

Joint Space Width Evaluation

1 Characteristics

This documentation applies to JSW V2.3.

JSW was developed in collaboration with the SPECTRA Group.

The algorithm is based on 3 independent approaches [1]–[3] to analyse the joint space width.

2 Goals

This document describes how to evaluate joint space width of the metacarpal (MCP) joints and optionally from the interphalangeal (PIP) joints of the hand using XtremeCT or XtremeCT II.

This document uses an MCP joint for illustration and description purpose. This evaluation is not exclusive to MCP or PIP joints and is applicable to other joints.

3 Tasks

3.1 Prepare holder & position hand

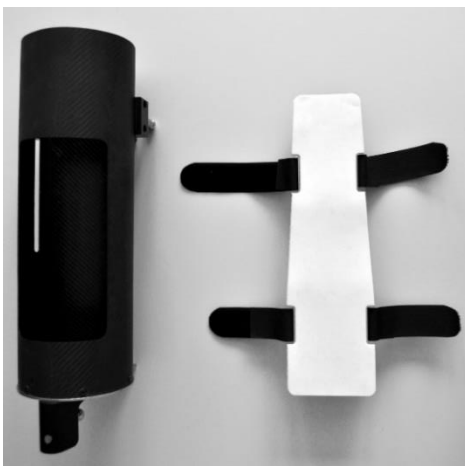


Figure 1- Carbon tube and hand support



Figure 2 - Hand strapped on support



Figure 3 - Support inserted in carbon tube

4 Scanning

More detail is available in Barnabe & Feehan 2012 publication [4].

4.1 Preparation

- Register patient
- Select Controlfile “Joint space width” or create control file with following settings ([Table 1](#))
- Condition patient to relax
- Run precalibration
- Place holder in bore with patient in comfortable position ([Figure 4](#))

	XtremeCT	XtremeCT II
Voxel size	82 um	61 um
High voltage	60 kVp	68 kVp
Current	900 uA	1470 uA
Integration time	100ms/projection	43 ms
Nb of Projections	750	900
Image matrix	1536 x 1536	2304 x 2304
Nb of slices (2 stacks)	220	336
Scout view angle	90 degrees	90 degrees

Table 1 - Scan settings

4.2 Scout view and reference line

- The initial reference line for the scout view should be the midpoint of the concave articular surface of the base of the 2nd or 3rd proximal phalanx, whichever is the most distal.
- Reference lines ([Figure 5](#)): The scan should start at a minimum 2 mm distal to this line and should include a minimum of 2 stacks to ensure that both the 2nd and 3rd MCP joint spaces are contained fully within the first 110 slices, in an effort to avoid any potential effect of stack artefact or discontinuity in the joint space. If a 3rd stack can also be done, the scan start location can be located more distally if needed, but it should still be ensured that the 2nd and 3rd MCP joint spaces are fully contained within 1 stack.
- Start Scan



Figure 4 - Patient positioning

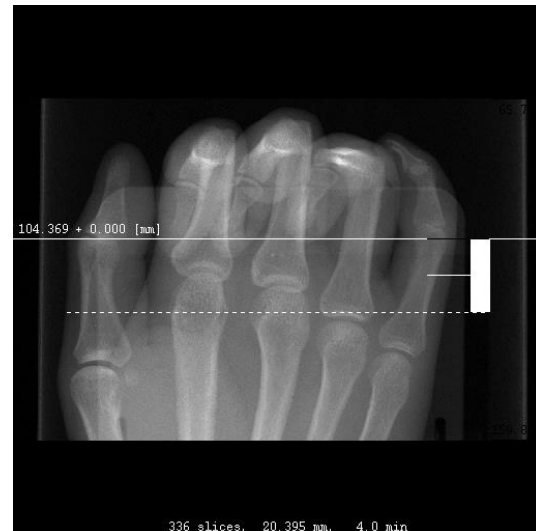


Figure 5 – Reference lines

5 Image quality assessment

Following the scan, assess the images for motion artefact ([Figure 6](#)), and exclude images of poor quality (grade >3). If possible, rescan.

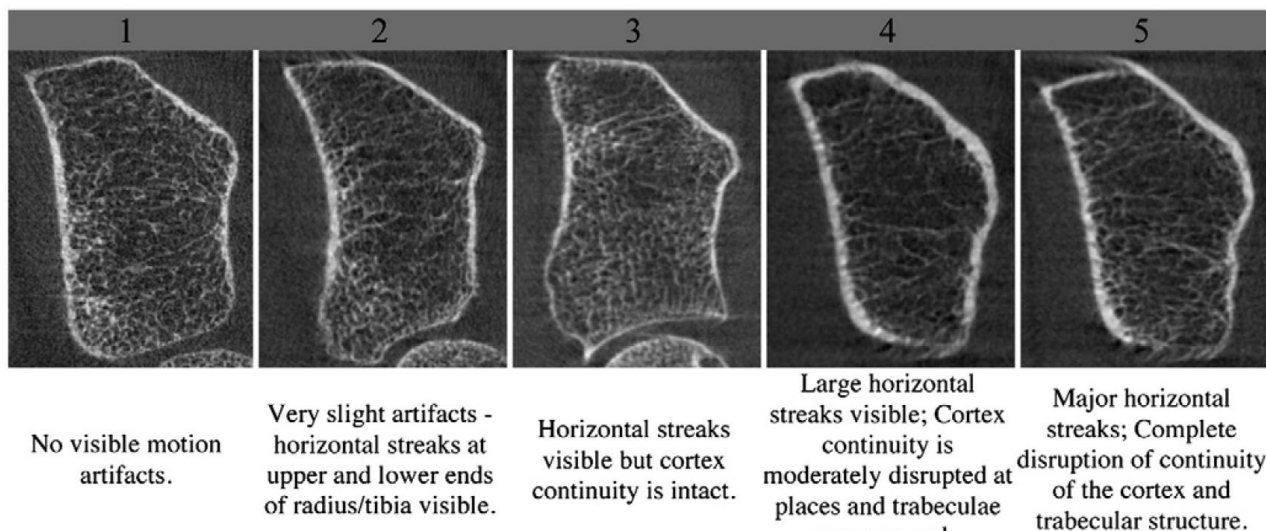


Figure 6 - Image quality grading guideline and representative reconstructed grayscale image of the distal radius for each grade et from Sode et al, 2011 [5]

6 Image processing

6.1 Identification of a joint of interest

The goal of this section is to define a region of interest for each identifiable joint (MCP or PIP). (Figure 7)

- Draw a contour in the most distal slice containing the phalange of interest (exclude other bones), and in the most proximal slice containing the metacarpal of interest. (Figure 8)
- **Make sure that the ROI contains more proximal bone than distal bone.**
The algorithm works under the assumption that within the ROI, the proximal bone volume will be bigger than the distal bone. Otherwise, the process may run into an error.
- Interpolates contours using use morphing. Exclude other bones. (Figure 9)
- Save GOBJ as C000XXXX.GOBJ

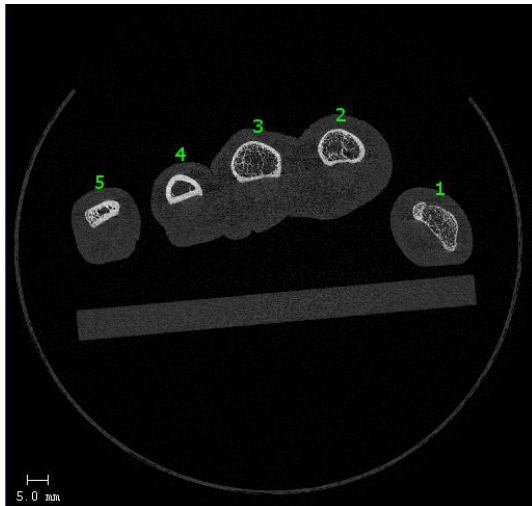


Figure 7 - The fingers are numerated 1 (thumb) to 5 (small finger)

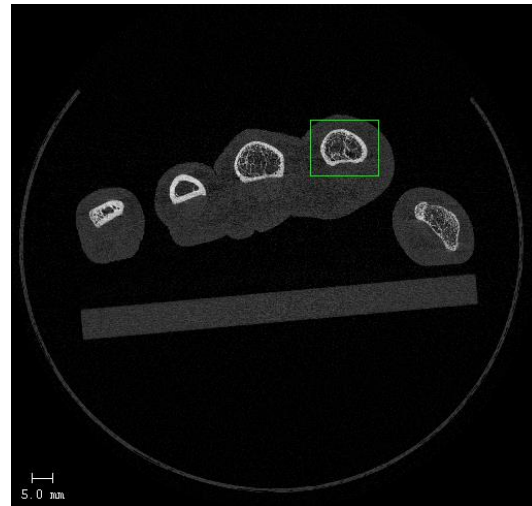


Figure 8 - Example drawing GOBJ for MCP2 (between metacarpal 2 and phalange 2)

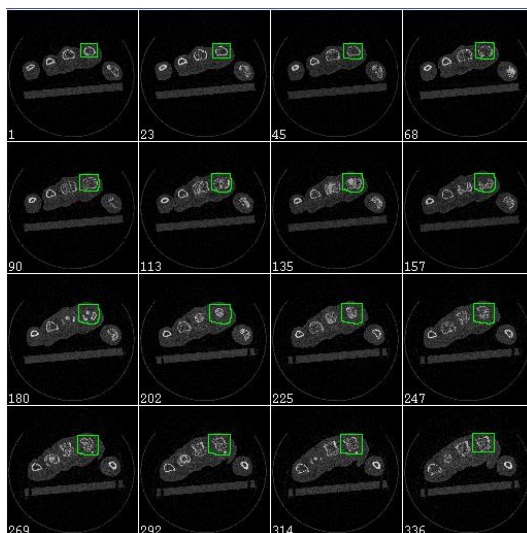


Figure 9 - Interpolated GOBJ for MCP2

6.2 Create separate measurement for the joint of interest

The isolated joint will be imported in a separate measurement.

- Select Tasks > "(JSW-XT2) Cut joint and reimport with ID"
- In the field "Joint ID" type in the joint ID (eg. MCP2, MCP3, PIP1. Keep some consistency in naming)
- Start evaluation
- A new measurement containing only the joint of interest will be generated.

6.3 Joint segmentation

- Open the ISQ of the newly created measurement with individual joint (*Figure 10*)
- Select Tasks > “(JSW-XT2) Joint Segmentation”
- Start evaluation.
- The segmentation result can be visualized by opening the file “XXX_ SEG.AIM” (*Figure 11*)

6.4 Joint autocontour

- Open the ISQ of the newly created measurement with individual joint (*Figure 10*)
- Select Tasks > “(JSW-XT2) Joint Autocontour”
- Start evaluation.
- The autocontour result can be visualized loading the GOBJ file “XXX_DST.GOBJ” or “XXX_PROX.GOBJ” (*Figure 12, Figure 13*)



Figure 10 - Isolated joint in a new measurement



Figure 11 - Segmented joint

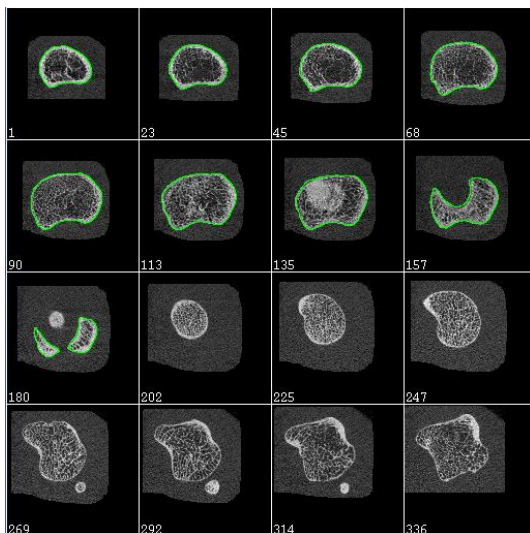


Figure 12 - Distal bone contour: XXX_DST.GOBJ

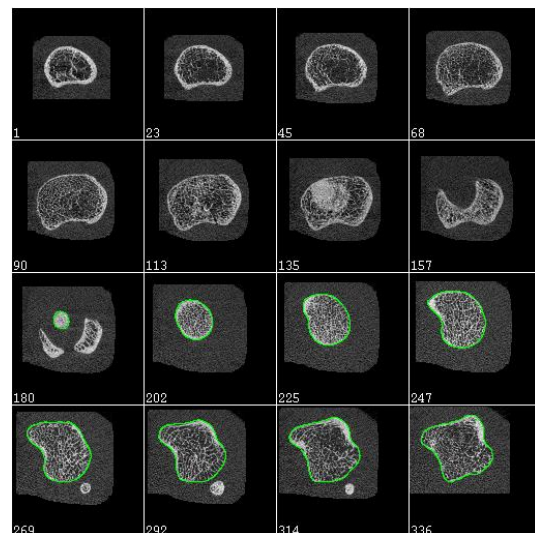


Figure 13 - Proximal bone contour: XXX_PROX.GOBJ

6.5 Solving Autocontour problems (optional)

In most cases, there is no need to execute the following paragraphs. They are typically applicable for cases of ankylosis or motion artefacts. Depending on the cases, only 6.5.1, only 6.5.2 or both could be needed.

Note: The algorithm is designed to allow modification of the bone contours only (6.5.1 and 6.5.2). The workflow does not allow manual modifications on the joint space contour JSMASK.GOBJ.

6.5.1 Separate proximal and distal bones

Sometimes, due to ankylosis in a joint, the proximal and distal parts of the joints are not separated during the autocontour process, because the bones are very close to each other or even fused within the joint space (*Error! Reference source not found.*). It is possible to use a manually drawn contour to force the splitting of the two bones.

- Open the ISQ of the individual joint
- Draw a contour that contains only the proximal bone (The contour does not need to be precise and fit to the bone edge, see [Figure 15](#))
- Save the contour as file "XXX_SPLIT.GOBJ"
- Resubmit the Task > "(JSW-XT2) Joint Autocontour". The SPLIT contour will be used as an input to label properly the DST and PROX contours.
- Start evaluation.
- The autocontour result can be visualized loading the GOBJ file "XXX_DST.GOBJ" or "XXX_PROX.GOBJ"

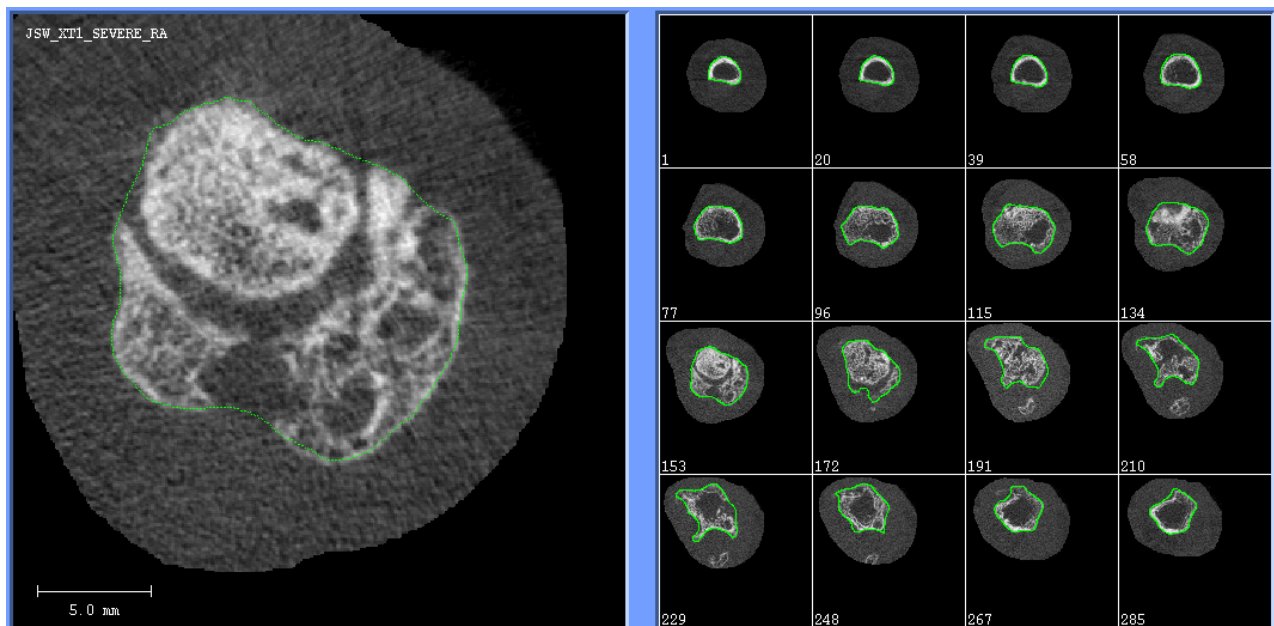


Figure 14 - In the example the joint space is so tight that autocontour could not distinguish proximal from distal. As illustrated by the XXX_DST.GOBJ contour which contains both bones.

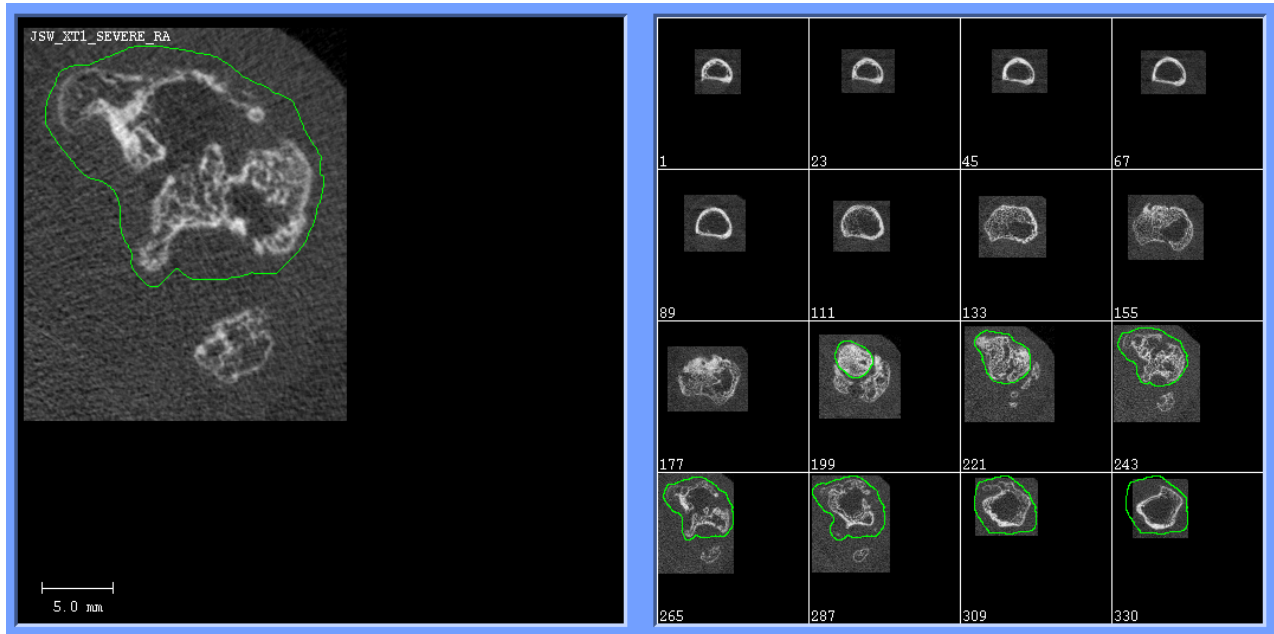


Figure 15 - XXX_SPLIT.GOBJ contour of the proximal bone to force separation of proximal and distal bones.

6.5.2 Manual corrections after autocontour

Sometimes the contours produced automatically may be inaccurate. If it happens outside the joint space (Figure 16) the effect is limited or null on the JSW results. If the approximation of the contour lies within the joint space, it may influence the results and it is advised to correct the contour manually.

- Open the ISQ of the individual joint
- Open the XXX_PROX.GOBJ contour that contains only the proximal bone
- Make manual corrections to the contour slice by slice (Figure 16, Figure 17, Figure 18)
- Save the contour
- Repeat for the XXX_DST.GOBJ
- Select Tasks > "(JSW-XT2) Corrections after autocontour"
- Start evaluation.

This script will update all files with the manual corrections.

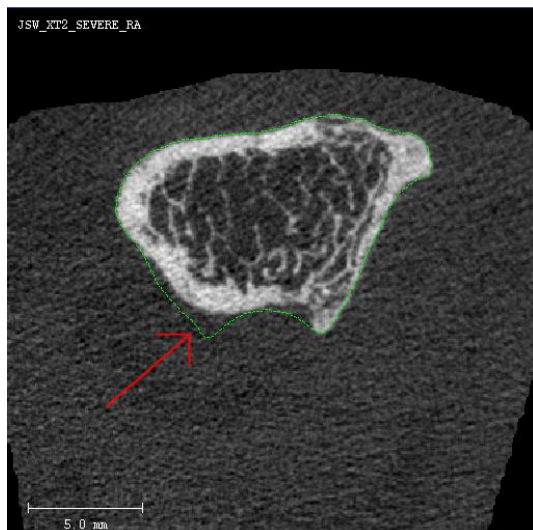


Figure 16 - Imperfect contouring outside joint space

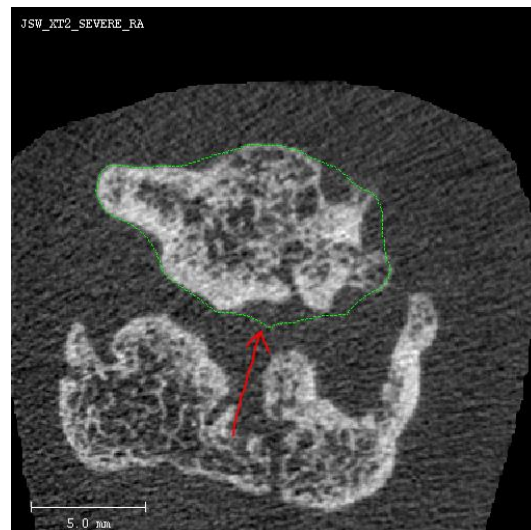


Figure 17 - Approximal contour with joint space

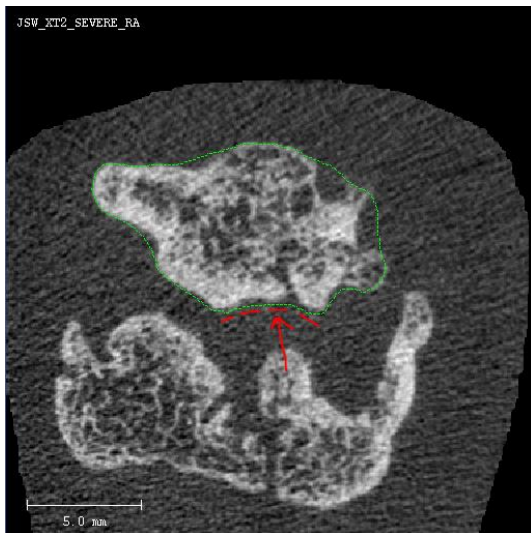


Figure 18 - Manual correction of the contour

6.6 Joint space analysis

The joint space ROI is created and the JSW distribution is computed.

- Select Tasks > “(JSW-XT2) Joint Space Analysis”
- Start evaluation.
- The results can be visualized in the pdf file XXX_JSW.pdf (*Figure 23*)
- The summarized data can be found in
DISK1: [MICROCT.RESULTS]UCT_LIST_3DLOG_JSW_ANALYSIS_XT2.TXT

Note: The evaluation task “Joint Space Analysis” is described in the manuscript “Approach for 3D joint space width of metacarpophalangeal joints of rheumatoid arthritis patients using high-resolution peripheral quantitative computed tomography”, in review

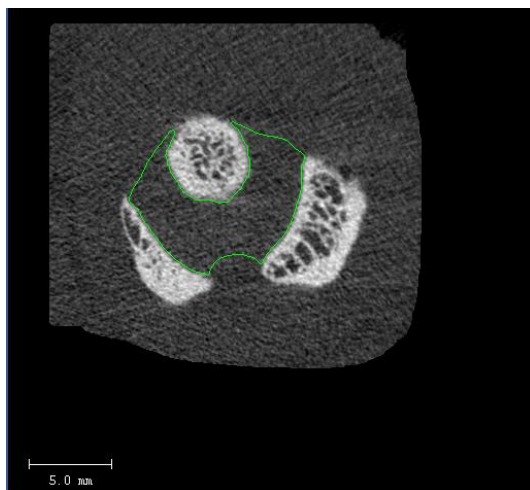


Figure 19 - Joint space GOBJ

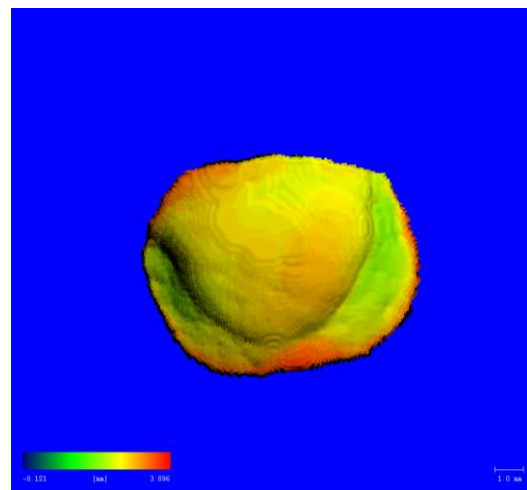


Figure 20 - Joint space thickness map

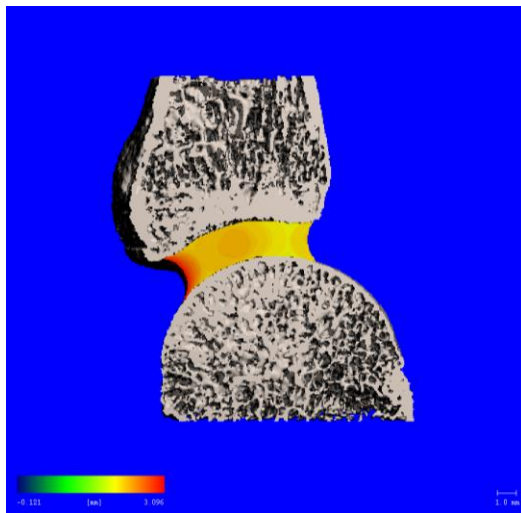


Figure 21 - Joint space analysis

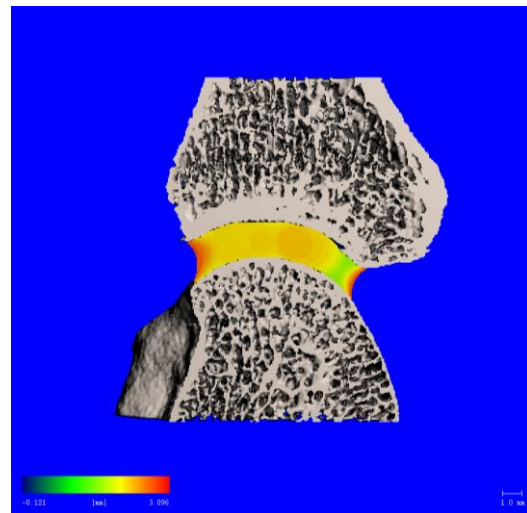


Figure 22 - Joint space analysis (profile)

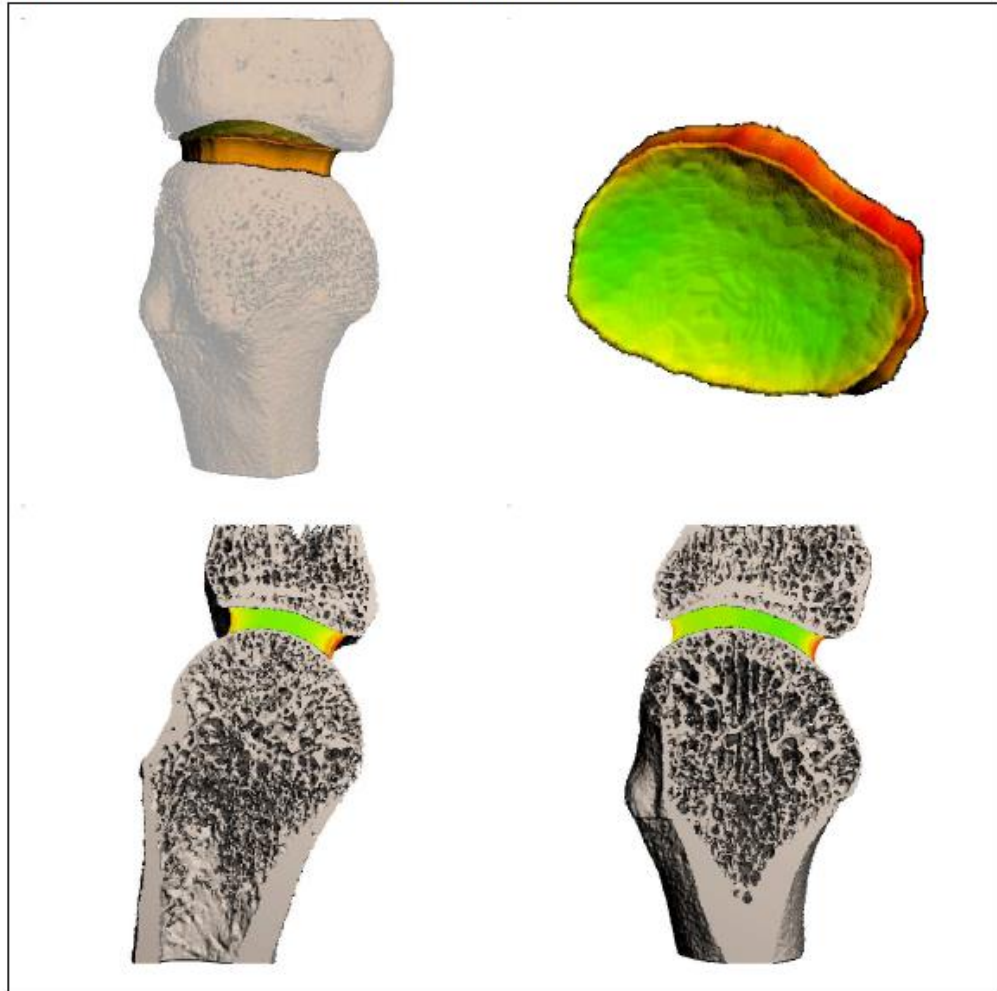
JSW_XT2_HEALTHY

SCANCO MEDICAL

Joint-ID: MCP3

S-No.: 21 Filename: J0007661

M-No.: 55 Date: 26-OCT-2017 08:29



VOI		X	Y	Z
Position	[p]	2	1	1
Dimension	[p]	410	438	504
Element Size	[mm]	0.0607	0.0607	0.0607

Joint Space Width Analysis

JS.V	[mm ³]	94.7371	Process log: Original MeasNo: 33 JointID: MCP3 Original Gobj: D0007661_MCP3.GOBJ;4 Date re-import: 17-APR-2019 17:39:19.73 New MeasNo: 55
JS.W	[mm]	1.5551	
JS.W_SD	[mm]	0.2938	
JS.W_MAX	[mm]	2.6708	
JS.W_MIN	[mm]	1.0926	
JS.W_AS	[-]	2.444444444	

Figure 23 - Example of print sheet

7 References

- [1] C. Barnabe *et al.*, 'Reproducible metacarpal joint space width measurements using 3D analysis of images acquired with high-resolution peripheral quantitative computed tomography.', *Med. Eng. Phys.*, vol. 35, no. 10, pp. 1540–1544, Oct. 2013.
- [2] A. J. Burghardt *et al.*, 'Quantitative in vivo HR-pQCT imaging of 3D wrist and metacarpophalangeal joint space width in rheumatoid arthritis.', *Ann. Biomed. Eng.*, vol. 41, no. 12, pp. 2553–2564, Dec. 2013.
- [3] S. Boutroy *et al.*, 'Importance Of Hand Positioning In 3D Joint Space Morphology Assessment', in *ACR Meeting Abstracts*, 2013.
- [4] C. Barnabe, L. Feehan, and 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.*, vol. 39, no. 7, pp. 1494–1495, Jul. 2012.
- [5] M. Sode, A. J. Burghardt, J.-B. Pialat, T. M. Link, and S. Majumdar, 'Quantitative characterization of subject motion in HR-pQCT images of the distal radius and tibia.', *Bone*, vol. 48, no. 6, pp. 1291–1297, Jun. 2011.

8 Additional Information:

8.1 Re-import: traceability

Upon cut and re-import processing two files are created to facilitate traceability:

CXXXXXXXX_REIMPORT_LOG.TXT in the original scan directory contains a list of all sub-scans. One can read it in a Terminal using:

```
$ type CXXXXXXXX_REIMPORT_LOG.TXT

JointID,      New MeasNo, Date
MCP1,         205,      22-JUN-2017 14:58:24.40
MCP2,         206,      22-JUN-2017 15:06:08.40
MCP3,         207,      22-JUN-2017 15:53:49.98
MCP4,         208,      22-JUN-2017 15:57:32.41
```

In this case 4 sub-regions (MCP1 to MCP4) were cut and re-imported from the original scan into measurement numbers 205 to 208.

JXXXXXXXX_JOINT_ID.TXT is created in the re-imported scan directory (for example n°208 from above):

```
$ type JXXXXXXXX_JOINT_ID.TXT

!! JSW Process log:
JSW_SAMPNO  == 64
JSW_MEASNO  == 208
JSW_JOINTID == MCP2
JSW_ORGMEASNO == 190
JSW_ORGGOBJ == C0010013_MCP2.GOBJ;8
JSW_REIMPDATE == 22-JUN-2017 15:57:32.41
```

In this case, the file shows that measurement n° 208 of patient 64, comes originally from measurement n°190. The original cutting ROI can be viewed in the original scan by loading the GOBJ CXXXXXXXX_MCP2.GOBJ;8