An automated pipeline based on computational algorithms to extract Imaging Biomarkers and integrate them to calculate a new parameter to assess bone fracture: Quality of Trabecular Structure (QTS)

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Abstract

The characterization of the bone microarchitecture from MR or CT is significantly relevant in order to predict the risk of bone fracture. Our purpose was to evaluate the accuracy of the our bone pipeline based on computational algorithms extracting Imaging Biomarkers and integrate them in a new parameter to asses bone fracture: Quality of Trabecular Structure (QTS) and compare it to the reference standard under different imaging modalities. The reference is based on synthetic bones, consisting of 10 samples, 5 with 15% and 5 with 30% of material density that were acquired from SAWBONES® (Washington, USA) with known mass, density and pore size and were scanned using X-Ray, MDCT and MR. The voxel size (mm) in MDCT was of 0.234x0.236x0.67. The MR sequence was a T2-GRE with a voxel of 0.146x0.146x0.5 mm. The image processing steps were a bit different in X-Ray, MDCT and MR, according to a methodology developed in our group. Bone Volume to Total Volume (BV/TV) were measured in order to define the bone percentage in the volume. Trabecular Separation (Tb.Sp) was quantified by taking into account consecutive voxels corresponding to marrow cavities. MR and MDCT measurements of trabecular bone volume percentage and pore size were calibrated against the known ground truth from synthetic bones. These results add insight into the validation of bone microarchitecture imaging biomarkers.

1. Introduction

The osteoporotic disease carries a high risk of bone fracture, which, besides health issues, represents millions in hospitalization and treatment. Therefore, being able to predict the risk of bone fracture is a common goal in modern medicine [1].

FRAX® (Fracture Risk Assessment tool), TBS (Trabecular Bone Score) and BMD (Bone Mineral Density) are the most common methods used currently to predict the risk of bone fracture. However, each of these methods present shortcomings that hinder their accuracy. In this scenario, new methods based on the characterization of bone micro architecture are needed in order to properly understand the bone quality.

The main goal of this work is to implement an automated pipeline based on computational algorithms to evaluate the accuracy of the characterization of bone micro architecture through imaging modalities like X-ray, Magnetic Resonance (MR) and Computed Tomography (CT) by their comparison against a reference based on synthetic bones with known properties

2. Material and Methods

2.1. Samples

Synthetic bones from Sawbone® (SAWBONES EUROPE AB, Malmo, Sweden) with known density, mass and cell size were used as acquisition samples for this research. The samples are built with an open cell rigid foam that resembles the structure of human trabecular bone, with a cell size of 1.5 to 2.5 mm [2]. Ten samples with different densities were acquired, 5 samples with 15 PCF (pounds per cubic foot) and 5 samples with 30 PCF.

2.2. Data acquisition

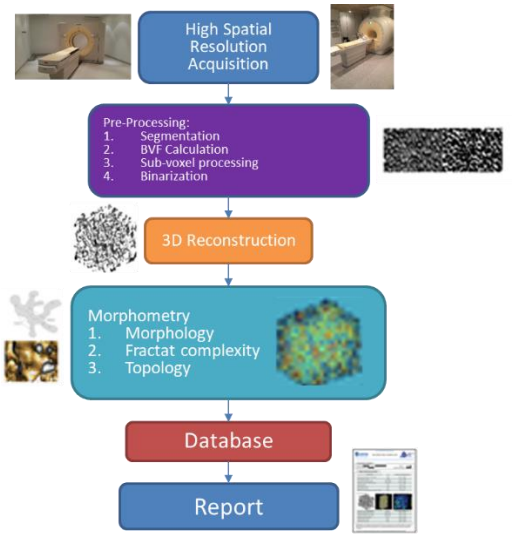
X-Ray images were acquired in a Philips Optimus 80 system with the following configuration: 66KV, 16,7mAs, 25 ms, focus distance: 102cm

CT acquisition was performed in a Philips Brilliance system with 64 detectors and the following parameters: slice thickness=0.67mm, KVP=120, spacing between slices=0.67mm, pixel spacing=0.234mm.

MR scans were acquired in a Philips Achieva 3T system with an 8 channel sense head coil with the following geometry parameters: slice thickness=0.5mm, spacing between slices=0.25mm, pixel spacing=0.146mm. The bones were included in a recipient of methacrylate that was filled with water in order to have contrast in the MR acquisition. The sequence consisted on a 3D turbo spin-echo (TSE) sequence with T2 weighting (TE=0.1, TR=1.5s).

2.3. Pipeline analysis

After the acquisition was completed, the imaging studies were sent to the Picture Archiving and Communication System (PACS), and analyzed with the Quibim (QUIBIM SL, Valencia, Spain) quidBone® pipeline accessible at www.quibim.com. Results of the analysis are shown on structural report.



The pipeline implements several algorithms to measure bone properties. Analysis algorithms are analogous across all imaging modalities, mainly differing on the pre-processing steps and on the lack of 3D geometry on plain X-rays.

MR scans need to be pre-processed, since trabecular bone appears black, and the only signal is that of bone marrow (i.e. emulated by water in the phantom). A Bone Volume Fraction (BVF) algorithm was used to correct signal heterogeneities and obtain the bone map through Laplacian thresholding [4].

$$\langle L \rangle_{\vec{r}}(I) \tag{1}$$

A binarization step was performed next for all imaging modalities with Otsu's thresholding method, which minimizes intra-class variance, helping achieve an optimal differentiation of trabecular bone and water [5]. Once the images were pre-processed, several imaging biomarkers were extracted. Bone volume to total volume (BV/TV) defines the ratio of bone contained in the volume:

$$\frac{BV}{TV} = \frac{n_{bone\ voxels}}{n_{total\ voxels}} \tag{2}$$

Trabecular thickness (Tb.Th) and trabecular separation (Tb.Sp) were calculated in a complimentary way, using the distance transform to compute the distance from the skeleton to the contour pixels(6):

$$Tb.Th = \frac{\sum_c \frac{\sum_{p \in Sk} 2 \cdot d_{min}}{|Sk|} \cdot \rho}{|c|} \tag{3}$$

Trabecular index (Tb.N) is a ratio between BV/TV and Tb.Th:

$$Tb.N = \frac{BV/TV}{Tb.Th} \tag{4}$$

A fractal dimension analysis was performed to assess the bone irregularity. This analysis was performed in 2D (D2D) and 3D (D3D) for each sample.

$$\log(N) = -D^{2D} \cdot \log(\lambda) + k \tag{5}$$
$$\log(N) = -D^{3D} \cdot \log(\lambda) + k \tag{6}$$

A multivariate parameter provided by the analysis pipeline was also taken into account, the Quality of Trabecular Structure (QTS) parameter. It summarizes trabecular bone morphometry and complexity imaging biomarkers in a single score to grade bone quality.

3. Results

Results from X-Ray, MDCT and MR analysis are collected in a Table 1, 2 and 3 respectively. (D3D value is not calculated from X-Ray analysis.)

Sample	BVTV (%)	TbTh-mean (µm)	TbSp-mean (µm)	TbN-Value	D2D-Value	QTS-Value
30PCF_1	32.828	334.771	530.110	0.981	1.769	2.634
30PCF_2	35.067	329.091	468.721	1.066	1.826	2.863
30PCF_3	35.167	322.543	455.133	1.090	1.839	2.809
30PCF_4	33.131	334.628	500.853	0.990	1.823	2.740
30PCF_5	34.839	325.764	482.800	1.069	1.829	2.791
15PCF_6	33.305	331.520	528.129	1.005	1.803	2.671
15PCF_7	34.188	334.444	487.612	1.022	1.819	2.836
15PCF_8	35.490	331.103	485.188	1.072	1.846	2.937
15PCF_9	33.863	336.113	520.833	1.007	1.829	2.816
15PCF_10	34.793	332.951	515.551	1.045	1.855	2.887

Table 1 *Results from X-Ray analysis*

Sample	BVTV (%)	TbTh-mean (µm)	TbSp-mean (µm)	TbN-Value	D2D-Value	D3D-Value	QTS-Value
30PCF_1	31.317	918.863	1685.177	0.341	1.589	2.554	9.414
30PCF_2	32.730	998.919	1766.154	0.328	1.613	2.538	10.662
30PCF_3	24.316	960.227	2.040.900	0.253	1.553	2.449	9.267
30PCF_4	21.178	856.802	1846.500	0.317	1.573	2.477	8.088
30PCF_5	28.602	873.640	1772.603	0.327	1.631	2.627	8.529
15PCF_6	18.744	677.680	1999.867	0.277	1.501	2.523	4.643
15PCF_7	17.079	803.136	2232.285	0.213	1.574	2.394	6.318
15PCF_8	15.063	682.401	2247.882	0.221	1.479	2.400	4.258
15PCF_9	14.514	620.699	2055.197	0.234	1.512	2.474	3.477
15PCF_10	16.710	628.125	1922.105	0.266	1.563	2.462	3.911

Table 2 *Results from MDCT analysis*

Sample	BVTV (%)	TbTh-mean (µm)	TbSp-mean (µm)	TbN-Value	D2D-Value	D3D-Value	QTS-Value
30PCF_1	32.879	456.407	936.030	0.720	1.598	2.502	3.481
30PCF_2	27.217	350.659	896.929	0.776	1.600	2.386	1.674
30PCF_3	25.116	333.546	955.316	0.753	1.640	2.415	1.268
30PCF_4	27.726	457.624	1075.781	0.606	1.579	2.391	2.983
30PCF_5	26.940	376.397	950.282	0.716	1.687	2.431	2.037
15PCF_6	21.504	537.755	1411.454	0.399	1.563	2.363	3.361
15PCF_7	19.845	387.572	1187.688	0.512	1.561	2.417	1.268
15PCF_8	16.890	389.777	1339.316	0.433	1.555	2.415	0.929
15PCF_9	19.853	439.574	1288.658	0.452	1.575	2.405	1.934
15PCF_10	17.838	409.906	1348.856	0.435	1.553	2.421	1.279

Table 3 *Results from MR analysis*

4. Discussion

The results obtained seem to indicate that there is a good correlation between the morphology analysis obtained from CT and MR scans, with a higher accuracy of CT, Table 4 is an example of the good correlation regarding

BVTV in both modalities and Figure 2 shows how different modalities are able to reproduce equals structures.

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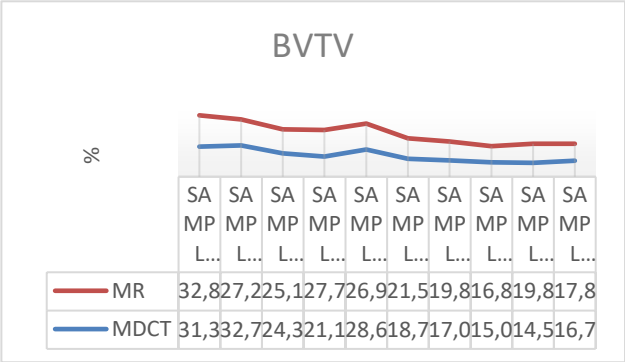

Table 4 *BVTV from MR and MDCT*

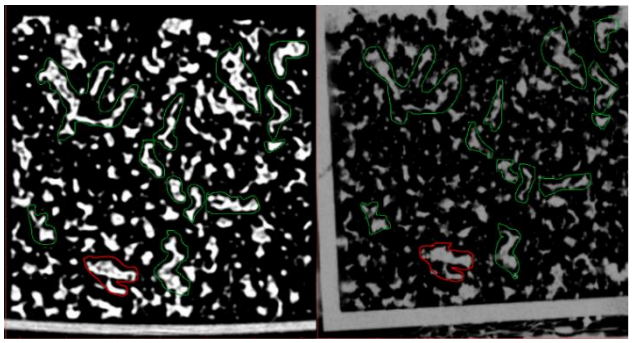

Figure: 1 *The image corresponds to the same slice obtained from MDCT (left) and MR with inverted signal (right) and it is possible to identify several structures in both acquisitions*

X-ray derived results remained similar with different bone porosities, demonstrating the lack of reliability of 2D techniques based on projection in the characterization of human bone quality. These data add insight into the existing knowledge on the behavior of the different imaging modalities with trabecular bone changing properties in patients with osteoporosis.

5. Acknowledgements

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