16Second_Anatomical_Stitch Study

GE Locus Ultra (“vct”)

- **Login** 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:**
  - Enter scanner room, mount pink, foam, custom designed bed (for 5-segment scans) on scanner table [FIX - DESCRIBE AND TAKE PICTURE OF POSITIONING]
  - Secure object on custom-designed bed using tape or velcro
  - Turn on alignment lasers - press “*Toggle Lasers*” soft key button on STC monitor (on the front face of the scanner)
  - 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
  - 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**
  - highlight desired scan sequence from the list of scan Names on main scanner console
  - click “*Execute*” (bottom right corner of main menu)
    - “Scan” field in lower right corner must read “Bright Dark”
  - press “*Start Scan*” button on main console keyboard after it glows green
  - Wait for scan to complete (approx. 40 seconds)

- **Acquire Segment 1 Scan**
  - Highlight desired scan sequence
    - eg. *free_16spr_100vpr_102mm_680rows, 80kVp, 50mA*
  - In the sequences table, ensure that the:
    - “*Start*” field shows “0.0” and
    - “Bright/Dark” field reads “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

- **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 no 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

  - Open a terminal on a UNIX/LINUX computer (likely one of: darkness, hampton or mingus)
  - 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*
  -
  - Make appropriate directory tree under target directory (/darkness/data/vct, /hampton/data
  - 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/*
  - Delete data off of vct scanner only after the reconstruction and post-processing are complete

- **Offline Reconstruction & Volume Stitching**
  - 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:
  - 16 second Anatomical
  - 16 second 80kv
- choose specimen:
  - Stitch_Object