PROCEDURE MANUAL FOR MROS

VISIT 4 HR-PQCT EXAMS:

CROSS-CALIBRATION PHANTOM ANALYSIS

UCSF

Protocol v0.1

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1   Introduction

The phantom imaging experiments for the UCSF Extremity Bone Structure Phantom result in long acquisitions of the four phantoms, each of which contain five individual bone sections. Analysis of those phantom measurements follows several main steps. First individual sample entries must be created in the database that correspond to the individual specimen sections. Second the four phantom measurements must be divided into individual sections and imported as unique measurements. Finally the post processing of the new measurements is performed that mimics the standard UPAT-style analysis. Each of these steps are described in the following sections.

2   Phantom Descriptions

2.1   UCSF Extremity Bone Structure (EBS) Phantoms

The EBS phantoms designed and manufactured by UCSF (Figure 2-3) consist of a series of polyethylene-resin cylinders with embedded human tibia and radius sections. The bone sections are approximately 1cm thick and were extracted at an anatomical site consistent with the standard XtremeCT clinical acquisition protocol (9.5mm and 22.5 mm proximal from the distal endplates for the radius and tibia respectively). The tissue was acquired from a non-profit, NIH-funded American tissue bank (NDRI). Each tissue specimen tested negative in serological screening for common blood-borne pathogens (HIV, Hepatitis, tuberculosis, etc). The specimens were fixed in 100% ethanol prior to embedment and therefore pose no biological risk.
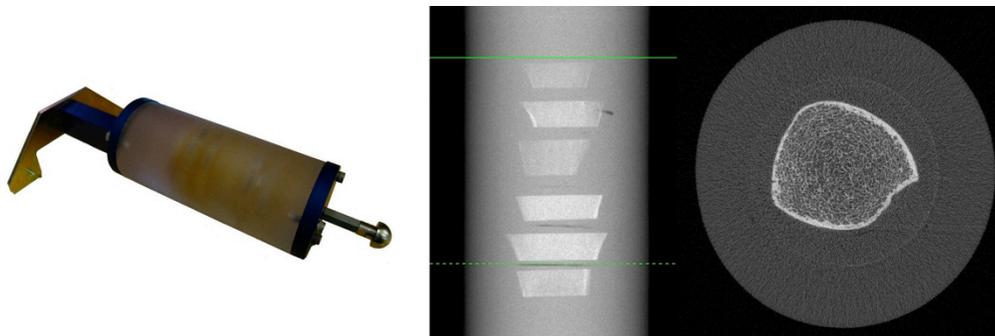

Figure 2-1: UCSF structure phantom for cross-calibration

3   Database setup

NOTE: The steps described in the grey-out Section 3 are only required the first time you are to import and process UCSF-EBS Phantom scans. For subsequent imaging and analysis of the phantom measurements, you will simply use the existing database entries created in this section and recorded in the appendix (and elsewhere presumably), proceeding directions to Section 4.

3.1   Create Database Entries

The first step of the process is to create new sample entries in the database that correspond to the individual sections of bone in the phantoms, for each clinical site. Each phantom serial number was previously used for the Sample Name when scanning the four phantoms (i.e. "UCSF-SP-02", "UCSF-SP-03", etc.). We will use this serial ID and add a two-digit number corresponding to the individual bone section within each phantom, such that the section at the beginning of the volume is 01 and the section at the bottom is 05. In addition the two character clinical center code will be appended (i.e. "UCSF-SP-02.03-BI"):

3.1.1   Create a new sample

Create new sample names/numbers for importing the individual sections from each of the four UCSF EBS phantoms. Complete the subject biographical information according to the procedures below:

- In the patient registration program of the XtremeCT scanner (see XtremeCT User's Guide, page 8 in "**Name**" field), enter the following, for Birmingham:

> Name: **UCSF-SP-02.01-BI**

- In the "**Date of Birth**" field, enter the first scan date of the phantom scan in the date formats supported by your scanner such as: **DD-MMM-YYYY**
  Here is an example of how the Date of Birth field may appear:

> Date of Birth: **01-MAR-2009**

- The "**Remarks**" field is not used for the study; you may enter any information for your own purpose.

- In the Samples window click "Save" to finalize the entry and then "New" to initiate a new entry

- Record the **Sample Number** in table A.1 of Appendix A

- Repeat this step for each phantom and each clinical center, using the appropriate coding:

Site	Center Code
Birmingham	BI
Minneapolis	MN
Palo Alto	PA
Pittsburgh	PI
Portland	PO
San Diego	SD

3.1.2   Alternative command-line steps to Create sample entries

The following steps are intended as an ***alternative to section 2.2.1*** to create the necessary entries in the database for the individual bone sections of the UCSF-EBS phantom. This procedure may not work if you do not have the program UT:UCT_DEFINE_SAMPLES.EXE available on your system:

```
$ run ut:uct_define_samples

Use '\' + any # of 'x' to be replaced by continuous numbers
e.g.:  Sample Test \xxx Study A
 or:  A\xxxxxxx
inline format: new_sample "Test \xxx Study A" 23 2
 where 2nd arg = start-no, 3rd arg = count
 creates Test 023 Study A
      Test 024 Study A
      Test 025 Study A

Sample Name (use any 'x' for Nr) []: UCSF-SP-02.\xx-BI
Number to start with [0]: 1
# of DB entries to create [0]: 5
UCSF-SP-02.01
UCSF-SP-02.02
UCSF-SP-02.03
UCSF-SP-02.04
UCSF-SP-02.05
Update DB [Y]: Y
.
$
```

- Record the **Sample Numbers** created in table A.1 of Appendix A

NOTE: Section 3.1.2 is an ALTERNATIVE to section 3.1.1. You do not, and should not, perform both sections, but decide which approach you are most comfortable with to create the necessary Sample entries in the database.

NOTE: Per the "Sample Name" specification entered above, this example creates five entries for Phantom UCSF-SP-02 for Birmingham.

3.1.3   Repeat for each individual section

Section 3.1.1 (or the alternative 3.1.2 should be repeated to create five individual Sample entries for each of the four phantoms, and then again for each clinical center. For example, Birmingham's set of entries would be:

- UCSF-SP-02.01-BI, UCSF-SP-02.02-BI, … UCSF-SP-02.05-BI

- UCSF-SP-03.01-BI, UCSF-SP-03.02-BI, … UCSF-SP-03.05-BI

- UCSF-SP-04.01-BI, UCSF-SP-04.02-BI, … UCSF-SP-04.05-BI

- UCSF-SP-05.01-BI, UCSF-SP-05.02-BI, … UCSF-SP-05.05-BI

4   Import New Measurements

In the following step a script will be customized to import the new measurements into the Sample entries created in Section 3. First this involves modifying the import script, then visually determining and recording the slice immediately before the first section of bone is seen for each of the four phantoms. Next, the import script is executed for each of the phantom measurements.

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4.1   Import Script

The import script UT:UCSF_SP_IMPORT.COM contains a number of hard coded parameters that must be customized for your local system:

4.1.1   Sample numbers

Most import, you must enter the Patient/Sample Number for the individual bone sections that were created in Section 3.1.1 to 3.1.3:

```
$! ------------------------------
$! Local Customization
$! ------------------------------
$!
$! Change to local Sample Nos. created for the individual sections
$!
$!SP-02
$ SAMPNO_0201 = 1189
$ SAMPNO_0202 = 1192
$ SAMPNO_0203 = 1193
$ SAMPNO_0204 = 1194
$ SAMPNO_0205 = 1195
  .
  .
  .
```

- In the example above Sample Number 1189 corresponds to UCSF-SP-02.01, 1192 to UCSF-SP-02.02, etc
- Complete the sections for SP-2 through SP-05

4.1.2   Queue and script location

It is also necessary to customize the batch queue used to run the import script. This should be done on a single dedicated queue, not a Generic Queue (i.e. not SYS$FAST) so that the measurements are imported in a linear fashion:

```
$! Batch queue submit command – CHANGE AS APPROPRIATE
$!   NOTE: SUGGEST NOT A GENERIC QUEUE SO IMPORTING IS LINEAR
$!
$ SUBMIT_QUEUE := SC3314_FAST
$ QQ = "SUBMIT/NOPRINT/QUE=''SUBMIT_QUEUE'/NOTIFY
UT:IPL_UCSF_SP_IMPORT.COM"
  .
  .
  .
```

- In the example above I use the FAST queue on the SC3314 node (selected because our RAID controller is on this host, so presumably will have faster i/o
- If the IPL script that performs the import was installed somewhere other than in UT:, then change that here

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4.1.3   Log files

By default the log of the import job is written to SYS$SCRATCH:. If you prefer it to go to a custom location, edit that here:

```
$!
$! Directory configuration – CHANGE AS NEEDED
$!
$ LOGDIR := SYS$SCRATCH:
.
.
.
```

- In the example above I use the FAST queue on the SC3314 node (selected because our RAID controller is on this host, so presumably will have faster i/o

- If the IPL script that performs the import was installed somewhere other than in UT:, then change that here

4.1.4   Final notes on the import script configuration

- Below the logdir configuration line, there are a number of hard coded values for the dimensions and relative positions of each section of bone. These should NOT be changed unless you are absolutely sure they need to be in order for the images to be extracted correctly. An example situation would be for a different resolution acquisition (the values are all hardcoded in slices, not absolute distances)

- The script relies on the fact that the original full phantom measurements (i.e. scan for UCSF-SP-02) used the recommended Patient/Sample Name scheme described in the phantom measurement protocol. Specifically the script searches the Patient Name field from the ISQ header for a string matching UCSF-SP-?? in order to identify the specific phantom so that the correct sample numbers and slice positions are used for import. If a different naming convention (and any slight variation (underscore instead of hyphen) was used, the following string search call would need to be modified according to your naming scheme:

```
$    UCSF_SP_ID = F$EXTRACT(F$LOCATE("UCSF-SP-",line_sym)+8,2,line_sym)
```

- A useful tip to verify the customizations are set correctly is to execute the script with all but the final import being executed. To do this comment out the final line in the IPL script (UT:IPL_UCSF_SP_IMPORT.COM) which executes the import task:

```
$! Comment out following line to not execute the import (For testing)
$! @'DEV''DIR''FILENAME'_IMPORT_'SAMPNO'.COM
```

4.2   Slice location

Unfortunately, due to small differences in scanner alignment and geometric calibration, it is difficult to predict the exact slice location of each bone section. Therefore each section is imported with some slice padding on either side to ensure the entire section is included. However, the import task only requires identification of the first slice of the first section

- In XImage or the Evaluation program, open the ISQ/Measurement corresponding to the full phantom scan to be imported (i.e. start with UCSF-SP-02)
- Locate the last slice from the beginning with a no visible partial volume from bone apparent
   - record the zero-based number (so one less than the slice number reported in the GUI).
   - typically this is somewhere around slice 20-40 or so
   - if you use the Eval program and you have the LUT set to scale each slice independently, the correct slice should appear much brighter once bone partial volume is no longer present (unless some artifactual values obscure this)
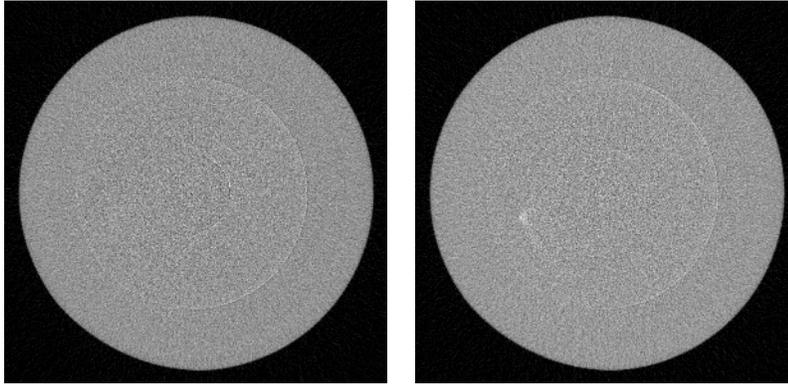

Figure 4-1: Phantom slice with no partial volume (left) and very minimal partial volume (right).

- Repeat this process for *each* of the four full phantom scans (UCSF-SP-02 to UCSF-SP-05)

4.3   Execute

Executing the import job is straightforward and requires two input parameters: The full filename specification of the ISQ file to be processed, and the corresponding, zero-based slice identified in section 4.2:

```
$ @UT:UCSF_SP_IMPORT <ISQ_FILE> <START_SLICE>
```

- This assumes that the import batch script was installed in UT:
- An example of this appears below for an ISQ corresponding to a scan of the UCSF-SP-02 phantom:

```
$ @UCSF_SP_IMPORT DK0:[MICROCT.DATA.00001185.00007311]C0006646.ISQ 21


Found: UCSF-SP-02


# ----------------------------------------------
# Initiating Import Processing for: UCSF_SP_02
# ----------------------------------------------

Job IPL_UCSF_SP_IMPORT (queue SC3314_FAST, entry 884) started on
SC3314_FAST
Job IPL_UCSF_SP_IMPORT (queue SC3314_FAST, entry 885) pending
     pending status caused by queue busy state
Job IPL_UCSF_SP_IMPORT (queue SC3314_FAST, entry 886) pending
     pending status caused by queue busy state
Job IPL_UCSF_SP_IMPORT (queue SC3314_FAST, entry 887) pending
     pending status caused by queue busy state
Job IPL_UCSF_SP_IMPORT (queue SC3314_FAST, entry 888) pending
     pending status caused by queue busy state
$
```

- Repeat this process for *each* of the four full phantom scans (UCSF-SP-02 to UCSF-SP-05)
- **NOTE:** The import process will create a new ISQ file for each corresponding subvolume. The filename convention used adapts the original full phantom scan filename, replacing the leading "C" with a "S" (indicating a "subvolume") and replaces the first digit of the 7-digit serial with a number (1-5) corresponding to the specific bone section. The remaining 6 digits of the original serial are retained. For example, the full phantom measurement in the example above has an ISQ file C0006646.ISQ. The corresponding bone section measurements imported from this scan would be S1006646.ISQ (UCSF-SP-02.01), S2006646.ISQ (UCSF-SP-02.02), and so on, through to S5006646.ISQ (UCSF-SP-02.05).

5 Image Analysis

In the final step the newly imported images will be processed to calculate bone density and structure measures analogous to those calculated using the standard patient analysis. An important difference between the automated processing here and the standard patient analysis is that automatic periosteal contours are used for the analysis, rather than relying on the operator-driven manual contouring process. This helps automate the procedure and minimizes operator variability from the cross-calibration experiment.

5.1 Slice Range Identification

As mentioned in section 4.2, each measurement is imported with some slice padding on either side to ensure the entire section is included. However, for the analysis we only want to process slices with complete axial cross-sections through bone:

- Open each newly created measurement in the evaluation program
- Locate the first slice with a complete axial cross section of bone with no partial voluming (Figure 5-1)
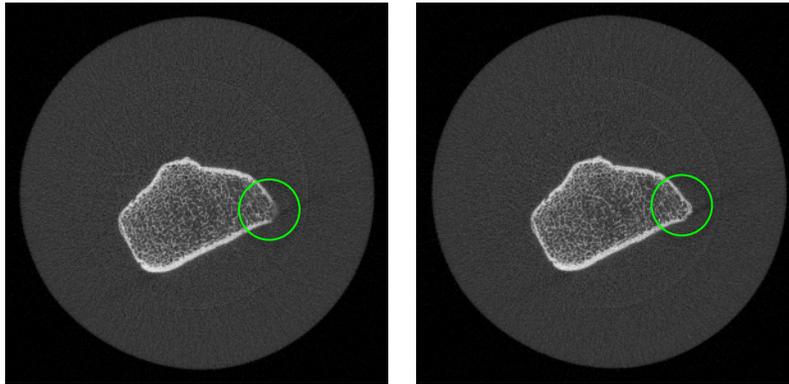
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Figure 5-1: Phantom slice still with some residual partial volume on the right corner due to the section boundary (left) and complete cross-section evident by full brightness in the cortex in the bottom corner (right)

5.2   Evaluation

All segmentation and measurements are performed through a custom evaluation script (UE:IPLV6_UCSF_SP_UPAT.COM). If this isn't installed, the analysis obviously will not work:

- With the measurement open in the eval tool, browse to Tasks> Evaluation 3D

- Select the task "Auto UPAT for UCSF EBS Phantom" which should be installed

- In VOI Start Z. enter the start slice identified in section 5.1 that contains the first complete cross section of bone

- For Dimension Z enter the value for DIM.Z in Appendix A, corresponding to phantom section of interest (e.g. UCSF-SP-02.01)

- Verify that the final slice covered by the white box contains no partial volume. If it does, adjust the start and dim accordingly (ideally this shouldn't be necessary)

- With the mouse adjust the X and Y dimensions of the white ROI box such that there it contains the entire bone, but is maybe 10-20 pixels from the bone edge (see Figure 5-2)
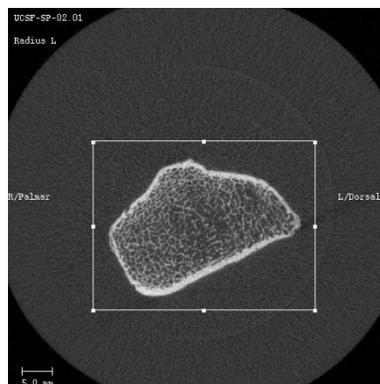
- Click "Start Evaluation" button.

Figure 5-2: Approximate positioning of the white ROI box for analysis. The bone should be entirely within, with some padding on all sides

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5.3   Extract Evaluation Results

Once the evaluation jobs have finished processing, the results can be extracted from the database. At a DEC terminal prompt, type "upat_list" to extract data from the patient database. Below is a sample terminal window with the parameters used. Several import points must be considered:

- It is recommended to extract data *without* slice-matching

- Replace the sample number passed to the "-b" flag with the sample number in your local database corresponding to UCSF-SP-02.01 and the "-e" flag with the sample number in your local database corresponding to UCSF-SP-05.05 (i.e. the first and last sample numbers for the phantoms sections):

```
$ upat_list –list –b=1189 –e=1216 –nomatch –
o=sys$scratch:eval_ucsf_ebs_upat.txt

Program: upat_print_list V1.9
Started: 27–MAR–2013 19:36:56.15

Written output file: sys$scratch:eval_ucsf_ebs_upat.txt
$
```

Appendix A

A.1: Bone Section Dimensions and Sample Numbers, by MrOS site

ID	DIM.Z	SC3412 (PA)	SC3413 (MN)	SC3414 (PI)	SC3415 (PO)	SC3416 (BI)
UCSF-SP-02.01	81					
UCSF-SP-02.02	81					
UCSF-SP-02.03	102					
UCSF-SP-02.04	90					
UCSF-SP-02.05	97					
UCSF-SP-03.01	100					
UCSF-SP-03.02	97					
UCSF-SP-03.03	122					
UCSF-SP-03.04	111					
UCSF-SP-03.05	79					
UCSF-SP-04.01	98					
UCSF-SP-04.02	100					
UCSF-SP-04.03	100					
UCSF-SP-04.04	136					
UCSF-SP-04.05	104					
UCSF-SP-05.01	107					
UCSF-SP-05.02	108					
UCSF-SP-05.03	112					
UCSF-SP-05.04	92					
UCSF-SP-05.05	104					