

This document outlines the workflow and scripts for the image processing steps after the second generation HR-pQCT (XtremeCT2, Scanco Medical) scans of the 2nd and 3rd MCP joints have been acquired (1). These are the scripts that were utilized in Brunet et al. BMC Med Imaging doi: 10.21203/rs.2.14575/v1.

1) STACK REGISTRATION

This script assumes that 3 stacks were acquired, with an overlap of 25%.

Step 1:

A contour must be drawn around the joint so that both the metacarpal and phalange are included. A new contour should be drawn approximately every ten slices, with the ‘morph’ used to fill in the rest of the contours. These contours should be drawn with space around the bone (Figure A-4). In the future, it would be valuable to use an auto-contouring algorithm and then dilating this contour by an equal number of voxels for each slice. This would improve the consistency of the contours and reduce the time required.

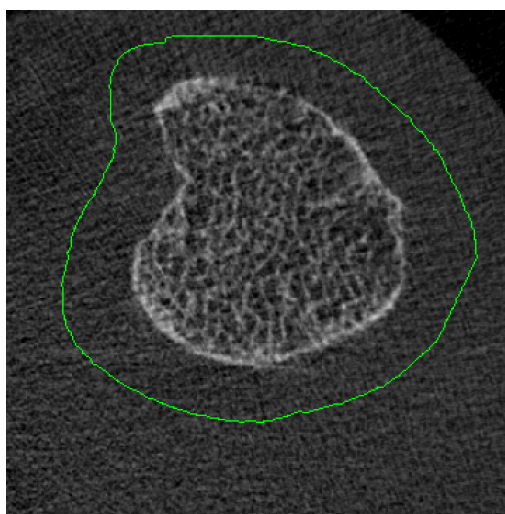


Figure A-4 Example of the manual contour drawn around the metacarpal bone for stack registration.

Once the contour has been made, save the ‘gobj’ file and run the script titled “3D Cutout of VOI, 1 solid object” script from the task bar. This will produce a new aim file of the cut-out bone.

Step 2:

Once the new aim files have been generated for each of the three stacks, copy and rename the aim and gobj files to a common directory you create. You should then have the following files in this directory:

<BASE>_DST.AIM	<BASE>_DST.GOBJ
<BASE>_MID.AIM	<BASE>_MID.GOBJ
<BASE>_PRX.AIM	<BASE>_PRX.GOBJ

Step 3:

You will need “SUBMIT_STACK_REGISTRATION.COM” which calls “STACK_REGISTRATION.COM”. To run the script for the desired joint change the input IN FILE1 in the submit script to: <BASE>. This will run the script and output a combined image titled: <BASE>_FINAL_IMAGE.AIM. This image will have all of the stacks combined and can be converted to an ISQ file for further analysis. To convert to an ISQ, the following functions were used in IPL interactively.

```
/read
  -name          in
  -filename      <BASE>_FINAL_IMAGE.AIM

/toisq_from_aim
  -aim_name      in
  -isq_filename  XX_XM_JX.ISQ
```

```
-square_flag          true
-original_position    false
```

This outputs a new ISQ file with the format XX_XM_JX.ISQ e.g. 01_0M_J2.ISQ.

2) AUTOCONTOUR

NOTE: The autocontour script is included in Scanco's Joint Space Width Analysis package (2).

We have created starter scripts to run this analysis from the command line rather than uct_evaluation.

Step 1:

Draw contours on the recently created ISQ file for the joint of interest that has all of the stacks combined together. Save this gobj file.

Step 2:

If the joint is fused, create a "SPLIT.GOBJ":

- i. Clear All BP
- ii. Set on most distal slice that shows only metacarpal and no phalange
- iii. Contour around the metacarpal in first image that shows both bones
- iv. Move backwards (in the distal direction) until there is phalange and no metacarpal in slice. Contour every 10 slices or so
- v. Select all in contouring toolbox – then click morph – this will fill in the contours you didn't do manually
- vi. Move to slice with no metacarpal – select backwards in contouring box – then delete. This will remove all contours on only the phalange.
- vii. Save as _SPLIT.GOBJ

Step 3:

Run the script “SUBMIT_SEG_AUTOK_JSW_RENAME.COM”. This calls the script “STARTER_SEG_AUTOK_JSW.COM”. This will contour the bones, separate the metacarpal from the phalange, and segment the bones.

3) LONGITUDINAL REGISTRATION

The longitudinal registration can be completed after successfully running the segmentation and autocontour steps above.

Step 1:

Run “SUBMIT_REGISTER_LONGITUDINAL” to call “REGISTER_LONGITUDINAL.COM” This step aligns the baseline and follow-up HR-pQCT images, and creates a transformed follow-up image. The script is currently designed to register the metacarpal bones. In order to register the proximal phalange bones, make the appropriate adjustments to the file naming and use the _DSTMASK as opposed to the _PRXMASK.

Inputs:

FILE1: <BASE> for the baseline image

FILE2: <BASE > for the follow-up image

FILE3: <BASE> _META

FILE4: <BASE> _PRXMASK for the baseline image

FILE4: <BASE> _PRXMASK for the follow-up image

Outputs:

<BASE_baseline> _META.AIM

<BASE_followup> _ROT.AIM

<BASE_followup> _ROT.GOBJ

<BASE_followup>_COMMON_REG.AIM

<BASE_baseline>_META_COMMON_REG_ALL.AIM

<BASE >.TXT (transform file)

<BASE>_META_REG.AIM

Step 2:

Once the follow-up image has been transformed to the baseline image space, bone loss and bone gain can be visualized. This is accomplished by running the “SUBMIT_BONE_REMODELLING.COM” script which calls the “BONE_REMODELLING.COM” script. This will produce a segmented bone loss and bone gain files, as well as a combined file with the segmented baseline image and the loss and gain.

Currently, the parameters for segmentation are set as follows:

Inputs:

File1: <BASE_baseline>_META

File2: <BASE_followup>_ROT

File3: <BASE>_META

File4: <BASE_baseline>_PRXMASK

Outputs:

<BASE>_DIF.AIM

<BASE>_DIF_MASK.AIM

<BASE>_FORMATION.AIM

<BASE>_RESORPTION.AIM

<BASE>_ADD_SEG.AIM

References

1. Barnabe C, Feehan L, SPECTRA (Study Group for XTrEme-CT in RA). High-resolution peripheral quantitative computed tomography imaging protocol for metacarpophalangeal joints in inflammatory arthritis: the SPECTRA collaboration. *J. Rheumatol. The Journal of Rheumatology*; 2012 Jul;39(7):1494–5.
2. Stok KS, Burghardt AJ, Boutroy S, Peters MPH, Manske SL, Stadelmann V, Vilayphiou N, Bergh JPVD, Geusens P, Li X, Marotte H, Rietbergen BV, Boyd SK, Barnabe C, Collaboration FTS. Consensus approach for 3D joint space width of metacarpophalangeal joints of rheumatoid arthritis patients using high-resolution peripheral quantitative computed tomography. *Quant Imaging Med Surg*. 2020 Nov 1;10(2):314–325–325.