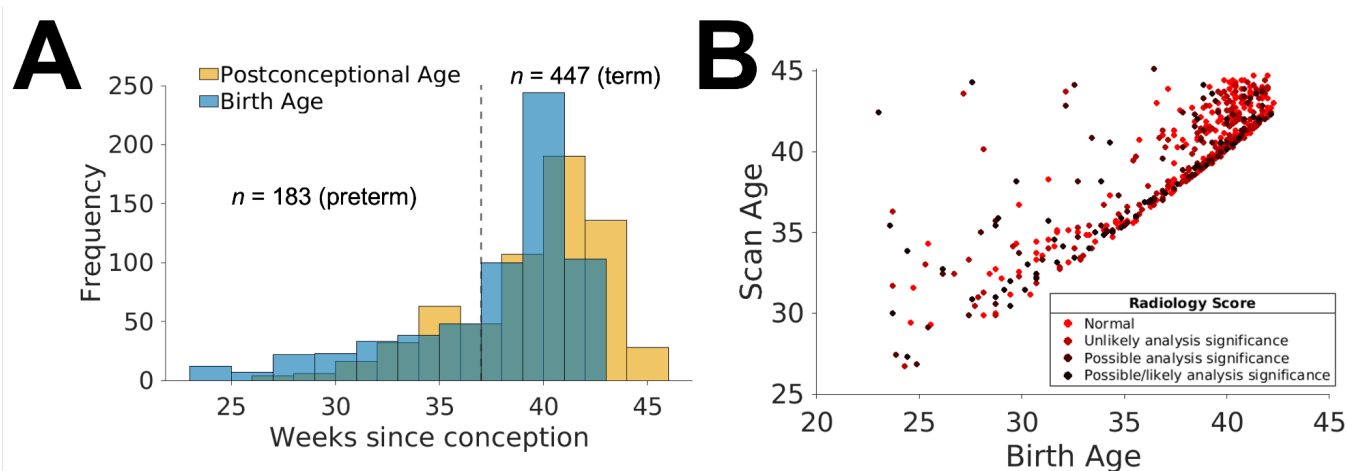
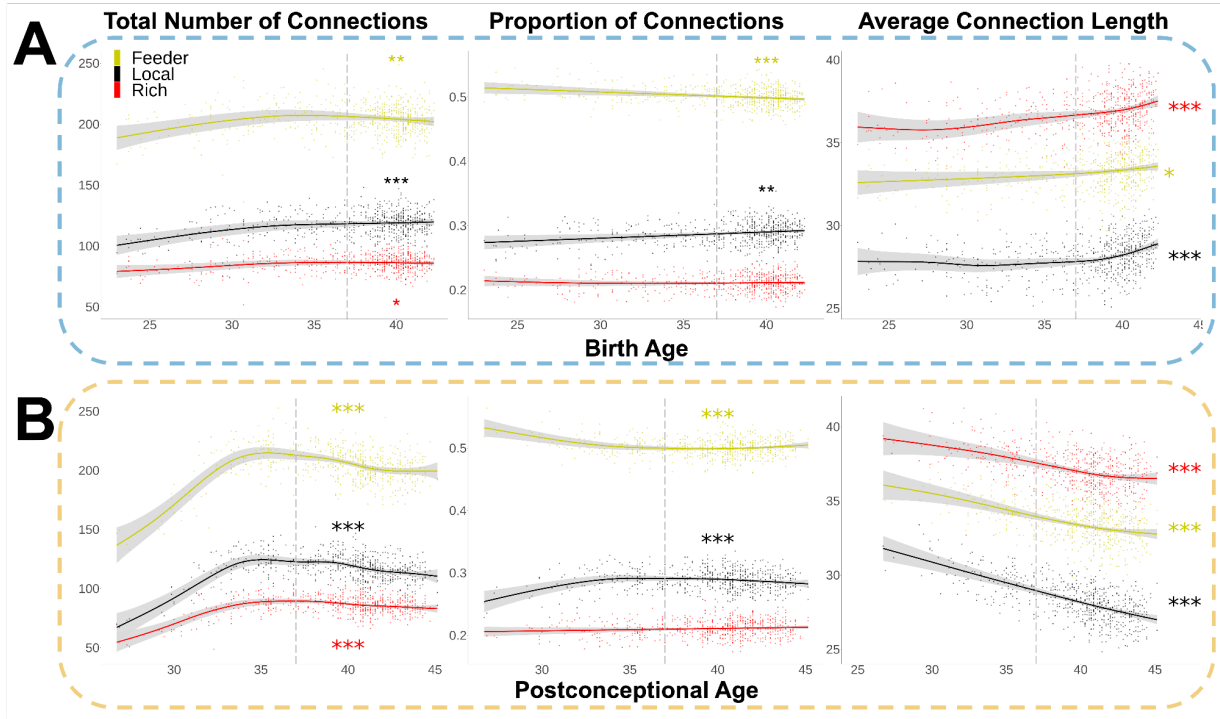
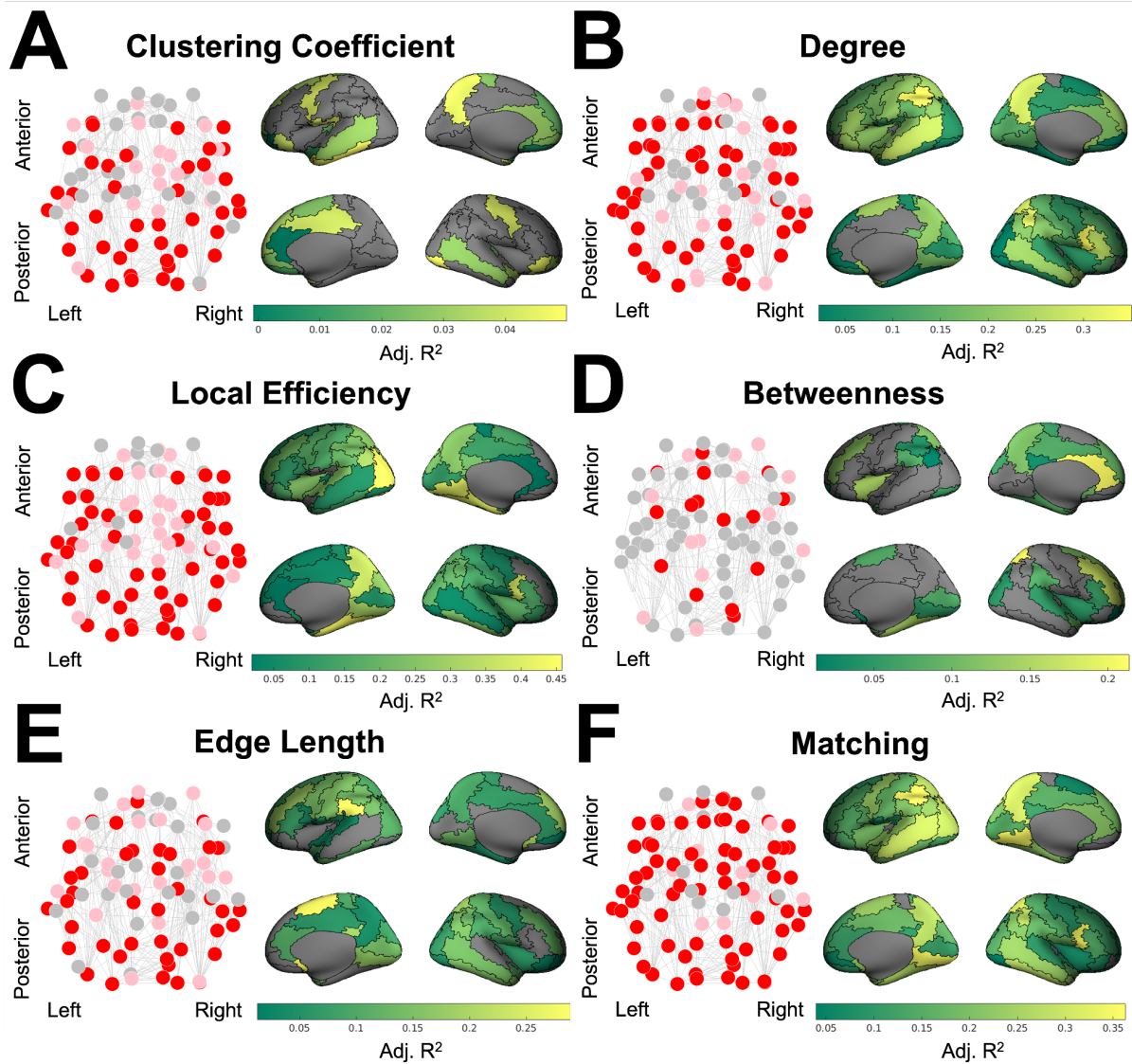




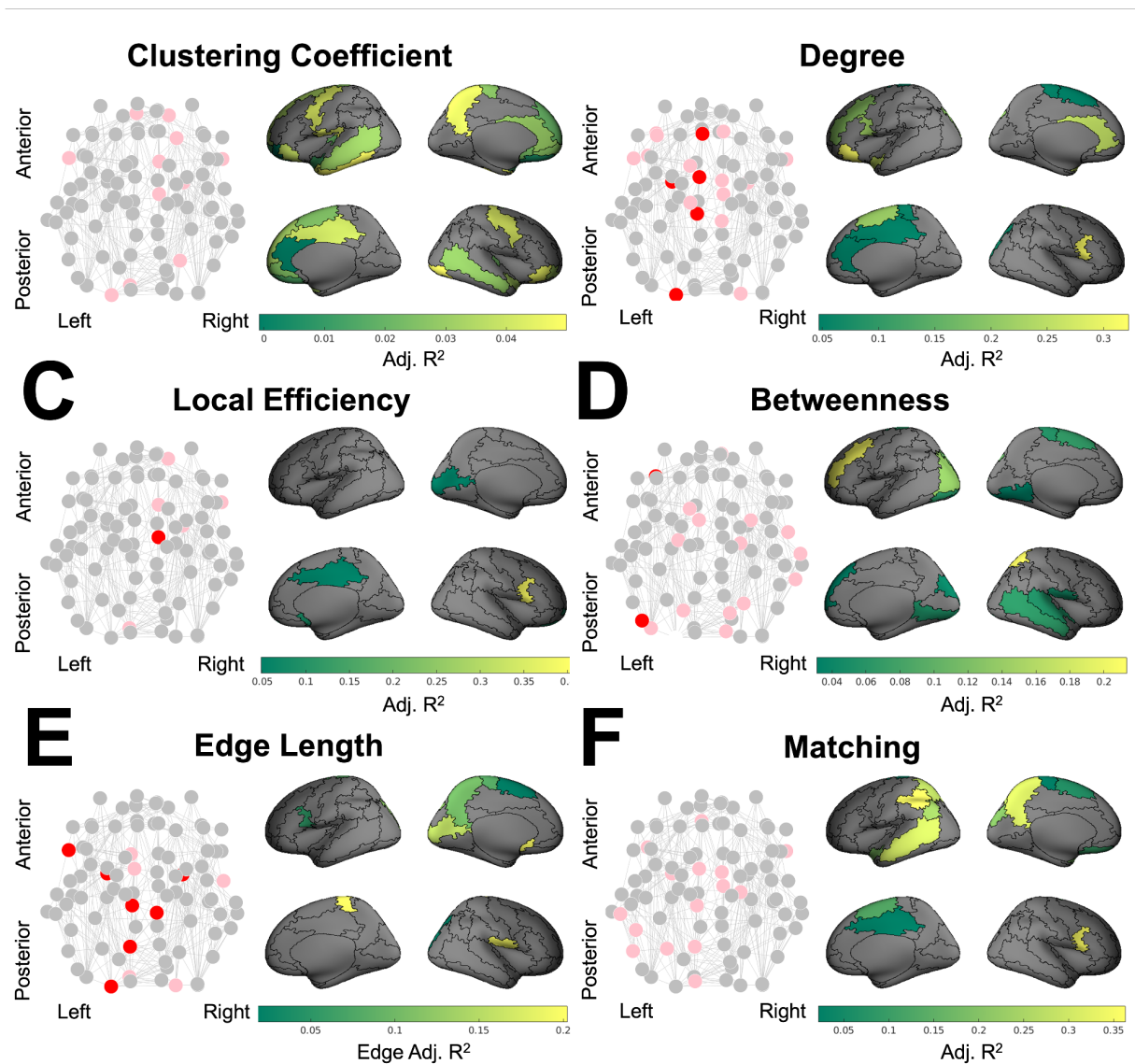
Supplementary Figure 1. Participant details. (A) Histogram depicting the distribution of birth and postconceptional ages in the sample. (B) Participants' birth age was plotted against their scan (postconceptional) age, grouped by the dHCP radiology score from their structural images.



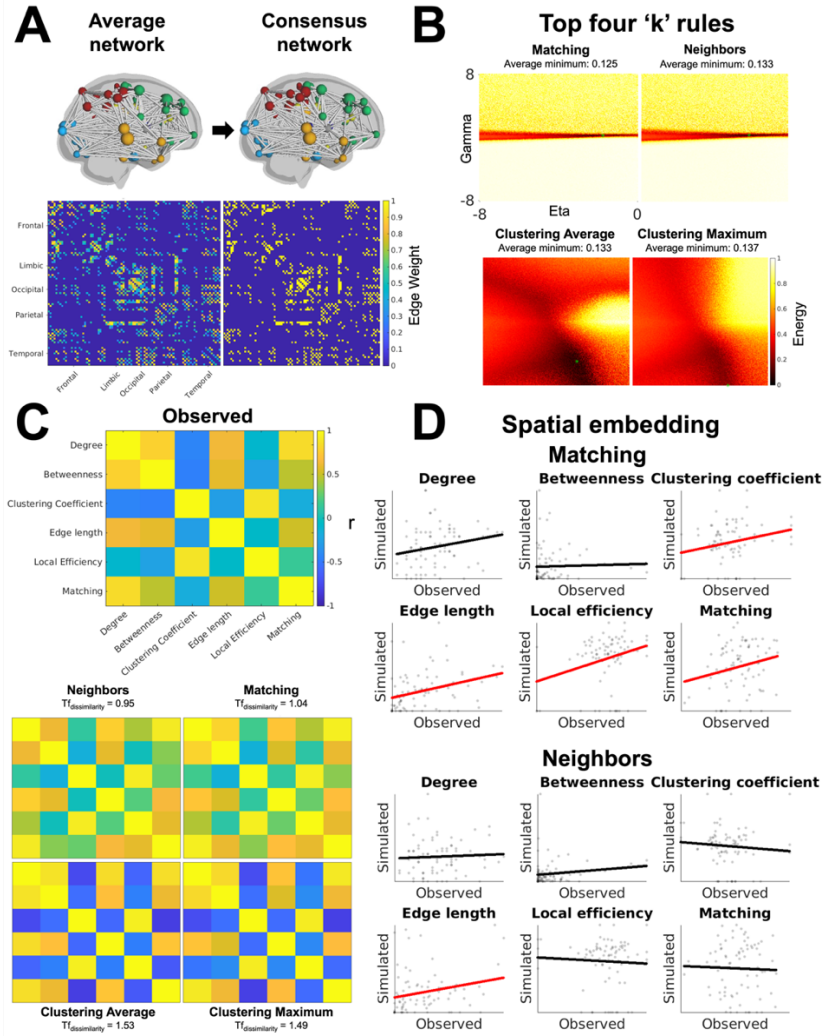
Supplementary Figure 2. Counts, proportions, and lengths of all connection types across postconceptional and birth age. (A) Across birth age, the total number of rich, feeder and local connections significantly increased ($F_{rich\ connections, birth\ age} = 3.05$, estimated $df = 2.69$, $p = 0.022$; $F_{feeder\ connections, birth\ age} = 3.55$, estimated $df = 3.04$, $p = 1.87 \times 10^{-3}$; $F_{local\ connections, birth\ age} = 6.94$, estimated $df = 2.79$, $p = 6.73 \times 10^{-5}$). However, proportional to the total number of connections in the network, feeder connections decreased, local connections increased and rich club connections do not significantly change ($F_{rich\ proportion, birth\ age} = 0.79$, estimated $df = 2.01$, $p = 0.623$; $F_{rich\ proportion, birth\ age} = 11.48$, estimated $df = 1.00$, $p = 7.42 \times 10^{-4}$; $F_{local\ proportion, birth\ age} = 8.98$, estimated $df = 1.00$, $p = 2.82 \times 10^{-3}$). The average length of connections increased for all connection types across birth age ($F_{rich\ length, birth\ age} = 5.37$, estimated $df = 3.82$, $p = 1.06 \times 10^{-4}$; $F_{feeder\ length, birth\ age} = 3.00$, estimated $df = 2.03$, $p = 0.031$; $F_{local\ length, birth\ age} = 6.36$, estimated $df = 4.25$, $p = 7.79 \times 10^{-6}$). **(B)** Across postconceptional age, the total number of rich, feeder and local connections significantly increased ($F_{rich\ connections, postconceptional\ age} = 16.62$, estimated $df = 5.92$, $p = 2.00 \times 10^{-16}$; $F_{feeder\ connections, postconceptional\ age} = 23.02$, estimated $df = 7.01$, $p = 2.00 \times 10^{-16}$; $F_{local\ connections, postconceptional\ age} = 20.57$, estimated $df = 7.16$, $p = 2.00 \times 10^{-16}$). However, proportional to the total number of connections in the network, feeder connections decreased, local connections increased and rich club connections do not significantly change ($F_{rich\ proportion, postconceptional\ age} = 1.87$, estimated $df = 1.00$, $p = 0.171$; $F_{rich\ proportion, postconceptional\ age} = 6.63$, estimated $df = 3.89$, $p = 7.01 \times 10^{-6}$; $F_{local\ proportion, postconceptional\ age} = 6.57$, estimated $df = 4.24$, $p = 3.71 \times 10^{-6}$). The average length of connections decreased for all connection types across postconceptional age ($F_{rich\ length, postconceptional\ age} = 11.92$, estimated $df = 3.04$, $p = 2.00 \times 10^{-16}$; $F_{feeder\ length, postconceptional\ age} = 19.15$, estimated $df = 2.77$, $p = 2.00 \times 10^{-16}$; $F_{local\ length, postconceptional\ age} = 59.70$, estimated $df = 1.85$, $p = 2.00 \times 10^{-16}$). *** indicates $p < 0.001$, ** indicates $p < 0.01$, * indicates $p < 0.05$



Supplementary Figure 3. Local measures changed significantly across postconceptional age. Significant effects of postconceptional age were found for (A) clustering coefficient, (B) degree, (C) local efficiency, (D) betweenness, (E) edge length (mm), and (F) matching. Red indicates $p < 0.001$ and pink indicates $p < 0.05$. Surface plots display the adjusted R^2 from GAMs.

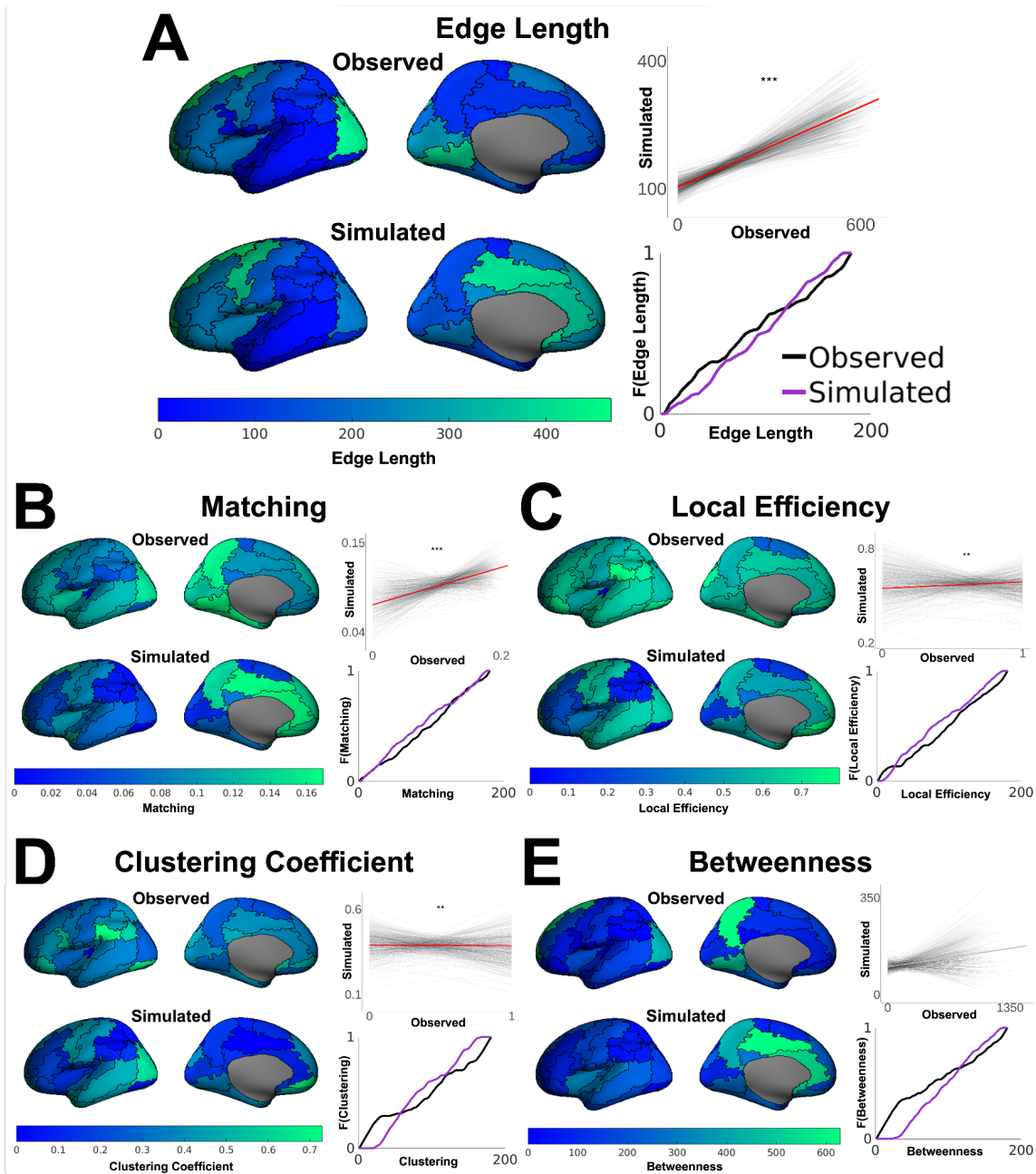


Supplementary Figure 4. Local measures changed significantly across birth age. Significant effects of birth age were found for (A) clustering coefficient, (B) degree, (C) local efficiency, (D) betweenness, (E) edge length (mm), and (F) matching. Red indicates $p < 0.001$ and pink indicates $p < 0.05$. Surface plots display the adjusted R^2 from GAMs.

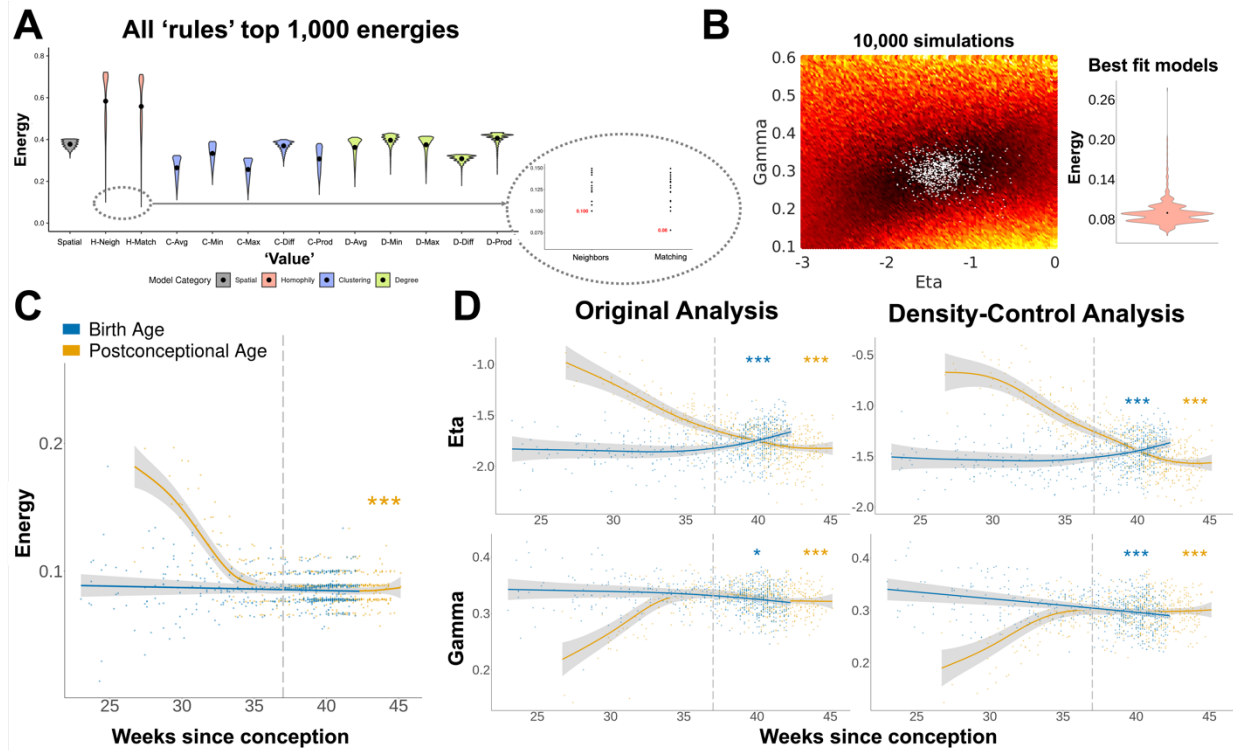


Supplementary Figure 5. 'Value' rule assessment through consensus network simulations.

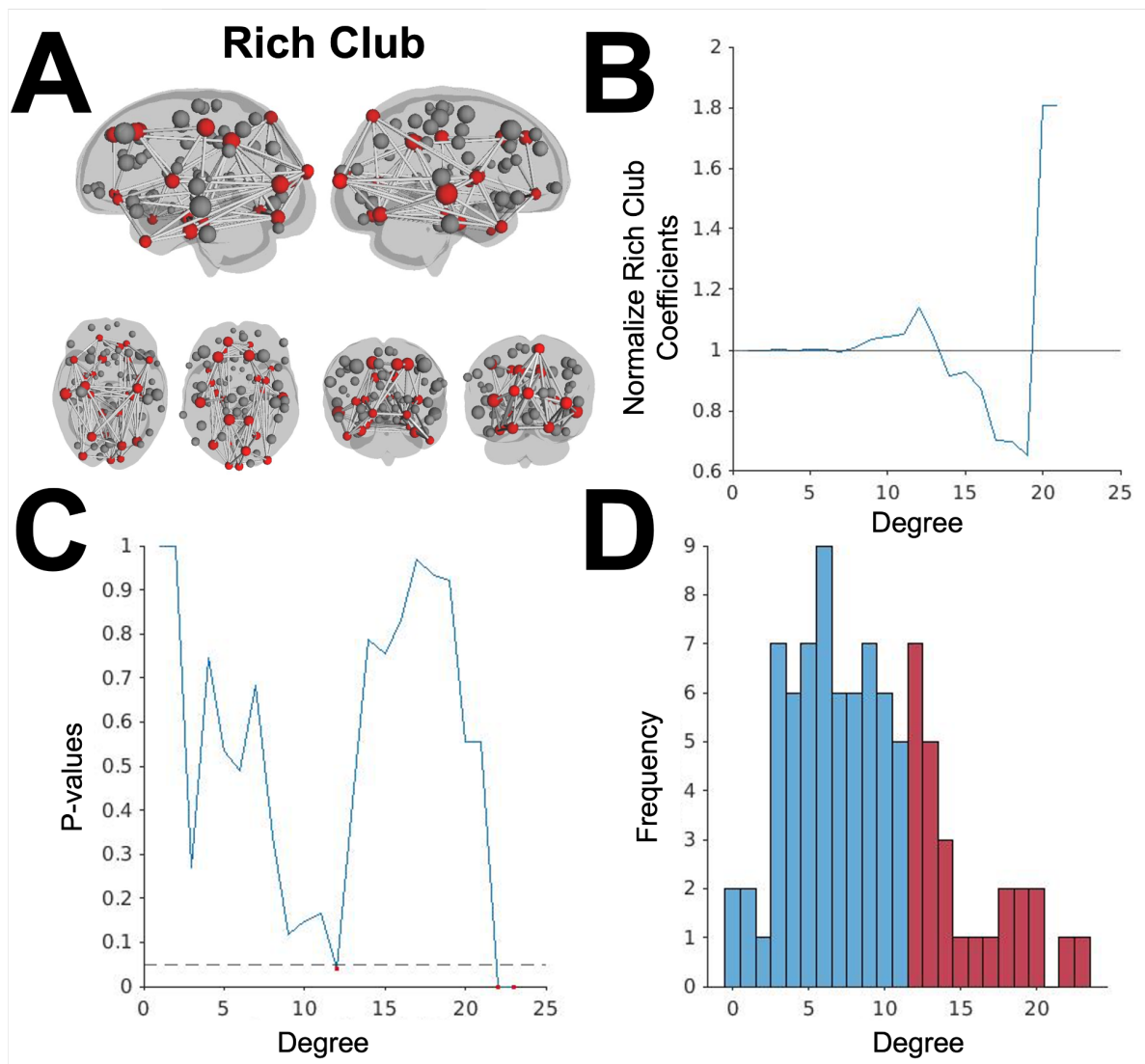
(A) Averaged weighted connectivity matrix compared to the binary matrix of the distant-dependent group representative consensus network. (B) The average energy landscapes of the top four rules (based on lowest energies) are plotted with a green asterisk (*) indicating the location of the best fitting model. Homophily models performed the best out of all rules. 'Neighbors' had the lowest overall energy. 'Matching' had the lowest energy average over the top 10 models. (C) The topological fingerprint of the observed network compared to the top four performing 'value' rules. 'Neighbors' had the lowest topological dissimilarity, followed by 'matching'. (D) 'Matching' displayed spatial embedding for four local organisation measures (degree: $p = 0.050$; betweenness: $p = 0.787$; clustering coefficient: $r_{pearson} = 0.23$; $p = 0.037$; edge length: $r_{pearson} = 0.33$; $p = 0.003$; local efficiency: $r_{pearson} = 0.30$; $p = 0.007$; matching: $r_{pearson} = 0.23$; $p = 0.043$). 'Neighbors' had significant spatial embedding for edge length ($r_{pearson} = 0.24$, $p = 0.035$) but not on the other five local measures assessed (degree: $p = 0.637$; betweenness: $p = 0.267$; clustering coefficient: $p = 0.400$; local efficiency: $p = 0.642$; matching: $p = 0.776$). Red lines indicate a significant correlation.



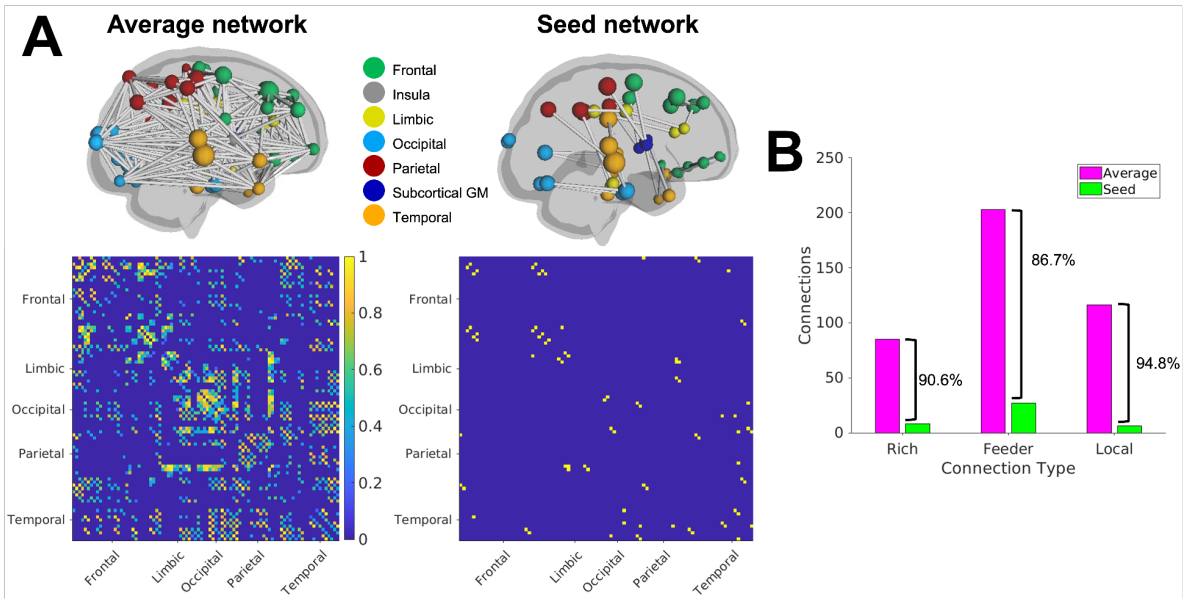
Supplementary Figure 6. Spatial embedding of optimized generative models. (A) Significant spatial embedding of local organisation appears for edge length, (B) matching, (C) local efficiency, (D) clustering coefficient, (E) but not for betweenness. *** indicates $p < 0.001$, ** indicates $p < 0.01$, * indicates $p < 0.05$. The top right graphs depict correlational data between observed and simulated measures in every region. A red line indicates a significant linear model, depicted as the average correlation and the grey lines show every participant's data. The bottom right graphs show the cumulative density function of the average observed (black) and simulated (purple) networks.



Supplementary Figure 7. Density-controlled analysis. (A) Energies from 90,000 simulations in $-8 \leq \eta \leq 0$ and $-8 \leq \gamma \leq 8$ sampling space fit to the density-controlled consensus network. The violin plot displays the lowest 1,000 energies for all 13 'value' rules. 'Matching' had the lowest overall energy (0.08) followed by 'neighbors' (0.10). (B) The average energy landscape of the density-controlled 'matching' models. The white dots indicate the location of the best-fit models for all participants. The violin plot demonstrates the disruption of energies of the best-fit models (maximum = 0.28, minimum = 0.06, $M = 0.09$, $SD = 0.02$). (C) Energy significantly decreased across postconceptional age ($F_{\text{energy, postconceptional age}} = 32.88$, estimated $df = 7.46$, $p = 2 \times 10^{-16}$) but not birth age ($p = 0.38$). (D) The original analysis (repeated from Figure 5) demonstrates that η significantly decreases across postconceptional age but increases across birth age. The opposite relationship is present for γ , which significantly increases across postconceptional age and decreases across birth age. The density-controlled analysis replicates these results ($F_{\eta, \text{postconceptional age}} = 39.56$, estimated $df = 5.51$, $p = 2 \times 10^{-16}$; $F_{\eta, \text{birth age}} = 5.14$, estimated $df = 3.19$, $p = 4.06 \times 10^{-4}$; $F_{\gamma, \text{postconceptional age}} = 11.34$, estimated $df = 5.18$, $p = 2 \times 10^{-16}$; $F_{\gamma, \text{birth age}} = 14.67$, estimated $df = 1.12$, $p = 5.5 \times 10^{-5}$). The grey dotted line indicates the cut-off of term-born infants (37 weeks or later is term-born). *** indicates $p < 0.001$, ** indicates $p < 0.01$, * indicates $p < 0.05$.



Supplementary Figure 8. The definition of rich club nodes. (A) Visualization of the 27 rich club nodes (red) and connections in the consensus network. (B) The normalized rich club coefficients, with two distinct instances of coefficients > 1 . (C) The calculation null models demonstrate two instances where the consensus network rich club coefficients are significantly greater than would be expected at random (indicated by the red dots where $p < 0.05$). (D) Histogram of the distribution of degree in the consensus network. The red histogram indicates the nodes that have been defined as rich club nodes.



Supplementary Figure 9. Comparison of seed network for GNMs with average binarized network. (A) The average network across all participants and the sparse seed network calculated from edges present in 95% of all participants (total connections = 41). On average, the seed network is about 10% of the total connections for each individual (average total connections = 404.6). (B) The number of connections, separated by connection type, on average across all participants and for the seed network.