Perelman School of Medicine University of Pennsylvania

Penn Center for Musculoskeletal Disorders

PCMD MicroCT Imaging Core Learning Lunch Series

Innovations in Bone Marrow Adipose Tissue Imaging

Optimizing Computational Workflows

Introducing the New DXA Scanner

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PCMD MicroCT Imaging Core

PENN Center for Musculoskeletal Disorders

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Penn Center for Musculoskeletal Disorders (P30-AR069619)

Outlines

- Brief introduction of our core facility
- Bone Marrow Adipose Tissue Imaging
- Optimizing Computational Workflows
- Q & A

μCT Imaging Core Resources

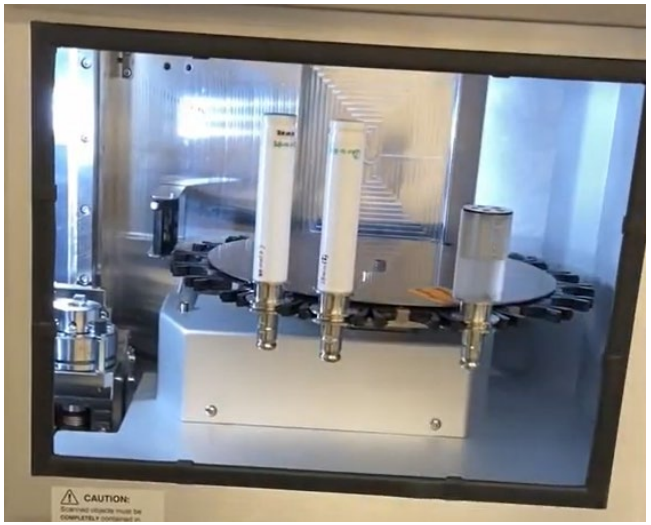
Model	Location	Scan Size (ØxL)	Voxel Size (μm)	Applications
μCT 35	Stemmler 335A	37.9 x 120	3.5-72	High resolution *ex vivo* scans
μCT 45	Stemmler 335A	50 x 120	3.0-100	High resolution *ex vivo* scans
vivaCT 80	Stemmler 368B	80 x 145	10.4-76	High resolution *in vivo* scans
New! DXA	Stemmler 368C	165 x 255	100	Full body 2D scan and analysis
μCT 50	PVAMC/TMRC	50 x 120	0.5-100	Ultra high resolution (sub-micron) *ex vivo* scans
vivaCT 75	PVAMC/TMRC	79.9 x 145	21-150	*In vivo* scans for small animals; *Ex vivo* scans for large specimens
XtremeCT II	CTRC	140 x 200	60-82	Clinical scans for peripheral skeleton

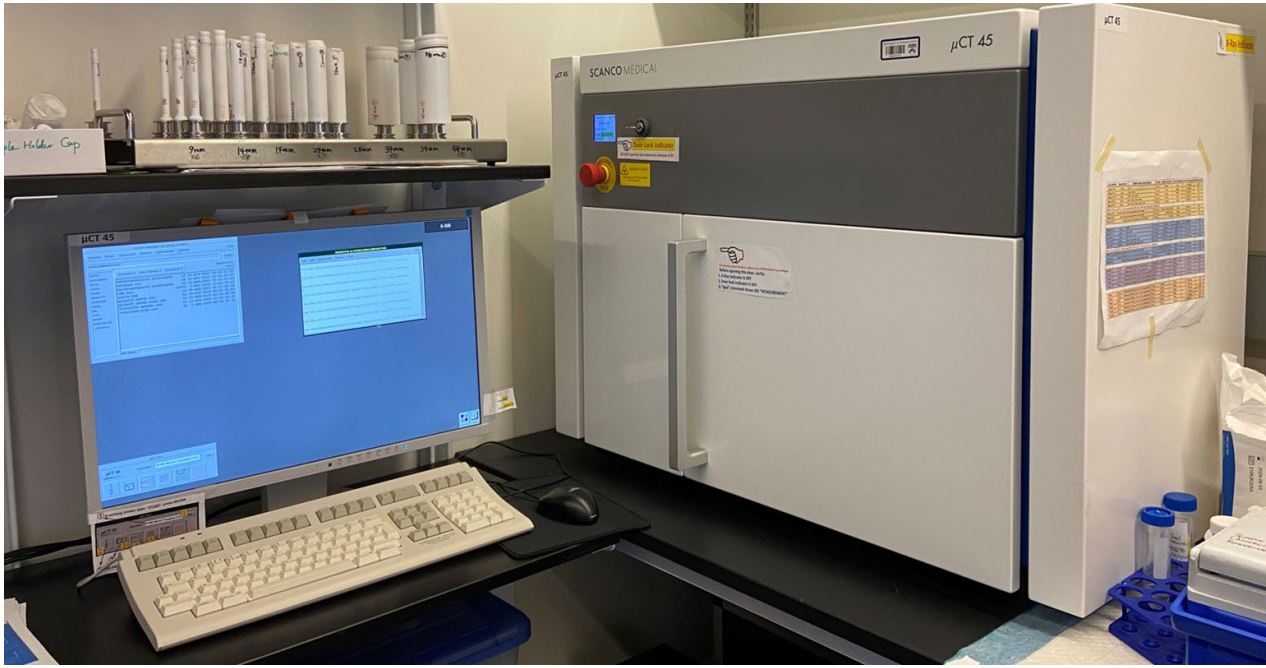
Ex vivo (Specimen) Scanners

- Scanco µCT 35 (Purchased in 2012)
  - Native voxel sizes: 3.5 µm, 6 µm, 10 µm, 15 µm, 18.5 µm

Ex vivo (Specimen) Scanners

- Scanco µCT 45 (Purchased in 2019)
  - Native voxel sizes: 3 µm, 4.5 µm, 7.4 µm, 10.4 µm, 14.6 µm
  - Carousel system supporting 20 sample holders
  - “Air” filter for scanning low density materials
  - “Copper” filter for scanning specimen with metal implants





In vivo Scanner

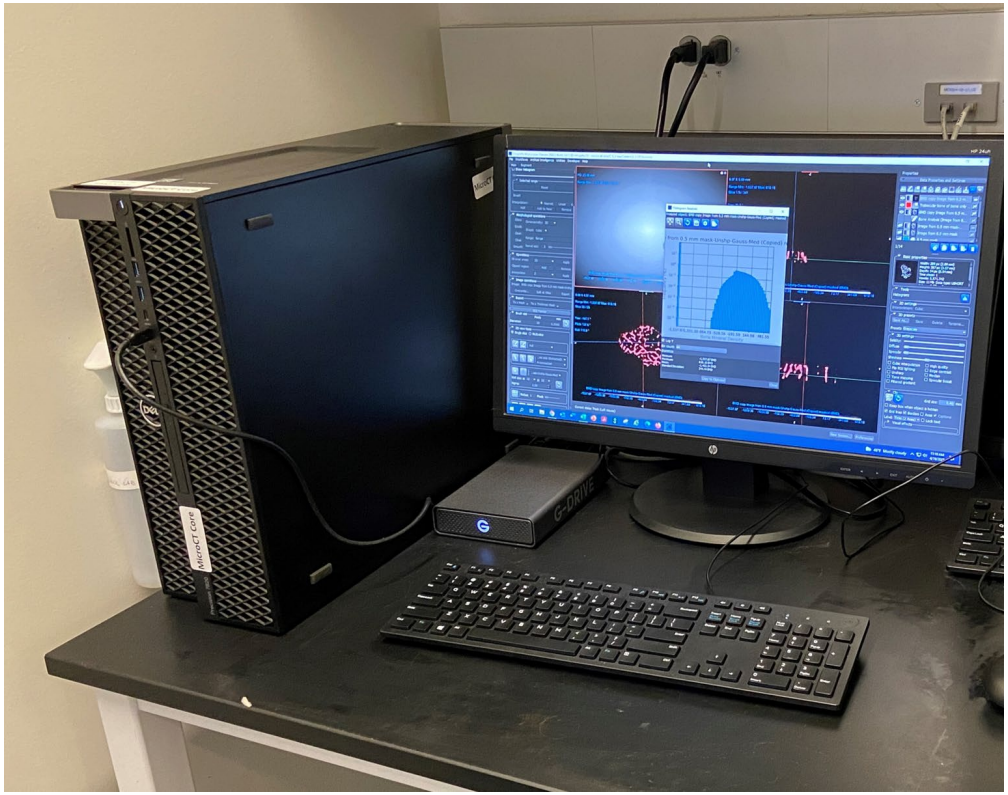
- Scanco vivaCT 80 (Purchased in 2018)
  - Voxel sizes: 10.4 µm, 11.6 µm, 13 µm, 16.1 µm, 20.8 µm, 26 µm
  - Internal heating device to keep animal warm
  - Internal camera to monitor animal's breathing
  - Ex vivo scan for specimen from large animals or human cadaver

MicroCT Analysis PC

- 2 PCs for MicroCT Analysis (315 Stemmler)
  - Windows 10 platform
  - Either remote or onsite access
  - Scanco software

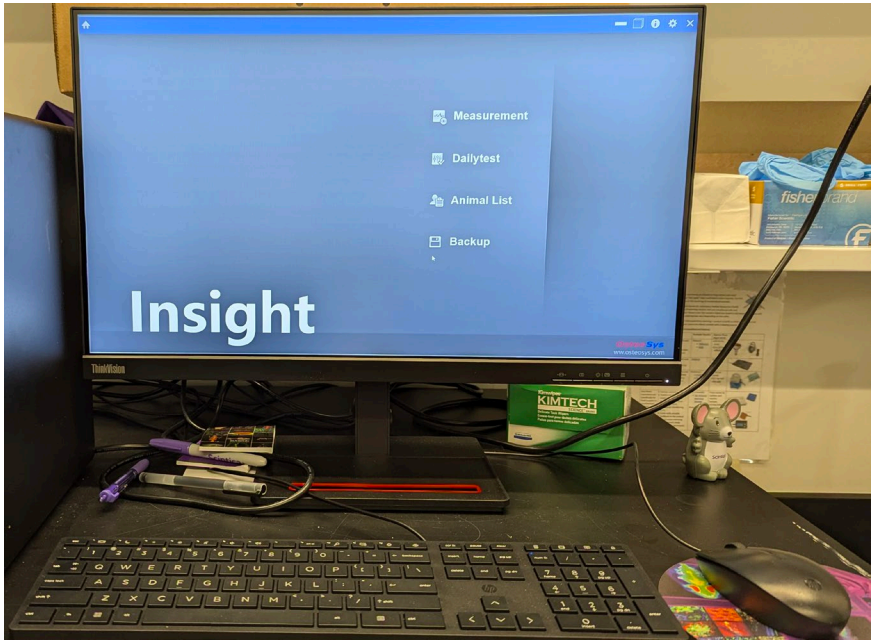
Dragonfly Workstation

- Workstation for Dragonfly software (324 Stemmler)
  - Windows 10 platform
  - PMACS account required (either remote or onsite access)
  - Deep learning assisted analysis
  - Training videos https://www.theobjects.com/dragonfly/tutorials.html



Scintica Insight DXA

- DXA system (368B Stemmler)
  - Windows 10 platform
  - In vivo / Ex vivo 2D scan and analysis
  - 25 sec per scan
  - Video tutorial: https://www.youtube.com/watch?v=ZRWOm7NnK1g



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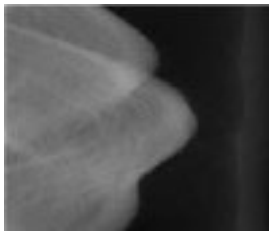
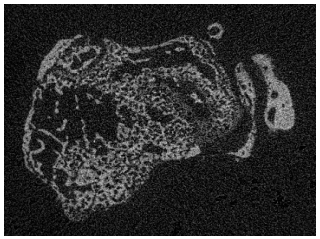
From Scan to Results

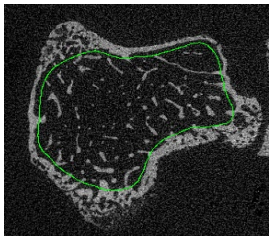
(Trabecular Morphometry, Midshaft Analysis)



Reconstruction



Contouring

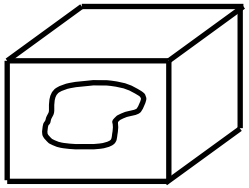


3D evaluation

.RSQ
RAW sequence data

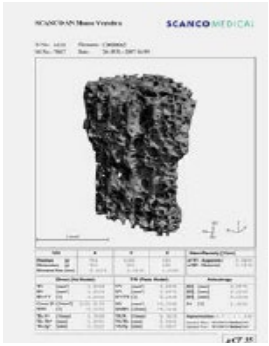
.ISQ
Image sequence data

.GOBJ
Graphical object



.AIM
White box
(gray scale)

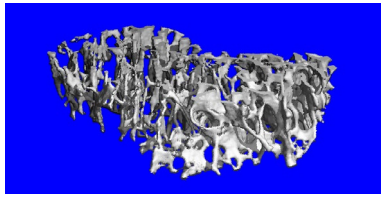
Thresholding (Gauss)



Final Results

- **Evaluation Sheet**
- **Trabecular Analysis**
  - **_TH.AIM**
  - **_SP.AIM**
  - **_TH.TXT**
  - **_SP.TXT**
- **Cortical Analysis**
  Midshaft Analysis
  - **_MOI_TXT**

Calculating Morphometry



_SEG.AIM
Segmented object
(binary file, black/white**)**

How to reduce evaluation time

- Server computational capacity
  - 5 evaluation tasks in parallel
- Pick a lower resolution
  - Mouse tibia/femur: 7.4 μm (ex vivo), 10 μm (in vivo)
  - Rat tibia/femur: 7.4 μm / 10 μm (ex vivo),
  - Full body skeleton: 50 – 100 μm
  - Imaging only (no quantification): 15 -
- Use a smaller VOI
  - Reduce the number of slices
  - Refine ROIs

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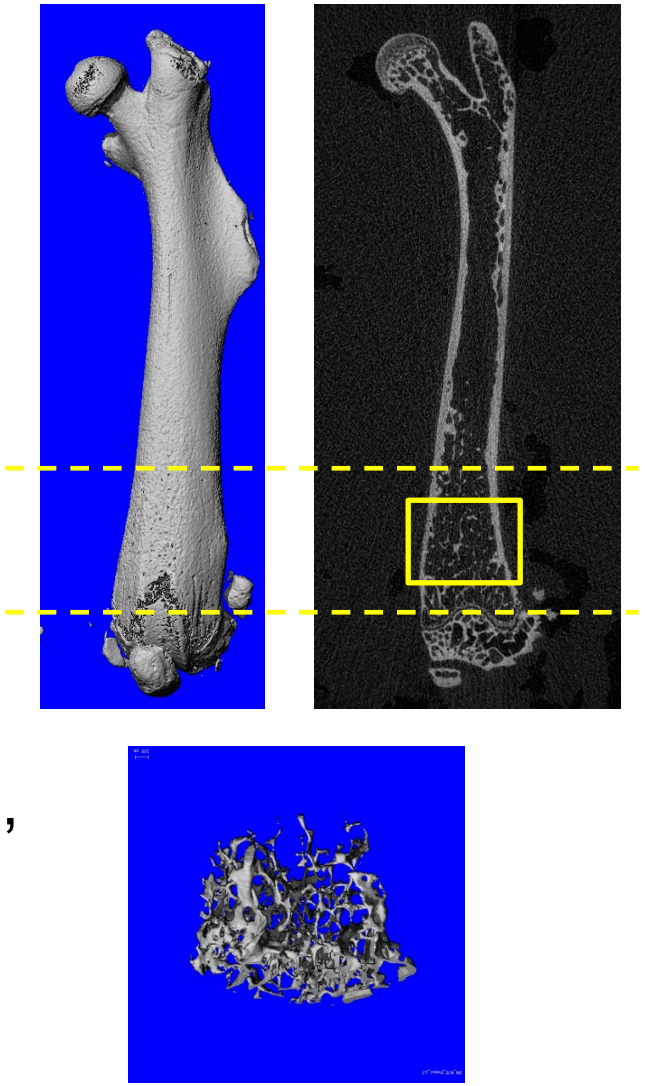
  - Imaging only (no quantification): 15 – 50 μm
- Use a smaller VOI
  - Reduce the number of slices
  - Refine ROIs

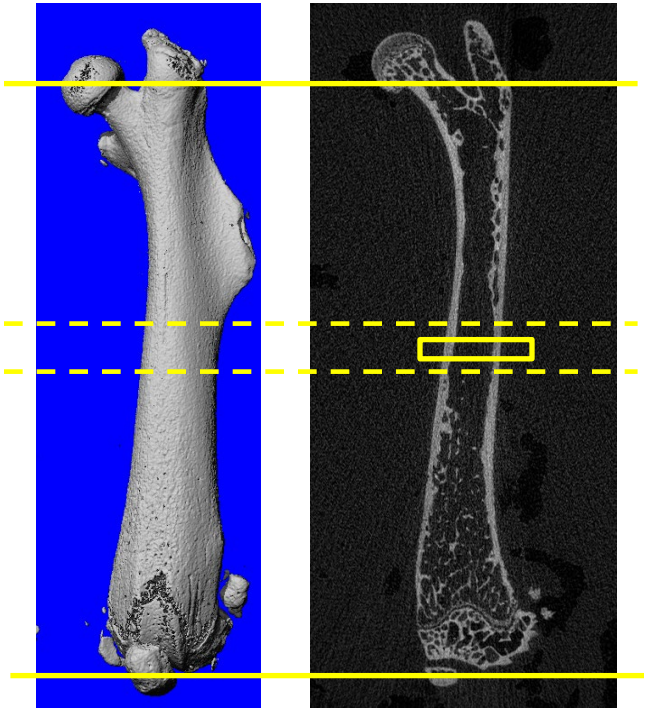
How to reduce evaluation time

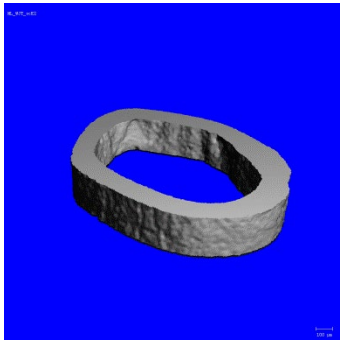
- Mouse trabecular bone analysis
  - Distal femur, proximal tibia
  - 6 μm isotropic voxel size
  - Scan Region
    - 1-2 stacks, ~210-420 slices
  - Average scan time: 24-48 mins
  - Analysis region
    - 100-200 slices, 0.5-1mm from the growth plate
  - Outcome measures: BV/TV, Tb.Th, Tb.N, Tb.Sp, SMI, Conn.D, BMD, TMD



How to reduce evaluation time

- Mouse cortical bone analysis
  - Midshaft of tibia or femur
  - 6-10 μm isotropic voxel size
  - Scan Region
    - 1 stack, ~210 slices
  - Average scan time: 24 mins
  - Analysis region
    - Middle 50 slices
  - Outcome measures: Ct.Area, Ct.Th, pMOI, Ct.Po, TMD



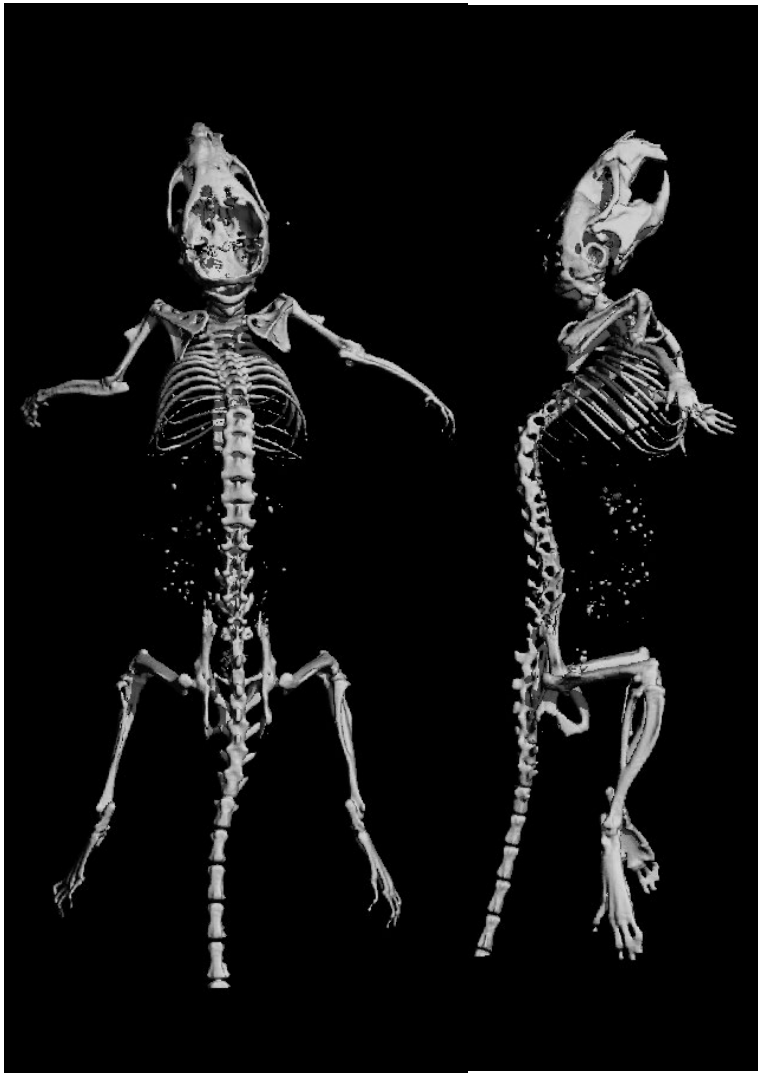


How to reduce evaluation time

- Mouse skeleton imaging
  - Scanner: microCT 45
  - 50 μm isotropic voxel size
  - Scan Region
    - 7-10 stacks, 1500 – 2000 slices
  - Average scan time: 120 mins

How to reduce evaluation time

- Rat skeleton imaging
  - Scanner: vivaCT 80
  - 100 μm isotropic voxel size
  - Scan Region
    - 12 – 13 stacks, 1000 – 1100 slices
  - Average scan time: 25 mins



What to do if an evaluation does not run through ?

- How to check if an evaluation task completes successfully
  - Google Spreadsheet
  - ‘Que’ command
  - Check txt / pdf file

```
$ que

QUEUE: SC2361_FAST
  324 EVAL_QC2_00000002_00024093 SC2361$DKC1:[MICROCT.SCRATCH]EVAL_QC2_00000002_
00024093.LOG;
1 job in SC2361_FAST
```

Evaluation Task

Sample Number

Measurement Number

What to do if an evaluation does not run through ?

(Trabecular Morphometry)

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Support Threshold	Unit	Data-Threshold
1.20	2	140

-Threshold	VOX-TV	VOX-BV	VOX-BV/TV	Conn
140		6	4587.000	

Conn-Dens.	TRI-SMI	DT-Tb.N	DT-Tb.Th
6.0222	0.0480		0.0080

TRI-SMI	DT-Tb.N	DT-Tb.Th	DT-Tb.Sp
0.0480	0.0080	-	-

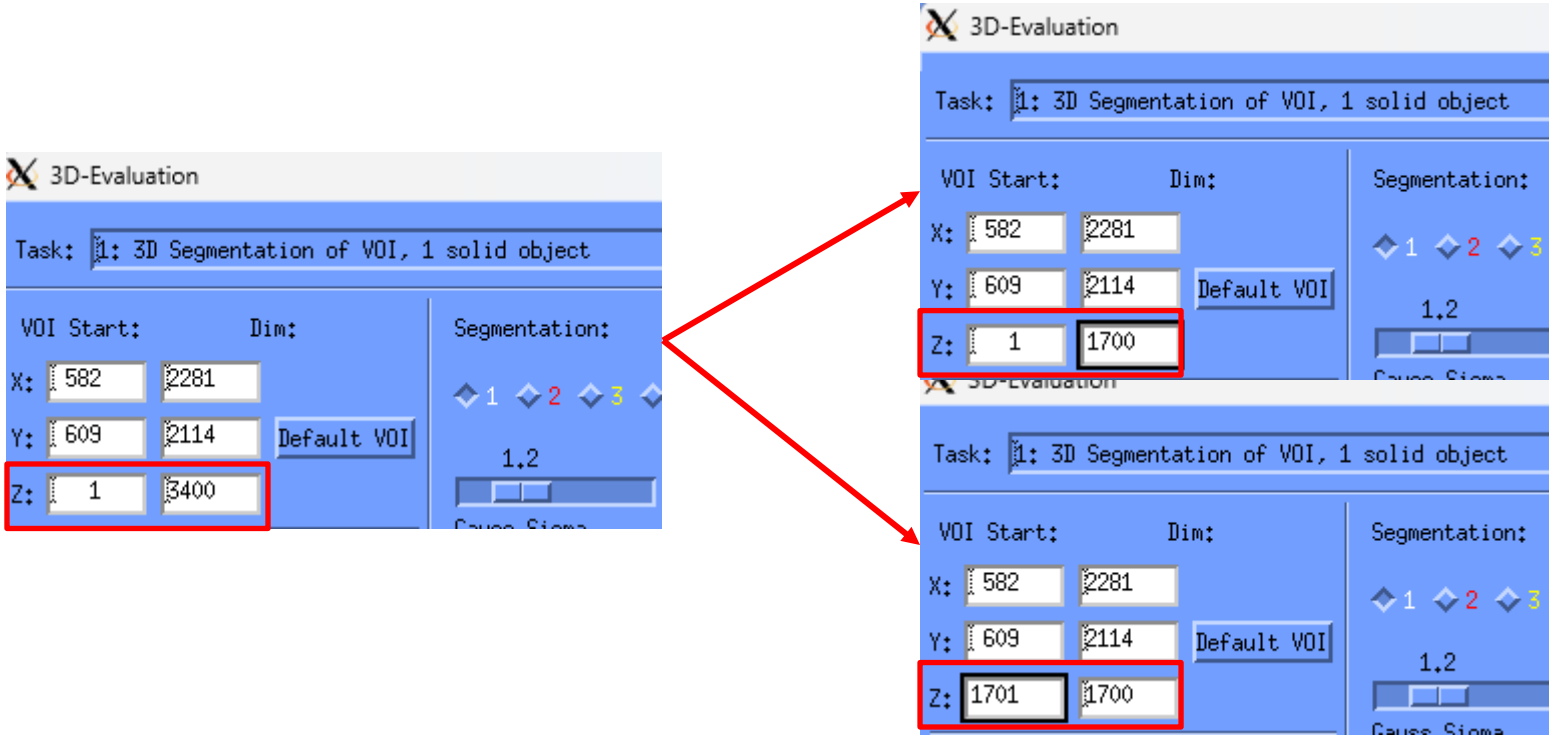
VOI	X	Y	Z	Mean/Density [mg HA/ccm]
Position [p]	1506	1029	704	of TV (Apparent) -24.4381
Dimension [p]	820	752	464	of BV (Material) 502.2062
Element Size [mm]	0.0030	0.0030	0.0030	

Direct (No Model)			TRI (Plate Model)			Anisotropy		
TV	[mm³]	6.0222	TV	[mm³]	–	|H1|	[mm]	–
BV	[mm³]	0.0480	BV	[mm³]	–	|H2|	[mm]	–
BV/TV	[1]	0.0080	BV/TV	[1]	–	|H3|	[mm]	–
Conn. D.	[1/mm³]	–	BS	[mm²]	–	DA	[1]	–
SMI	[1]	–	BS/BV	[1/mm]	–			
Tb.N*	[1/mm]	–	Tb.N	[1/mm]	–	Segmentation: 1.2 / 2 / 140		
Tb.Th*	[mm]	–	Tb.Th	[mm]	–	Operator Meas.: PCMD MicroCT Imaging		
Tb.Sp*	[mm]	–	Tb.Sp	[mm]	–	Operator Eval.:		

What to do if an evaluation does not run through ?

(Trabecular Morphometry)

- Task break up
  - Slice number < 3000
  - Statistics – combine the results by taking average
  - 3D image – align multiple images into a full view



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