

Machine Learning Enabled Brain Segmentation for Small Animal Neuroimaging Registration

Hendrik J. Klug¹, Berkan Lafci^{2,3}, Markus Rudin⁴, Daniel Razansky^{2,3}, Horea-Ioan Ioanas⁵

¹ ETHZ, Department of Information Technology and Electrical Engineering, Zurich, Switzerland

² UZH, Institute of Pharmacology and Toxicology and Institute for Biomedical Engineering, Faculty of Medicine, Zurich, Switzerland

³ ETHZ, Institute for Biomedical Engineering, Department of Information Technology and Electrical Engineering, Zurich, Switzerland

⁴ ETHZ, Center for Imaging Science and Technology, Zurich, Switzerland

⁵ Massachusetts Institute of Technology, Department of Biological Engineering, Cambridge, United States of America

Introduction

In biomedical imaging, between-subject comparability is attained at the voxel level via image registration. This process requires several data preparation steps, of which brain extraction is particularly problematic in preclinical applications. Current solutions rely on human brain extraction library adaptations, or full image processing — with introduce artefacts via rostrocaudal cropping and peripheral hyperintensities, respectively. We present a deep learning framework for multi-contrast MRI brain tissue segmentation, and benchmark its performance with respect to novel workflow advances.

Methods

The model was iteratively trained on 3D magnetic resonance images taken from an aggregation of multiple studies with high age heterogeneity, as well as supplementary novel data, acquired with similar parameters. For the model architecture, we leveraged the U-Net [2] native 3D implementation from Oktay [3]. The resulting auto-encoder type model was utilised for benchmarking, and can similarly be re-used as a parameterized preprocessing step in the “SAMRI Generic” registration workflow [1] — though a standalone version is also available. We publish both the resulting classifier and the training pipeline, thereby facilitating methods transfer to any biomedical use cases looking to iteratively improve classification of tissues in 3D.

Results/Discussion

In comparison to the reference SAMRI Generic registration workflow — which provides adequate and modular registration capabilities, yet does not constrain similarity metrics to brain tissue, specifically — our workflow shows significant improvements in multiple quality control read-outs. The Volume Conservation Factor (VCF) [1] which measures the registration-induced volume deformation, and is optimal at a value of 1, favours the brain-extraction extended workflow, with a root mean squared error ratio of $RMSE_M(\text{extended})/RMSE_G = 0.66$. Further, the extended workflow exhibits an inter-sample VCF variance decrease (0.44-fold), indicating not only increased accuracy, but increased precision and reproducibility. Evaluating the Smoothness Conservation Factor (SCF) [1], which expresses the ratio between smoothness of the image before and after registration, we also find notable improvement, with $RMSE_M(\text{extended})/RMSE_G = 0.93$.

Conclusions

We present a novel preclinical brain tissue classifier, providing brain extraction in a simple drop-in fashion in the modular state-of-the-art SAMRI Generic workflow. We benchmark this extension against metrics highlighted in the original publication, finding significant improvements. Conceptually, this showcases the feasibility of iterative classifier refinement based on imperfect input data and endogenous features — a key biomedical challenge.

Disclosure

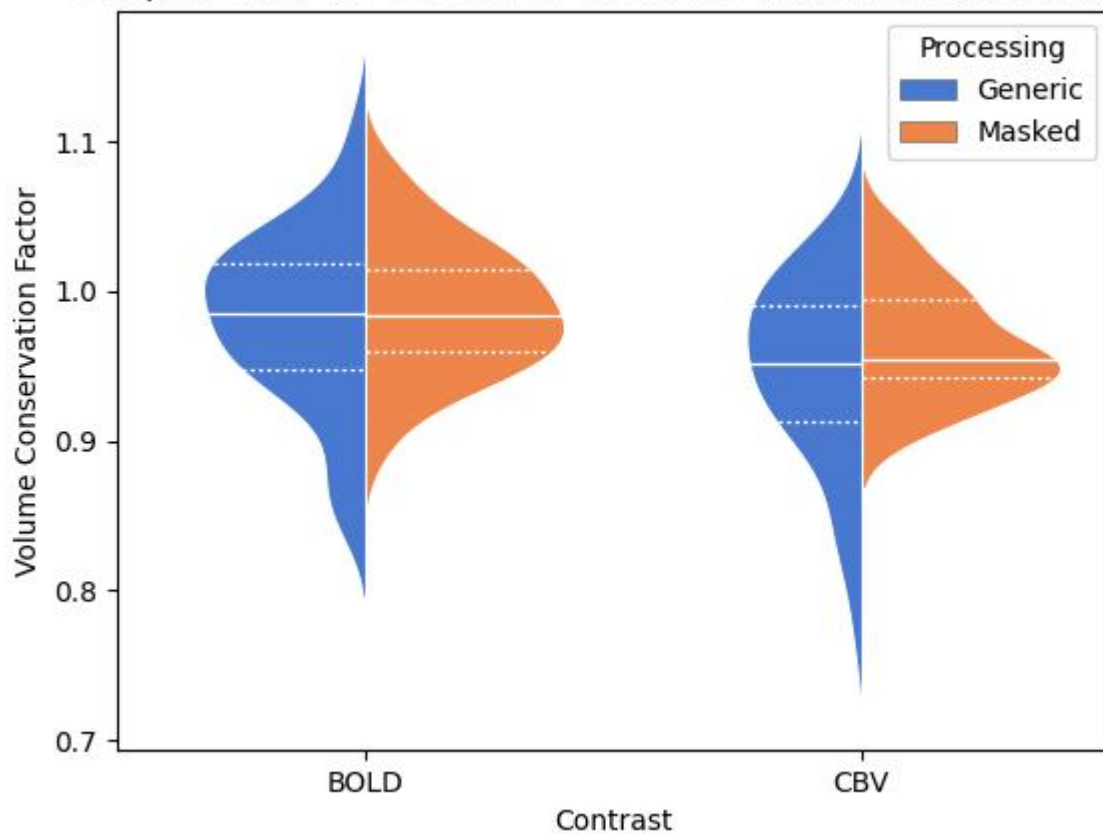
I or one of my co-authors have **no financial interest** or **relationship** to disclose regarding the subject matter of this presentation.

Affix

References

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Comparison of the VCF across workflows and functional contrasts



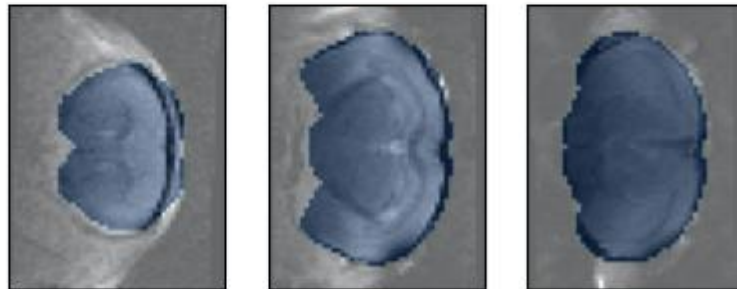
Comparison of the VCF across workflows and functional contrasts.

Plot showing the distribution of the Volume Conservation Factor. Solid lines in the colored distribution densities indicate the sample mean and dashed lines the inner quartiles.

Generic



Masked



Qualitative comparison between the Masked (ours) and the Generic workflow

The Masked workflow prevents the shifting of outer-brain region voxels into the template-brain region (in blue). Comparison of slices from 3 different volumes, registered with the Generic (first row) and the Masked (second row) workflow.