Predicting Brain Connectivity Mapping Using Radiomics Features in Anatomical MRI

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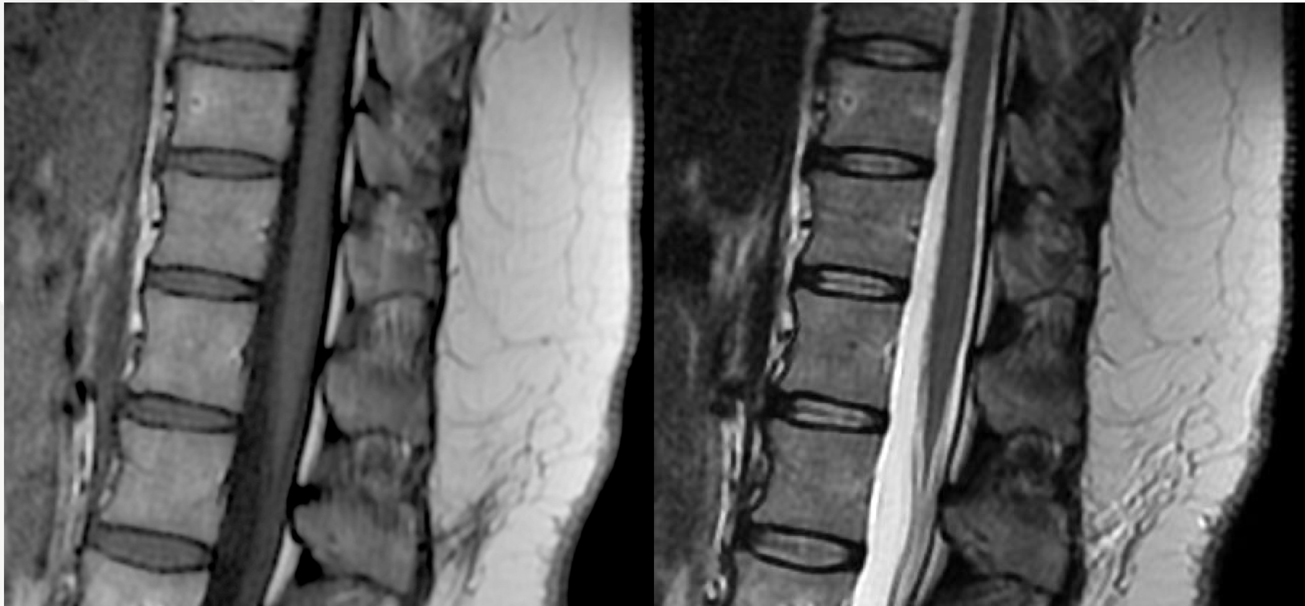
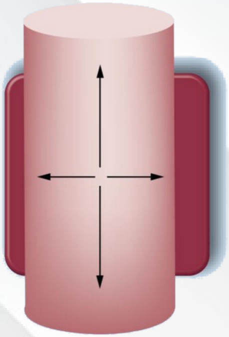
Magnetic Resonance Imaging

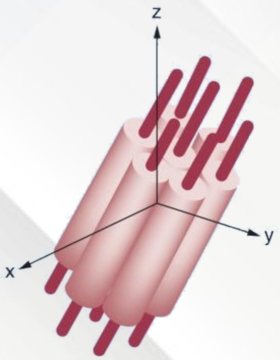
- volumetric imaging technique
- can highlight distinct tissue properties
- T1 and T2

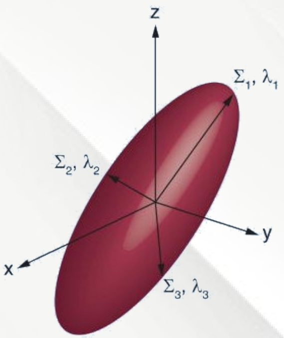


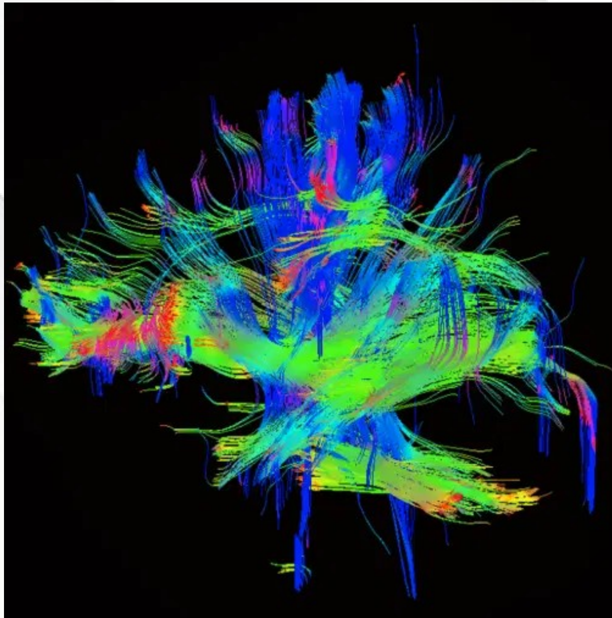
Diffusion Tensor Imaging

- cells impose anisotropy on water diffusion
- FA, MD and Relative Connectivity









State of the Art

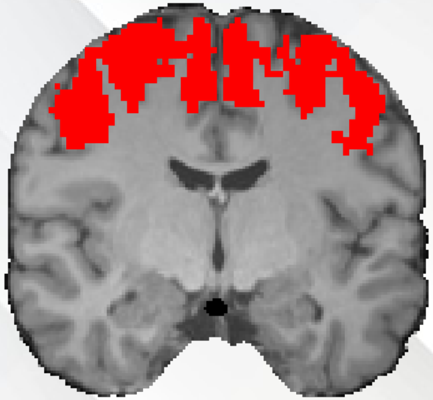
- T1/T2 and Myelin
- Radiomics
- Neural Networks

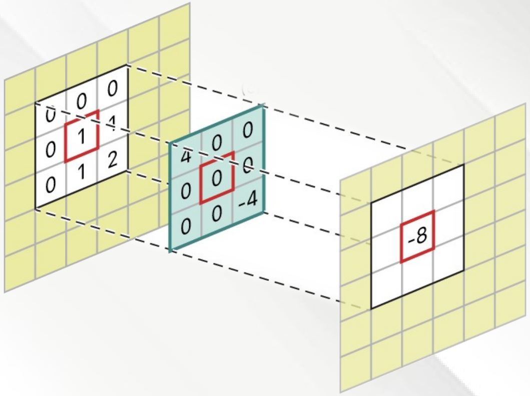
T1/T2 and Myelin

- T1/T2 => cortical myelin maps (more robust than R1)
- mapping cortical areas
- direct correlation to MFW

Radiomics

- quantitative information from diagnostic images
- voxel and non-voxel based



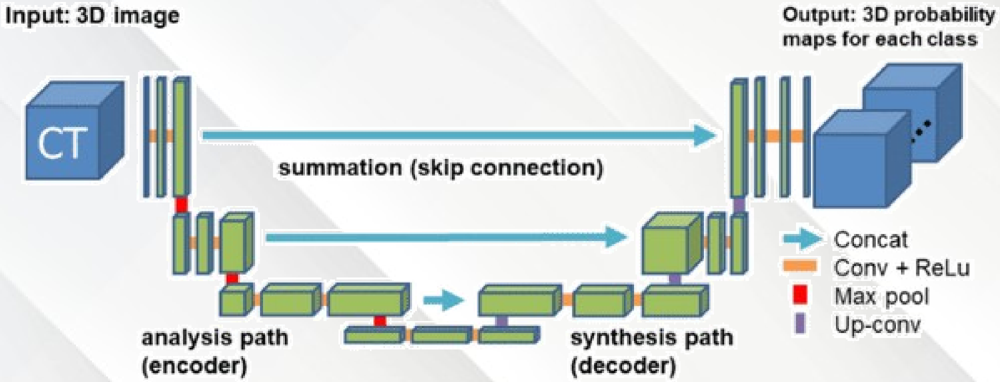


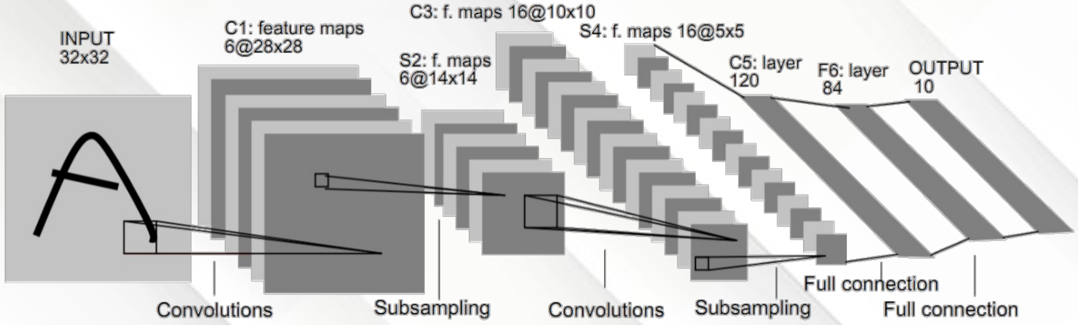
GLRLM at θ = 0

$$\mathbf{I} = \begin{bmatrix} 5 & 2 & 5 & 4 & 4 \\ 3 & 3 & 3 & 1 & 3 \\ 2 & 1 & 1 & 1 & 3 \\ 4 & 2 & 2 & 2 & 3 \\ 3 & 5 & 3 & 3 & 2 \end{bmatrix} \quad \mathbf{P} = \begin{bmatrix} 1 & 0 & 1 & 0 & 0 \\ 3 & 0 & 1 & 0 & 0 \\ 4 & 1 & 1 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 \\ 3 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Neural Networks

- FNNs have great performance on large, high-dimensional datasets
- FCNNs & CNNs for handling spatial data



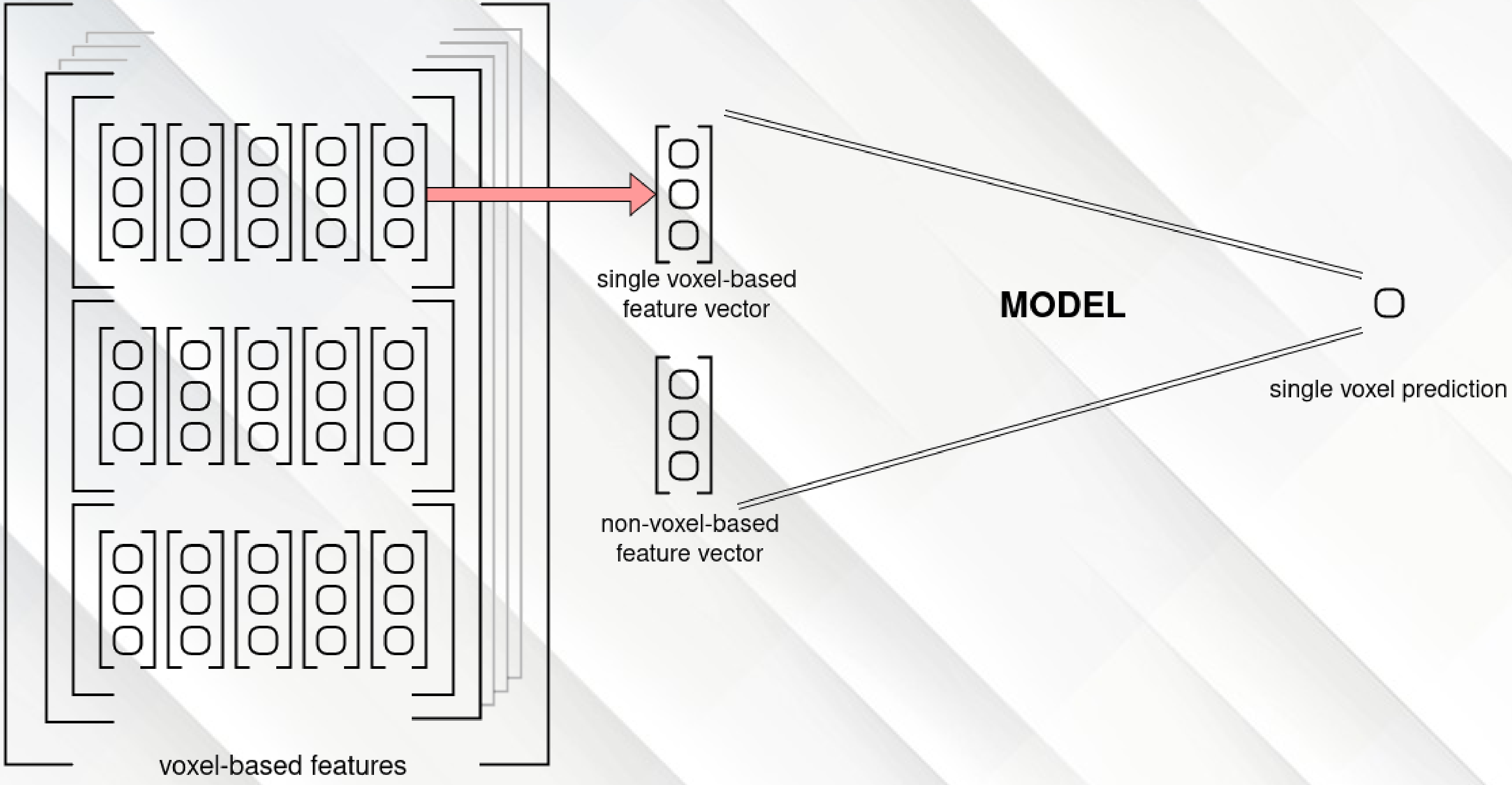


Motivation & Objectives

Can structural connectivity images be synthesized directly from anatomical images using machine learning?

- use radiomics for feature extraction
  - replace 3D convolutional backbone
- use FNN classification/regression head
- increase performance with T1/T2

Proposed Solution

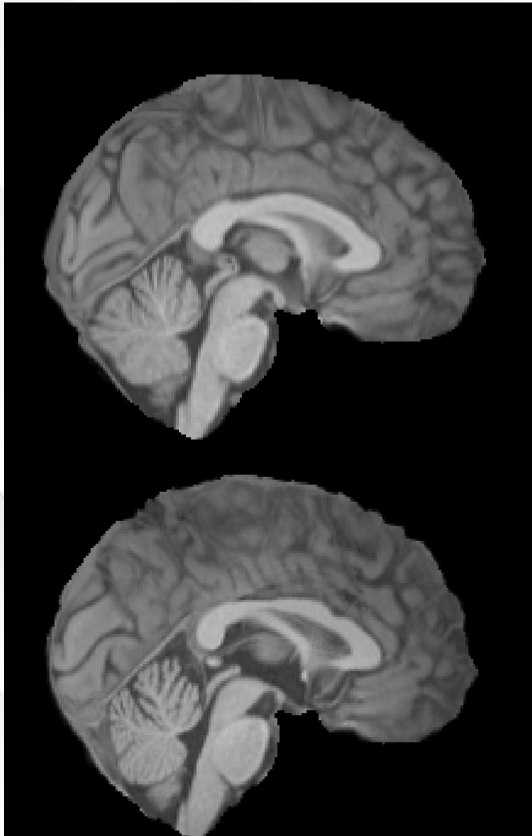


Limitations and Robustness

- Basal Ganglia => ROI
- Huntington’s Disease
- 32 control + 38 patient records

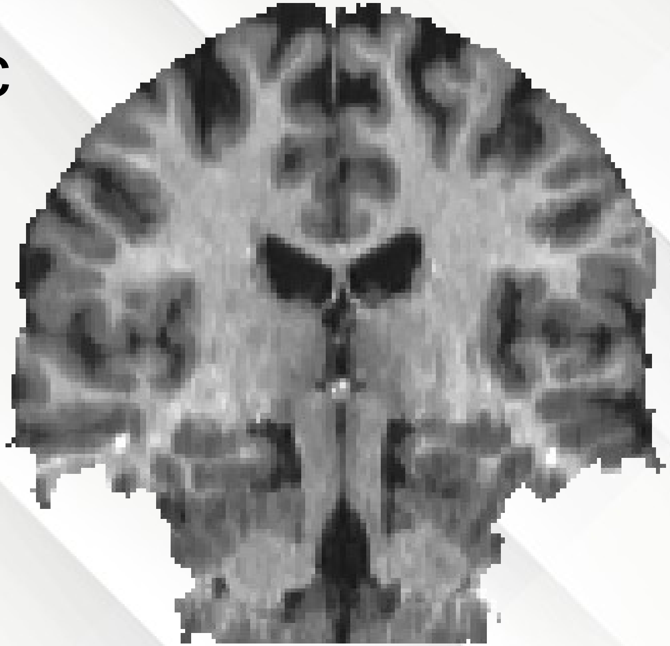
Native or Normalized Space

- brains are unique
- non-linear registration
- lowers variance



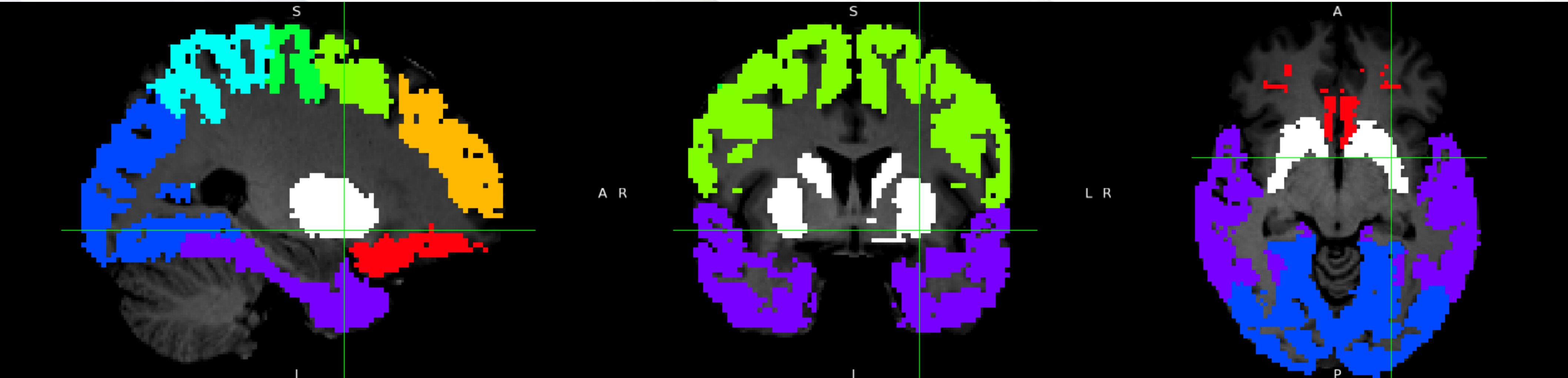
T1 or T1/T2 Input Image

- myelin proxy
- additional noise!!!
  - T2 is anisotropic



Non-Voxel Based Features

- Cortical Targets
- Basal Ganglia
- Entire Brain

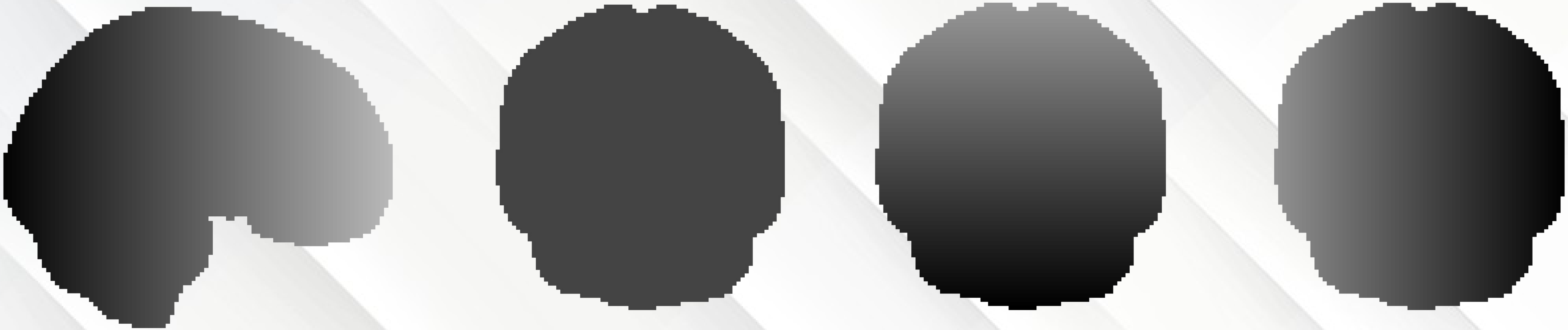


Kernel Size and Bin Size

- kernel size => same as in a CNN
- absolute binning
- relative binning

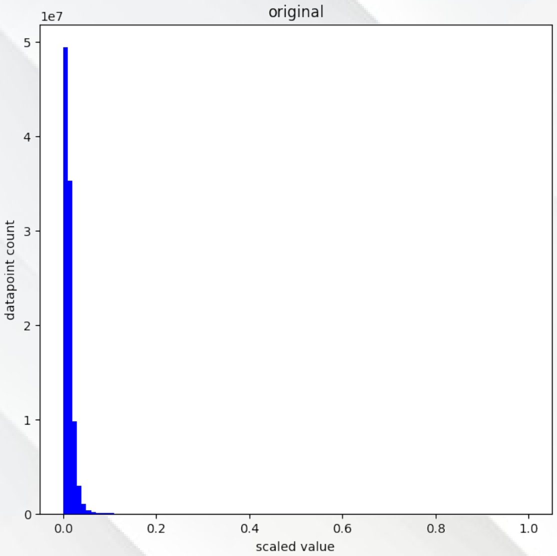
Coordinate Map

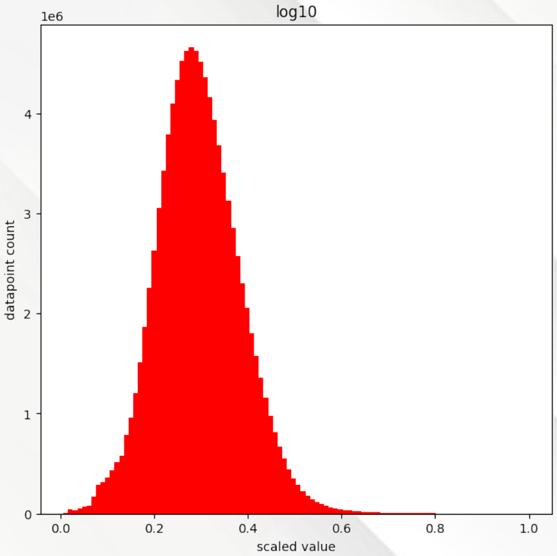
- global context
- normalized space
- de-normalization => native space

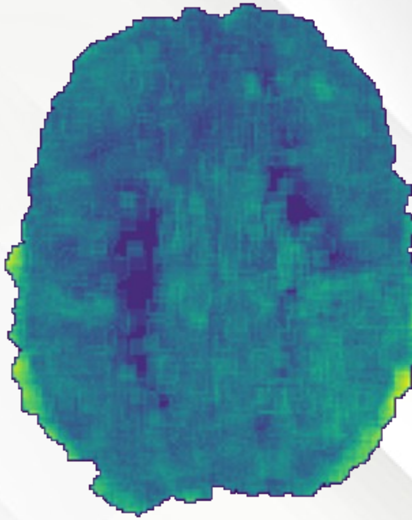


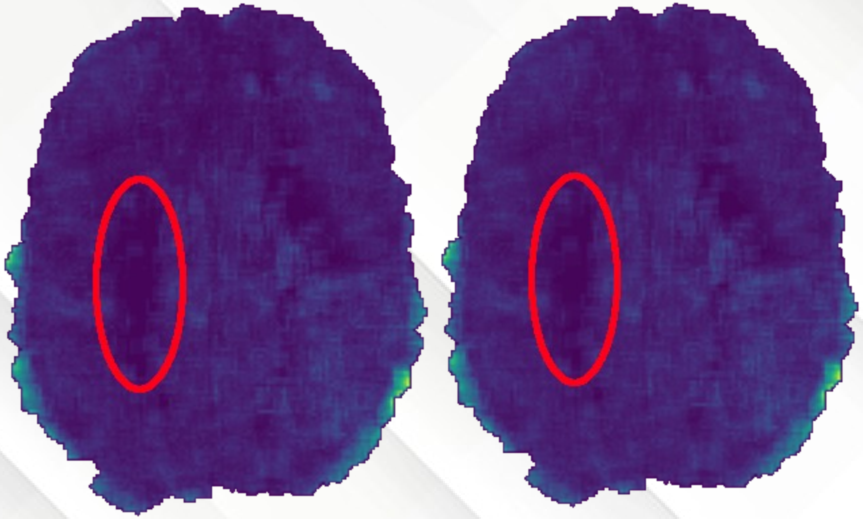
Scaling and Normalization

- min-max scaling
- left skewed features => log



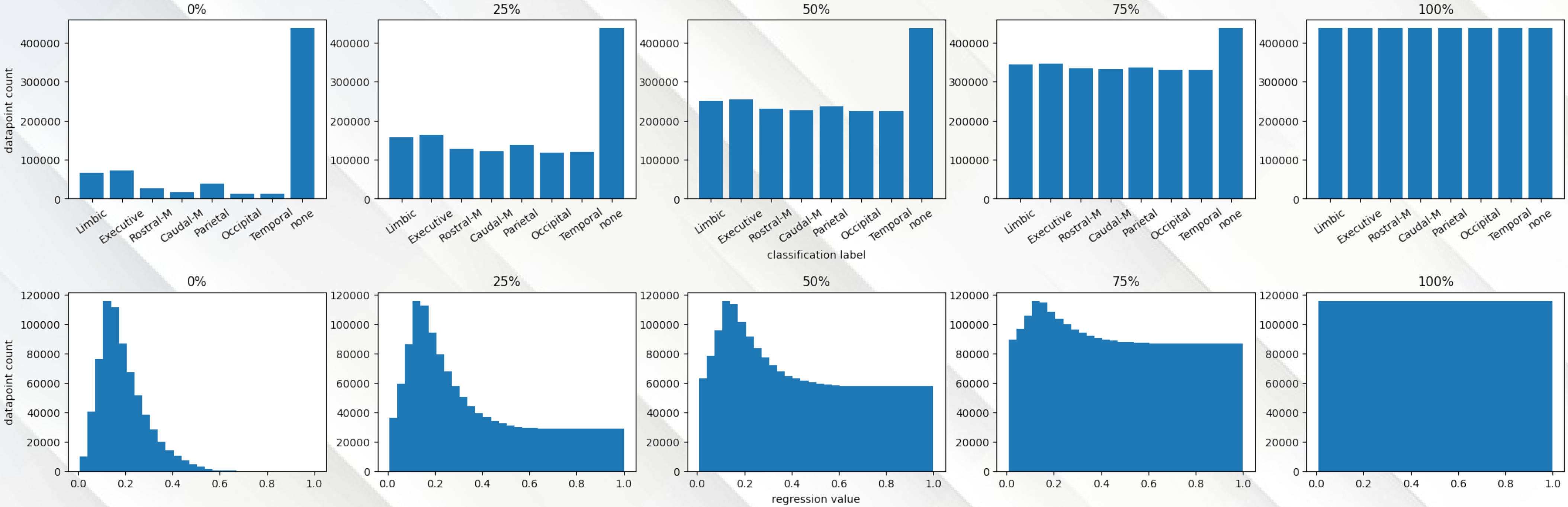






Balance Ratios

- Partially balanced data
- 0 => unbalanced; 1 => balanced



Exhaustive Sequential Backwards Feature Selection

- target metric => validation accuracy
- stopping criteria => target metric 2% decrease
- stopped after 41 features (92 total)
- Maximum accuracy increase of 2% (peaked at iteration 35)

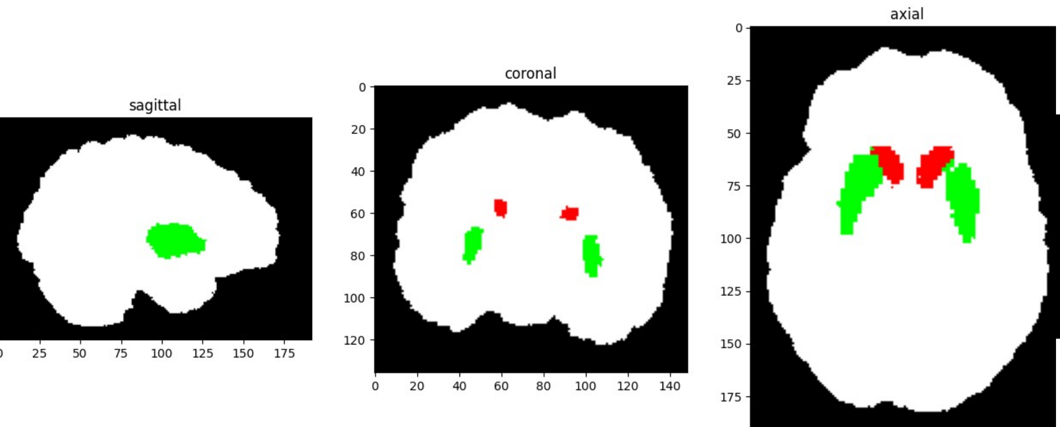
Additional Aspects

- Single/Many Different Kernel Sizes
- Single/Many Different Bin Sizes
- Control/Patient/Both Records
- Left/Right/Both Hemisphere Datapoints
- Additional Clinical Features for Patient Records
- Data Augmentation in Native Space

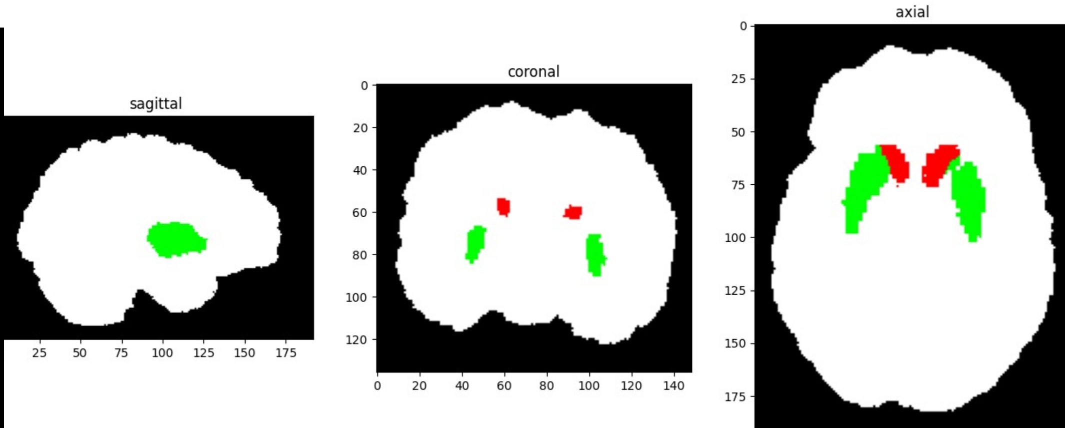
Subcortical Segmentation Results

- Minimal tuning required
- 96% accuracy

true



predicted

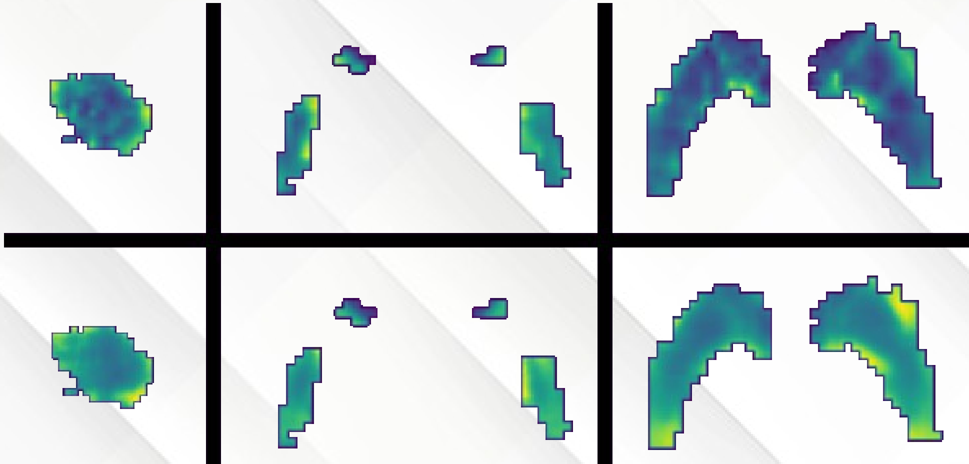


Fractional Anisotropy Results

- T1-Normalized space
- Patients records 0.1 correlation decrease
- Mixed records only 0.03 decrease
- 0.85 pearson

true

predicted

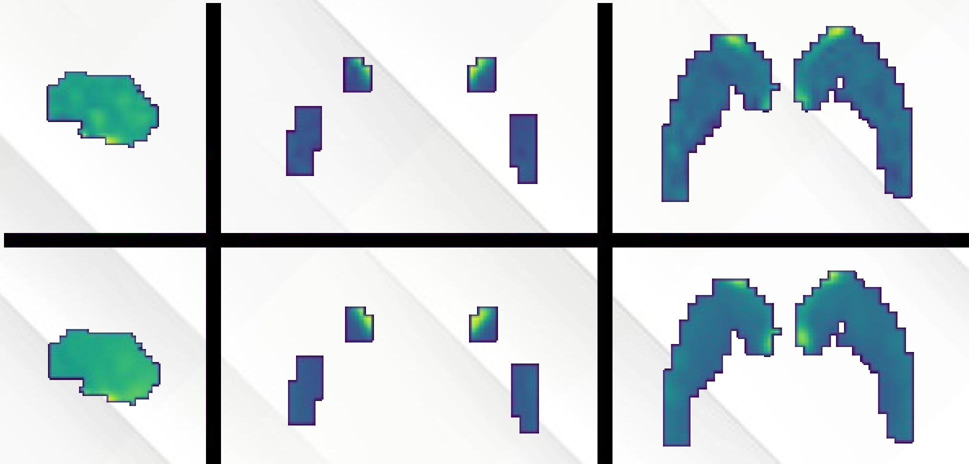


Mean Diffusivity Results

- Very similar results between modalities
- Patients records 0.04 correlation decrease
- Mixed records only 0.02 decrease
- 0.95 pearson

true

predicted



Relative Connectivity Results

- T1-Normalized space
- Patients records 4% accuracy decrease
- Mixed records only 2% decrease
- 73% accuracy

true

predicted

Conclusions

- normalized space is preferred over native space
- T1 generally better than T1/T2
  - T1/T2 better performance with less input data
  - possible explanation => T2 is anisotropic
- substantial performance drop with patients only
  - marginal decrease with mixed records
  - clinical features did compensate for patients records
- augmentation did not affect performance
- log transforming the left skewed features did help
- right hemisphere datapoints better performance
  - Mixed hemisphere data no performance drop

Future Improvements

- feature selection re-run
- constant gender ratio
- optimize binning, kernel size and feature class combinations

Project Future

- expand FA and MD models for the whole brain
- improve relative connectivity model