm	40.9	mm	40.9	mm	40.9	mm	40.0	
Radius of Curve of Spee	mm	56.2	mm	56.0	mm	56.0	mm	56.3	
Lip Embrace	0.0 mm	-1.1	1+*	0.0 mm	-1.1	1+*	0.0 mm	-1.3	1+*
Occlusal Plane X Distance	3.4 mm	-1.1	2+**	3.4 mm	-1.1	2+**	3.4 mm	-1.3	2+**
Functional Measurement									
Sagittal Condyle Inclination (right)	mm	65.1	mm	60.1	mm	60.1	mm	61.3	
Sagittal Condyle Inclination (left)	mm	57.2	mm	63.7	mm	63.7	mm	54.5	

### 7.2.14 Calculation options

Using the menu item *Options* → *Calculation options*, you can configure various settings regarding the calculation of condylar inclination values and the norm values provided by the application.



You can find detailed explanations of the available calculation options in the following chapters.

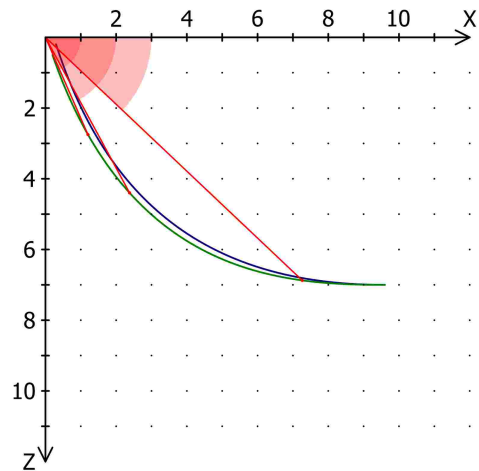


**i** You can save the current settings as default for new CADIAS analysis objects in GDSW classic by checking the respective check box before pressing OK. However, if CADIAS Analyzer has been started from GAMMA Document Browser, it will always use the calculation options that were defined as properties of the CADIAS analysis in the Workspace (refer to chapter "Creating a CADIAS analysis").

### 7.2.14.1 SCI excursion distance

By setting an SCI excursion distance (SCI = Sagittal Condylar Inclination), you can specify the location on the selected condylography curve at which to measure the SCI angle for the numerical analysis. Thus, this setting also affects the values dependent on the SCI angle, such as the relative condylar inclination RCI.

In most cases, the excursion distance specified here corresponds to one of the excursion distances used for articulator programming in the CADIAX module, i.e. 3 mm, 5 mm, or 10 mm (refer to chapter "Articulator Settings" <sup>148</sup>).

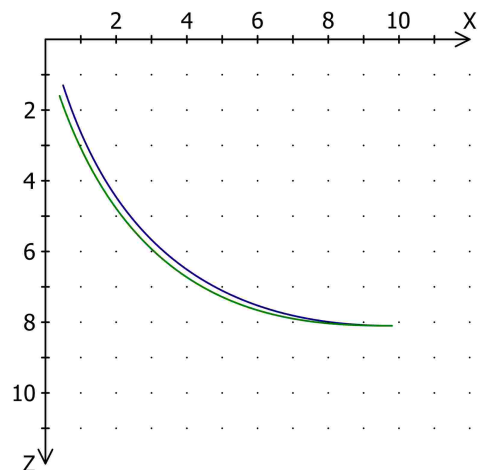


If the selected condylography curve is shorter than the specified excursion distance, the SCI angle and dependent values in the numerical analysis will remain blank. To fall back to the angle at the most excursive point of the curve in those cases, you can activate the option for automatically determining the SCI excursion distance in the calculation options.

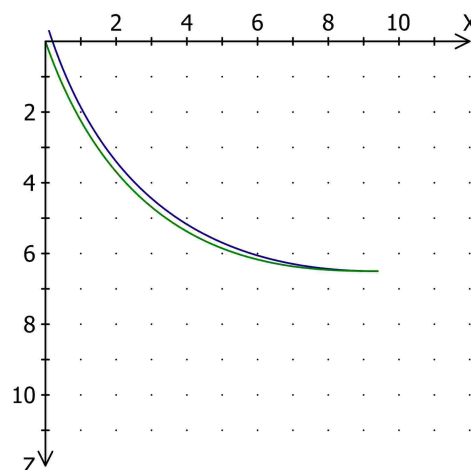
**i** The SCI excursion distance is measured from the origin of the coordinate system, which does not necessarily coincide with the starting point of the condylography curve. To align the curve with the coordinate system origin, use the respective calculation option (refer to chapter "Zeroing of condylography curves" <sup>232</sup>) or the zero point adjustment in the CADIAX module (refer to chapter "Zero point adjustment" <sup>141</sup>).

### 7.2.14.2 Zeroing of condylography curves

In some recordings, for example on patients with an unstable reference position, the starting point of the condylography curve might not coincide with the origin of the coordinate system.



For such cases, you can activate an automatic zeroing of condylography curves in the calculation options, which will move the starting point of the curve to the origin of the coordinate system. Alternatively, you could also carry out such a correction manually using the corresponding function in the CADIAX module (refer to chapter "Zero point adjustment [141]").



### 7.2.14.3 Selecting race-specific norm values

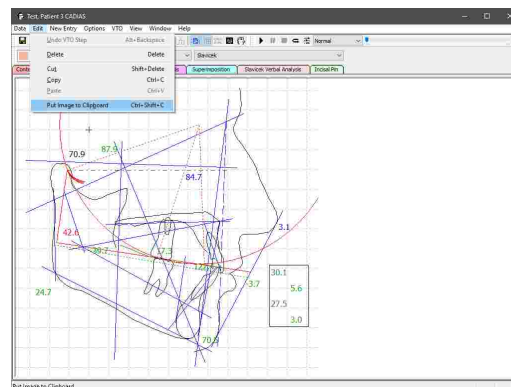
For the evaluation of race-specific cephalometric values, the CADIAS module provides norm values for Caucasian and Asian facial types, between which you can switch in the calculation options. After changing the norm values to be used, the deviations and trend values displayed in the analyses will be recalculated automatically (refer to chapter "Display of numerical values [214]").

## 7.2.15 Display options

### 7.2.15.1 Copying the view to the clipboard

To copy the current view as an image to the clipboard, use the menu entry *Edit* → *Put Image to Clipboard*.

You can then paste the copied image for further editing or for creating presentations into external applications such as Microsoft Paint or Microsoft PowerPoint.



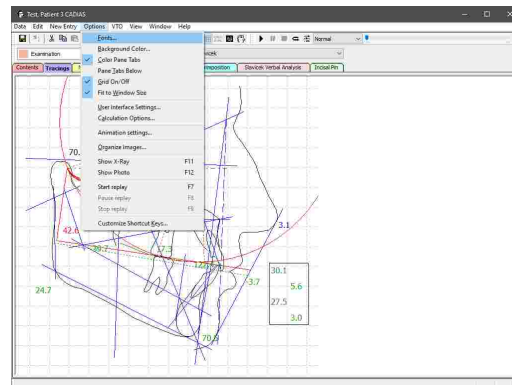
### 7.2.15.2 Copying values to the clipboard

To easily export the values displayed by the software to external applications, you can copy them to the clipboard by right-clicking any of the displayed tables and choosing *Copy values* in the context menu. This functionality is available in the numerical analysis, the Slavicek verbal analysis, the incisal pin table, as well as in the diagnostic sheet.

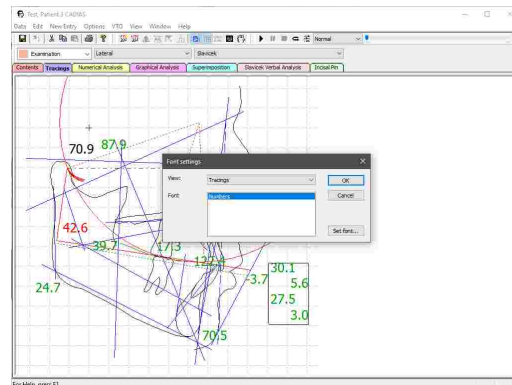
Statistical Measurement	Norm	Value	Trend
Facial Axis	80.0°	87.9°	
Facial Depth	69.0°	84.7	1-*
Horizontal Plane	24.0°	24.7	
Facial Taper	68.0°	70.5	
HandBulge Ang	29.0°	42.6	89***
Maxillary Protrusion	65.0°	69.8	
Corneality	0.0 mm	3.0	10*
Lower Facial Height (By S Slavicek)	43.6°	38.4	
Lower Facial Height (by HOFED)	50.3°	48.3	
Dental Measurement			
Interincisal Angle	130.4°	122.4	
Upper Incisor Protrusion	mm	5.6	
Upper Incisor Vertical	mm	2.6	
Lower Incisor Protrusion	mm	3.0	
Lower Incisor Endination	-21.1°	27.5	
Upper Molar Endination	19.0 mm	17.1	
Occlusal plane			
Occlusal Plane - Axis (Optical Plane (OPNS))	mm	8.6	
Identified Occlusal Plane - Axis (Optical Plane)	mm	10.5	
Distance - Occlusal plane - Axis (EPO)	40.0 mm	26.0	
Radius of Curve of Spee	mm	70.9	
Lip Embrasure	0.0 mm	0.7	
Occlusal Plane (I) Distance	-1.4 mm	0.2	
Functional Measurement			
Sagittal Condyle Inclination (right)	Norm	Value	Trend
Sagittal Condyle Inclination (left)	mm	53.9	

### 7.2.15.3 Changing the font

To change the settings of the fonts used for the analyses, such as type face, color, and size, use the menu entry *Options* → *Fonts*.

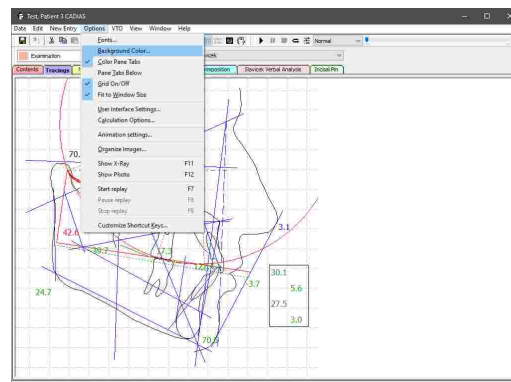


In the subsequent dialog, you will be able to select the analysis and the elements for which you want to customize the font. For example, in the case of a numerical analysis, you can set a different font for the title and the individual values of the table. Press the button *Set font* to set the font to be used for the specified section.

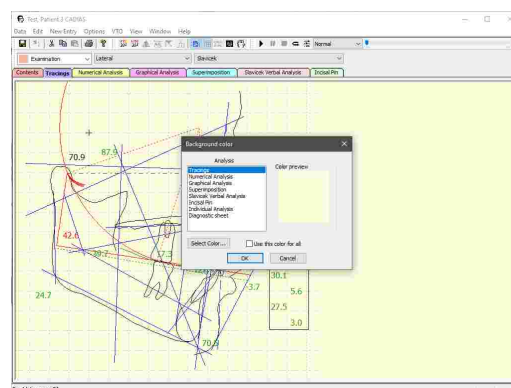


### 7.2.15.4 Changing the background color

To change the background color of the analyses, use the menu entry *Options* → *Background Color*.

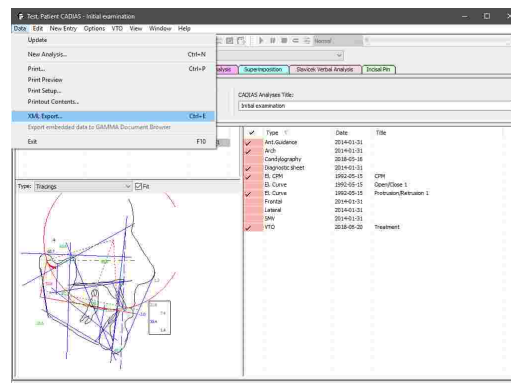


In the following dialog, you can specify a distinct background color for each analysis. By checking the provided check box, you can have the selected color be applied to all analyses at once.

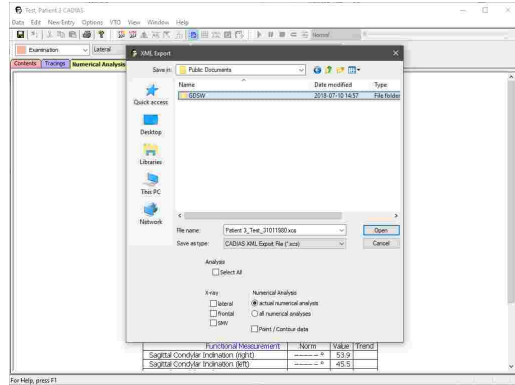


### 7.2.16 XML export

To export the cephalometric data of the CADIAS module for custom evaluations, CADIAS Analyzer provides a feature for exporting this data in the human- and machine-readable XML format. To do so, use the menu item *Data* → *XML Export*.

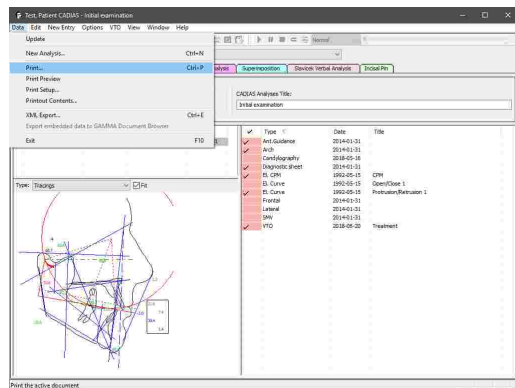


In the subsequent dialog, you can choose which analyses, digitizings, and numerical analyses should be included in the export. Furthermore, you can specify whether the coordinates of the digitized points and contours should be included.

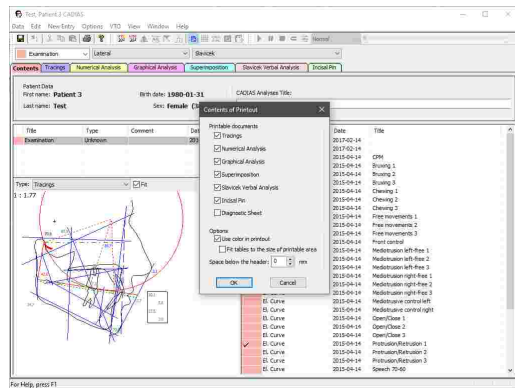


### 7.2.17 Printing

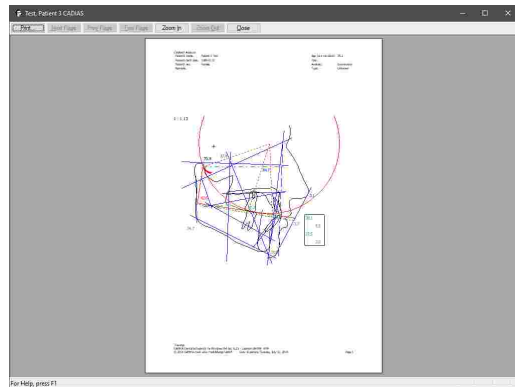
To print particular CADIAS analyses, show a print preview, or change the page format of the printout, use the respective entries in the *Data* menu.



Prior to printing, you will be shown a dialog in which you can select the analyses to be printed and specify other printing-related settings. The following analyses are available for selection:

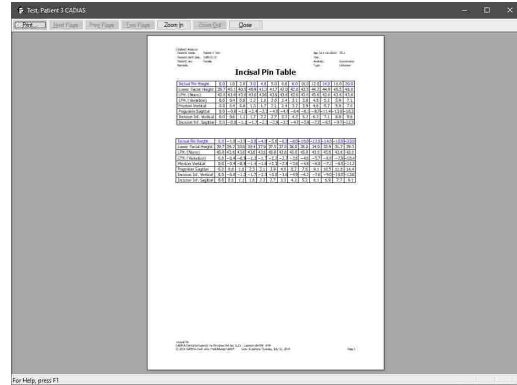


- Tracing

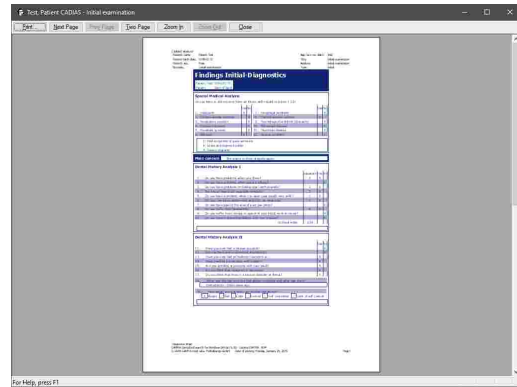




- Incisal pin table

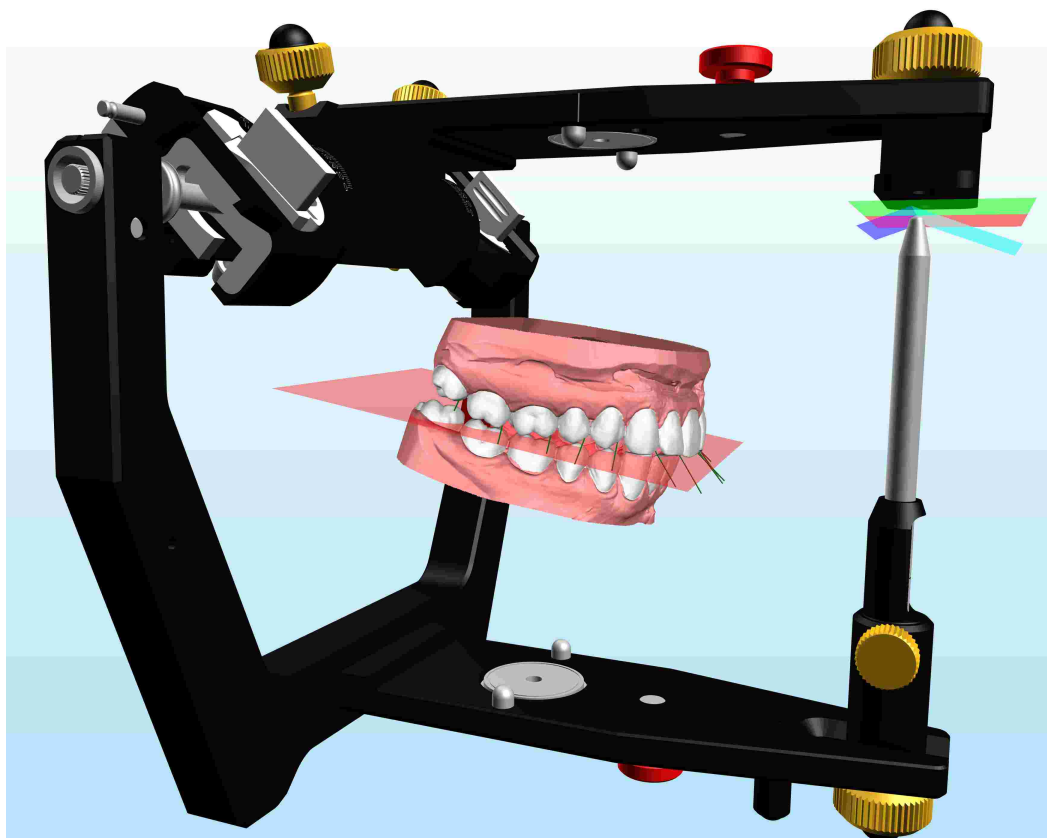


- Diagnostic sheet: Only available if CADIAS Analyzer has been started from GDSW classic. If the application has been started from GAMMA Document Browser, the diagnostic sheet input takes place in the form editor integrated therein (refer to chapter "Entering a diagnostic sheet<sup>65</sup>").



## 8 CADIAS 3D

The software module **CADIAS 3D** is a tool for static and dynamic occlusion analysis based on 3D dental models in a virtual articulator. Lower jaw movements can be simulated using either the patient's actual CADIAX recordings or approximative articulator settings (refer to chapter "CADIAX<sup>114</sup>"). CADIAS 3D supports the digital CAD/CAM workflow of modern dentistry and aids in the production of prosthetic appliances in the dental laboratory.

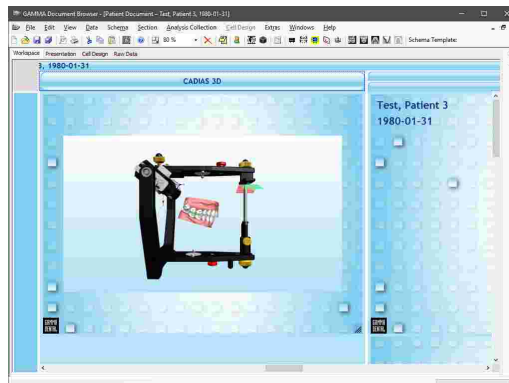


CADIAS 3D is not included in all software licenses and may not be available in your software. Please refer to chapter "Compare editions<sup>16</sup>" for more information.

### 8.1 Starting the application

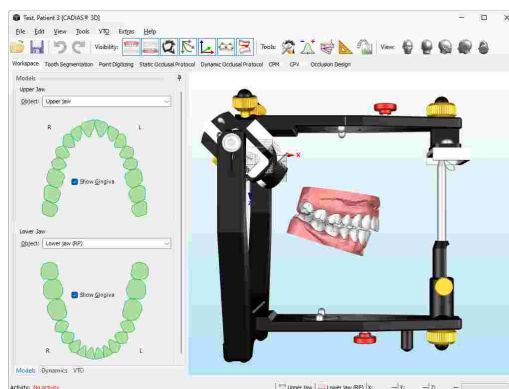
CADIAS 3D is an integral part of GAMMA Document Browser and not available from GDSW classic. For more information regarding GAMMA Document Browser, please refer to chapter "GAMMA Document Browser<sup>34</sup>".



You can start CADIAS 3D from GAMMA Document Browser by double-clicking one of the CADIAS 3D data areas. For more information about creating a CADIAS 3D data area, please refer to chapter "Importing CADIAS 3D data" <sup>82</sup>.



## 8.2 User interface

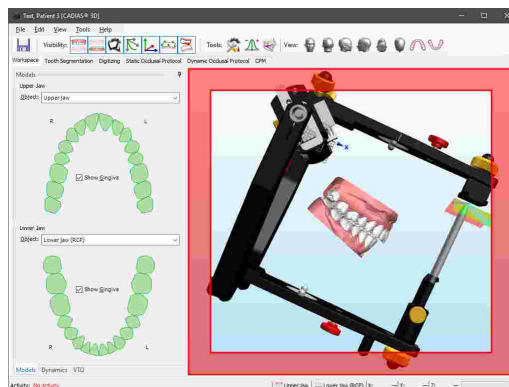
You will find the features of CADIAS 3D separated on panes that you can switch between via the horizontal register bar that is located below the tool bar. Each pane provides its primary functionalities via panels on the left side of the window. Additional tools can be shown on the right side of the window as needed (refer to chapter "Tools" <sup>273</sup>).



 All side panels in CADIAS 3D may be collapsed and switched into auto-expanding mode by clicking on the pin needle icon . This gives more real estate to the 3D environment, which can be especially important on smaller screens.

Use the mouse buttons and the mouse wheel to navigate within the 3D environment. You can move the view by pressing and holding the left or middle mouse button, rotate it with the right mouse button, and zoom in and out by scrolling with the mouse wheel.








In addition, you can rotate the view around the view axis by pressing and holding the right mouse button at the borders of the 3D display. This area is marked **red** in the accompanying picture.








You can control the visibility of individual objects in the 3D environment by using the following toolbar buttons:









Shows or hides the upper jaw model. Make sure that you have selected a model on the *Models* panel of the Workspace (refer to chapter "Objects" <sup>254</sup>).

-  Shows or hides the lower jaw model. Make sure that you have selected a model on the *Models* panel of the Workspace (refer to chapter "Objects" [254](#)).
-  Shows or hides the virtual Reference SL articulator.
-  Shows or hides the condylar coordinate systems and the currently selected condylography curve (refer to chapter "Dynamics" [255](#)).
-  Shows or hides the origin and the axes of the articulator's coordinate system. The X axis is displayed in blue, the Y axis green, and the Z axis red.
-  Shows or hides the points that have been digitized on the models (refer to chapter "Point digitizing" [260](#)).
-  Shows or hides the functional guidance paths that have been specified as part of the dynamic occlusal protocol (refer to chapter "Dynamic occlusal protocol" [263](#)).
-  Shows or hides the occlusal distances between upper and lower jaw model.

Some panes provide additional tools that can be docked to the right border of the window as needed. Use the following toolbar buttons to show the respective side panel:

-  Articulator settings (refer to chapter "Articulator settings" [273](#))
-  Numerical analysis (refer to chapter "Numerical analysis" [274](#))
-  Graphical analysis (refer to chapter "Graphical analysis" [274](#))
-  Custom measurements (refer to chapter "Custom measurements" [274](#))
-  3D image overlay (refer to chapter "3D image overlay" [275](#))

By using the following buttons in the toolbar, you can quickly jump to a predefined view from the indicated direction:

-  Frontal view
-  Back view
-  Lateral right view
-  Lateral left view
-  Top view
-  Bottom view



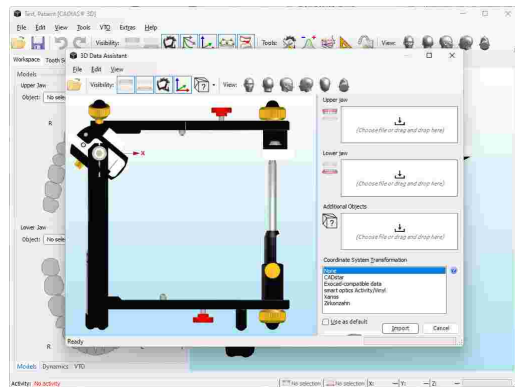
Occlusal view of the upper jaw model. Other objects are hidden automatically.



Occlusal view of the lower jaw model. Other objects are hidden automatically.

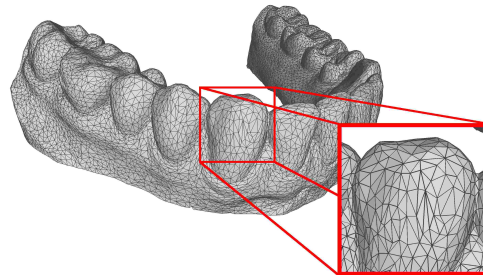
### 8.3 Importing 3D data


Importing 3D data is carried out using the **3D Data Assistant**, which you can start either from GAMMA Document Browser (refer to chapter "Importing CADIAS 3D data") or directly in CADIAS 3D via the menu *File* → *Open*. The 3D Data Assistant allows loading the 3D models from files, transforming them into GAMMA's axis-orbital coordinate system, and performing basic mesh editing tasks.



#### 8.3.1 Supported 3D file formats

A 3D dental model in general is a representation of the hollow surface of the patient's dentition. During a 3D scanning procedure, many thousand points are measured on the physical model and subsequently connected to form a triangle mesh that approximates the true model's surface. Raising the scan resolution will increase the density of point measurements and thus also the number of triangles, resulting in a more accurate approximation of the true model. A corresponding setting is typically also provided when exporting data from third-party CAD/CAM software.



 Please note that increasing the model resolution will result in an increase of the software's demands on performance and memory due to the greater amounts of data being processed. Experience has shown that the resolution of models with around 500,000 triangles is sufficient for most use cases. This equates to a file size of about 25 MB in case of the binary STL file format. Having imported a model in the 3D Data Assistant, the actual number of triangles will be displayed in the status bar.


For importing data in the 3D Data Assistant, the following file formats are supported:

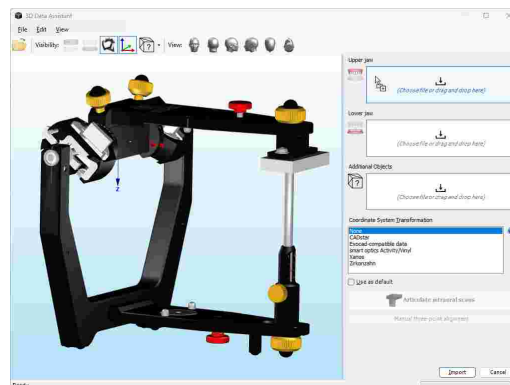
- STL (text-based or binary)
- OBJ (text-based)
- PLY (text-based or binary)
- OFF (text-based or binary)

The 3D coordinate values of the vertices in the triangle mesh are expected in millimeter units. Besides the surface topology of the dental model, the file formats stated above may also specify auxiliary

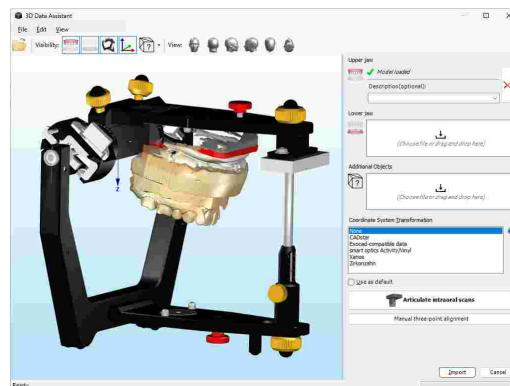
information such as color, materials, textures, or normal vectors. If the imported file includes color information or a texture, you will be able to use the a special display mode in CADIAS 3D for visualizing the true surface color of the 3D model (refer to chapter "Visual settings for 3D objects [277]").


### 8.3.2 Importing upper and lower jaw model

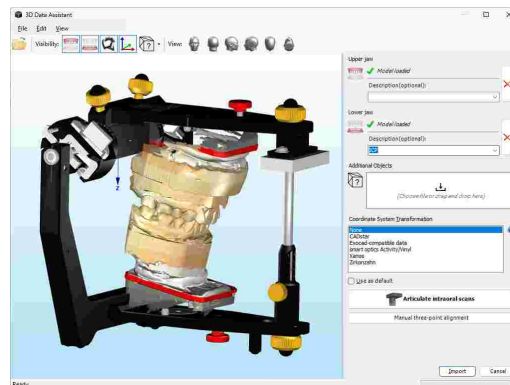
To import an upper and lower jaw model, simply drag and drop the corresponding files from your file explorer onto the areas indicated by the icon . Alternatively, open a regular file dialog by clicking those areas or press *Ctrl+V* to paste a copied file from the clipboard.




If a 3D model loaded from file has been created for GAMMA's coordinate system, it will be placed in the correct position in the virtual articulator automatically. Otherwise, it needs to be transformed as appropriate for the 3D scanner or software that created the data. Refer to the following chapter "Coordinate system transformation [244]" for more information.

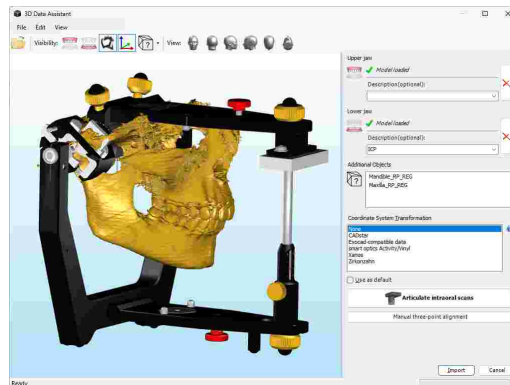


If you intend to load multiple models of the same type, for example, two lower jaw models in both reference position (RP) and intercuspation (ICP), you can enter a description in the corresponding input box. The last used descriptions are provided for selection via the drop-down menu. To unload a previously loaded model from the 3D scene, use the respective  *Remove* button.



### 8.3.3 Importing additional objects

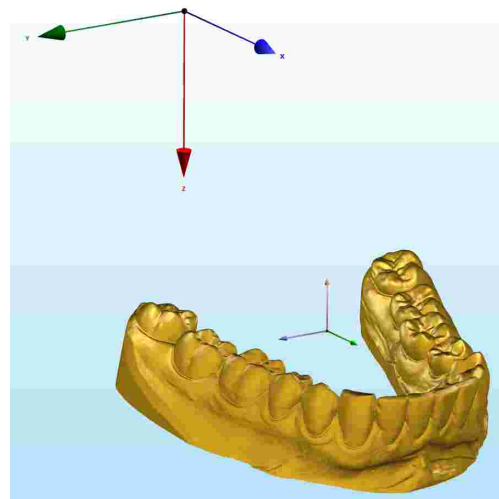
In addition to loading an upper and lower jaw model, it is also possible to load an arbitrary number of additional objects in the 3D Data Assistant. Loaded objects are listed in the side panel and can be shown or hidden using the  *Show Additional Objects* drop-down button in the toolbar. You can load, rename, or remove additional objects using the context menu of the list in the side panel.




### 8.3.4 Coordinate system transformation

Typically, the 3D model data created by 3D scanners and CAD/CAM software will use the respective manufacturer's proprietary coordinate system. In order to correctly position a dental model in the virtual articulator of CADIAS 3D, the model needs to be aligned with GAMMA's axis-orbital coordinate system beforehand (refer to chapter "The reference coordinate system<sup>[299]</sup>").

This alignment can be carried out by applying an appropriate **Transformation Template** during the import, which describes the 3D transformation that converts the model data from one coordinate system to the other. An installation of GAMMA Dental Software comes with several predefined transformation templates, which can be extended or adapted to your particular workflow as needed (refer to chapter "Transformation Templates<sup>[249]</sup>").



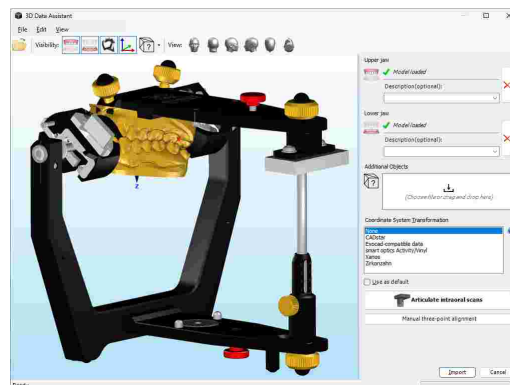
 For the import of 3D dental models in the CADIAS 3D module it is essential that the models are correctly positioned in the virtual articulator. This does not only concern the relation of upper and lower jaw models to one another, but also their relation to the hinge axis of the temporomandibular joint. The latter is especially important because even minor positional deviations can lead to significantly different tooth contacts in dynamic occlusion.

Verify the correct model position prior to your first use of the CADIAS 3D module as well as subsequently in regular time intervals and adapt the used transformation template as needed.

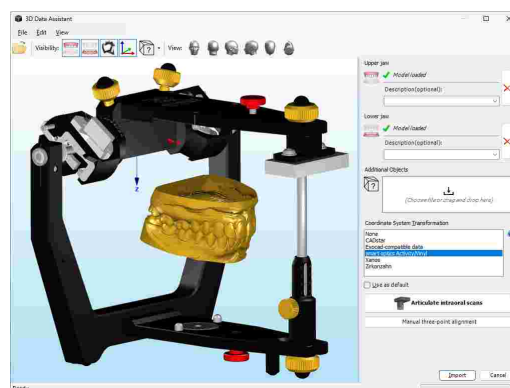
#### 8.3.4.1 Articulating laboratory scans or CAD/CAM data

When scanning articulated plaster models in a laboratory scanner or when exporting scan data from an external CAD/CAM application, the resulting data will always use an exactly defined coordinate system. The transformation required to position the model scans correctly in the virtual articulator will thus always be the same. To correctly articulate this type of data, GAMMA Dental Software comes with several predefined **transformation templates** for various laboratory scanners and CAD/CAM applications. You may extend or modify these templates as appropriate for your workflow (refer to chapter "Transformation templates<sup>[249]</sup>").

Following the import of 3D models, these are by default displayed in their own respective coordinate system. Oftentimes, the origin of this coordinate system lies centrally between the upper and lower jaw, resulting in the models being displayed near the origin of the articulator coordinate system.



To apply a transformation template, select the item appropriate for your scanner or software from the list box in the side panel. If you want the selected template to be applied automatically for all models imported in the future, activate the option *Use as default* before finishing the import.

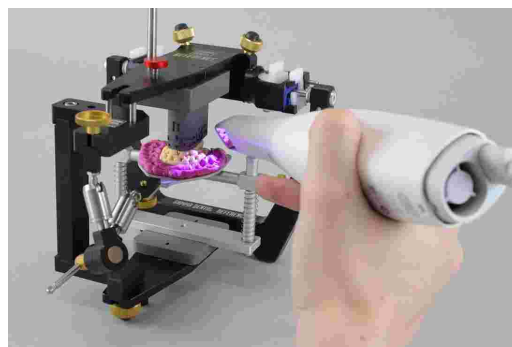


If you use a 3D scanner for creating the 3D dental models, make sure that it is intended to be used in the dental sector and achieves a minimum accuracy of 10  $\mu\text{m}$  in accordance with ISO 12836. Follow the manufacturer's instructions regarding the calibration of the scanner system.

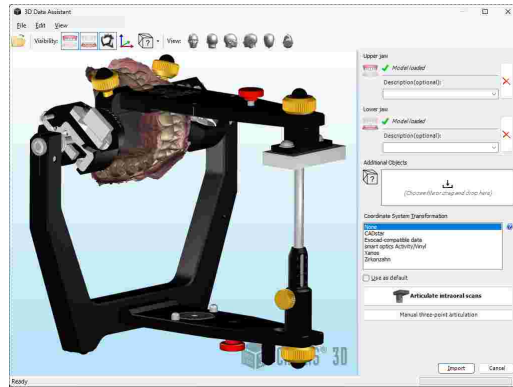
### 8.3.4.2 Articulating intraoral scans (Digital Workflow)

Unlike laboratory scans of articulated plaster models, intraorally scanned 3D models have no defined relationship to the hinge axis of the temporomandibular joint or a cranial reference plane. To address this issue, GAMMA has developed a digital workflow that allows transferring intraoral scans into the virtual articulator using either the anatomic or the exact kinematic hinge axis. This workflow requires an additional scan of the bite fork with the upper jaw impressions together with a digital transfer block (order number 06-230950) to be performed with the intraoral scanner.

For more information regarding the usage of the digital transfer blocks, please refer to the corresponding instructions for use.



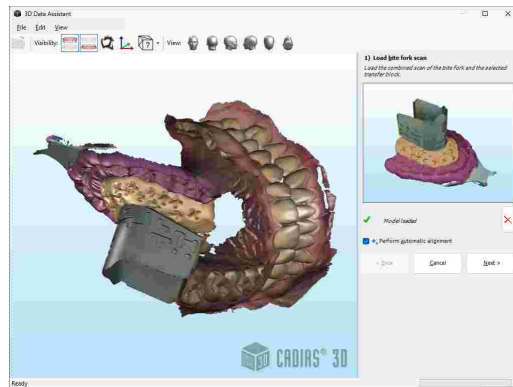
First, load the intraoral scans of upper and lower jaw in the 3D Data Assistant. Press the button **Articulate intraoral scans** to start the digital workflow. This workflow will guide you step-by-step through the procedure of aligning the 3D data.



**Step 1: Load bite fork scan**

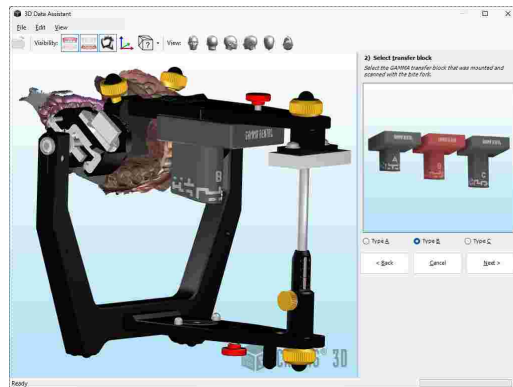
Load the scan of the bite fork that shows both the upper jaw impressions and the transfer block.

Here, the **Perform automatic alignment** check box allows you to choose between performing the subsequent alignment steps automatically or manually by marking three corresponding points. Automatic alignment skips the manual steps and speeds up the articulation process substantially.



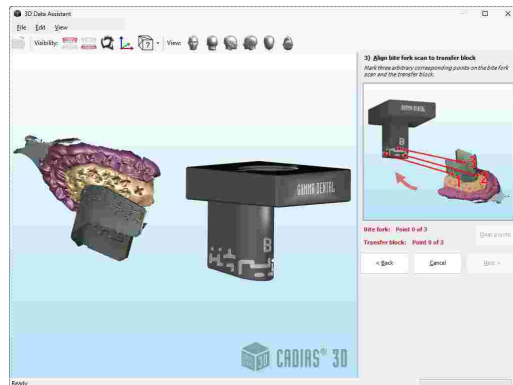
**Step 2: Select transfer block**

Select the type of transfer block that was used to scan the bite fork in the articulator or transfer stand.



**Step 3: Align bite fork scan to transfer block**

Mark three points on the transfer block and the same three points on the bite fork scan. If necessary, you can clear already digitized points using the corresponding button in the side panel. Upon pressing **Next**, the software will carry out a precise surface alignment of the two 3D datasets.



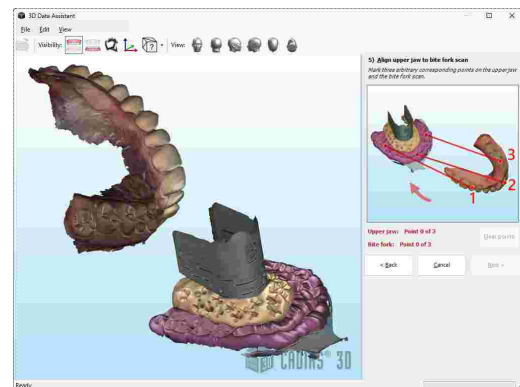
**Step 4: Check alignment of bite fork scan**

Verify the result of the surface alignment. Ideally, the two surfaces are perfectly superimposed. The average deviation of the superimposed surfaces in millimeters is given in the side panel.



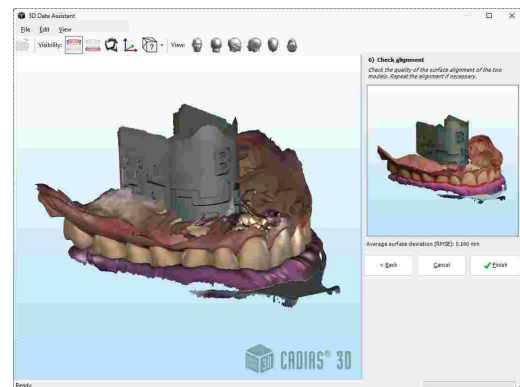
**Step 5: Align upper jaw to bite fork scan**

Again, mark three corresponding points on the upper jaw impressions of the bite fork and on the intraoral scan of the upper jaw. The upper jaw will thus be aligned to the bite fork.

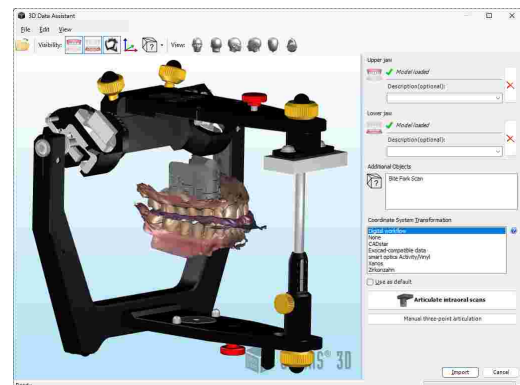


**Step 6: Check alignment of upper jaw**

Verify the alignment of the upper jaw. The model should be placed firmly in the impressions of the bite fork. You may now finish the digital workflow.



After finishing the digital workflow, both upper and lower jaw models will be shown in the virtual articulator. The data is now correctly positioned and ready for import.



### 8.3.4.3 Performing a three-point alignment

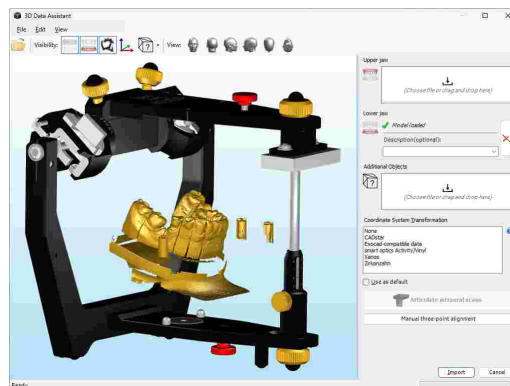
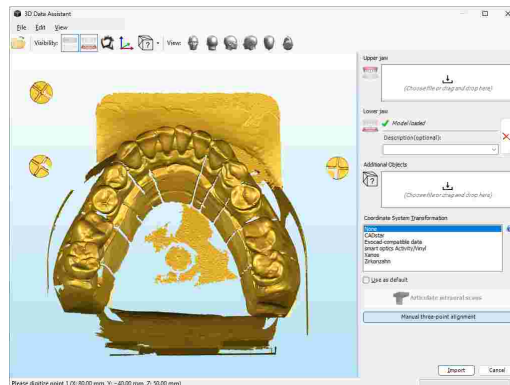
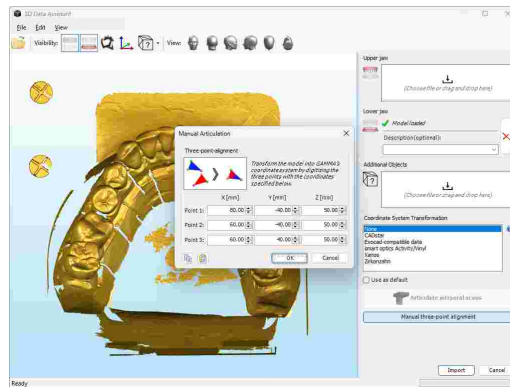
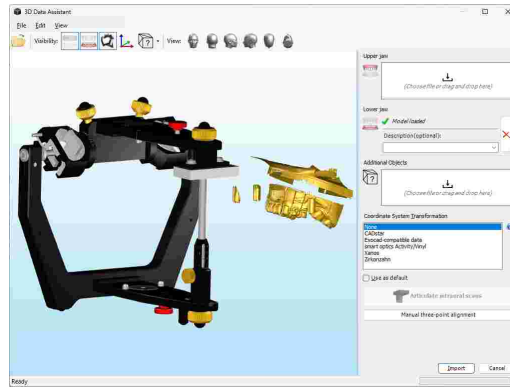
It is also possible to manually position a model in the virtual articulator by digitizing three points with known coordinates on the model surface. The software can thus transform the model in a way to optimally align the digitized points with their nominal coordinates.

To start the manual three-point alignment, press the corresponding button in the side panel. In the appearing dialog, enter the nominal *X/Y/Z* coordinates of the three articulation points that you are going to digitize in the next step. Confirm by pressing *OK*.

Now, you can move your mouse cursor over the model's surface and click the left mouse button to digitize the three articulation points. Make sure to digitize them in the same order in which you specified their coordinates in the previous dialog.

Once all points have been digitized, press the right mouse button to confirm and have the software transform the model to its nominal position.

The model will now be positioned so that the articulation points are as close as possible to their previously entered coordinates. During the transformation, the model will only be moved and rotated, but not scaled. This can cause the digitized points to not be exactly at the entered coordinates, depending on the quality of the model data and the accuracy of the digitizing.



### 8.3.4.4 Transformation templates

Transformation templates are stored as XML-files in the definition files folder of GAMMA Dental Software (refer to chapter "Definition files"<sup>[297]</sup>), which makes it easy to create your own. Predefined transformation templates for the following 3D scanner and CAD/CAM software solutions are provided with a standard installation of GAMMA Dental Software:

- smart optics  
<https://www.smartoptics.de/>
- Zirkonzahn  
<https://www.zirkonzahn.com/>
- CADstar  
<https://www.cadstar.dental/>
- Xanos (equivalent to DOF)  
<https://www.dentag-italia.com/en/products/cad-cam/scanning/>
- Exocad  
<https://exocad.com/>

Each transformation template must specify a display name for how the template should be listed in the 3D Data Assistant as well as an arbitrary combination of the following transformation operations. Each operation is represented by an XML-Element with or without attributes.

#### Translation

The `<Translate>` element moves the model by the specified offset along one or more axes of the coordinate system. Omitted coordinate values are assumed to be zero.

The following example translates the model by 80 mm along the X axis, by -30 mm along the Y axis, and by 60 mm along the Z axis:

```
<Translate X="80.0" Y="-30.0" Z="60.0" />
```

#### Rotation

The `<Rotate>` element rotates the model around an arbitrary axis specified by two points. The angle of rotation is specified in degrees and applied using the right-hand rule. Omitted coordinate values are assumed to be zero.

The following example rotates the model by -90° around the Z axis:

```
<Rotate X1="0.0" Y1="0.0" Z1="0.0"
X2="0.0" Y2="0.0" Z2="1.0"
Angle="-90.0" />
```

Or, simplified:

```
<Rotate Z2="1.0" Angle="-90.0" />
```

#### Scale

The `<Scale>` element scales the model by the specified scaling factors along one or more axes. Omitted coordinate values are assumed to be one.

The following example scales the model by factor two along Y axis:

```
<Scale X="1.0" Y="2.0" Z="1.0" />
```

Or, simplified:

```
<Scale Y="2.0" />
```

### Exchange axes

The `<Exchange>` element swaps the coordinate values of two coordinate system axes, effectively mirroring the model and simultaneously rotating it by 90°.

The following example exchanges the coordinate values of X and Z axis:

```
<Exchange Axis1="X" Axis2="Z" />
```

### Matrix multiplication

The `<MultiplyMatrix>` element applies a specific 4×4 transformation matrix, which may be composed of several transformation operations such as translation, rotation, and scale. Omitted matrix elements are assumed to correspond to the respective element in an identity matrix.

The following example translates the model by 80 mm along the X axis, by -30 mm along the Y axis, and by 60 mm along the Z axis, as well as rotating it by -90° around the Z axis and scaling the Y axis by factor two:

```
<MultiplyMatrix
  R0C0="0.0" R0C1="1.0" R0C2="0.0" R0C3="80.0"
  R1C0="-2.0" R1C1="0.0" R1C2="0.0" R1C3="-30.0"
  R2C0="0.0" R2C1="0.0" R2C2="1.0" R2C3="60.0"
  R3C0="0.0" R3C1="0.0" R3C2="0.0" R3C3="1.0" />
```


### Invert normal vectors

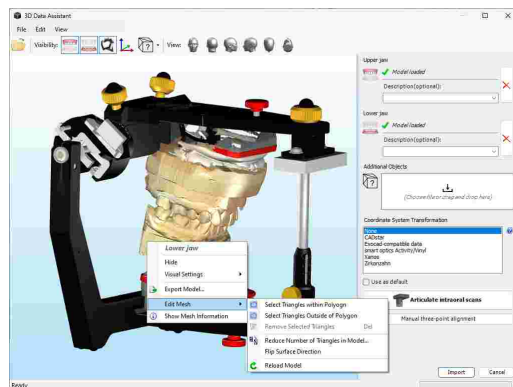
The `<InvertNormals>` element inverts the normal vector directions of the model's triangle mesh, effectively turning the model inside out. This element does not have any attributes and should appear at most once within a transformation template.

The following example inverts the normal vectors of the model:

```
<InvertNormals />
```




## 8.3.5 Editing 3D meshes

The 3D Data Assistant allows the rudimentary editing of imported 3D mesh data using the context menu in the 3D view. For instance, to cut or to reduce the resolution of loaded models. To revert the changes made to a model, use the context menu entry  *Reload Model*.

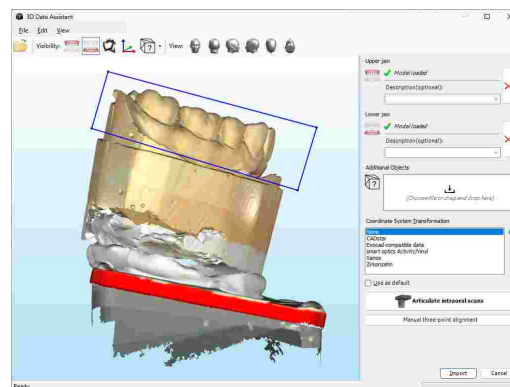


### 8.3.5.1 Cutting of 3D data

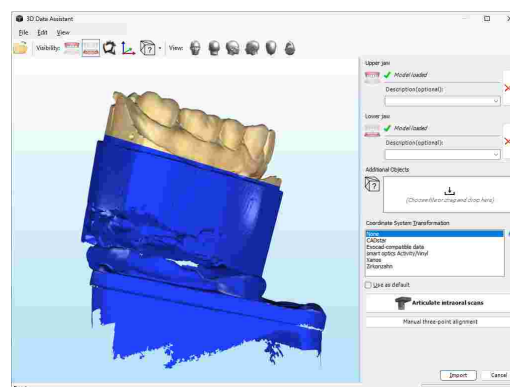
Sometimes a 3D model may include unwanted and for analytical purposes irrelevant surfaces, such as the mounting base of the plaster model. These areas can be cut away prior to the import in order to reduce the amount of data and improve application performance. The 3D Data Assistant provides the following mesh editing functions for this purpose:

-  Draw a polygon on the 3D display, within which all triangles will become selected.
-  Draw a polygon on the 3D display, outside of which all triangles will become selected.
-  Removes the selected triangles from the model. Selected triangles are colored blue.

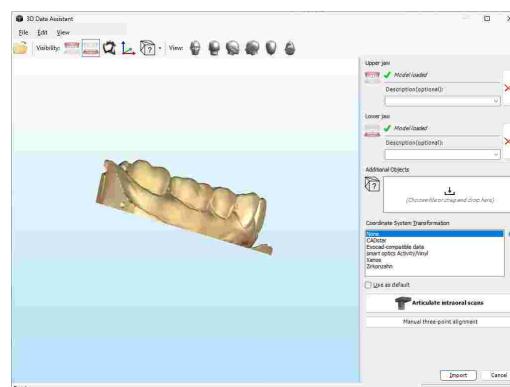
To cut away a part of the model, first activate the desired function for drawing a polygon on the 3D display. Subsequently, you can specify the shape of the polygon by pressing the left mouse button at its corner points. Once you are finished, confirm by pressing the right mouse button.




The selected triangles will now be indicated in blue color. You can move and rotate the model in the 3D view to verify the selection. If necessary, press the *Esc* key to discard it and start again.




To remove the selected triangles, either press the corresponding context menu item or the *Del* key on your keyboard.



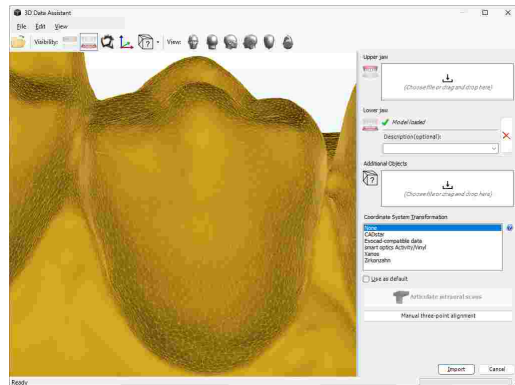
 When removing triangles from a model, always make sure to avoid removing areas that could be of relevance for occlusal function. Especially the unintended removal of tooth surfaces leads to a poor representation of the true dental situation and can compromise the quality of the analyses carried out in CADIAS 3D.

### 8.3.5.2 Reducing the resolution of 3D data

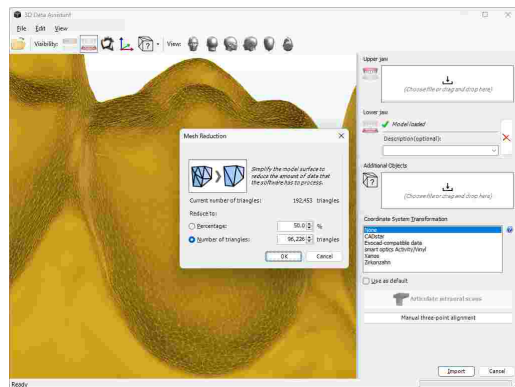
Another way to reduce file size and improve the performance of the application is to lower the resolution of the 3D model through surface simplification. During this process, the small triangles that make up the surface of the model are gradually fused together, increasing their size while reducing their number. The 3D Data Assistant provides the following mesh editing function for this purpose:

 Reduce the number of triangles in the loaded model.

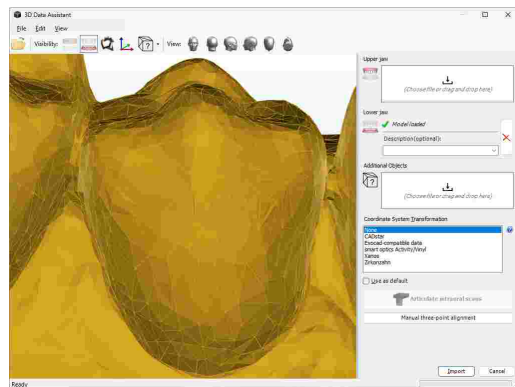
To reduce a currently loaded 3D model, use the appropriate entry in the context menu.





In the appearing dialog, you can choose whether you want to simplify the model to a specified number of triangles or to a certain percentage of the actual size. Press OK to confirm.



You will notice that the surface of the model becomes coarser after each simplification process. In addition, the number of triangles displayed at the lower border of the 3D Data Assistant will decrease accordingly.

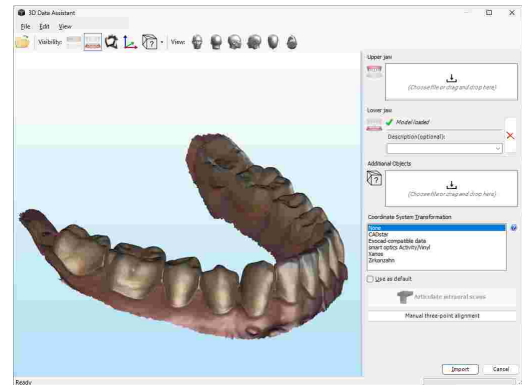


 When simplifying the surface of a model, always make sure to preserve a resolution adequate for your particular use case. Excessive simplification leads to a poor representation of the true dental situation and can compromise the quality of the analyses carried out in CADIAS 3D.

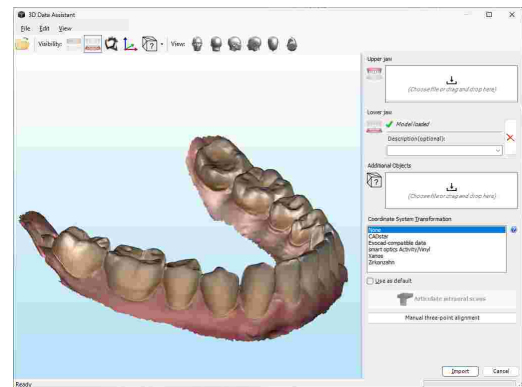
 You can visualize the outlines of the model's triangle mesh by activating the wireframe display mode via the context menu (refer to chapter "Visual settings for 3D objects [277]").

### 8.3.5.3 Flipping the surface direction

In some error cases, the data created by 3D scanners or external CAD/CAM software may be exported incorrectly, resulting in the mesh surface being turned inside-out. This can be apparent based on the visualization of the data in the 3D view.

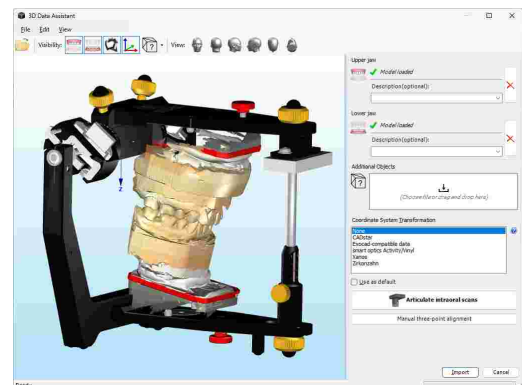


To flip the direction of the surface of a model, use the appropriate mesh editing function provided in the context menu.

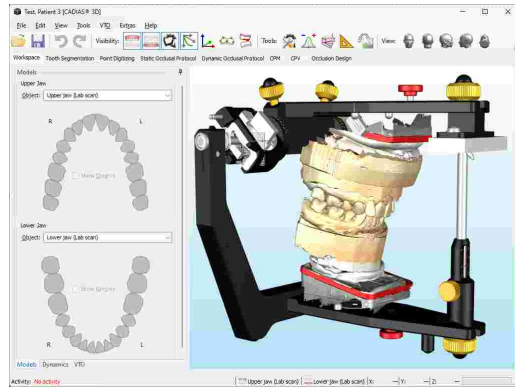


### 8.3.6 Finishing the data import

To finish the data import following the articulation and editing of the models in the 3D Data Assistant, simply press the button *Import*.

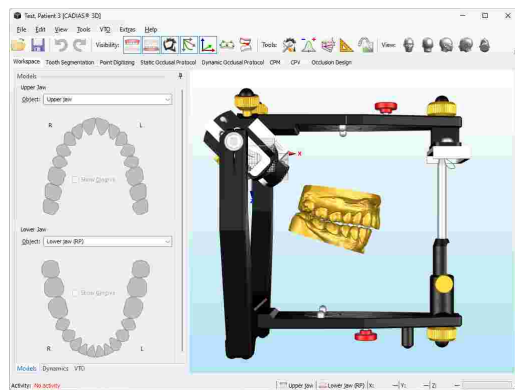


The models are thus saved in the patient file. If the 3D Data Assistant has been started from CADIAS 3D, the models will automatically appear in the Workspace view.



## 8.4 Workspace

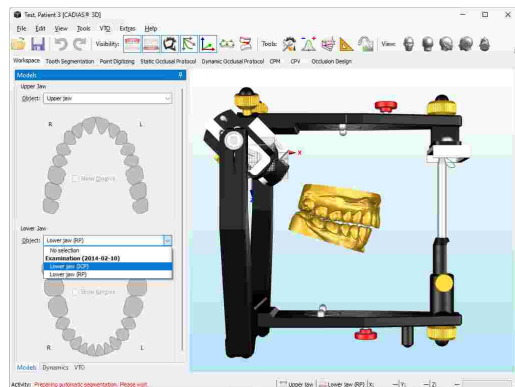
After opening the CADIAS 3D analysis from the Workspace of GAMMA Document Browser, you will find yourself in the Workspace of CADIAS 3D. Most activity in CADIAS 3D will take place in this view.



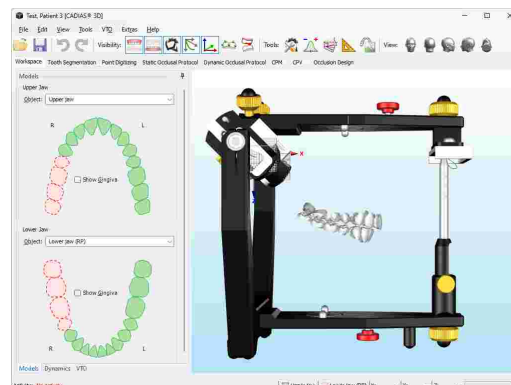
**i** Using the buttons labeled *Tools* in the toolbar, you can adjust the settings of the virtual Reference SL articulator (refer to chapter "Articulator settings<sup>[273]</sup>"), show a numerical analysis of the anatomical measurements as well as graphical visualizations thereof (refer to chapters "Numerical analysis<sup>[274]</sup>" and "Graphical analysis<sup>[274]</sup>", respectively).

### 8.4.1 Objects

On the *Objects* panel of the Workspace, you can select the 3D models that the application will use for display and calculations. Once the selected model has been segmented (see chapter "Tooth segmentation<sup>[258]</sup>"), you can also control the visibility of its individual teeth and the gingiva.



For segmented models, the dental arches will indicate the available and displayed teeth with green color. To toggle their visibility, simply click them with the left mouse button. Teeth that have not been segmented will be treated as missing and therefore appear grayed out.

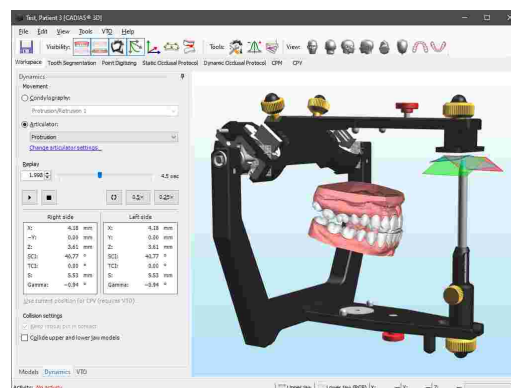


**!** Please note changing the model selection is only possible while VTO mode for that model is deactivated (refer to chapter "Visualized Treatment Objectives (VTOs)"<sup>[256]</sup>).

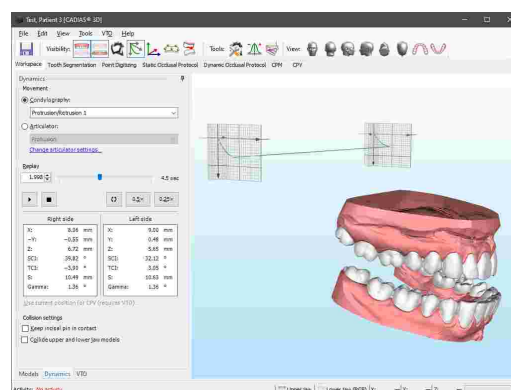
### 8.4.2 Dynamics

By using the *Dynamics* panel on the *Workspace*, you can animate the lower jaw model according to a recorded condylography movement or a mechanical movement created from the articulator settings specified on the *Articulator settings* side panel (refer to chapter "Articulator settings"<sup>[273]</sup>).

After selecting the movement to be replayed, you can have it replayed in real time by pressing the **▶ Play** button. To replay the movement at half or quarter speed, activate the respective option. Furthermore, you can replay the movement in a continuous loop by activating the option **↻ Loop replay**.



When the option to show condylography information is activated via the toolbar button, you can see the tracks of the replayed movement as well as the axis movement in the condylar coordinate systems.



During a replay, the side panel displays the following values of the current time position, for right and left side:

- **X/Y/Z** coordinates, measured from the origin of the respective condylar coordinate system.

- Angle values for **SCI** (Sagittal condylar inclination; measured on the X/Z plane) and **TCI** (Transversal condylar inclination; measured on the X/Y plane), calculated from the origin of the respective coordinate system.
- The two-dimensional distance **S** from the origin of the respective coordinate system, measured on the X/Z plane.
- The **Gamma** rotation angle around the hinge axis.

**i** You can copy the values of the current time position into the clipboard using the context menu. These values can also be transferred to the CPV pane using the link label provided below, e.g. for realizing a therapeutic position (refer to chapter "Condyle Position Variator (CPV)<sup>[267]</sup>"). This requires the VTO mode of the model to be repositioned to be active (refer to chapter "Visualized Treatment Objectives (VTOs)<sup>[266]</sup>").

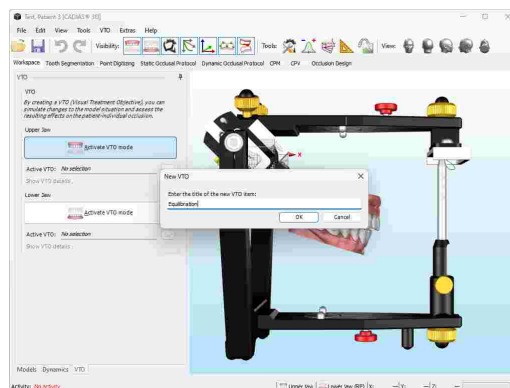
The *Dynamics* panel also provides options for controlling the types of collision that may occur during a curve replay. Activating *Keep incisal pin in contact* will enforce incisal guidance by keeping the incisal pin in contact with the incisal table, while *Collide upper and lower jaw model* will prevent the two models from intersecting each other. This is realized by opening the lower jaw model as far as necessary to prevent intersections, which overrides the rotation that has been recorded during condylography.

**!** Please note that the functionality for colliding upper and lower jaw models requires the models to be segmented beforehand (see chapter "Tooth segmentation<sup>[258]</sup>"). Movements defined by the articulator are guided by the incisal table and thus have the respective collision setting always activated.

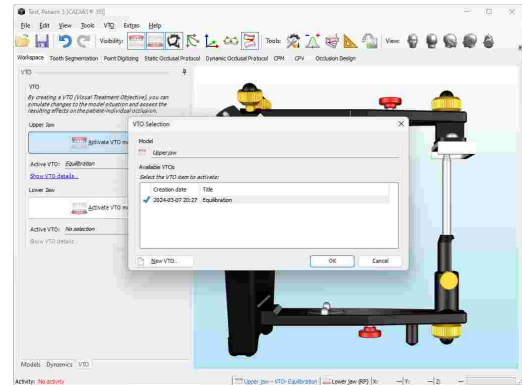
### 8.4.3 Visualized Treatment Objectives (VTOs)

CADIAS 3D allows the visualization of planned treatment objectives in the form of so-called **VTO** items (Visualized Treatment Objective). Every VTO is associated with either the upper or lower jaw model and describes the repositioning operations that were applied to the model and its individual teeth. Based on the new occlusal situation described by a VTO, the application will immediately recalculate its static and dynamic analyses, visualizing the consequences of each change in real-time.

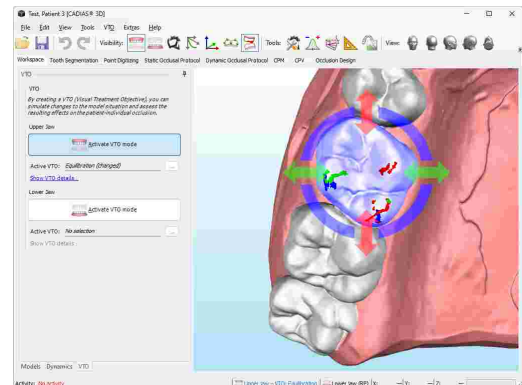
To create a new VTO item, switch to the VTO side panel in the Workspace view and activate VTO mode for the upper or lower jaw. If you have already created a VTO item for the model, that item will become active automatically. Otherwise, the application will ask you to specify the title of the new VTO item.



To show the available VTO items for a model, use the respective ... button. In the appearing dialog, you can activate one of the items by selecting it and pressing OK. In this dialog you can also create new VTOs and rename or delete the existing ones using the context menu in the list.

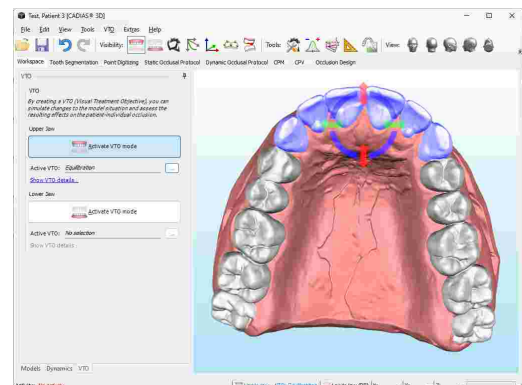




Once VTO mode is activated, you can click any part of the corresponding model in the 3D environment to show an interactive modification widget. By dragging one of the arrows or the circular elements with the mouse, you can move or rotate the object along or around the X, Y, and Z axes of the coordinate system. Holding down the *Shift* key while doing so will snap to predefined intervals.

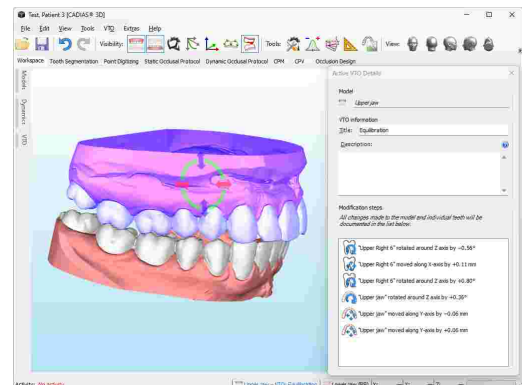


While doing so, the points that were digitized on the surface of the object as well as the numerical and graphical analyses calculated from these points will adjust to the new position immediately. Likewise, the functional guidance paths created using the dynamic occlusal protocol will be recalculated to show the new guidance pattern.

By holding down the *Ctrl* or *Shift* keys during selection, it is possible to select both upper and lower jaw model or multiple teeth on a single model simultaneously. This allows the selected objects to be moved or rotated as a group.




Using the buttons  *Undo* and  *Redo* in the toolbar, you can revert and restore the previously applied VTO modifications. To show the modification steps that were applied as part of the active VTO, click on *Show VTO details*. Here, you can also modify the title of the VTO item and optionally enter a short description of the visualized treatment objective.

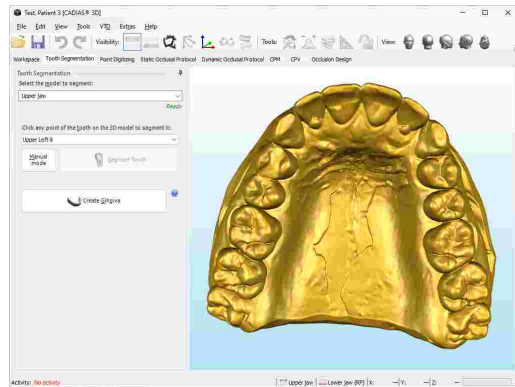


## 8.5 Tooth segmentation

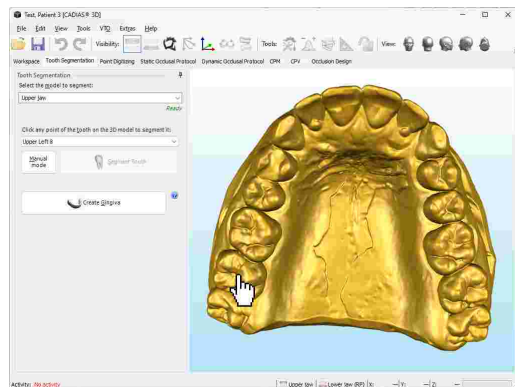
As the 3D data of a dental model is typically represented as one solid surface, it is required to separate the teeth from the gingiva before the software can use the individual teeth for calculations such as the static or dynamic occlusal protocol. This separation process is referred to as **Tooth Segmentation**.

 Please note that segmenting a model is only possible while VTO mode is deactivated (refer to chapter "Visualized Treatment Objectives (VTOs)"<sup>256</sup>).

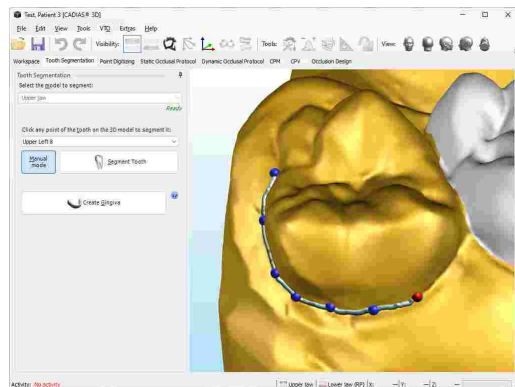
You can start tooth segmentation by activating the *Tooth Segmentation* view. First, select the model to segment from the combo box at the top of the panel. This will initiate the preparation for automatic segmentation, which may take a few seconds.



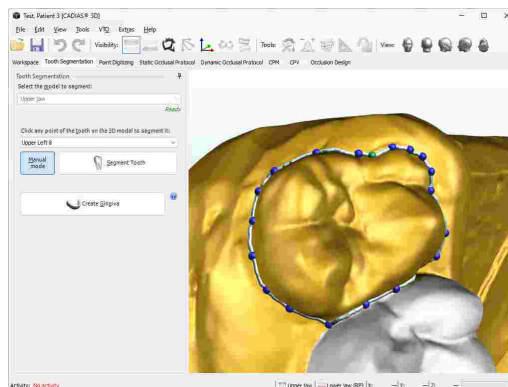
Subsequently, moving your mouse cursor over the model will show the "hand" cursor (☞) for segmentable teeth and the "not available" cursor (⊘) for other areas that cannot be segmented. Select the first tooth to be segmented in the side panel and proceed with segmentation from the right molars to the left molars.




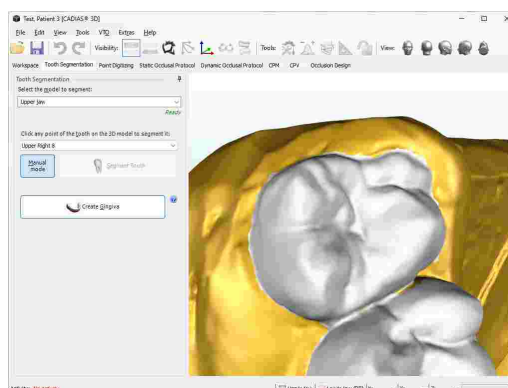
For teeth that could not be segmented automatically, you can switch to manual segmentation mode using the corresponding button. If you now move your mouse cursor over the displayed 3D model, you will see a red ball on its surface. By clicking the left mouse button, you can draw a contour around the previously specified tooth. The individual contour points will be connected automatically, including the first and last one.




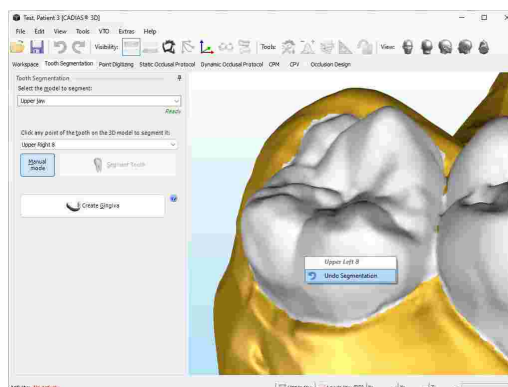
You can correct the location of digitized contour points by dragging them with the left mouse button. To add a new contour point between two existing ones, move your mouse cursor over the contour until the cursor changes its appearance, and then press and hold the left mouse button.




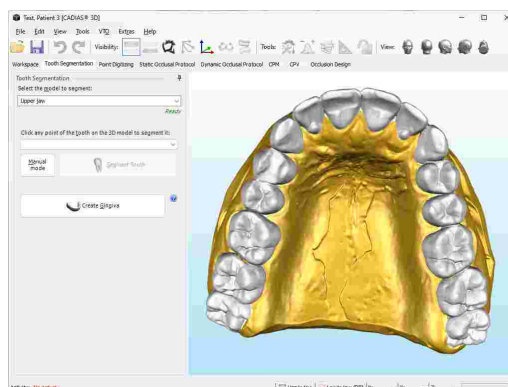
Once the contour is closed around the tooth, press the button  *Segment tooth* on the side panel. This will separate the tooth from the model's surface and its color will change to white.



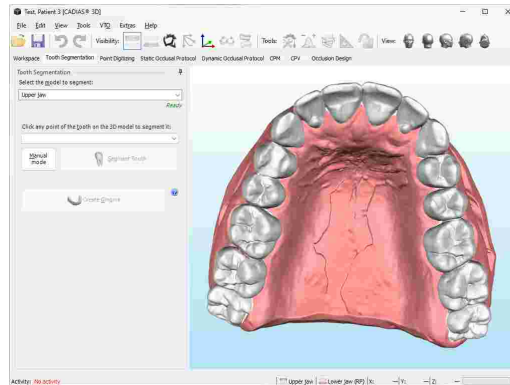
If you notice that the contour has been entered incorrectly, you can undo the segmentation by clicking on the tooth with the right mouse button and choosing  *Undo Segmentation* from the context menu.



After all teeth have been segmented, press the button  *Create gingiva* on the side panel to create the gingiva from the remaining, unsegmented part of the model.



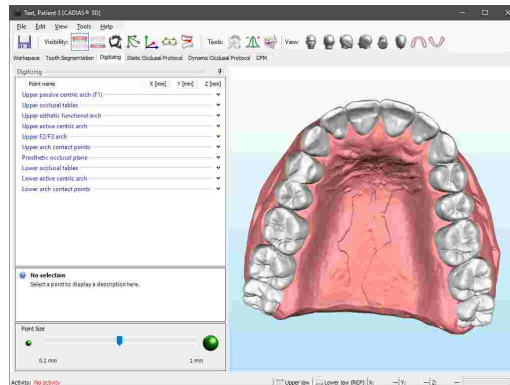
The gingiva of the model will become colored pink, indicating that segmentation of the model has been completed.



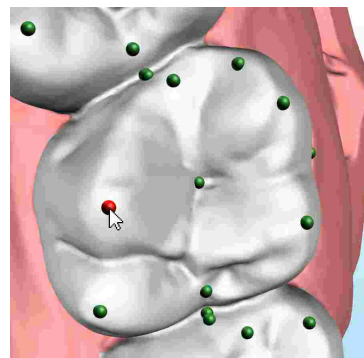
## 8.6 Point digitizing

The *Point digitizing* view provides functionality for measuring and analyzing the anatomical structures of the upper and lower jaw models. Based on these measurements, the software is able to calculate values such as angles, distances, relations, etc., and to visualize those in the 3D environment.

The side panel on the left side of the *Point digitizing* pane lists the points that can be digitized on the surface of the displayed models, logically divided into groups. Upon measurement, each point will be assigned its *XYZ* coordinates in the axis-orbital reference coordinate system. If certain points cannot be digitized, e.g. because the respective teeth are missing, you can skip them by selecting one of the following points in the list.



Now, if you move your mouse cursor over the surface of the model, you will see a red ball that indicates where the point will be digitized when you press the left mouse button. Already digitized points are displayed in green color.



**i** The *XYZ* coordinates of the current mouse cursor location are displayed in real-time at the bottom border of the window.

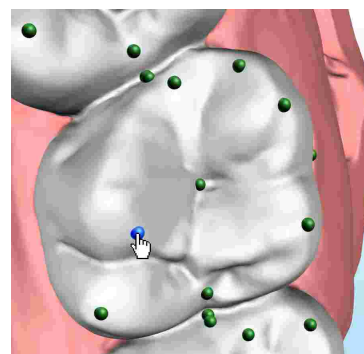
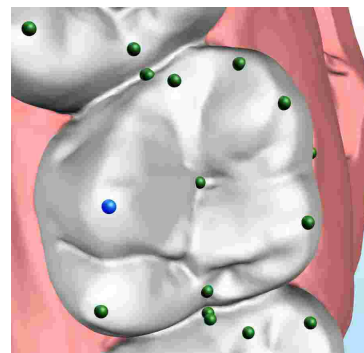
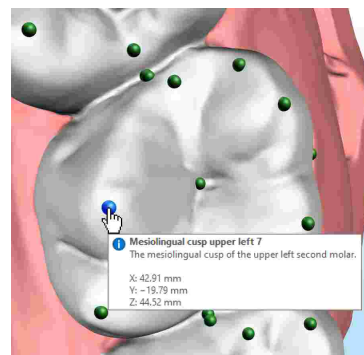
**!** If you find that the already digitized points are not being displayed, ensure that the display of digitized points is activated via the button in the toolbar.

Below the list of digitized points, you can find an explanatory description of the currently selected point and the possibility to change the size with which the digitized points are displayed.

By moving your mouse cursor over a digitized point, you can furthermore display a tooltip with the name, description, and coordinates of that point. This functionality is also provided in the other views.

By selecting an already digitized point in the list, you can have it highlighted with blue color in the 3D environment.

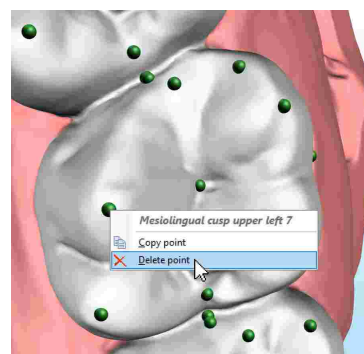
To correct the location of an incorrectly digitized point, simply drag it in the 3D environment while keeping the left mouse button pressed. Of course you can also re-select the corresponding entry in the list and digitize the point again.



**i** If you move an already digitized point to a new position, the numerical and graphical analyses based on that point will be updated in real-time. You can show these analyses via the buttons labeled *Tools* in the toolbar (refer to chapters "Numerical analysis<sup>[274]</sup>" and "Graphical analysis<sup>[274]</sup>").

To delete individual points, right-click them in the 3D environment and choose the appropriate entry from the context menu.

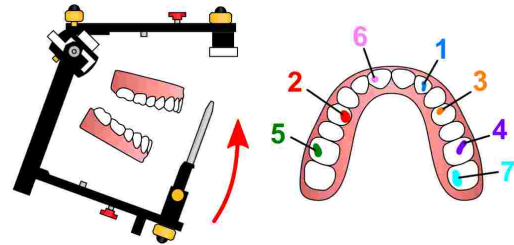
You can use the context menu of the list to delete entire point groups or to copy the coordinates of points to the clipboard for transferring them to another application.



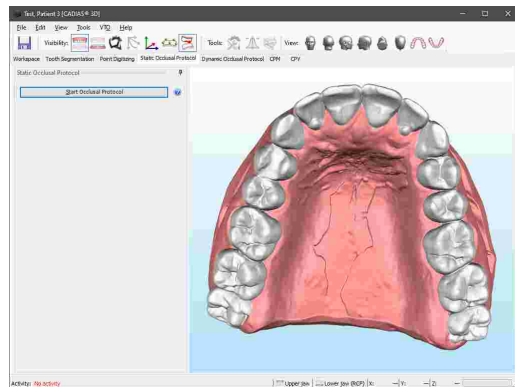
**i** The definitions of digitized points are defined in an XML-file that is located in the definition files folder of GAMMA Dental Software, which makes it easy to add your own. Please contact GAMMA for further instructions on how to do so.

### 8.7 Static occlusal protocol

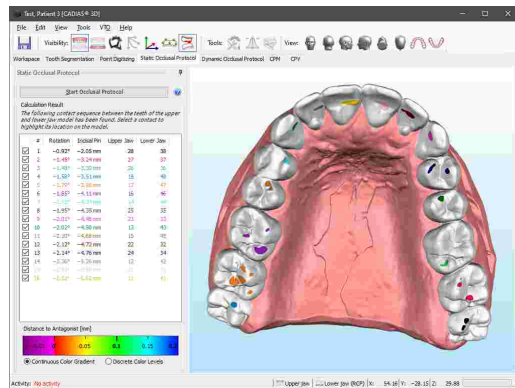
As its name implies, you can carry out a virtual occlusal protocol on the *Static Occlusal Protocol* pane. During this process, the lower jaw is slowly rotated towards the upper jaw, and the sequence in which the contacts occur on the individual teeth, as well as their locations, is documented.



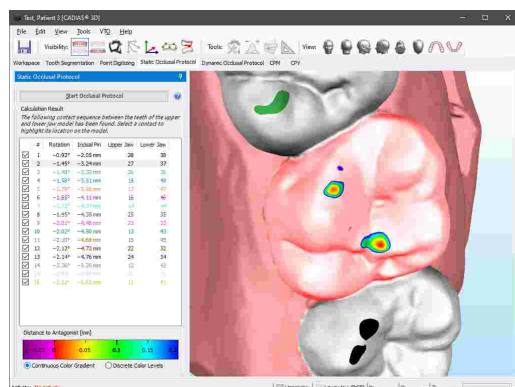
The computation of the static occlusal protocol is fully automated. Simply press the button *Start Occlusal Protocol*.



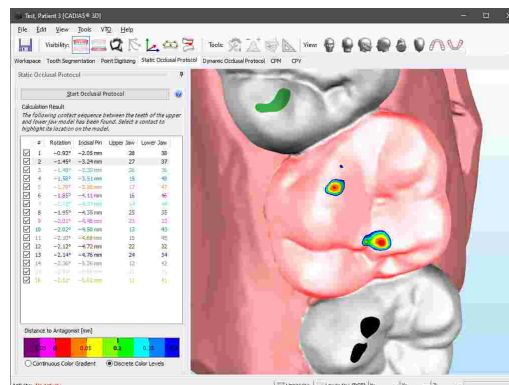
Once calculation is completed, the list displays the individual teeth contacts in their order of occurrence. For each contact, it also shows the angle of hinge axis rotation, the corresponding incisal pin height, as well as the contacting upper and lower jaw teeth. The color of the list entries represents the coloring of the contact areas on the surface of the upper jaw model.



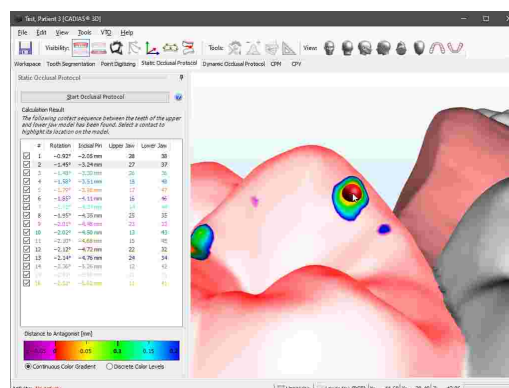
To analyze a specific tooth contact in detail, you can select it in the list, which will highlight the contacting teeth in red color and turn the plain surface coloring into a distance map. The colors indicate the distance between the contacting teeth at the time that the contact occurred. You can read the millimeter distance associated with a particular color from the color scale at the bottom of the side panel.



You can switch this distance map from a continuous color gradient to discrete color levels using the radio buttons below the color scale. The resulting color bands can make it easier to identify which areas fall within a certain distance interval.



While having selected a contact, you can move the mouse cursor over the model surface to measure the spatial coordinates of specific points. Clicking the left mouse button will copy the actual contact information together with the coordinate values to the clipboard for easy transfer to external applications.



### 8.8 Dynamic occlusal protocol

A dynamic occlusal protocol is used to determine the real functional guidance paths on the teeth of the upper jaw model. This feature takes the dynamic aspect into account, which comes into play due to patient-individual jaw movements. Compare this to the static occlusal protocol functionality (see chapter "Static occlusal protocol<sup>262</sup>"), which evaluates the static tooth contact sequence during a simple closing rotation. Below we want to provide you a simplified description of the calculation method used for the dynamic occlusal protocol.



The calculation starts with the upper and lower jaw models in reference position. Depending on how the models were mounted in the articulator, this will typically be Retral Contact Position (RCP) or intercuspal position (ICP).

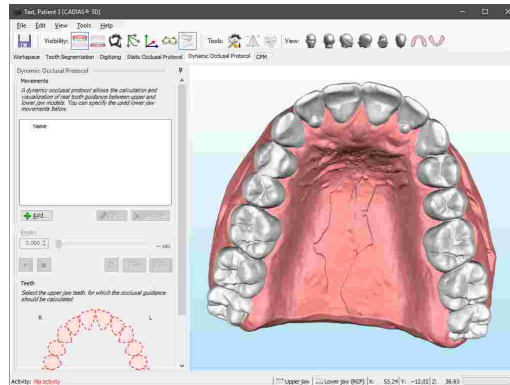


Starting from this position, the lower jaw model is closed until the first contact for the upper jaw tooth in question has been found. This position marks the beginning of the guidance paths calculated in the next step.

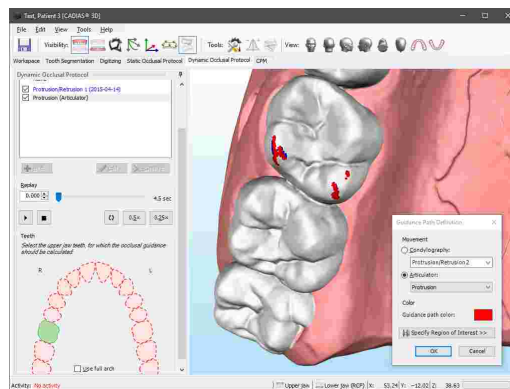


Finally, the lower jaw model is animated according to a condylography or articulator-defined movement while preserving contact with the upper jaw. Keeping track of the contact position during the animation results in a path on the surface of the upper jaw tooth that represents the occlusal guidance during this particular movement.

To perform a dynamic occlusal protocol, switch to the *Dynamic Occlusal Protocol* pane. On the left-hand side, the application provides a list in which you can add an arbitrary number of condylography- or articulator-defined movements, for which a guidance path should be calculated. Below that, you can select the teeth of the upper jaw to be included in the calculation. Selected teeth will appear green. Check *Use full arch* to combine all individual teeth into a rigid model. If this option is activated, the selection of teeth above will be ignored.

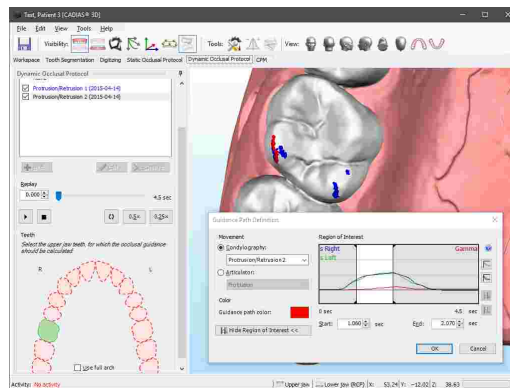


After selecting at least one tooth, press the **+** *Add* button to specify a movement to calculate the guidance path for. Once the background calculation has been finished, the path will be visualized on the upper jaw teeth. Note that you can still freely navigate the 3D environment even while the movement definition dialog is opened.



For editing or removing a movement later on, use the buttons **E** *Edit* and **X** *Remove*, respectively. By checking the check box next to every list entry, you can control the visibility of the corresponding guidance paths.

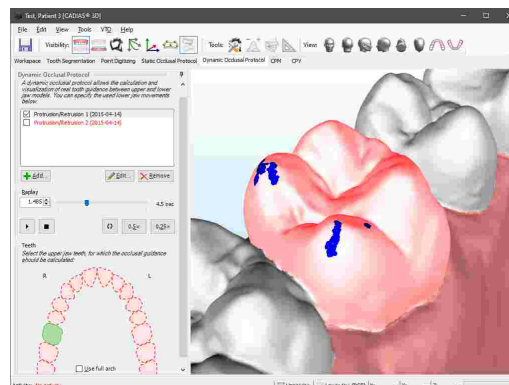
Within the movement definition dialog, you have the possibility to select any condylography movement stored in the patient database or a movement defined by the articulator settings. You can also select the color to visualize the path with, and trim the movement to a specific time region of interest. This can be useful when you want to limit the guidance path to a certain section of the movement, e.g. the part in which the F1-F2 guidance can be observed. By default, the software uses the whole excursion movement and ignores the incursion.



**i** To adjust the settings of the articulator, you can open the associated tool window using the button under the *Tools* label in the toolbar (refer to chapter "Articulator settings" <sup>273</sup>).

By selecting a movement in the list, you can animate the lower jaw accordingly using the replay controls. For replaying the movement in real-time, use the ▶ *Play* button. For doing so at half or quarter speed, activate the respective option. Furthermore, you can replay the movement in a continuous loop by activating the option ⌂ *Loop replay*. During the animation, the models will be kept in contact and the guidance path drawn on the upper jaw model's surface will trace the current and past contact points. The teeth that are currently in contact are additionally highlighted in red color.

Please note that replaying a movement guided by tooth contact is only possible when just a single tooth is selected.



For inspecting the timely progression of the guidance path while the lower jaw is being animated, it is recommended to switch the lower jaw model to a transparent display mode (refer to chapter "Visual settings for 3D objects" [277]).



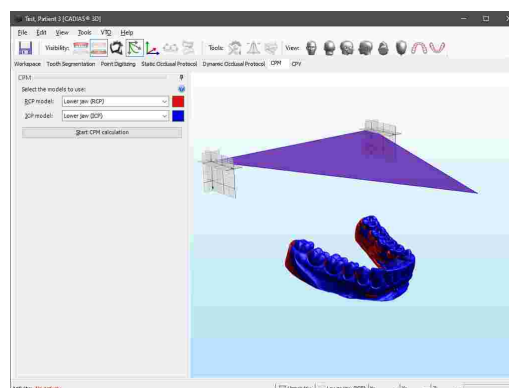
Please note that the occlusal protocol functionality requires both upper and lower jaw models to be segmented beforehand (see chapter "Tooth segmentation" [258]).

## 8.9 Condyle Position Measurement (CPM)

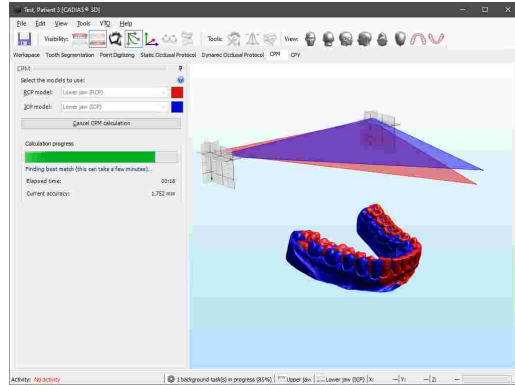
A Condyle Position Measurement (CPM) describes the condylar movement that occurs in the temporomandibular joint when the lower jaw moves from one position to another, e.g., from retral contact position (RCP) to intercuspation (ICP). CADIAS 3D supports the fully automated calculation of a CPM by matching the spatial position of two lower jaw models. For this purpose, it is necessary to import two versions of the lower jaw that were scanned in the respective positions.

Calculated CPM values are stored persistently in the CADIAS 3D analysis, wherefore it is not necessary to repeat the calculation when the analysis is opened the next time.

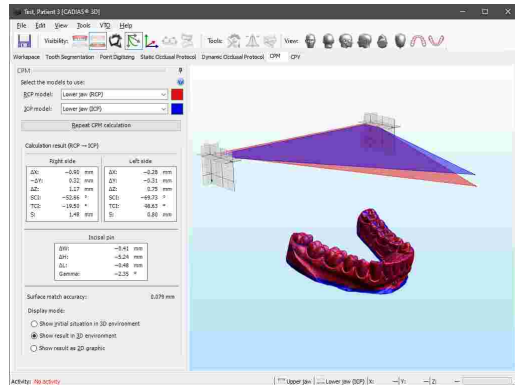
To calculate a CPM, switch to the *CPM* pane of CADIAS 3D. If two lower jaw models with appropriate descriptions indicating RCP and ICP are already present in the database of GAMMA Document Browser, these will be selected automatically.



Press *Start CPM Calculation* to start the calculation. Depending on the resolution of the models, this process can take several minutes. Since calculation it is carried out in the background, you can continue using the software in the meantime.

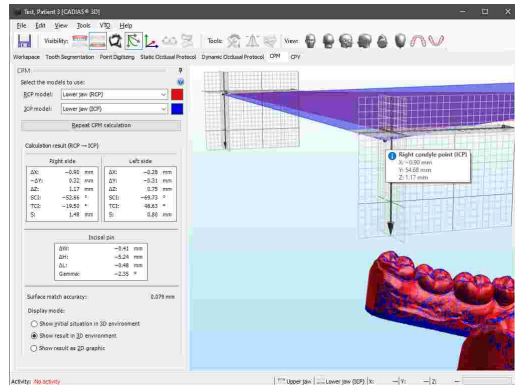


Once calculation is finished, the amount of movement determined for right and left condyle will be displayed. You can display the surface match between the two models by choosing the option *Show result in 3D environment*.

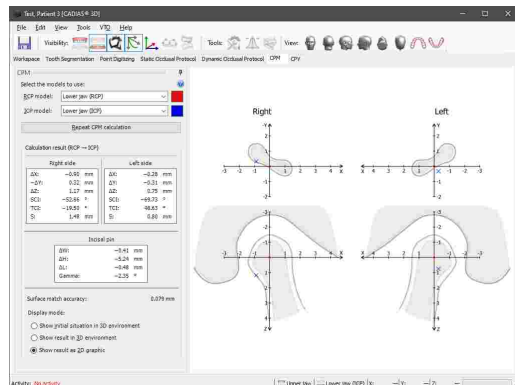


To quickly invert the calculation results, you can swap the two selected models using the button *Swap*.

When the display of condylography is activated via the toolbar button, the calculated movements will be indicated in the condylar coordinate systems.



By choosing *Show result as 2D graphic*, you can display a simple 2D graphic that indicates the calculated movement.



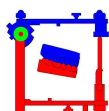
## 8.10 Condylar Position Variator (CPV)

The condylar position variator device (CPV; order number 06-230750) is used for the controlled repositioning of already articulated upper and lower jaw models. This allows, for example, the realization of the patient's individual therapeutic position during splint therapy.

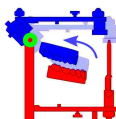
To do so, the desired condylar shift and incisal pin height would be set in the device, the mounting plaster of the model to be repositioned would be separated, and the model would be rearticulated using a previously obtained bite registration. CADIAS 3D provides a virtual counterpart to the functionality of the mechanical CPV.



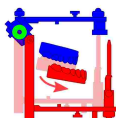
To reposition an upper or lower jaw model using CADIAS 3D, switch to the *CPV* pane. On the very top of the side panel you will find two radio buttons for selecting which model is to be repositioned:



As initial situation, the application always assumes the current relation of upper and lower jaw model. Depending on the articulation procedure, this may for example be the reference position (RP) or intercuspal position (ICP).



When remounting the upper jaw, the relation between lower jaw and hinge axis will be preserved. Current school of thought advises to use this approach as said relation is prescribed by the anatomic connection between mandibular dentition and the temporomandibular condyles. When this option is selected, the offset values entered below will be applied in inverted form to the upper jaw model.



When remounting the lower jaw, the relation between upper jaw and hinge axis will be preserved. When this option is selected, the offset values entered below will be applied to the lower jaw model unchanged.



CADIAS 3D processes the model repositioning applied using the CPV as part of the VTO system (refer to chapter "Visualized Treatment Objectives (VTOs)"<sup>[256]</sup>). This means that all static and dynamic analyses provided by the application, such as the numerical analysis or the dynamic guidance paths, will be recalculated and visualized immediately after each change of a model's position. When selecting the model to be repositioned, the corresponding VTO mode will be activated automatically.

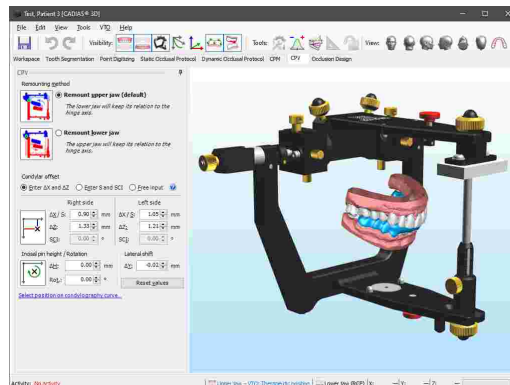
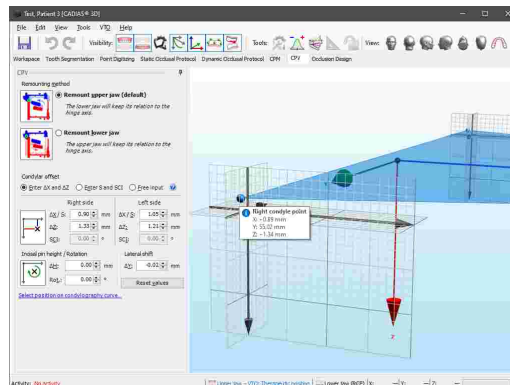
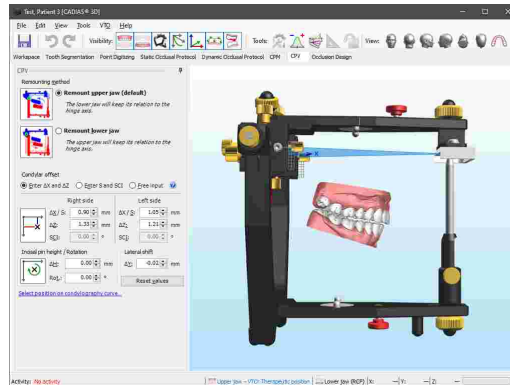


Please note that each VTO item may only contain at most one CPV-based model repositioning. The model position realized this way will itself be used as the basis for subsequent VTO modification steps, such as manual repositioning of models or individual teeth.

Following the selection of the model to be repositioned, you may enter the desired offset values in the input fields provided below. Here, you can choose between entering condylar shift as a combination of horizontal X offset and vertical Z offset or as a combination of excursion distance and SCI angle. Likewise for changing the vertical dimension, you can either enter the change to the incisal pin height or directly as the angle of opening rotation. Due to the rigidity of the mandibular bone, lateral Y shift is applied symmetrically on right and left side.

The effects of the entered repositioning parameters on the original hinge axis points and the anterior reference point (tip of incisal pin) are illustrated by means of a semi-transparent blue triangle. Move the mouse cursor over one of its corners to show the new X/Y/Z coordinates of the respective point.

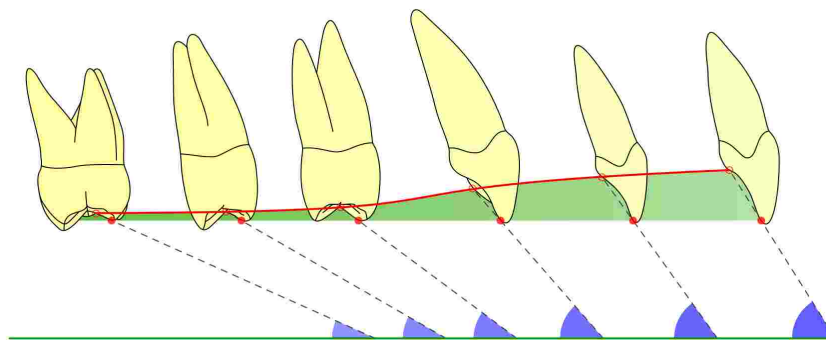
Following a repositioning, you can export upper and lower jaw models via their right-click context menu (refer to chapter "Data export[280]"). The exported model pair may then be used for designing and manufacturing a bite or relaxation splint in 3D CAD/CAM software of third-parties, such as Exocad.



### 8.11 Occlusion design

The Sequence incisal table makes it possible to create a wax-up according to the concept of sequential occlusion in the Reference SL articulator. This concept describes incrementally steepening inclination of guidance surfaces from the first molar to the canine (refer to chapters "The concept of sequential occlusion<sup>[152]</sup>" and "Sequence incisal table settings<sup>[155]</sup>").

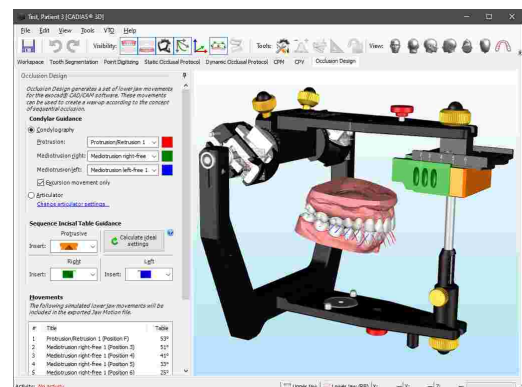
The *Occlusion Design* pane allows simulating articulator movements guided by the Sequence incisal table as well as the subsequent export of these movement data to external CAD/CAM applications. It is thus possible to take into account the morphological occlusal guidance sequence that naturally occurs in human dentition when designing and manufacturing functional dental prostheses.



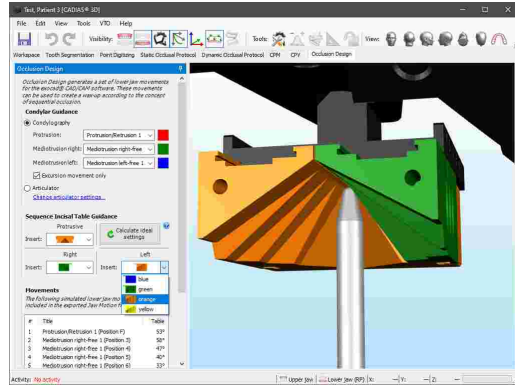
**i** The movement data created using this feature can be imported in Exocad version 2.4 (Plodiv) or higher. A license that permits using the "Jaw Motion Import" module is required.

In the upper section of the left side panel, you can define the condylar guidance to use when generating the movements. This guidance may be based on the settings of the virtual articulator on on the patient's true mandibular movements as recorded with CADIAX. The selected protrusion movement will be displayed in the 3D environment with red color, the mediotrusion right movement in green, and the mediotrusion left movement in blue.

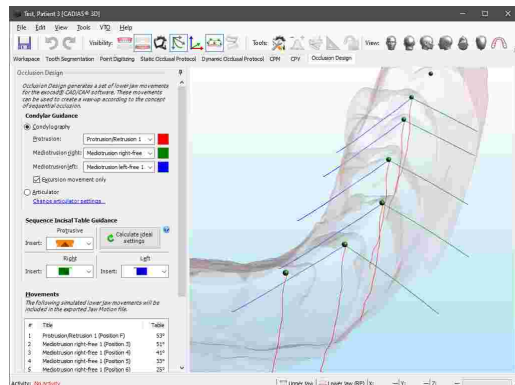
Changing the articulator settings using the corresponding tool window (refer to chapter "Articulator settings<sup>[273]</sup>") will immediately update the movements displayed in the 3D environment as appropriate.



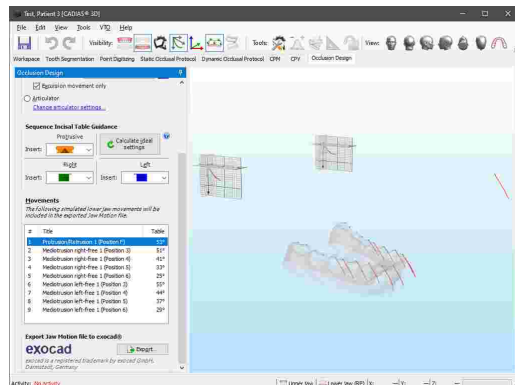
In the next step, you can choose the inserts to use for the Sequence incisal table either manually or have the optimal setting calculated based on the condylar guidance specified above. The calculation method used here matches that used for the articulator calculation in CADIAX Analyzer.



The 3D environment will display the movement tracks of all dental cusps of the lower active centric that have been digitized on the model (refer to chapter "Point digitizing<sub>2601</sub>"). The colors used here match those of the corresponding condylar movement.

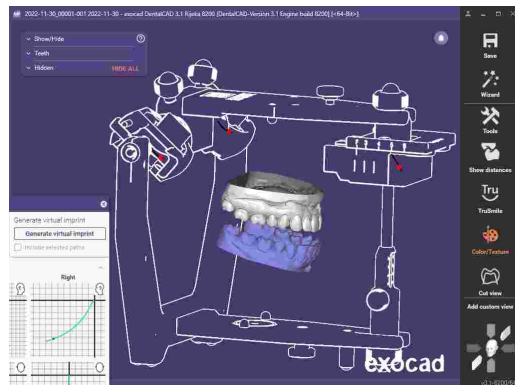


The protrusive movement tracks of all cusps illustrate a single protrusion movement. The mediotrusion movements for the cusps of teeth 3 to 6 on both sides are however guided with the Sequence incisal table in the respective position.



The list in the lower part of the side panel shows the movement data as it will be written to the exported file. Column *Table* indicates the corresponding guidance angle on the Sequence incisal table (protrusive or mediotrusive, as appropriate).

To reduce the displayed movement tracks to just a single articulator movement, you can select that movement in the list. Doing so will also show the movement track of the incisal pin, which illustrates the guidance angle stated in the list.



Finally, using the button *Export*, you can export the generated movement data to a Jaw Motion file in order to transfer it to the Exocad CAD/CAM application. In addition, the movement tracks of the lower active centric cusps can be exported by checking the respective option.

For further instructions regarding the operation of Exocad and usage of the movement data, please refer to the corresponding instructions for use.

## 8.12 3D model printing

A fully digital workflow usually entails the absence of physical models, which complicates crucial steps such as the final functional verification of digitally designed restorations. The Reference Print&Click Set (order number 06-230960) solves this problem by facilitating the accurate articulator mounting of 3D-printed dental models.

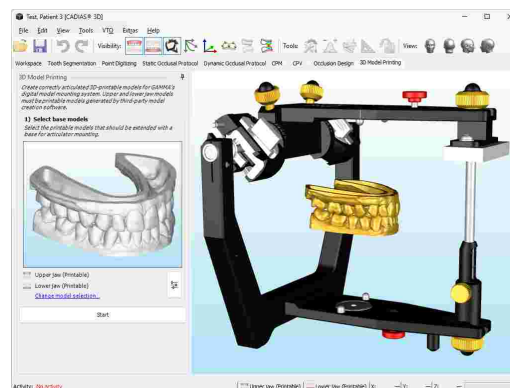
The *3D Model Printing* pane provides a step-by-step workflow to guide you through the creation of models for the Reference Print&Click mounting system.



**i** For using the *3D Model Printing* pane, it is necessary that you converted the scan data into printable models. For this purpose, you may use external model creation software such as exocad Model Creator, Medit Model Builder or 3Shape Model Builder. If the scan data has already been articulated virtually, please ensure not to change the coordinate system.

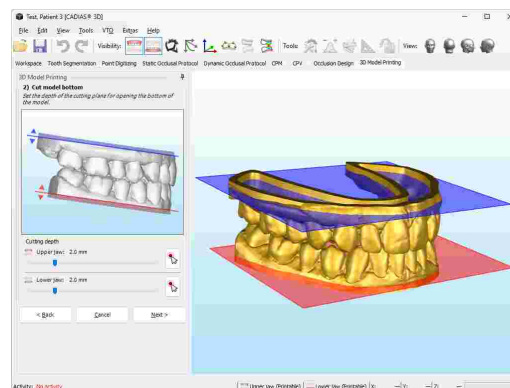
### Step 1: Select base models

Make sure that you have selected the printable models in the *Objects* panel of the Workspace (refer to chapter "Objects" 254").



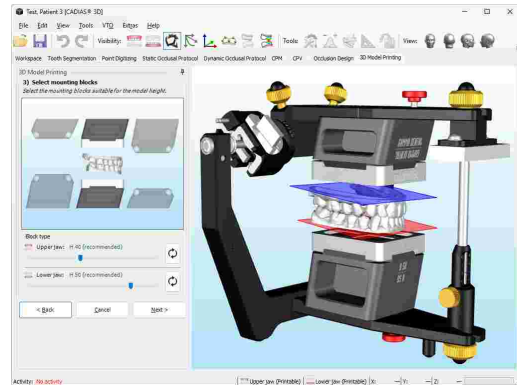
### Step 2: Cut model bottom

Adjust the depth of the cutting plane for the upper and lower jaw model as necessary to cut the bottom of the models.



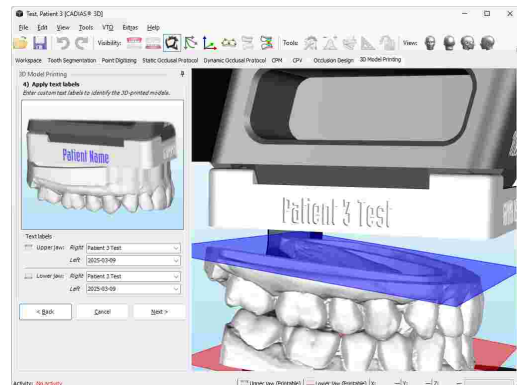
### Step 3: Select mounting blocks

The software will automatically determine the optimal height of the Print&Click mounting blocks as appropriate for the position of the upper and lower jaw models.



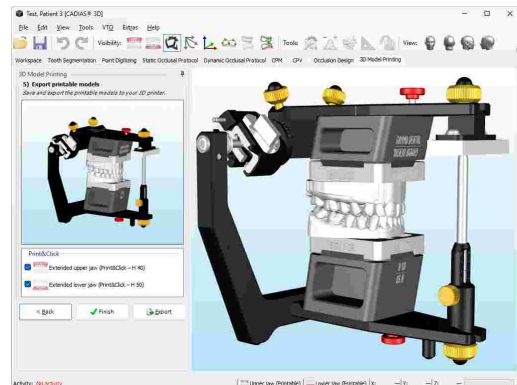
### Step 4: Apply text labels

Optionally, you may also apply text labels on the lateral faces of the base plate to identify the patient case, the date of 3D-printing, or the user of the software.



### Step 5: Export printable models

Finally, you can export the models, now attached to a base plate, to your 3D printer in a desired format.



Following the 3D printing and post-processing, the printed models can be clicked into the appropriate mounting block right away. The required block height and mounting direction is permanently indicated in the printed parts.






Please be aware that the quality of 3D-printed models is highly dependent on the 3D-printing process. It is therefore essential to calibrate and validate your workflow before putting the system into practice.

## 8.13 Tools

Each pane in CADIAS 3D provides a predefined set of functionality in the side panels on the left border of the window. Certain panes additionally provide complementary tool windows that can be opened or closed as needed. These tool windows can be activated via the buttons labeled *Tools* in the toolbar.

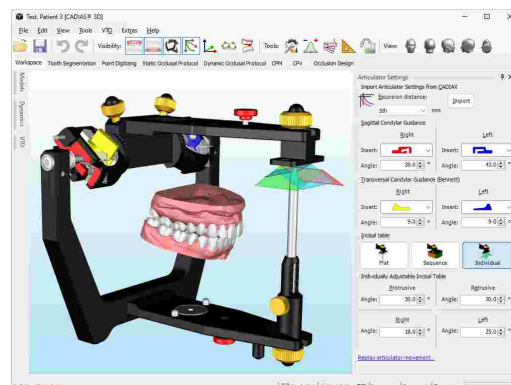
### 8.13.1 Articulator settings

The tool window  *Articulator Settings* allows you to change the settings of the virtual Reference SL articulator. This fully-adjustable articulator provides the following settings:

- Both **sagittal condylar guidance (SCI)** and **transversal condylar guidance (TCI)** of left and right side can be adjusted by selecting the insert to use, which defines the shape of the movement curve as well as its angulation.
- The **incisal table guidance** can be adjusted with respect to the type of incisal table being used, and, where available, the guidance angles for all directions of movement (protrusive, retrusive, laterotrusive right and left).


Instead of specifying custom values for SCI and TCI, you can also import these settings from the articulator calculation of CADIAX for a specified millimeter of excursion.

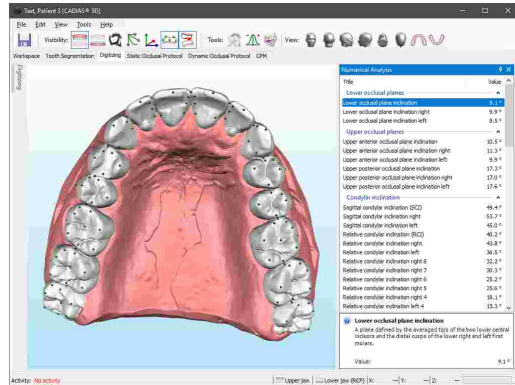
Changing any of the above settings will visualize them immediately on the virtual articulator. If you have chosen to use an articulator-defined curve for animation in the *Dynamics* panel of the Workspace (refer to chapter "Dynamics<sup>[255]</sup>") or for the computation of a functional guidance path (refer to chapter "Dynamic occlusal protocol<sup>[263]</sup>"), those movements will be regenerated automatically.



### 8.13.2 Numerical analysis


Based on the points that were digitized on the surface of the model (refer to chapter "Point digitizing [260]"), CADIAS 3D can calculate numerous anatomical and morphological measurements and display them in tabular form. Some of the values, such as occlusal plane inclination and F1-F2 guidance angles, can also be visualized in the 3D environment (refer to chapter "Graphical analysis [274]").

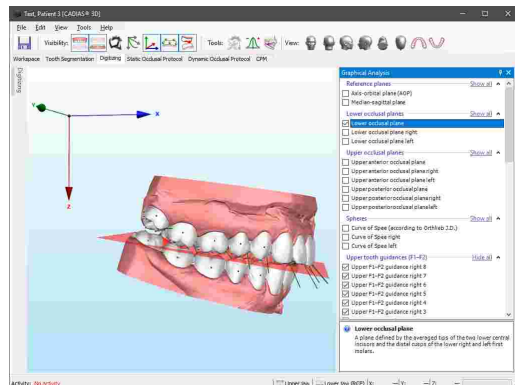
To show the available measurements, activate the  *Numerical Analysis* tool window using the button in the toolbar. The values and value groups displayed in this window can be copied to the clipboard using the context menu. By selecting a particular value, you can have the application display a description of that value below the list.




### 8.13.3 Graphical analysis

Based on the points that were digitized on the surface of the model (refer to chapter "Point digitizing [260]"), CADIAS 3D can visualize graphical elements such as planes, lines, and dental arches, which can also aid the understanding of the associated measurements in the numerical analysis (refer to chapter "Numerical analysis [274]").

To select the graphical elements to be displayed, activate the  *Graphical Analysis* tool window using the corresponding button in the toolbar. Items for which required points have not yet been digitized are grayed out. If you select an item, a short explanatory description will be displayed below the list.



### 8.13.4 Custom measurements

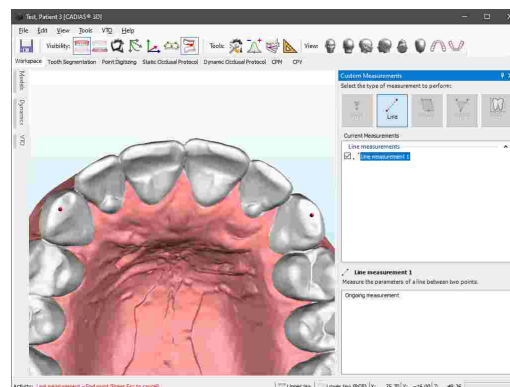
The tool window  *Custom Measurements* allows performing basic measurements on any object displayed in the 3D scene, including the Reference SL articulator and undefined objects. This functionality is independent of the anatomical point landmarks digitized on the upper and lower jaw models (refer to chapter "Point digitizing [260]").

The following types of custom measurements can be carried out:

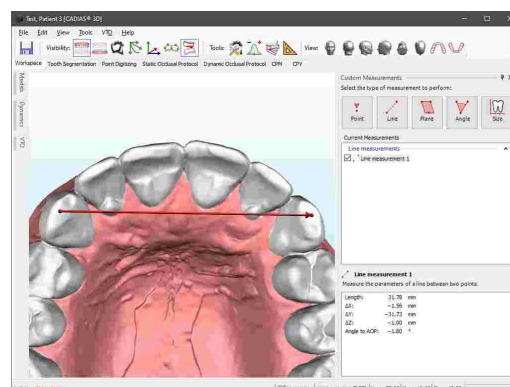
- **Point:** Coordinate measurement of a single point on the object surface.
- **Line:** Distance measurement between two points.
- **Plane:** Measurement of a plane defined by three points.
- **Angle:** Measurement of an angle defined by three points.

- **Size:** Dimensions of a selected object.

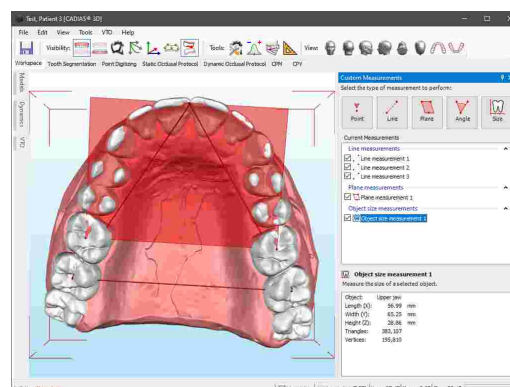
To start a measurement, select the type of measurement to be performed using the buttons provided in the tool window and digitize the appropriate number of points on the surface of any displayed 3D object. The point to be digitized next is indicated in the status bar.



After digitizing the required number of points, the measurement will be illustrated in the 3D scene and the corresponding measurement values will be displayed in the lower section of the side panel. You can copy these values to the clipboard by clicking them with the right mouse button and choosing **Copy**.



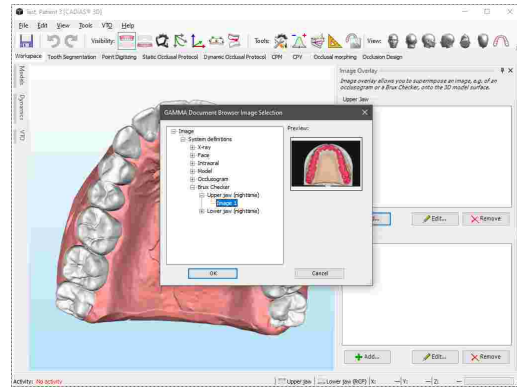
You can perform an arbitrary number of measurements of each type and have them visualized simultaneously. To hide individual measurements or entire groups, simply uncheck them in the list of measurements.



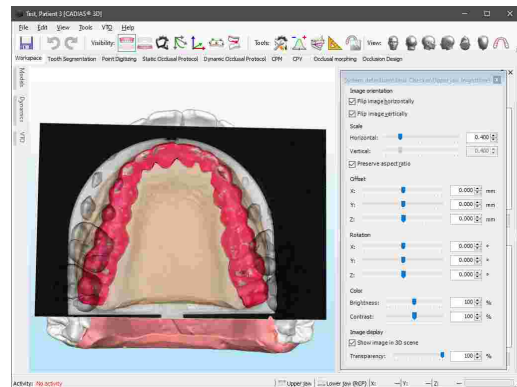
### 8.13.5 3D image overlay

The tool window **3D Image Overlay** enables the superimposition of images such as Brux Checker or occlusogram pictures onto the 3D models of upper or lower jaw. Areas of bruxing and function can thus be associated with corresponding surface areas on the 3D data. For each model, you can superimpose any number of images and display them independently.

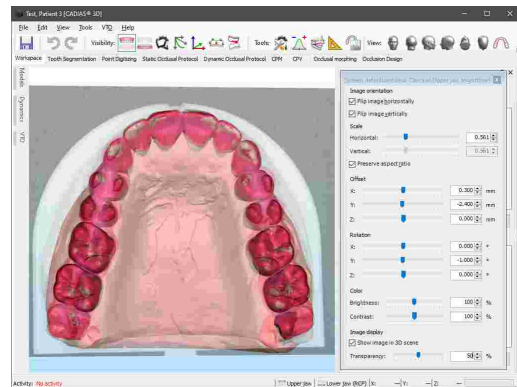
To create a new image overlay, press the button **+** Add. Select the image to superimpose and press **OK**.



The selected image will subsequently be displayed in the 3D environment. In the dialog window that appears, you can fine-adjust the size, position, and rotation of the image to achieve the best possible superimposition.

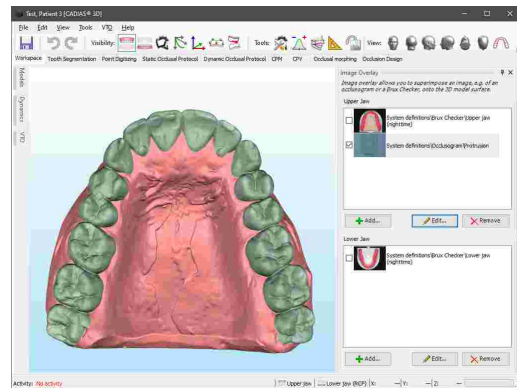


Further adjustments can be made to the image's brightness and contrast as well as to the transparency of the image in the 3D environment.



Upon finishing the image alignment, simply close the dialog window.

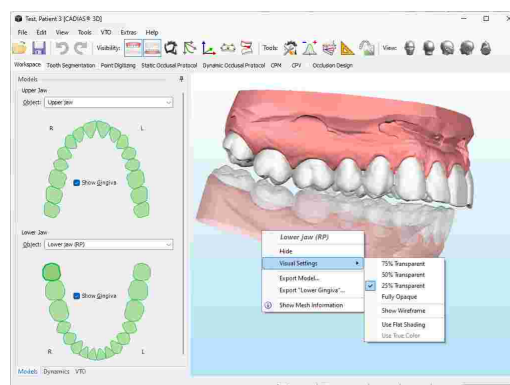
By checking the check mark in the list of image overlays, you can set their visibility. In addition, you can assign custom names and edit or remove previously created image overlays.



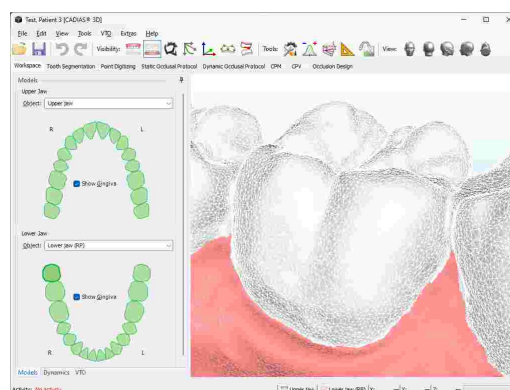
## 8.14 Display settings

### 8.14.1 Visual settings for 3D objects

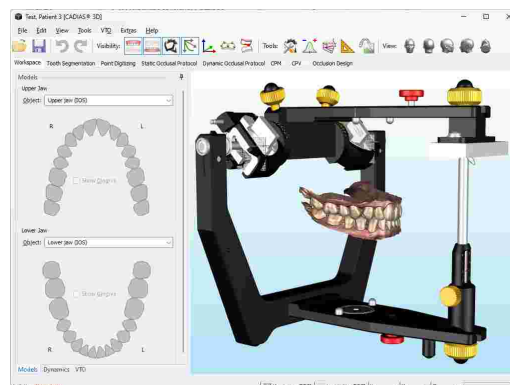
Using the context menu of 3D objects, you can specify various visual settings, such as a desired transparency level.



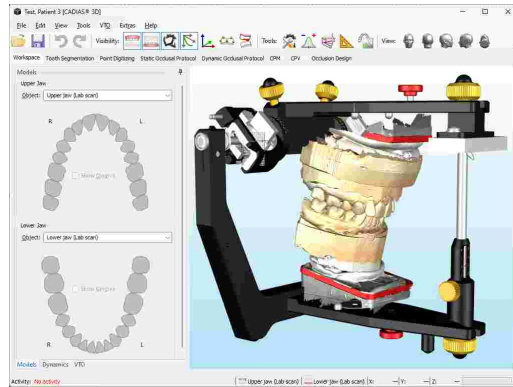
By activating the wireframe option, you can have the software visualize the triangle mesh that represents the surface of the 3D object.



Models that contain color information or textures, such as intraoral scans, are by default displayed with true surface color, as acquired by the scanner. This option can be disabled via the context menu, which can be useful to better highlight the occlusal contacts determined by the software.



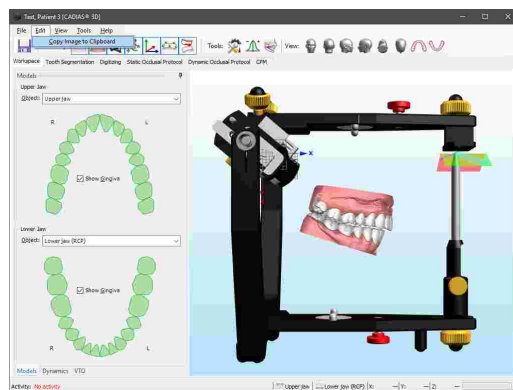
Some laboratory scanners are also capable of capturing this color information, which can be useful to digitize color markings made on the plaster models.



### 8.14.2 Copying the view to the clipboard

To copy the current view as an image to the clipboard, use the menu entry *Edit* → *Put Image to Clipboard*.

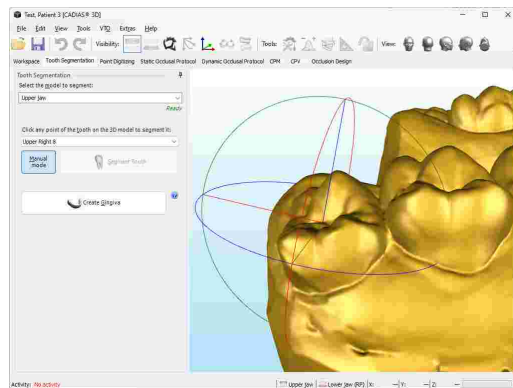
You can then paste the copied image for further editing or for creating presentations into external applications such as Microsoft Paint or Microsoft PowerPoint.



### 8.14.3 Setting the camera rotation center

By pressing the mouse wheel while the cursor is over the surface of a model, you can set that position as the new rotation center for the virtual camera. Afterwards, rotating the camera with the right mouse button pressed will keep the specified position in the center of the screen, which can be especially when you want to put the focus on individual teeth, such as during tooth segmentation or point digitizing.

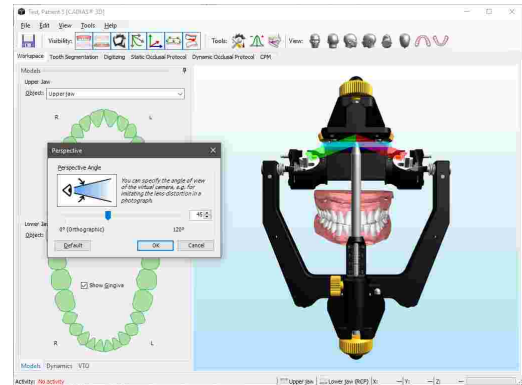
You can reset the camera's rotation center to its default location by pressing the mouse wheel while the cursor is on the background of the 3D environment.



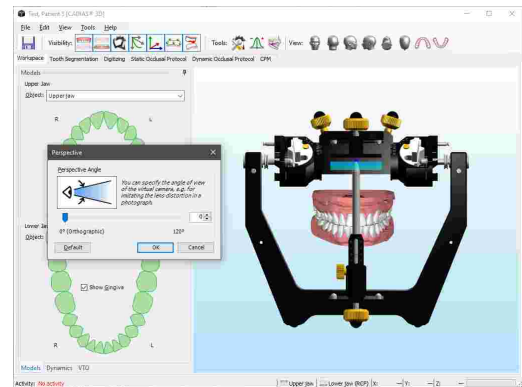
### 8.14.4 Adjusting the camera perspective

Similar to the objective of a real camera, the virtual camera used in 3D applications uses a specific opening angle. However, in the latter case, this angle can be adjusted freely, which can be useful for a 1:1 comparison of the virtual models' appearance with photographs of the actual plaster models.

In CADIAS 3D, you can adjust this perspective angle via the menu *View* → *Change Perspective*. Every change of this value is immediately visualized in the 3D view and can be applied persistently by pressing *OK*.

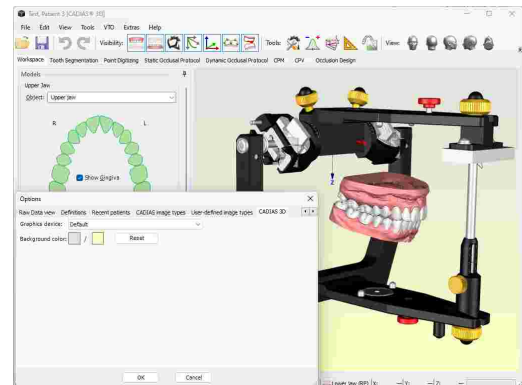


Here, an angle of 0° is used for the special case of parallel projection, in which the apparent size of an object is independent from its distance to the camera. This method of visualization is often used in CAD/CAM applications.



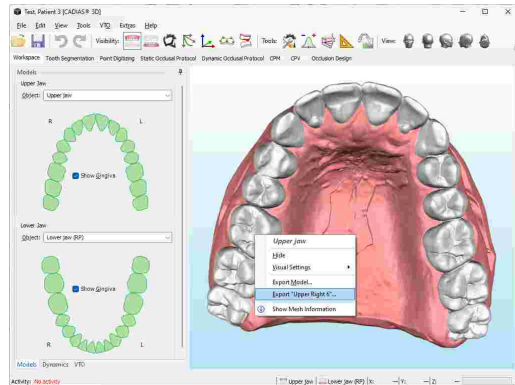
### 8.14.5 Changing the background color

The background color of the 3D environment can be adjusted in the Options dialog. You can open this dialog using the menu entry *Extras* → *Options*.

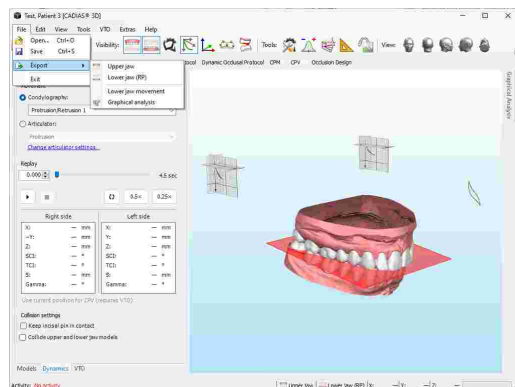


## 8.15 Data export

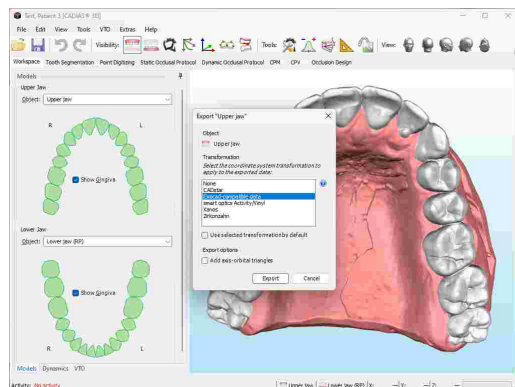
To export an object displayed in CADIAS 3D to external applications, use the menu *File* → *Export* or simply right-click the object in the 3D environment.



In the same menu, you can export the lower jaw movement that is selected on the Dynamics tool window (refer to chapter "Dynamics [255]") as a Jaw Motion file for CAD/CAM applications such as Exocad. Here, it is also possible to export the currently displayed items of graphical analysis (refer to chapter "Graphical analysis [274]") as individual 3D objects.

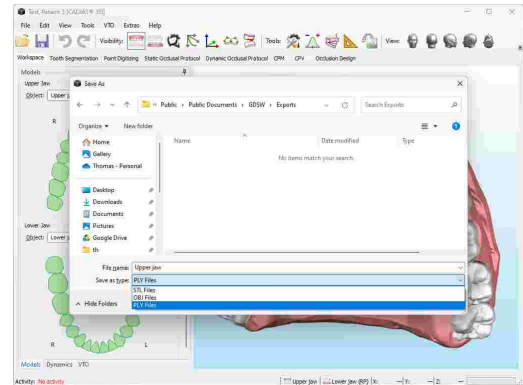


Upon invoking the export, a dialog will appear, in which you can choose a coordinate system transformation to be applied to the exported data. Selecting the transformation appropriate for the target third-party software is essential as it ensures that the 3D data will keep its relation to the hinge axis when imported. By default, data is exported in the axis-orbital coordinate system (refer to chapter "The reference coordinate system [299]"). By checking the corresponding option in this dialog, you can specify that the currently selected transformation will automatically be used for future exports.



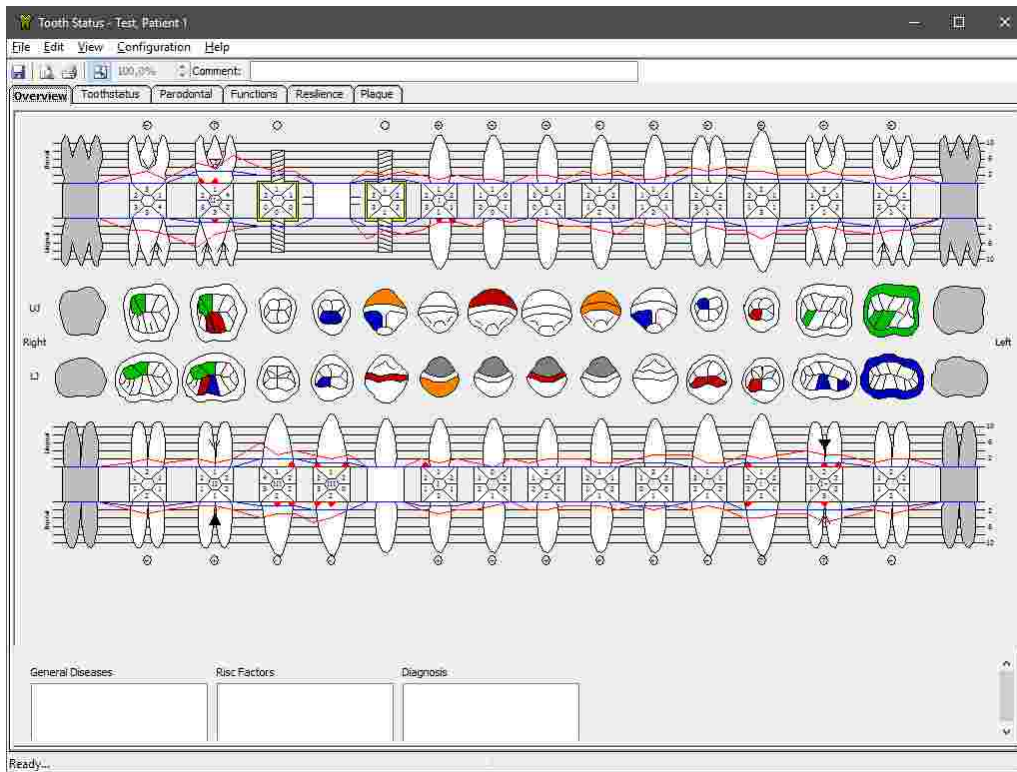
In the export options below, you can furthermore choose to have the application append three reference triangles to the exported data, indicating the locations of right and left hinge axis points as well as the anterior reference point.

You can choose between several file formats in the subsequent save dialog. The application will remember and restore the last used export directory during the next export operation.



## 9 Tooth status

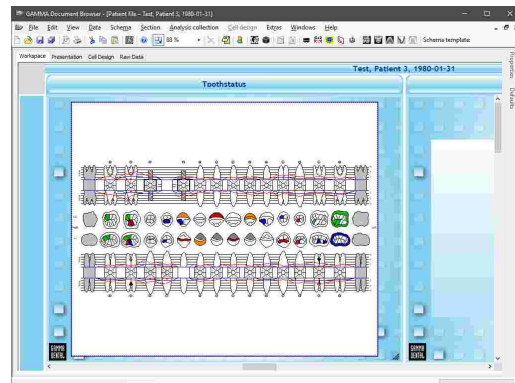
The **Tooth Status** module allows the documentation of the patient's dental condition. Within the application, you can specify missing teeth, implants, gum diseases, misalignment of teeth, and much more. The user interface is separated into several registers, each with its own graphical representation and input controls for various dental parameters. On the register *Overview*, you can find a comprehensive summary of the entered information.




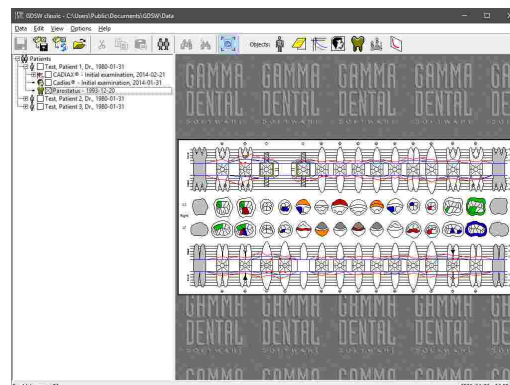
### 9.1 Starting the application

The Tooth Status module is an integral part of GAMMA Dental Software and can be started from GAMMA Document Browser as well as from GDSW classic:

- You can start the Tooth Status application from GAMMA Document Browser by double-clicking one of the Tooth Status data areas. Please refer to chapter "Entering tooth status information" for more information.



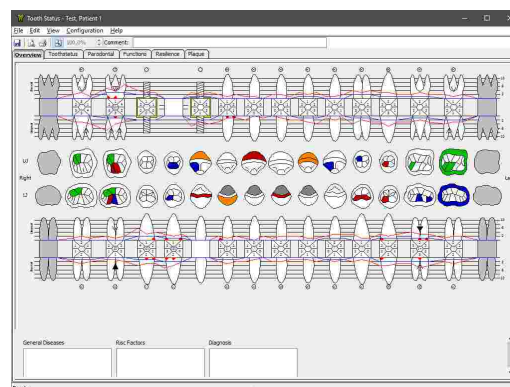
- In GDSW classic, you can create a new Tooth Status analysis via the button  *Tooth Status* in the toolbar. Please refer to chapter "Entering tooth status information<sup>107</sup>" for more information.



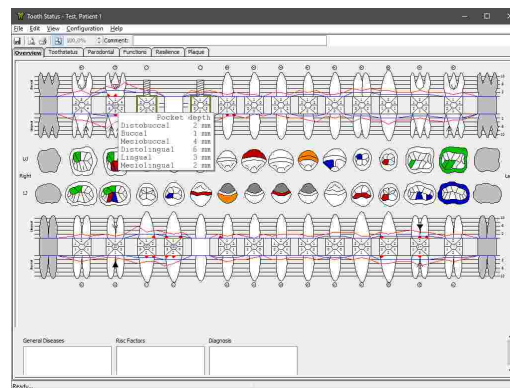
## 9.2 Overview


The *Overview* combines most of the information that was entered on the other registers into a single, comprehensive graphic. To make changes or view specific information in detail, you can always switch to the respective register.

On this register itself, you can enter arbitrary textual information regarding the patient's general diseases, risk factors, or diagnostic remarks.



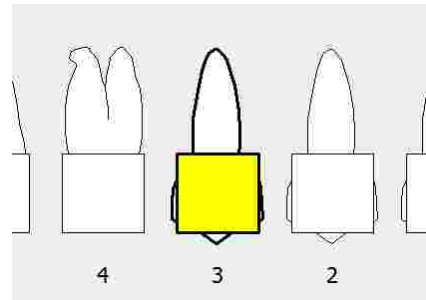
You can view additional information for a specific tooth by moving your mouse cursor over its center.



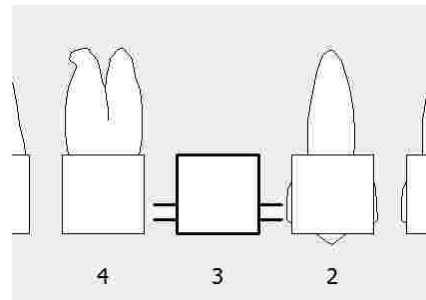
 The *Overview* combines elements from the other registers. For detailed explanations regarding the visualizations used in the graphic, please see the following chapters.



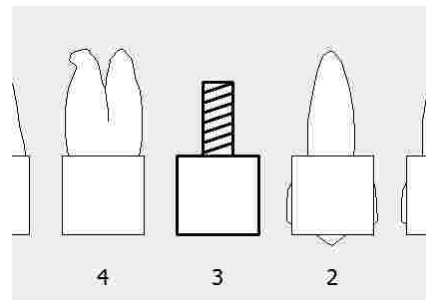
- **Crown:** A crown of any type is bonded to the tooth.



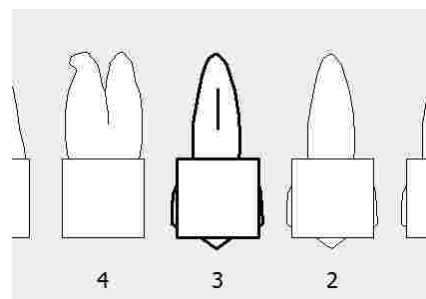
- **Pontic or denture:** The tooth has been replaced with a dummy that is held in place by adjacent crowns, implants, or as part of a denture.



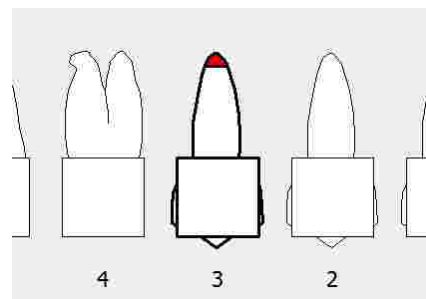
- **Implant:** The tooth has been replaced by a dental implant that is fixated in the bone of the mandible or the maxilla.



- **Root canal:** The tooth had its pulp cleaned out, disinfected, and filled with inert material as part of an endodontic therapy.



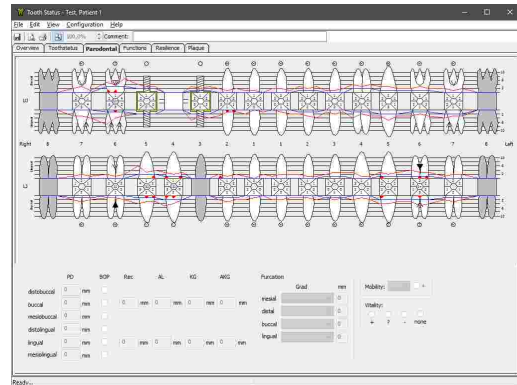
- **Apical problem:** The tooth causes complications at one or more root apices.



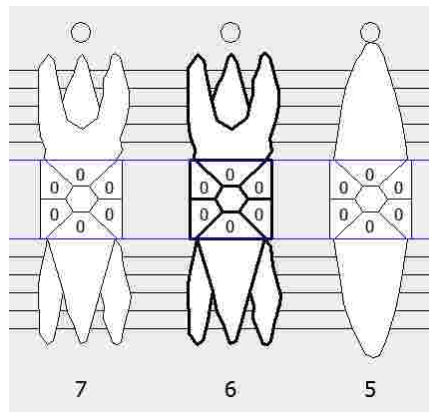
Please note that some combinations of multiple parameters are allowed, while others are mutually exclusive, such as implant and root canal.

## 9.4 Parodontal

In the *Parodontal* view, you can specify information regarding the periodontal tissues and structures that support the teeth.



To do so, select a tooth by clicking on it with the left mouse button. The currently selected tooth will always be highlighted with a bold outline.



### 9.4.1 Attachment

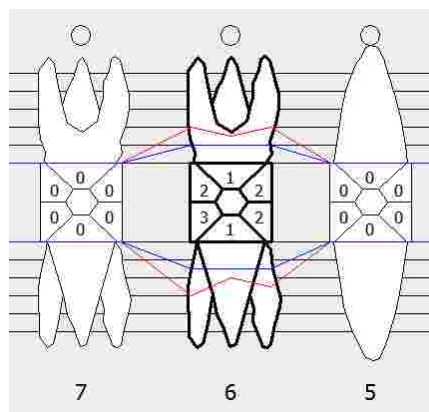
The tissues that connect and fixate a tooth to the surrounding bone are referred to as **Attachment**. In case of a gum disease like periodontitis, the attachment can recede or lose its strength, which can eventually lead to tooth loss if left untreated.

If the gingival margin has receded below the crown of the tooth, this amount of recession can be measured and entered as gingival recession **Rec**. In the graphic, this value is indicated by a **blue line**.

The actual attachment however may have receded even further. This height difference between the visible gingival margin and the actual attachment is referred to as probing depth **PD**. It can be measured at six locations around a tooth using a periodontal probe and then entered in the software. These six values are displayed in the center of the visualized tooth.

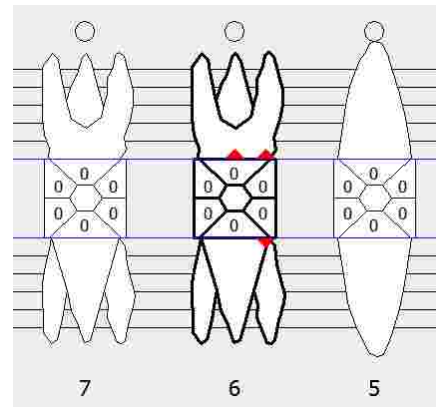
The sum of the gingival recession and probing depth is the overall clinical attachment loss **AL** and is indicated by a **red line**.

For reference, the application displays horizontal lines behind the tooth roots that indicate steps of 2 mm. The entered probing depth values are displayed in the visualized crown of the tooth. The software



also allows entering height of the keratinized gingiva **KG** and can thus calculate the amount of attached keratinized gingiva **AKG**. This value is the difference of probing depth and height of keratinized gingiva.

If measuring the periodontal pocket depth causes the tissue to bleed, this can be documented using the check boxes labeled with **BOP** ("bleeding on probe"). In the graphic, it will then be indicated by small red triangles on the lingual and/or buccal side of the tooth.

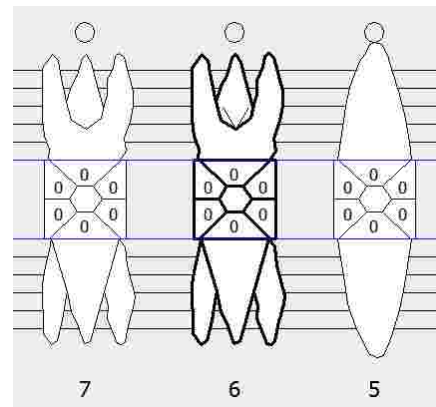


### 9.4.2 Furcation

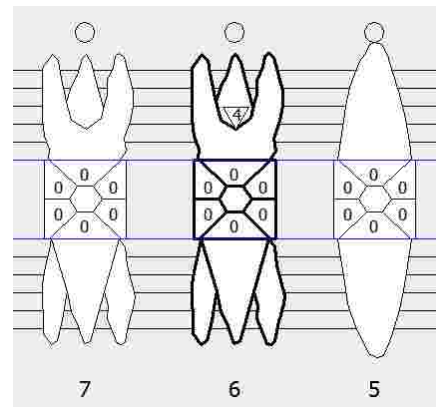
Furcations are the branching points of teeth that have multiple roots. Periodontal disease can lead to bone loss and gingival recession in the surrounding area, which in turn can cause the furcation to become exposed. Due to the compromised accessibility, this area can be difficult to clean during oral hygiene and can lead to an accumulation of harmful bacteria.

In the *Parodontal* view, you can enter the severity of such a furcation defect using the provided combo boxes. The following classifications are available, according to Rateitschak et al., 1984:

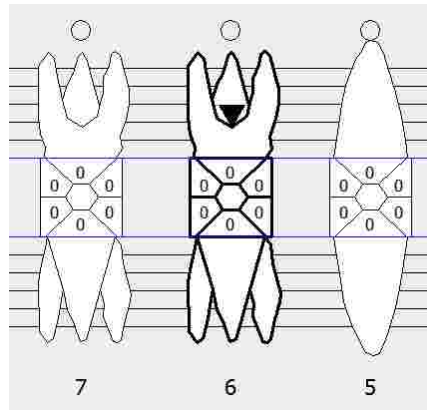
- **Class I (palpable):** The furcation defect can be probed horizontally to less than 3 mm in depth.



- **Class II (measurable):** The furcation defect can be probed horizontally to more than 3 mm in depth, but not all the way through. In this case you can enter the measured depth numerically.



- **Class III (through):** The furcation defect can be probed all the way through to the opposite side.



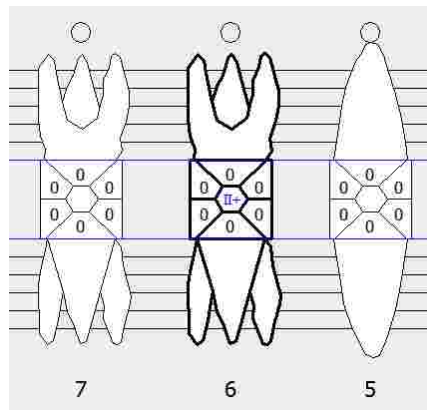
**i** Naturally, the furcation input is only available for teeth that have more than one root.

### 9.4.3 Mobility

In the *Parodontal* view, you can furthermore enter a degree of mobility for each tooth. The following classifications are available, according to Miller PD Jr., 1985:

- (No selection): Normal physiological mobility.
- **Class I:** Palpable horizontal mobility (< 1 mm).
- **Class II:** Visible horizontal mobility (> 1 mm).
- **Class III:** Horizontal and vertical mobility.

The selected class is displayed in the center of the visualized tooth crown. For special intermediate cases, a plus sign can be appended.



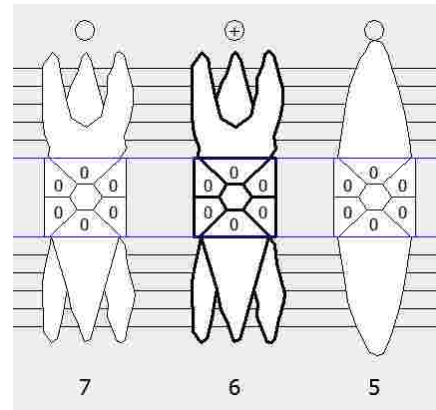
### 9.4.4 Vitality

Finally, the *Parodontal* view also allows entering the vitality of each tooth. In endodontics, the vitality of the dental pulp can be determined with sensitivity tests that assess whether there is a response to a thermal or electric stimulus.

The vitality of a tooth can be entered as one of the following categories:

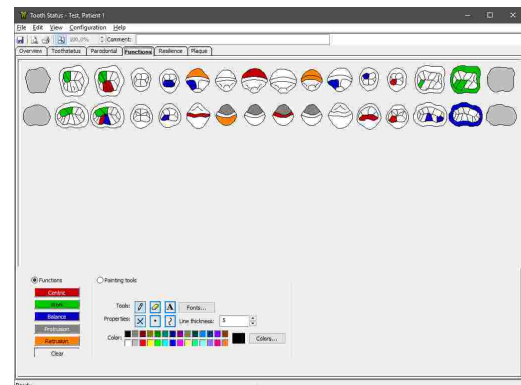
- +: Vital.
- ?: Unknown.
- -: Not vital.

In the graphic, the selected category is displayed in a circle next to the buccal side of the respective tooth root.













## 9.5 Functions


In the *Functions* view, you can specify the occlusal function of each morphological tooth area. To do so, select the function to apply by pressing the appropriate button in the *Functions* group box and then click the respective tooth areas in the graphic. The *Clear* button allows you to clear an assigned function in the same way.



The individual functions are color-coded as follows:

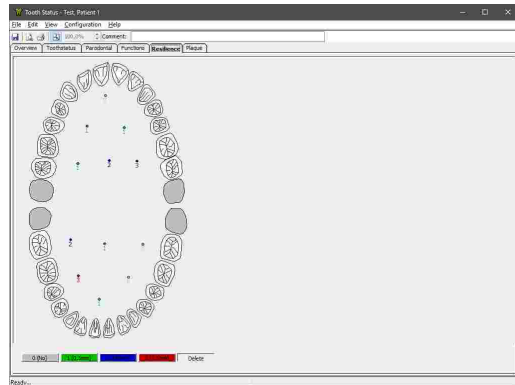
-  Centric
-  Work
-  Balance
-  Protrusion
-  Retrusion

Using the painting tools, you can highlight certain areas or add arbitrary remarks in the graphic. To do so, select the shape to add, which can be crosses with , dots with , lines with , or text fields with . Then, you can draw by clicking at the desired position in the graphic or by holding down the left mouse button in case of lines and text fields. You can also adjust the font, line thickness, and color using the provided controls. To delete a shape, activate the eraser  and then click on the shape in the graphic.

 Please note that shapes drawn using the painting tools will only be displayed in the *Functions* view, and not on the *Overview* register.

## 9.6 Resilience

In the *Resilience* view, you can enter the resilience of the upper and lower palate area. To do so, select the appropriate button for the measured amount of resilience on the bottom of the window and then click at the location of measurement in the graphic. The *Delete* button allows you to remove a placed marker in the same way.



Measured resilience points are color-coded as follows:

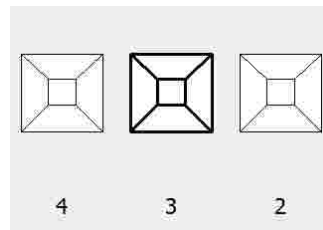
-  0: No resilience.
-  1: 0.5 mm resilience.
-  2: 1.0 mm resilience.
-  3: 1.5 mm resilience.

## 9.7 Plaque

In the *Plaque* view, you can specify the hygiene and plaque status for each tooth.



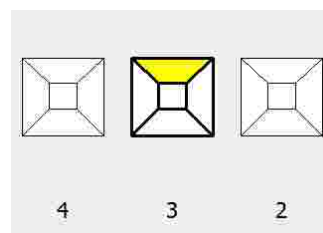
To do so, select a tooth by clicking on it with the left mouse button. The currently selected tooth will always be highlighted with a bold outline.



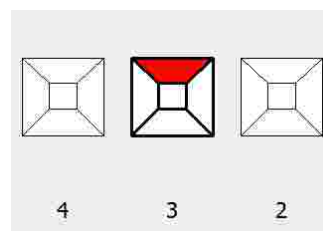
### 9.7.1 Plaque

In the *Plaque* view, you can document the severity of plaque formation for all five sides of a tooth. The following values can be entered. The default value is 0, indicating no plaque.

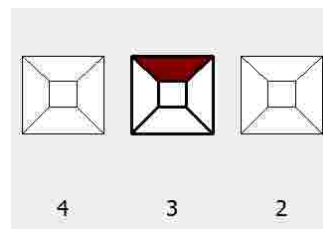
- **1 (Low):** Thin film of plaque on the gingival edge. Can be scraped off with the probe.



- **2 (Moderate):** Visible amounts of plaque along the gingival edge.



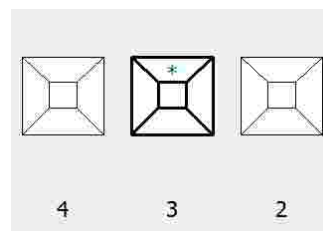
- **3 (Severe):** Large amounts of plaque, interdental spaces are filled with plaque.



### 9.7.2 Retention

Retention spots are locations where a higher plaque accumulation can be expected. This particularly concerns teeth that have cavities, tartars, porous or overhanging fillings, as well as teeth that are partially impacted or misaligned.

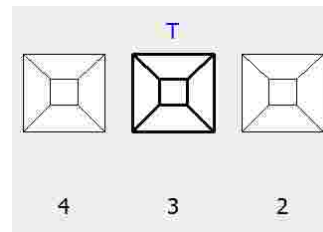
Similar to the plaque input, retention spots can be marked for all five sides of the tooth. In the graphic, these will appear as green stars on the respective tooth area.



### 9.7.3 Tartar

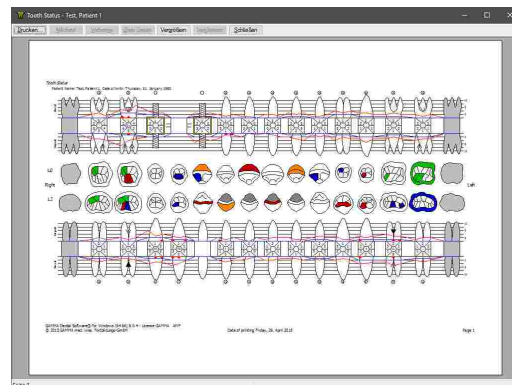
Tartar or calculus is a hardened form of dental plaque that can cause the accumulation of harmful bacteria that compromise the health of the periodontal system. It may form along the gumline or the narrow sulcus that exists between the teeth and the gingiva.

For each tooth, you can specify whether a tartar has formed on the lingual or the buccal side using the respective check boxes. If a tartar is present, the graphic will indicate this with a blue **T** next to the tooth.



## 9.8 Printing

To print the tooth status overview, show a print preview, or to change the page format of the printout, use the respective entries in the *File* menu.




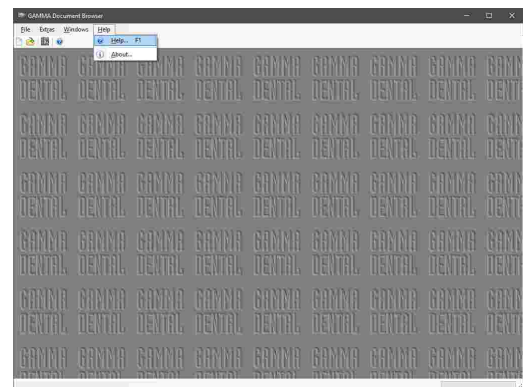
## 10 General software functions

In this chapter you will find a description of general software functions that are not specific to any particular software module.

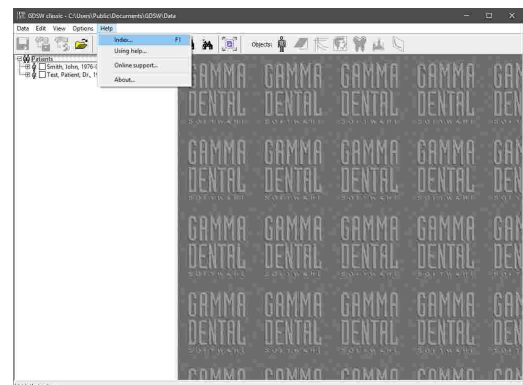
### 10.1 Opening the on-screen help

You can open this manual also as on-screen help from within the software. The corresponding menu item is provided in the *Help* menu of all applications of GAMMA Dental Software.

To launch the on-screen help from GAMMA Document Browser, use the menu *Help* →  *Help*.



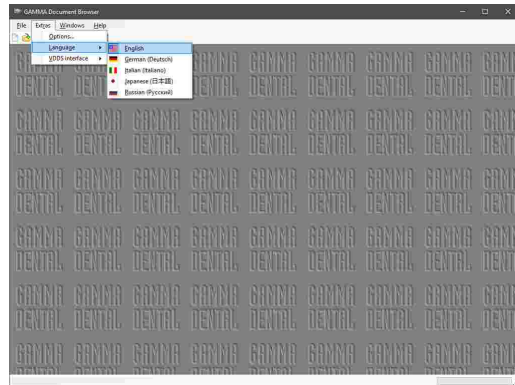
To launch the on-screen help from GDSW classic, use the menu *Help* → *Index*.



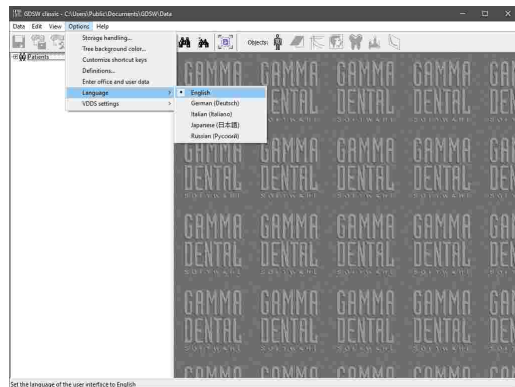
### 10.2 Changing the language

The language of the user interface that was selected during installation can be changed at a later time in GAMMA Document Browser or GDSW classic. To apply the changes, the software has to be closed and restarted.

In GAMMA Document Browser, use the entries in the menu *Extras* → *Language*.



In GDSW classic, use the entries in the menu *Options* → *Language*.



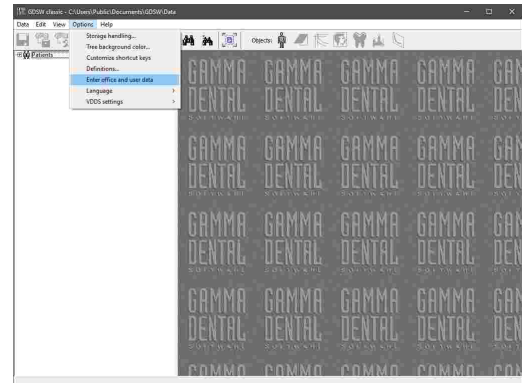
**!** Changing the language of the software after installation will only apply the new language to the elements of the user interface. Any language-specific definition files, such as predefined templates for the Workspace layout in GAMMA Document Browser, will remain localized to the language selected during installation. Should you need those files in the new language as well, it is recommended to uninstall the software and carry out a new installation.

### 10.3 Changing user information

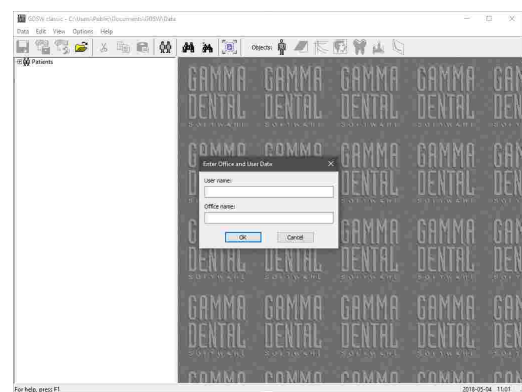
The user information entered during installation is printed on the top right corner of the printouts created by GAMMA Dental Software. You can change this information at any time.

**!** Changing the user information entered during installation requires GDSW classic to be started with administrative privileges. To do so, right-click the shortcut on your desktop or in your start menu and choose *Run as administrator*.

To open the dialog for changing the user information in GDSW classic, use the menu *Options* → *Change office and user data*.

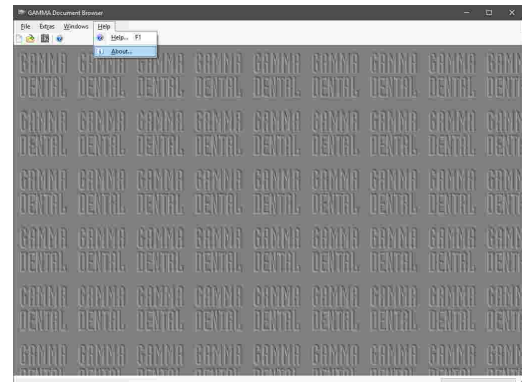


In the appearing dialog you can adjust the name of the user or office as needed. Confirm your changes by pressing *OK*.

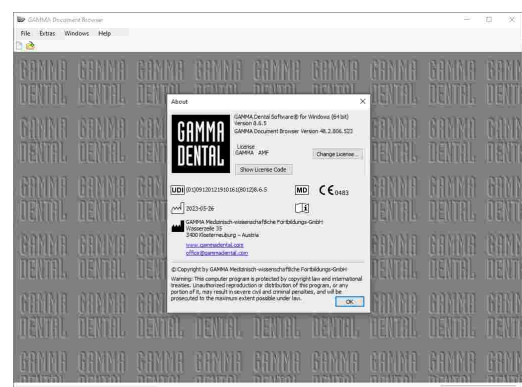


### 10.4 Viewing the licensing information

To view the license that was used for activating the software, use the menu item *Help* → *About*.



This dialog additionally displays the version of the software as well as GAMMA's contact details. If the software has been activated with a time license, this expiration dialog will be displayed here as well.

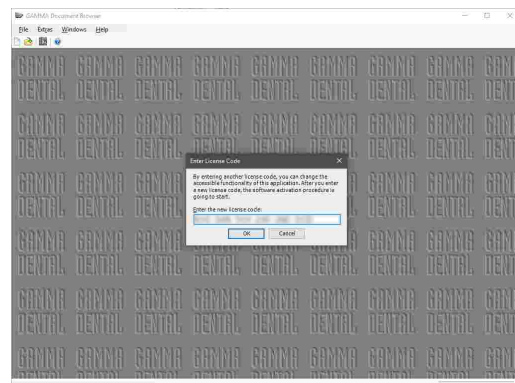


## 10.5 Changing the license code

To change the license code that has been entered during installation, firstly open the About dialog via the menu item *Help* → *About*. Then, press the button *Change license* next to the licensing information.



Enter the new license code in the appearing dialog and confirm by pressing *OK*.



**i** The procedure for changing the license code starts automatically if the software has been activated with a time license of which the expiration date has passed.

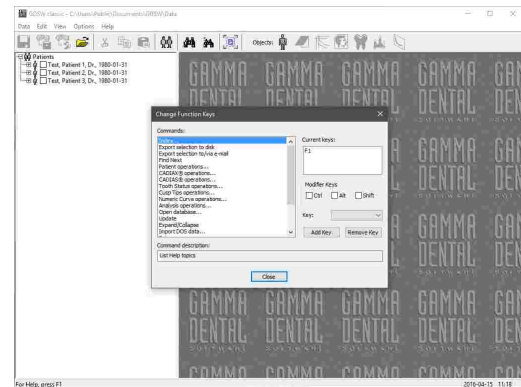
**!** Please note that the number of computers that the software can be activated on with any particular license code is limited. Once the software has been installed and activated, it is bound to that specific computer. Changing the license code of an already activated software will not free the activation used by the old license code.

If you plan to upgrade or exchange a computer on which you have activated the software, please contact GAMMA to assist you in migrating or restoring the license. Should you need to reinstall the software on the same computer without changing its hardware, the previously issued activation will be reused automatically.

## 10.6 Configuring shortcut keys

To provide quick and easy access to specific operations, most software modules allow you to associate them with shortcut keys. By pressing the defined shortcut key combination on your keyboard, the specified operation will be executed immediately.

The most commonly used functions already have default shortcut keys assigned after installation. These will be displayed next to the respective items in the menu.



## 10.7 Definition files

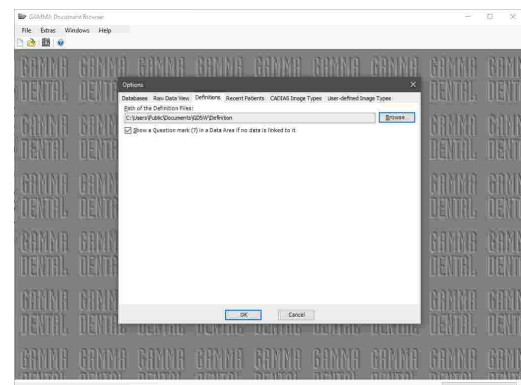
Definition files are files that are essential for the operation of GAMMA Dental Software. These include x-ray tracing definitions for the CADIAS applications, macro files for CADIAX Recorder, schema design templates for GAMMA Document Browser, and many more. These files are installed together with the software itself, by default into the following directory:

*C:\Users\Public\Documents\GDSW\Definition\*

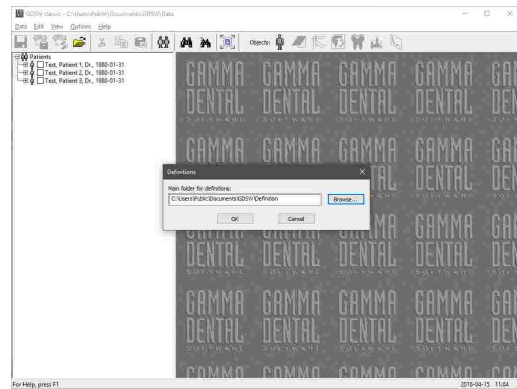
To move definition files from one computer to another, you can simply copy this directory and paste it on the target computer. However, please note that both computers should use the same software version in this case. Files that have been created by a newer version are not necessarily readable by an older version.

Since it is possible to create custom definition files and, within limits, customize the existing ones, you may want to move this folder to a network storage that is accessible from multiple workstations. To do that, you will have to configure the software on every workstation to use the shared path.

In GAMMA Document Browser, you can do so via the menu *Extras* → *Options*, on the register *Definitions*. Browse for the directory to use and confirm by pressing *OK*.



In GDSW classic, you can change the directory from which the software will access the definition files via the menu *Options* → *Definitions*. Browse for the directory to use or enter it manually, and confirm by pressing *OK*.



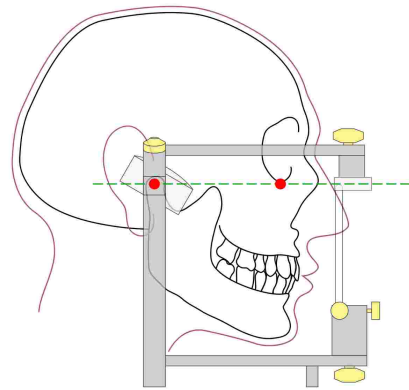
## 11 Background information

In this chapter you will find explanations regarding the terminology and backgrounds of the GAMMA concept.

### 11.1 The reference coordinate system

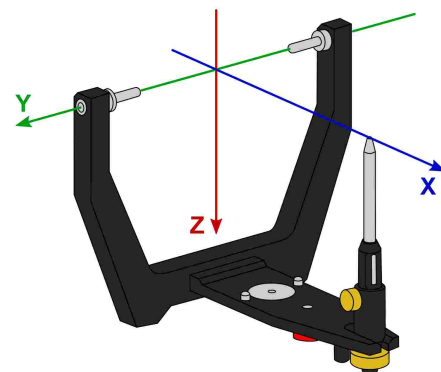
In order to aggregate CADIAX condylography data and CADIAS cephalometry tracings, all GAMMA products use the hinge-axis-orbital coordinate system as reference. This allows the reproducible and standardized transfer of recorded data in the analog or virtual articulator.

The basis for the axis-orbital coordinate system is the axis-orbital-plane (AOP), which is defined by the left and right hinge axis points and the left orbital point (lowest point of the orbit's anterior margin). Before a lateral radiography, usually lead markers are placed on these three points to indicate their location in the x-ray image.



The axis-orbital-plane on the cranium and in the articulator. The visible axis point and the orbital point are marked red.

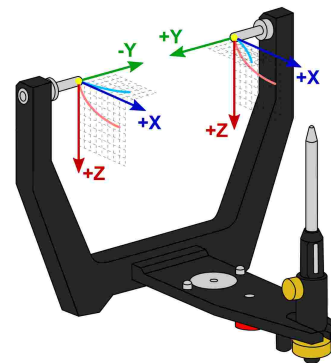
The origin of the coordinate system is located centrally on the hinge axis between right and left condyle. From this origin, the positive X axis extends anterior towards the orbital point, the positive Z axis downwards, and the positive Y axis to the right, from the patient's point of view. The median-sagittal plane coincides with the X and Z axis, the transversal plane with the X and Y axis, and the frontal plane with the Y and Z axis.



The origin of the axis-orbital coordinate system in the articulator.

The movements of the right and left condyle recorded during condylography are visualized in symmetric sub-coordinate systems with identical axis definitions.

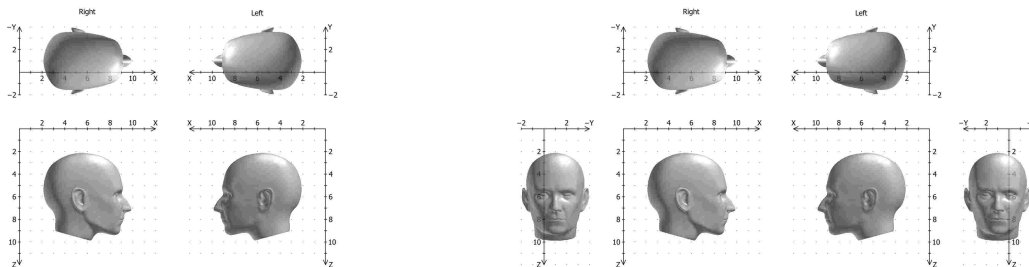
When recording movements on the patient, the distance between left and right measurement electronics is naturally greater than the distance between the right and left condylar guidance elements in the articulator. It is for this reason that recordings have to be recalculated to the smaller distance before the software can calculate articulator settings.



The zero points of right and left condyle used when recording condylography.

**i** The reference position set during recording represents the zero point of these sub-coordinate systems. Ideally, the reference position is located on the hinge axis and remains fixed for the duration of the recording. However, due to physiological reasons, most patients are unable to return to the precise starting position after a movement. In these cases it can happen that recordings do not start in the zero point, unless the reference position has been re-fixed before each individual recording.

Besides viewing condylographic recordings in sagittal (X/Z) or transversal (X/Y) projection, the CADIAX applications can also display additional coordinate systems for frontal projection (Y/Z):



The coordinate system with sagittal and transversal view.

Extended coordinate system with sagittal, transversal, and frontal view.

## 11.2 Exact and anatomic hinge axis

A CADIAX condylography recording can be carried out based on either the exact or the anatomic hinge axis of the temporomandibular joint, depending on the used recording system. In both cases, the measurement takes place in close proximity to the joint itself.

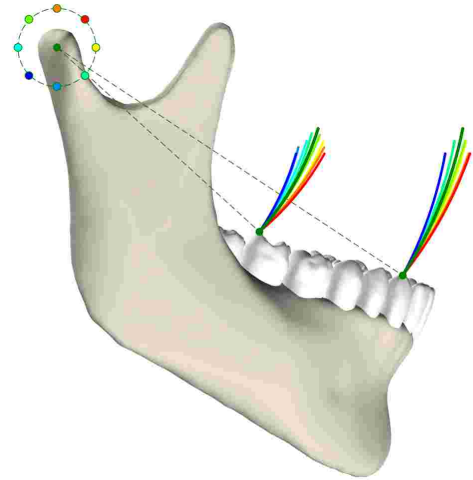
The exact hinge axis (also referred to as kinematic or individual hinge axis) is determined during the recording on the patient. Here, the joint is fixated in retral position and the rotation center of stationary open/close movements is observed. Subsequently, the measurement electronics are adjusted to that position and the reference position is set. For recording on exact hinge axis without limitations, a CADIAX 4 or CADIAX diagnostic device is required.

In contrast to the exact hinge axis, the anatomic hinge axis (also referred to as arbitrary hinge axis) is not ascertained for each individual patient. Rather, its location is given through the empirically determined distance of 10 mm anterior to the ear canal. This position is indicated on the Reference AB face bow that is usually used for anatomic recordings and therefore easy to find and adjust to.

Recordings on the anatomical hinge axis can be carried out with the devices CADIAX compact 2 as well as CADIAX 4.

The advantage of recording on the anatomic hinge axis is in its simple and quick application. While the deviation from the exact hinge axis inevitably leads to a distortion of the curve characteristics, its effects on the movements used for articulator programming, namely protrusion and mediotrusion, are tolerable.

However, when recording condylography for the purpose of functional diagnostics and occlusion analysis, the exact determination of the patient's individual hinge axis is imperative. In this use case, hinge axis deviations of just a few millimeters in combination with the rotational component can cause significantly different movement patterns in the tooth area.

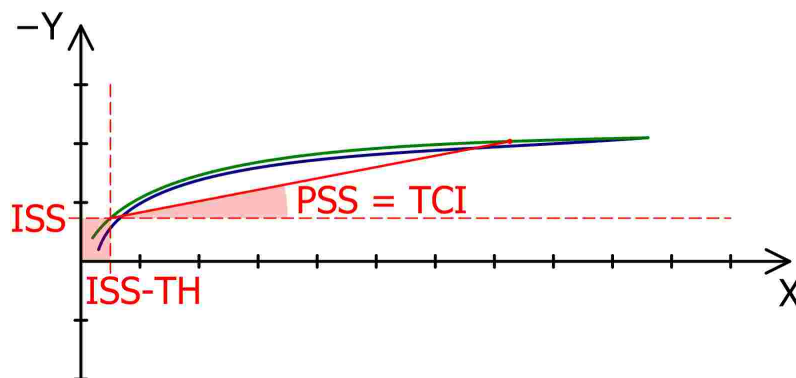


The effects of various deviations from the exact hinge axis onto the movements of dental cusps.

### 11.3 Immediate side shift (ISS)

Some articulator systems divide the transversal Bennett curve into an immediate and a subsequent progressive side shift movement. These two phases of the movement are referred to as "immediate side shift" (ISS) and "progressive side shift" (PSS), respectively. The separation is made at a particular distance measured in X direction, which is referred to as "ISS threshold" (ISS-TH).

In the articulator settings calculated by the software, the ISS describes the maximum transversal displacement up to the specified threshold distance. The PSS however is an angle value equatable to the transversal condylar inclination (TCI), not including the initial displacement.




The ISS threshold (ISS, here: 0.5 mm) separates the Bennett movement in immediate (ISS) and progressive side shift (PSS).





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The logo consists of a solid black square. Inside the square, the words "GAMMA" and "DENTAL" are stacked vertically in a white, bold, sans-serif font. The letters are widely spaced, giving the logo a modern and clean appearance.

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