

uCT 35 Weekly (QC1) and Monthly (QC2) Calibration

The weekly and monthly calibration scans are performed as checks of the system. The operator must verify that the density and geometry values are within an acceptable range. If the values are not within range, the operator must contact Scanco Medical and will be required to perform repeated calibration scans and update the system to bring it back into range.

Notes: Calibration phantoms are specific to the scanner. Consistent sample positioning is critical.

Locate the calibration phantom for the uCT35 system. The phantom is stored in a plastic sample holder, usually on top of the scanner.

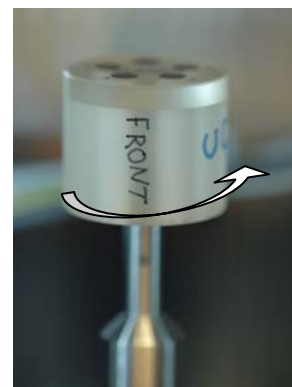


Remove the calibration phantom from the holder. Notice that the phantom is labeled and must be positioned in the scanner in a particular orientation (this is so that the pre-made gobj files are properly aligned).

Note: The metal spindle must be fixed to the epoxy to ensure consistent positioning of the sample. If the spindle becomes loose, it must be re-glued together and the pre-made gobj files must be updated.



Position the phantom in the scanner so that the front" label is facing towards you and the sample has dropped into place (i.e. the slot in the spindle locks the sample in position). The phantom should not be able to rotate, however, it does about one degree due to slack. Very gently rotate the sample counter-clockwise to ensure it will align with the gobj. You should not be rotating so much that you feel the resistance of the motor (if you do, the gobj will not be aligned).



Start the scanning program. For QC1, select sample 1 and run control files 2 (QC1 55 kVp, 1200 mg HA) and 24 (QC1 55 kVp, 200 mg HA). For QC2, select sample 2 and run control file 4 (QC2).

Alternatively, you can close the scanning program and run the measurements from the command line on Workstation 3:

```
$ @um:uct_batch_measurement 1 1 2 116 135.0 n
$ @um:uct_batch_measurement 1 1 24 116 135.0 n
$ @um:uct_batch_measurement 1 2 4 150 126.0 n
```

In general: \$ @um:uct_batch_measurement P1 P2 P3 P4 P5 P6

where: P1: Operator
P2: Sample
P3: Controlfile
P4: Number of slices*
P5: Position of 1st slice in mm with decimal point*
P6: Shutdown x-ray tube
*get values for P4 and P5 from the controlfile

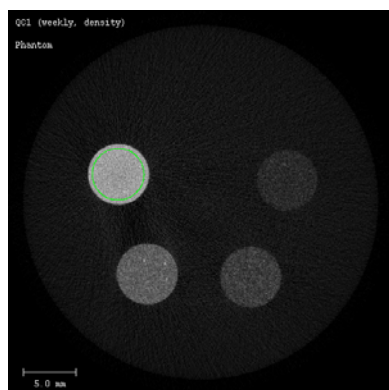
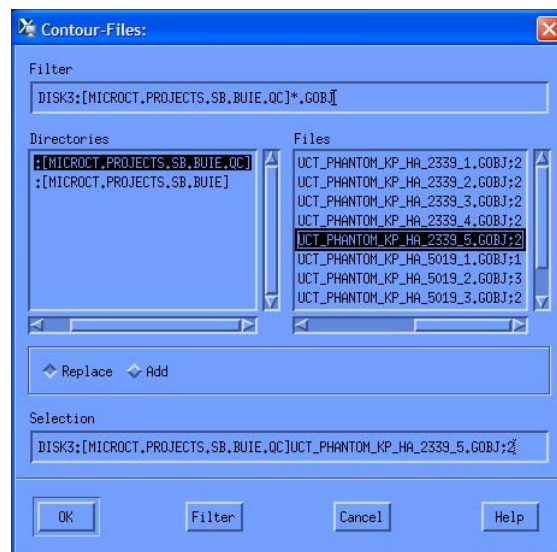
When the QC1 and/or QC2 scans have reconstructed, they must be analyzed.

If you suspect the sample may not be aligned, load one of the gobj files used for the analysis.

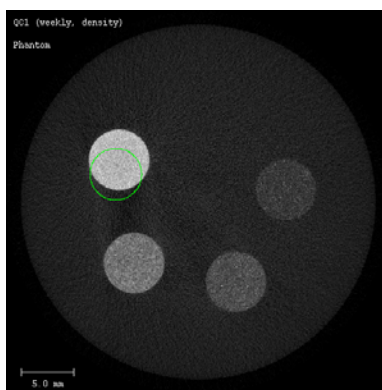
**DISK3: [MICROCT.PROJECTS.SB.BUIE.QC]
UCT_PHANTOM_KP_HA_2339_5.GOBJ**

The contour should be centered on the brightest rod. If it is not, reposition and rescan the calibration phantom.

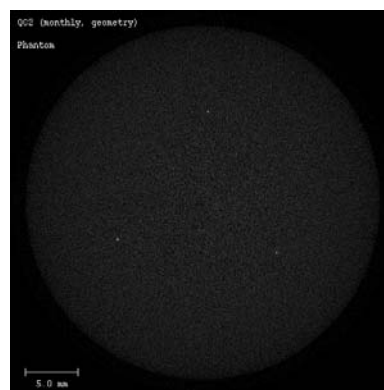
DO NOT SAVE OVER THE GOBJ!!!



QC1 (aligned)



QC1 (not aligned)

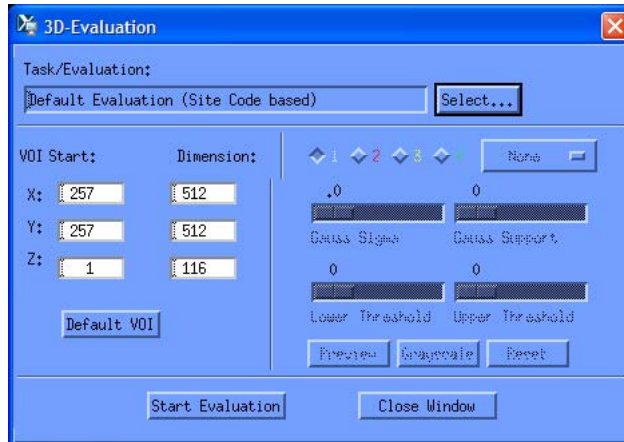


QC2

On Workstation 3:

Run the evaluation program (uct_evaluation, cutout). Load the measurement.

Top menu → Tasks → Evaluation 3D...



Press the Select... button. Choose the **QC1** or **QC2 for microct 40**, depending on which calibration check you are running.

It is not necessary to adjust the white box on the screen that's usually used to cut out an aim.

Start Evaluation.

When the evaluation is complete, check the results.

\$ uct_list P1
where: **P1: Measurement Number**

For QC1 evaluations, check and record the value of Mean 5. Acceptable range: 764-806 mg HA/ccm.

For QC2 evaluations, check and record the value of BV. Watch for consistency in values.

Example: Extracting Mean 5 value for QC1 analysis

\$ uct_list 8367

Processing measurement 8367

Name :C0001433
 Sample-Name :QC1 (weekly, density)
 Sample-Nr :1
 Meas-Nr :8367
 Meas-Date :09-OCT-2008 09:58
 Oper Meas, Eval :Helen Buie, Wei
 Date of Birth :
 Sample-Remarks :
 Meas-Remarks :
 Site :Phantom
 Meas-NrofSlices :116
 Scanner ID :2339
 RAW Location :DK0:[MICROCT.DATA.00000001.00008367]
 IMA Location :DK0:[MICROCT.DATA.00000001.00008367]

Segmentation: -----
 Sigma : -
 Support : -
 Threshold : -
 in Units : -

Direct: -----
 TV : -
 BV : -
 BV/TV : -
 Conn.Dens.: -
 SMI : -
 Tb.N* : -
 Tb.Th* : -
 Tb.Sp* : -
 Tb.1/N.SD* : -
 Tb.Th.SD* : -
 Tb.Sp.SD* : -
 Mean1 ±SD : -10.9799 +- 53.1333 [mg HA/ccm]
 Mean2 ±SD : 105.5392 +- 72.5993 [mg HA/ccm]
 Mean3 ±SD : 214.0918 +- 85.7614 [mg HA/ccm]
 Mean4 ±SD : 418.2428 +- 95.9447 [mg HA/ccm]
 Mean5 ±SD : 802.3682 +- 96.7759 [mg HA/ccm]

TRI (Plate Model): -----
 TV : -
 BV : -
 BS : -
 BV/TV : -
 BS/BV : -
 Tb.Th : -
 Tb.Sp : -
 Tb.N : -

Anisotropy: -----
 |H1| : - H1x: - H1y: - H1z: -
 |H2| : - H2x: - H2y: - H2z: -
 |H3| : - H3x: - H3y: - H3z: -
 DA : -
 Dim X : 0
 Dim Y : 0
 Dim Z : 0
 Pos X : 1
 Pos Y : 1
 Pos Z : 1
 El-Siz X : -
 El-Siz Y : -
 El-Siz Z : -

Example: Extracting BV value for QC2 analysis

\$ uct_list 8372

Processing measurement 8372

Name : C0001436
 Sample-Name : QC2 (monthly, geometry)
 Sample-Nr : 2
 Meas-Nr : 8372
 Meas-Date : 09-OCT-2008 12:07
 Oper Meas, Eval : Wei,
 Date of Birth :
 Sample-Remarks :
 Meas-Remarks :
 Site : Phantom
 Meas-NrofSlices : 150
 Scanner ID : 2339
 RAW Location : DK0:[MICROCT.DATA.00000002.00008372]
 IMA Location : DK0:[MICROCT.DATA.00000002.00008372]

Segmentation: -----
 Sigma : 0.00
 Support : 0
 Threshold : 230
 in Units : 6
 Direct: -----
 TV : 3983.5144

BV : 0.1053

BV/TV : 0.0000
 Conn.Dens.: -
 SMI : -
 Tb.N* : -
 Tb.Th* : -
 Tb.Sp* : -
 Tb.1/N.SD* : -
 Tb.Th.SD* : -
 Tb.Sp.SD* : -
 Mean1 ±SD : - +- - [mg HA/ccm]
 Mean2 ±SD : - +- - [mg HA/ccm]
 Mean3 ±SD : - +- - [mg HA/ccm]
 Mean4 ±SD : - +- - [mg HA/ccm]
 Mean5 ±SD : - +- - [mg HA/ccm]

TRI (Plate Model): -----
 TV : -
 BV : -
 BS : -
 BV/TV : -
 BS/BV : -
 Tb.Th : -
 Tb.Sp : -
 Tb.N : -

Anisotropy: -----
 |H1| : - H1x: - H1y: - H1z: -
 |H2| : - H2x: - H2y: - H2z: -
 |H3| : - H3x: - H3y: - H3z: -

DA : -
 Dim X : 2048
 Dim Y : 2048
 Dim Z : 150
 Pos X : 1
 Pos Y : 1
 Pos Z : 1
 El-Siz X : 0.0185
 El-Siz Y : 0.0185
 El-Siz Z : 0.0185