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Disentangling cortical function and its spatial topography reveals divergent roles of genes and environment

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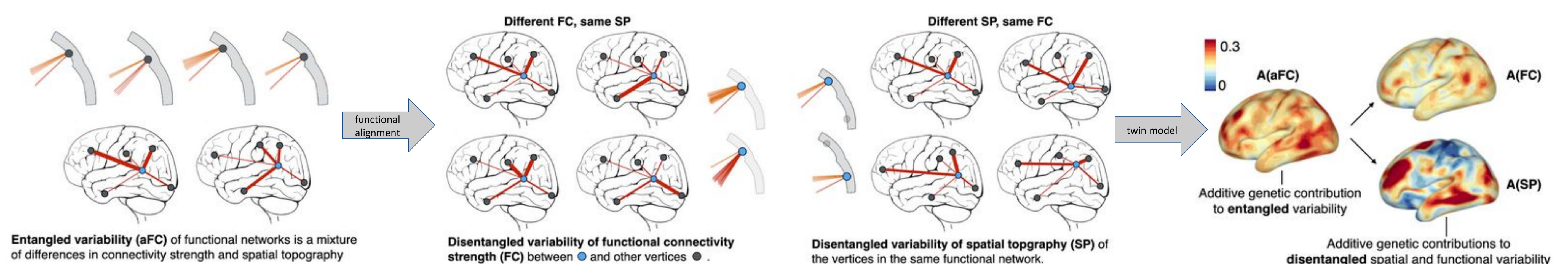
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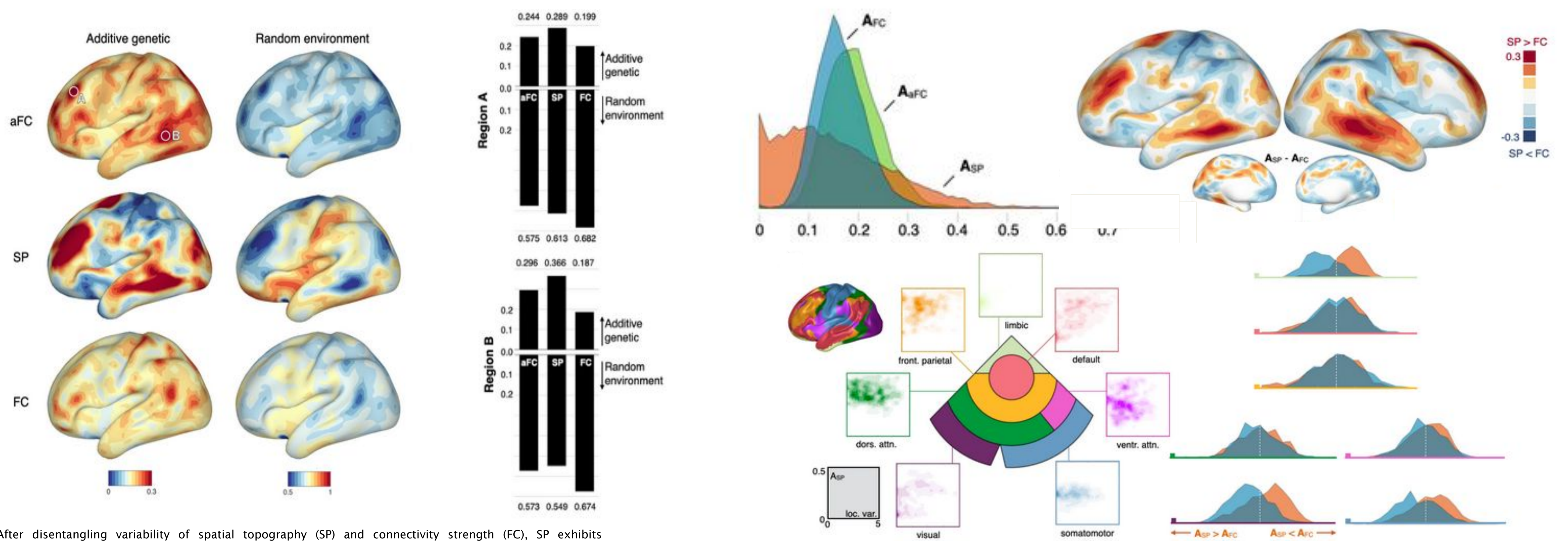
Objective

The human brain varies across individuals in its morphology, function and cognitive capacities. Variability is particularly high in areas associated with higher order cognitive abilities. In this study we investigated genetic and environmental influence on two key features of functional connectivity on the cortex: connectivity strength and topography.

Material and Methods

To investigate genetic and random environmental influence, we used functional magnetic resonance imaging (fMRI) data of 231 young healthy adults, labeled either as monozygotic or dizygotic twins from the HCP S1200 ICA-FIX denoised dataset. To examine disentangled connectivity strength and topography, we used a technique for functional alignment of subjects. This allowed us to observe variability in topography and functional connectivity strength of corresponding functional regions independently. Twin models were then applied to each of the two cortical features.

Entangled variability (aFC) of functional networks is a mixture of differences in connectivity strength and spatial topography

Disentangled variability of functional connectivity strength (FC) between 🔵 and other vertices ⚫.

Disentangled variability of spatial topgraphy (SP) of the vertices in the same functional network.

Additive genetic contribution to **entangled** variability

Additive genetic contributions to **disentangled** spatial and functional variability

Results

After disentangling variability of spatial topography (SP) and connectivity strength (FC), SP exhibits pronounced peaks of genetic contribution of at least 30%, whereas the genetic contribution to FC has mainly decreased compared to entangled functional variability (aFC). For two regions of interest indicated in the aFC map, quantitative values are shown. Compared to aFC, genetic contribution is lower for FC and higher for SP. The contribution of random environment is highest for disentangled connectivity strength FC.

Distribution of genetic influence on topography (A_{SP}) is much broader than distribution of genetic influence on connectivity strength before (A_{aFC}) and after (A_{FC}) disentanglement (top left). As indicated by the density plots (bottom), A_{SP} increases from primary areas (visual, somatomotor) to intermediate and high association areas (front-parietal, default). At peaks A_{SP} dominates over A_{FC} (top right). A_{FC} dominates in primary areas, such as the visual cortex and somatomotor cortex.

Conclusion

In intermediate to higher association areas genetic influence observed on entangled connectivity variability mainly shapes topography. A recent study showed that most predictive information of behaviour in entangled functional connectivity strength is actually also reflected in topographical organisation. This means that differences in behaviour might be caused by differences in genetically coded variability of topography.

References

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