Figures and figure supplements

The heritability of multi-modal connectivity in human brain activity

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**Figure 1.** Contribution of genetic factors to functional connectivity outweighs that of the environment shared between twins. A. Grand average functional connectome for fMRI and for the theta, alpha and beta MEG oscillatory bands. The coloured edge maps show group-average network matrices for correlations in oscillatory amplitude in each band, and partial correlations in BOLD response, thresholded for visualisation. Nodes are annotated by cortical region, and labelled in Supplementary file 1. 3D renderings of these connectomes are shown in Figure 1—videos 1 to 4. B. Similarity of pairs of network matrices, separated by the relationship status of each pair. Subjects with a shared environment, and a greater proportion of shared genetics, have more similar organisation of neuronal coupling. Violin plots show distributions of distance values between pairs of network matrices for correlations in oscillatory amplitude in each band, and partial correlations in BOLD response, thresholded for visualisation. Nodes are separated by the relationship status of each pair. Subjects with a shared environment, and a greater proportion of shared genetics, have more similar organisation of neuronal coupling. Violin plots show distributions of distance values between pairs of network matrices for correlations in oscillatory amplitude in each band, and partial correlations in BOLD response, thresholded for visualisation. C. Average genetic and shared environmental contributions to the variability of functional connectivity. The bar charts show the mean genetic component (heritability, h²) and mean shared environment component (c²) from a variance decomposition model fitted on each network edge, with 95% bootstrapped confidence intervals on the mean. Annotations indicate the difference in contribution between genes and the shared or developmental environment. The values of h² and c² are expressed as proportions of the total variance. The difference between their total and unity is e², the remaining environmental and measurement noise component. D. Average genetic and shared environmental contributions to the variability of oscillatory power, or BOLD response, in each ROI. Stars indicate significant differences in mean value for each of the displayed comparisons. Figure 1 continued on next page.
***p<0.001; **p<0.01; *p<0.05; n.s., not significant. The non-parametric p-values were computed by permutation and corrected for multiple comparisons over the 21 tests performed.

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Figure 1—figure supplement 1. Heritabilities of fMRI connection strengths. Parameter estimates for the influence of additive genetics, $h^2$, on each individual network connection, for partial correlations in BOLD time courses derived from each ROI.

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Figure 1—figure supplement 2. Heritability of cortical curvature, and spatial profile of the heritability of functional connections. Top left: mean heritability of cortical curvature within each ROI. Bottom left: heritability of each fMRI network connection, averaged onto each relevant ROI. Right, top to bottom: heritability of each MEG network connection in beta, alpha and theta bands, averaged onto each relevant ROI.

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Figure 2. Regions of interest used for functional connectivity estimation. (A) Primary parcellation of 39 contiguous clusters, identified from a resting-state 100-dimensional group-ICA decomposition of fMRI data from the first 200 subjects of the HCP project. (B) The 15-dimensional fMRI ICA parcellation computed by the HCP as part of the S900 data release.

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Figure 3. Illustration of pipeline for MEG functional connectivity estimation. From a whole-brain source-reconstruction, a single time-course is extracted to represent each ROI. These time-courses are bandpass filtered, then orthogonalised to remove shared signal which is potentially attributable to spatial leakage effects. The power envelope of each time-course is computed, then correlated to form the network matrix.

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