Facilitating manual segmentation of 3D datasets using contour and intensity guided interpolation

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Motivation

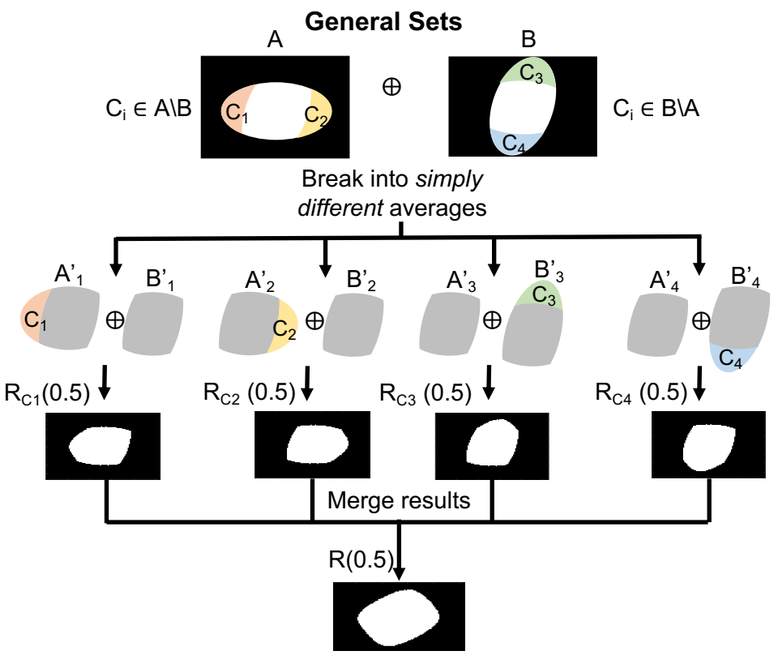
- Manual segmentation of anatomical structures in 3D datasets is laborious and time consuming
- Interpolation can be used to propagate labels from partially annotated datasets to the remaining unlabeled slices, allowing manual segmentation of small subset of slices

We propose integrating contour and intensity information for an improved interpolation which better handles complex shape deformations and minimizes intensity-related artifacts

Method

BINARY-WEIGHTED AVERAGE (BWA) FOR CONTOUR-BASED INTERPOLATION

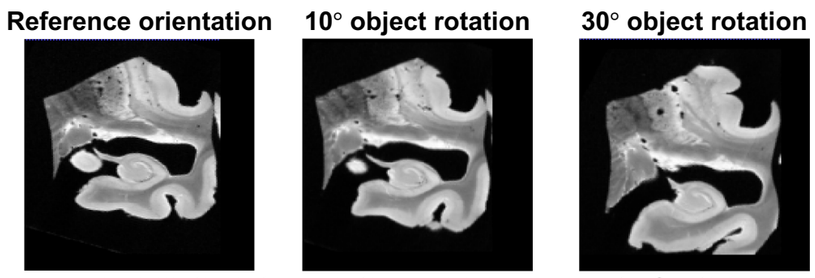
- Segmentation is represented by its signed distance transform
- Interpolate between two images, A and B, by thresholding the weighted average of their signed distance transforms ⟶ $R(t) = tA \oplus (1-t)B$



- Introduce non-linear reparameterization of averaging parameter proposed by Kels et al. [1]
- Piece-wise interpolation required when difference set between two images contains multiple connected components (*general sets*)

PROBABILISTIC WEIGHTED AVERAGING

- Slice plane in which manual segmentations are drawn is arbitrary relative to the object's orientation



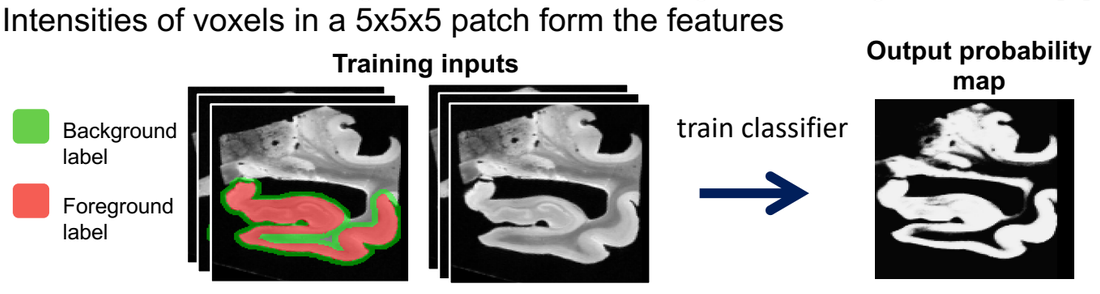
- Can provide a probabilistic interpolation which accounts for this variability in the slice plane direction by:
  - Approximating these transformations using small translations and performing multiple interpolations per pair of segmentations

OR

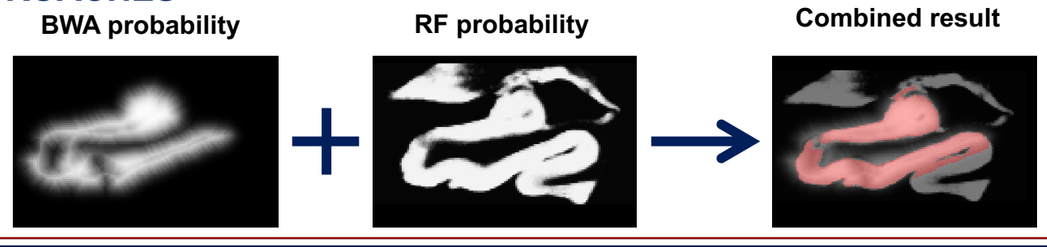
  - Applying a smoothing transformation to the interpolated distance function

RANDOM FOREST (RF) FOR INTENSITY-BASED CLASSIFICATION

- RF classifier trained using set of slices containing manual segmentations [2]
- Intensities of voxels in a 5x5x5 patch form the features



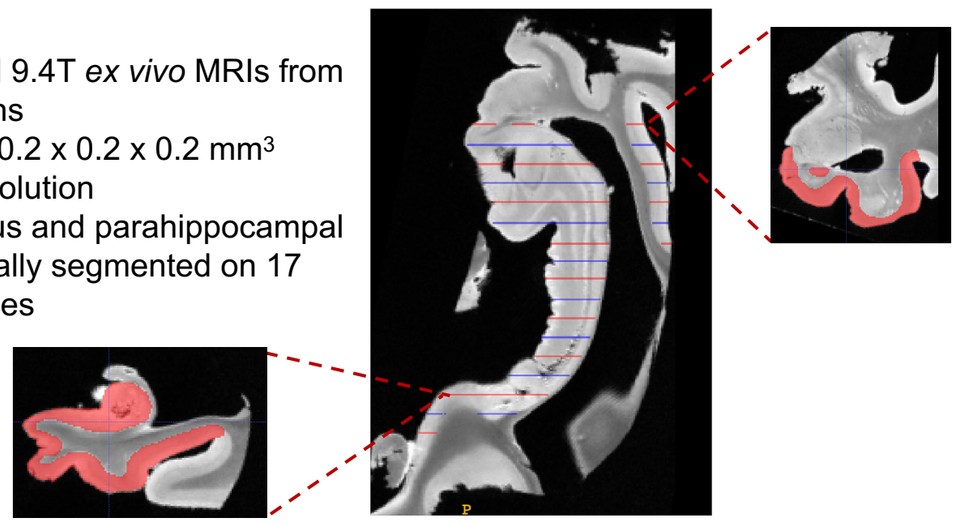
VOXEL-WISE AVERAGE OF PROBABILITY MAPS TO COMBINE APPROACHES



Evaluation

DATASET

- T2-weighted 9.4T *ex vivo* MRIs from 10 specimens
- Scanned at 0.2 x 0.2 x 0.2 mm^3 isotropic resolution
- Hippocampus and parahippocampal gyrus manually segmented on 17 selected slices



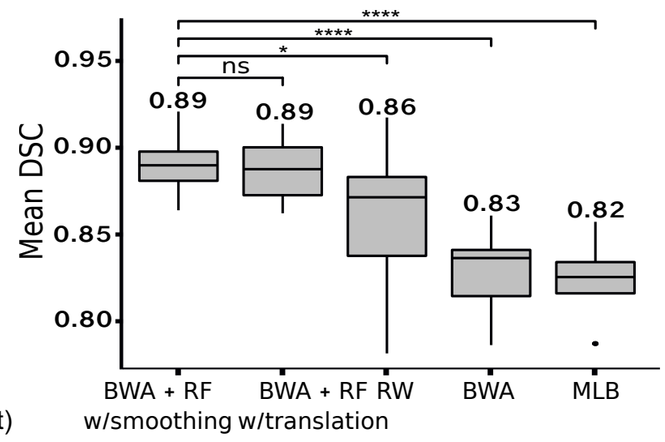
- Every other slice withheld for testing (blue)
- Remaining 9 slices (red) used to interpolate segmentations across the entire volume (~200 slices)
- Computed mean Dice Score Coefficient (DSC) between interpolated segmentation and manual segmentation on withheld test slices

COMPARATIVE METHODS

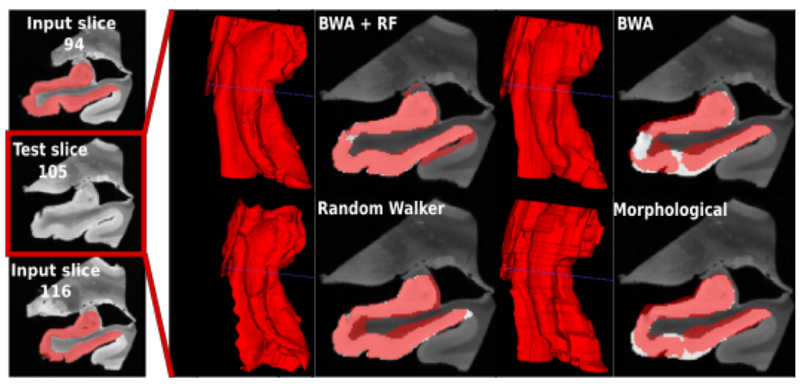
- Binary weighted averaging only [1]
- Random walker (RW) algorithm [3]
- Morphology-based interpolation (MLB) [4]

Results

- Proposed method achieves a higher mean DSC of 0.89 ± 0.16 compared to RW, MLB and BWA
- The smoothing approach to generate a probabilistic interpolation is computationally faster and produces comparable results to the translation-based approach



paired t-test (*: p-value < 0.05, ****: p-value < 0.0001, ns = not significant)



- BWA and MLB produce sharp turns and visible steps between layers
- Combining contour and intensity information results in a smoother reconstruction

Conclusion

- We propose a novel interpolation technique which uses both contour and intensity information from manually segmented slices to annotate unlabeled slices in the dataset
- Implemented using the Insight Registration and Segmentation Toolkit (ITK) and code is available on GitHub
- Incorporated in ITK-SNAP as an interactive tool for semi-automated segmentation. Allows the user to iteratively refine the interpolation using a multi-step approach

GitHub

References:
[1] Kels,Shay & Dyn,Nira. *Computers & Graphics* (2011)
[2] Yushkevich, PA et al. *Neuroinformatics* (2018)
[3] Grady, Leo. *IEEE Transactions on Pattern Analysis and Machine Intelligence* (2006).
[4] Albu, AB et al. *IEEE Transactions on Biomedical Engineering* (2008)

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