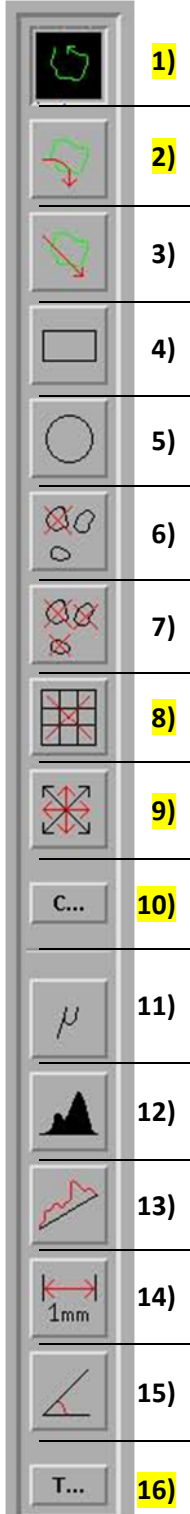


Contouring Tools:

Contouring is important step to delineate the region of interest and is performed before the segmentation.



1) Use this tool to **draw contour** around the region of interest. The region enclosed by contour drawn **counter-clockwise** will **be included** for analysis; while the region enclosed by contour drawn **clockwise** will be **excluded** from analysis.

2) **Free hand correction:** Allows user to correct/edit drawn contour. The contour to be corrected must be crossed at two places. The part lying in between these crossing points will be replaced by new contour. Correction must follow the same direction as the drawn contours.

3) **Straight line correction:** Allows the user to correct/edit contours in straight lines only.

4) Draws rectangular contour or square (hold SHIFT key) contour

5) Draws elliptical contour or circular (hold SHIFT key) contour

6) Allow user to **delete one contour** on the selected slice. Intersect red line on the desired contour to delete.

7) Allow user to **delete all contours of CURRENT (single) slice only.**

8) Allow user to **delete all contours of ALL slices.**

9) Selecting this tool will bring eight end points on the current slice. *Holding* one of the end points via **left-mouse button** will help **to move** contour around in the window. *Holding* one of the end points via **middle-mouse button** will help **to resize** contour in the window. Not selecting any white-end points will move the zoomed region in the slice

10) **Opens up the Contouring** sub-window and also **highlights** the slices with drawn contour in the *image selection area* (left-bottom corner of the evaluation program).

11) **Linear-attenuation coefficient (μ):** Provides point-by-point information of the linear-attenuation coefficient value of the pixel represented by current cursor position. This value can be useful to derive Hounsfield unit / number (HU).

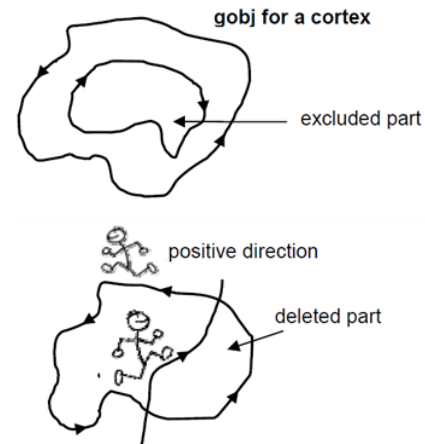
12) Displays histogram of the current view of the slice or selected contoured region.

13) Displays straight-line histogram of the drawn line on the slice.

14) Displays point-to-point distance of drawn line on the screen. Move each end-point to change the length or position of the line.


15) Displays angle between two lines on the screen. Move each end-point /angle-point to change the position of the line or angel between them.

16) **Opens the 3D-Evaluation sub-window**




Contouring sub-window:

Contouring sub-window can be opened using 'C...' or 'Tasks', 'Contouring'. Opening the contouring sub-window will highlight the image selection area with three types of markers with different representation.

Green  represents slices with *hand-drawn contours* or *iterated contours*

Yellow  represents *morphed slices*

Red  represents sliced that were re-morphing because of user corrections in morphed or original contours

Manual drawing of contours for every slice is time-taking and user-biased, but the contouring option provides a semi-automated option for contouring the region of interest. There are three ways to semi-automate the contouring process but the user must correct after drawing contours using semi-automated options.

Iterate Option:

Double clicking a hand-drawn contour automatically adapt to OUTER or INNER boundaries depending on the selection of contouring (outer and inner values).

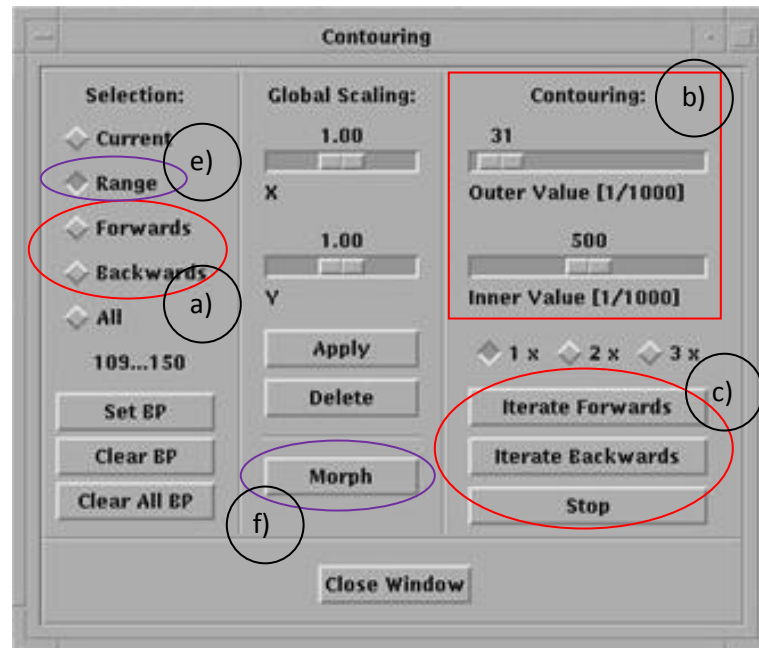
To adapt **OUTER boundary** (e.g. Periosteum surface for cortical-bone analysis): smaller '**Outer Value**' (e.g. 31) & large '**Inner Value**' (e.g. 500).

To adapt **INNER boundary** (e.g. Endosteum surface for trabecular-bone analysis): larger '**Outer Value**' (e.g. 1000) & smaller '**Inner Value**' (e.g. 150).

Select **1x**, **2x**, or **3x** to increase the # of iterations/slice.

Iterate Forward / Backwards: Iterate option can be automatically repeated on forwarding / back-warding slices after Iterating/drawing contour on one slice.

- Select '**Forward**' or '**Backward**' in the selection region.
- Select proper **INNER** and **OUTER** value.
- Click on '**Iterate Forward**' or '**Iterate Backward**' and Click '**Stop**' to interrupt the iterate process.



Morphing Option:

Use this option to "morph" or to extrude the missing objects between two reference slices. The program interpolates the slices in between. To create complex shapes, repeat the morphing step for different ranges. Morphing only occurs between two drawn contours.

- Draw contours on the slices you want to start (e.g Slice 1) & to end (e.g Slice 10).
- Select any slice that is falling in between the start & end slice, and select '**Range**' option in Selection region.
- Click on '**Morph**'.
- Correct contours in between (highlighting will change) slices and repeat morph steps to adjust with corrected contours.



Use of Auto-contouring scripts to contour cortical and trabecular ROI

Easy-to-follow steps:

- 1) Open your scan in the evaluation program.
- 2) Click on **"T..."** (Last toolbar button) to opens the 3D-Evaluation sub-window.
- 3) On the drawing field, **manually** make the white box big enough such that it is nicely around the bone/ROI, with a little margin. Using **"Select..."** button (you will be directed to **Evaluation Script Selection** window) script, select one of the following scripts from task/evaluation script.
 - a. *Calculate Auto Contour Cortical Bone* (to draw contour for cortical bone)
 - b. *Calculate Auto Contour Trabecular Bone* (to draw contour for trabecular bone)
- 4) To select slices: enter the starting slice number of in "Z box of VOI Start" and enter the total number of slices to be analyzed in "Z box of Dimension".

e.g. I have set of 100 slices and I want to analyze slices 75 to 90. So, my 'Z box of **VOI Start**' will be 75 and 'Z box of **Dimension**' will be 15. (Z box of Dimension is the number of **slices**, not 'end slice number')
- 5) Upon completion of the evaluation; go to **'File', 'Load Gobj...'**

You will be directed to the **Contour-Files** Window.
- 6) You will be automatically filtered in your directory sub window (if not, change directory in the directory selection area using your associated sample and measurements number). In the files sub-window, you will see different files with extension of Cxxxxxxx.gobj;1, Cxxxxxxx_cortex.gobj;1, Cxxxxxxx_Trab.gobj;1, Cxxxxxxx_Trab_NOPEEL.gobj;1.

By default, the standard gobj file will be saved for the selected evaluation script

For example:

When, the evaluation script is chosen for *Calculate Auto Contour Cortical Bone*, the Cxxxxxxx.gobj;1 belong to the cortical bone analysis.

When, the evaluation script is chosen for *Calculate Auto Contour Trabecular Bone*, the Cxxxxxxx.gobj;1 belong to the trabecular bone analysis.
- 7) Select associated Graphical Object (gobj) file by changing the number and hit **"OK"**
- 8) On the display window, you will find your appropriate contours drawn on the slices.
- 9) Select your appropriate Gaussian and thresholding parameters and perform 3D Evaluation to see your results (as normally you do after drawing your contours).