Tiops Cephalometric Analysis:
Superimposing Serial Headfilms for Growth- and Treatment Analysis

Analysis of serial headfilms can be done effectively with the Tiops4 program. The program makes it possible to perform analysis of general facial growth, maxillary and mandibular growth and dentoalveolar change based on serial headfilms. The TIOPS program is designed to perform "structural" superimpositions as described by Björk (1983) using a set of three reference lines, representing stable structures in the cranial base, the maxilla and mandible, respectively. These reference lines are placed on the first film, in a series, and carried forward after superimposing the second and subsequent headfilm on the stable structures in the same areas.
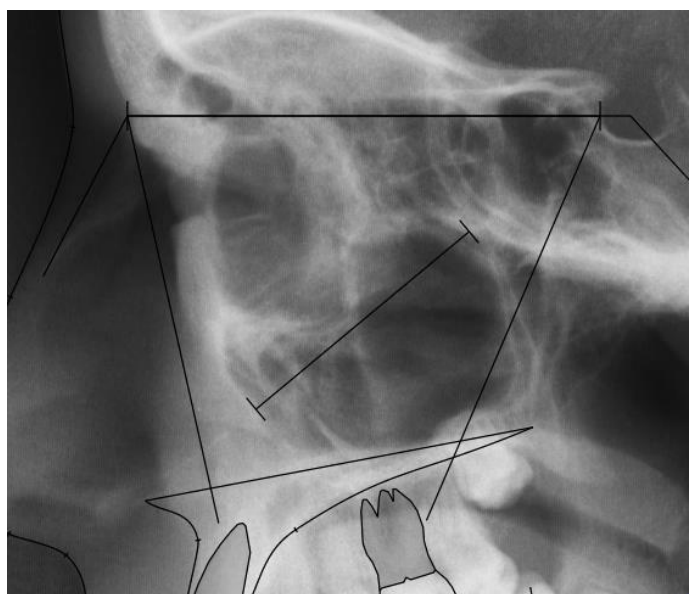
Additionally, TIOPS can also align sets of occlusograms correctly after the respective headfilms have been digitized and saved. The maxillary and mandibular occlusograms are automatically oriented to the incisors in the respective jaw at the two stages as described by Björk et al (1983).

Procedure

1. Before starting the superimposing procedure make sure all headfilms have been saved in either .jpg or .bmp format and that they aresuperimposing located in an easily accessible location on the computer.

2. Check that the initial headfilm has been correctly digitized and that the landmarks are correctly located. You should also check the x-ray enlargement of the initial headfilm once more to make sure it is correct. If you have entered the picture resolution yourself check it as well. These two factors can now be changed without having to redo the analysis. Then adjust the brightness and contrast of the initial headfilm as needed.

    Note: The picture should not be too dark.

3. In order to correctly orient the image of the second headfilm to the initial or any subsequent headfilm, already digitized and saved in Tiops4, a new stage is added by clicking on the "New Stage" Icon or by pressing <Ctrl> and<A>simultaneously. This opens a new Stage under the same case number. The Stage Type and the Date are then entered in the menu located on the left side of the screen.
See: http://www.tiops.com/downloads/T4UG/T4UGStageData_NewStage.pdf

4. Now press <Ctrl> and <Q> simultaneously to create a new lateral Analysis.

5. Under the heading Lateral enter the Date of the film (is defaulted as the Stage Date). Then move down, using the down arrow key <↓> to the box labeled Xray. Open Xray using the right arrow key <→>.

6. In the box Filename click on the [...] or press <Ctrl> and <→> simultaneously and an Open Dialog window pops up showing the content of the X-Ray folder. Browse to the relevant file at this location (or an alternative place) and click Open.

7. Now click the Consolidate icon under the File Menu to place the X-Ray file in the designated X-Ray folder. This will also at the same time save the patients file.

About RESOLUTION
See: http://www.tiops.com/downloads/T4UG/T4UGProgramBasics_DigitalImageFiles.pdf
A standard .jpg file has a built in resolution factor and most commercial programs will provide you with a correct .jpg file. However, some medical Xray systems unfortunately do not create a file with this information. Instead you may experience resolution values of 1 or something similar. When you suspect that the correct factor has not been provided it has to be calculated by means of the file pixel properties and your knowledge about the picture size using the formula below.
Normally the X- and Y-Resolution are equal and will change simultaneously.
The unit of resolution to be entered in the program is indicated in Pixels/Inch.
A .bmp file does normally provide you with a resolution value. If not, it has to be calculated and entered using this formula:

$$\text{Number of pixels}_{\text{picture height}} / \text{Picture height}_{\text{inch}}$$

8. The second headfilm is now seen together with the Tracing of the initial film. Make sure the two stages to be compared are showing in the top menu bar ⭐ and that the relevant second stage is selected as active. ⭐
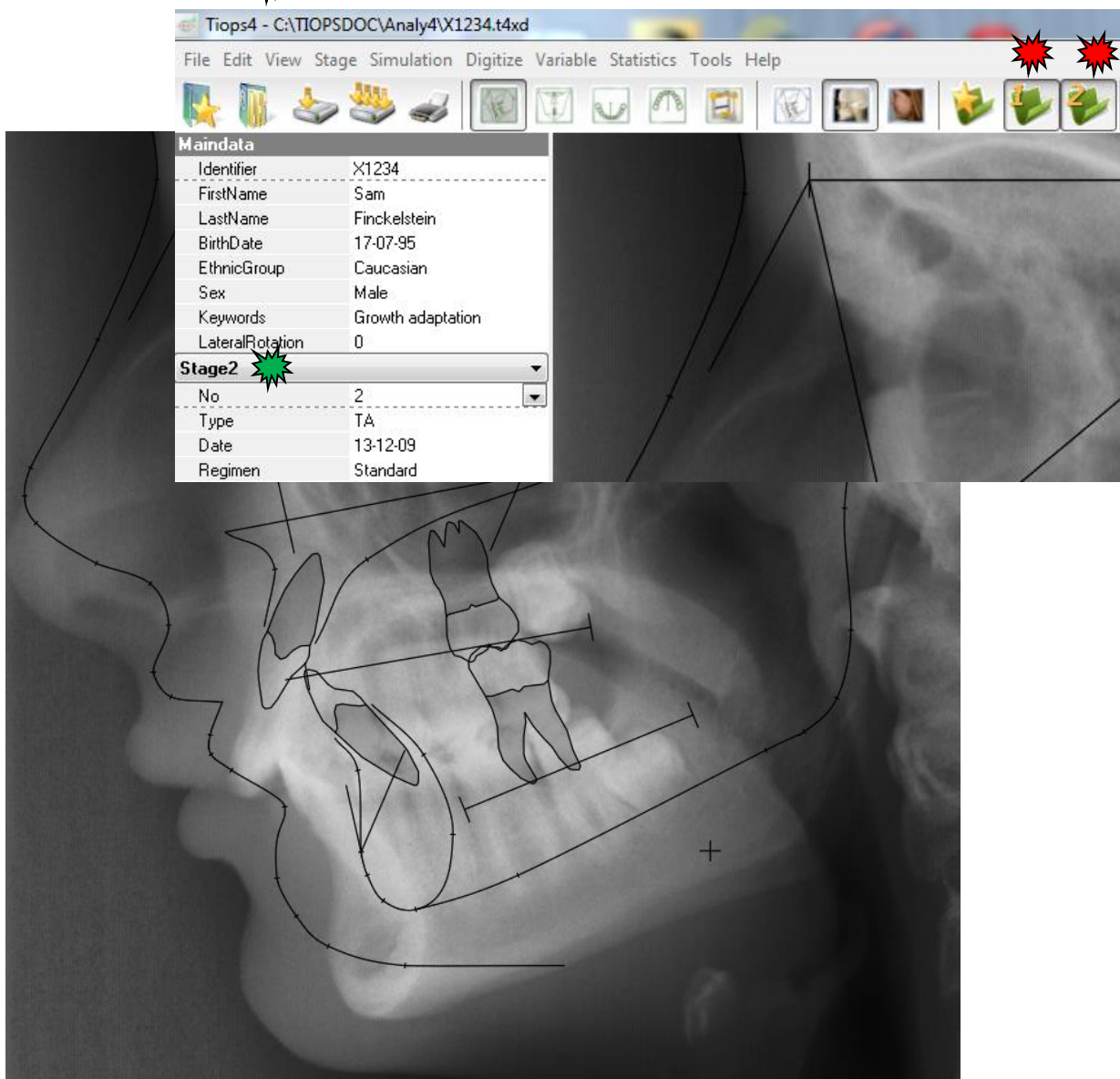
9. The process of aligning headfilms begins by pressing <Ctrl> and <D> or by clicking the Digitizer Start icon in the upper tools bar to initiate the digitizing process.

Digitizer Start (Ctrl+D)
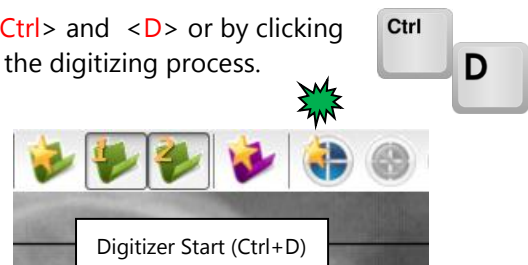
10. You will now see the two films together with the initial tracing aligned with the first film. Some of the tool icons are inactivated to prevent you from performing incorrect procedures. However, some additional icons will now appear (see next page) and a help guide is displayed on the right bottom of the screen.
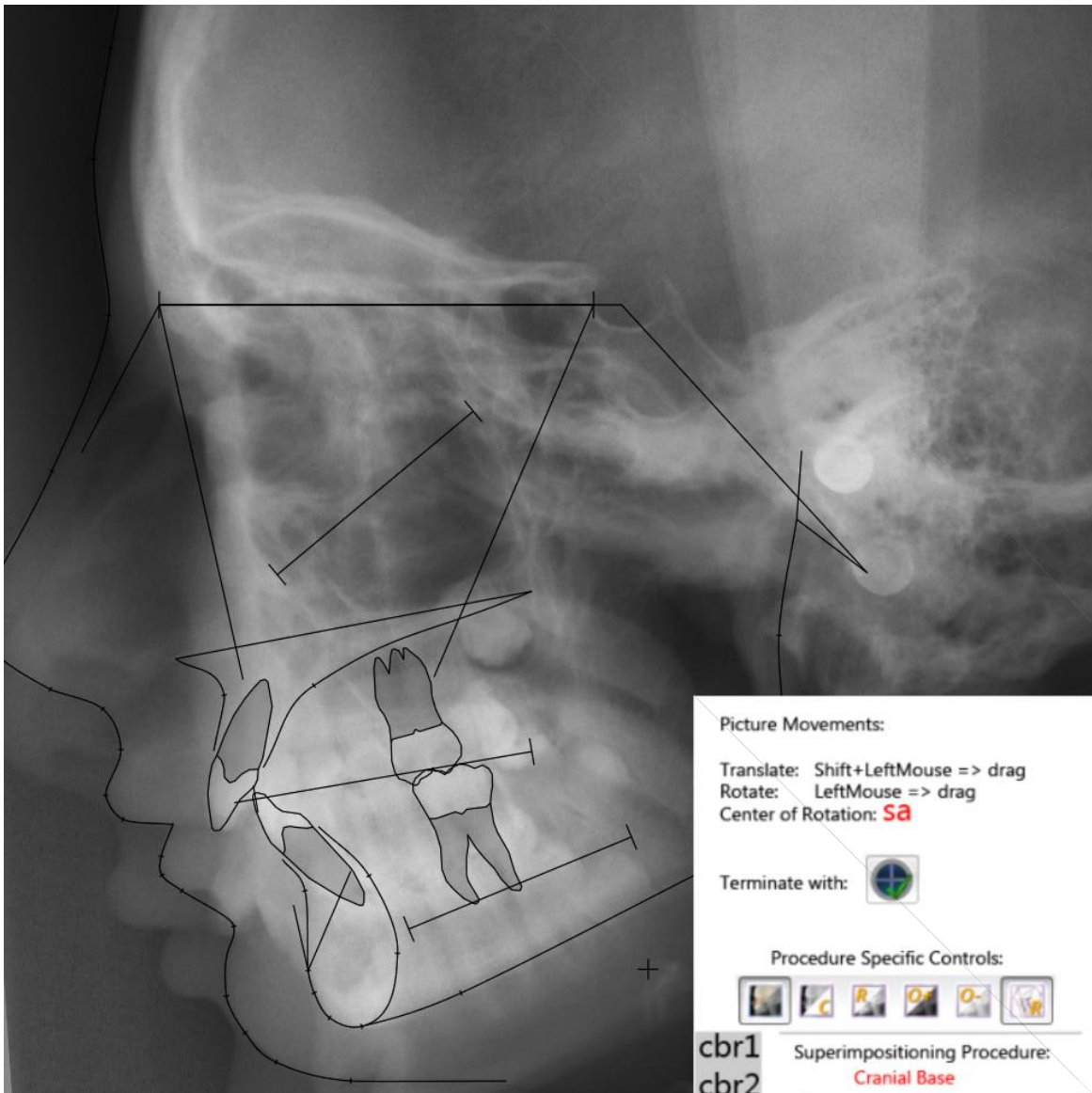
11. The next step is to move the second film so it aligns with the structures in the anterior and median cranial base on the first film, as described by Björk (1983).
   See: http://www.tiops.com/downloads/Articles/BjorkCephalometricGrowthAnalysis.pdf

    ➢ To translate the second film hold down the <Shift> key, hold down the left mouse button and release the <Shift> key. The picture can then be translated when you move the mouse while continuing to hold down the left mouse button at the same time.

    ➢ You can rotate the second film by moving the mouse while holding down the left mouse button. The center of rotation is located at Sella Anterior (sa) on the first film, once the films are lined up on the cranial base structures

Note: All the standard functions for manipulating the films are still available during the superimposing procedure.
See: http://www.tiops.com/downloads/T4UG/T4UGProgramBasics_ManeuveringImages.pdf

12. This somewhat difficult superimposing procedure can be made easier by using the following tools:
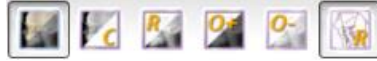
A. Click to display both headfilms   <F4>

B. Click to display the current headfilm only   <F5> toggles between B. and C

C. Click to display the reference headfilm only   <F5> toggles between C. and B

A. Click to increase the opacity of the current headfilm in increments of 10%   <F6>

A. Click to decrease the opacity of the current headfilm in increments of 10%   <F7>

B. Click to remove the reference tracing   <F8>

C. Additionally you can use the zoom functions: <F9-F10-F11>

13. Once you have aligned the structures in the cranial base that are considered stable, press <Ctrl> and <R> or click on the Accept Reference icon:

This locks the films together on the cranial base reference line (n(cb1) – sa) which is used for the general superimposition.

About the Snake Regimen

If you wish to mark certain bony structures on the headfilm to ease the superimposing process, then select the Snake regimen for that stage and choose Digitize / Add/Remove Structures. Check the boxes for the number of Snakes you may wish to place.
The corresponding number of w-figures, each defined by 5 landmarks, will now appear near the cervical vertebrae. They can then be repositioned to the desired location using the landmark correction procedure.
You may want to identify similar bony structures on subsequent headplates, i.e the mandibular canal.
If you plan to use this procedure for a patient then select the Snake regimen when you begin digitizing. The snakes can then be digitized directly and later hidden by choosing a Regimen different from Snake.
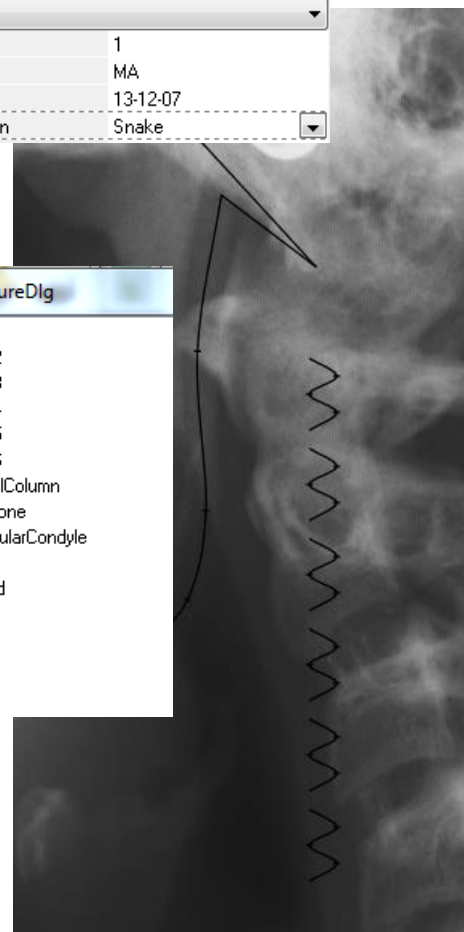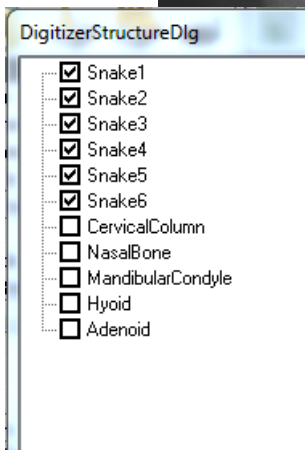
14. After you have clicked the Accept Reference icon the first (reference) film will disappear and only the second (current) film is visible. A sequence of points are then to be digitized beginning with Nasion (n), followed by Sella Center (s). After this follows the normal sequence of points located on this second film. The pognonion (spg) is recorded automatically.

15. When you have digitized the posterior symphysis point (sym), the reference film appears again and the films can be superimposed on the stable mandibular structures. Move the second headfilm in the same manner as before so as to fit the reference film. The rotation center is point supra pognonion (spg) on the initial film. It is usually a good idea to first translate the films until the chins are aligned and then rotate the second film until stable structures (the mandibular canal and other) align. Then once again click on the Accept Reference icon and the films are locked together.
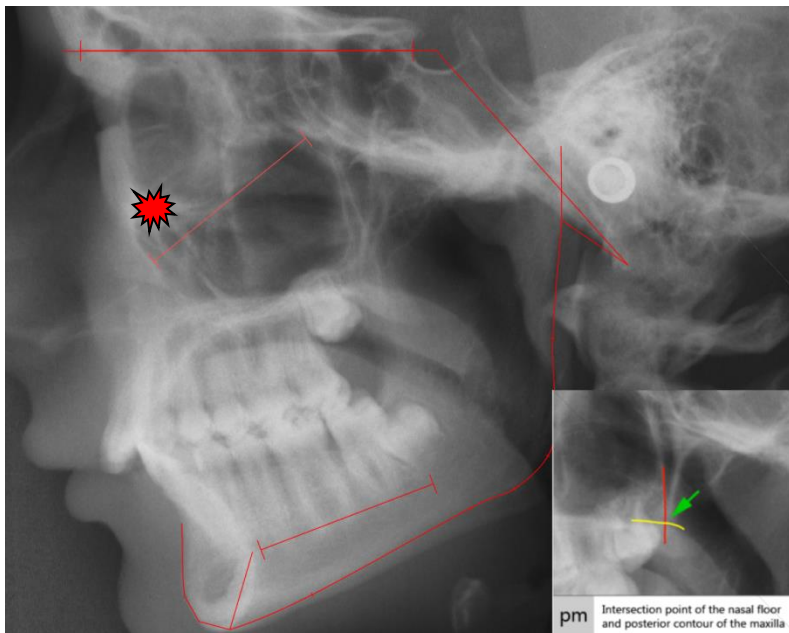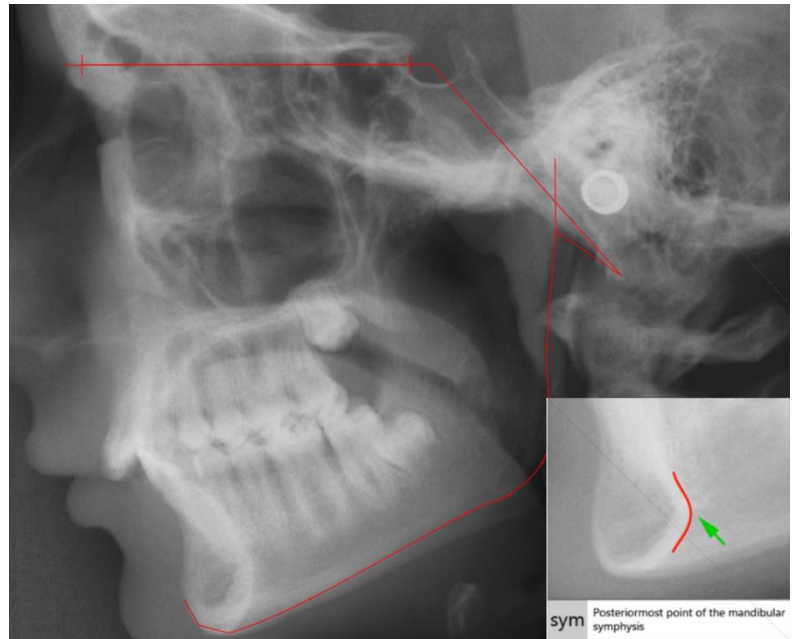
16. The program has at this point calculated a theoretical maxillary reference line (shadow colored) to ease the superimposing procedure of the maxilla.

    The theoretical maxillary reference is calculated using the same algorithms as used by the simulation procedure.
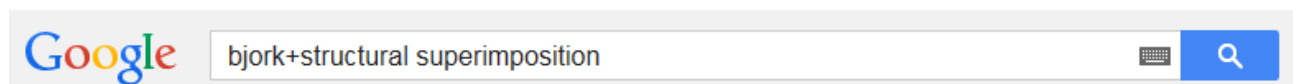
17. Now move to the next point in sequence; posterior nasal spine (pm), followed by the points (ss), (pal) and (sp). The films can now be superimposed on the maxillary structures. In this procedure the center of rotation is located at the first maxillary reference landmark (ma1) on the first film. This rather tricky procedure can be initiated by moving the second (current) headfilm image so that the light red theoretical maxillary reference line lines up with the black on the initial (reference) film. This makes a good starting point for further adjustment.
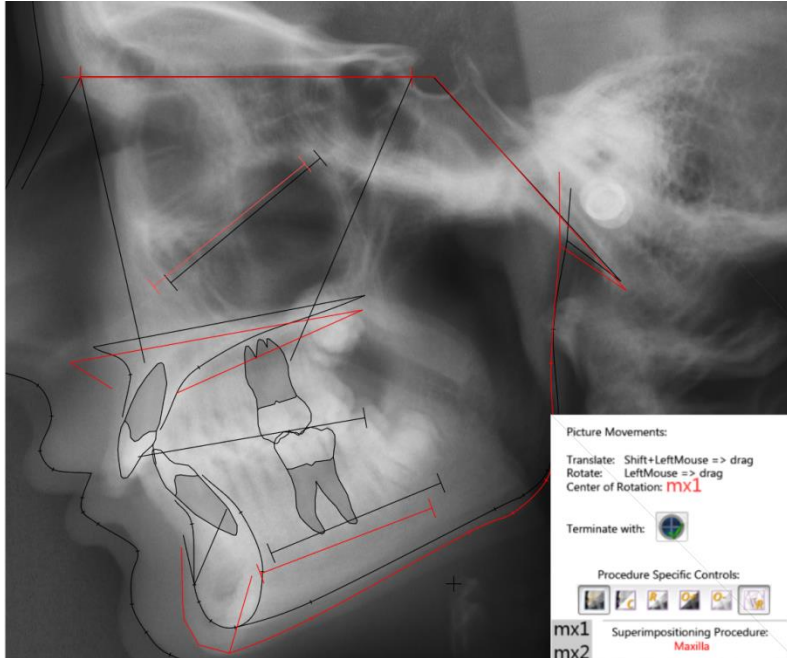
18. After alignment the films are locked together by clicking on the accept reference icon.

19. Now the remaining landmarks are digitized as usual.

20. Continue to digitize all points. When the End of point sequence message is accepted the Points list is opened for eventual correction of wrongly registered landmarks. Individual landmarks as well as the three References can also be corrected later by selecting the actual landmark respectively the cbr1, ma1 and mx1 points from the Points list

Note: The correct maxillary and mandibular superimposing cannot be seen in their correct positions until the whole procedure has been completed.

http://www.tiops.com/downloads/Articles/BjorkCephalometricGrowthAnalysis.pdf

http://www.angle-society.com/case/guide.pdf

http://www.americanboardortho.com/professionals/clinicalexam/casereportpresentation/preparation/superimpositions.aspx#