Supplementary Information

Imaging data preprocessing

Preprocessing was carried out using the open-source, Nipype-based, automated Configurable Pipeline for the Analysis of Connectomes v0.3.9 (https://github.com/FCP-INDI/C-PAC/tree/v0.3.9; http://dx.doi.org/10.5281/zenodo.16557). In light of our previous work,[1,2] after discarding the first 4 time-points of each functional run to allow for magnetization to reach steady state, preprocessing individual resting-state functional scans consisted of (I) 3D motion correction (realignment using 3 translational and 3 rotational parameters), (II) mean-based intensity normalization, (III) nuisance regression (detailed below), (IV) temporal band-pass filtering (0.01–0.1 Hz), (V) registration (detailed below), and (VI) spatial smoothing using a 6-mm Gaussian kernel at full-width half maximum.

Nuisance regression

The subject-level nuisance regression strategy involved application of CompCor[3] with five principal components derived from white matter and cerebrospinal fluid using subject-specific masks with tissue type probability threshold of 0.6, along with regressing out preprocessed data on the 24 parameters generated from the motion correction procedure (i.e., 3 translational and 3 rotational parameters, their values from the previous time-point, and the squared values of these 12 items).[4]

Registration

We adopted an unbiased pairwise approach[5] to ensure robust image registration. Specifically, using the Advanced Normalization Tools (ANTs) algorithm,[6] for every participant, pairwise registration was performed with the common “midway” points calculated in three steps: once per each scan pair, and then between the resulting mid-points of paired registered images. Following functional-to-anatomical image co-registration, images were transformed into MNI152 (Montreal Neurological Institute) space at 2 mm^3 isotropic resolution using ANTs.[6]

Statistical inference

In light of recent demonstrations that parametric statistical inference tends to inflate false discovery rates[7] we performed group-level non-parametric statistical inference. We opted for the threshold-free cluster enhancement (TFCE) algorithm implemented in FSL v5.0.8’s Randomise tool (http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/Randomise)[8] with 5,000 permutations to obviate issues of spatial smoothing, threshold dependence and localization inherent to cluster-based inference. TFCE controls for multiple comparisons (familywise error rate at α=0.05). In the general linear model, each of the two resting-state scans per condition was modeled separately. Central results were corroborated in a confirmatory analysis that used the average of resting-state scans within each condition (data not shown).

Head motion data

Head motion was indexed by Jenkinson’s mean frame-wise displacement (FD), computed separately for each resting-state run for every participant.[9] The mean FD across participants and runs was 0.07±0.03 mm. The maximum FD for any run was 0.16 mm,

which is below the standard cut-off of 0.20 mm.[1] Therefore, no data were discarded due to unacceptably high head motion. Finally, there were no significant differences in mean FD across the 4 study phases for either resting-state run (first run: $F_{3,12}$=0.06, p=0.98; second $F_{3,12}$=0.39, p=0.77).

Sleep duration data

Wrist actigraphy was used to estimate sleep duration. For one of the five study completers with imaging data, sleep duration data was unavailable for two phases. Sleep duration was on average 7.05±0.44h with no significant differences across the 4 study phases ($F_{3,8}$=0.76, p=0.55).

References

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