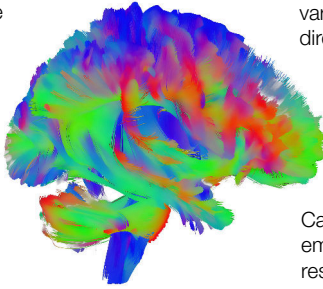


Background and Research Questions

Tractography maps brain white matter (WM) pathways as polylines



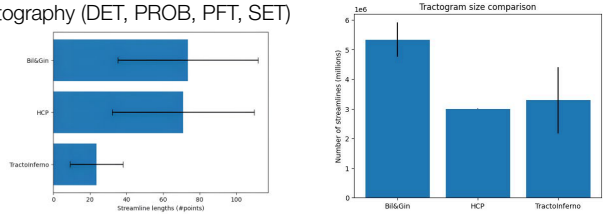
Pathways (streamlines) vary in length, preventing direct comparison

Current models (e.g., FINTA [1]) require uniform resampling, distorting the original shape

Can we learn better embeddings without resampling?

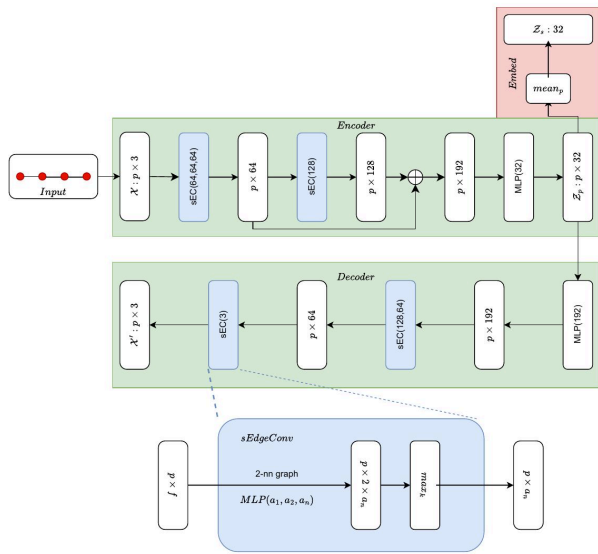
Data

- Bil&Gin [2]: A subsample of the Bil&Gin dataset, 206 subjects with streamline labelled based on anatomical plausibility
- HCP [3]: A subsample of 41 subjects of the test-retest release of the HCP dataset. Gold-standard for tractography analyses
- TractoInferno [4]: A subsample of 20 subjects, each with 4 types of tractography (DET, PROB, PFT, SET)



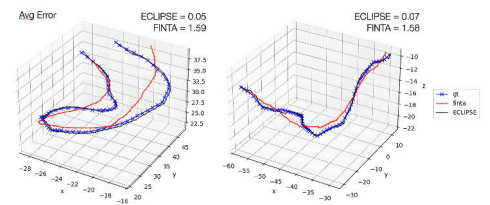
Model & Results

Our model, ECLIPSE, has an autoencoder-like architecture based on edge convolution

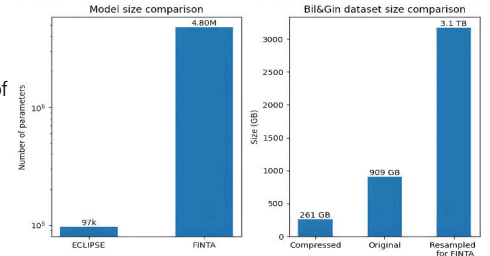


- ECLIPSE has a substantially lower reconstruction error than FINTA

- FINTA tends to over-smooth streamlines, while ECLIPSE keeps the reconstruction closer to the original



- ECLIPSE has ~50 times less parameters than FINTA. The size of the Bil&Gin dataset preprocessed for FINTA was 3.1 Tb, while the original version was 909 Gb, and the compressed version 261 Gb.



Generalization

- ECLIPSE shows generalization capabilities to different datasets, step sizes and tractography types

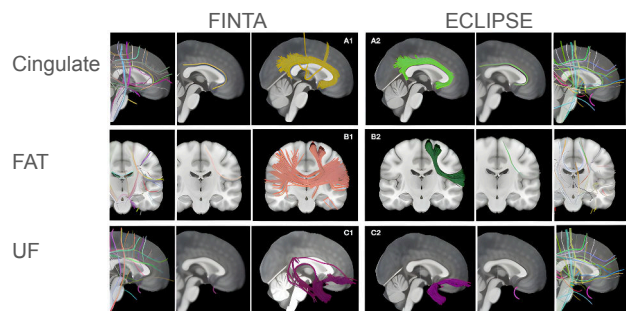
Model	fixed step size		flexible step size		
	1 mm	2 mm	3 mm	const	mixed
FINTA (padding)	0.47	4.11	13.02	45.77	22.45
FINTA (resampled)				0.28	
ECLIPSE (DEC)	0.14	2.36	15.73	0.09	81.59
ECLIPSE	0.06	0.24	1.58	0.07	5.98

Model	B&G HCP		TractoInferno			
	PROB	PROB	DET	PROB	PFT	SET
FINTA (padding)	0.82	0.83	49.23	15.29	16.64	20.28
ECLIPSE (DEC)	0.28	0.29	238.45	78.31	58.07	107.50
ECLIPSE	0.08	0.07	27.85	3.83	5.57	13.68

MSE of the models in different settings

Downstream task

- Qualitative analysis on downstream tasks, show that ECLIPSE embeddings achieve better discrimination between different streamline bundles: Cingulate, Front Aslant Tract (FAT), Uncinate Fasciculus (UF)



References

[1] Legarreta, Jon Haltz, et al. "Filtering in tractography using autoencoders (FINTA)." *Medical Image Analysis* 72 (2021): 102126.

[2] Mazoyer, Bernard, et al. "BIL&GIN: A neuroimaging, cognitive, behavioral, and genetic database for the study of human brain lateralization." *Neuroimage* 124 (2016): 1225-1231.

[3] Van Essen, David C., et al. "The WU-Minn human connectome project: an overview." *Neuroimage* 80 (2013): 62-79.

[4] Poulin, Philippe, et al. "TractoInferno-A large-scale, open-source, multi-site database for machine learning dMRI tractography." *Scientific Data* 9.1 (2022): 725.