

CT ANALYSIS PROCEDURES FOR HABC SPINAL BMD MEASUREMENTS

Prepared by:

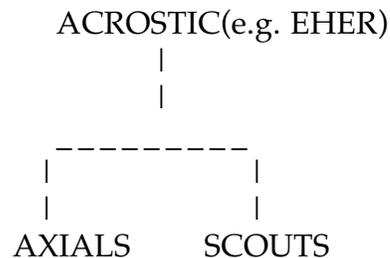
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I. Receipt of Data and Transfer to Workstation for BMD Analysis

Spinal CT images (see U of Colorado Operations Manual for acquisition procedures) are acquired at the Pittsburgh Computerized Tomography Center and are archived along with the soft tissue images obtained for the main arm of the HABC study. The archive medium is 9-track GE-9800 CT tape. The tapes, along with the patient logsheets giving the acrostic and ID number of the patient, are sent to the University of Colorado Health Sciences Center for soft-tissue analysis. The Pittsburgh images are then loaded on to a GE-Advantage MR Workstation for subsequent transfer to another computer for soft-tissue analysis. Once they are loaded on the Advantage Workstation, the images are archived onto 4-mm DAT tapes, which are sent along with photocopies of the corresponding worksheets to Thomas Lang, PhD at UCSF.

Data are then transferred from DAT using a script which rewinds the DAT tape, and copies all of the files to an optical disk. Another script then reads these files, determines the Patient Name acrostic, and creates a directory structure on the optical disk as follows:



If an image from a given patient is a CT slice, it is copied into the AXIALS subdirectory; if it is a scoutview, it is copied into SCOUTS.

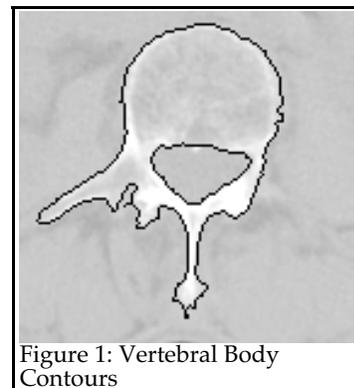
Data are transferred to UCSF every week.

II. Analysis of Images and Archival of Results

Images are analyzed using the AVS (Advanced Visualization Systems, Waltham, MA) image processing environment run on a network of Sun Sparcstations.

The image analysis program has three phases.

1. Contouring of the vertebra: The contours of the vertebral body are derived using an automatic threshold-driven contouring algorithm operated at a threshold of 126 hounsfield units. Two contours are derived: the external contour and the spinal canal. Vertebral BMD is computed for those



pixels inside the vertebral contour, but outside that of the spinal canal (See Figure 1). The program is activating by clicking a cursor next to the vertebral body. Any errors in the automatically-derived contour are corrected using an interactive editing procedure.

2. Determination of principal axis of the vertebral body: A cross-hair is centered at the anterior edge of the spinal canal as shown in Figure 2. The long axis of the cross-hair is angled so as to bisect the area of the vertebral body. This information on the orientation of the vertebral body is used to guide the program which determines regions of interest for BMD computations.

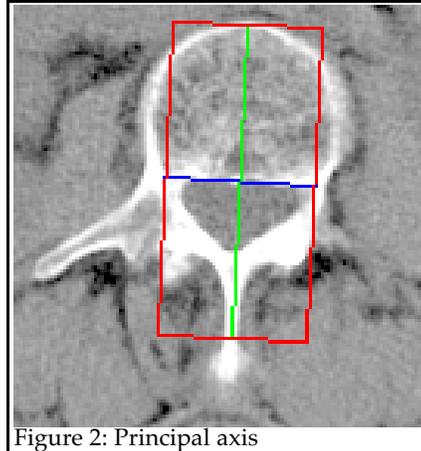


Figure 2: Principal axis

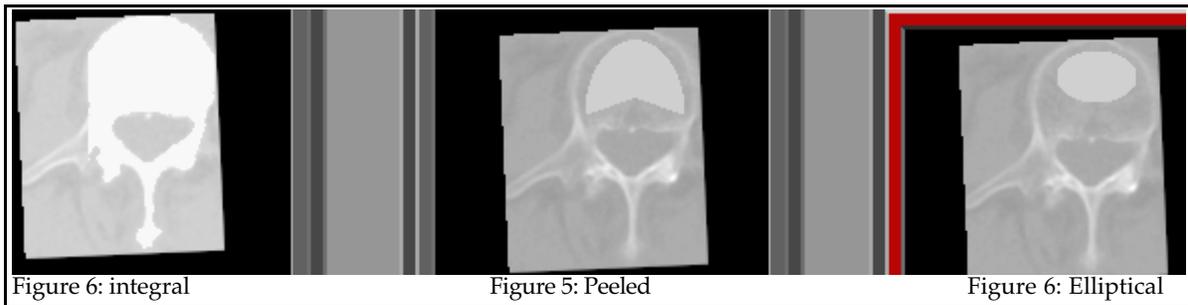
3. Calibration: The user marks the three calibration objects in the Image Analysis hydroxyapatite (HA) calibration phantom, as indicated in Figure 3. The program places circular regions of interest in the three objects (200, 100 and 50 mg/cc known HA densities), and a fourth region in the background material (0mg/cc). The measured CT numbers are then linearly regressed against the known HA densities; the resulting calibration equation is used to convert the measured CT numbers in the vertebral regions to HA equivalent densities.



Figure 3: Calibration regions of interest

4. Vertebral ROI analysis. The vertebral ROI program searches along the anteroposterior axis defined in step 2. Two landmarks are located on this axis: The anterior edge of the vertebral body and the anterior edge of the spinal canal. Utilizing these two landmarks: regions of interest are determined based on the definitions of Steiger et al [Steiger, 1987 #1126]. These regions of interest are shown below in Figures 4-6. The elliptical and peeled regions are measures of trabecular BMD; the integral region also contains the cortical

component associated with the cortical rim of the vertebral body and the posterior elements.



5. Archival of results: The patient information section of the program is shown in Figure 7. The patient acrostic and ID are extracted from the image header. After carrying out the image analysis and determining that the regions of interest are appropriately placed as shown in Figures 4-6, the operator enters information in each of three type-in boxes. After entering the information, the SAVE_RESULTS button adds the patient information and density results as a new line in the specified database file.

DBfile	
Dir : /home/thomas	
File: .../thomas/HABC_SPINE2	
../ (home) Body_Comp Calibration_Results Cortical_Thickness	
<input type="button" value="New Dir"/> <input type="button" value="New File"/>	
Patient Name	AFLC
Patient ID	HB5014
QC_code	000
Clinical_Abnormalities	001
ANALYSIS_ID	TFL
<input type="button" value="save_results"/>	

Figure 7: Patient information

QC_CODE: Problems related to imaging

- 000: No problems
- 001: Image artifact (primarily striping through phantom)
- 002: Phantom mispositioned (off center of patient axis)
- 003: Patient mispositioned (patient is rotated)
- 004: Gap between bolus bag and patient
- 005: Patient has severe bowel gas.
- 006: Other

CLINICAL_ABNORMALITY: Problems related to patient vertebral anatomy

- 000: No problems
- 001: Mild osteophyte
- 002: Moderate to severe OA
- 003: Hemangioma
- 004: Other

ANALYSIS: Initials of operator running program.

6. Database structure and transfer to Central Coordinating site: The database consists of the following measures:

NAME:	patient name acoustic
ID:	eg HB5032
ACQ_DATE:	Date of acquisition-note this comes out to be <u>1 day behind</u> true acquisition date
OPERATOR:	Pittsburg CT tech code, B26 or B27
ANALYSIS:	Initials of UCSF image analysis operator
ANALYSIS DATE:	This date is correct.
LEVEL:	Assumed to be L3 unless otherwise noted
QC CODE:	As shown in section 5
CLINICAL CODE	As shown in section 5 (clinical abnormality)
ELLIPSE BMD:	mean BMD mg/cc HA in ellipse region (Figure 3)
ELLIPSE SD:	standard deviation of mean BMD in ellipse region
ELLIPSE VOL:	volume in cc of ellipse region
TRAB2D BMD:	mean BMD mg/cc HA in peeled region (Figure 4)
TRAB2D SD:	standard deviation of mean BMD in peeled region
TRAB2D VOL:	volume in cc of peeled region
INTGL_2D BMD:	mean BMD mg/cc HA in integral region (Figure 5)
INTGL_2D SD:	standard deviation of mean BMD in integral region
INTGL_2D VOL:	volume in cc of integral region
ELLIPSE_HU:	mean CT number of ellipse region
ELLIPSE_HU_SD	standard deviation of above
TRAB2D_HU:	mean CT number of peeled region
TRAB2D_HU_SD	standard deviation of above
INTGL_2D_HU:	mean CT number of integral region
ELLIPSE_HU_SD	standard deviation of above
SLOPE:	slope of calibration equation
INCPT:	intercept of calibration equation
SEE:	RMS error of calibration line (mg/cc)
PIXEL_SIZE:	size of reconstructed pixel (mm)
XFOV:	Diameter of field of view (mm)
YFOV:	Always same as XFOV
GANTRY_ANG:	gantry angle (deg) required to correct for L3 lordosis

SLI_THI: Thickness of slice: should always be 10-mm
KVP: should always be 80 kilovolts
MA: should always be 70 mA
EXP_TIME: exposure time should always be 2 seconds.

The rows of the database are for each patient and are delineated by new lines. Fields are separated by commas. The database is sent electronically to the Coordinating Center in a text format. The title of each transmission is:

ctmmdyy.txt. For a file shipped on June 23, 1997, the title would be:
ct062397.txt

7. Severe clinical abnormalities: If an abnormality possibly affecting the health of the patient is detected, a radiologist is asked to review the image, and a brief report is issued. This report is sent to the Coordinating Center (Nevitt) for transmission to the clinical recruitment site.