

Deep Active Learning for Segmentation of Biodegradable Bone Implants in High Resolution Synchrotron Radiation Microtomograms

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With the increasing success of deep learning techniques in many applications, researchers also use it for segmentation of biodegradable implants in high resolution synchrotron radiation microtomograms (SR μ CT). Deep learning models, however, require lots of annotated training examples in order to generalize and perform well on new data. Manual annotation of high resolution SR μ CT is a very time-consuming, and expensive task. Moreover, domain expertise is required for accurate segmentation of biodegradable bone implants. We leverage deep active learning techniques in this research to alleviate the need for annotating a large dataset, yet achieve a similar performance. A small number of annotated tomograms are used to train a model. The trained model and a so-called acquisition function are used to propose new tomograms to manually annotate and include in the training set which could potentially improve the performance of the deep learning model the most. The new annotated tomograms are added to the training set and the process is repeated, evaluating the trained model on a separate test dataset after each round. The process is halted when the increase in performance on the test dataset between two successive rounds is negligible. Experiments are conducted on an annotated dataset of biodegradable implants. There are 6 samples (5591 tomograms) for validation, and 6 samples (6000 tomograms) for testing. Even though 8 samples (6878 tomograms) are allocated for training, initially, only 8 tomograms (1 from each sample) from the training set are used to train the model in the first round. After each round, 8 new tomograms are added to the training set based on the scores calculated using the acquisition function. After 10 rounds of active learning and only 80 annotated tomograms for training, the model achieves a mean intersection over union (mIoU) score of 80.51% on the test dataset. Training a model on the whole dataset, i.e., 6787 annotated tomograms, in a vanilla supervised fashion yields a mIoU score of 82.91%, only ~2% higher, on the test dataset.

Primary author: KAZIMI, Bashir (Hereon (Helmholtz-Zentrum Hereon))

Co-authors: BALTRUSCHAT, Ivo (Research and Innovation in Scientific Computing, DESY); MOOSMANN, Julian (Helmholtz-Zentrum Hereon); HEUSER, Philipp (DESY/Helmholtz Imaging); KAKAVAND, Sahar (IT (Research and Innovation in Scientific Co))

Presenter: KAZIMI, Bashir (Hereon (Helmholtz-Zentrum Hereon))