one another. Interestingly, the parameters η and γ appear to trade off with one another (Figure 3D), suggesting that the more an individual's connectome is shaped by geometry (large amplitude of η), the less it is shaped by non-geometric constraints and vice versa. On average, the MI model outperformed the geometric model in reducing discrepancies along all four components of the energy function: $KS_k = 0.10 \pm 0.03$, $KS_b = 0.10 \pm 0.02$, $KS_e = 0.10 \pm 0.03$ and $KS_c = 0.11 \pm 0.02$ (maximum p-value for all KS statistics and energy was $p \approx 10^{-7}$, Wilcoxon signed-rank test). Whereas the geometric model's performance was limited primarily by mismatches in clustering and edge length, the MI model's performance was more evenly limited. The best-fitting synthetic networks had energies equal to KS_k, KS_b, KS_c, and KS_e around 21%, 25%, 29%, and 25% of the time, respectively.

3.3. Evaluating synthetic networks using additional measures

Our analyses to this point consisted of tuning the parameters of generative models to ranges where the synthetic networks achieved low energy, which identified the MI model as the best fitting model. The form of the energy function, however, may be considered *ad hoc*; it represents only one of many alternative ways to evaluate a synthetic network's fitness. For this reason it was important to establish that the best-fitting synthetic networks generated by the MI model matched observed connectomes across additional dimensions that were not part of the energy function used for optimization. To that end, we subjected the lowest-energy synthetic networks to a series of additional tests to determine whether they could also reproduce other properties of the human connectome.

3.3.1. Graph theoretic measures

The first test involved evaluating the best-fitting synthetic networks in terms of how well they matched graph-theoretical properties of observed connectomes,