

## Publication

Automatic histology registration in application to X-ray modalities

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ID 3786397 Author(s) Chicherova, Natalia; Hieber, Simone E.; Schulz, Georg; Khimchenko, Anna; Bikis, Christos; Cattin, Philippe C.; Mueller, Bert Author(s) at UniBasel Cattin, Philippe Claude ; Year 2016 Title Automatic histology registration in application to X-ray modalities Editor(s) Stock, Stuart R.; Müller, Bert; Wang, Ge Book title (Conference Proceedings) Developments in X-Ray Tomography X Volume 9967 Place of Conference San Francisco Publisher SPIE Place of Publication Bellingham Pages 9967-9968 ISSN/ISBN 978-1-5106-0325-7

Registration of microscope images to Computed Tomography (CT) 3D volumes is a challenging task because it requires not only multi-modal similarity measure but also 2D-3D or slice-to-volume correspondence. This type of registration is usually done manually which is very time-consuming and prone to errors. Recently we have developed the first automatic approach to localize histological sections in  $\mu$ CT data of a jaw bone. The median distance between the automatically found slices and the ground truth was below 35  $\mu$ m. Here we explore the limitations of the method by applying it to three tomography datasets acquired with grating interferometry, laboratory-based  $\mu$ CT and single-distance phase retrieval. Moreover, we compare the performance of three feature detectors in the proposed framework, i.e. Speeded Up Robust Features (SURF), Scale Invariant Feature Transform (SIFT) and Affine SIFT (ASIFT). Our results show that all the feature detectors performed significantly better on the grating interferometry dataset than on other modalities. The median accuracy for the vertical position was 0.06 mm. Across the feature detector types the smallest error was achieved by the SURF-based feature detector (0.29 mm). Furthermore, the SURF-based method was computationally the most efficient. Thus, we recommend to use the SURF feature detector for the proposed framework.

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