Tiops2005 user guide

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These guidelines are intended to help you make the most efficient use of the TIOPS program. The program is designed to facilitate morphological analysis of an individual headfilm (digital or analog) as well as growth and treatment analysis of serial headfilms.

Occlusograms from digital and analog pictures can be fitted to the cephalometric tracings.

The program also permits the clinician to develop simulations of facial growth, --orthodontic treatment and treatment combining orthodontics and orthognathic surgery.

The links
will guide you
through

Contents

Program Basics

To access the TIOPS program double click the icon on the desk top. The program then opens and you can either enter data for a new patient analysis or access an old .txd file saved in the Analy2005 folder, by default. This folder is placed on the C: drive, or in any defined location on a network drive: DriveLetter:\AnyPath\…\Analy2005 .
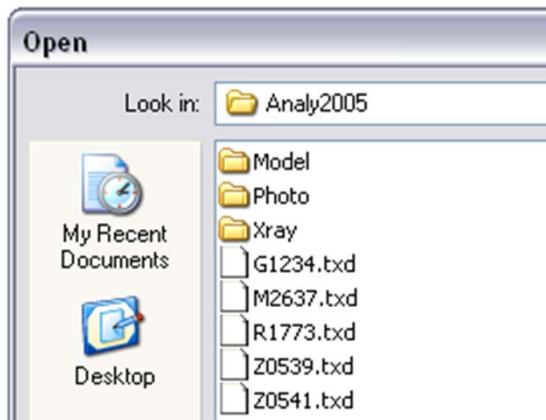
To perform an analysis of a digital X-ray, it has to be stored as a .jpg or .bmp file in the TIOPS programs X-ray archive folder normally labeled C:\Analy2005\Xray. You can define any folder as your X-ray destinationfolder.
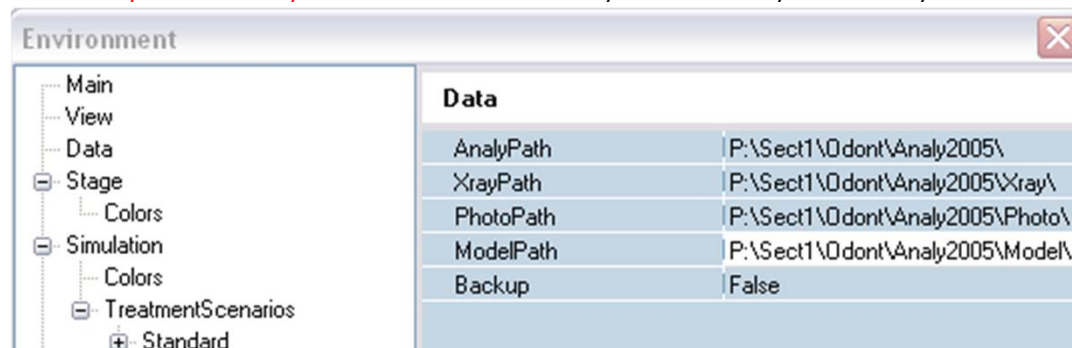
Most digital X-ray systems have the capability to export the picture in these formats. Tiops2005 has some built in possibilities for adjustment of the image. You can adjust brightness and contrast using the TIOPS program. You can also make adjustments using the digital X-ray program that came with the digital x-ray equipment to make more elaborated adjustments of specific features and then export the improved image in either jpg or .bmp format, to the x-ray folder.

Imaging programs like Photoshop™ can also be used to create and improve a .jpg file if you are scanning a conventional headfilm.

Analog (conventional) headfilms can also be analyzed using a conventional digitizer.
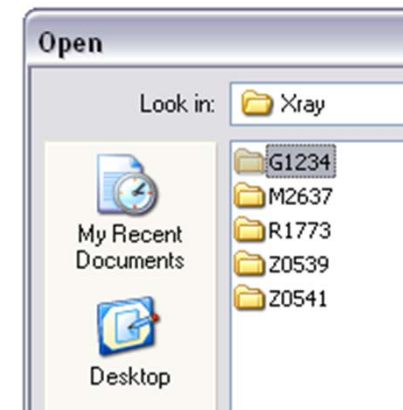
Image folders
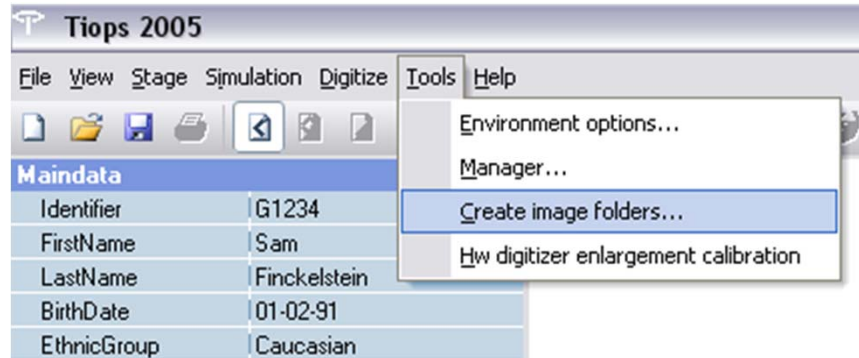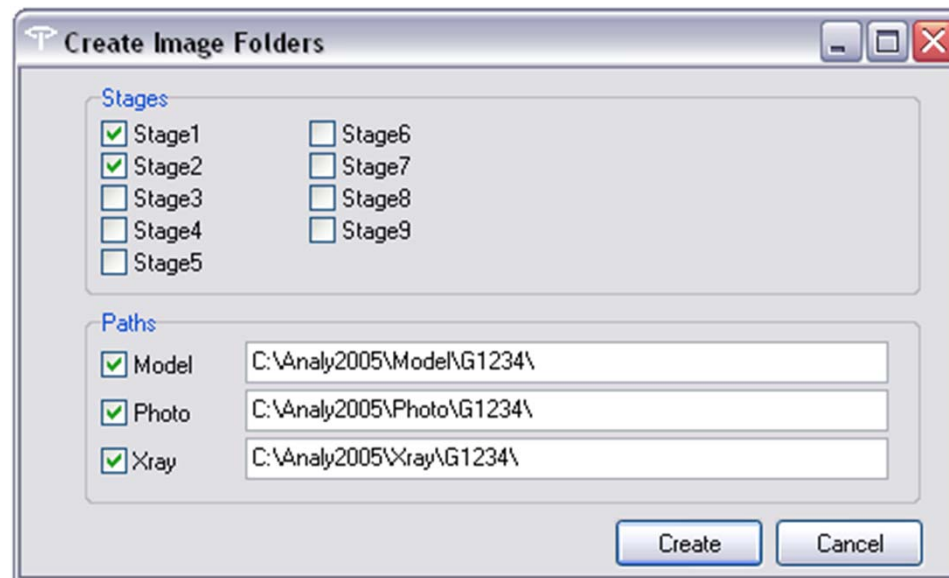
All image files of a patient are stored in the appropriate subfolder in the Analy2005 directory so they can be accessed by the TIOPS program.
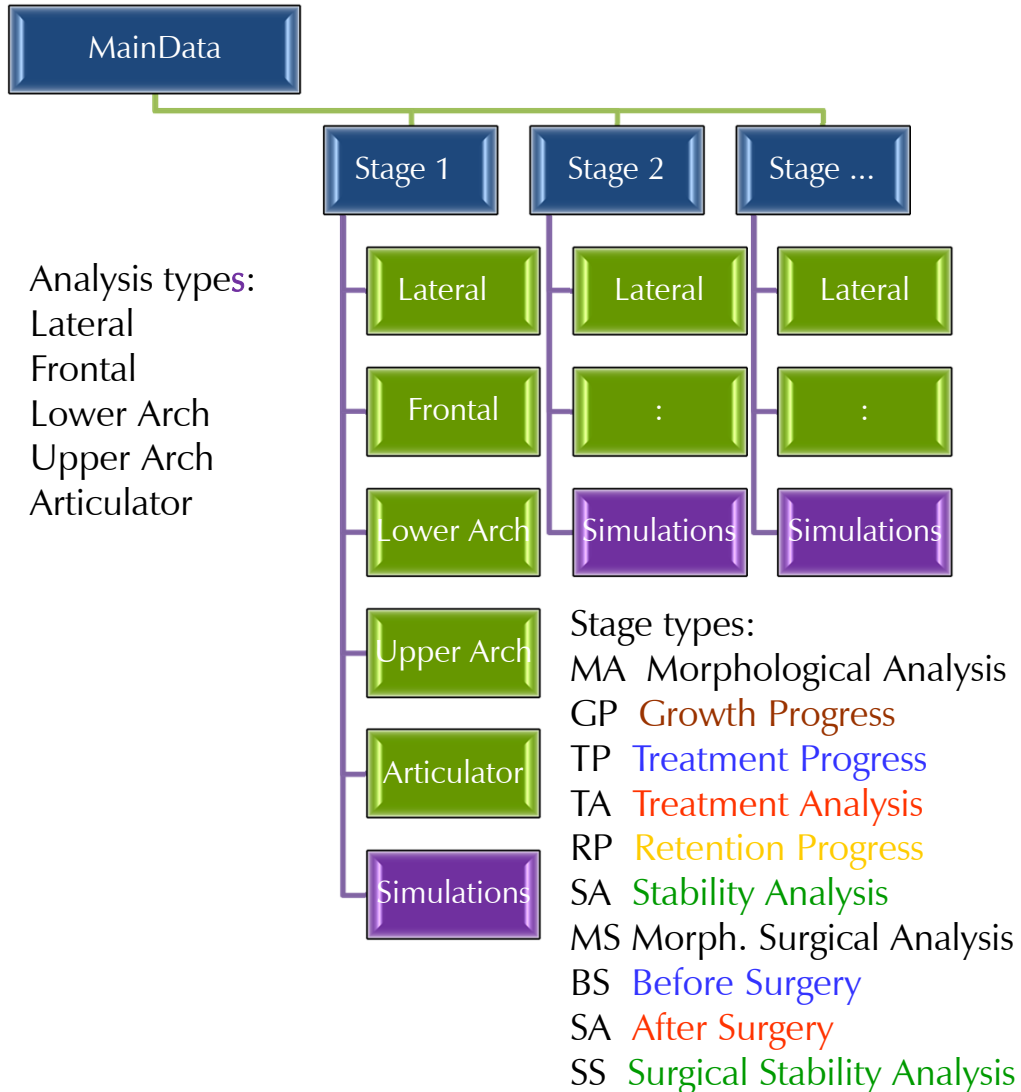
If you have several X-rays, images of the study casts and photos of the same patient, you may find it convenient to make sub folders to organize your image files.

Create Image Folders does this automatically, just check the appropriate boxes.

Patient file structure and management

MainData

Stage 1 — **Stage 2** — **Stage ...**

Analysis types:
Lateral
Frontal
Lower Arch
Upper Arch
Articulator

Stage 1: Lateral, Frontal, Lower Arch, Upper Arch, Articulator, Simulations

Stage 2: Lateral, :, Simulations

Stage ...: Lateral, :, Simulations

Stage types:
MA Morphological Analysis
GP Growth Progress
TP Treatment Progress
TA Treatment Analysis
RP Retention Progress
SA Stability Analysis
MS Morph. Surgical Analysis
BS Before Surgery
SA After Surgery
SS Surgical Stability Analysis

Using the Tools/Manager... it is possible to remove parts af the a patients file that are not wanted or corrupted.

Click the icon of the part to be removed and press Delete.
The program will keep track of the parts that are used by other components of the program.
Note: These can not be deleted.

ManagerDlg

Stage No	1
Stage Type	MA

Delete   Close
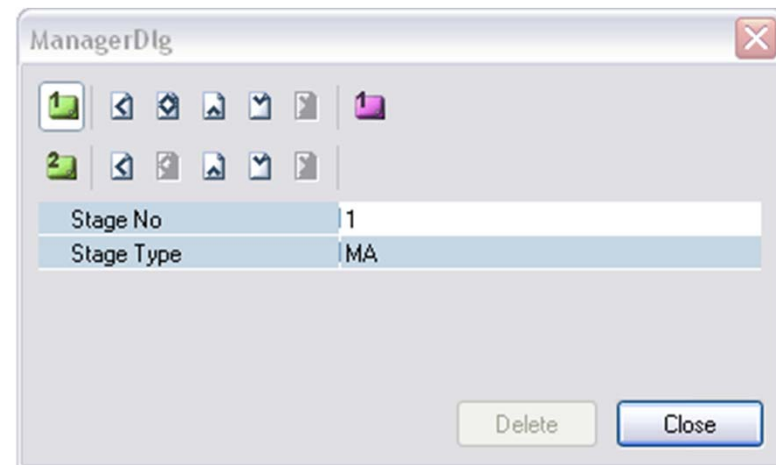
Entering a new patient (1:2)

To enter a new patient into the program fill in the MainData area seen below. To move from one menu box to the next, up or down the list, use the arrow keys (↓↑). To move from one rubric to another use the mouse.

The first line in the Maindata area identifies the patient by a unique label. One possible convention is to enter a letter followed by the last four digits of the patients chart number, but you can choose between several different IdMasks.

Hint: Choose the same IdMask format for all your files

Changes to the default setting of the IdentifierMask and the IdSettings can be made by going to Tools/Environment options and select the box labeled IdMask/IdSettings under Main. The changes do not take effect until the program is restarted.
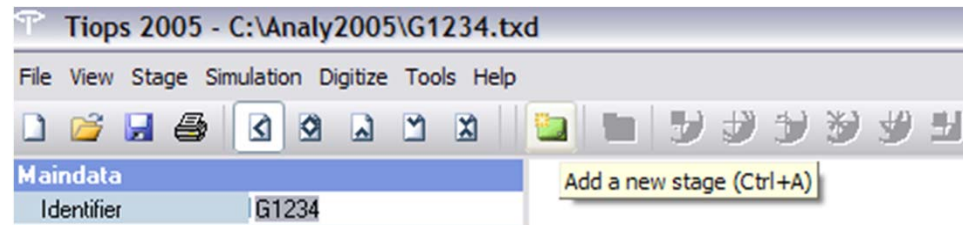
Following the identifier enter First and Last Name and DOB as well as Sex. (No values have been entered for other Ethnic Groups at this time).

The information is automatically stored in the program when you move down to the next field using the down arrow key <↓> key - (if you use <Enter> the data will be accepted but the focus will not move to the next field).

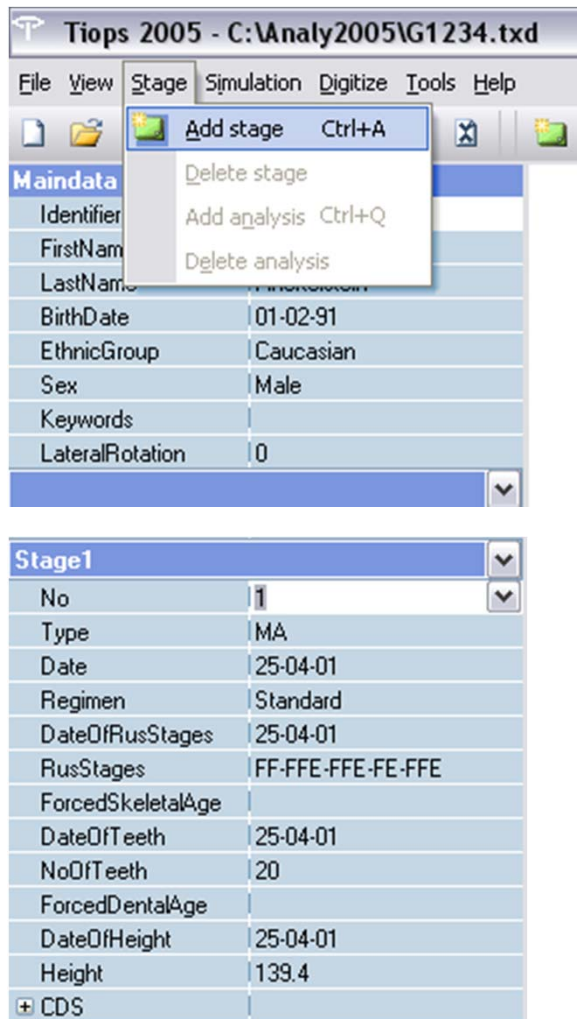The field Keywords may be used for patient group search.

The Menu Bar

When you hold the mouse arrow over an icon in the menu bar the function and the shortcut associated with that icon is indicated. Icons that are grey are not active at this stage in the program.

Entering a new stage (1:2)

To continue in the program press <Ctrl> and <A> together. This opens the next series of information under the heading Stage1 and automatically creates a new Stage.
Alternatively you can click the button   located on the menu bar.

Or use the Stage pull down menu and click Add stage.
With the arrow key <↓> key you scroll down the list, while checking or entering information.

To determine the skeletal age of a patient the so-called RUS data can be entered. The program uses this information to further calculate the variable means used in the simulation procedure. The program then assigns a condylar growth value using the subjects skeletal age. If no RUS data is entered, you can individually set the skeletal age (yy:mm) derived from other sources. If no RUS data is entered or any skeletal Age is set the program will use the chronological age calculated from the Stage Date.

NoOfTeeth refers to the number of the number of erupted permanent teeth. If no number is entered, you can set a dental age (yy:mm) derived from other sources.

You now reach a box labeled CDS - Chronological, Dental and Skeletal Age Relations. The sub menus can be accessed by using the right arrow key <→> or by clicking at the [+] sign.

If you previously entered RUS values and/or the number of erupted permanent teeth as well as body height (cm) the calculated variables are listed under Chronological, Dental and Skeletal Age.

The average height (cm) based on the patient's sex and the predicted (estimated) height at completion of growth is also listed.

Any of the submenu boxes can be closed again using either the left arrow key <←>; or click on [+] next to the menu.

Adding a lateral digital headfilm (1:6)
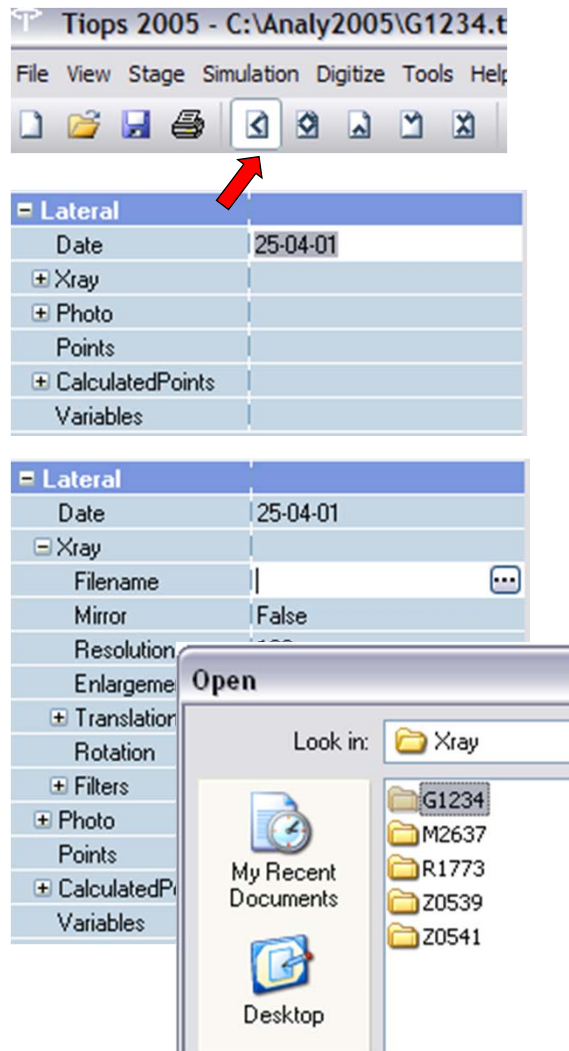
You are now ready to perform the lateral analysis. Make sure that the lateral view icon is selected (see arrow).

At this point you can open the next sets of menus by pressing <Ctrl> and <Q> together which adds a new Analysis. A set of sub menus now opens up. Check that the Date of the headfilm is correct as the program uses the entered Stage Date as a default. The two dates should be the same.

You now proceed through the listing using the down arrow key <↓> and when reaching the sub menu Xray, open it by clicking on the plus sign [+] next to it. The box sign changes to a [-] and a new list is revealed.

Scroll down to Filename and either click the radio button ⋯ or type <Ctrl> and <→> together. This opens the Xray folder in the Analy2005 directory where your headfilms should be stored as .jpg or .bmp files either directly in the Xray folder or in the patient sub folders.

Select the appropriate .jpg or .bmp file and the image is automatically loaded into the analysis program.

Adding a lateral digital headfilm (2:6)

The headfilm will now appear in the window ready to digitize, but check before the entries:
Mirror, Enlargement and Filters. When the profile faces to the left then set Mirror to True. Resolution, Translation and Rotation are set automatically.

Adding a lateral digital headfilm (3:6)

Lateral	
Date	25-04-01
Xray	
Filename	C:\Analy2005\Xray\G1234.j
Mirror	False
Resolution	191
Enlargement	5.6
Translation	
Rotation	0
Filters		
Invert	False
Brightness	0
Contrast	0
SharpenPercent	0

Hint:
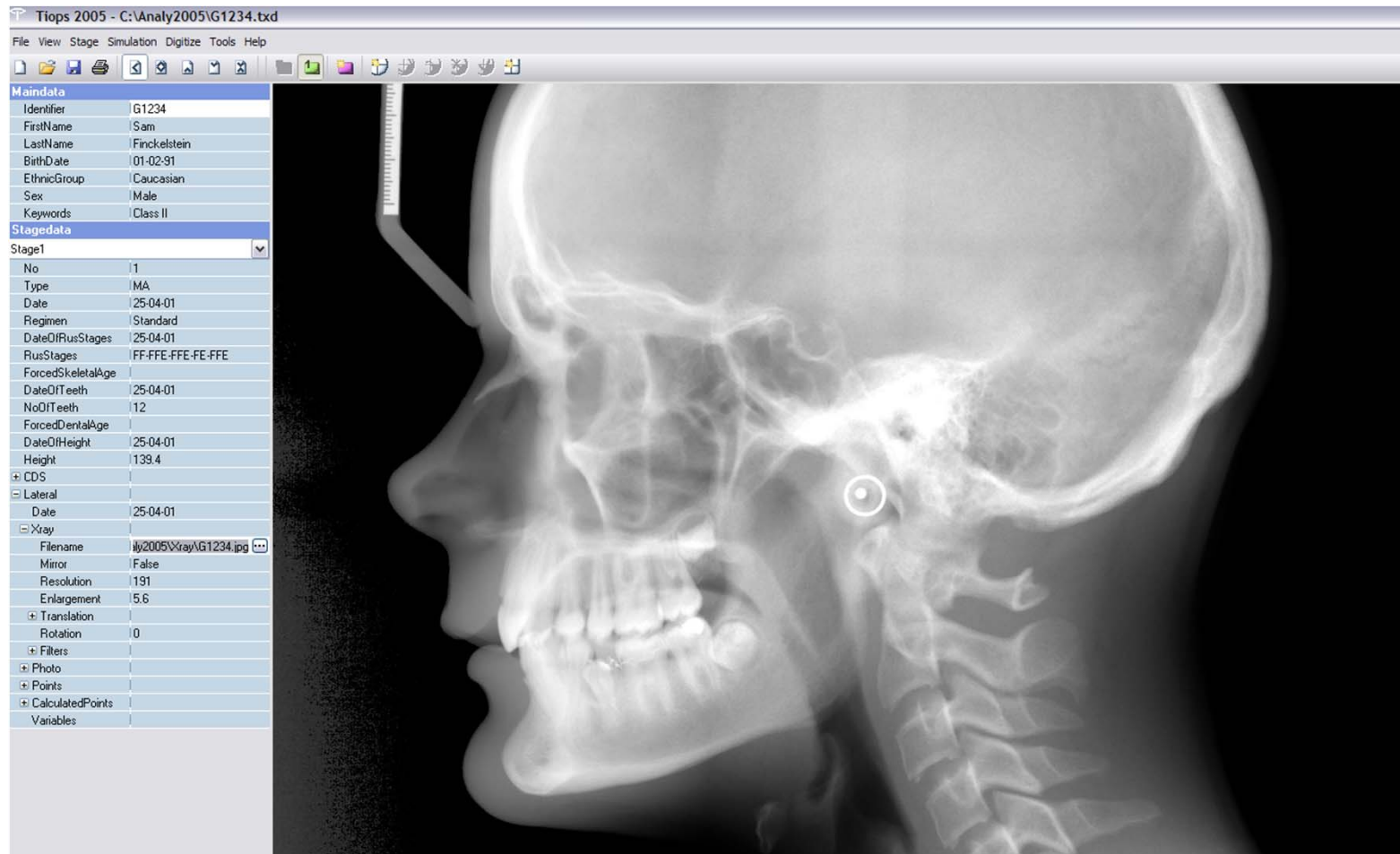If you have a 50 mm scale on the headfilm, the program can calculate the enlargement. Point at the 0 mm mark, hold down the left mouse button and draw a line to the 50 mm mark. The enlargement is listed on the bottom left of the screen. For any other scale size the enlargement can be calculated using the measured length using the formula: ((Measured distance/Actual distance)-1)*100

MeasureLength: |(28,-29.5) (26.75,-79.5)| = 50.02mm XrayEnlargement (for 50mm reference): 13%

Start

Mirror
It is possible to change the horizontal orientation of an imported image select True instead of False. This flips the image horizontally.

Resolution
Do not change the resolution as it is detected automatically from the .jpg file. Some .jpg do not have this information and .bmp files never have it. In those instances the resolution can be calculated and entered using the following formula: $\text{Number of pixels}_{\text{picture height}} / \text{Picture height}_{\text{inch}}$

Enlargement
The Xray Enlargement is a system variable preset in Environment/Stage. Change if not appropriate. All images on the screen are adjusted to zero enlargement.

Translation and Rotation
Do not change these settings. The values are calculated by the program when the points n(cb1) and sa(cb2) are entered and thereafter the headfilm is aligned with the nasion sella line horizontal. When the headfilm is registered in natural balanced head position, the variable NSL/HOR can be used to show the tracing and the headfilm aligned in this orientation. Enter the negative value of this variable in the Maindata field labeled LateralRotation to change the orientation.

Filters
It is possible to change the normal negative image to a positive choosing True instead of False in the heading Invert.
You can adjust the brightness of an image, the contrast and even sharpen the image as needed, using the sliders. The program remembers the changes when you open the file the next time, but the file itself is not modified.

Standard regimen – the basic regimen

Blueprint regimen – including the cervical vertebrae – the regimen used at the Post Graduate Orthodontic Program in Copenhagen

LatFron regimen – including the possibility of both right and left landmarks for the posterior part of the mandible and the upper and lower molars and functional occlusal plane.

Snake regimen – is explained separately.

Complete regimen – all the landmarks from the list. This regimen is the basis for creating individualized regimens.
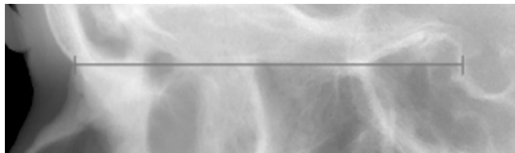
Select the Regimen

from this drop down box:

Hint: The landmark sequence for the different regimens can be seen in the file TiopsLandmarks.xls, which can be downloaded from the www.tiops.com/Documentation.

Stage1		
No	1	
Type	MA	
Date	03-10-07	
Regimen	Standard	

Start digitizing

by pressing <Ctrl> and <D> together or click:

Entering digital cephalometric landmark data into Tiops

With a new image opened you are now ready to start the digitizing process. Use the left mouse button and click on the anatomical point Nasion(n) followed by Sella Anterior(sa), located at the intersection of the anterior wall of Sella Tursica and the Anterior Clinoid process. A line will be drawn between these two points and the picture is oriented horizontally.

The digitizing sequence

The next point to be digitized is listed in the lower left area of the computer screen (above the Windows Start menu).

Sella [s] in MedBas (s-ba)

Then follow by clicking on Sella(s) then Basion(ba), once again a line connecting the two is drawn.

To skip a point, in this case Condylion (cd), click on the white circle with a black cross and a sad blue arrow in the Tools bar.

Proceed through the list of points until you get to the lower incisor.

Condyleon [cd] in MandibularCondyle (cd) (skip)

Hint: According the regimen chosen, some points are mandatory but others can be passed (skipped).

Entering teeth into Tiops
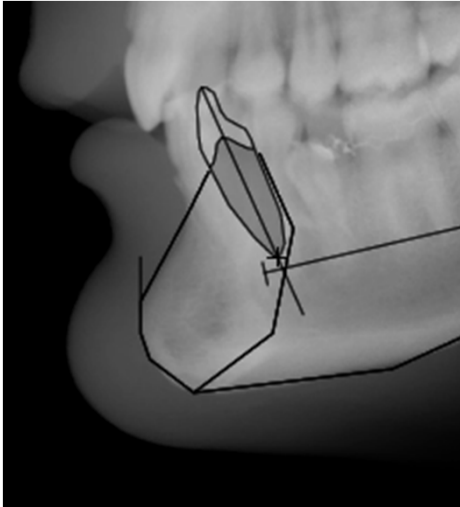
When you have entered the second maxillary reference point (mx2) you will see a lower incisor floating when you move the mouse. The tooth will continue to "float" until you anchor the incisal edge by clicking after it has been placed a short distance away from the correct location.

The inclination can now be changed by moving the mouse sideways (Do not click!!).

When the correct inclination is present the tooth can then be translated to the correct position of the incisal edge by simultaneously holding down the <shift> key and sliding the mouse until the correct position is achieved. The correct tooth length and the final inclination is determined by placing the cursor cross in the apical area of the tooth template and clicking the left button of the mouse. This locks the tooth into place.

If at any time a mistake is made you can go back step by step by clicking the red circle with a X in the tools bar.

The next tooth to be entered is the lower first molar. Then the upper central incisor is digitized and lastly the upper first molar.

Once the teeth are placed continue with the premolar occlusal point (pop) located at the tip of the lower first bicuspid. This determines together with the medial cusp of the first lower molar the so-called functional occlusal plane OLf (Ricketts/Tiops).

The final landmarks
Now follows a series of soft tissue points and after completing these you will here a "blip sound" indicating you need to digitize or skip the hyoid bone (hy) next.

This is then followed by three additional points. First, a point on the most posterior outline of the Maxilla (tu), is digitized. Second, a point opposite to (tu) located on the soft tissues at the back of the naso pharynx (ad1), is entered.
These two points are defining the shortest distance between the maxillary tuberosity and the adenoid tissue.
The third and last point is located at the back of the naso pharynx (ad2), at the intersection of a line from pm to the midpoint of the Sella-Basion line, where it crosses the soft tissues of the pharynx.
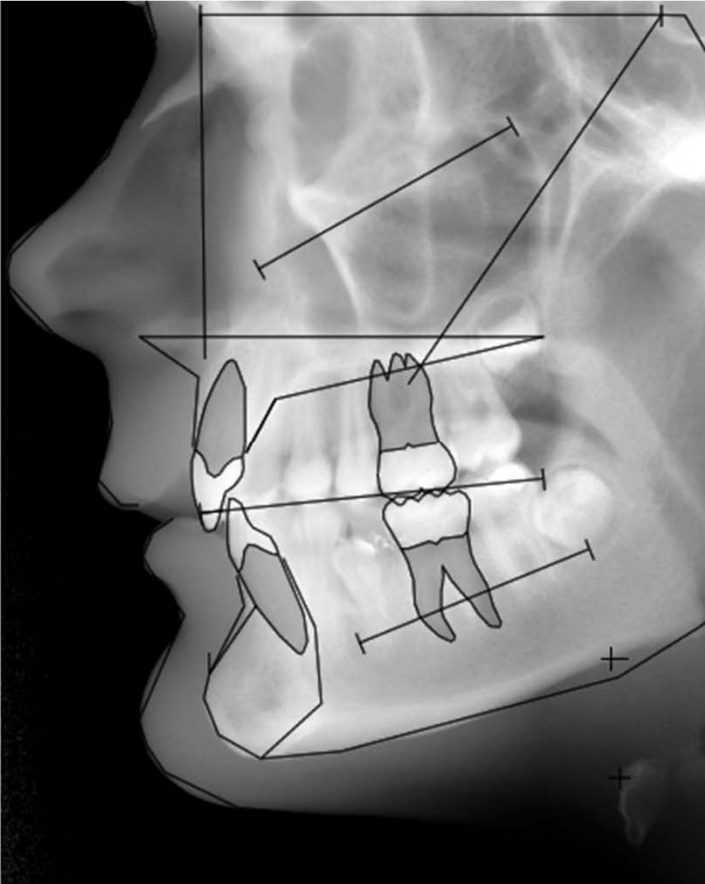
This completes the digitization process and now you must save the data. Go to the dropdown menu File/save or click the save icon:

If you try to close the program without saving the date you will be prompted to do so.
It is a bright idea to save your data after completing each step of the analysis.

Digital landmark correction

Landmark correction:
If you have made a mistake that does not appear until the final data is saved, you can open the point list by clicking the plus next to Point [+]. Scroll down to the point and re enter it with the left mouse button on the tracing. When all points are correct you should close the Point entry and remember to save the file again.

Working with regimens

This function is further developed and
described in the Tiops4 program.
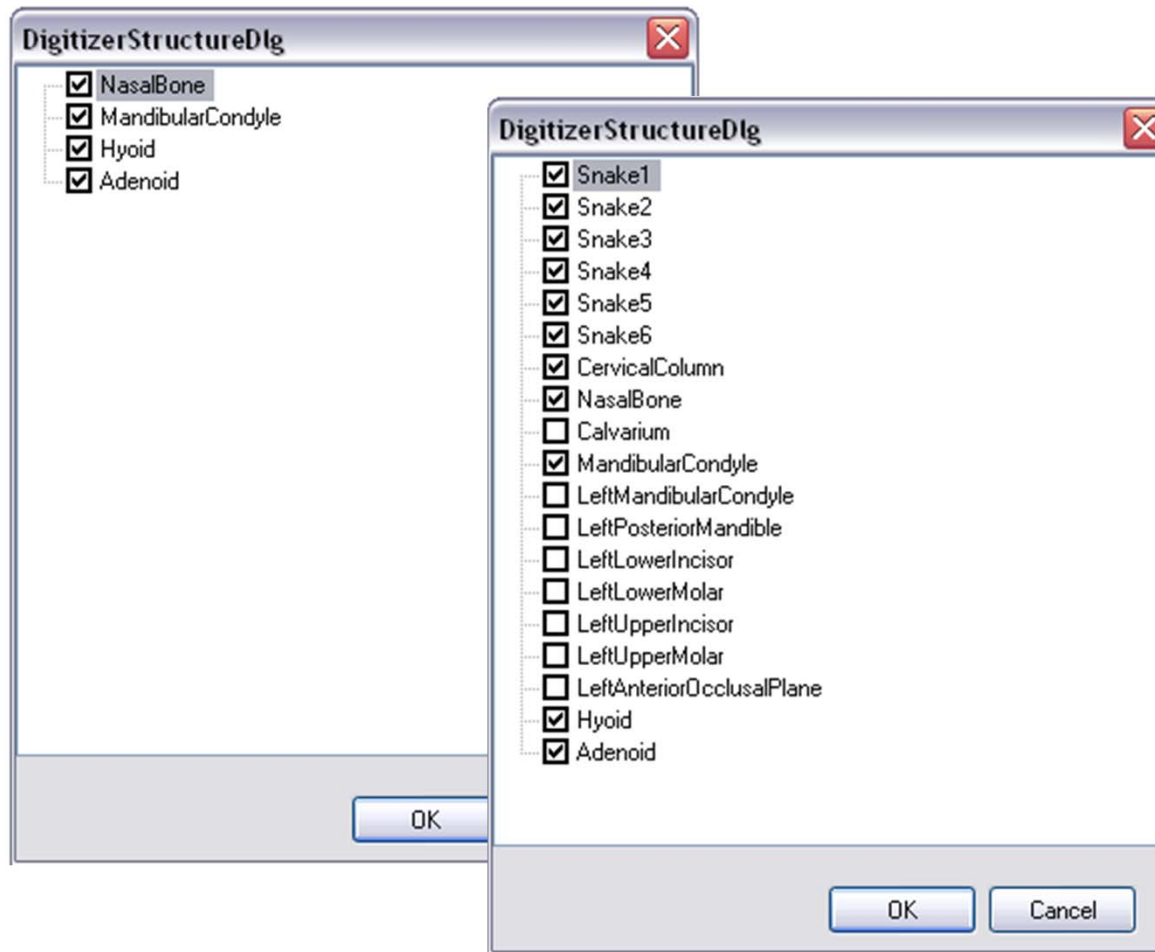
□ Lateral	
Date	25-04-01
□ Xray	
Filename	
Mirror	False
Resolution	100
Enlargement	5.6
⊞ Translation	
Rotation	0
⊞ Filters	

After entering the stage data you are now ready to perform the lateral analysis. Make sure that the lateral view is selected.

At this point you can open the next menu by pressing <Ctrl> and <Q> together to add a new Analysis. A new set of sub menus then opens up. Check that the Date of the headfilm is correct as the program uses the entered Stage Date as a default. The two dates should be the same.

Enlargement
The Xray Enlargement is a system variable preset in Environment/Stage. Change if not appropriate.
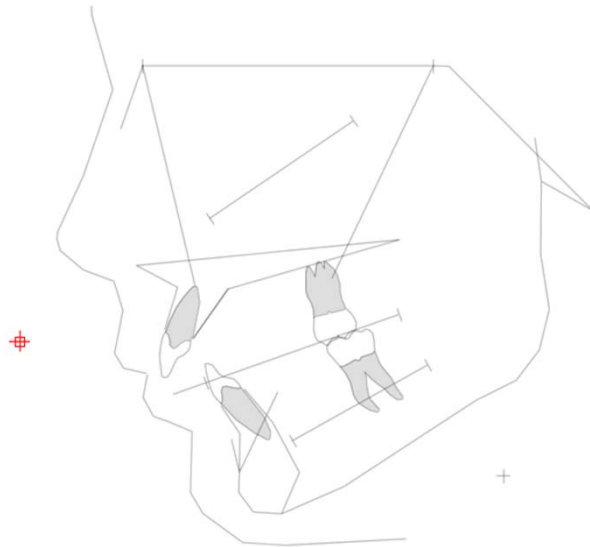
Start digitizing
by pressing <Ctrl> and <H> together or click:
A headfilm tracing appears and you will see a small red area indicating re1. This is an important reference point for the program so you digitize this and then re2.

Continue digitizing

Following re1 and re2 continue through all the standard cephalometric points, as shown on the tracing and listed on the lower left portion of the screen. As you reach certain points you will hear a different noise indicating that you can skip the next sequence if you wish. By pressing button <2> on the cursor (the second button from the left) you will automatically advance to the next important point in the predetermined sequence. The first time you encounter this is after digitizing basion(ba) you can now skip condylion (cd), if you wish, and go straight to the point articulare(ar). Thereafter you proceed in the order indicated on the tracing.

What if I make a mistake when digitizing??

Should you miss a point or digitze the wrong point it can be corrected in one of two ways. The program has a fail-safe as you can go back at any time by pressing the number <4> key on the cursor (3rd.button from the left) this will take you back one step at a time. This procedure can be repeated as often as necessary to get you back to where you made the mistake. In most cases this is the easiest way to correct a mistake.

Analog landmark correction
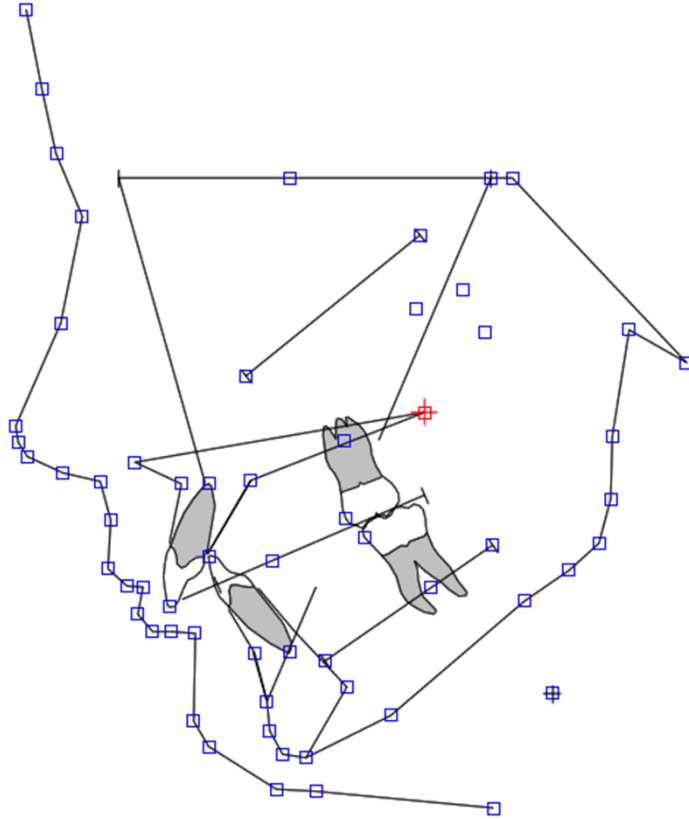
However, it is also possible later after you have saved your work, to recall all the digitized points and then to correct the problem.
If this is your choice, then open the headfilm tracing by pressing <Ctrl> and <H> together or click:

A headfilm tracing appears and you will see a small red area indicating re1. Digitize the reference points re1 and re2. A tracing with small blue squares will appear.
Select the point in question by clicking with the mouse (it will show in red) and register the point with the digitizer.
To finish and leave the process of correcting points you must click the red cross on the task bar:

The program automatically saves the changes as you make them.

After completing digitization of the headfilm you save it using the File/Save command under the file menu or pressing <Ctr> and <S> together.

Adding a frontal analysis

Contents

This function is further developed and described in the Tiops4 program.

Adding an occlusogram

The program allows the user to add occlusogram data into the file of a patient. There are two ways to do this:

The first is to use a digital (photo or scan) occlusogram. To facilitate the correct calculation of the magnification a ruler should always be placed next to the study model before the picture is made. Remember the model photo or scan must be saved as a .jpg file in the Model folder in Analy2005.

A second method for acquiring model data is to digitize a photo or photocopy of the model on a digitizer. Remember to include a ruler.

Before entering the occlusogram you should first digitize the lateral headfilm of the patient into the TIOPS program and save the data.

On the tracings of the upper and lower jaws the occlusograms are correctly related to the jaws. The same is the case when analyzing growth and treatment changes or if a simulation is performed. To ensure this it is important that the first reference point(ref1) registered on the occlusogram must corresponds with the landmark defining the tip af the incisor on the lateral analysis. It should also define the symmetry axis of the arch.

The program will also automaticcally adjust the magnification of the occlusograms to the headfilm on the tracings.

Entering model data

To enter the occlusograms into the data bank you need to click on the lower arch icon to open the lower arch view.

With this view selected press <Ctrl> and <Q> together to add a LowerArch analysis.

You now proceed through the listing using the using the down arrow key <↓>, open the sub menu Model by clicking on the plus sign [+] next to it or using the right arrow key <→>. The box sign changes to a [-] and a new list is revealed.
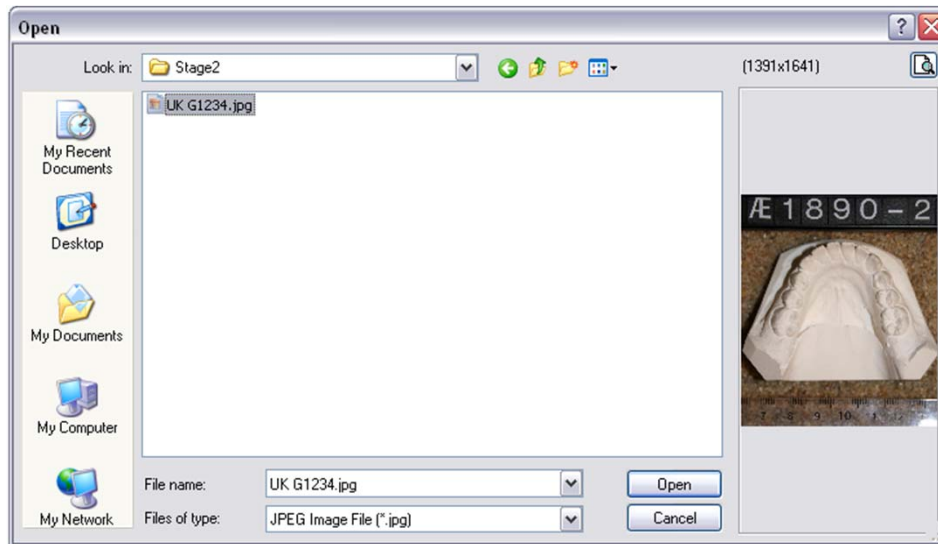
Scroll down to Filename and either click the radio button or type <Ctrl> and <→>. together.

This opens the Model folder in the Analy2005 directory where your occlusogram pictures should be stored as .jpg files either directly or in the patient sub folders.

The model image must be rotated to show the incisors facing towards the top of the screen

ÆE 1890 - 2

Magnification adjustment

In order to ensure an accurate drawing of the teeth and arch form the picture or scan of the model must be corrected for a possible magnification factor. To make this possible place a ruler next to the study cast. The magnification can then be adjusted by the following procedure:

With the model displayed click the left mouse button on the ruler at 70 mm hold the left button down drag a line 50 mm long across the ruler and release the mouse. The actual distance measured is seen on the right bottom part of the screen.

Now enter the value and the program now automatically corrects the enlargement to match the measurement. Normally the model will appear slightly reduced.

Date	25-04-01
⊟ Model	
Filename	C:\Analy2005\Model\G1234
Resolution	72
Enlargement	115.8

MeasureLength: |(30.62,-172.5) (138.52,-171.08)| = 107.9mm XrayEnlargement (for 50mm reference): 115.8%
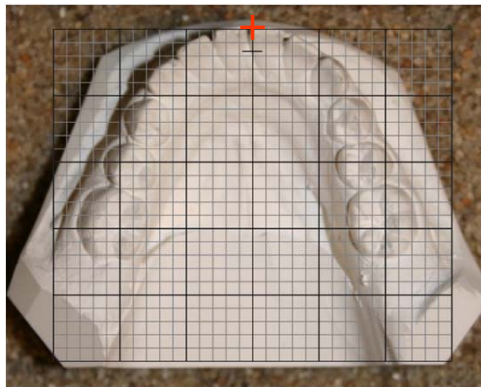
start

Adding a digital occlusogram (3:5)

To facilitate digitizing the model you can zoom in by placing a frame around the model by clicking and holding down the right mouse button, then drag the frame around the model and release the button. This does not affect the magnification adjustment but will enlarge the picture.
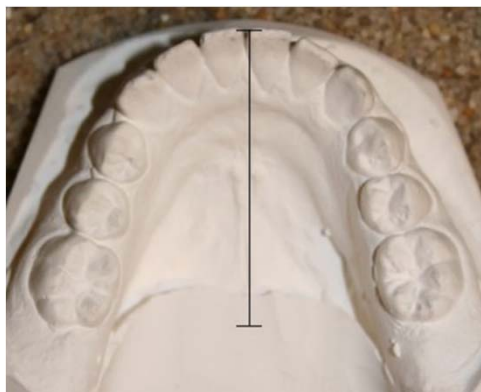
Start digitizing
by pressing <Ctrl> and <D> together or click:

You can now start digitizing by placing the edge of the grid that materializes where ref1 should be. This first reference point registered on the occlusogram must correspond with the landmark defining the tip af the incisor on the lateral analysis.
Once you have entered ref1 you proceed to ref2 after aligning the grid to match the models symmetry axis. The grid will rotate when the mouse is moved. The grid can be translated by simultaneously holding down the <shift> key and slide the mouse sideways until the correct position is achieved. Now enter ref2 in the midline of the grid at the height of the molars.
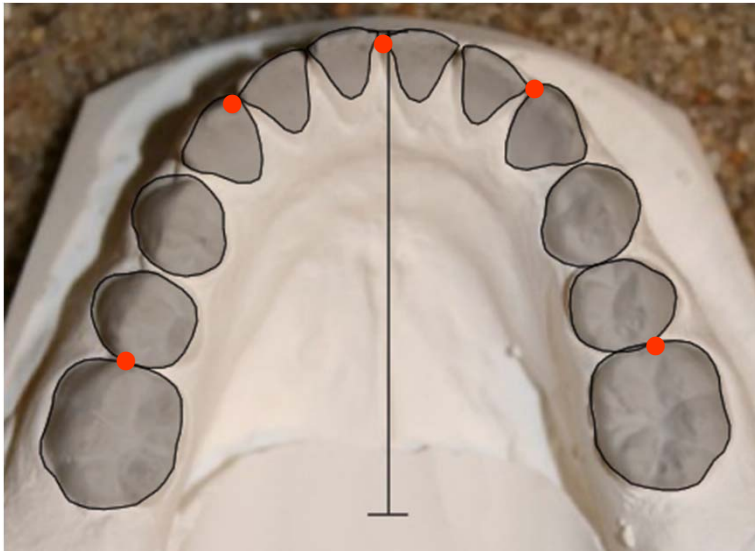The ref1and ref2 landmarks should be placed defining the symmetry axix of the arch.

These two points can not be changed now but any corrections, including that of the midline, can be done after the digitization process is completed

Point list for occlusograms

Now follows a series of points as shown in the point listing on the lower left side of the computer screen.

Unique is a series of arch perimeter points that are included to allow defining the arch length for measuring the space conditions. These points are located between the first molar and second bicuspid, the cuspid and the lateral incisor and in the midline between the incisors. They are marked in the illustration above with Red Dots. These points are listed with capital letters when you reach any of them. (LMM, LCM, LIM, RCM, RMM)
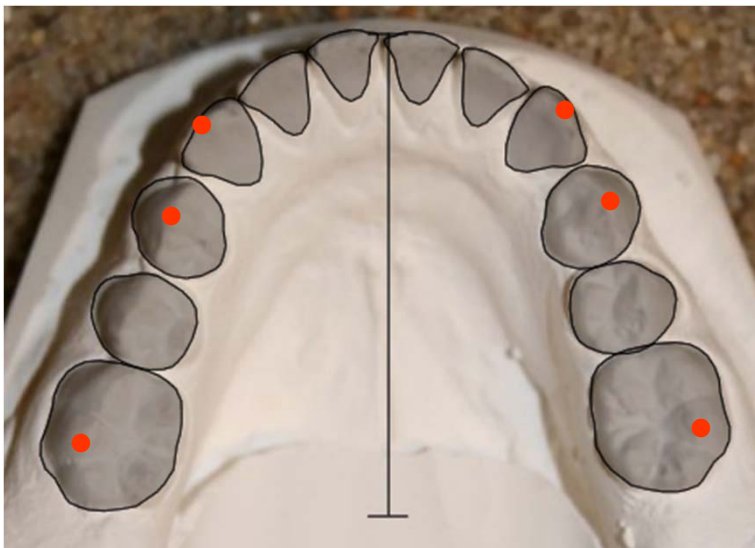
Six occlusion contact points between the upper and lower teeth are defined on the next picture. They too are indicated with a capital letters as you reach them. (L6C, LPC, L3C, R3C, RPC, R6C)
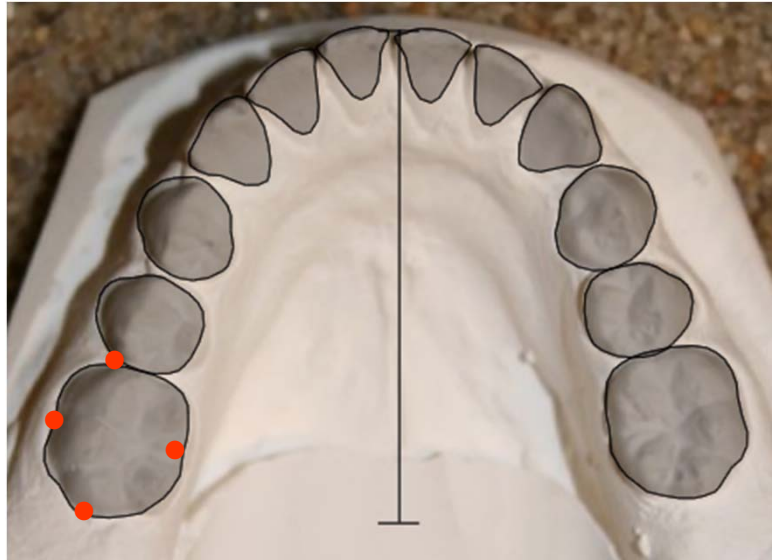
The two red sets of points are mandatory, L3C and R3C only when the cuspids are present.

LPC and RPC should be registered too, when the premolars are preceded by the primary teeth.
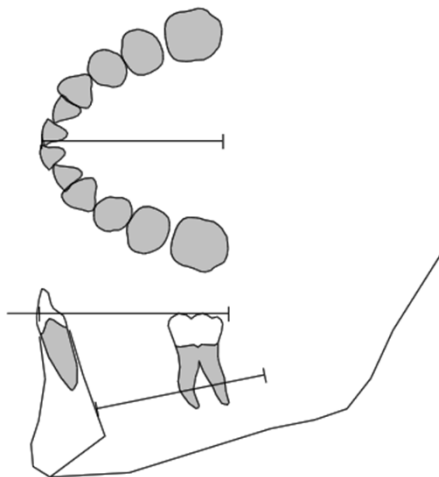
Adding a digital occlusogram (5:5)

The digitization of the dental landmarks starts with the distal of the lower left molar. This is followed by the labial, mesial and so on.. (l6d, l6b, l6m, l6l). The process is complete when the distal point on the first molar on the right side has been entered.

Hint: The dental landmarks are mixed with the arch perimeter points and the occlusion contact points in the digitization sequence.

The premolars and the cuspids can be skipped individually when not erupted, You will hear a special sound when you are reaching these teeth in the procedure.

At this point the program shows the occlusogram with the teeth shaded on the right side of the screen. Remember to save the file again before proceeding further.

On the tracing the occlusogram is correctly positioned to the jaw view.

Fixing digital occlusogram mistakes

Delete point (Ctrl+X)

Correcting mistakes in occlusogram entry
If you have made a mistake during entry of a given point you can correct it by clicking on the round icon with the red X . This will take you back one step for each click.

Information

Stop and delete points?

Yes   No

Clicking on the round icon with the red cross lets you start all over again.

LowerArch	
Date	25-04-01
Model	
Filename	C:\Analy2005\Model\G1
Resolution	72
Enlargement	116
Translation	
Rotation	1.35289999999998
Points	
re1	[-4271,1808]
re2	[-4035,-8190]
ref1	[0,0]
ref2	[0,-3600]
l6d	[-2302,-3533]
l6b	[-2496,-2784]
l6m	[-2000,-2458]

If you have made a mistake that does not appear until the final data is saved, you can open the point list by clicking the plus next to Point [+]. Scroll down to the point and re enter it with the left mouse button on the occlusogram. When all points are correct you should close the Point entry and remember to save the file again.

The midline can also be corrected at this time, when necessary by scrolling to ref1 or ref2 and entering the new position. Note that you can not change re1 and re2 as they are part of the computer programs system points. They are entered automatically registered when the file is reopened.

After entering the LowerArch analysis data you are now ready to perform the UpperArch analysis. Make sure that the upper arch wiew is selected by clicking on the upper model icon in the menu bar.

With this view selected press <Ctrl> and <Q> together to add a UpperArch analysis.

The six occlusal contact points between the upper and lower teeth are defined on the next picture. They are too indicated with a capital letters as you reach each of them. (L6C, LPF, L3C, R3C, RPC, R6F)

Then the process is similar to the lower model with digitization of the reference points first followed the landmarks in the same order as previously. Check that the Enlargement is correct before entering data. Once again save the data before proceeding further.

Adding a analog occlusogram

After entering the lateral analysis data you are now ready to perform the lower arch analysis. Make sure that the lower arch wiew is selected.

At this point you can open the next menu by pressing <Ctrl> and <Q> together to add a new LowerArch analysis. A new set of sub menus then opens up. Check that the Date of the occlusogram is correct as the program uses the entered Stage Date as a default.

Enlargement
In order to get an accurate drawing of the teeth and arch form it may be a help to make the picture or photocopy of the model with some (>2) magnification, but as mentioned you should place a ruler beside the model. The magnification should then be adjusted by the following procedure:
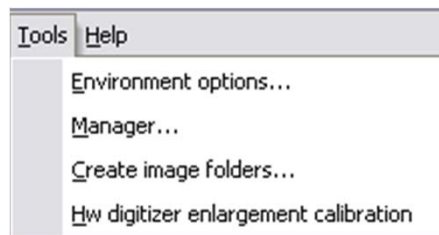
Place the occlusogram picture on the digitizer and Select Tools/Hw digitizer … . Then digitize two points with a distance of 50mm. The actual distance measured is seen on the right bottom part of the screen. Now enter the enlargement value and the program now automatically corrects for the enlargement when the occlusogram is digitized.

MeasureLength: |(30.62,-172.5) (138.52,-171.08)| = 107.9mm XrayEnlargement (for 50mm reference): 115.8%