A Keypoint Framework for Multimodal Registration

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Abstract

Histology and micro-computed tomography (µCT) are key methods for studying tissues and diseases. Their registration supports the development of pathological applications. However, challenges remain due to the poor image quality of soft tissue in µCT and deformations in histological images. In this work, a robust and accurate method is proposed for registering histology slices to µCT.

19 skeletal muscle sample pairs were used; preprocessing of the 3D µCT volumes began by extracting, from each volume, a slice corresponding to the related histology section. Histology images were normalized and gamma-corrected to enhance contrast. Additionally, both image types were divided into 64×64-pixel patches. Keypoints were detected using the Scale-Invariant Feature Transform (SIFT), a feature-based method that efficiently identifies stable local keypoints. At each keypoint, texture descriptors (standard deviation, entropy, gradient mean, Gabor response) were computed to filter the best candidates. They were then clustered using k-means, and the two keypoints nearest each centroid were retained. Candidate pairs were matched by distance, refined with local affine corrections, and globally aligned using an affine transformation.

The proposed method registers histology slices to µCT images by matching keypoints. Local residual error (the Euclidean distance between each transformed µCT keypoint and its histology counterpart) was, in pixels: Pair 1: 13.2, 18.6, 27.6; Pair 2: 3.4, 11.7, 12.0; Pair 3: 2.7, 3.0, 9.5.

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