Integrated Processing System for *In Vivo* MR Images of Trabecular Bone Networks

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Introduction

The standard method for evaluating structural implications of bone diseases such as renal osteodystrophy, hyperparathyroidism and osteomalacia, is histomorphometry based on the iliac crest bone biopsy (1). During recent years progress in peripheral computed tomography (2) and MR imaging technology (3) have made possible the noninvasive structural analysis of trabecular bone by means of image processing (4). Limited spatial resolution, subject motion and SNR, however, pose significant challenges and require a number of image restoration and processing steps. Here, we report on a distributed processing system that allows analysis of these images with minimal user intervention.

Methods

The cascade of processing steps follows the transfer of the complex k-space and navigator data from the scanner (General Electric Signa Echospeed™) utilizing file transfer protocol (FTP). Step 1 comprises navigator correction and Fourier reconstruction of the 3D spin-echo images (5). In step 2 noiseless bone volume fraction (BVF) maps are generated by means of a histogram deconvolution method (6). BVF is obtained by computing an average over the VOI or different subregions. In step 3 the images are resolution-enhanced using a method termed "subvoxel processing" (7). At this stage images of 69x69x87 micron^3 voxel size are ready for structural analysis and the processed data files can reach up to 20 Mbytes in size. To accommodate the se large file sizes the system incorporates file compression, large-capacity hard disks, and CD recorders for archival. In step 4 all voxels of the subvoxel-processed BVF maps are binarized, skeletonized and topologically classified. This operation determines the voxel's local topological class (8) (e.g. surface, curve, junction, etc.) as a means to quantitatively characterize the trabecular network. Finally, a projection image from an automatically selected cylindrical region ("virtual bone biopsy") is created to provide a qualitative visual impression of trabecular network integrity.

System control and interface has been written in IDL (Research Systems, Inc. Boulder CO, USA), but the actual processing is distributed between the IDL system, command-line programs, and a Unix-based processing subsystem accessed through FTP and telnet connections. This system allows integration of algorithms from multiple investigators working in different environments and facilitates addition of new analysis techniques in the future. The results are compiled into a Microsoft Excel spreadsheet and transferred automatically to a Microsoft Word document for display and printing. The entire system is designed for high throughput by distributing the workload among multiple computers (PC, Mac, or Unix) on a network and consolidating the spreadsheet results on a single machine, enabling the large scale processing needed for epidemiological studies and clinical trials. The final output of the system is a 2-page clinical report that provides a qualitative and quantitative summary of the subject's bone quality.

Results and Conclusion

The images of Fig. 1 show the progression of a typical scan from the raw data through the various stages of processing and analysis. The total time for analysis was 150 minutes for the radius and 420 minutes for the tibia on a 400 MHz Intel Pentium II based computer with 320 MB of RAM. The longer processing time for the tibia was due to the more complex processing of the phased array surface coil data, which was motion corrected and reconstructed separately for each coil element and then combined (root mean square method), doubling the time needed for a volume coil. Finally, the marrow region of the tibia is 50-100% larger than for the radius.

Based on the initial experience from processing 12 scans each from the distal radius and distal tibia, the system is easy to use and requires little operator intervention. The only manual processes in the system are delineation of the marrow and background regions needed for the deconvolution process, taking about 5 minutes. The processing time for the remaining automated operations is expected to decrease linearly with processor speed, for example to 30 and 84 minutes in the radius and tibia, respectively, on a dual 1 GHz Pentium III processor computer.

Future expansions of the system include automatic trabecular orientation analysis, automatic cortical thickness analysis, and a more automated user-guided VOI delineation. Reproducibility per FDA guidelines is preserved by archiving the data and individual programs, enabling manual reproduction of the analysis at any time without reproducing the complete system.

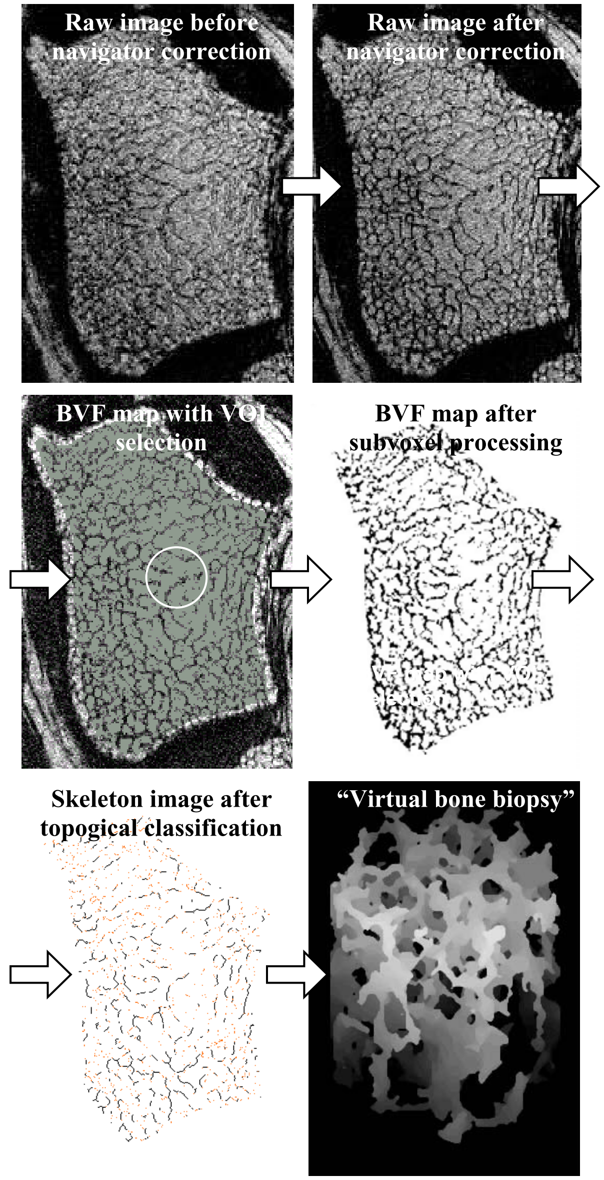

Figure 1: Stages of processing and analysis of the trabecular bone images.

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