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- An extensive comparison between diffusion approaches based on brain age predictions and the identification of the driving white matter (WM) regions in human ageing is still lacking.
- This study was performed to close this knowledge gap by mapping WM features across the lifespan and identifying regions driving global estimates of brain age.

Methods

- Tract-based spatial statistics were used to extract region-wise (John Hopkins University atlas) and global diffusion metrics for six different diffusion approaches¹ using UK Biobank diffusion-weighted MRI data N=35,749, 44.57 to 82.75 years (Figure 1).

Figure 10: Performance of the proposed model as a function of training data percentage. The graph shows four metrics: MAE/10, r, R2, and RMSE/10. The x-axis represents Training Data Percentage (0 to 50), and the y-axis represents Value (0.4 to 0.8). The metrics generally improve as training data percentage increases, with r and R2 showing the most significant improvement and reaching a plateau around 0.8 and 0.65 respectively.

Training Data Percentage	MAE/10	r	R2	RMSE/10
2	0.39	0.77	0.59	0.48
4	0.38	0.79	0.63	0.46
6	0.38	0.80	0.64	0.47
8	0.38	0.79	0.61	0.48
10	0.37	0.80	0.64	0.46
20	0.37	0.80	0.64	0.46
30	0.37	0.80	0.64	0.46
40	0.38	0.79	0.63	0.47
50	0.37	0.80	0.64	0.46

- Differences in correlations between predicted and chronological age across diffusion approaches were small for corrected ($r \leq 0.02$) and uncorrected age predictions ($r < 0.05$).

- Brain age gaps (BAG) were strongly correlated across models, with $r > 0.7$ (Fig. 3).
- Of all white matter regions, fornix features were strongest correlated with age (Fig. 4) and having the highest feature gain in brain age predictions (Table 1).

BRIA	DKI	DTI	SMT	mcSMT	WMTI	Multimodal
Micro FA fornix (54957)	MK fornix (39662)	MD fornix (50535)	MD fornix (43563)	Intra fornix (38043)	AWF fornix (52531)	Micro FA Fornix (67749)
Micro RD right external capsule (22860)	RK fornix (26954)	RD FMIN (18386)	MD right anterior corona radiata (24675)	Extra trans Fornix (35799)	RadEAD ATRL (12328)	RD Fornix right Striatoterminals (17664)
Micro FA FMIN (10081)	AK right anterior limb of internal capsule (16340)	RD fornix right stria terminalis (15431)	MD SLFR (19451)	Extratrans right external capsule (15369)	RadEAD right anterior corona radiata	AK anterior right limb of internal capsule (17664)
Micro FA fornix right stria terminalis (9853)	AK fornix	AD fornix (9637)	MD FMIN (13527)	Extra MD anterior left limb of internal capsule (6254)	RadEAD IFOFR (9828)	RadEAD right anterior corona radiata (17375)
Micro RD Fornix right stria terminalis (9812)	AK left superior frontooccipital fasciculus	FA fornix left striatoterminals (9283)	FA fornix (12011)	Extra trans anterior right limb of internal capsule (12722)	RadEAD right external capsule (9793)	RadEAD SLFR (15840)

[illegible]

Heatmap showing the correlation of gene expression across various tissues and developmental stages. The color scale ranges from blue (low correlation) to red (high correlation). The tissues are grouped into two main clusters: one with high correlation (red) and one with low correlation (blue). The developmental stages are grouped into two main clusters: one with high correlation (red) and one with low correlation (blue).

- Global fornix features are highly correlated in clearly distinguishable clusters (Fig. 5).
- Predicting global diffusion features from age, sex and scanner site produces clear curvilinear trends across approaches (Fig. 6).
 - Fig. 6A-B: predicted scores
 - Fig. 6C-D: raw scores
 - Fig. 6E: R^2 (bars) and SE (below bars) for 6A-B

Figure 2: Variance explained by linear models predicting mean model metrics.

Panel A: BRIA, DKI, and DTI Metrics

Panel B: SMT, mcSMT, and WMTI Metrics

Panel C: Free Value

Panel D: Free Value

Panel E: Variance Explained by Linear Models Predicting Mean Model Metrics

Metric	Variance Explained (R^2)
Free Value	0.012
Free Value	0.047
Free Value	0.081
Free Value	0.126
Free Value	0.133
Free Value	0.136
Free Value	0.211
Free Value	0.227
Free Value	0.249
Free Value	0.093
Free Value	0.116
Free Value	0.142
Free Value	0.149
Free Value	0.221
Free Value	0.225
Free Value	0.24
Free Value	0.176
Free Value	0.177
Free Value	0.182
Free Value	0.007
Free Value	0.101
Free Value	0.122
Free Value	0.157
Free Value	0.176
Free Value	0.037
Free Value	0.026
Free Value	0.013

- Conventional and advanced diffusion models perform concordant with each other on brain age predictions, with fornix being the key region for these predictions.
- Fornix features were not only strongest correlated with age, but formed also a unique, strong correlation structure across diffusion approaches indicating similarities in metrics of different diffusion approaches.
- Age curves of global WM features showed similarities in slopes for features of different approaches, indicating that advanced diffusion approaches can be useful in addition to conventional DTI when examining age-WM associations.

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