3D Slicer Erosion Analysis Extension Guide

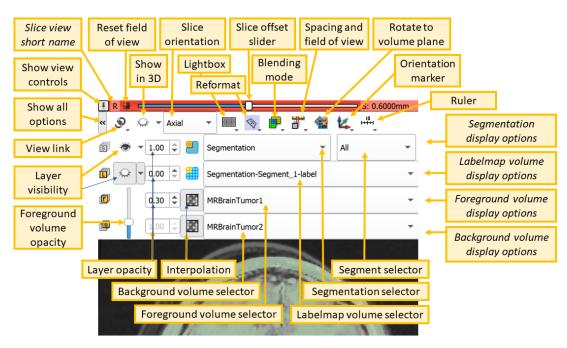
This 3D Slicer extension measures the volume, surface area, and shape of bone erosions using high-resolution peripheral quantitative computed tomography (HR-pQCT). Erosions are identified by placing seed points in each of them. Two modules were designed, each solving a specific task. The first module "Automatic Contour" draws the periosteal bone surface. The second module "Erosion Detection" identifies erosions based on the periosteal bone surface, and the seed points plotted by the user.

This guide has four sections:

- 1. 3D Slicer Built-In Tools
- 2. Erosion Definition
- 3. Erosion Analysis User Instructions
- 4. References

3D Slicer Built-In Tools

Viewer Windows [1]



Three default slice views are provided (with Red, Yellow and Green colored bars). The colored bar across any slice view shows a pushpin icon on its left (**Show view controls**). When the mouse rolls over this icon, a panel for configuring the slice view is displayed. The panel is hidden when the mouse moves away. For more options, click the double-arrow icon (**Show all options**). To display a different image, select a different image at one of the selectors (**Background volume selector** or **Foreground volume selector** for greyscale images, **Labelmap volume selector** for masks).

Segment Editor [2]

Add segment: Add a new segment to the segmentation and select it.

Remove segment: Select the segment you would like to delete then click Remove segment to delete from the segmentation.

Segments table: Displays list of all segments.

Eye icon: Toggle segment's visibility.

Color swatch: set color.

Effects: Select the desired effect here. See below for more information about each effect.

Masking: These options allow you to define the editable areas and whether or not certain segments can be overwritten.

Editable area: Changes will be limited to the selected area. This can be used for drawing inside a specific region or split a segment into multiple segments.

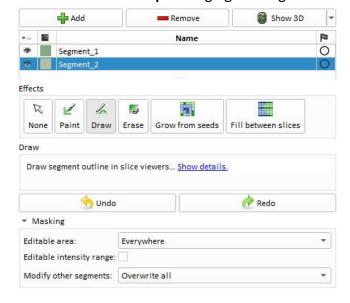
Editable intensity range: Changes will be limited to areas where the master volume's voxels are in the selected intensity range. It is useful when locally an intensity threshold separates well between different regions. Intensity range can be previewed by using Threshold effect.

Modify other segments: Select which segments will be overwritten rather than overlapped.

Overwrite all: Segment will not overlap (default).

Overwrite visible: Visible segments will not overlap with each other. Hidden segments will not be overwritten by changes done to visible segments.

Allow overlap: Changing one segment will not change any other.



Effects:

Paint:

- Left click to apply single circle
- Left click and drag to fill a region
- A trace of circles is left which are applied when the mouse button is released
- Sphere mode applies the radius to slices above and below the current slice.

Draw:

- Polygon tool
- Left click to lay individual points of an outline
- Left drag to lay down a continuous line of points
- Right click to apply segment

Erase:

Same as the Paint effect, but the highlighted regions are removed from the selected segment instead of added.

Grow from seeds:

Draw/Paint segment inside each anatomical structure first. You can skip any number of slices between segmented slices. This method will start from these "seeds" and grow them to achieve complete segmentation.

Initialize: Click this button after initial segmentation is completed (by using other editor effects, e.g. **Draw**, **Paint**). Initial computation may take more time than subsequent updates. The result will be a preview. You will need to hit the **Apply** button to save the result to the segments.

Update: Update completed segmentation based on changed inputs.

Auto-update: activate this option to automatically update result preview when segmentation is changed.

Cancel: Remove result preview. Seeds are kept unchanged, so parameters can be changed and segmentation can be restarted by clicking Initialize.

Apply: Overwrite seeds segments with previewed results.

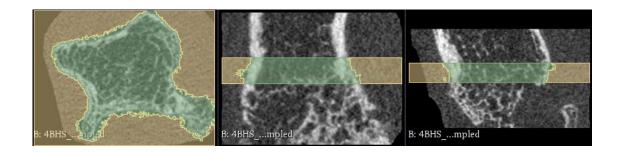
Notes:

This method takes into account the intensities of the image.

Only visible segments are used by this effect.

At least two segments are required.

The growth region only extends between slices that have been labeled. For example, if the seeds are initially labeled on two slices, slice 84 and slice 101, then the labels will only grow between slice 84 and slice 101 (See image below). You can make the growth region arbitrarily large by adding seeds as far as you want the segments to grow.



Fill between slices:

Create complete segmentation on selected slices using any editor effect. You can skip any number of slices between segmented slices. This method will fill the skipped slices by interpolating between segmented slices.

Initialize: Click this button after initial segmentation is completed (by using other editor effects, e.g. **Draw**, **Paint**). Initial computation may take more time than subsequent updates. The result will be a preview. You will need to hit the Apply button to save the result to the segments.

Update: Update completed segmentation based on changed inputs.

Auto-update: activate this option to automatically update result preview when segmentation is changed.

Cancel: Remove result preview. Seeds are kept unchanged, so parameters can be changed and segmentation can be restarted by clicking Initialize.

Apply: Overwrite seeds segments with previewed results.

Notes:

This method only considers the shape of the specified segments, not the intensities of the image.

Only visible segments are used by this effect.

The fill region only extends between the first and last slices that have been labeled. For example, if slice 84, slice 90 and slice 101 are initially labeled, then only slices between 84 and 101 are filled. Initially label the first and last slice of the image to fill the entire image.

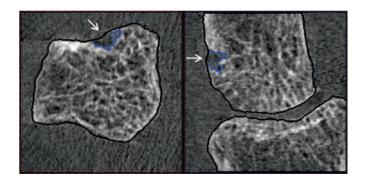
Erosion Definition

The SPECTRA collaboration developed the following definition of an erosion on HR-pQCT images [3]:

- Clear cortical interruption.
- The cortical break spans over at least two consecutive slices, and is visible in two perpendicular planes
- Loss of underlying trabecular bone
- Nonlinear in shape

This extension follows the same major steps in segmentation as outlined by another erosion analysis program, MIAF [4]:

- 1. Segmentation of periosteal bone surface (black lines in the images below)
- 2. Segmentation of erosions (blue lines in the images below) by placing seed points in each of them



Erosion Analysis User Instructions

Load Files

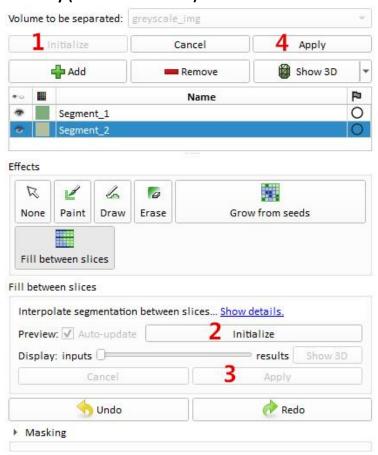
Load a greyscale scan to 3D Slicer. Either drag-and-drop the files to the application window or hit the Add Data button and select the files. There are three viewer windows coloured in red, yellow, and green. The axial slices of the scan should fall in the red window. If not so, the scan has to be resampled to have that orientation, for the extension to work properly.

Step 1 - Bone Separation

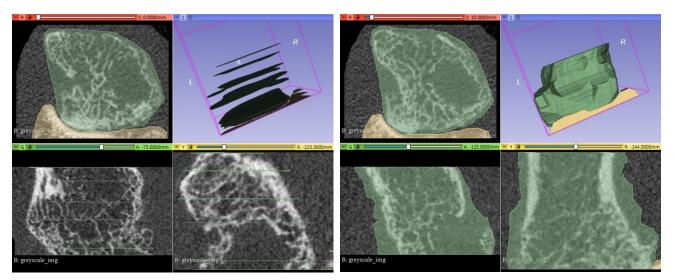
This step is only necessary if multiple bones in the scan appear to be close or connected to each

other. The purpose is to manually separate the bones. If the bones are clearly not connected, then they will be automatically separated by a connectivity component filter in the future steps. In this step, the user will use the editor tools to completely cover each bone with a different label.

First way (Fill between slices):



- Select the loaded scan at **Volume to be separated**.
- Hit the Initialize button #1, and the editor tools will be activated. To switch to a
 different greyscale image, hit the Cancel button and select a different image at Volume
 to be separated.
- Hit the Add or the Remove buttons to add or remove segments.
- Using the **Draw** tool, completely cover each bone on the first slice, the last slice, and a few middle slices with a different label. Skip any number of slices in between.
- Switch to the **Fill between slices** tool. Hit the **Initialize** button **#2** below **Fill between slices**. A previewed result will be initialized.
- Hit the **Apply** button #3 below the Initialize button to save the result in the segments.
- Once completed editing, hit the Apply button #4.

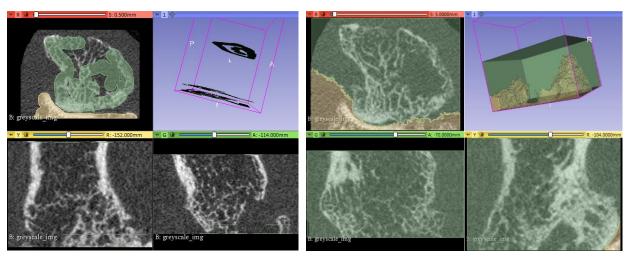


Initial segmentation

Output from Fill between slices

Second way (Grow from seeds):

- Select the loaded scan at Volume to be separated.
- Hit the **Initialize** button **#1**, and the editor tools will be activated.
- Hit the **Add** or the **Remove** buttons to add or remove segments.
- Roughly label each bone on the first slice, the last slice, and a few middle slices with **Paint** or **Draw** tools. Skip any number of slices in between.
- Switch to the **Grow from seeds** tool. Hit the **Initialize** button #2 below **Grow from seeds**. A previewed result will be initialized.
- Hit the **Apply** button #3 below the Initialize button to save the result in the segments.
- Once completed editing, hit the **Apply** button #4.



Initial seeds

Output from Grow from seeds

The result will be a label map named with a post-fix "_separated".

Step 2 – Automatic Contour

This step is to identify the periosteal bone surface. It will attempt to fill the voids in the bone.

Parameters:

- **Input Volume**: the greyscale scan
- Output Contour: each separate bone in the output will be labeled differently
- **Lower Threshold/Upper Threshold**: global thresholds
- Number of Bones: will be used if no bone separation map is provided
- **Bone Separation Map**: the output from the previous step. If none, the method will use a connectivity filter to automatically separate the bones.

Hit the **Get Contour** button. It will take around one minute to process each bone.



Step 3 – Manual Correction

The user will be able to manually correct the periosteal bone surface in this step.

Select the output from Step 2 at Contour to be Corrected, and the greyscale scan at Master Volume.

Hit the Initialize button #1, and the editor tools will be activated.

Select the contour segment and edit.

Once completed editing, hit the **Apply** button #2.

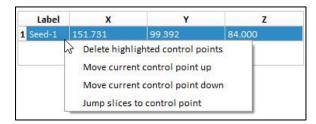


Step 4 – Erosions

In this step, erosions will be identified by placing seed points in each of them. Large and small erosions will be identified separately, so the user will run this step multiple times. Each time, the seed points are plotted in erosions of similar size.

Parameters:

- **Input Volume**: the greyscale scan
- **Input Contour**: the output contour from the previous steps
- Output Volume: each erosion will be labeled differently
- **Seed Points**: Each time when placing a seed point, hit the placement button * , and left click in the viewer windows where the seed point should go. Manage the seed points using the seed point table, and right click the table to access more actions. Place one or more seed points in the middle of each erosion. Try to keep all the seed points as middle in the erosions as possible.



- **Large Erosion**: Check this box if the seed points are plotted in "large" erosions. This determines the internal parameters used in the segmentation.
- **Advanced parameters**: further adjust the internal parameters used in the segmentation.

Hit the **Get Erosions** button. It will take around half a minute to produce the result.

Rerun this step for erosions of different sizes. Plot seed points in different erosions. Create new **Output Volumes** to store erosions of different sizes.

If the output contains trabecular leakage, increase the values of the **Advanced** parameters. If some erosions are missing, modify the seed points or decrease the values of the **Advanced** parameters.



Step 5 - Manual Correction

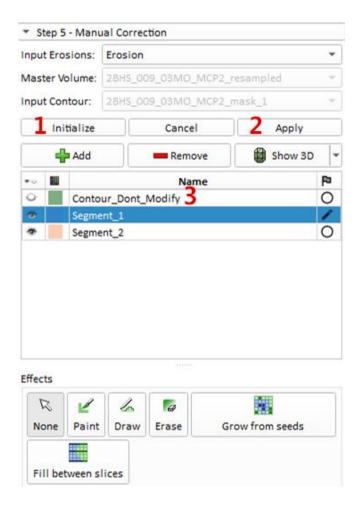
The user will be able to manually correct the erosions in this step. Since large and small erosions were identified separately, the erosions scatter among multiple outputs. This step also allows for combining those erosions into a single output.

Parameters:

Input Erosions: the output from Step 4

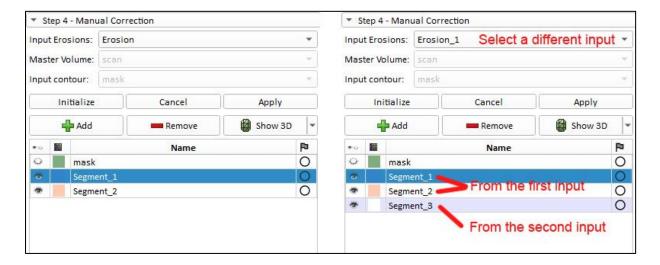
- Master Volume: the greyscale scan

- **Input Contour:** the periosteal bone surface



Hit the **Initialize** button **#1**, and the editor tools will be activated. The editor is set so that only voxels with low intensities and voxels inside the bone surface are editable. The first segment **#3** will be the Input Contour. Leave it invisible and do not modify.

To add erosions from a different output, change the **Input Erosions**, and hit the **Initialize** button #1. The goal is to combine all the large and small erosions from Step 4 into a single output.



Once completed editing, hit the **Apply** button #2. The changes will be applied to the selected **Input Erosions**.

Step 6 – Statistics

Parameters:

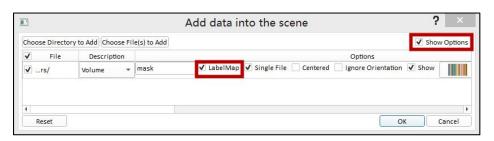
- Input Erosions
- **Output Table**: Only the erosions in the selected **Input Erosions** will appear in the output table

Hit the **Get Statistics** button. The statistics include volume, surface area, roundness, and centroid (the coordinates of each erosion).

Save and Reload Files

Hit the Save button in the tool bar in , and select the files to be saved.

When reloading files, the masks, i.e. the periosteal bone surface and the erosion segmentations, need to be loaded as **LabelMapVolumes**. To do so, check the **Show Options** check box at the top right corner of the Add Data prompt window, and then check the **LabelMap** option.



References

- [1] Lasso A, Pieper S, Fillion-Robin JC. User Interface. 3D Slicer's Documentation (2020). https://slicer.readthedocs.io/en/latest/user_guide/user_interface.html
- [2] Lasso A, Sunderland K. Segment editor. 3D Slicer's Documentation (2020). https://slicer.readthedocs.io/en/latest/user_guide/modules/segmenteditor.html
- [3] Barnabe C, Toepfer D, Marotte H, Hauge EM, Scharmga A, Kocijan R, Kraus S, Boutroy S, Schett G, Keller KK, et al. Definition for rheumatoid arthritis erosions imaged with high resolution peripheral quantitative computed tomography and interreader reliability for detection and measurement. J Rheumatol (2016) 43:1935–1940. doi:10.3899/jrheum.160648
- [4] Töpfer D, Finzel S, Museyko O, Schett G, Engelke K. Segmentation and quantification of bone erosions in high-resolution peripheral quantitative computed tomography datasets of the metacarpophalangeal joints of patients with rheumatoid arthritis. Rheumatology (Oxford) (2014) 53:65–71. doi:10.1093/rheumatology/ket259