Supplementary Material for:

Cross-sectional and longitudinal trajectories of structural connectome aging diverge: a diffusion MRI study across the adult lifespan

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S1 Sample-construction flow

The analytic sample was derived from the public Dallas Lifespan Brain Study (OpenNeuro ds004856) by the following sequence of filters applied to the per-scan tractography output:

- All diffusion-weighted scans for which the deterministic CSD tractography pipeline ran to completion: 405 scans across 200 subjects.
- Restriction to scans whose post-resampling AAL parcellation contained the full 116 regions: 377 scans across 194 subjects (28 scans dropped, all due to incomplete parcellation after non-linear interpolation).
- Restriction to scans for which the streamline-count connectivity matrix was non-empty and all summary network metrics were available: 377 scans across 194 subjects (no additional rows dropped at this step).

The 28 excluded scans correspond predominantly to a small subset of older participants in whom the resampled atlas lost one or more peripheral regions; these scans were not directly comparable to the 116-region majority and were excluded from all analyses.

S2 Linear mixed-effects model specification

For each network metric y_{ij} (subject i, wave j), we fit:

$$y_{ij} \;=\; \beta_0 \;+\; \beta_{\text{time}}\, t_{ij} \;+\; \beta_{\text{age0}}\, \text{age}_{i,0} \;+\; u_{0i} \;+\; \varepsilon_{ij},$$

$$u_{0i} \sim \mathcal{N}(0, \sigma_u^2), \qquad \varepsilon_{ij} \sim \mathcal{N}(0, \sigma_\varepsilon^2),$$

where t_{ij} is the time elapsed from each subject's baseline scan (in years; assumed approximately 2 years between waves following the DLBS protocol), $\text{age}_{i,0}$ is the subject's baseline age, and u_{0i} is a per-subject random intercept. Models were fitted by REML using `statsmodels.MixedLM` with the

BFGS optimizer, with Powell and conjugate-gradient as fallbacks. The fixed effect of interest was β_{time}, reported with its z-statistic and p-value.

We did not include a random slope for time, both because the longitudinal subsample is modest in size ($n = 115$) and because exploratory fits with a random slope produced near-singular variance components for several metrics. The reported random-intercept fits are the most parsimonious specification consistent with the data.

S3 Sex differences (full table)

Table S1. Welch t-tests on baseline data comparing male ($n = 74$) and female ($n = 120$) participants. Effect sizes (Cohen's d) and uncorrected p-values are reported.

Metric	**Male**	**Female**	d	t	p
Mean FA	0.268	0.267	+0.03	—	0.82
Threshold h_{50}	0.155	0.143	+0.23	—	0.13
Threshold AUC	0.173	0.165	+0.18	—	0.24
Targeted-att. h_{50}	0.441	0.426	+0.30	—	0.04
Clustering	0.518	0.526	−0.25	—	0.09
Connection density	0.224	0.227	−0.07	—	0.61
Mean node strength	1.167	1.125	+0.12	—	0.42

S4 Machine-learning model performance (full)

Table S2. Cross-validated classification of younger (< 50 yr) vs older (≥ 50 yr) adults from baseline-only data ($n = 194$, 10-fold stratified CV). All pipelines included in-fold standardization. Permutation testing on the best model (logistic regression) used 1,000 label-shuffling iterations.

Model	**Accuracy (mean±SD)**	**Balanced accuracy**	**AUC**
Logistic regression	0.777 ± 0.094	0.769	0.848
SVM (RBF)	0.777 ± 0.129	0.770	0.830
Random forest	0.746 ± 0.123	0.741	0.819
Gradient boosting	0.756 ± 0.094	0.754	0.816
k-NN ($k = 7$)	0.700 ± 0.098	0.703	0.761

Permutation test on logistic regression ($n_{\text{perm}} = 1{,}000$):
actual accuracy = 0.7774; permuted mean = 0.5318; $p_{\text{perm}} = 0.001$.

S5 Random-forest feature importance

S6 Code, data, and reproducibility

The Dallas Lifespan Brain Study is publicly available on OpenNeuro under accession ds004856. Per-scan tractography output (CSV with one row per scan, including all summary network metrics, FA, streamline counts, and processing metadata) and the analysis notebook used to produce all numbers reported in the main text are available from the corresponding author upon reasonable request. The notebook is

Table S3. Random-forest feature importance (mean decrease in impurity) from a model fit on the full baseline sample.

Feature	**Importance**
Mean FA	0.314
Clustering coefficient	0.134
Number of streamlines	0.110
Threshold AUC	0.096
Mean node strength	0.082
Connection density	0.081
Number of edges	0.080
Targeted-attack h_{50}	0.069
Threshold h_{50}	0.034

single-file Python and runs in approximately 10 minutes on a standard laptop. The random seed for all stochastic procedures (bootstrap, permutation, cross-validation) was set to 42.