VALIDATION OF A MULTIMODAL 2D-3D REGISTRATION ALGORITHM USING UNIMODAL SYNTHETIC EXPERIMENTS

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Introduction

Bone is a hierarchical tissue whose mechanobiological processes span several temporal and spatial scales. Recently, we have developed a correlative multimodal imaging (CMI) approach to correlate *in vivo* 3D micro-computed tomography (micro-CT) images with *ex vivo* 2D histological sections from the same bone sample [1], enabling a holistic analysis of this multiscale system. We analysed a mouse femur dataset of histological sections obtained along the samples' longitudinal axis (LO), but it is not clear how cross-sectional (CS) images would perform. Further, an initial guess (IG) is required for the 2D-3D registration step, but its influence on the accuracy and convergence of the registration has not been quantified. Therefore, in this work, we developed a validation toolkit to perform synthetic experiments with known ground-truth (GT) transformations to evaluate the performance of our CMI approach. We compared the accuracy of 2D-3D registration for synthetic datasets containing CS and LO images of a mouse femur and quantified the convergence success of the registration depending on the IG considered.

Methods

The data used here was collected in a previous study [2], where 20-week-old C57BL/6J mice underwent femur defect surgery and were imaged weekly with *in vivo* micro-CT (10.5 µm, vivaCT 40) over seven weeks after surgery. Images were Gauss-filtered (sigma 1.2) and binarized at 395 mgHA/cm^3. To mimic formalin-fixed paraffin-embedded LO and CS sections, three GT orientations were randomly sampled per condition and synthetic 2D datasets containing 25 parallel sections each were generated from 3D micro-CT at the last time-point (Figure 1A). Sections were 2D-3D registered iteratively based on binary image similarity. For each section, IG transforms were defined between 0-100% (step 25%) of their GT rotation and translation. Each registration ran for a maximum of 50 iterations, converging if the root sum squared error between GT and optimised parameters reached 1. The accuracy of the registration was assessed with mean dense registration error [3], normalised by the voxel size (in %).

Results

LO sections consistently achieved better performance than CS, with a convergence rate above 80% for sections initialised from 25% of the GT transform (Figure 1B). Additionally, successful registrations achieved sub-voxel accuracy, with mean DRE values below 3.5 % for all configurations (Figure 1C). At last, IG with deviations in translations were retrieved more successfuly than rotations (Figure 1D).

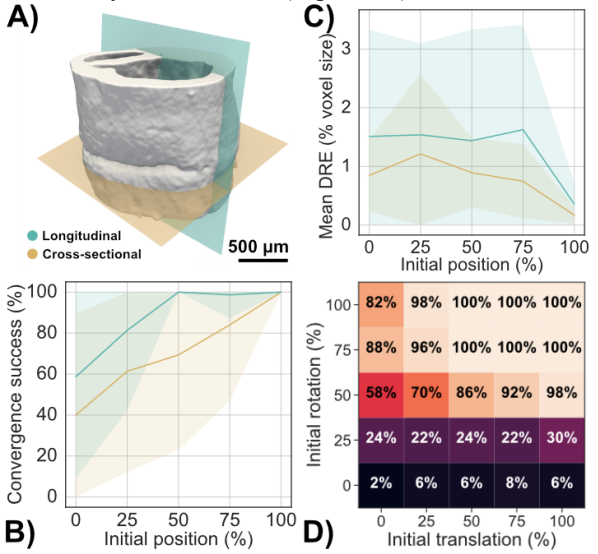

Figure 1: A) Synthetic dataset generation of LO and CS sections. B) Convergence success for varying IG based on the GT transform. C) Mean DRE (% voxel size) for successful registrations of LO and CS. D) Convergence success for varying IG for LO datasets, for rotation and translation.

Discussion

The validation of CMI approaches can be challenging due to limited multimodal GT datasets available. As our 2D-3D CMI approach relies on binary images, synthetic experiments using a single modality (micro-CT) are a viable alternative to assess its capabilities. Notably, our validation toolkit can reproduce realistic histological datasets, even image deformations that typically occur during sectioning (data not shown). Importantly, these findings are directly applicable to support the preparation of histological sections in future studies. Besides, its modular architecture provides a fast and versatile approach to benchmark new image similarity metrics and registration algorithms or repeat the analysis with datasets of other established preclinical models used in bone research, like the mouse caudal vertebra.

References

1. Marques et al., ESB Congress 2022.
2. Wehrle et al., Sci Rep 11, 23037, 2021.
3. Lundin et al., Bone, 105:173-183, 2017.

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