

# A 3D electron microscopy segmentation pipeline for hyper-realistic diffusion simulations

Michiel Kleinnijenhuis<sup>1</sup>, Errin Johnson<sup>2</sup>, Jeroen Mollink<sup>1,3</sup>, Saad Jbabdi<sup>1</sup>, Karla Miller<sup>1</sup>

<sup>1</sup> FMRIB Centre, University of Oxford, Oxford, United Kingdom

<sup>2</sup> Sir William Dunn School of Pathology, University of Oxford, Oxford, United Kingdom

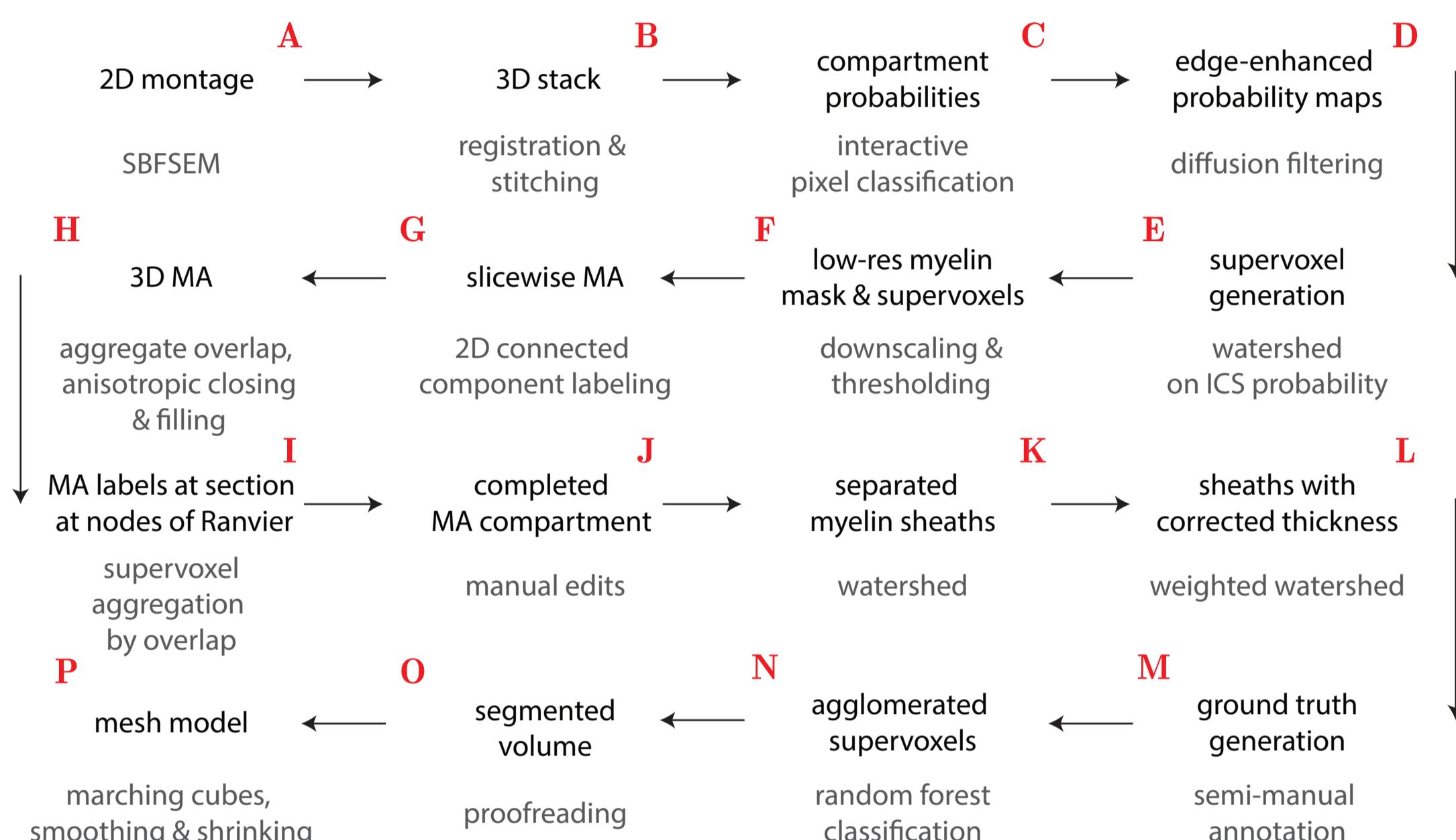
<sup>3</sup> Department of Anatomy, Donders Institute for Brain, Cognition & Behaviour,

Radboud University Medical Center, Nijmegen, The Netherlands

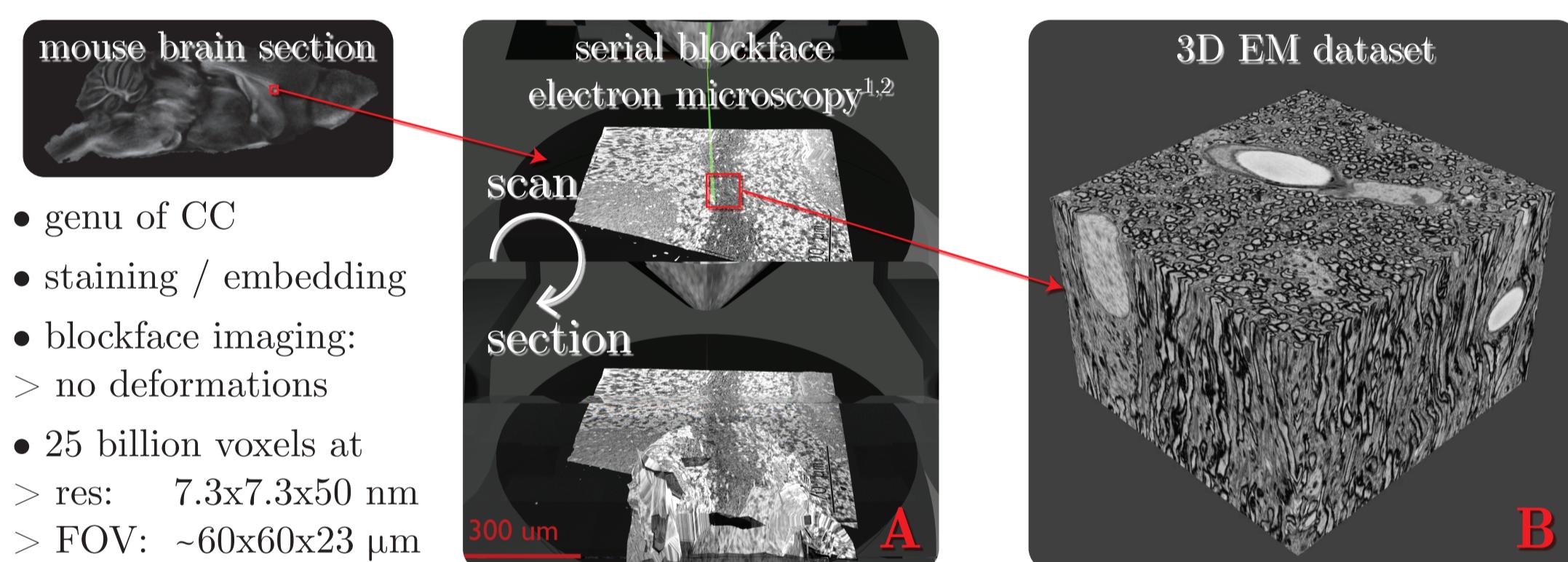
## background

- problem: diffusion MRI lacks specificity to tissue features, e.g. myelination
- goal: identify signature MRI signal components specific to tissue compartments
- approach: hyper-realistic simulations based on microscopy data
  - essence of microstructure => MRI signal relation
  - flexibility to manipulate the model

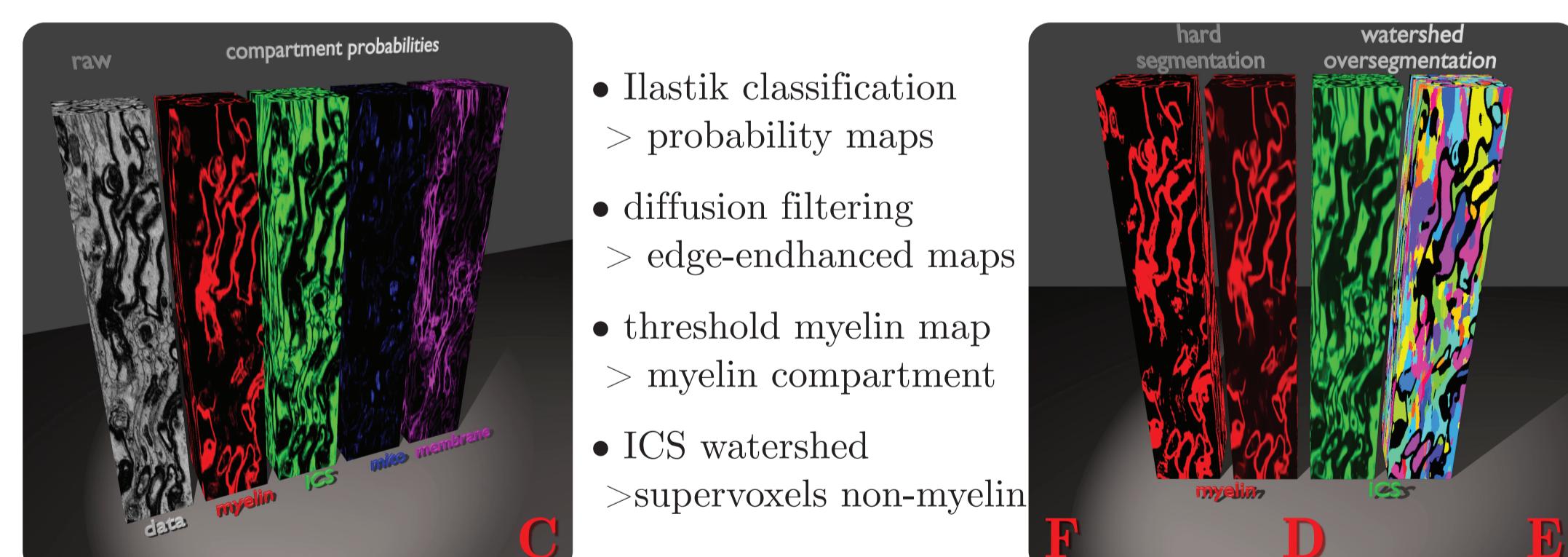
## segmentation pipeline overview



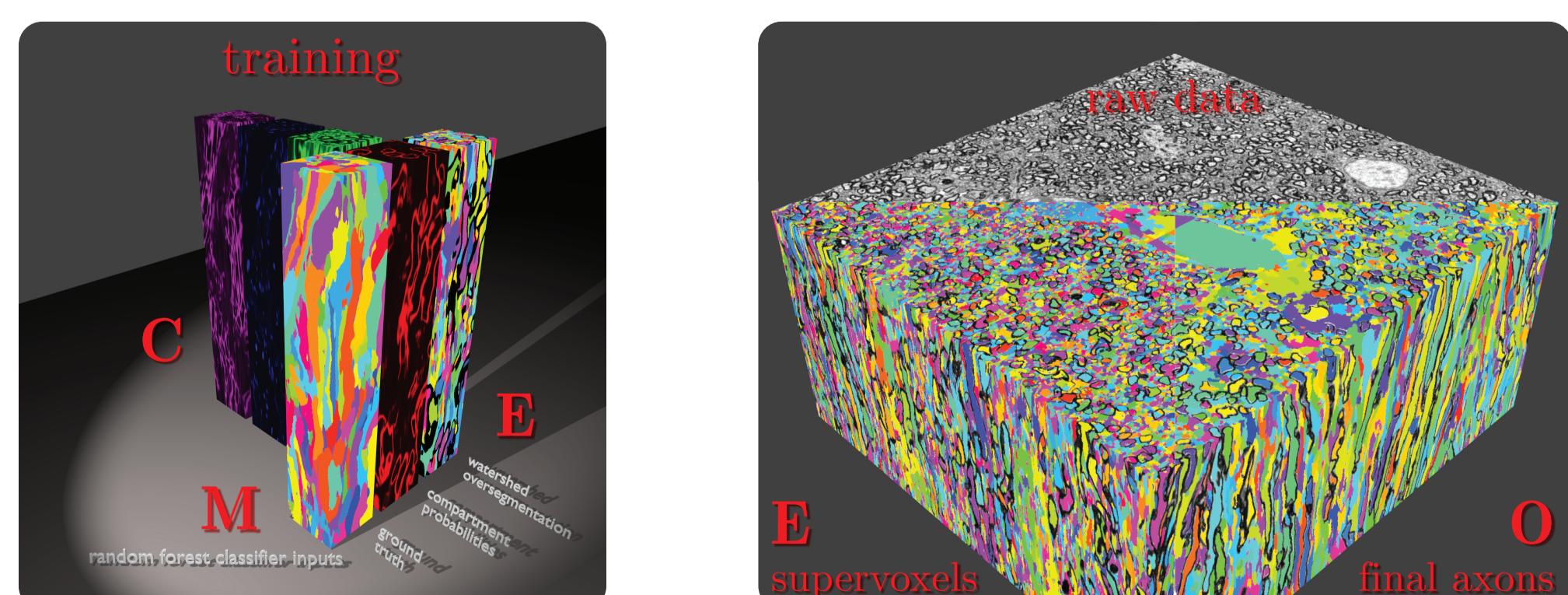
## 3D EM data acquisition (Gatan 3View)



## pixel classification (Ilastik<sup>3</sup>)

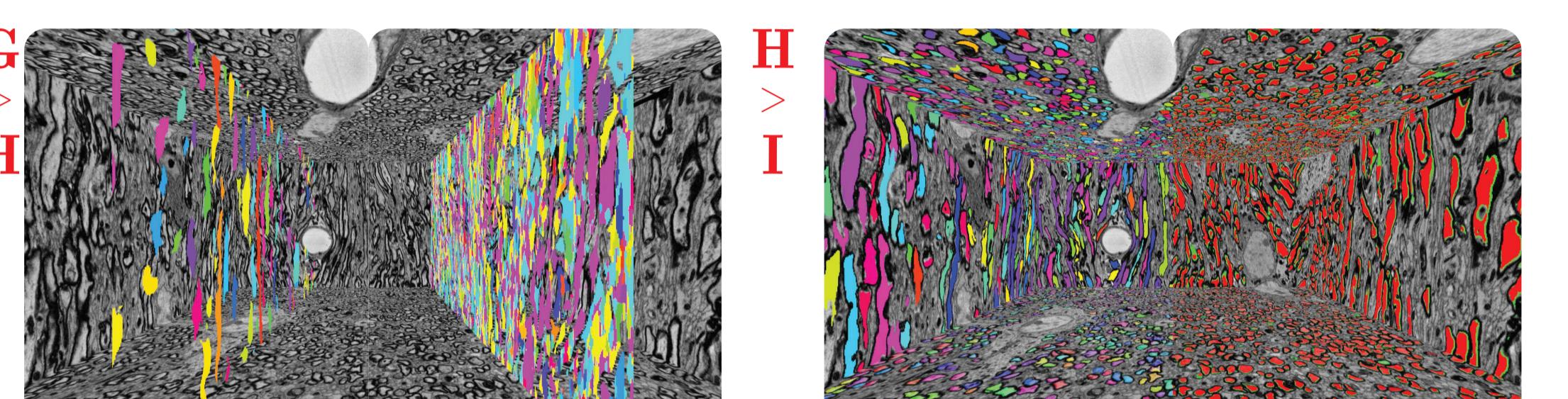
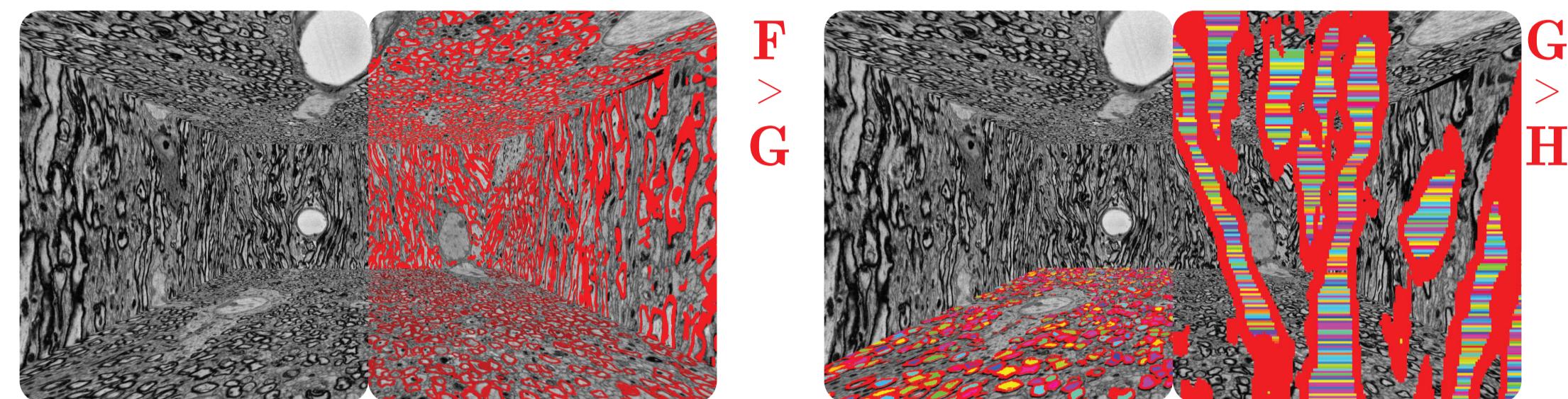


## axon classification (Neuroproof<sup>4</sup>)

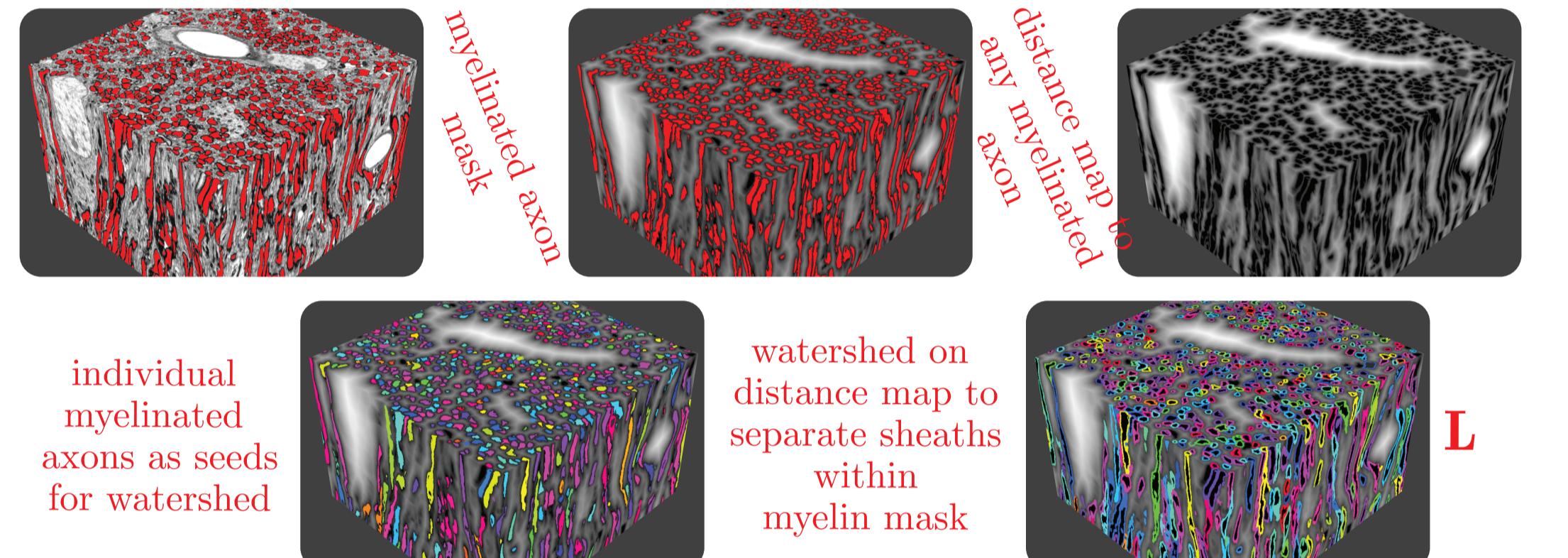


## methods

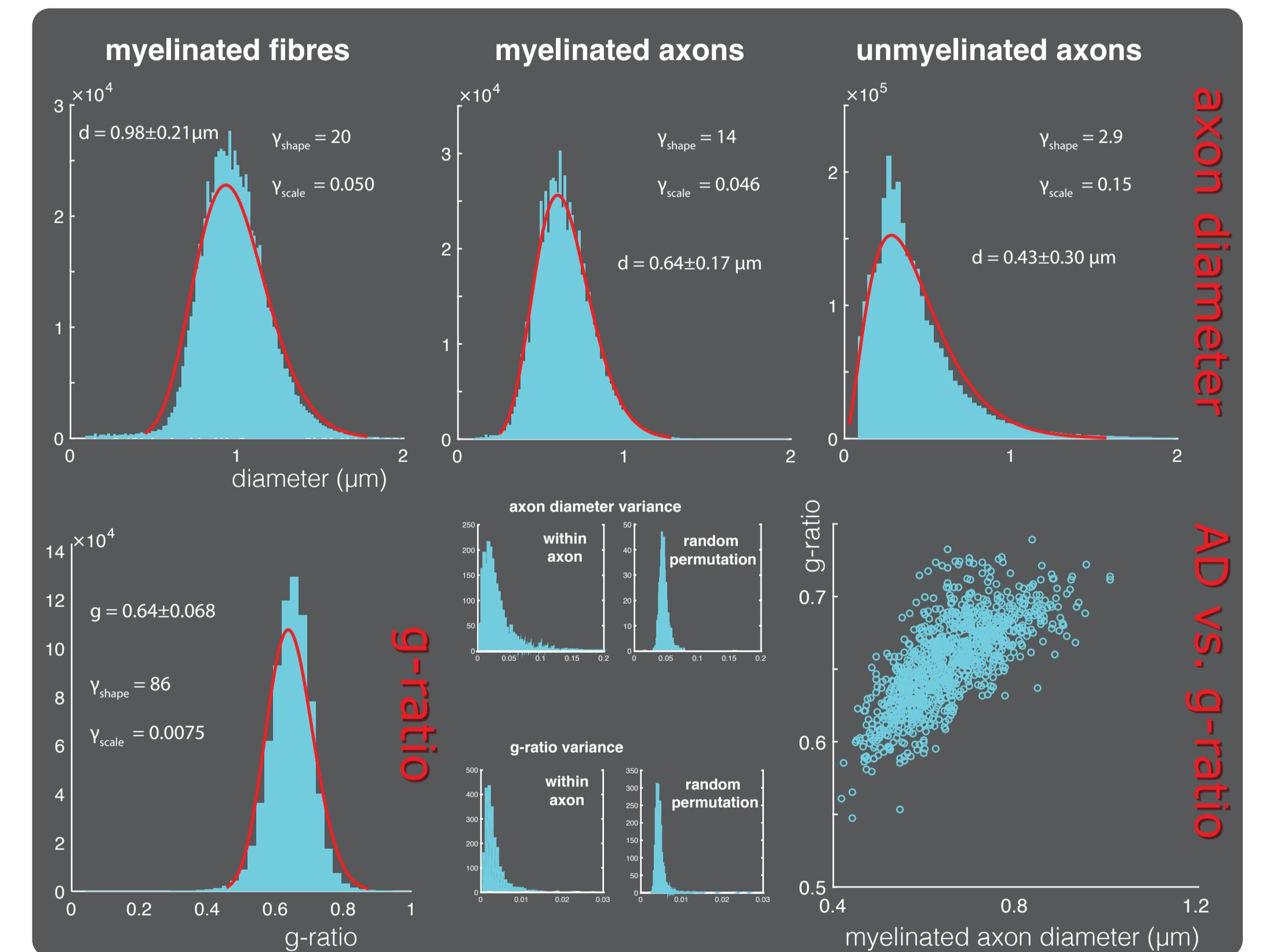
## myelinated axon segmentation



## myelin sheath separation



## tissue properties histograms



## conclusions

- we have developed a method for segmenting large 3D electron microscopy datasets of the white matter
  - minimal manual intervention, yet still fairly laborious
- remaining issues:
  - complex myelin loops
  - split/merge errors automated segmentation
- utility:
  - flexible mesh models for realistic simulations of diffusion MRI
  - informative benchmark statistics of tissue microstructure
  - a way to robustly quantify subtle changes in myelination

## conclusion