Automatic matching of grating-based phase tomography dataset with histology

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INTRODUCTION: Identifying a histological slice in a three-dimensional dataset corresponds to a challenging 2D-3D matching problem. Recently, we developed an automatic algorithm that was successfully applied to micro computed tomography (μCT) data acquired in absorption contrast mode and histology images of the jaw bone biopsy.[2] To explore how the method generalizes, here we evaluated its performance on another modality for tissue, namely grating-based phase contrast tomography of the human cerebellum.

METHODS: The sample data used for this study originates from a human cerebellum extracted post mortem. The 3D volume scan of the specimen was acquired using grating-based phase tomography at the beamline ID 19 (ESRF, Grenoble, France) at a photon energy of 19.5 keV and an effective pixel size of 5 μm. The diameter of the specimen is 6 mm. Our automatic algorithm is based on the rotation- and scale-invariant edge detector SURF (Speeded Up Robust Features[3]). In a first step corresponding feature points are detected between each slice in the 3D data set and the histology image using SURF. The coordinates of all matching points from 3D data are subconsequently saved relative to its axial position. Based on these coordinates, we build a 3D point cloud, where the third dimension corresponds to the slice number in the dataset. Finally, to find the best matching tomography slice to histology, we filter the points based on their density distribution and use RANSAC algorithm to robustly fit a plane in a noisy point cloud. For this particular dataset, we added an additional parameter for robustness, namely filter radius for matched keypoints. The specimen borders usually produce high edge response. To remove it, we cropped the points by taking only those lying inside a circle with a radius less than the radius of the specimen. Other parameters were the same as in the previous study[1].

RESULTS: We observed reasonable performance of the method for four histology slices. Thus, the method shows a potential for generalization to other imaging modalities. The figure shows the results for the best found match of a histological slice in the tomography data. The high similarity between the two images indicates that the algorithm performed well in this case. In total we analysed four histology slices and visually evaluated the similarity between the automatically found images. The algorithm found good matching pairs in all four cases.

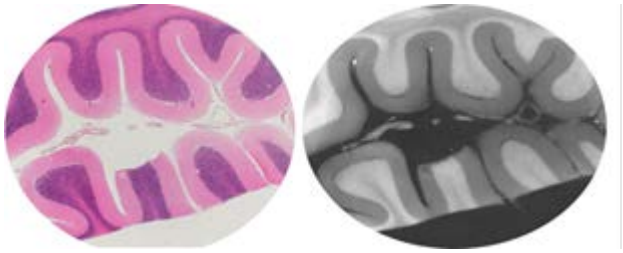

Fig. 1: Automatically registered slice from the 3D tomography dataset (right) and the reference histology image (left).

DISCUSSION & CONCLUSIONS: The results indicate that our method can be applied to datasets of other modalities. Even though the SURF descriptor is usually not considered to be multi-modal, it shows good performance when applied to this density problem. The main advantage of the detector is a property of detecting borders of two images for matching. Therefore, we believe that our approach will work with other modalities with high intensity contrast and corresponding tissue borders. However, this property is also a limitation which can potentially lead to incorrect registration. Currently, we are working on improving the method using sparse modality invariant descriptors.

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