

We repeated stages 1, 2, and 3 a total of five times and varied  $\alpha$  with each repetition, going from  $\alpha = \{0.0, 0.5, 1.0, 1.5, 2.0\}$ . Early on, the low values of  $\alpha$  meant that we searched the parameter space randomly, while the larger values at later repetitions allowed us to focus in on the low energy regions. We emphasize that alternative optimization schemes could be used to minimize  $E$  (e.g. simulated annealing); the approach used here was chosen because it allowed us to not only converge to good solutions, but also to explore the energy landscape.

### 3. Results

We fit generative models to the connectomes of individual participants. In the main text, we focus on 40 adults (ages 18-40 years) scanned at the Department of Radiology, University Hospital Center and University of Lausanne (CHUV), Lausanne, Switzerland. The Appendix contains results from replication cohorts of 214 and 126 participants from the Human Connectome Project (HCP) (Van Essen et al., 2012; Glasser et al., 2013) and the Nathan Kline Institute, Rockland, New York (NKI) cohort (Nooner et al., 2012), respectively. In the same Appendix we also investigate the sensitivity of our results to alternative processing streams.

#### 3.1. Geometric model

It is well known that the connectome’s physical embedding shapes its topology by promoting the formation of low-cost connections (Bullmore and Sporns, 2012). On the other hand, forming only the shortest connections produces a skewed edge length distribution lacking long-distance connections (Kaiser and Hilgetag, 2006), resulting in increased characteristic path length, thereby reducing the efficiency with which information can flow between distant brain regions.