

Supplementary Materials : 2D/3D Deep Registration Along Trajectories With Spatiotemporal Context: Application To Prostate Biopsy Navigation

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1 Data Generation for "partial" experiment

For "part" experiments, the given input volume for each time t is now a subpart of the reference volume, defined as $V_{sub,t}$. This sub-volume is obtained after transforming and orienting the reference volume V_{ref} according to a transform $T_{sub,t}$, which relies on the estimated previous slice localization S_{t-1} (see Fig. 1). This restricts the search space, centered and cropped around a close position. The ground-truth slice localization is now computed relatively to the intermediate sub-volume ($T_t = T_{S_t \rightarrow V_{sub,t}}$) as described in eq. 1a. Then, successive relative transformations toward each sub-volume are successively composed (eq. 1b) to obtain a final global transformation toward the initial reference volume (as defined in eq. 1c). This is convenient for always resampling from the initial full reference volume and for keeping the same range of transformation values as other experiments.

$$T_t = T_{S_t \rightarrow V_{sub,t}} = T_{sub,t}^{-1} * T_{S_t \rightarrow V_{ref}} \quad (1a)$$

$$\text{with } T_{sub,t} = T_{S_{t-1} \rightarrow V_{sub,(t-1)}} * T_{sub,t-1} \quad (1b)$$

$$\text{and } T_{sub,0} = T_0 = T_{S_0 \rightarrow V_{ref}} \quad (1c)$$

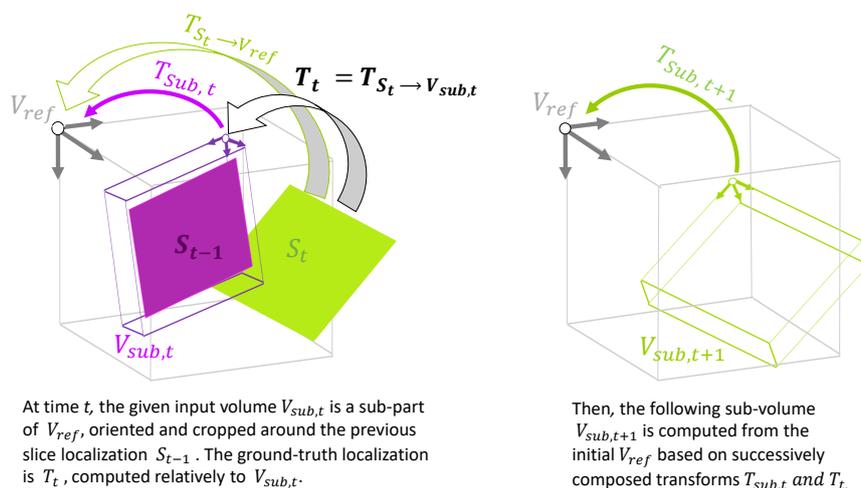


Figure 1: Sub-volume generation and computation of the corresponding ground-truth slice localization.

2 Datasets

We simulated sweep trajectories (as described in "Data generation process") that we applied to a large database composed of 600 TRUS volumes, coming from biopsy sessions of 100 different patients. The datasets for the two different studies (described in sections III-A.1 and III-A.2) are structured in two different ways, described just below.

For the ablation study, each tested experiment is trained, validated and tested on the same datasets. The ratio splits, applied on samples, are summarized in Table 1. We took care to keep unseen patients in the testing set, to evaluate the good generalization capabilities of the model on new anatomies.

For the comparison study (with a more manageable number of experiences), we used a 5-fold validation strategy, where results were then averaged for all folds to increase the reliability of the results. The different folds are divided according to the number of patients (and not samples) to preserve a diversity of represented anatomies. This cross-validation procedure leads to new data splits described in in Table 2.

Table 1: Description of the dataset splits (on samples) used for the ablation study.

Datasets	Training & Validation (75 % and 8 %)	Testing (17 %)
" S_i to V_i "	5 V_i x 80 patients \approx 30 000 samples	5 V_i x 20 patients \approx 6 000 samples
" S_i to V_j "	10 $V_{i,j}$ x 50 patients \approx 16 000 samples	10 $V_{i,j}$ x 8 patients \approx 3 000 samples

Table 2: Description of the 5-fold splits (on patients) used for the comparison study.

Datasets	Training 4-folds	Testing last-fold
" S_i to V_i "	5 V_i x 80 patients \approx 30 000 samples	5 V_i x 20 patients \approx 6 000 samples
" S_i to V_j "	10 $V_{i,j}$ x 44 patients \approx 14 500 samples	10 $V_{i,j}$ x 11 patients \approx 4 500 samples