Hidden geometry of human connectomes: a key to higher-order brain functional differences

With its complex circuits, the brain enables the entire human activity, psychology, and behaviour. Its evolutionary adaptation evolved towards a complex structure that supports its functional features. Studies have shown that information processing relies on mechanisms of self-organized criticality (self-regulated bursting dynamics with long-range temporal correlations) supported by the specific organization of brain connections. Hence, quantifying the brain functional structure holds excellent prospects for understanding brain dynamics, psychology, pathology, and cognition.

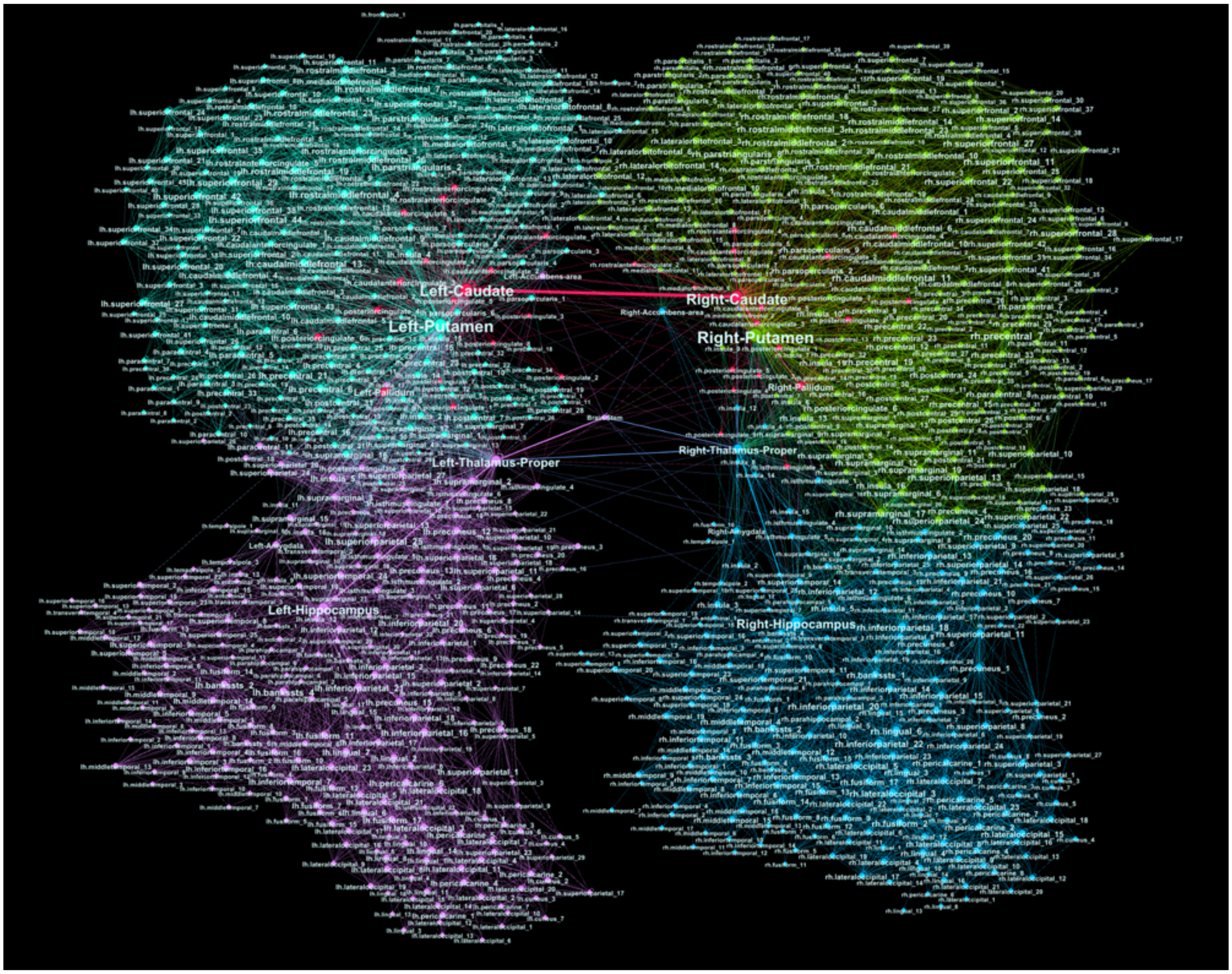

Fig. 1. Consensus Female Connectome consisting of the edges common to 100 healthy individuals is generated by applying the brain mapping tools at the Budapest reference connectome server (https://pitgroup.org/connectome/) based on the diffusion imaging data from Human Connectome Project. Nodes are 1015 anatomical brain regions, indicated by the labels, while 11339 edges are white-matter connections established by one million fibres tracked; colours indicate different

mesoscopic-scale communities—the image by BT, using Gephi (https://gephi.org/) graph visualization.

Mathematical modelling of the brain involves a range of algorithms that help interpret the imaging data. Diffusion tensor imaging data have been readily mapped onto the structural brain network (connectome). The network nodes are anatomical grey-matter regions interconnected via white-matter fibre bundles, cf. Figure 1. In recent years, network mapping opened up a new research avenue of brain structure-function interdependences, using advanced graph theory and algebraic topology methods. Our study extends the standard network's theory beyond pairwise connections to determine patterns of higher-order structures. They are geometrically described as triangles, tetrahedrons and higher cliques involving different brain regions. At a larger scale, these simplicial complexes are arranged into five functionally different brain segments, corresponding to the network's communities, as shown in Figure 1. Deciphering how these geometrical descriptors of all sizes are mutually interconnected reveals the entire hierarchical organisation of human connectomes.

Knowing the complete architecture of the human connectome helps elucidate some fundamental features of the brain's functional geometry. Specifically, the graph is 3/2-hyperbolic with short paths, enabling efficient transmissions of information between distant brain areas. The topology hubs (nodes with the most significant connectivity and weights of edges, and the number of simplexes of all orders attached to them) appear to be eight central brain regions (Putamen, Caudate, Hippocampus and Thalamus-Proper in the left and right cerebral hemispheres), making a "rich-club structure". The identified core network around these hubs represents the part of the human connectome through which the hubs connect distinct parts of the brain via simplexes of different sizes. Moreover, beyond the mere number of edges, the structure of simplicial complexes of female and male connectomes unveils the essential sex-related differences. Notably, the female consensus connectome appears better connected in all topology measures than the corresponding male connectome. Potentially, the structural differences between the connectomes in specific neurological disorders (vs. healthy individuals) can be identified using these topological measures. Finally, the precise architecture of simplicial complexes in the human connectome provides a basis for realistic modelling towards the emergent brain dynamics with the higher-order interactions embedded in the underlying geometry.

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