Searching the counterpart of histology in micro tomography data to approach the regenerative capacity of bone grafting materials

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INTRODUCTION: Analysing biopsies after bone grafting, both the conventional histology and advanced micro computed tomography (µCT) exhibit the architecture of the trabecular bone and the shape of remaining biomaterial. Whereas µCT yields local X-ray absorption, the histology represents functional information on bone formation. Therefore, the two techniques can be regarded as complementary [1]. The size of a dataset from µCT is often orders of magnitudes larger than the size of a single histology slice. As a consequence it is a challenging task to identify the exact location of the two-dimensional (2D) histology counterpart within the huge three-dimensional (3D) data set.

METHODS: Synchrotron radiation-based µCT measurements of a biopsy containing the bone grafting material Bio-Oss® (Geistlich Pharma AG, Wolhusen, Switzerland) were performed at the beamline W2 (DORIS, Hamburg, Germany) that was operated by the Helmholtz Zentrum Geesthacht [2]. The following parameters were selected: photon energy 25 keV, pixel size 2.2 µm, and number of radiographs 721 aquiangular between 0 and 180°. The data were reconstructed using a filtered back-projection algorithm after fourfold binning to increase the density resolution. Subsequent to µCT 300 µm-thin histological sections were prepared using a saw (Leica 1SP 1600, Leica Instruments GmbH, Germany). Thinning was achieved through grinding (EXAKT 400 CS, EXAKT Apparatebau GmbH, Germany). The polished sections were etched by formic acid and stained with toluidine blue.

RESULTS: The protocol of the histological sectioning provides hints for the localization of the counterpart within the µCT data. The counterpart identification is a challenging task even for experienced personnel and was performed by a time-consuming visual inspection. For example, one can use the visualization software VG Studio Max 2.0 (Volume Graphics, Heidelberg, Germany) to inspect the µCT data slice by slice with the aim to find characteristic visual landmarks. In detail, Figure 1 displays the histology slice. It contains morphological features of bone and biomaterial, as the entire 3D µCT data.

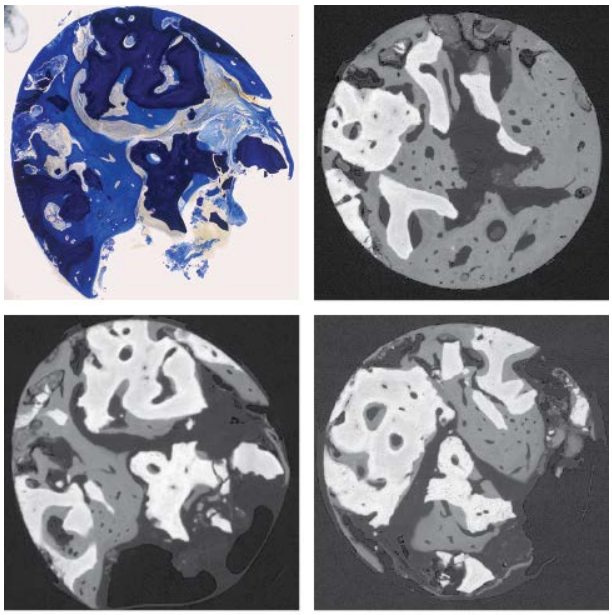

Fig. 1: Manual determination of the counterpart to the histology slice (top, left) within µCT data by landmark identification. The two images on the right are virtual cuts with characteristic features similar to the ones in the histology slice. Intentionally tilting and mirroring the µCT data one iteratively searches for the best suitable cut through the µCT data set. The X-ray absorption image below histology is a characteristic result of such a manual registration.

Evaluating the µCT-data perpendicular to the axis of the cylindrical biopsy, one finds the images given on the right of Figure 1. They contain a very few features (top-left and centre) similar to histology. Note the mirror symmetry. The elliptical shape of the histology slice further indicates the tilt. These observations result in the counterpart of histology given just below the histology slice.

DISCUSSION & CONCLUSIONS: The results of the manual search depend on the personal perspective, but they can be used as the starting point for automatic registration algorithms [1,3].

REFERENCES: [1] A. Stalder et al. (2014) *Int J Mater Res* **105**:679-691. [2] B. Ilgenstein et al. (2012) *Proc SPIE* **8506**:85060M. [3] N. Chicherova et al. (2014) *LNCS* **8673**:243-250.