

We have a connectome dataset $D = \{G_1, G_2, \dots, G_i, \dots, G_n\}$, each $G_i(V, E_i, W)$ has the same number of vertices (could be voxels) which associated with same sets of vertex attribute $W = \{M1, S1, dorsal\ hippocampus, ventral\ hippocampus, \dots\}^k$, and E_i describes the connection between each vertex pair $E_i \in \{0, 1\}^{n \times n}$

Fit $SBM_k(\vec{p}, \vec{B})$ to D , where k equals the number of categories in W and the vertices are clustered accordingly. Using maximum likelihood method to find $\vec{\theta}_i$ in $\vec{B}_i \sim \text{Bern}(\vec{\theta}_i)$

Assuming the prior distribution $\vec{\theta} \sim \text{Beta}(\vec{a}, \vec{b})$, where hyperparameters \vec{a} and \vec{b} can be estimated from connectomes of people who have been identified as normal.

Decision rule δ using Bayesian inference. $\delta(D) = p(\vec{\theta} | D) = \text{Beta}(\vec{\theta} | \vec{a} + \vec{n}_1, \vec{b} + \vec{n}_0)$, where \vec{n}_1 are the total number of occurrence of edge for every pair of clusters, while \vec{n}_0 are that of the absence of edge.

Risk function: $E[L(\vec{\theta}, \vec{\delta})] = r(\vec{\theta}, \delta(D))$