<div align="center">16Second_Anatomical_Stitch Study</div>

GE Locus Ultra ("vct")

- **Login (Console)** uid:*vct*, pwd:*vct@pci*
- **Login (Application)** uid:*sysadmin*, pwd:*guest*
- Choose "*Scan*" **Mode** from LHS main screen menu
- Use **Study**: *16Second_Anatomical_Stitch_86mm_Table_Translation*
- Choose The **Protocol** you want to use (Must be selected before creating exam in the next step) (For now, choices are "16 second Anatomical" and "16 second 80kV")
- [FIX] Cradle choices
- **Create Exam** Named: *YYYYMMDD_MyObject*; click "*Create*" button
- **Landmark the object:**
  o Enter scanner room, mount pink, foam, custom designed bed (for 5-segment scans) on scanner table [FIX - DESCRIBE AND TAKE PICTURE OF POSITIONING]
  o Secure object on custom-designed bed using tape or velcro
  o Turn on alignment lasers - press "*Toggle Lasers*" soft key button on STC monitor (on the front face of the scanner)
  o Align internal laser marker with custom bed markers (between bed-edge slots outlined in black marker – as shown FIX TAKE PICTURE) using "*Fast Advance*", "*Advance Table*", "*Retract Table*", and "*Fast Retract*" soft kwy buttons on STC monitor
  o Set the "zero" scan position - press "*Set*" on the internal (or external) Landmarks soft key button on the STC monitor

- **Acquire Brightfield And Darkfield Images**
  o highlight desired scan sequence from the list of scan Names on main scanner console
  o click "*Execute*" (bottom right corner of main menu)
    ▪ "Scan" field in lower right corner must read "Bright Dark"
  o press "*Start Scan*" button on main console keyboard after it glows green
  o Wait for scan to complete (approx. 40 seconds)

- **Acquire Segment 1 Scan**
  o Highlight desired scan sequence
    ▪ eg. *free_16spr_100vpr_102mm_680rows, 80kVp, 50mA*
  o In the sequences table, ensure that the:
    ▪ "*Start*" field shows "0.0" and
    ▪ "Bright/Dark" field reads "Completed"
  o click "*Execute*" (bottom right corner of main menu)
    ▪ "Scan" field in lower right corner must read "Sequence"
  o press "*Start Scan*" button on main console keyboard after it glows green
  o Wait for scan to complete (approx. 90 seconds)
  o NB: Make note of Scan Series Number for all acquisitions

- **Acquire Segment 2 Scan**
  - Highlight desired scan sequence (in this case, the sam one)
    - eg. *free_16spr_100vpr_102mm_680rows, 80kVp, 50mA*
  - In the sequences table, change the "Start" field to "*-86.0*".
  - In the sequences table, ensure that the
    - "Start" field shows "-86.0" and
    - "Bright/Dark" says "Completed"
  - click "*Execute*" (bottom right corner of main menu)
    - "Scan" field in lower right corner must read "Sequence"
  - press "*Start Scan*" button on main console keyboard after it glows green
  - Wait for scan to complete (approx. 90 seconds)
  - NB: Make note of Scan Series Number for all acquisitions
  - Repeat for Segment 3 (or additional) Scans or Click "*Close Exam*" button

- **Acquire Segment 3 (or additional) Scan(s)**
  - Highlight desired scan sequence (in this case, the same one)
    - eg. *free_16spr_100vpr_102mm_680rows, 80kVp, 50mA*
  - In the sequences table, change the "Start" field to "-172.0".

    Uber-Geek Table Translation Notes:

    - *Segment 1 translation = 0.0 mm*
      Segment 2 translation = -86.0 mm
      Segment 3 translation = -172.1 mm
      Segment 4 translation = -258.1 mm
      Segment 5 translation = -344.1 mm
      Segment 6 translation = -516.1 mm
      Segment 7 translation = -602.2 mm (likely not possible)

    - *Useable axial FOV per acquisition volume (559 voxels)*
        = 559 voxels x 0.153884 mm/voxel
        = 86.02156 mm
    - *Table displacement for N^{th} scan is (N-1) x 86.02156 mm*
        - *Round to the nearest integer mm*
          Scanner does not support sub-mm bed translation
    - *Maximum landmark-able table travel is 531.8 mm*

  - In the sequences table, ensure that the
    - "Start" field shows "-172.0" and
    - "Bright/Dark" says "Completed"
  - click "*Execute*" (bottom right corner of main menu)
    - "Scan" field in lower right corner must read "Sequence"
  - press "*Start Scan*" button on main console keyboard after it glows green
  - Wait for scan to complete (approx. 90 seconds)
  - Click "*Close Exam*" button

Transfer Data for Offline Reconstruction and Post-Processing

- o Open a terminal on a UNIX/LINUX computer (likely one of: darkness, hampton or mingus)
- o Check for available space on a data drive (such as /darkness/data, /hampton/data, or /hampton/data2) using UNIX 'df' command
    - ▪ *df –k* or *df -h*
- o
- o Make appropriate directory tree under target directory (/darkness/data/vct, /hampton/data
- o Use secure copy 'scp' to copy all
    - ▪ Eg. *scp -r /vol/data/vct/4392[1-2] youruserID@hampton.imaging.robarts.ca:/hampton/data/vct/bio_ specimen/ morphology/moth/mothra/20110819/*
- o Delete data off of vct scanner only after the reconstruction and post-processing are complete

- **Offline Reconstruction & Volume Stitching**
    - o Run the recon and stitching script (both are integrated into the script) from the parent directory to where the scan series directories reside:
        - ▪ *cd /hampton/data/vct/bio_specimen/morphology/moth/mothra/20110819/* (you should see the acquired scan series number directories within this parent directory)
        - ▪ */mingus/data2/spollman/bin/proclog.vCT_Recon_Stitch_16sec.sh*
            - • bed translation distance is editable (TABLE_TRANSLATION_MM=86)
            - • reconstructed voxel spacing is editable (VOXEL_SPACING=0.153884)

POSSIBLY ADD TO SOP LATER

- choose protocols to add to study:
    - o 16 second Anatomical
    - o 16 second 80kv
- choose specimen:
    - o Stitch_Object