Software tools for MR and pQCT bone quantification

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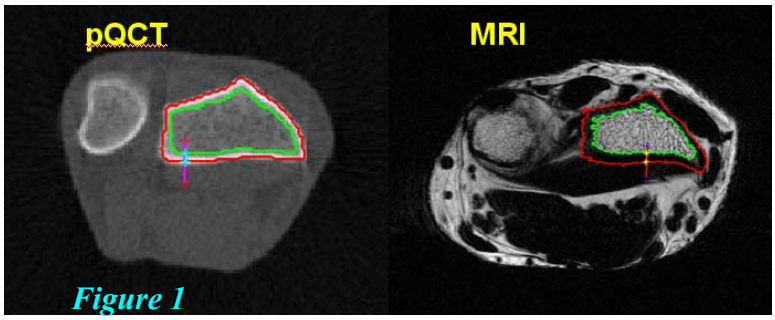
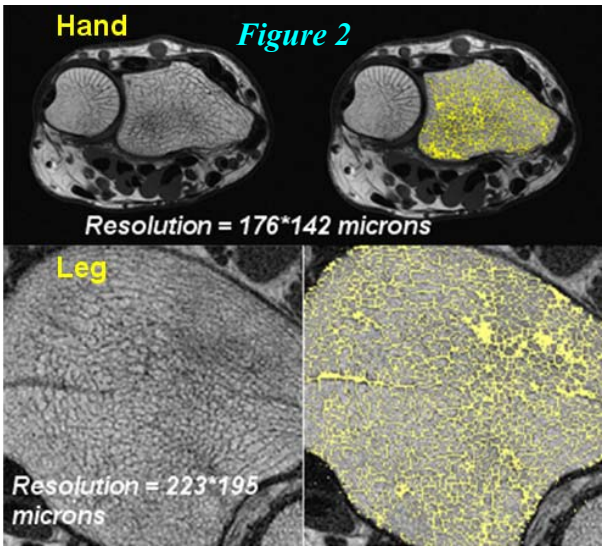
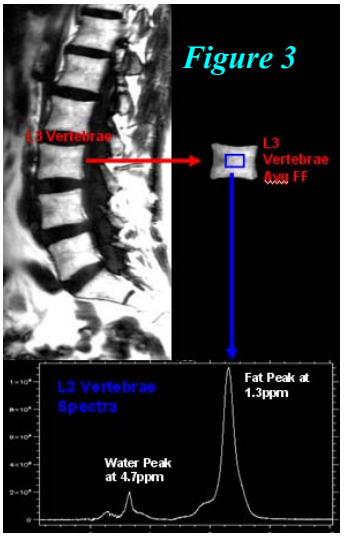
Purpose: Peripheral Quantitative Computed Tomography (pQCT) and Dual Energy X-Ray Absorptiometry (DEXA) are the current gold standards for the measurement of bone density and structure, in the research and clinical setting respectively. However, Magnetic Resonance Imaging (MRI) and unsuppressed ^{1}H Magnetic Resonance Spectroscopy (MRS) can also offer several advantages including the ability to quantify bone marrow content and structure. As part of a Wellcome-funded study to characterise high bone mass (HBM) we recruited around 169 individuals for this project. In-house software was developed to process and evaluate cortical and trabecular bone structure, marrow composition and vertebrae segmentation using data from MRI/MRS and structural details from pQCT. 43 individuals were selected from the total pQCT population for data acquisitions with MR.

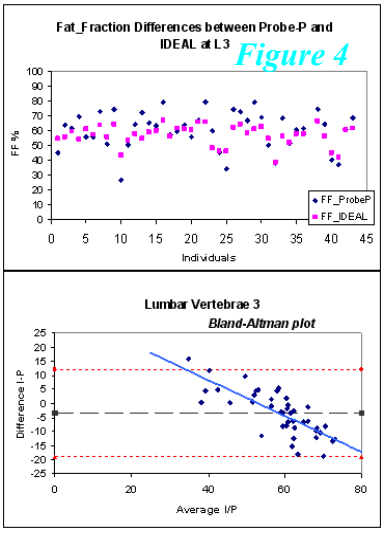




Materials and Methods: A 3.0 Tesla whole-body GE Signa system (HDx then with MR750) was used to acquire MRI data from distal leg, wrist and lumbar vertebrae, and MRS data from lumbar vertebrae only, in 43 individuals HBM. A three point Dixon technique (IDEAL) was used to acquire separate water and fat images to analyse fat-fraction (FF = fat signal / sum of fat signal and water signal). High resolution T_1 images were acquired to study the trabecular structure and ^{1}H single voxel point-resolved spectroscopy (PRESS) were acquired on individual vertebrae of L1, L3 and L5. pQCT measurements were acquired using a XCT-2000 Stratec scanner. In-house software was developed (using MATLAB) to process these images and perform a variety of structural and composition measurements in one user-friendly environment, enabling the additional benefits of MRI to be critically evaluated. Spectra were processed using GE's SAGE/IDL package and later by linear combination LCModel.

Results: The software enabled the automatic segmentation of cortical and trabecular bone permitting the user independent evaluation of structure and FF measurements. An example of a fat only image used in the determination of FF is illustrated in *Figure 1* (right) & *Figure 3* (top). In addition the software was able to analyse pQCT data to provide a comparison with MRI as illustrated in *Figure 1* (left). The high resolution T_1 images demonstrated excellent bone architecture which enabled measurement of the bone volume fraction (BVF) in the trabeculae, as illustrated in *Figure 2*. MRS from individual vertebrae provided effective chemical composition for evaluation as illustrated in *Figure 3* (bottom). A comparison between IDEAL FF and spectroscopy FF was performed on around 43 individuals at L3 vertebrae *Figure 4* (top), this data provides a non-random difference between IDEAL and spectroscopy data which is illustrated in *Figure 4* (bottom) as a Bland-Altman plot. Work is ongoing to study this difference and further work is ongoing to process the pQCT data and high resolution images from the distal hand and leg as a factor of quantification using different processing methods.





Conclusions: MRI and MRS show great potential to measure bone structure as well as marrow composition. Software has been successfully developed which permits an effective evaluation of this potentially useful modality for bone studies. Work is ongoing to test these tools for in-vivo quantification. In the future, further image analysis tools could be incorporated including textural analysis and this software could be used to assess bone abnormalities.

References: 1. G.P. Liney, *et al*., *JMRI* 26:787-793 (2007)
2. P.Gibbs, *et al*., *MRM* 50: 92-98 (2003)