
Human lifespan changes in the brain's functional connectome

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Supplementary Methods

1. Image quality control process

In this study, we employed a comprehensive four-step data quality control framework that combined automated assessment approaches and expert manual review to assess both structural and functional images (Supplementary Figs 1 and 2). This rigorous framework effectively identified imaging artifacts or errors, ensuring the accuracy and reliability of the neuroimaging data.

Step 1: Quality control of the raw images. First, we performed a preliminary quality control to filter out low-quality scans with problematic acquisitions. For several publicly available datasets (dHCP, HCP-Development, HCP-Aging, HCP-Young Adult, and ABCD) that provide information on image quality, we performed initial quality control according to their recommended inclusion criteria. For the BCP dataset, each scan was visually reviewed by two neuroradiologists experienced in pediatric MRI. For the other datasets, we conducted automated quality assessment using the MRI Quality Control (MRIQC) tool¹, which extracted non-reference quality metrics for each structural (T1w and T2w) and fMRI image. In each dataset, structural images were excluded if they were marked as outliers (more than 1.5 times the interquartile range (IQR) in the adverse direction) in at least three of the following quality metrics: entropy-focus criterion (EFC), foreground-background energy ratio (FBER), coefficient of joint variation (CJV), contrast-to-noise ratio (CNR), signal-to-noise ratio (SNR), and Dietrich's SNR (SNRd). Similarly, functional images were excluded if they were marked as outliers in three or more of the following quality metrics: AFNI's outlier ratio (AOR), AFNI's quality index (AQI), DVARS_std, DVARS_vstd, SNR, and temporal signal-to-noise ratio (tSNR). This step resulted in the exclusion of 822 structural and 951 functional images.

Step 2: Determination of whether to pass the entire processing pipeline. Following the initial quality control step, the images were submitted to the pre- and post-processing pipelines. A detailed description of the latter is provided in the “**Data processing pipeline**” section. Any scan that could not pass the entire data processing pipeline was excluded, resulting in the removal of 2,731 structural and 2,816 functional images.

Step 3: Surface quality control and head motion control. For structural images, the Euler number was employed to assess the quality of the reconstructed cortical surface. The Euler number is a mathematical concept that summarizes the topological complexity of a surface and, can be calculated as $2-2n$, where n represents the number of defects such as holes or handles. A high Euler number represents a surface with fewer defects, indicating high-quality cortical surface reconstruction. The Euler number is a reliable and quantitative measure that can be used to identify images unsuitable for analysis²⁻⁴. Similarly, the images with an Euler number magnitude less than 1.5 times the IQR in the adverse direction from the study-specific distribution ($Q1-1.5*IQR$) were identified as outliers and excluded. For functional images, scans with large head motion (mean FD > 0.5 mm, or frames with FD over 0.5 mm > 20%) were excluded, along with scans with fewer than 100 final time points or a ratio of final time points to original time points < 90%. In total, 2,012 structural images and 3,442 functional images were excluded.

Step 4: Visual double-check. During the initial three QC steps using automated assessment approaches, 5,565 scans with structural imaging problems and 7,209 scans with functional imaging problems were excluded. To further ensure the quality of the remaining scans, we performed a detailed and comprehensive visual check QC. (1) A visual QC team was assembled, comprising of four anatomically trained experts: Q.W., Q.Y., C.P., and L.S.. For each participant who had passed the automated QC steps, three 2D pictures were generated (one for structural MRI images and two for functional MRI images). (2) Based on these images, L.S. conducted the initial round of visual QC on both structural and functional data for all participants, recording the IDs of those with quality errors. (3) The pictures were then distributed evenly among Q.W., Q.Y., and C.P. for a secondary evaluation. The IDs of the participants exhibiting quality defects were documented. The final list of participants who were excluded was determined based on the combination of these records. Throughout the process, the QC team engaged in in-depth discussions to ensure that the exclusion criteria were consistently applied across members. The exclusion criteria were as follows: The T1-weighted structural images were primarily evaluated for artifacts and quality of cortical segmentation, reconstruction, and registration. For participants with T2-weighted images, those with abnormal myelination distribution (as measured by the T1/T2 ratio) were also excluded. Functional images were assessed for brain coverage, functional-to-structural and functional-to-standard space registration quality, and volume-to-surface mapping quality. Participants were excluded if any of these issues were present. A comprehensive tutorial on visual QC procedures is available at <https://github.com/sunlianglong/BrainChart-FC-Lifespan/blob/main/QC/README.md>. In this step, 636 structural images and 1,103 functional images were excluded. Finally, only scans that successfully passed QC for both functional and structural images were retained.

2. Data processing pipeline

(i) Structural data preprocessing. For individuals aged two years and older, we utilized the publicly available, containerized HCP structural preprocessing pipelines (v4.4.0-rc-MOD-e7a6af9)⁵, which have been standardized through the QuNex platform (v0.93.2)⁶. Briefly, this pipeline consists of three stages: (1) The PreFreeSurfer stage focused on the normalization of anatomical MRI data and involved a sequence of preprocessing steps that included brain extraction, denoising, and bias field correction on anatomical T1 weighted (T1w) and T2 weighted (T2w) MRI data (if T2w data were available). (2) The FreeSurfer stage aimed to create cortical surfaces from the normalized anatomical data, including anatomical segmentation; the construction of pial, white, and mid-thickness surfaces; and surface registration to the standard atlas. (3) The PostFreeSurfer stage converted the outputs from the previous steps into the HCP format (CIFTI). The volumes were transformed to the standard MNI space using nonlinear registration, while the surfaces were mapped to the standard fs_LR_32k space using spherical registration and surface downsampling. To mitigate the computational burden of processing the large ABCD dataset, we chose to use the community-shared, preprocessed data released through the ABCD-BIDS Community Collection⁷ (ABCD collection 3165; <https://github.com/ABCD-STUDY/nda-abcd-collection-3165>). The multimodal neuroimaging data were preprocessed using the ABCD-HCP pipeline, a variant of the HCP pipeline adapted to better suit the ABCD dataset. Modifications to the ABCD-HCP structural pipeline include volume registration algorithms and bias field correction methods. Further details of these modifications can be found in the online document (<https://collection3165.readthedocs.io/en/stable/pipelines/>).

For participants in the postmenstrual age range of 32 to 44 weeks from the dHCP study, we applied the officially recommended dHCP structural pipelines⁸, which have been specifically designed to account for the substantial differences between neonatal and adult MRI data. This HCP-style pipeline included the following steps: (1) bias correction and brain extraction, which were performed on the motion-corrected, reconstructed T2w images; (2) tissue segmentation; (3) cortical reconstruction of the white matter surface; (4) surface topology correction; (5) generation of pial and mid-thickness surfaces; (6) generation of inflated surfaces derived from the white matter surface through an expansion-based smoothing process; and (7) projection of the inflated surface onto a sphere for surface registration. Furthermore, we used the officially recommended iBEAT V2.0 pipelines⁹ for participants aged from 0-2 years (all from the BCP study). This pipeline, which is optimized for preprocessing early-age neuroimaging data based on advanced algorithms, has shown superior performance in tissue segmentation and cortical reconstruction for BCP datasets compared to alternative approaches⁹. The main steps of this pipeline included (1) inhomogeneity correction of T1w/T2w images; (2) skull stripping and cerebellum removal (for participants with incomplete cerebellum removal, frame-by-frame manual corrections were performed); (3) tissue segmentation; (4) cortical surface reconstruction; (5) topological correction of the white matter surface; and (6) final reconstruction of the inner and outer cortical surfaces. To ensure consistency in data preprocessing, we employed the iBEAT pipeline for structural image preprocessing of participants aged 2-6 years (53 scans, representing 13% of the total BCP cohort) from the BCP cohort.

The individual cortical surface obtained from the dHCP and iBEAT V2.0 structural pipelines were aligned with the adult fs_LR_32k standard space using a three-step registration method (Supplementary Fig. 3). For participants aged 32 to 44 postmenstrual weeks, the following steps were implemented. (1) Individual surfaces were registered to their respective postmenstrual week templates¹⁰. (2) Templates for 32-39 postmenstrual weeks and 41-44 postmenstrual weeks were registered to the 40-week template. (3) The 40-week template was then registered to the fs_LR_32k surface template. For participants aged 1-24 months, the following steps were undertaken. (1) Individual surfaces were registered to their corresponding monthly age templates¹¹. (2) All monthly templates were registered to the 12-month template. (3) The 12-month template was then registered to the fs_LR_32k surface template. A supplementary analysis was conducted to validate the normative growth pattern of the global functional connectome, which involved avoiding cross-age surface registration (Supplementary Result 7 and Supplementary Fig. 18).

(ii) Functional data preprocessing in volumetric space. For individuals aged two years and older, the HCP functional preprocessing pipelines were employed⁵. The fMRIVolume stage consisted of the following steps. (1) Slice timing correction: This step was applied to single-band acquisitions, as multi-band acquisitions did not require slice timing correction. (2) Motion correction: EPI images were aligned to the single-band reference image using 6 DOF FLIRT registration. In cases where the single-band imaging data were not available, the first frame of the fMRI data was used as the reference. The motion parameters, including translations, rotations, and their derivatives were recorded. Additionally, the demeaned and linearly detrended parameter was provided for nuisance regression analysis. (3) EPI distortion correction: Geometric distortion correction was conducted using either the opposite-phase encoded spin-echo images (when LR-RL or AP-PA encoded acquisitions were available) or the regular (gradient-echo) fieldmap images (when fieldmap acquisitions were available). If neither image

was available, this step was skipped. (4) Anatomical registration: The fMRI images were registered to the T1w image using 6 DOF FLIRT with boundary-based registration (BBR). (5) Intensity normalization: The fMRI data, masked by the final brain mask generated by the PostFreeSurfer structural pipeline, were normalized to a 4D whole-brain average of 10,000.

For participants in the postmenstrual age range of 32 to 44 weeks from the dHCP study, we applied the dHCP functional pipelines¹². Building on the foundation of the HCP pipeline and the FSL FEAT pipeline, this pipeline was tailored to address the unique challenges associated with neonatal fMRI data. The key components of the pipeline included the following steps. (1) Fieldmap preprocessing, which included estimation of the susceptibility distortion field based on the opposite-phase encoded spin-echo images and subsequent alignment of this field to the functional data. (2) Registration, which included BBR of the fieldmap magnitude to the T2w image, BBR of the single-band reference image to the T2w image with incorporation of field map-based distortion correction, and 6 DOF FLIRT registration of the first volume of the functional multiband EPI to the single-band reference image. (3) Susceptibility and motion correction, which included slice-to-volume motion correction, motion-by-susceptibility distortion correction, and estimation of motion nuisance regressors. These steps resulted in distortion-corrected and motion-corrected 4D multiband EPI images in the T2w native volumetric space. For participants from the BCP cohort, we implemented several steps to obtain preprocessed volumetric fMRI data. (1) Motion correction: functional images were aligned to the single-band reference image using 6 DOF FLIRT registration. In the absence of a single-band reference, the mean functional images (with all frames aligned to the first frame) were employed as the reference. (2) Distortion correction: we performed distortion correction based on the opposite-phase encoding (AP-PA) spin-echo images. This step was only performed for participants with available images. (3) EPI to anatomical registration: the reference image was aligned to the anatomical image (T1w or T2w) using 6 DOF FLIRT registration.

(iii) Functional data preprocessing in surface space. In the fMRISurface stage of the HCP functional pipeline, the goal was to project the volume time series onto the standard CIFTI grayordinates space. For the data from the dHCP and BCP cohorts, we followed the same steps of the HCP preprocessing pipeline to achieve an accurate representation of cortical BOLD signals on the surface. Specifically, the fMRI volumetric data in the cortical cortex were separated into left and right hemispheres and mapped onto each participant's mid-thickness surfaces using a partial-volume weighted, ribbon-constrained volume-to-surface mapping algorithm⁵. Subsequently, the time courses were then transferred from the individual's native space to the fs_LR_32k standard space using each participant's surface registration transformations from the structural preprocessing stage.

Supplementary Results

1. Lifespan growth patterns of interindividual variability in the functional connectome

The GAMLSS framework permitted the utilization of models that account for multiple moments in the outcome distribution, including central tendency and dispersion that are represented by the mean (μ parameter) and variance (σ parameter), respectively. This flexible statistical modeling approach enabled us to chart age-related growth patterns in functional brain phenotypes, as captured by the μ parameter, and to model the interindividual variabilities of these phenotypes over time, as captured by the σ parameter. Our analyses indicated that across the lifespan, interindividual variabilities in functional brain metrics demonstrated nonlinear growth curves at both the global and system levels. The individual variability in most functional connectome metrics initially decreased, then gradually increased, and decreased again, with the greatest variability occurring at the middle and older ages (Extended Data Fig. 2). This result was generally consistent with previous studies showing that individual variability in functional connectivity decreases from 31 to 42 postmenstrual weeks of age¹³ and increases with age during adulthood¹⁴. The peak values of individual variability in both the global connectome mean and variance were observed in the middle of the sixth decade of life (55.0 years, 95% CI [53.7, 55.8] for global mean; 56.6 years, 95% CI [54.9, 57.9] for global variance). For system-specific segregation, the peak values of individual variability in the VIS, DA, VA, LIM, DM, and SM networks were observed from the middle of the sixth decade of life to 80 years. Specifically, the peak values were observed in the VIS network at 60.1 years (95% CI [58.2, 61.5]), in the DA network at 56.9 years (95% CI [55.0, 58.0]), in the VA network at 62.6 years (95% CI [58.5, 65.9]), in the LIM network at 55.5 years (95% CI [54.0, 56.7]), in the DM network at 64.3 years (95% CI [55.9, 80.0]), and in the SM network at 80.0 years (95% CI [66.5, 80.0]). The FP network exhibited its peak individual variability at 32 postmenstrual weeks.

2. Lifespan growth patterns of within-system and between-system connectivity

Based on the individual-based functional atlas, we calculated within-system and between-system connectivity for each network. Within-system connectivity was defined as the average of all pairwise connections among vertices within the same system. The within-system connectivity of all networks exhibited a nonlinear increase followed by a decrease across the lifespan, with the exception of the LIM network (Extended Data Fig. 5). When the connections were categorized by distance (short: 10-40 mm, middle: 40-75 mm, long: > 75 mm), the VIS, DA, VA, FP, and DM networks displayed comparable growth patterns for each distance bin as the overall within-system connectivity (Supplementary Fig. 8). In contrast, the overall growth pattern of within-system connectivity in the SM network was mainly influenced by long-distance connectivity. These results collectively indicate an enhanced within-system connectivity during early development, which facilitates the emergence and maturation of functional specialization, and an accelerated decline during aging, which reflects a reduction in functional specialization.

Between-system connectivity was defined as the average of all connections between vertices in one system and vertices in another system. During early development, the FP network exhibited a typical pattern of decreased between-system connectivity with all other networks (Extended Data Fig. 5). The DM network also exhibited a similar growth pattern of between-system connectivity (except for the DM-SM) (Extended Data Fig. 5). This general decoupling reflects the differentiation of the higher-order networks from other networks. Such patterns were also observed in all short- and medium-distance connectivity, and some long-distance connectivity

(Supplementary Fig. 8). However, several long-distance between-system connectivity, such as the DM-SM and FP-VA networks, were observed to be increased during early development (Supplementary Fig. 8). For the DA and VA networks, they decoupled from higher-order networks during early development, but both showed increased connectivity with the VIS network (Extended Data Fig. 5). This growth pattern was observed across short-, medium-, and long-distance connectivity (Supplementary Fig. 8). Finally, the VIS-SM network showed a pattern of initial decline followed by an increase across the lifespan, with consistent growth across different distances (Extended Data Fig. 5 and Supplementary Fig. 8). These results reveal the intricate patterns of lifespan growth observed in between-system connectivity, which represent a reorganization of network connectivity towards the balance of functional segregation and integration.

3. Sex differences in interindividual variability curves across the lifespan

In GAMLSS modeling, we incorporated sex as a variable to explore its effect on lifespan curves. The μ and σ coefficients indicate the adjusted mean and variance effect of sex on the functional metrics, accounting for confounding variables such as age, head motion (mean FD), and scanner site. We characterized the sex-stratified growth curves and interindividual variability curves of the functional connectome (Extended Data Fig. 6 and Supplementary Fig. 9) and found significant differences between males and females in various functional metrics (Supplementary Tables 3 and 4). The sex differences in growth curves are described in the Results section of the main text. Here, we focus on the interindividual variability curves. For the global variance of the connectome, the interindividual variability curve showed higher values in females than in males ($p_{FDR} < 0.01$), which is similar to the sex difference observed in the growth curve. For system segregation, females showed greater individual variability in the VIS and LIM networks (both $p_{FDR} < 0.01$) but lower individual variability in the VA, FP, and DM networks (all $p_{FDR} < 0.001$) than males. At the regional level, the angular gyrus, visual cortex, and lateral prefrontal cortex showed greater individual variability of functional connectivity strength (FCS) in females, whereas the sensorimotor cortex, medial prefrontal cortex, and superior temporal gyrus showed greater individual variability of FCS in males ($p_{FDR} < 0.05$).

4. Removing site effects using ComBat-GAM before construction of normative modeling

In studies involving multisite datasets, it is critical to account for and remove site-specific effects to ensure that the measurements across different sites are directly comparable. The ComBAT method¹⁵ and its variants^{16, 17} are increasingly used to harmonize neuroimaging data across multiple sites. However, employing ComBat for site effect removal in lifespan normative modeling introduces certain limitations^{3, 18, 19}. (1) It assumes homoskedasticity across different ages, potentially oversimplifying the normative variance structure. (2) The model's outcomes can be disproportionately influenced by sample characteristics, with larger sites having a greater contribution to shaping the normative growth curves. (3) Normative models based on ComBAT exhibit limitations when applied to out-of-sample data, potentially affecting generalizability. (4) ComBAT is constrained by its Bayesian foundation to Gaussian distributions, while GAMLSS offers a more flexible maximum likelihood approach, accommodating various distributions. This approach is particularly beneficial for data that significantly deviate from normality, including distributions with pronounced skewness or kurtosis. This flexibility is crucial for accurately modeling complex neuroimaging data across diverse developmental and aging stages. Therefore, we conservatively selected GAMLSS with site as a random effect for data harmonization in the main results. Additionally, we also conducted a supplementary analysis with the ComBat-related

harmonization method. We employed ComBAT with the generalized additive model (GAM) for each functional metric, with age and sex designed as the biological variables to be protected, and age as a smoothing term¹⁶.

We found that the absolute values of the fitted curves based on ComBAT-GAM differed from those obtained using the random effects approach. This may be attributed to ComBAT being more susceptible to influence from sites with large samples. This confirmed the aforementioned limitation (1). The growth centiles based on ComBAT-GAM showed little variation in variance across different ages, validating the limitation (2). However, the nonlinear growth patterns and age ranges of the peak points based on the ComBAT-GAM approach are aligned with those in the main results (Supplementary Fig. 15). To quantitatively assess the similarity in growth trends between the curves and those in the main results, we sampled 80 points at one-year intervals for each growth curve and growth rate and calculated the Pearson's correlation coefficients between them. All the metrics demonstrated a high degree of similarity to the main results (all $r > 0.9$, $p < 0.0001$). Consistent conclusions were also observed when sampling was conducted at six-month intervals (160 points) and monthly intervals (1,000 points) (all $r > 0.9$, $p < 0.0001$). For regional-level functional connectivity, we also observed high spatial similarity of the lifespan growth axis with that of the main results ($r = 0.98$, $p_{\text{spin}} < 0.0001$).

5. Lifespan growth patterns of negative connectivity in the functional connectome

We modeled the normative curves of negative functional connectivity at the global, system, and regional levels. The global mean of negative connectivity demonstrated a nonlinear increase from 32 postmenstrual weeks, stabilizing later in the second decade (Extended Data Fig. 8a). The within- and between-system negative connectivity were presented in Supplementary Fig. 16-I. The anticorrelations between the DM and task-positive networks (DA, VA, and FP) have been extensively reported in previous research^{20, 21}. In our study, we noted that the negative connectivity between the DM network and the DA/VA/FP networks continuously increased, extending into midlife. For nearly all vertices, the most notable changes in negative connectivity occurred within the first decade of life (Extended Data Fig. 8c), with a similar growth pattern to positive connectivity. Regions showing significant increases in negative connectivity were primarily located in the medial and lateral parietal cortex regions, which are pivotal components of the DM network. We then sought to ascertain whether the growth curves of negative connectivity across the cortex also spatially varied with the primary-to-transmodal axis. Using the PCA analysis, we identified a dominant growth axis of regional-level negative functional connectivity strength (Extended Data Fig. 8d and 8e). The first PC accounted for 53.5% of the variance. Intriguingly, we found that this lifespan growth axis also exhibited a significant association with the S-A axis ($r = -0.49$, $P_{\text{spin}} < 0.0001$, one-sided) (Extended Data Fig. 8f).

Additionally, we established the normative growth curves for the number of positive and negative connections across the lifespan (Supplementary Fig. 16-II) and performed case-control comparisons for three disorders. As expected, we initially observed that the growth curves for the number of positive and negative connections consistently showed opposite trends throughout the lifespan. Specifically, the number of positive connections initially decreased, reaching its lowest point during adolescence (12.9 years, 95% bootstrap CI 12.4-13.4), and subsequently increased, stabilizing during midlife. Notably, we reported that the global mean of positive connectivity increased from birth to adolescence (Fig. 1a). These results collectively suggest that the number of positive connections was decreasing while their strength was rapidly increasing. The number of negative connections initially increased, peaking during adolescence (12.9 years, 95%

bootstrap CI 12.3-13.4), and then decreased, also stabilizing during midlife.

6. Lifespan growth patterns of regional segregation in the subcortical cortex

In this study, we focused mainly on cortical surface-based analysis, which has several advantages over volume-based methods^{10, 22-25} and is increasingly recognized as a preferred approach. First, it respects the topological properties of the cortex, thereby enhancing the accuracy of anatomical and functional alignments^{22, 23}. Traditional volumetric registration may result in a reduction of statistical power due to residual misalignment between cortical folds^{10, 25}. It can also lead to the leakage of blood-oxygen-level-dependent (BOLD) signals across adjacent folds in fMRI studies²⁶. Second, it can minimize geometric distortion and improve the localization of functional signals^{22, 27}. Third, it allows for precise measurement of distinct cortical properties, including thickness, surface area, folding, and myelin content²³. Given these advantages, cortical surface-based analysis is an effective method for capturing dynamic and complex neurobiological changes during early development and for accurately representing the anatomical and functional correspondence between individuals throughout the entire lifespan.

In terms of surface space, integrating cortical and subcortical analyses presents significant methodological challenges. First, numerous tools have been developed for cortical surface reconstruction and registration across different developmental stages, including the neonatal stage^{8, 10, 23}, infant and early childhood^{9, 23}, and adulthood^{5, 28, 29}. However, robust tools for subcortical surface reconstruction and registration are notably lacking. Existing tools support hippocampal surface reconstruction in adult brains³⁰, yet their applicability across the entire lifespan, particularly during early developmental stages, remains unconfirmed. Second, the absence of subcortical reconstruction tools necessitates volume-based registration of subcortical nuclei, leading to less precise outcomes compared with cortical surface alignments based on folding information^{22, 24}. Third, even with usable subcortical surfaces, mapping functional signals poses challenges. Compared to mapping BOLD signals from the cortical ribbon (the area between the pial surface and the white matter surface), projecting the BOLD signal from the three-dimensional structure of subcortical nuclei onto their surfaces could result in significant signal loss from deeper voxels within the nuclei. This is a critical concern in maintaining the integrity of functional signals in subcortical regions.

Given the substantial morphological changes that the brain undergoes throughout the lifespan and the advantages of surface-based cortical registration, we focused on the cortical functional connectome using surface-based methodologies in our main results. Given the importance of subcortical structure, we have separately analyzed the lifelong growth patterns of functional connectivity in subcortical structures in the volume space, consistent with prior research^{5, 31, 32}

(i) Registering preprocessed fMRI to Montreal Neurological Institute (MNI) standard space.

In accordance with prior research^{5, 31, 32}, we analyzed the functional connectivity of subcortical nuclei in the volume space. In the “Data processing pipeline” section of Methods, we detailed the preprocessing and the registration process for structural and functional images in individual spaces. Building on this foundation, the fMRI volumes of all participants were resampled to a 3×3×3 mm resolution. Subsequently, a volume registration of the individual’s structural images was conducted (Supplementary Fig. 17-I), maintaining a consistent framework with the surface-based registration approach (Supplementary Fig. 3). Specifically, for participants aged 32 to 44 postmenstrual weeks, a three-step volume registration procedure was employed. (1) Individual

T2w images were mapped to their corresponding postmenstrual week templates. (2) The 32-39 and 41-44 postmenstrual week templates were registered to the 40-week template³³. (3) The 40-week template was registered to the MNI template³⁴. For participants aged 1-24 months, the following steps were implemented. (1) Individual T2w or T1w images were aligned with their monthly age templates³⁵. For individuals aged 6 months or younger, T2w images were used, whereas for those older than 6 months, T1w images were used. (2) All monthly templates were registered into the 12-month template. (3) This 12-month template was then registered to the MNI template³⁴. The deformation fields from these multi-step registrations were integrated using the Advanced Normalization Tools (ANTs) software to avoid multiple resampling of the functional signals. For participants aged more than two years, the individual structural images were registered to the standard MNI space. Using the deformation fields, we mapped each individual's fMRI volume to the MNI standard space.

(ii) *Extracting BOLD signals using subcortical parcellation.* A recent study introduced a robust multiscale subcortical parcellation³⁶. By developing a 'gradientography' approach, Tian and colleagues³⁶ effectively demarcated functional boundaries within subcortical structures of the in vivo human brain. This novel atlas, featuring four scales, captures the well-established anatomical nuclei at the coarsest scale. Given the extensive age range of the participants and to ensure functional comparability across various age groups, we used the coarsest scale (scale 1) atlas, which includes eight distinct regions: the hippocampus, amygdala, posterior thalamus, anterior thalamus, nucleus accumbens, globus pallidus, putamen, caudate nucleus (Extended Data Fig. 9a). This atlas was then resampled to a 3×3×3 mm resolution, encompassing 2354 voxels. For each participant, the time series for each voxel within these subcortical nuclei were extracted.

(iii) *Functional postprocessing of subcortical data.* For the ABCD dataset, the ABCD-HCP functional pipeline used DCANBOLDProcessing software (<https://collection3165.readthedocs.io/en/stable/pipelines/>) to reduce spurious variance that is unlikely to reflect neural activity. For other datasets, the preprocessed fMRI data were post-processed using SPM12 (v6470) and GREYNA (v2.0.0) with a uniform pipeline. Specifically, the following steps were initially conducted on the time series for each voxel of subcortical regions (2,354 vertices in total): linear trend removal, regression of nuisance signals (24 head motion parameters, white matter signal, cerebrospinal fluid signal, and global signal), and temporal bandpass filtering (0.01–0.08 Hz). To mitigate the effects of head motion, the motion censoring was further implemented. This process involved discarding volumes with an FD greater than 0.5 mm and adjacent volumes (one before and two after). To maintain the temporal continuity of the fMRI time series, we subsequently filled these censored frames using a linear interpolation. Participants with more than 20% of frames exceeding the 0.5 mm FD threshold were excluded from our study. Volume-based smoothing was then performed using a 6-mm full-width at half-maximum (FWHM) kernel.

(iv) *Calculating the regional segregation of subcortical nuclei.* For a given subcortical region, we calculated the functional connectivity between all pairs of voxels within the region using Pearson's correlation coefficient. All negative connectivity values were set to zero. The within-region functional connectivity, denoted as FC_w , was defined as the average connectivity of all pairs of voxels. Subsequently, we calculated the pairwise connectivity between all voxels within the region and voxels in all other regions. The between-region connectivity, denoted as FC_b , was

represented by the average strength of connections between this region and all other regions. System segregation³⁷ was determined by calculating the difference between FC_w and FC_b , normalized by FC_w , as described in the following formula:

$$\text{System segregation} = \frac{FC_w - FC_b}{FC_w}$$

Similarly, mean system segregation across the whole subcortex was defined as the difference between the whole-subcortex mean within-region connectivity and the whole-subcortex mean between-region connectivity, normalized by the whole-subcortex mean within-region connectivity.

The intra- and inter-regional connections for eight subcortical regions were shown in Supplementary Fig. 17-II. The mean segregation across the entire subcortex reached its peak in the early fourth decade of life (32.1 years, 95% bootstrap CI 31.0–33.2) (Extended Data Fig. 9b). The nonlinear growth curves of regional segregation of the hippocampus, amygdala, posterior thalamus, anterior thalamus, putamen, and caudate nucleus peaked in the late third decade or early fourth decade of life (Extended Data Fig. 9c). The nucleus accumbens peaked during adolescence, while the globus pallidus exhibited a steady increase across the lifespan.

7. Lifespan growth patterns of global functional connectome using a different surface registration strategy

Ensuring functional alignment across participants necessitates registering all participants to a standard space, which is an unavoidable step in neuroimaging analyses. For participants in early development, we designed a multistep, refined registration process (Supplementary Fig. 3). This approach reduces errors associated with single-step registration, allowing for more accurate alignment of functional signals across different participants^{10, 38}. To explore whether our results were influenced by the registration process, we conducted a supplementary analysis. We reconstructed the functional connectome for all participants by only aligning each participant's cortical surface to age-specific templates (Supplementary Fig. 18-I). Subsequently, we mapped the individual functional signals to these age-specific standard templates using deformation fields, followed by a uniform postprocessing procedure without downsampling. This approach allowed us to avoid potential age biases that might arise from cross-age template registration and resampling. Specifically, for participants aged 32 to 44 postmenstrual weeks, the individual surfaces were mapped directly to the template for the specific week, resulting in the 59412×59412 functional connectomes. For participants aged 0-24 months, the surfaces were aligned with the monthly age templates, creating the 74846×74846 functional connectomes. For participants older than two years, the surfaces were mapped to the fs_LR_32k standard space, producing the 59412×59412 functional connectomes. Due to the non-correspondence of nodes in the high-resolution brain network between participants, we only calculated normative growth patterns of global mean and variance of the connectome (Supplementary Fig. 18-II). The growth curves were found to be similar to those reported in the main text (Fig. 1c) ($r = 0.85$, $p < 10^{-23}$ for the global mean; $r = 0.97$, $p < 10^{-47}$ for the global variance).

8. Lifespan growth patterns of global mean of the connectome using different averaging methods

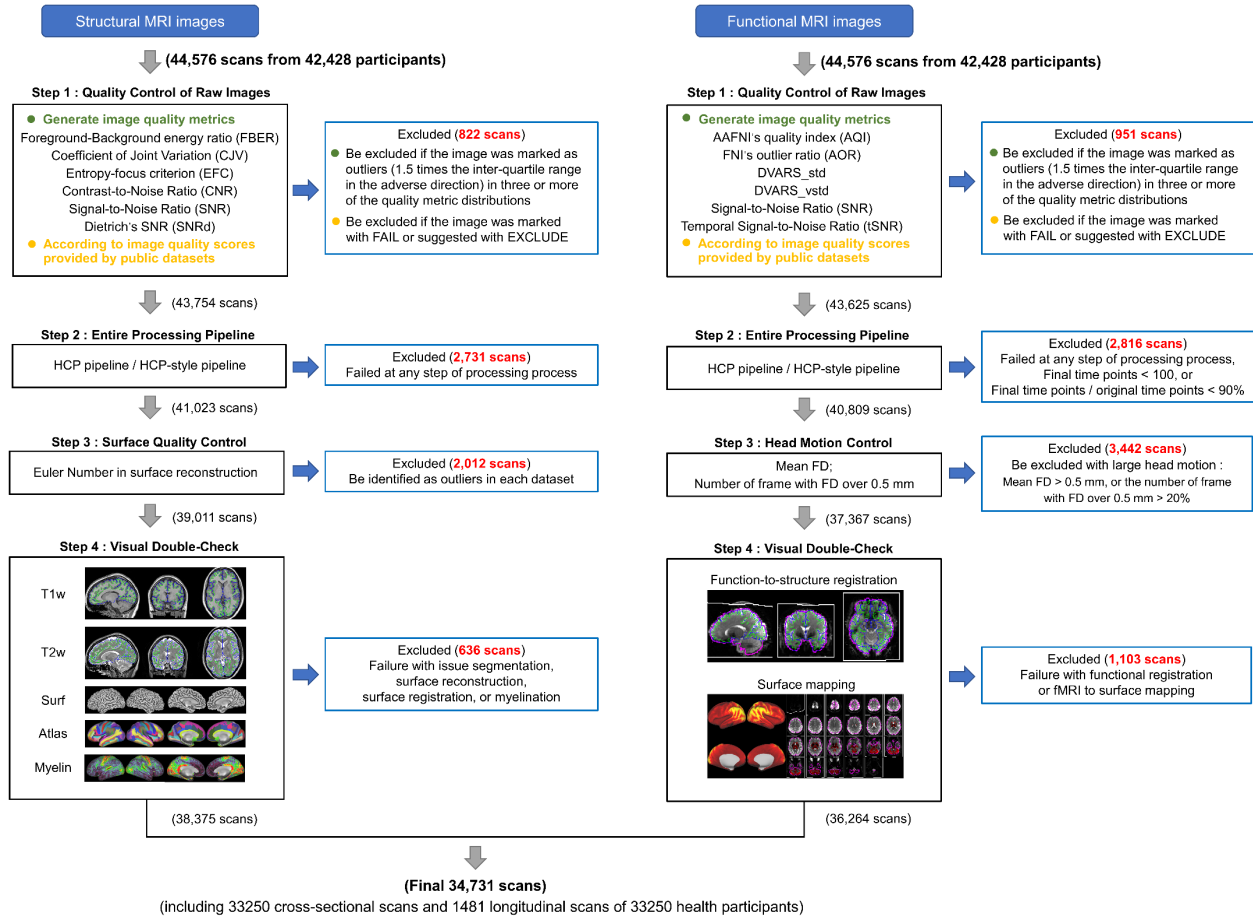
When calculating the global mean of the connectome, it is important to consider whether to use the total number of existing edges or the total number of only the nonzero weighted edges as the

denominator. At the global level, averaging across all edges is crucial for identifying low connectivity patterns, especially in participants with sparse functional connectomes. In contrast, averaging across only nonzero edges fails to capture this critical characteristic. At the regional level, the number of nonzero edges varies across vertices. Therefore, using a nonzero edge averaging method could lead to misleading results. For example, nodes with 1,000 edges may appear to have similar functional connectivity strength to nodes with only a few edges. Therefore, we calculated the global mean of the connectome based on the total number of existing edges in the main results. Nonetheless, we established the normative model of the global mean of the connectome using this alternative averaging method (Supplementary Fig. 19). Although there are differences in the absolute values of the growth curves (reflected by the varying scales on the y-axis), the nonlinear pattern of the global mean of the connectome by this method is similar to that of the main results (Fig. 1c) ($r = 0.92$, $p < 10^{-32}$ for the growth curve; $r < 0.73$, $p < 10^{-13}$ for the growth rate).

9. Longitudinal connectome changes in participants with different ages based on connectome-based growth modeling

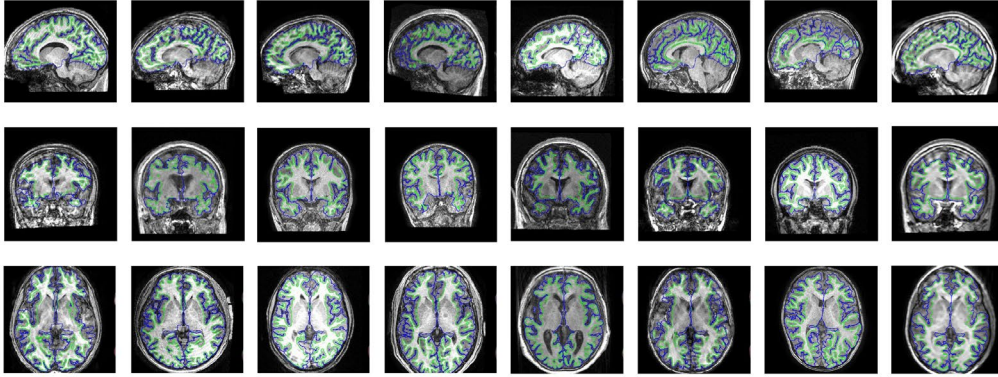
We generated individual longitudinal changes in the raw values and deviation scores based on the connectome-based normative model for several participants with longitudinal scans. Specifically, after training the normative models on the cross-sectional cohort of 33,250 participants, we used longitudinal scan data as the testing set to estimate age-related predictions and deviation scores. The 1,077 participants with longitudinal scans primarily comprised one follow-up scan for 67.8% of the participants and two follow-up scans for 27.5% of the participants. As shown in Supplementary Fig. 25, several selected participants were visualized, demonstrating substantial heterogeneity in individual longitudinal changes in both raw values and deviation scores. This variability may be attributed to interindividual differences, age-related variations, or a combination of both.

Supplementary Figures

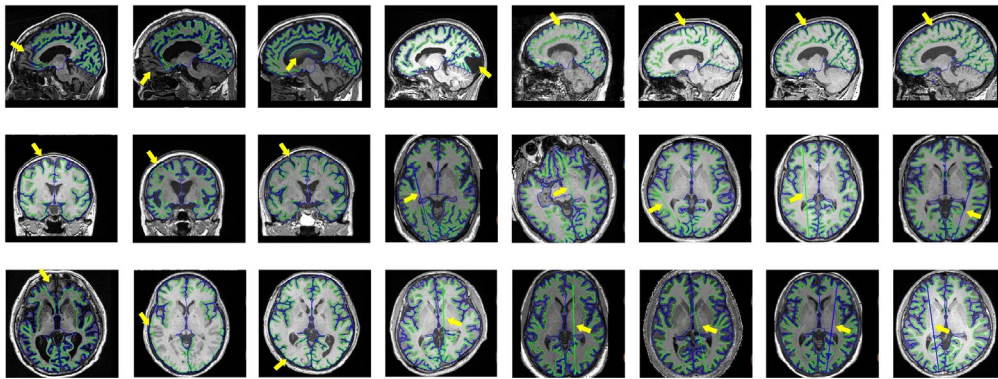


Supplementary Fig. 1 | A framework for quality control of structural MRI and task-free functional MRI data. The four-step rigorous quality control process resulted in the total exclusion of 9,845 scans from 9,178 participants. The final sample included 33,250 healthy participants (33,250 cross-sectional scans and 1,481 longitudinal scans) with high-quality functional and structural images.

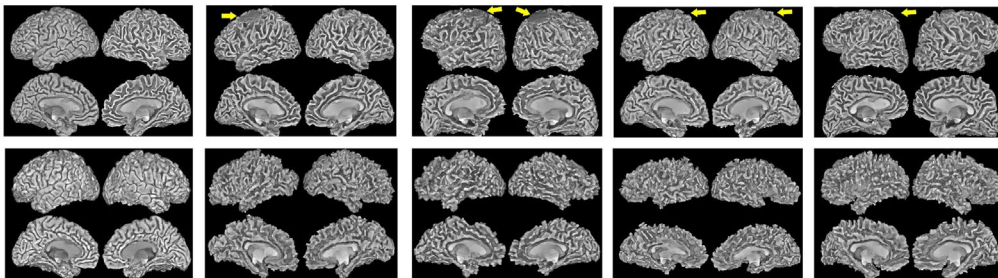
a. Structural MRI with artifacts



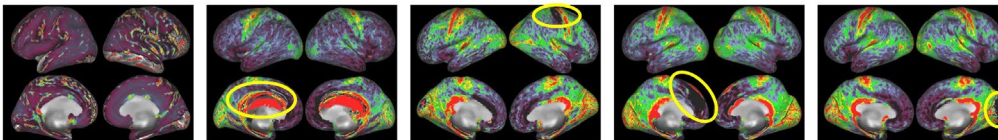
b. Issues with tissue segmentation



c. Issues with surface reconstruction

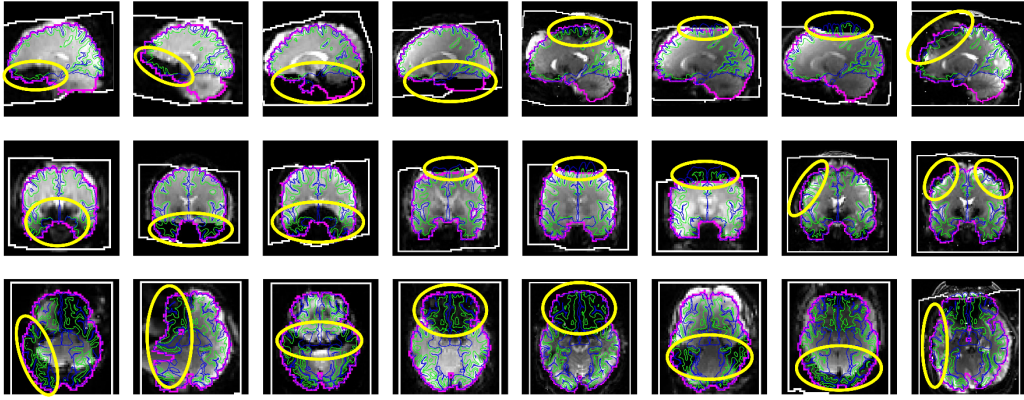


d. Issues with myelination distribution

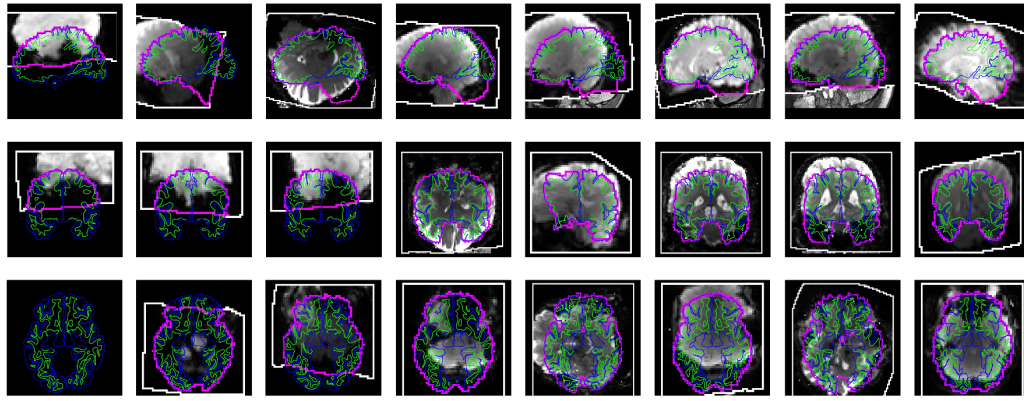


Supplementary Fig. 2-I | Instances of exclusion during the visual-check quality control procedure: structural MRI data. **a.** Examples of data were excluded if artifacts interfered with brain tissue segmentation. The blue lines represent the gray matter boundary, and the green lines represent the white-gray matter interface. **b.** Examples of cortical segmentation/reconstruction in participants with quality issues. Common issues included unrecognizable brain tissues, missing brain tissues, indistinguishable gray and white matter, indistinguishable gray matter and skull, and problems with surface-to-volume mapping. **c.** Examples of cortical surface in participants with quality issues. Each subplot shows the visualization of the mid-thickness surface across four views: left lateral, right lateral, left medial, and right medial. **d.** Examples of participants with problematic myelination distribution. The detailed tutorial on visual QC procedures is accessible at <https://github.com/sunlianglong/BrainChart-FC-Lifespan/blob/main/QC/README.md>.

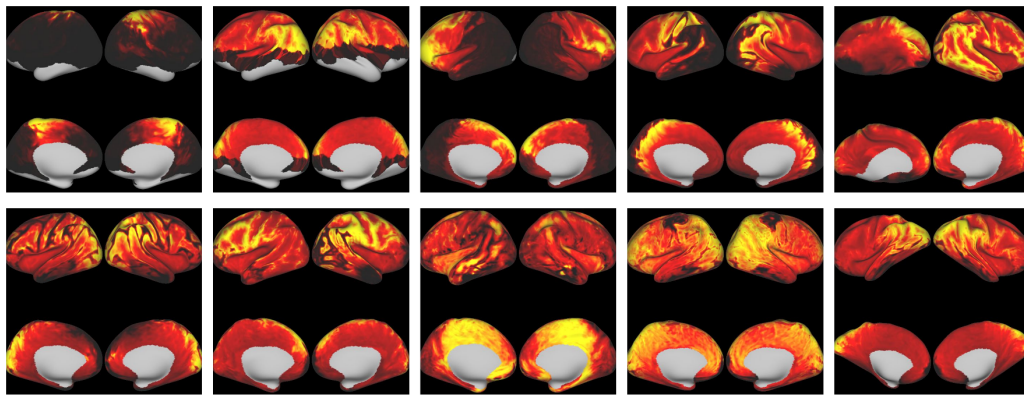
a. Incomplete brain coverage



b. Registration failures from functional to structural data or from functional to standard space

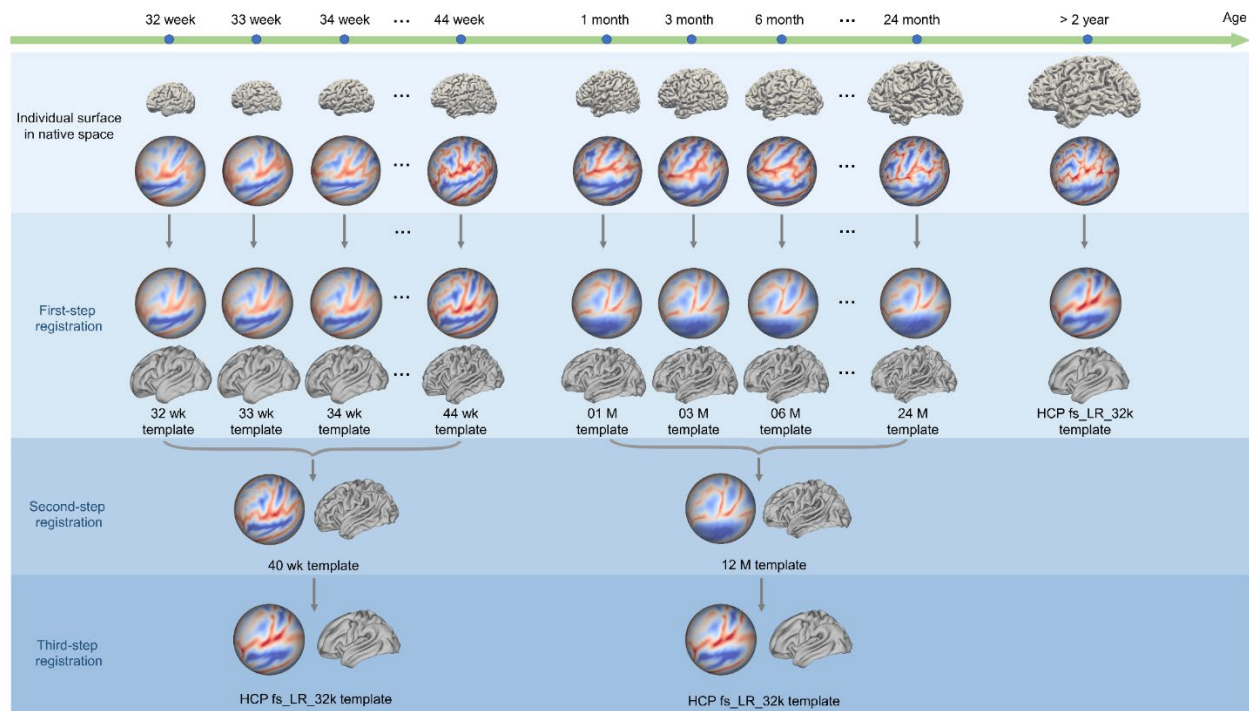


c. Issues with volume-to-surface mapping



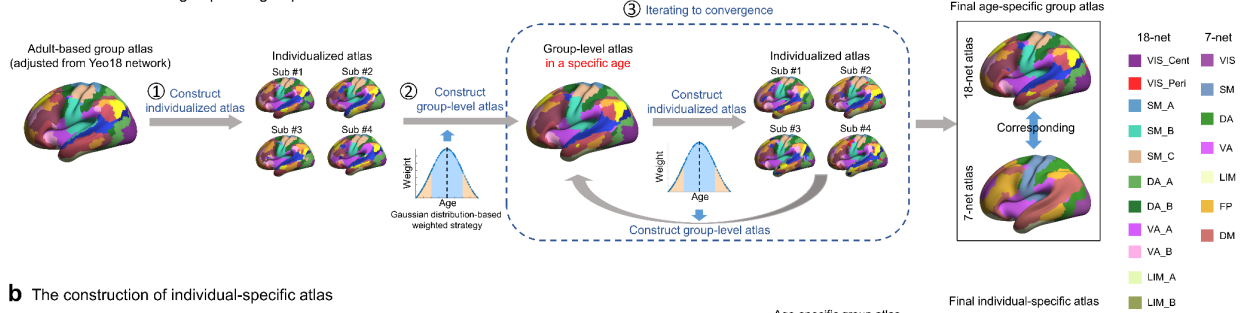
Supplementary Fig. 2-II | Instances of exclusion during the visual-check quality control procedure:

fMRI data. **a.** Examples of data with incomplete BOLD signal coverage. **b.** Individual fMRI data were first registered to native structural space, and then to standard space. The registration quality was assessed by visualizing the averaged fMRI images (background), fMRI image masks (purple outlines), and boundaries of gray and white matter in structural images. Examples of data that failed to pass the quality control process are depicted. **c.** The visualization of mean BOLD data, mapped from volume space to the surface, demonstrating examples that failed the quality check. The detailed tutorial on visual QC procedures is accessible at <https://github.com/sunlianglong/BrainChart-FC-Lifespan/blob/main/QC/README.md>.

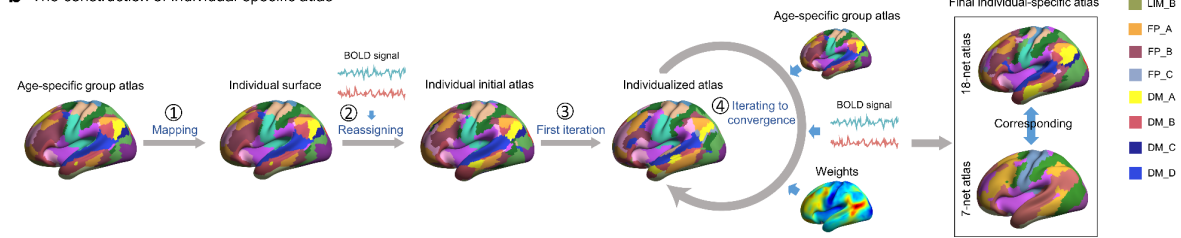


Supplementary Fig. 3 | A schematic overview of cortical surface registration. The surface registration process aimed for precise alignment with the fs_LR_32k standard space. For participants aged 32 to 44 postmenstrual weeks, a three-step procedure was employed. (1) Individual surfaces were mapped to their corresponding postmenstrual week templates. (2) The 32-39 and 41-44 postmenstrual week templates were registered to the 40-week template¹⁰. (3) The 40-week template was registered to the fs_LR_32k surface template⁵. For participants aged 1-24 months, the following steps were undertaken. (1) Surfaces were aligned with their monthly age templates¹¹. (2) All monthly templates were registered into the 12-month template. (3) The 12-month template was then mapped to the fs_LR_32k surface template. For participants older than two years, the individual surfaces were mapped to the fs_LR_32k space. The transformations involving adult templates, namely from individual to fsaverage space, then from fsaverage space to Conte69 space, and finally downsampled to the fs_LR_32k space, are not illustrated in the figure. wk, week; M, month.

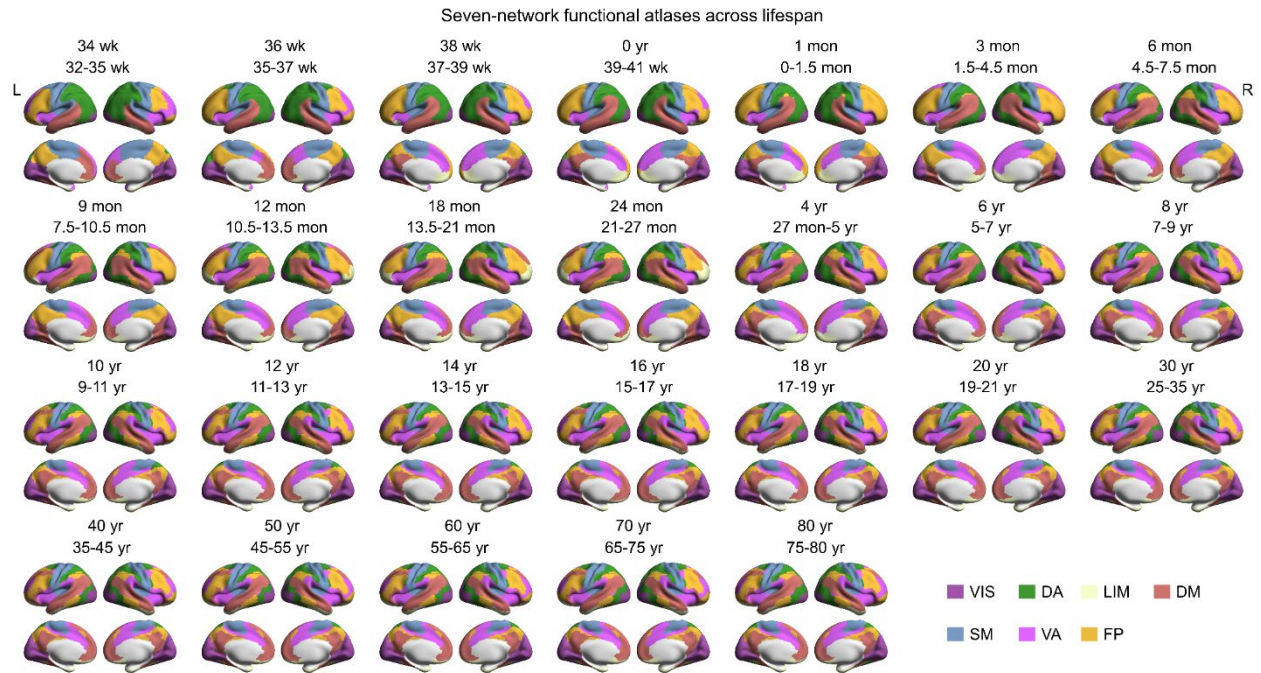
a The construction of age-specific group atlases



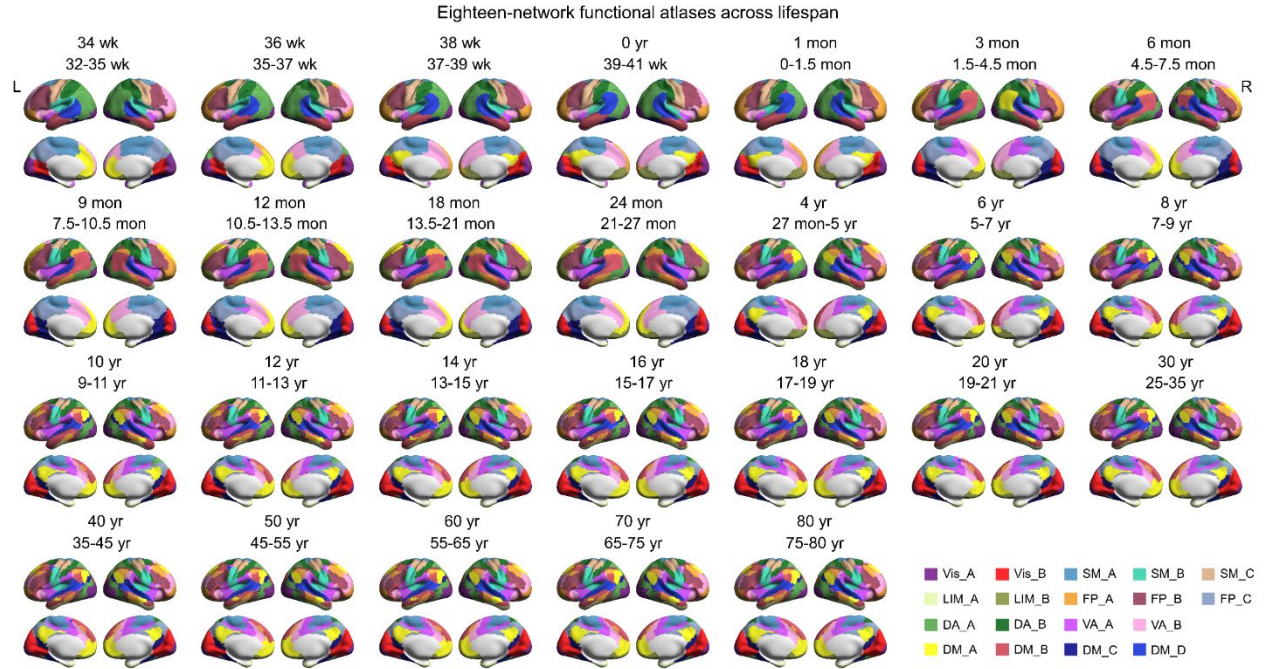
b The construction of individual-specific atlas



Supplementary Fig. 4 | A schematic overview of the construction of age-specific group atlas and individual-specific atlas. a, Construction of age-specific group atlas. We segmented participants into 26 age intervals according to their age. The atlas generation process involved the following steps for a given age interval. (1) Constructing an individualized atlas. We used an individualized parcellation iteration algorithm³⁹ to map the adult 18-network atlas to each participant. (2) Constructing a population-level atlas. An age-weighted population-level atlas generation method was proposed based on a Gaussian probability distribution. The weight assigned to each participant was determined based on their age within a Gaussian distribution (mean $\mu = 0$ and standard deviation $\sigma = 1$). The weight quantified the participant's contribution to the construction of the population-level atlas, with proximity to the target age of the atlas resulting in a greater contribution. For each cortical vertex, we calculated the across-participant cumulative probability of belonging to each network and assigned vertex labels to the network with the highest cumulative probability. These processes resulted in an initial age-specific population-level atlas. (3) Iteration to convergence. Steps 1 and 2 were iteratively repeated until the overlap between the current and previous atlases exceeded 95% or the total number of iterations over 10. Finally, according to the correspondence between 18 and 7 networks, we obtained the age-specific 7-network atlas. **b,** Construction of individualized atlas. (1) Personalized mapping and reference establishment. The age-specific population-level atlas was mapped onto an individual's cortical surface. The mean BOLD signal time series of a network was averaged across all vertices in this network, providing atlas-based reference signals essential for the subsequent optimization phase. (2) Correlation and vertex reassignment. For a given vertex, the BOLD signal underwent a correlation analysis with the 18 reference signals. The network with the highest correlation was assigned to this vertex. (3) Signal averaging and iterative refinement. A combined reference signal was generated by weighted averaging of the signal from step (2) and the initial reference signals from step (1). Factors weighted in this averaging process included interindividual variability map, tSNR map, and iteration count. This combined signal then served as an updated reference, guiding the reassignment of cortical vertices to their most suitable networks. (4) Iterative convergence. The procedures in steps (2) and (3) were iteratively executed until reaching a predefined stopping criterion (the overlap between the current and previous atlases exceeded 98%, or the total number of iterations over 50). More information on this iterative functional parcellation approach can be found in previous study³⁹. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode.



Supplementary Fig. 5 | Lifespan set of 7-network age-specific group atlases from 32 postmenstrual weeks to 80 years (left and right hemispheres). VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode; wk, week; mon, month; yr, year.

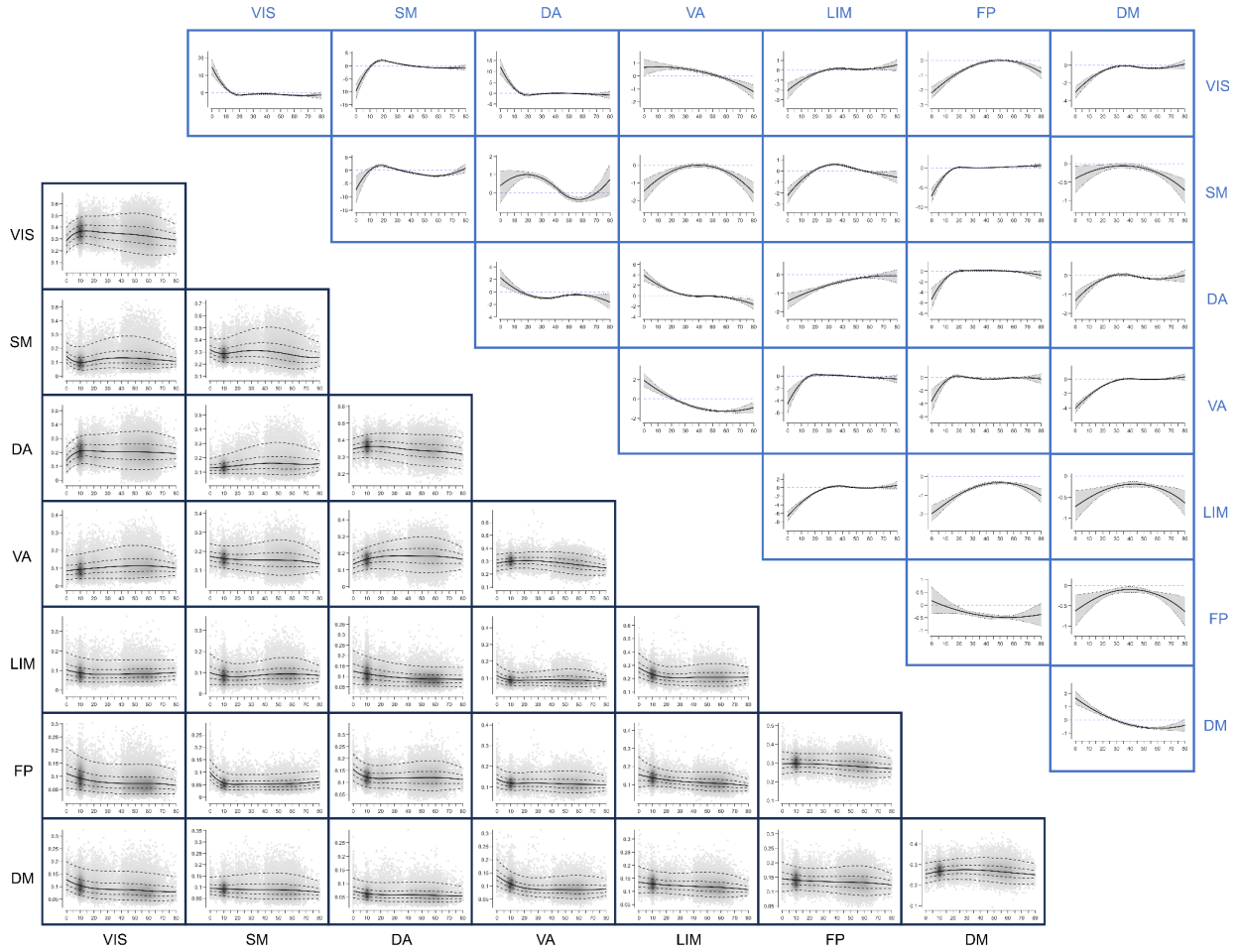


Supplementary Fig. 6 | Lifespan set of 18-network age-specific group atlases from 32 postmenstrual weeks to 80 years. VIS_A, VIS_B, visual; SM_A, SM_B, SM_C, somatomotor; DA_A, DA_B, dorsal attention; VA_A, VA_B, ventral attention; LIM_A, LIM_B, limbic; FP_A, FP_B, FP_C, frontoparietal; DM_A, DM_B, DM_C, DM_D, default mode; wk, week; mon, month; yr, year.



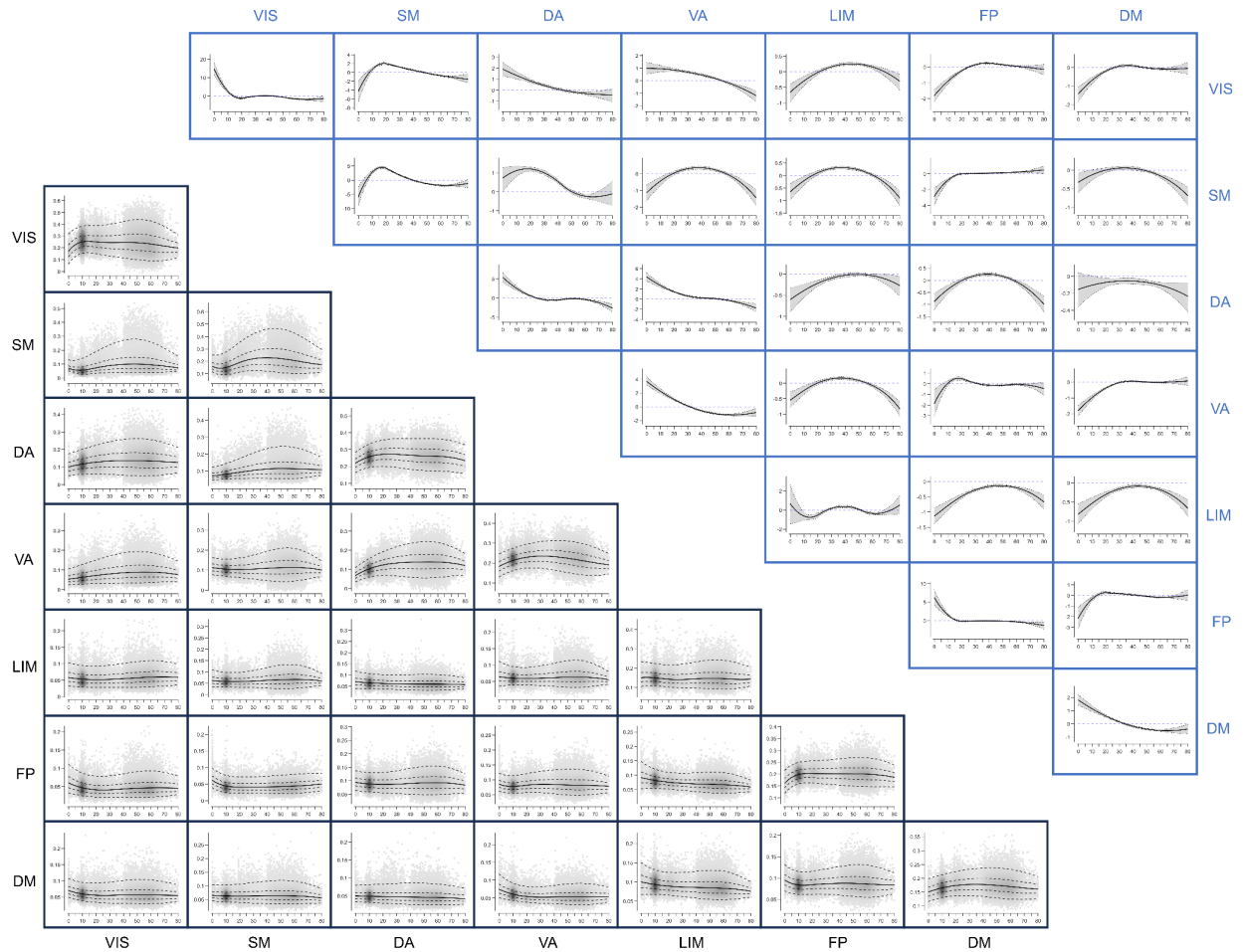
Supplementary Fig. 7 | Statistical differences in functional homogeneity of connectivity profiles among three atlases. a, One-way repeated analysis of variance (RANOVA) of functional homogeneity for each age group. Here, the functional homogeneity of a system is defined as Pearson's correlations between the “connectivity profiles” of vertices within this system^{40,41}. A connectivity profile was generated for each vertex by correlating it with all other vertices. We calculated the global homogeneity by averaging the homogeneity values across all systems⁴¹. The RANOVA revealed significant differences in the global homogeneity among atlases for any given age group (all $F > 255$, $p < 10^{-25}$, two-sided). The blue, green, and orange colors represent the functional homogeneity in individual-specific atlas, age-specific group atlas, and adult-based group atlas, respectively. The gray lines connect the three atlases for the same participant. ***, $p < 10^{-25}$. **b**, Post-hoc differences in the homogeneity of connectivity profiles between each pair of atlases. The post-hoc analyses revealed significant differences (all $p < 10^{-8}$, two-sided, Bonferroni-corrected) between any pairs of atlases. The bars for each age group represent the mean difference in global functional homogeneity between two atlases for all participants in that group. wk, week; mon, month; yr, year.

Normative growth curves and growth rates of within-system and between-system functional connectivity (short distance [10 mm – 40 mm])



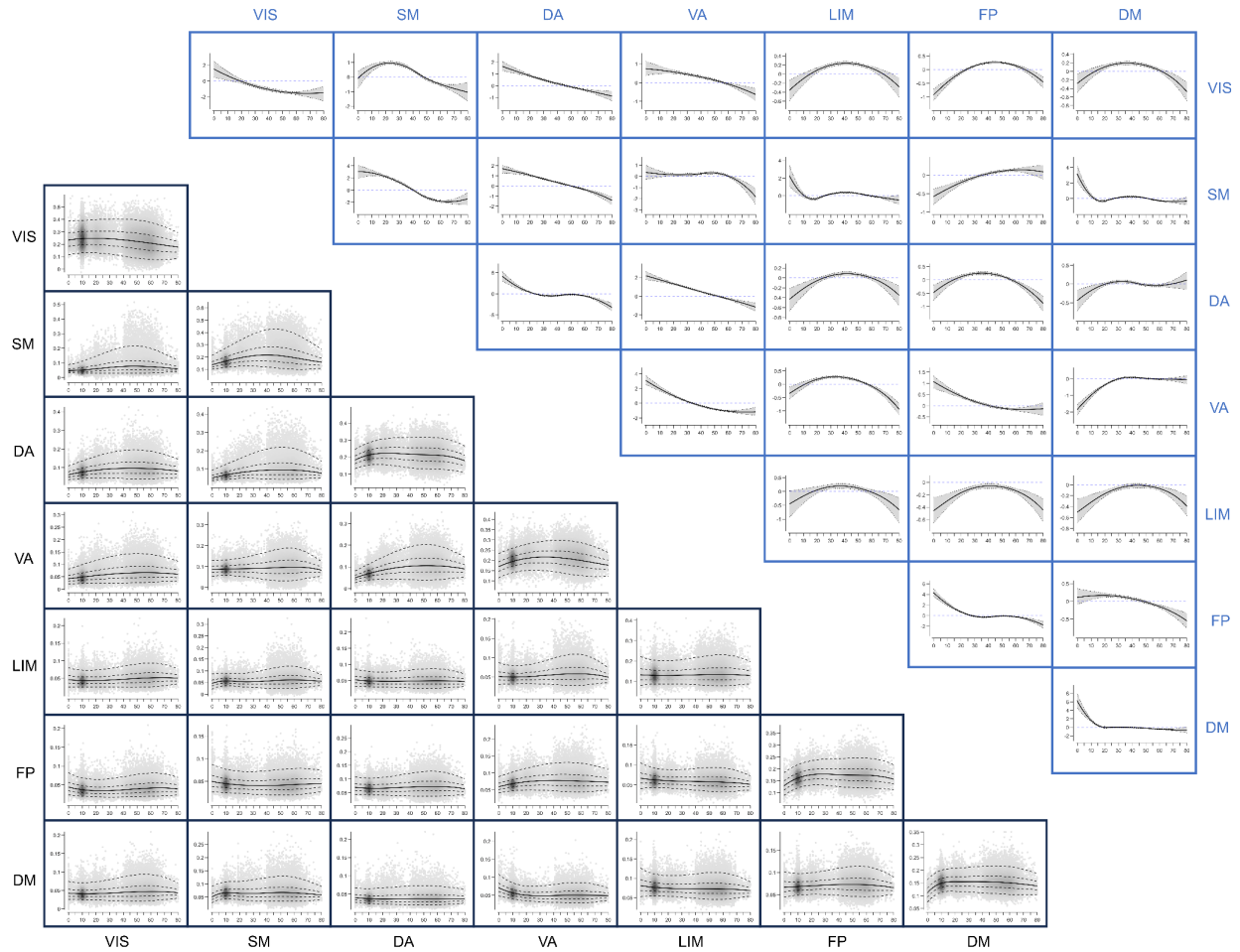
Supplementary Fig. 8-I | Lifespan growth patterns of within-system and between-system functional connectivity (short range, 10 mm – 40 mm). The lower triangular matrix (shown in black) represents the normative growth curves for within-system and between-system FC, while the upper triangular matrix (shown in blue) represents the growth rates for these FC measures. The diagonal of the matrix shows the growth curves and growth rates of within-system FC; the off-diagonal elements represent the growth curves and growth rates of between-system FC. For the growth curve, the median (50th) centile is shown as a solid line, and the 5th, 25th, 75th, and 95th centiles are represented by dotted lines. The growth rate (showed as the central line) is characterized by the first derivative of the median centile. The gray shaded areas denote the 95% confidence interval, estimated through bootstrapping 1,000 times. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode; FC, functional connectivity.

Normative growth curves and growth rates of within-system and between-system functional connectivity (middle distance [40 mm – 70 mm])

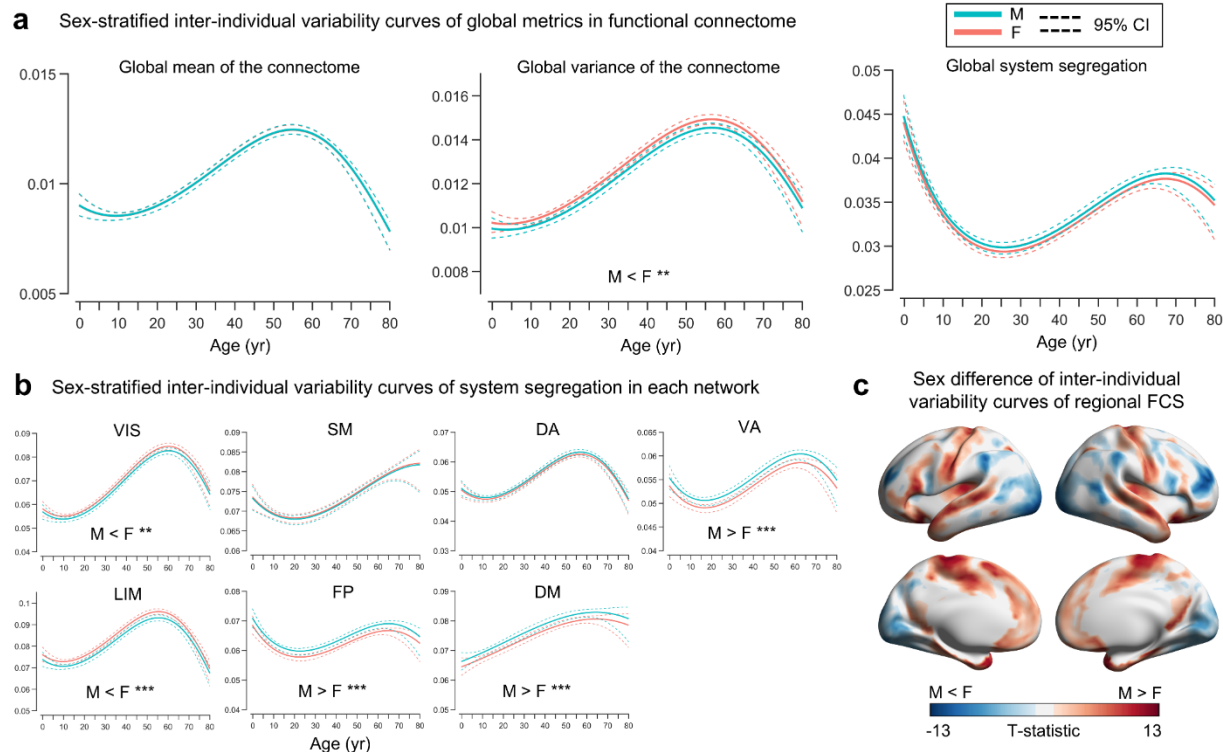


Supplementary Fig. 8-II | Lifespan growth patterns of within-system and between-system functional connectivity (middle range, 40 mm – 75 mm). The lower triangular matrix (shown in black) represents the normative growth curves for within-system and between-system FC, while the upper triangular matrix (shown in blue) represents the growth rates for these FC measures. The diagonal of the matrix shows the growth curves and growth rates of within-system FC; the off-diagonal elements represent the growth curves and growth rates of between-system FC. For the growth curve, the median (50th) centile is shown as a solid line, and the 5th, 25th, 75th, and 95th centiles are represented by dotted lines. The growth rate (showed as the central line) is characterized by the first derivative of the median centile. The gray shaded areas denote the 95% confidence interval, estimated through bootstrapping 1,000 times. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode; FC, functional connectivity.

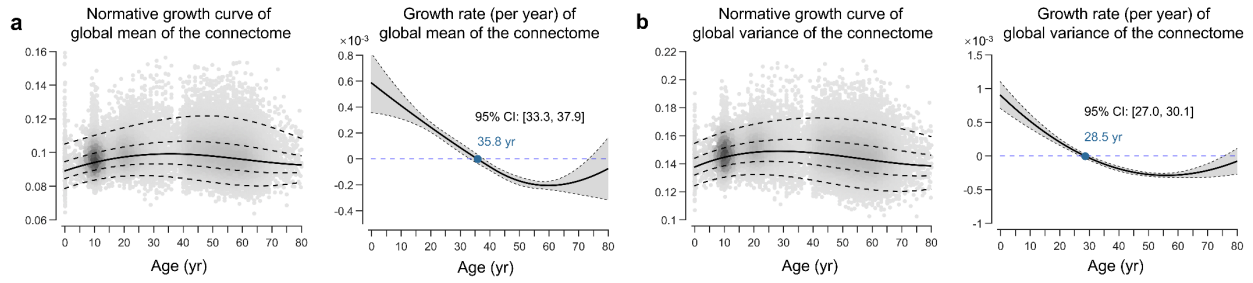
Normative growth curves and growth rates of within-system and between-system functional connectivity (long distance > 75 mm)



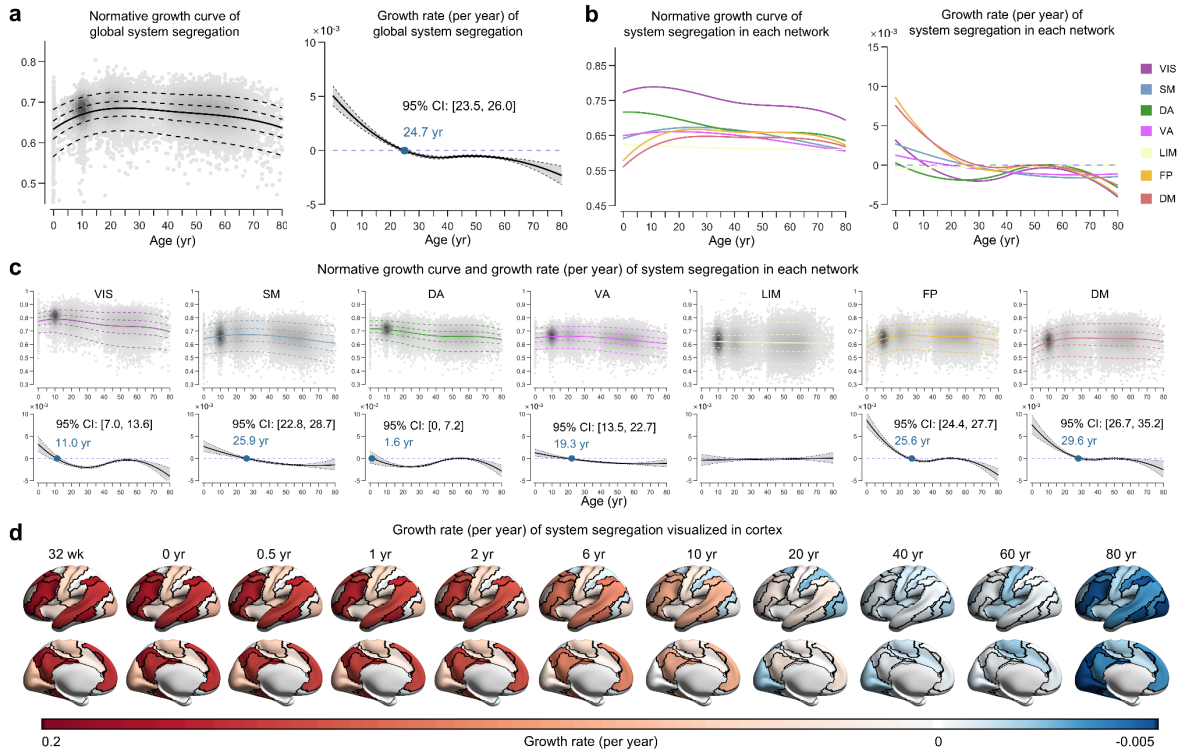
Supplementary Fig. 8-III | Lifespan growth patterns of within-system and between-system functional connectivity (long range, > 75 mm). The lower triangular matrix (shown in black) represents the normative growth curves for within-system and between-system FC, while the upper triangular matrix (shown in blue) represents the growth rates for these FC measures. The diagonal of the matrix shows the growth curves and growth rates of within-system FC; the off-diagonal elements represent the growth curves and growth rates of between-system FC. For the growth curve, the median (50th) centile is shown as a solid line, and the 5th, 25th, 75th, and 95th centiles are represented by dotted lines. The growth rate (showed as the central line) is characterized by the first derivative of the median centile. The gray shaded areas denote the 95% confidence interval, estimated through bootstrapping 1,000 times. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode; FC, functional connectivity.



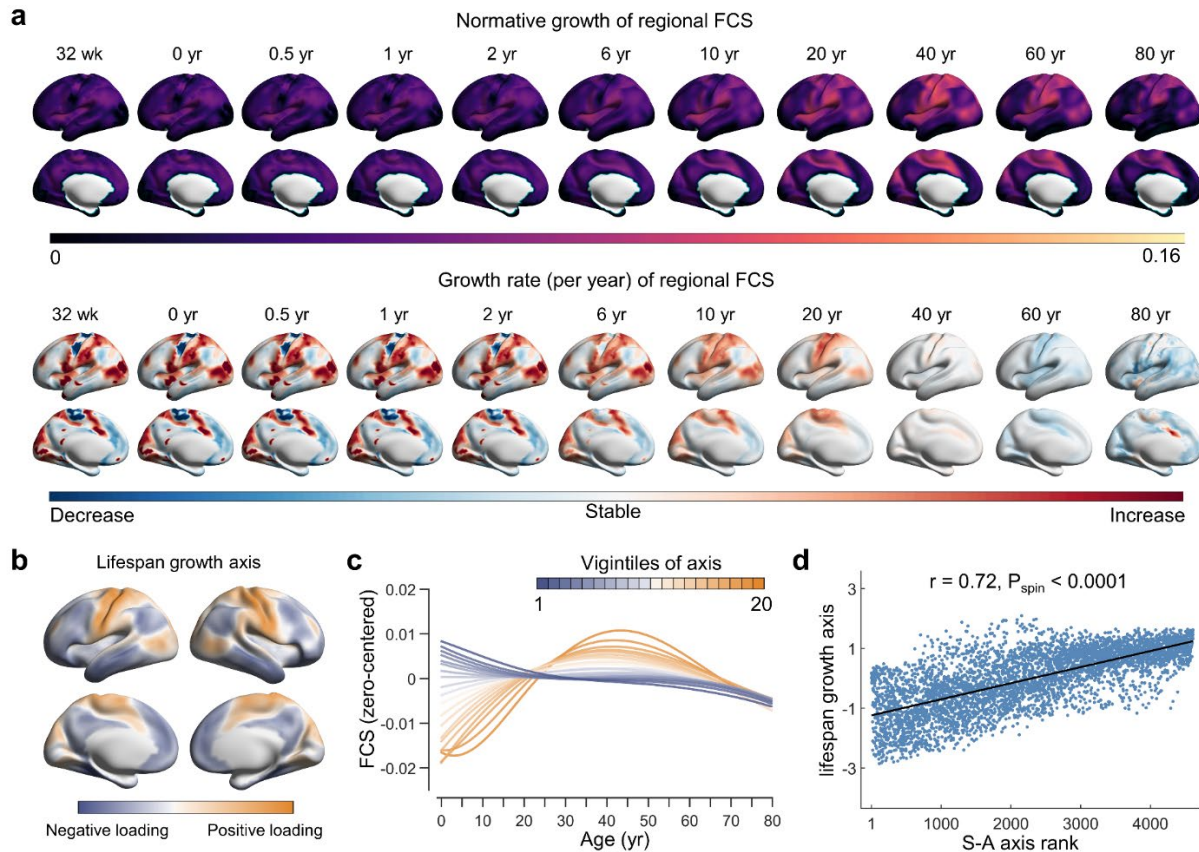
Supplementary Fig. 9 | Sex differences in the normative curves of interindividual variability in the functional connectome. **a**, Sex-stratified interindividual variability curves for global functional metrics. The solid line represents the 50th centile, with the two surrounding dotted lines denoting the 95% confidence interval, which was estimated by bootstrapping 1,000 times. The subplots from left to right represent the global mean of the connectome, global variance of the connectome, and global system segregation, respectively. **b**, Sex-specific interindividual variability curves for system segregation in each network. The solid line represents the 50th centile, with the two surrounding dotted lines denoting the 95% confidence interval. **c**, Sex differences in the interindividual variability curves of regional-level FCS. Red colors indicate that the values of males are significantly higher than those of females, and blue colors denote that the values of females are significantly higher than those of males. Out of the 4,609 vertices, 2,995 exhibited significant sex differences ($p < 0.05$, Benjamini-Hochberg FDR corrected). FCS, functional connectivity strength; VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode. M, male; F, female. **, $p < 0.01$, ***, $p < 0.001$, Benjamini-Hochberg FDR corrected. The exact p-values is provided in Supplementary Table 4.



Supplementary Fig. 10-I | Sensitivity analyses: with stricter head motion threshold (mean FD threshold < 0.2 mm), for global functional connectome. A sample of 24,494 participants (with a mean FD threshold of 0.2 mm) was used to validate the lifespan growth curve of the global functional connectome. **a**, Normative curve and growth rate of the global mean of the connectome as estimated by GAMLSS. **b**, Normative growth curve and growth rate of global variance of the connectome. In each panel, the left panel shows the median (50th) centile as a solid line, while the 5th, 25th, 75th, and 95th centiles are indicated by dotted lines. The growth rate (right panel, showed as the central line) is characterized by the first derivative of the median centile. The gray shaded areas represent the 95% confidence interval, which were estimated by bootstrapping 1,000 times. FD, framewise displacement.



Supplementary Fig. 10-II | Sensitivity analyses: with stricter head motion threshold (mean FD threshold < 0.2 mm), for system segregation. A sample of 24,494 participants (with a mean FD threshold of 0.2 mm) was used to validate the lifespan growth curves of the system segregation. **a**, Normative growth curve (left panel, showed as centile lines) and growth rate (right panel, showed as the central line) of global system segregation. The gray shaded areas represent the 95% confidence interval, which were estimated by bootstrapping 1,000 times. **b-c**, Normative growth curve (showed as centile lines) and growth rate (showed as the central line) of system-specific segregation for each network. The median (50th) centile is represented by a solid line, while the 5th, 25th, 75th, and 95th centiles are indicated by dotted lines. The gray shaded areas represent the 95% confidence interval. The key inflection points are marked in blue font. **d**, Growth rate of system-specific segregation visualized in the cortex, with black lines depicting system boundaries. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode; wk, week; yr, year.



Supplementary Fig. 10-III | Sensitivity analyses: with stricter head motion threshold (mean FD threshold < 0.2 mm), for regional functional connectivity strength. A sample of 24,494 participants (with a mean FD threshold of 0.2 mm) was used to validate the lifespan growth curves of regional functional connectivity strength. **a**, The fitted 50% centiles (top panel) and their growth rates (bottom panel) for all vertices at representative ages. **b**, The lifespan growth axis of brain functional connectivity, represented by the first principal component (accounting for 60.4% of the variance) from a PCA on regional-level FCS curves. **c**, Based on the lifespan principal axis, all vertices across the brain were equally divided into 20 bins. The zero-centered curves of all vertices within each bin were averaged. The first vigintile (depicted in darkest blue) represents one pole of the axis, while the twentieth vigintile represents the opposite pole (depicted in darkest yellow). The patterns of growth curves vary continuously along the axis, with the greatest differences observed between the two poles. **d**, A strong correlation was observed between the lifespan principal growth axis and the sensorimotor-association (S-A) axis ($r = 0.72$, $p_{\text{spin}} < 0.0001$, one-sided). The central line represents the linear fit and the gray shaded areas shows a 95% confidence interval. FCS, functional connectivity strength; wk, week; yr, year.

a

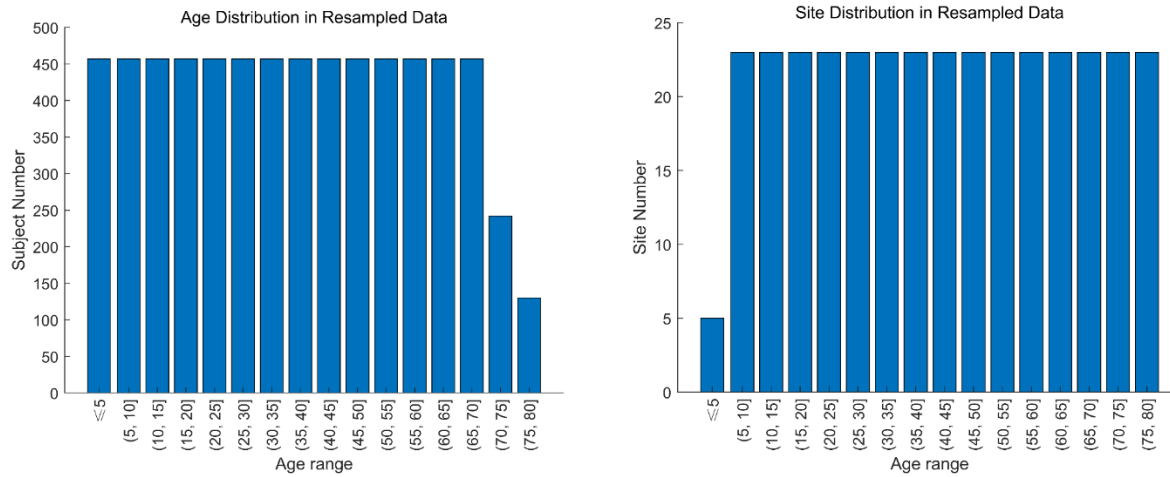
Sample and site distribution in each age group before resampling

Age (yr)	≤5	(5-10]	(10-15]	(15-20]	(20-25]	(25-30]	(30-35]	(35-40]	(40-45]	(45-50]	(50-55]	(55-60]	(60-65]	(65-70]	(70-75]	(75-80]
Sample	692	4439	4287	1766	2250	911	636	464	2528	3063	3466	3937	3142	1231	283	155
Sites	5	48	60	49	44	38	29	29	23	24	27	36	36	52	45	41

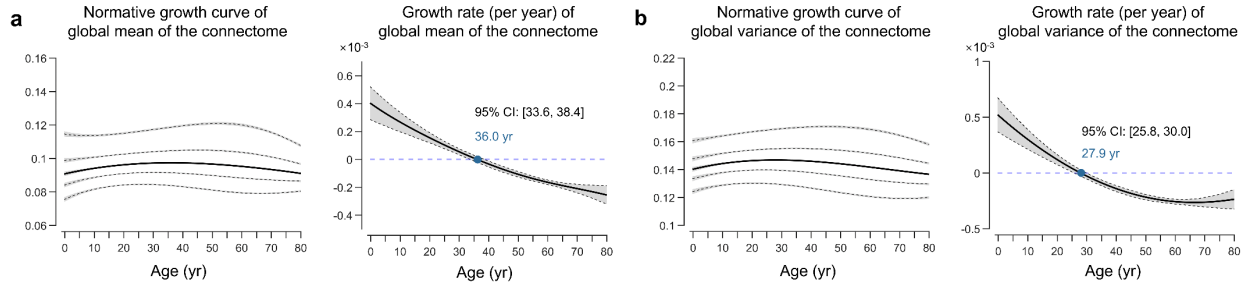
b

Sample and site distribution in each age group after resampling

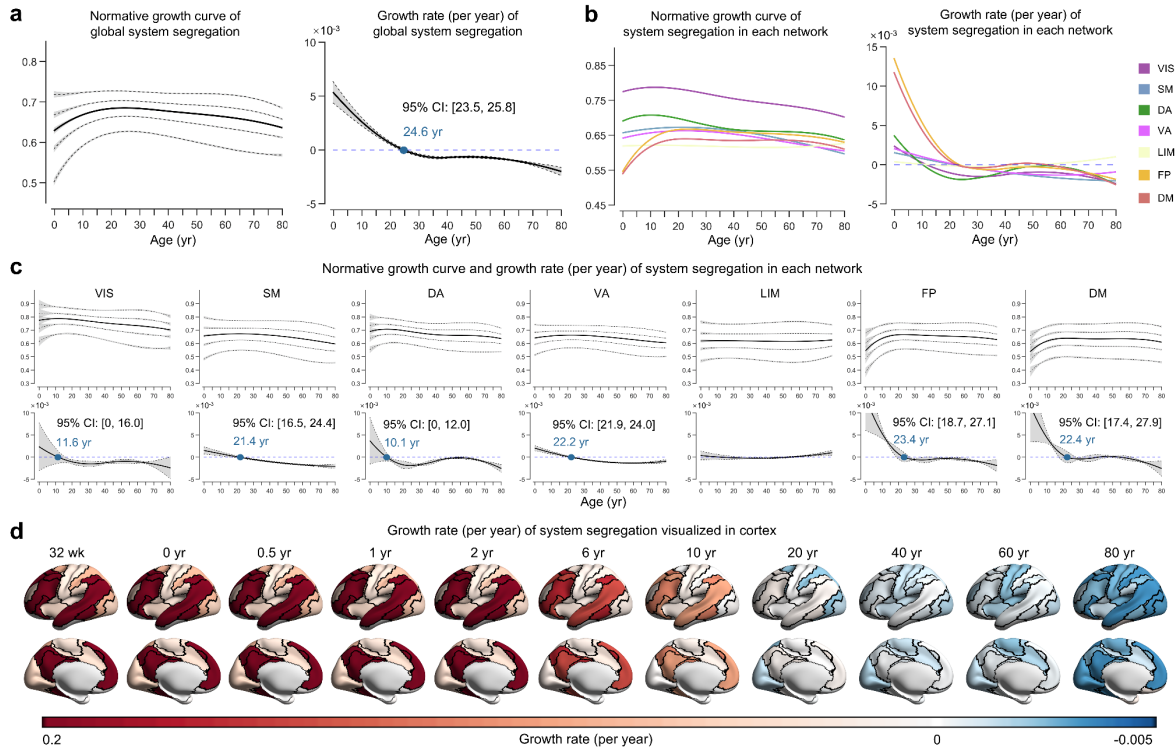
Age (yr)	≤5	(5-10]	(10-15]	(15-20]	(20-25]	(25-30]	(30-35]	(35-40]	(40-45]	(45-50]	(50-55]	(55-60]	(60-65]	(65-70]	(70-75]	(75-80]
Sample	457	457	457	457	457	457	457	457	457	457	457	457	457	457	242	130
Sites	5	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23



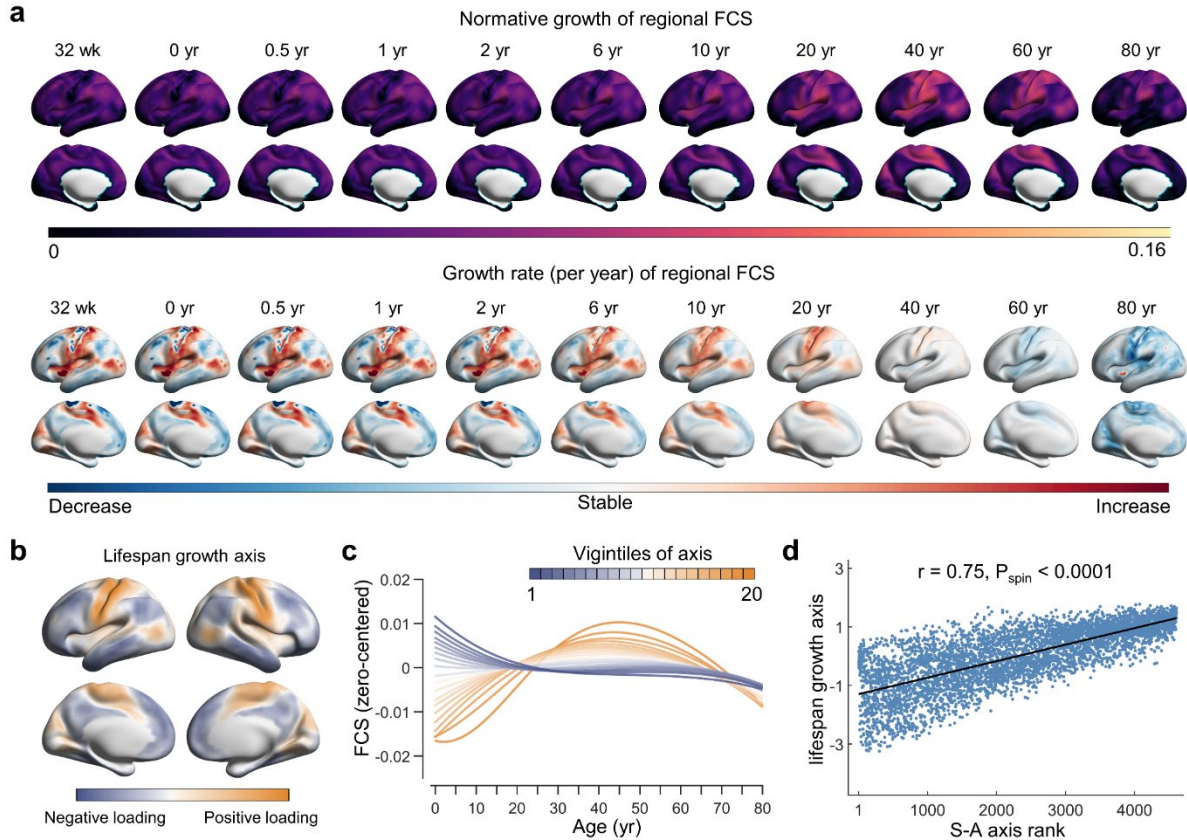
Supplementary Fig. 11-I | Balanced resampling of the samples and sites across the lifespan. The entire age range across the lifespan was divided into sixteen age groups. **a.** The sample and site distribution in each age group before resampling. The (35, 40] age group had the fewest participants at 464 and the (40, 45] age group had the fewest sites at 23 after excluding age groups under 5 years of age or over 70. **b.** The sample and site distribution in each age group after resampling. yr, year.



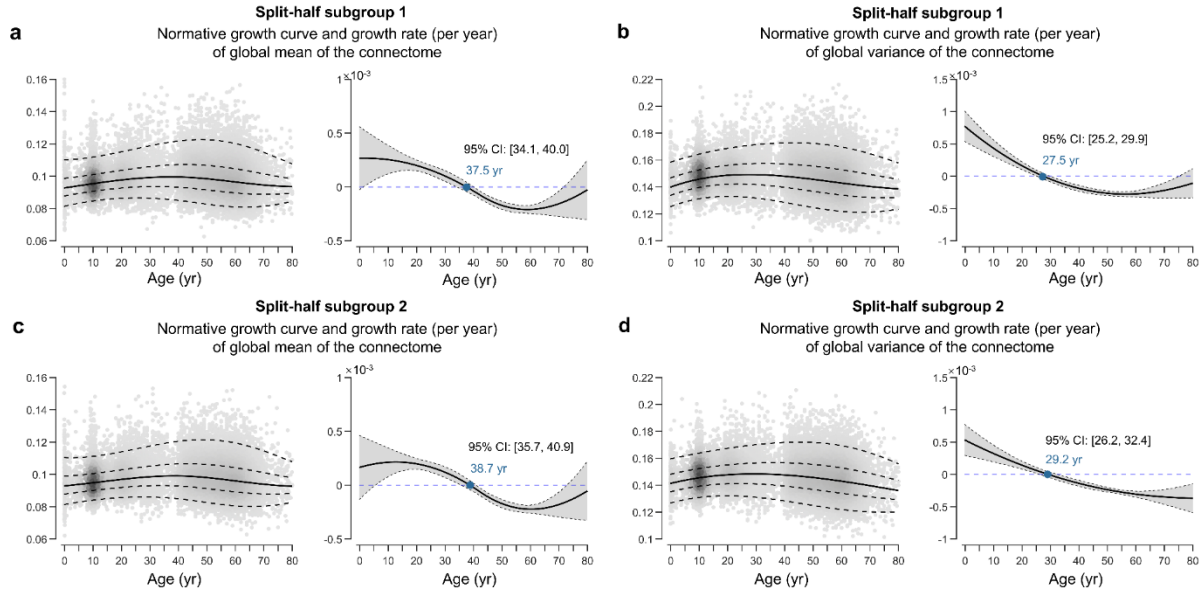
Supplementary Fig. 11-II | Sensitivity analyses: with the balanced resampling strategy (N = 6,770), for global functional connectome. a, Normative growth curve (left panel, showed as centile lines) and growth rate (right panel, showed as the central line) of global mean of the connectome. Using a balanced resampling strategy, we recalculated the GAMLSS model 1,000 times, yielding 1,000 sets of normative growth curves and growth rates. The left panel shows the averaged median (50th) centile as a solid line, surrounded by the averaged 5th, 25th, 75th, and 95th centiles as dotted lines. The gray shaded areas surrounding each centile represent the 95% confidence interval. In the right panel, the solid line illustrates the growth rate of the averaged median centile, with its 95% confidence interval highlighted by gray shaded areas. **b**, Normative curve (left panel) and growth rate (right panel) of global variance of the connectome. The left panel shows the averaged median (50th) centile as a solid line, surrounded by the averaged 5th, 25th, 75th, and 95th centiles as dotted lines. The gray shaded areas surrounding each centile represent the 95% confidence interval. In the right panel, the solid line illustrates the growth rate of the averaged median centile, with its 95% confidence interval highlighted by gray shaded areas. yr, year.



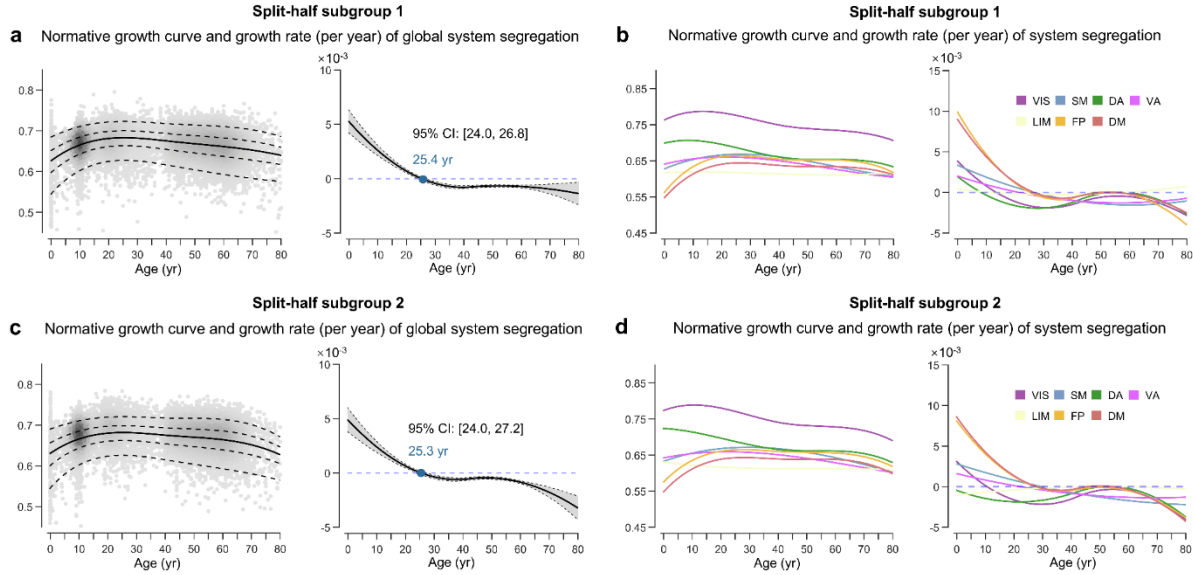
Supplementary Fig. 11-III | Sensitivity analyses: with the balanced resampling strategy (N = 6,770), for lifespan system segregation. **a**, Normative growth curve (left panel, showed as centile lines) and growth rate (right panel, showed as the central line) of global system segregation. The averaged median (50th) centile as a solid line, surrounded by the averaged 5th, 25th, 75th, and 95th centiles as dotted lines. The gray shaded areas surrounding each centile represent the 95% confidence interval. **b-c**, Normative growth curve (showed as centile lines) and growth rate (showed as the central line) of system-specific segregation for each network. The averaged median (50th) centile as a solid line, surrounded by the averaged 5th, 25th, 75th, and 95th centiles as dotted lines. The gray shaded areas surrounding each centile represent the 95% confidence interval. **d**, Growth rate of the averaged curve of system-specific segregation visualized in the cortex, with black lines depicting system boundaries. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode; wk, week; yr, year.



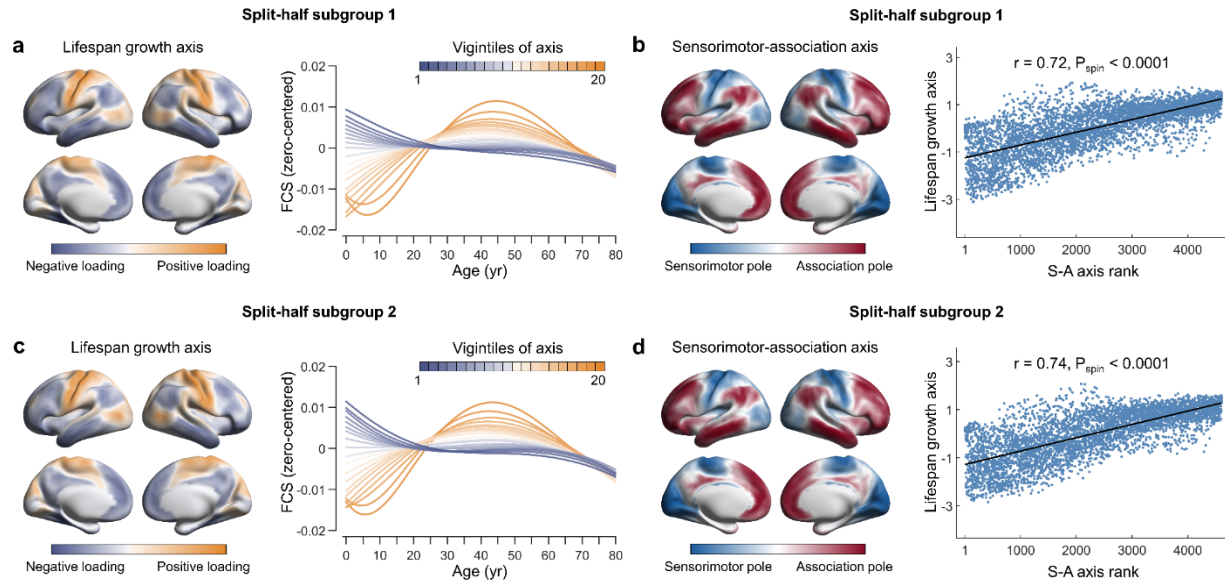
Supplementary Fig. 11-IV | Sensitivity analyses: with the balanced resampling strategy (N = 6,770), for regional functional connectivity strength. Due to computational constraints, at the regional level, we performed a single random sampling analysis and reran the normative modeling for all 4,609 vertices, yielding consistent results with the main analysis. **a**, The median centiles (top panel) and their growth rates (bottom panel) for all vertices at representative ages. **b**, The lifespan growth axis of brain functional connectivity, represented by the first principal component (accounting for 61.3% of the variance) from a PCA on regional-level FCS curves. **c**, Based on the lifespan principal axis, all vertices across the brain were equally divided into 20 bins. The zero-centered curves of all vertices within each bin were averaged. The first vigintile (depicted in darkest blue) represents one pole of the axis, while the twentieth vigintile represents the opposite pole (depicted in darkest yellow). The patterns of growth curves vary continuously along the axis, with the greatest differences observed between the two poles. **d**, A strong correlation was observed between the lifespan principal growth axis and the sensorimotor-association (S-A) axis ($r = 0.75$, $p_{\text{spin}} < 0.0001$, one-sided). The central line represents the linear fit and the gray shaded areas shows a 95% confidence interval. FCS, functional connectivity strength; PCA, principal component analysis; wk, week; yr, year.



Supplementary Fig. 12-I | Sensitivity analyses: replicating growth patterns in independent samples based on a split half approach, for global functional connectome. We randomly divided all participants into two subgroups, each comprising 50% of the participants ($N_{\text{subgroup1}} = 16,663$, $N_{\text{subgroup2}} = 16,587$), with stratification by site. **a**, Normative growth curve and growth rate of global mean of the connectome using samples of subgroup 1. **b**, Normative curve and growth rate of global variance of the connectome using samples of subgroup 1. **c**, Normative curve and growth rate of global mean of the connectome using samples of subgroup 2. **d**, Normative curve and growth rate of global variance of the connectome using samples of subgroup 2. In each panel, the left panel shows the median (50th) centile as a solid line, while the 5th, 25th, 75th, and 95th centiles are indicated by dotted lines. The growth rate (right panel, showed as the central line) is characterized by the first derivative of the median centile. The gray shaded areas represent the 95% confidence interval, which were estimated by bootstrapping 1,000 times. yr, year.

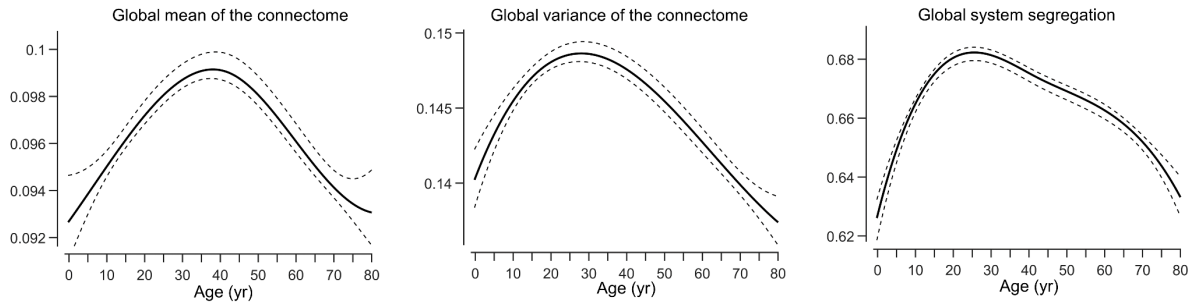


Supplementary Fig. 12-II | Sensitivity analyses: replicating growth patterns in independent samples based on a split half approach, for system segregation. We randomly divided all participants into two subgroups, each comprising 50% of the participants ($N_{\text{subgroup1}} = 16,663$, $N_{\text{subgroup2}} = 16,587$), with stratification by site. **a**, Normative growth curve and growth rate of global system segregation using samples of subgroup 1. The left panel shows the median (50th) centile as a solid line, while the 5th, 25th, 75th, and 95th centiles are indicated by dotted lines. The growth rate (right panel, showed as the central line) is characterized by the first derivative of the median centile. The gray shaded areas represent the 95% confidence interval, which were estimated by bootstrapping 1,000 times. **b**, Normative curve and growth rate of system segregation for each network using samples of subgroup 1. **c**, Normative curve and growth rate of global system segregation using samples of subgroup 2. The left panel shows the median (50th) centile as a solid line, while the 5th, 25th, 75th, and 95th centiles are indicated by dotted lines. The growth rate (right panel, showed as the central line) is characterized by the first derivative of the median centile. The gray shaded areas represent the 95% confidence interval. **d**, Normative curve and growth rate of system segregation for each network using samples of subgroup 2. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode; yr, year.

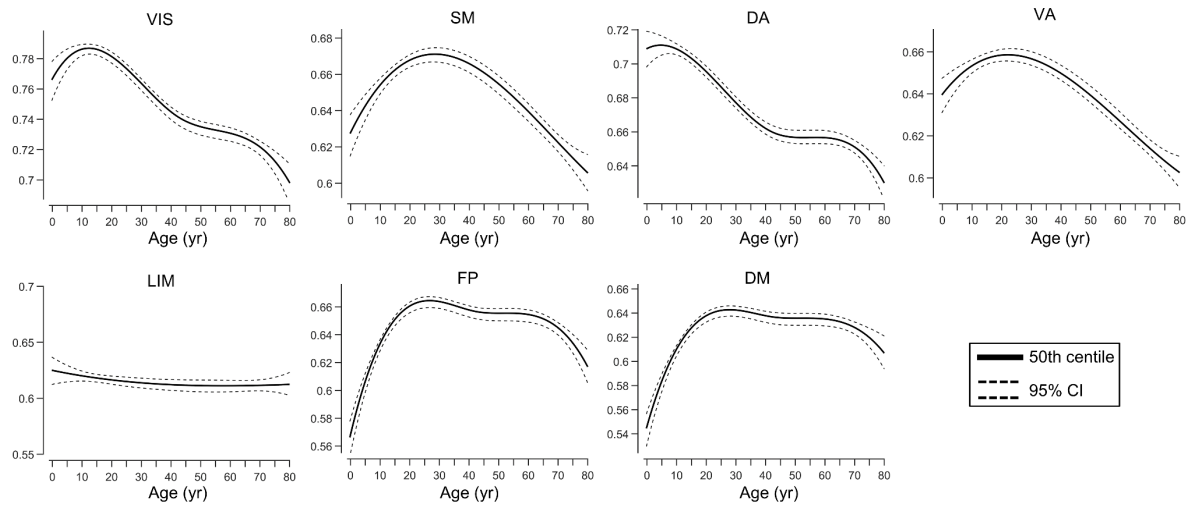


Supplementary Fig. 12-III | Sensitivity analyses: replicating growth patterns in independent samples based on split half approach, for regional functional connectivity strength. We randomly divided all participants into two subgroups, each comprising 50% of the participants ($N_{\text{subgroup1}} = 16,663$, $N_{\text{subgroup2}} = 16,587$), with stratification by site. **a**, The left panel showed the lifespan growth axis using samples of subgroup 1, represented by the first principal component (accounting for 60.4% of the variance) from a PCA on regional-level FCS curves. The right panel showed the averaged zero-centered curves of all vertices within each age bin. **b**, A strong correlation was observed between the lifespan principal growth axis (subgroup 1) and the sensorimotor-association (S-A) axis ($r = 0.72$, $p_{\text{spin}} < 0.0001$, one-sided). The central line represents the linear fit and the gray shaded areas shows a 95% confidence interval. **c**, The left panel showed the lifespan growth axis using samples of subgroup 2, with the first principal component accounting for 60.1% of the variance. **d**, The correlation between the lifespan principal growth axis (subgroup 1) and the S-A axis ($r = 0.74$, $p_{\text{spin}} < 0.0001$, one-sided). The central line represents the linear fit and the gray shaded areas shows a 95% confidence interval. FCS, functional connectivity strength; PCA, principal component analysis; yr, year.

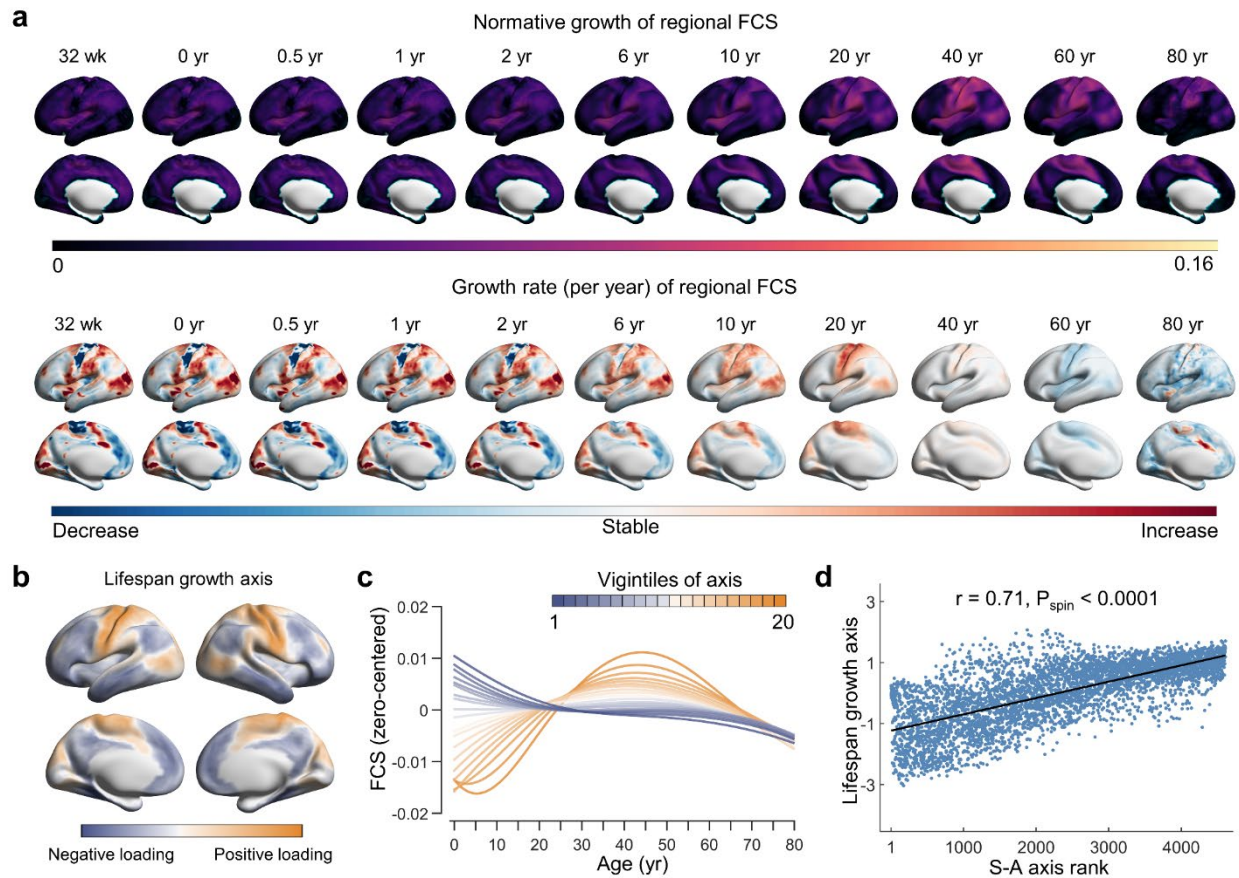
a Bootstrapping analysis for normative growth curves of global metrics in functional connectome



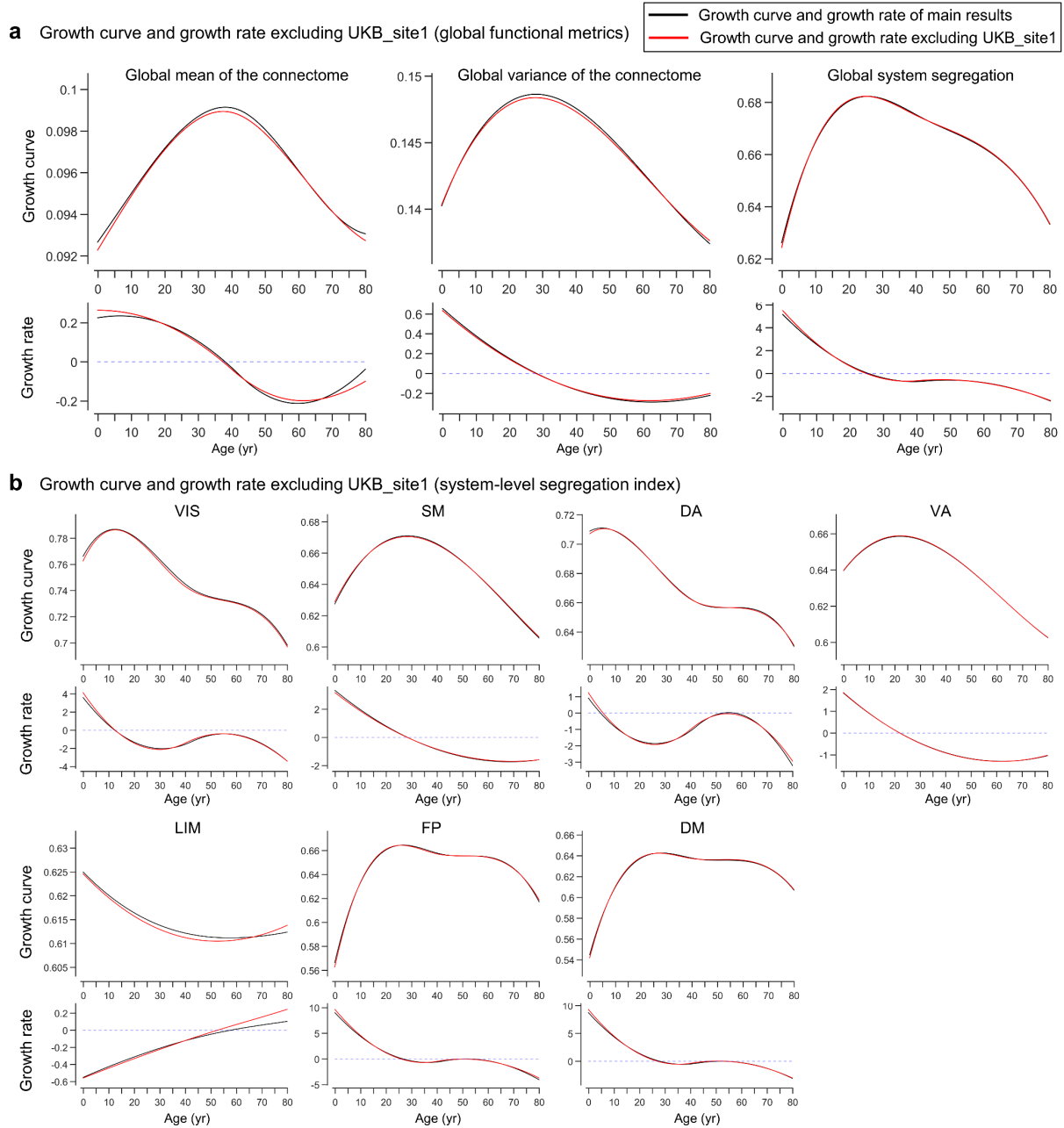
b Bootstrapping analysis for normative growth curves of system segregation in each network



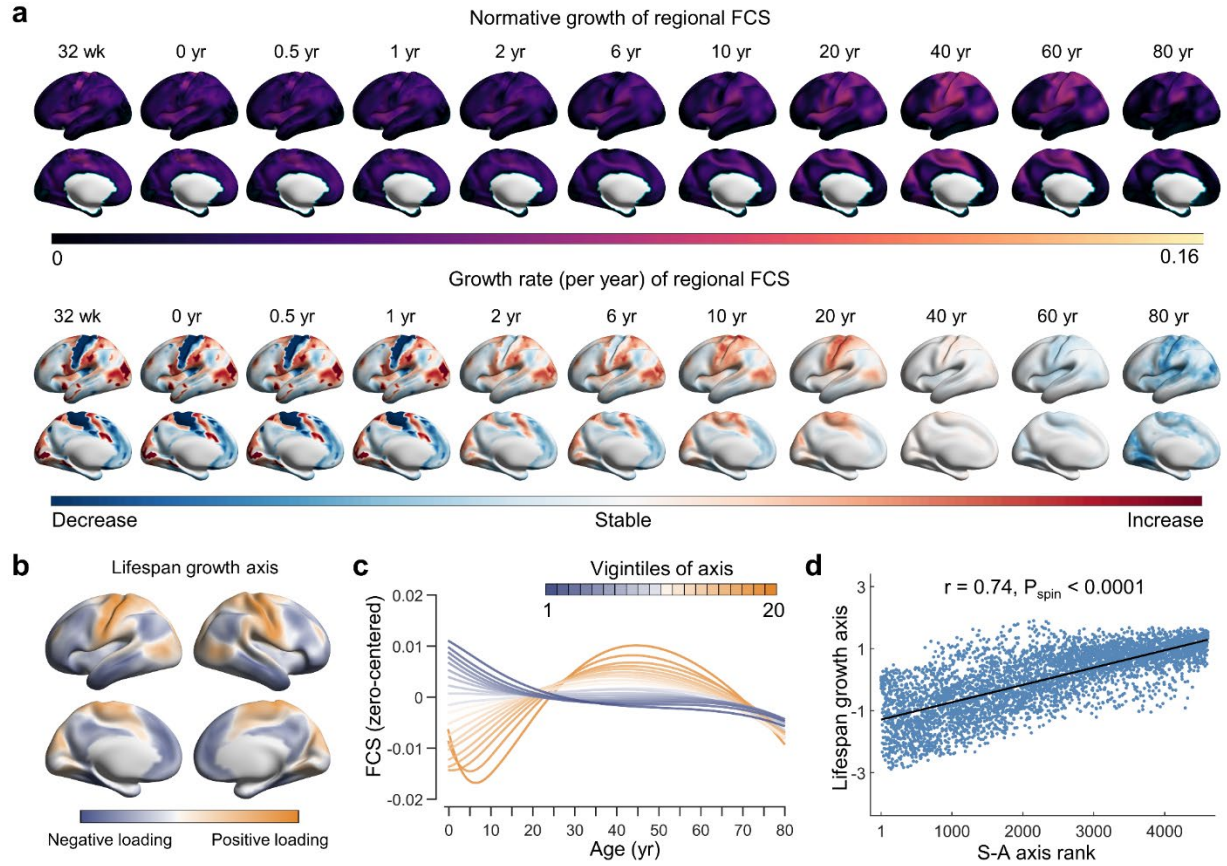
Supplementary Fig. 13-I | Sensitivity analyses: bootstrap resampling analysis for global- and system-level metrics. To assess the reliability of the lifespan growth curves, we performed 1,000 bootstrap iterations using replacement sampling. **a**, The 95% confidence interval (dotted lines) for the 50th centile curve (solid line) of global functional metrics. **b**, The 95% confidence interval for the 50th centile of system segregation in each network. yr, year.



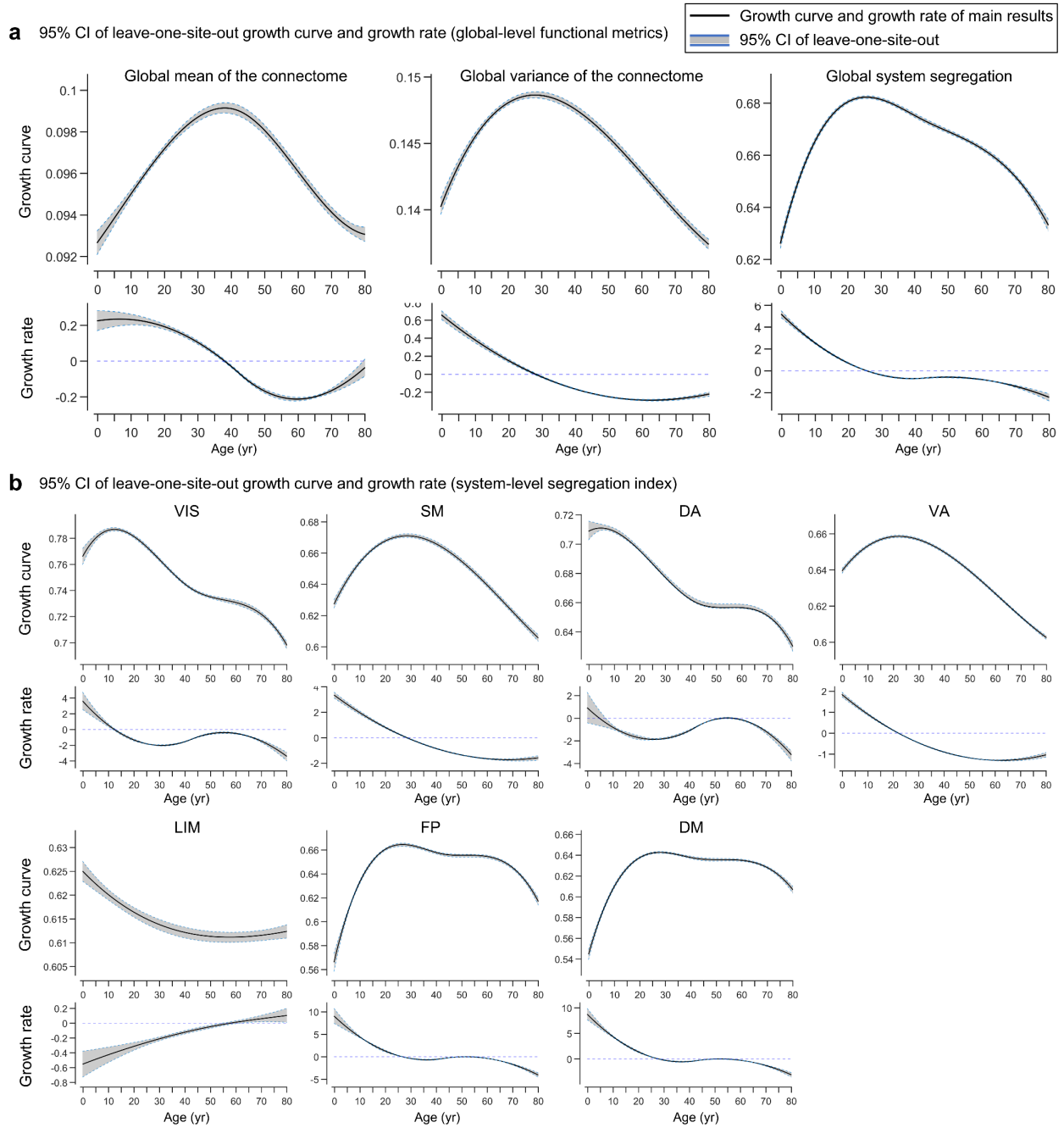
Supplementary Fig. 13-II | Sensitivity analyses: bootstrap resampling analysis for regional functional connectivity strength. Due to computational constraints, at the regional level, we performed a single bootstrap sampling analysis and rerun the normative modeling for all 4,609 vertices, yielding consistent results with the main analysis. **a**, The median centiles (top panel) and their growth rates (bottom panel) for all vertices at representative ages. **b**, The lifespan growth axis, represented by the first principal component (accounting for 59.7% of the variance) from a PCA on regional-level FCS curves. **c**, Based on the lifespan principal axis, all vertices across the brain were equally divided into 20 bins. The zero-centered curves of all vertices within each bin were averaged. The first vigintile (depicted in darkest blue) represents one pole of the axis, while the twentieth vigintile represents the opposite pole (depicted in darkest yellow). The patterns of growth curves vary continuously along the axis, with the greatest differences observed between the two poles. **d**, A strong correlation was observed between the lifespan principal growth axis and the sensorimotor-association (S-A) axis ($r = 0.71$, $p_{\text{spin}} < 0.0001$, one-sided). The central line represents the linear fit and the gray shaded areas shows a 95% confidence interval. FCS, functional connectivity strength; PCA, principal component analysis; wk, week; yr, year.



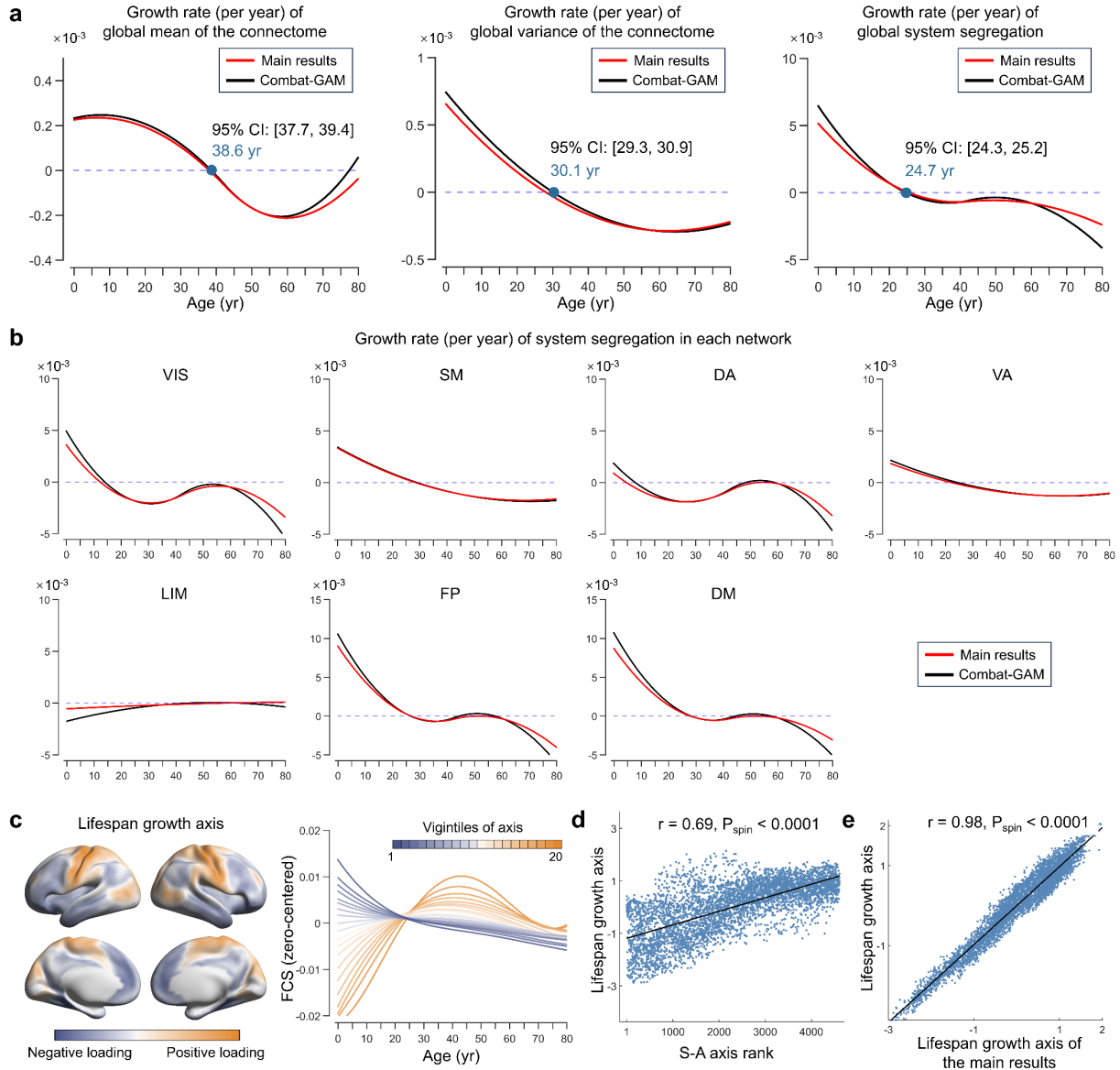
Supplementary Fig. 14-I | Sensitivity analyses: removing the site with the largest sample size (UKB site 1) from the whole dataset ($N_{\text{remaining}} = 20,373$), for global- and system-level metrics. Site 1 in the UK Biobank dataset includes the largest cohort, comprising 12,877 participants. After excluding Site 1 from the UK Biobank dataset, the normative curves and growth rates for the global functional metrics (**a**) and system-specific segregation metrics (**b**) are depicted by the red line. The normative curves and growth rates from the main results are represented by the black line. yr, year.



Supplementary Fig. 14-II | Sensitivity analyses: removing the site with the largest sample size (the UKB site) from the whole dataset ($N_{\text{remaining}} = 20,373$), for regional functional connectivity strength. **a**, The median centiles (top panel) and their growth rates (bottom panel) for all vertices at representative ages. **b**, The lifespan growth axis, represented by the first principal component (accounting for 62.6% of the variance) from a PCA on regional-level FCS curves. **c**, Based on the lifespan principal axis, all vertices across the brain were equally divided into 20 bins. The zero-centered curves of all vertices within each bin were averaged. The first vigintile (depicted in darkest blue) represents one pole of the axis, while the twentieth vigintile represents the opposite pole (depicted in darkest yellow). The patterns of growth curves vary continuously along the axis, with the greatest differences observed between the two poles. **d**, A strong correlation was observed between the lifespan principal growth axis and the sensorimotor-association (S-A) axis ($r = 0.74, p_{\text{spin}} < 0.0001$, one-sided). The central line represents the linear fit and the gray shaded areas shows a 95% confidence interval. FCS, functional connectivity strength; PCA, principal component analysis; wk, week; yr, year.

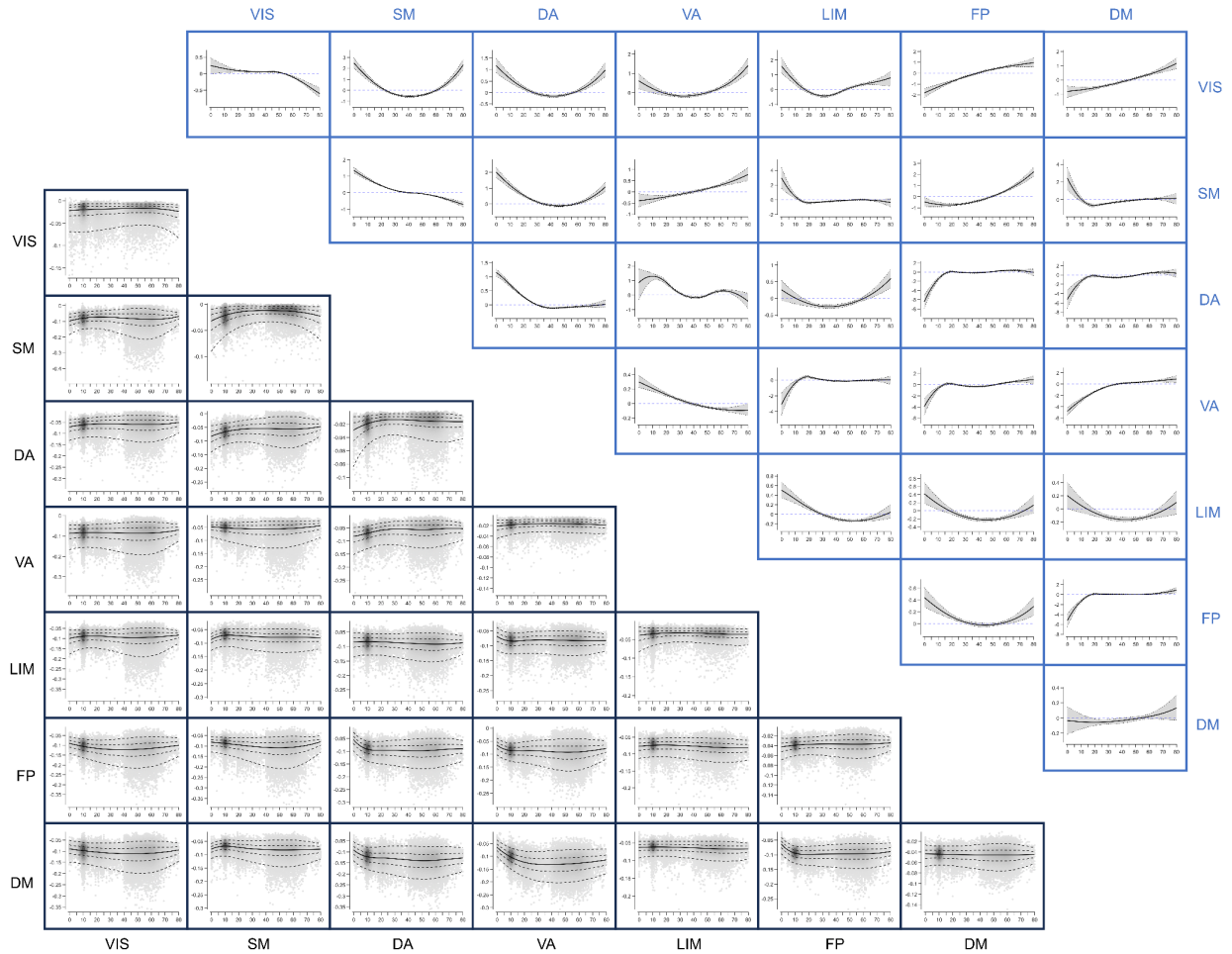


Supplementary Fig. 14-III | Sensitivity analyses: leave-one-site-out (LOSO). **a**, The top panel showed the LOSO 95% confidence intervals (CIs) for normative median curves (showed as central line) of global functional metrics, depicted as gray shaded areas. These CIs were obtained from the mean and standard deviation of the 50th centile lines, which were calculated repeatedly after sequentially excluding each site. The bottom panel showed the LOSO 95% confidence interval of growth rates (showed as central line) of global functional metrics. **b**, The LOSO 95% confidence interval of normative median curves (top panel, showed as central line) and growth rates (bottom panel, showed as central line) of system-specific segregation. yr, year.

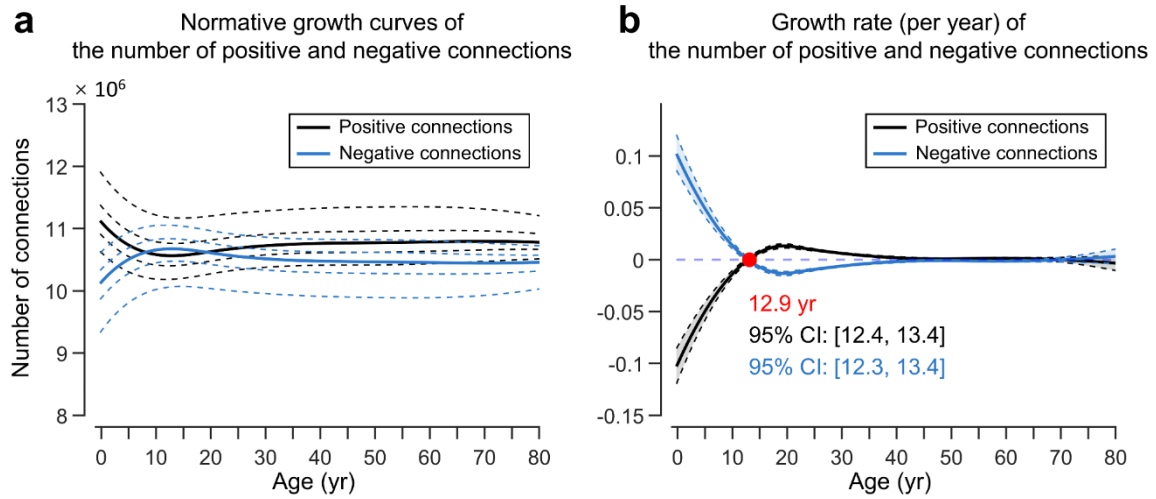


Supplementary Fig. 15 | Removing site effects using ComBAT-GAM method. **a**, Normative growth rate of global mean of the connectome, global variance of the connectome, and global system segregation. Each panel shows the growth rate of the median curve as a black solid line. The growth rate lines of the main results are shown as red solid lines. **b**, The growth rate of system segregation for each network. **c**, The left panel showed the lifespan growth axis of functional brain connectivity, represented by the first principal component (accounting for 64.3% of the variance) from a PCA on regional-level FCS curves. Right panel: based on the lifespan principal axis, all vertices across the brain were equally divided into 20 bins. The zero-centered curves of all vertices within each bin were averaged. The first vigintile (depicted in darkest blue) represents one pole of the axis, while the twentieth vigintile represents the opposite pole (depicted in darkest yellow). **d**, A strong correlation was observed between the lifespan principal growth axis and the sensorimotor-association (S-A) axis ($r = 0.69$, $p_{\text{spin}} < 0.0001$, one-sided). The central line represents the linear fit and the gray shaded areas shows a 95% confidence interval. **e**, The lifespan growth axis was highly similar with that of main results ($r = 0.98$, $p_{\text{spin}} < 0.0001$, one-sided). The central line represents the linear fit and the gray shaded areas shows a 95% confidence interval. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode; FCS, functional connectivity strength; PCA, principal component analysis; yr, year.

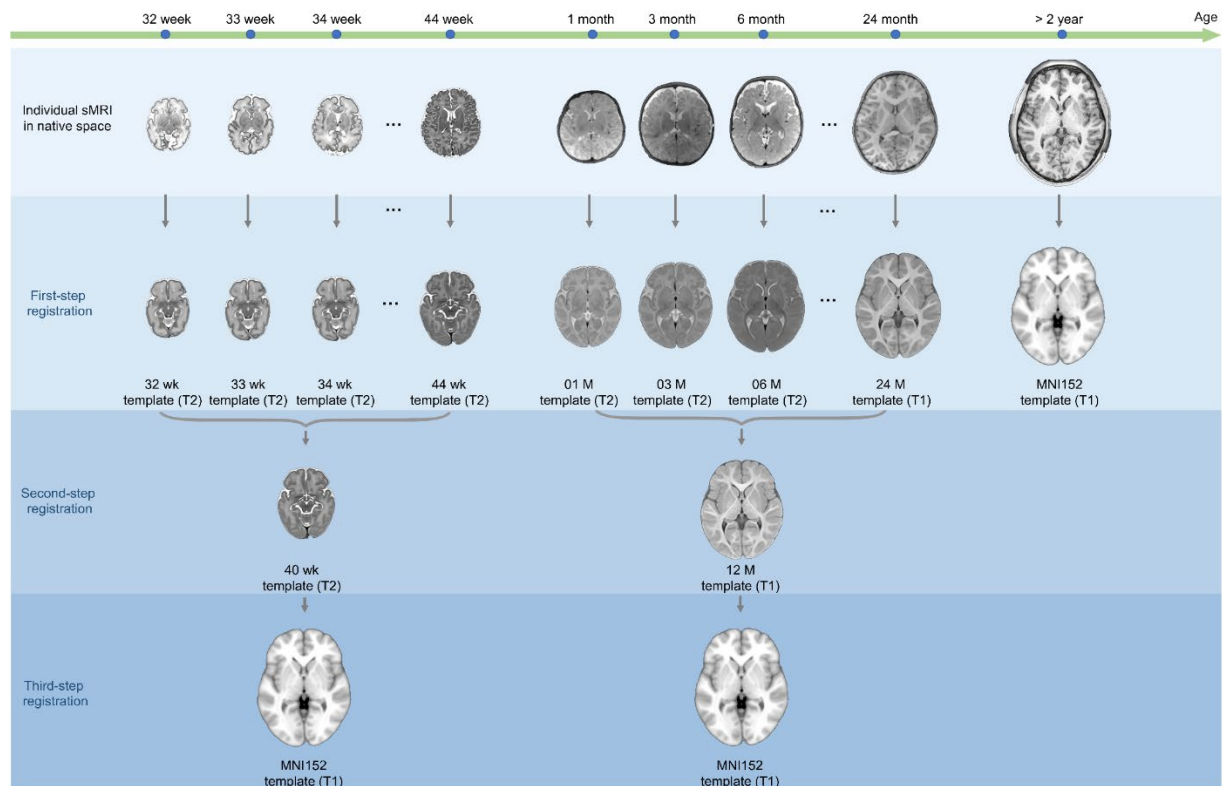
Normative growth curves and growth rates of within-system and between-system negative functional connectivity



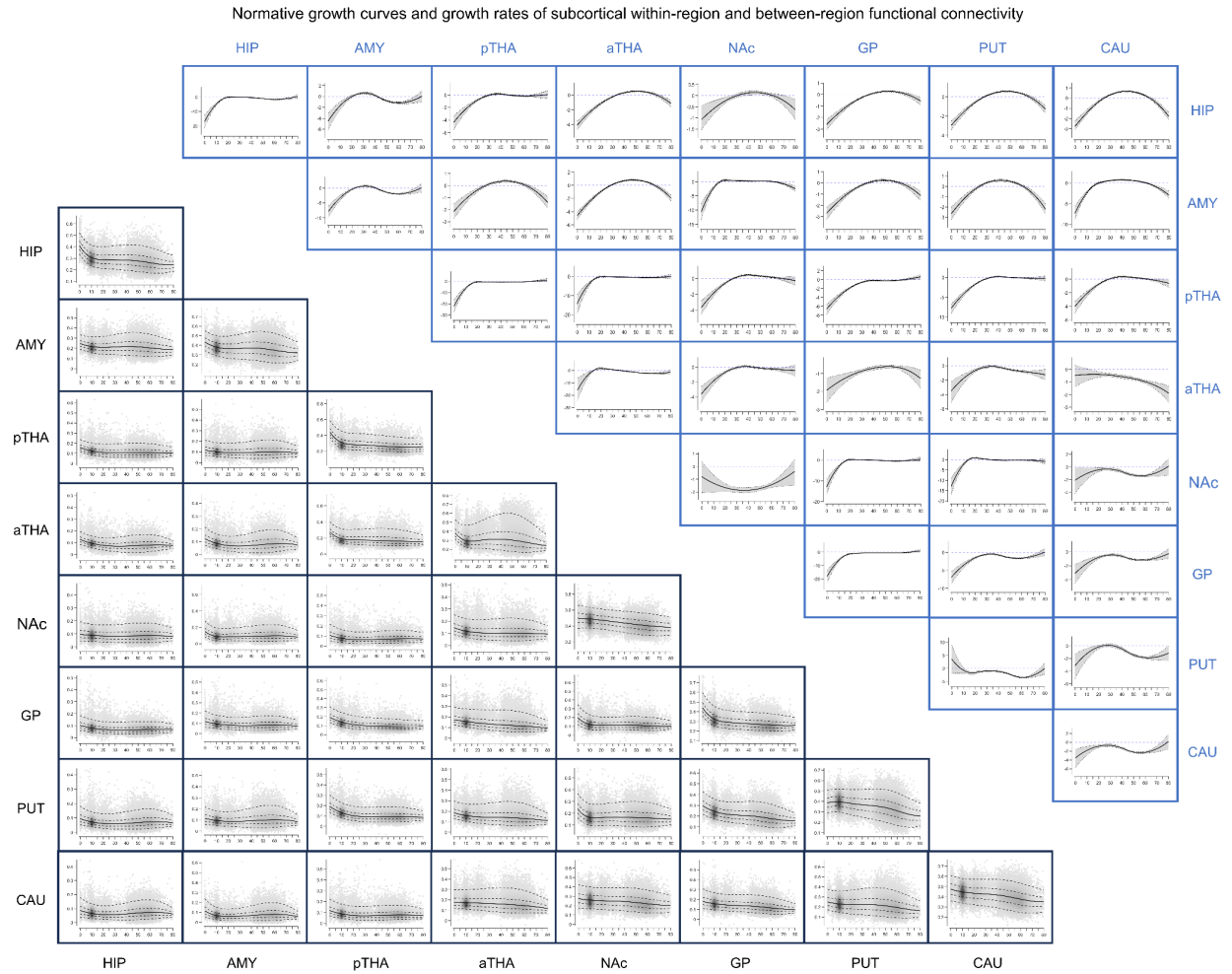
Supplementary Fig. 16-I | Lifespan growth patterns of within-system and between-system negative functional connectivity. The lower triangular matrix (shown in black) represents the normative growth curves for within-system and between-system negative connectivity, while the upper triangular matrix (shown in blue) represents the growth rate for these connectivity measures. The diagonal of the matrix shows the growth curves and growth rates of within-system negative connectivity; the off-diagonal elements represent the growth curves and growth rates of between-system negative connectivity. For the growth curve, the median (50th) percentile is shown as a solid line, and the 5th, 25th, 75th, and 95th percentiles are represented by dotted lines. The growth rate (showed as the central line) is characterized by the first derivative of the median centile line. The gray shaded areas denote the 95% confidence interval, estimated through bootstrapping 1,000 times. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode.



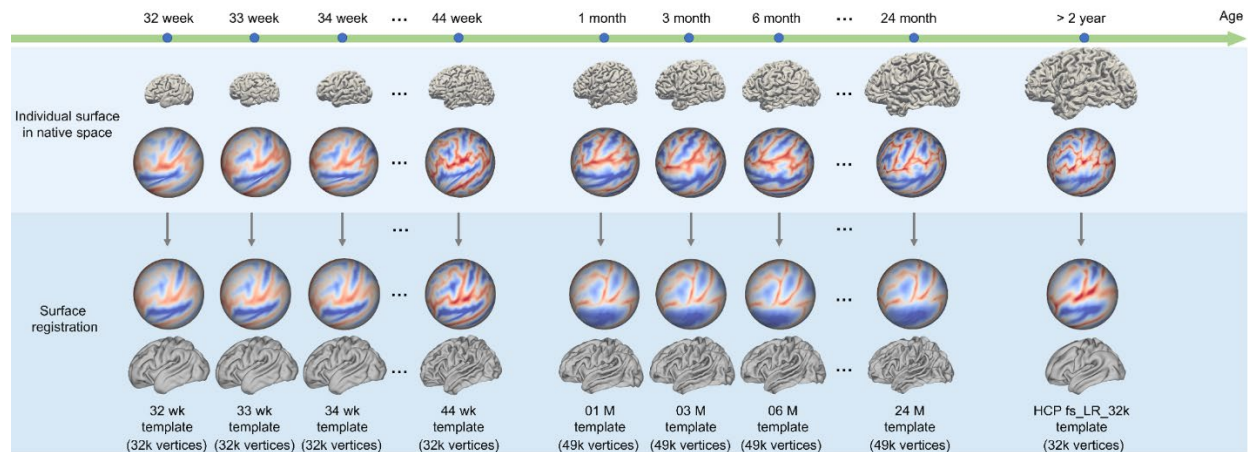
Supplementary Fig. 16-II | Lifespan normative curves and growth rate of the number of positive and negative connections. **a**, The curves for positive connections are depicted in black, while those for negative connections are shown in blue. The median (50th centile) curve is shown as a solid line, while the 5th, 25th, 75th, and 95th centiles are indicated by dotted lines. **b**, The growth rate (showed as the central line) is characterized by the first derivative of the median curve. The gray shaded areas represent the 95% confidence interval, which were estimated by bootstrapping 1,000 times. yr, year.



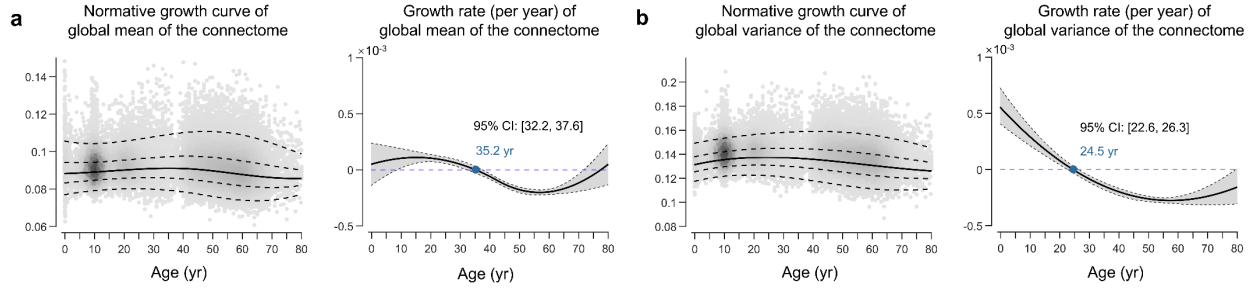
Supplementary Fig. 17-I | A schematic overview of the volume-based registration framework for sub-cortical analysis. For participants aged 32 to 44 postmenstrual weeks, a three-step volume registration procedure was employed: (1) individual T2w images were mapped to their corresponding postmenstrual week templates³³; (2) the 32-39 and 41-44 postmenstrual week templates were registered to the 40-week template; and (3) the 40-week template was registered to the MNI template³⁴. For participants aged 1-24 months, individual T2w or T1w images were aligned with their monthly age template³⁵. Specifically, for the individuals less than 6 months, T2w images were used, and for the individuals larger than 6 months, T1w images were used. All monthly templates were registered into the 12-month template, which was further registered to the MNI template. For participants aged larger than two years, the individual structural MRI were registered to the standard MNI space. wk, week; M, month.



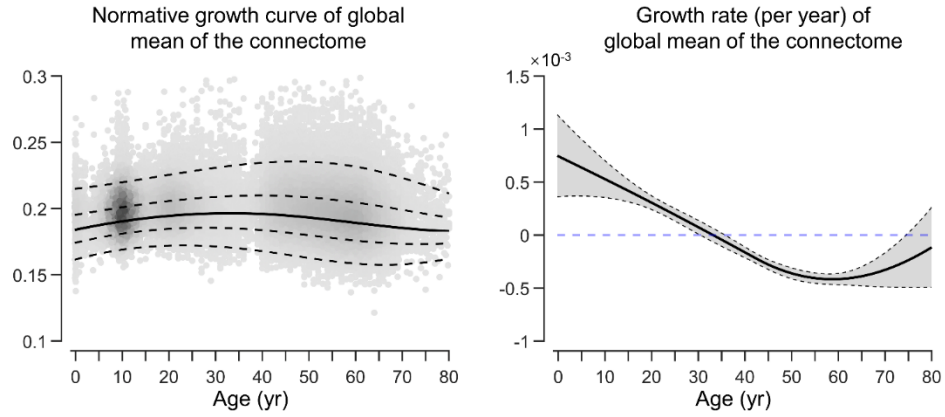
Supplementary Fig. 17-II | Lifespan growth patterns of within-region and between-region functional connectivity in subcortical structures. The lower triangular matrix (shown in black) represents the normative curves for within-region and between-region FC, while the upper triangular matrix (shown in blue) represents the growth rates for these FC measures. The diagonal of the matrix shows the growth curves and growth rates of within-region FC; the off-diagonal elements represent the growth curves and growth rates of between-region FC. For the growth curve, the median (50th) centile is shown as a solid line, and the 5th, 25th, 75th, and 95th centiles are represented by dotted lines. The growth rate (showed as the central line) is characterized by the first derivative of the median centile. The gray shaded areas denote the 95% confidence interval, estimated through bootstrapping 1,000 times. FC, functional connectivity; HIP, Hippocampus; AMY, Amygdala; pTHA, Posterior thalamus; aTHA, Anterior thalamus; NAc, Nucleus accumbens; GP, Globus pallidus; PUT, Putamen; CAU, Caudate nucleus.



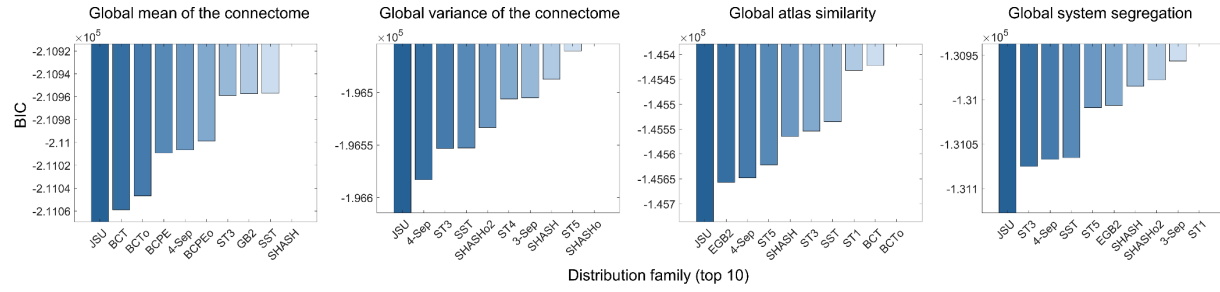
Supplementary Fig. 18-I | A surface registration strategy in which individual surfaces were registered only to the age-specific templates. To assess whether our main results were biased by the surface registration procedures to adult standard space, the fMRI data for all participants were re-preprocessed, with each participant's surface registered only to the corresponding age-specific template and without downsampling. For participants aged 32 to 44 postmenstrual weeks, the individual surfaces were mapped directly to their specific postmenstrual week templates³³. For participants aged 1-24 months, the individual surfaces were aligned with their monthly age templates¹¹. For participants aged larger than two years, the individual surfaces were mapped to the fs_LR_32k space⁵. wk, week; M, month.



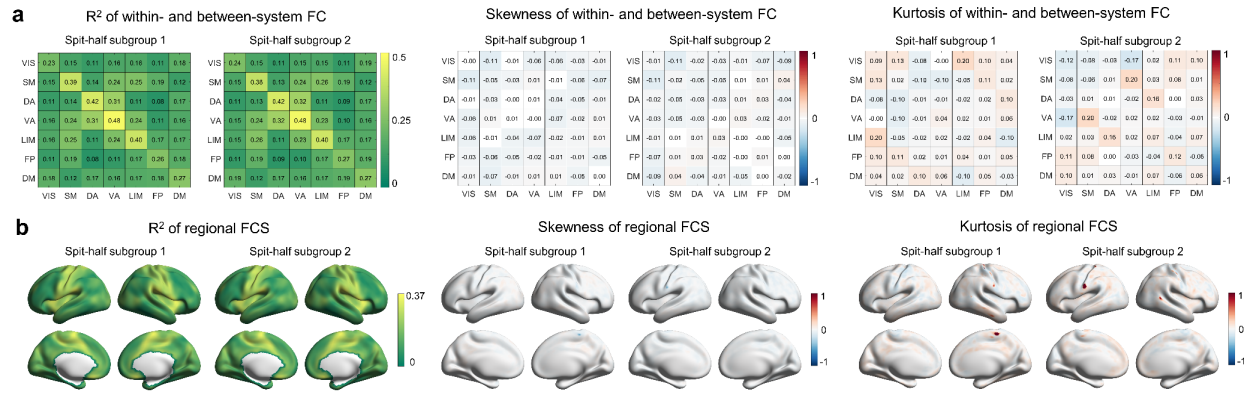
Supplementary Fig. 18-II | Lifespan growth patterns of the global functional connectome with employing different surface registration strategy. We re-analyzed the data for all participants by only aligning each participant's cortical surface to age-specific templates (see Supplementary Result 7 and Supplementary Fig. 18-I). Subsequently, we mapped the individual functional signals to these age-specific standard templates using deformation fields, followed by a uniform post-processing procedure without downsampling. **a**, Normative curve and growth rate of global mean of the connectome. **b**, Normative curve (left panel) and growth rate (right panel) of global variance of the connectome. For each panel, the left panel shows the median (50th) centile as a solid line, while the 5th, 25th, 75th, and 95th centiles are indicated by dotted lines. The growth rate (right panel, showed as the central line) is characterized by the first derivative of the median centile. The gray shaded areas represent the 95% confidence interval, which were estimated by bootstrapping 1,000 times. yr, year.



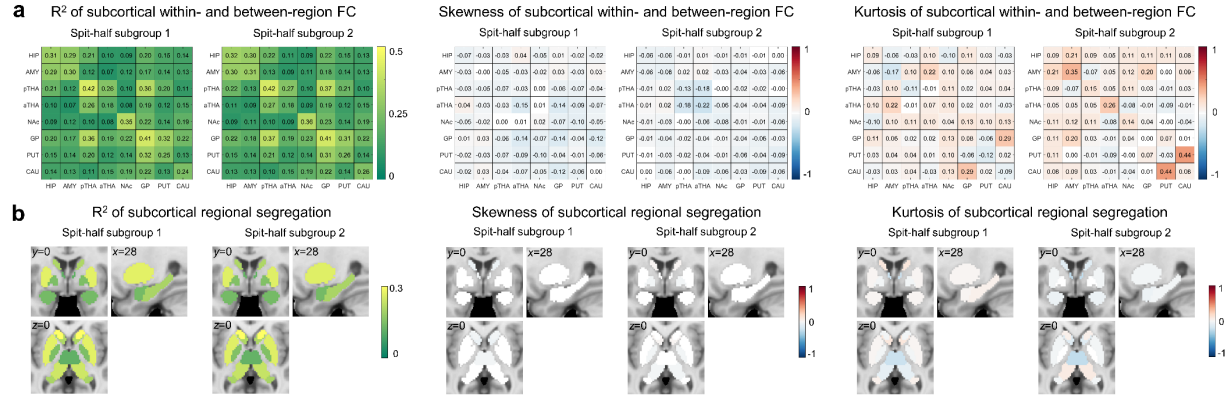
Supplementary Fig. 19 | Lifespan growth curve and growth rate of global mean of the connectome, by calculating averaged connectivity across only non-zero correlations. The left panel showed the averaged median (50th) centile as a solid line, surrounded by the averaged 5th, 25th, 75th, and 95th centiles as dotted lines. In the right panel, the solid line illustrated the growth rate of the averaged median centile, with its 95% confidence interval highlighted by gray shaded areas. yr, year.



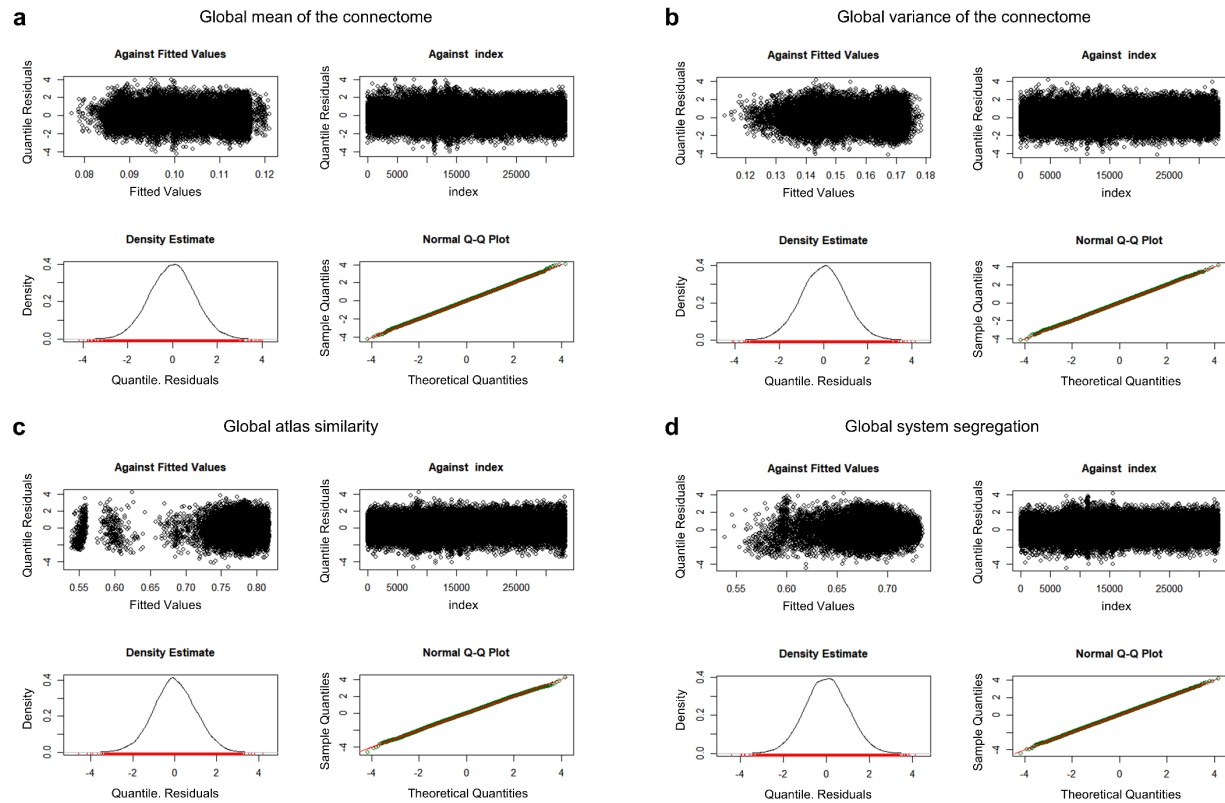
Supplementary Fig. 20 | Bayesian information criterion for each family of distributions. For each representative global-level functional phenotype, the top ten distributions with the lowest Bayesian information criterion (BIC) values were visualized. Among the evaluated distributions, Johnson's Su (JSU) consistently outperformed the others across all global phenotypes. The JSU distribution has four parameters: the median (μ), coefficient of variation (σ), skewness (ν), and kurtosis (τ). The distribution acronyms were in accordance with the GAMLSS package notation.



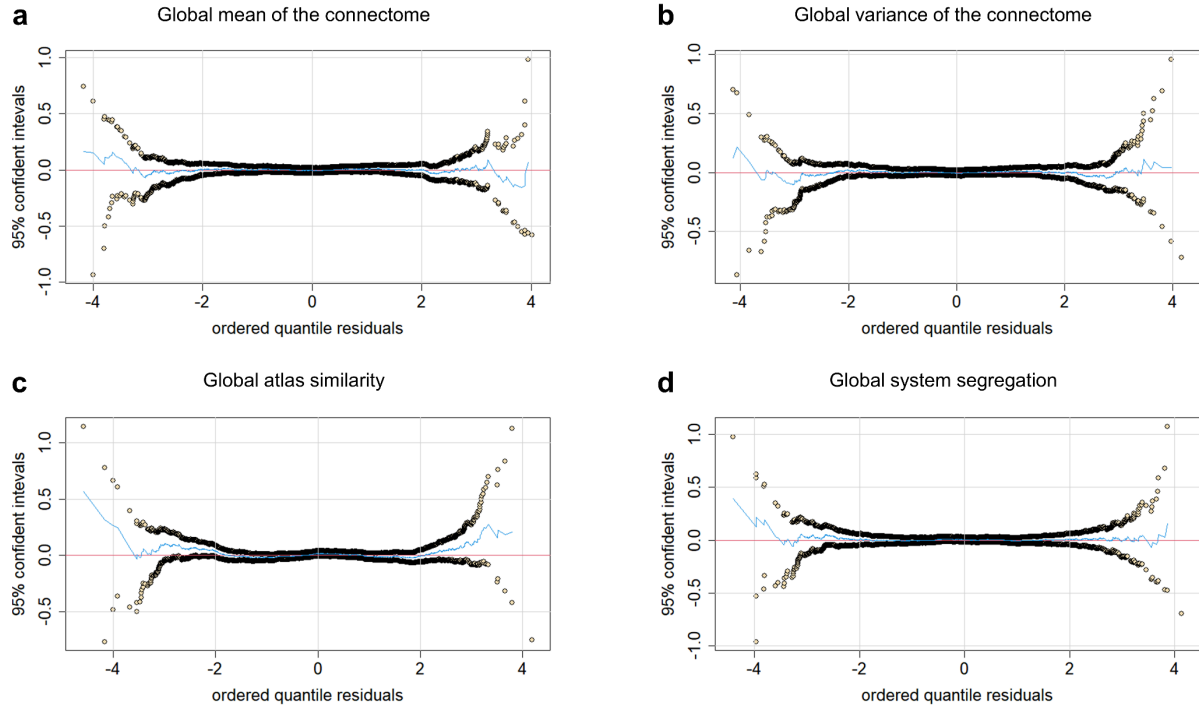
Supplementary Fig. 21 | Goodness of fit of the normative models of within-system FC, between-system FC, and regional FCS in the whole-cortex. All available data were split into two subgroups, with the GAMLSS model constructed using the training set (50%, $N_{\text{Subgroup1}} = 16,663$) and the goodness of fit of the models was evaluated using the testing set (50%, $N_{\text{Subgroup2}} = 16,587$). This process was replicated by swapping the roles of the training and testing sets. **a**, R -squared (R^2), skewness, and kurtosis of the normative model of within- and between-system FC. **b**, R -squared (R^2), skewness, and kurtosis of the normative model of regional-level FCS. For all models, the W values of the Shapiro-Wilk test were consistently greater than 0.99. FC, functional connectivity; FCS, functional connectivity strength; VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode.



Supplementary Fig. 22 | Goodness of fit of the normative models of within-region FC, between-region FC, and regional segregation in the subcortical structures. All available data were split into two subgroups, with the GAMLSS model constructed using the training set (50%, $N_{\text{Subgroup1}} = 16,663$) and the goodness of fit of the models was evaluated using the testing set (50%, $N_{\text{Subgroup2}} = 16,587$). This process was replicated by swapping the roles of the training and testing sets. **a**, R^2 , skewness, and kurtosis of the normative model of within- and between-region FC. **b**, R^2 , skewness, and kurtosis of the normative model of subcortical regional segregation. For all models, the W values of the Shapiro-Wilk test were consistently greater than 0.99. FC, functional connectivity.

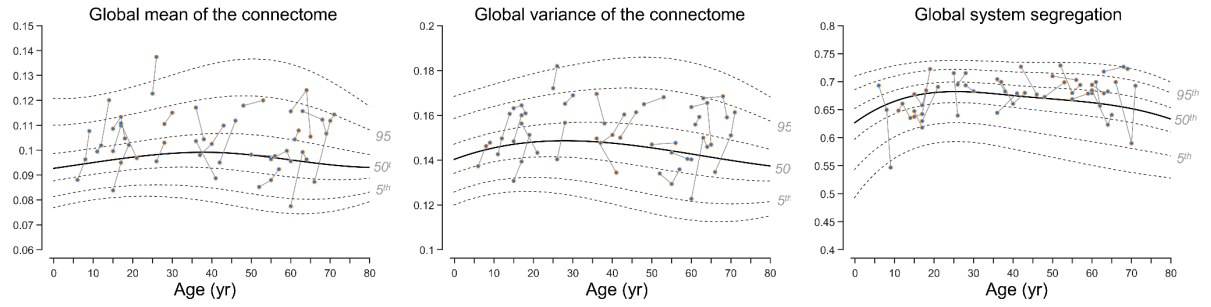


Supplementary Fig. 23 | Residual distribution plots of the GAMLSS models for global functional metrics. The plots showed that the model residuals of global mean of the connectome (**a**), global variance of the connectome (**b**), global atlas similarity (**c**), and global system segregation (**d**) were normally distributed.

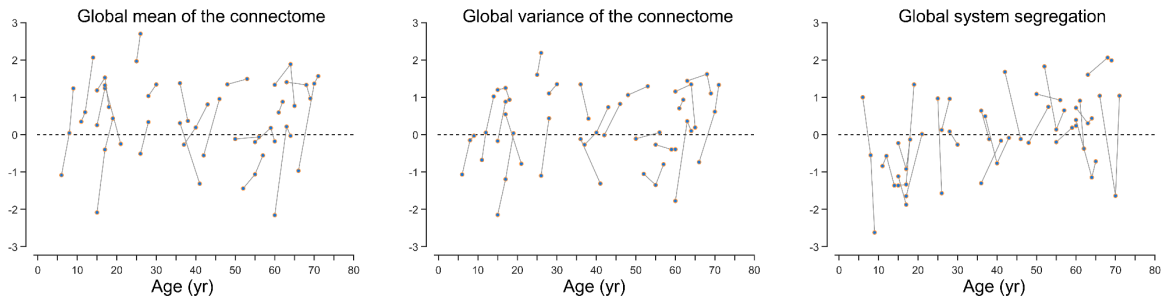


Supplementary Fig. 24 | Detrended transformed Owen's plots of the GAMLSS models for global connectome metrics. The zero horizontal line was within the confidence interval, suggesting that the residuals of global mean of the connectome (**a**), global variance of the connectome (**b**), global atlas similarity (**c**), and global system segregation (**d**) followed a normal distribution.

a Longitudinal age-related changes for some participants in the raw values



b Longitudinal age-related changes for some participants in the deviation scores



Supplementary Fig. 25 | Longitudinal age-related changes for some participants in the raw values and deviation scores based on the connectome-based normative model. Longitudinal scans were available for a subset of the participants included in the present study (1,481 longitudinal scans from 1,077 participants, representing 3.2% of the total cohort). Following the training of the normative models on the cross-sectional cohort of 33,250 participants, we used the longitudinal scan data as a testing set to estimate age-related predictions and deviation scores. For the purpose of illustrations, several example participants were selected to demonstrate the longitudinal changes in raw values and deviation scores. **a**, From left to right, the panel shows longitudinal changes in the raw values for the global mean of the connectome, global variance of the connectome, and global system segregation. The median (50th centile) curve is indicated by a solid line, while the 5th, 25th, 75th, and 95th centiles are indicated by dotted lines. The longitudinal changes are shown using solid lines connecting scatter points from the same participant's two or three scans. **b**, The longitudinal changes in deviation scores for the global mean of the connectome, global variance of the connectome, and global system segregation. The figure showed substantial heterogeneity in individual longitudinal changes in both raw values and deviation scores. This variability may be attributable to interindividual differences, age-related variations, or their combined effects.

Supplementary Tables

Supplementary Table 1. Demographic information of the participants for each site

Available in separate file, *SI_Table_1_2_Demographics_and_Image_Acquisition.xlsx*

Supplementary Table 2. Imaging scan parameters for each site

Available in separate file, *SI_Table_1_2_Demographics_and_Image_Acquisition.xlsx*

Supplementary Table 3. Sex differences in the Mu (μ) coefficients in GAMLSS models

Functional metric	μ Coefficients					
	Estimate	Std.Error	T value	P value	P _{FDR}	
Global mean of the connectome	0.0004	0.0001	3.828	0.0001	0.0002 ***	M > F
Global variance of the connectome	-0.0004	0.0001	-3.393	0.0007	0.0009 ***	M < F
Global system segregation	-0.0036	0.0003	-10.402	3e-25	7e-25 ***	M < F
System segregation of VIS network	-0.0026	0.0006	-3.965	0.00007	0.0001 ***	M < F
System segregation of SM network	0.0115	0.0008	14.735	5e-49	2e-48 ***	M > F
System segregation of DA network	0.0006	0.0006	1.111	0.267	0.267	
System segregation of VA network	-0.0104	0.0006	-18.121	5e-73	3e-72 ***	M < F
System segregation of LIM network	0.0109	0.0009	12.049	2e-33	6e-33 ***	M > F
System segregation of FP network	-0.0019	0.0007	-2.766	0.0056	0.0062 **	M < F
System segregation of DM network	-0.0171	0.0008	-21.82	1e-104	1e-103 ***	M < F

Abbreviations: VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode; FDR, false discovery rate; M, male; F, female.

Supplementary Table 4. Sex differences of the Sigma (σ) coefficients in GAMLSS models

Functional metric	σ Coefficients					
	Estimate	Std.Error	T value	P value	P _{FDR}	
Global mean of the connectome	0.0010	0.0081	0.120	0.905	0.905	
Global variance of the connectome	-0.0261	0.0082	-3.196	0.001	0.002 **	M < F
Global system segregation	0.0158	0.0083	1.914	0.056	0.088	
System segregation of VIS network	-0.0220	0.0078	-2.837	0.005	0.009 **	M < F
System segregation of SM network	-0.0045	0.0079	-0.577	0.564	0.689	
System segregation of DA network	0.0110	0.0081	1.356	0.175	0.241	
System segregation of VA network	0.0311	0.0082	3.809	0.0001	0.0006 ***	M > F
System segregation of LIM network	-0.0302	0.0081	-3.723	0.0002	0.0007 ***	M < F
System segregation of FP network	0.0344	0.0079	4.358	0.00001	0.0001 ***	M > F
System segregation of DM network	0.0276	0.0077	3.599	0.0003	0.0008 ***	M > F

Abbreviations: VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode; FDR, false discovery rate; M, male; F, female.

Supplementary Table 5. Similarity of lifespan normative growth curves between each sensitivity analysis and the main results (sampling 80 points at one-year intervals)

Sensitivity analysis	Global-level metrics			System segregation							Regional level metrics
	Global mean of the connectome	Global variance of the connectome	Global system segregation	VIS	SM	DA	VA	LIM	FP	DM	Lifespan growth axis
S_1	0.97	0.98	1.00	1.00	0.98	1.00	0.99	0.98	1.00	1.00	1.00
S_2	0.99	1.00	1.00	0.99	0.91	0.99	1.00	0.51	0.99	0.99	0.94
S_3	1.00	1.00	1.00	1.00	0.99	1.00	1.00	0.80	1.00	1.00	0.99
S_4	1.00	0.99	0.99	1.00	1.00	0.99	1.00	0.98	1.00	1.00	0.99
S_5	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99
S_6	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Abbreviations: S_1, Sensitivity analysis: with stricter head motion threshold (mean FD < 0.2mm, N = 24,494). S_2, Sensitivity analysis: Balanced resampling (N = 6,770). Similarity of mean curve was shown for global and system level metrics. Spatial correlation of the lifespan growth axis between a random balanced analysis and the main results was shown for regional level metrics. S_3, Sensitivity analysis: independent replication samples: split-half subgroup 1 (N = 16,663). S_4, Sensitivity analysis: independent replication samples: split-half subgroup 2 (N = 16,587). S_5, Sensitivity analysis: Bootstrapping. Similarity of mean curve was shown for global and system level metrics. Spatial correlation of the lifespan growth axis between a random bootstrapping analysis and the main results was shown for regional level metrics. S_6, Sensitivity analysis: leave-one-site-out (LOSO) analysis. Similarity of mean curve was shown for global and system level metrics. Spatial correlation of the lifespan growth axis between sensitivity analysis (removing the largest site [UKB site 1]) and the main results was shown for regional level metrics. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode.

Supplementary Table 6. Similarity of lifespan growth rate between each sensitivity analysis and the main results (sampling 80 points at six-month intervals)

Sensitivity analysis	Global-level metrics			System segregation						
	Global mean of the connectome	Global variance of the connectome	Global system segregation	VIS	SM	DA	VA	LIM	FP	DM
S_1	0.95	0.99	1.00	0.99	1.00	0.97	1.00	0.99	1.00	1.00
S_2	0.93	1.00	1.00	0.97	0.99	0.86	1.00	0.39	0.97	0.98
S_3	1.00	0.99	0.99	1.00	0.99	0.95	0.99	0.21	1.00	1.00
S_4	0.99	0.98	0.99	0.99	0.99	0.89	1.00	0.87	1.00	0.99
S_5	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
S_6	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Abbreviations: S_1, Sensitivity analysis: with stricter head motion threshold (mean FD < 0.2mm, N = 24,494). S_2, Sensitivity analysis: Balanced resampling (N = 6,770). Similarity of mean growth rate was shown for global and system level metrics. S_3, Sensitivity analysis: independent replication samples: split-half subgroup 1 (N = 16,663). S_4, Sensitivity analysis: independent replication samples: split-half subgroup 2 (N = 16,587). S_5, Sensitivity analysis: Bootstrapping. Similarity of mean growth rate was shown for global and system level metrics. S_6, Sensitivity analysis: leave-one-site-out (LOSO) analysis. Similarity of mean growth rate was shown for global and system level metrics. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode.

Supplementary Table 7. Similarity of lifespan normative growth curves between each sensitivity analysis and the main results (sampling 160 points at six-month intervals)

Sensitivity analysis	Global-level metrics			System segregation							Regional level metrics
	Global mean of the connectome	Global variance of the connectome	Global system segregation	VIS	SM	DA	VA	LIM	FP	DM	Lifespan growth axis
S_1	0.97	0.98	1.00	1.00	0.98	1.00	0.99	0.98	1.00	1.00	1.00
S_2	0.99	1.00	1.00	0.99	0.91	0.99	1.00	0.51	0.99	0.99	0.94
S_3	1.00	1.00	1.00	1.00	0.99	1.00	1.00	0.80	1.00	1.00	0.99
S_4	1.00	0.99	0.99	1.00	1.00	0.99	1.00	0.98	1.00	1.00	0.99
S_5	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99
S_6	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Abbreviations: S_1, Sensitivity analysis: with stricter head motion threshold (mean FD < 0.2mm, N = 24,494). S_2, Sensitivity analysis: Balanced resampling (N = 6,770). Similarity of mean curve was shown for global and system level metrics. Spatial correlation of the lifespan growth axis between a random balanced analysis and the main results was shown for regional level metrics. S_3, Sensitivity analysis: independent replication samples: split-half subgroup 1 (N = 16,663). S_4, Sensitivity analysis: independent replication samples: split-half subgroup 2 (N = 16,587). S_5, Sensitivity analysis: Bootstrapping. Similarity of mean curve was shown for global and system level metrics. Spatial correlation of the lifespan growth axis between a random bootstrapping analysis and the main results was shown for regional level metrics. S_6, Sensitivity analysis: leave-one-site-out (LOSO) analysis. Similarity of mean curve was shown for global and system level metrics. Spatial correlation of the lifespan growth axis between sensitivity analysis (removing the largest site [UKB site 1]) and the main results was shown for regional level metrics. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode.

Supplementary Table 8. Similarity of lifespan normative growth curves between each sensitivity analysis and the main results (sampling 1,000 points at one-month intervals)

Sensitivity analysis	Global-level metrics			System segregation							Regional level metrics
	Global mean of the connectome	Global variance of the connectome	Global system segregation	VIS	SM	DA	VA	LIM	FP	DM	Lifespan growth axis
S_1	0.97	0.98	1.00	1.00	0.98	1.00	0.99	0.98	1.00	1.00	1.00
S_2	0.99	1.00	1.00	0.99	0.91	0.99	1.00	0.51	0.99	0.99	0.94
S_3	1.00	1.00	1.00	1.00	0.99	1.00	1.00	0.80	1.00	1.00	0.99
S_4	1.00	0.99	0.99	1.00	1.00	0.99	1.00	0.98	1.00	1.00	0.99
S_5	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99
S_6	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Abbreviations: S_1, Sensitivity analysis: with stricter head motion threshold (mean FD < 0.2mm, N = 24,494). S_2, Sensitivity analysis: Balanced resampling (N = 6,770). Similarity of mean curve was shown for global and system level metrics. Spatial correlation of the lifespan growth axis between a random balanced analysis and the main results was shown for regional level metrics. S_3, Sensitivity analysis: independent replication samples: split-half subgroup 1 (N = 16,663). S_4, Sensitivity analysis: independent replication samples: split-half subgroup 2 (N = 16,587). S_5, Sensitivity analysis: Bootstrapping. Similarity of mean curve was shown for global and system level metrics. Spatial correlation of the lifespan growth axis between a random bootstrapping analysis and the main results was shown for regional level metrics. S_6, Sensitivity analysis: leave-one-site-out (LOSO) analysis. Similarity of mean curve was shown for global and system level metrics. Spatial correlation of the lifespan growth axis between sensitivity analysis (removing the largest site [UKB site 1]) and the main results was shown for regional level metrics. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode.

Supplementary Table 9. Similarity of lifespan growth rates between each sensitivity analysis and the main results (sampling 160 points)

Sensitivity analysis	Global-level metrics			System segregation						
	Global mean of the connectome	Global variance of the connectome	Global system segregation	VIS	SM	DA	VA	LIM	FP	DM
S_1	0.95	0.99	1.00	0.99	1.00	0.97	1.00	0.99	1.00	1.00
S_2	0.93	1.00	1.00	0.97	0.99	0.86	1.00	0.39	0.97	0.98
S_3	1.00	0.99	0.99	1.00	0.99	0.95	0.99	0.21	1.00	1.00
S_4	0.99	0.98	0.99	0.99	0.99	0.89	1.00	0.87	1.00	0.99
S_5	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
S_6	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Abbreviations: S_1, Sensitivity analysis: with stricter head motion threshold (mean FD < 0.2mm, N = 24,494). S_2, Sensitivity analysis: Balanced resampling (N = 6,770). Similarity of mean growth rate was shown for global and system level metrics. S_3, Sensitivity analysis: independent replication samples: split-half subgroup 1 (N = 16,663). S_4, Sensitivity analysis: independent replication samples: split-half subgroup 2 (N = 16,587). S_5, Sensitivity analysis: Bootstrapping. Similarity of mean growth rate was shown for global and system level metrics. S_6, Sensitivity analysis: leave-one-site-out (LOSO) analysis. Similarity of mean growth rate was shown for global and system level metrics. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode.

Supplementary Table 10. Similarity of lifespan growth rates between each sensitivity analysis and the main results (sampling 1,000 points)

Sensitivity analysis	Global-level metrics			System segregation						
	Global mean of the connectome	Global variance of the connectome	Global system segregation	VIS	SM	DA	VA	LIM	FP	DM
S_1	0.95	0.99	1.00	0.99	1.00	0.97	1.00	0.99	1.00	1.00
S_2	0.93	1.00	1.00	0.97	0.99	0.86	1.00	0.39	0.97	0.98
S_3	1.00	0.99	0.99	1.00	0.99	0.95	0.99	0.21	1.00	1.00
S_4	0.99	0.98	0.99	0.99	0.99	0.89	1.00	0.87	1.00	0.99
S_5	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
S_6	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

Abbreviations: S_1, Sensitivity analysis: with stricter head motion threshold (mean FD < 0.2mm, N = 24,494). S_2, Sensitivity analysis: Balanced resampling (N = 6,770). Similarity of mean growth rate was shown for global and system level metrics. S_3, Sensitivity analysis: independent replication samples: split-half subgroup 1 (N = 16,663). S_4, Sensitivity analysis: independent replication samples: split-half subgroup 2 (N = 16,587). S_5, Sensitivity analysis: Bootstrapping. Similarity of mean growth rate was shown for global and system level metrics. S_6, Sensitivity analysis: leave-one-site-out (LOSO) analysis. Similarity of mean growth rate was shown for global and system level metrics. VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode.

Supplementary Table 11. Detailed information of the age range, number of participants, and sex ratio for the construction of age-specific group atlases

Atlas name	Age range	Number of participants	Female (%)
34-week atlas	32-35 postmenstrual weeks	25	40.00
36-week atlas	35-37 postmenstrual weeks	29	31.03
38-week atlas	37-39 postmenstrual weeks	38	31.58
0-year (40-week) atlas	39-41 postmenstrual weeks	122	40.98
1-month atlas	0.25-1.5 months	167	50.30
3-month atlas	1.5-4.5 months	33	57.58
6-month atlas	4.5-7.5 months	47	57.45
9-month atlas	7.5-10.5 months	57	57.89
12-month atlas	10.5-13.5 months	60	58.33
18-month atlas	13.5-21 months	88	52.27
24-month atlas	21-27 months	59	55.93
4-year atlas	2.25-5 years	137	50.36
6-year atlas	5-7 years	122	48.36
8-year atlas	7-9 years	300	51.67
10-year atlas	9-11 years	300	43.67
12-year atlas	11-13 years	300	42.00
14-year atlas	13-15 years	300	42.00
16-year atlas	15-17 years	300	39.67
18-year atlas	17-19 years	300	51.00
20-year atlas	19-21 years	300	53.67
30-year atlas	25-35 years	300	45.67
40-year atlas	35-45 years	300	53.67
50-year atlas	45-55 years	300	62.33
60-year atlas	55-65 years	300	60.67
70-year atlas	65-75 years	300	56.00
80-year atlas	75-80 years	155	53.55

Supplementary Table 12. Fitting quality of the connectome-based normative models at global and system-level

Functional metric	Half 1				Half 2			
	R ²	W	Skewness	Kurtosis	R ²	W	Skewness	Kurtosis
Global mean of the connectome	0.49	1.00	-0.01	0.1	0.49	1.00	-0.02	-0.07
Global variance of the connectome	0.48	1.00	0.00	0.1	0.48	1.00	-0.02	-0.09
Global system segregation	0.36	1.00	0.05	0.02	0.35	1.00	-0.01	0.02
System segregation of VIS network	0.32	1.00	0.07	0.11	0.33	1.00	0.02	-0.13
System segregation of SM network	0.14	1.00	0.03	-0.05	0.14	1.00	0.00	-0.05
System segregation of DA network	0.28	1.00	0.05	0.01	0.27	1.00	-0.03	0.09
System segregation of VA network	0.19	1.00	-0.01	0.03	0.19	1.00	0.02	-0.02
System segregation of LIM network	0.24	1.00	0.05	-0.06	0.24	1.00	-0.04	0.11
System segregation of FP network	0.23	1.00	0.03	0.07	0.24	1.00	0.00	-0.06
System segregation of DM network	0.20	1.00	-0.03	0.01	0.20	1.00	0.07	0.03

Abbreviations: VIS, visual; SM, somatomotor; DA, dorsal attention; VA, ventral attention; LIM, limbic; FP, frontoparietal; DM, default mode.

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