



Background

- Recent advancements in neuroimaging and computational neuroscience have facilitated the assessment of individual connectomes, the organization of a brain’s structural network.
- Mounting data from the connectome of patients with focal epilepsy have changed our understanding of the disease, revealing abnormalities throughout the brain network, well beyond the area of seizure focus.
- Whether these changes are cause or consequence of seizure onset and propagation is still matter of debate, but deriving quantitative measures to characterize different features of a brain’s network may help identify personalized biomarkers useful in predicting clinical outcomes.
- Here, we focused on betweenness centrality (BC), a measure of a node’s influence on the network, and its association with post-surgical seizure control among patients with refractory medial temporal lobe epilepsy (MTLE).

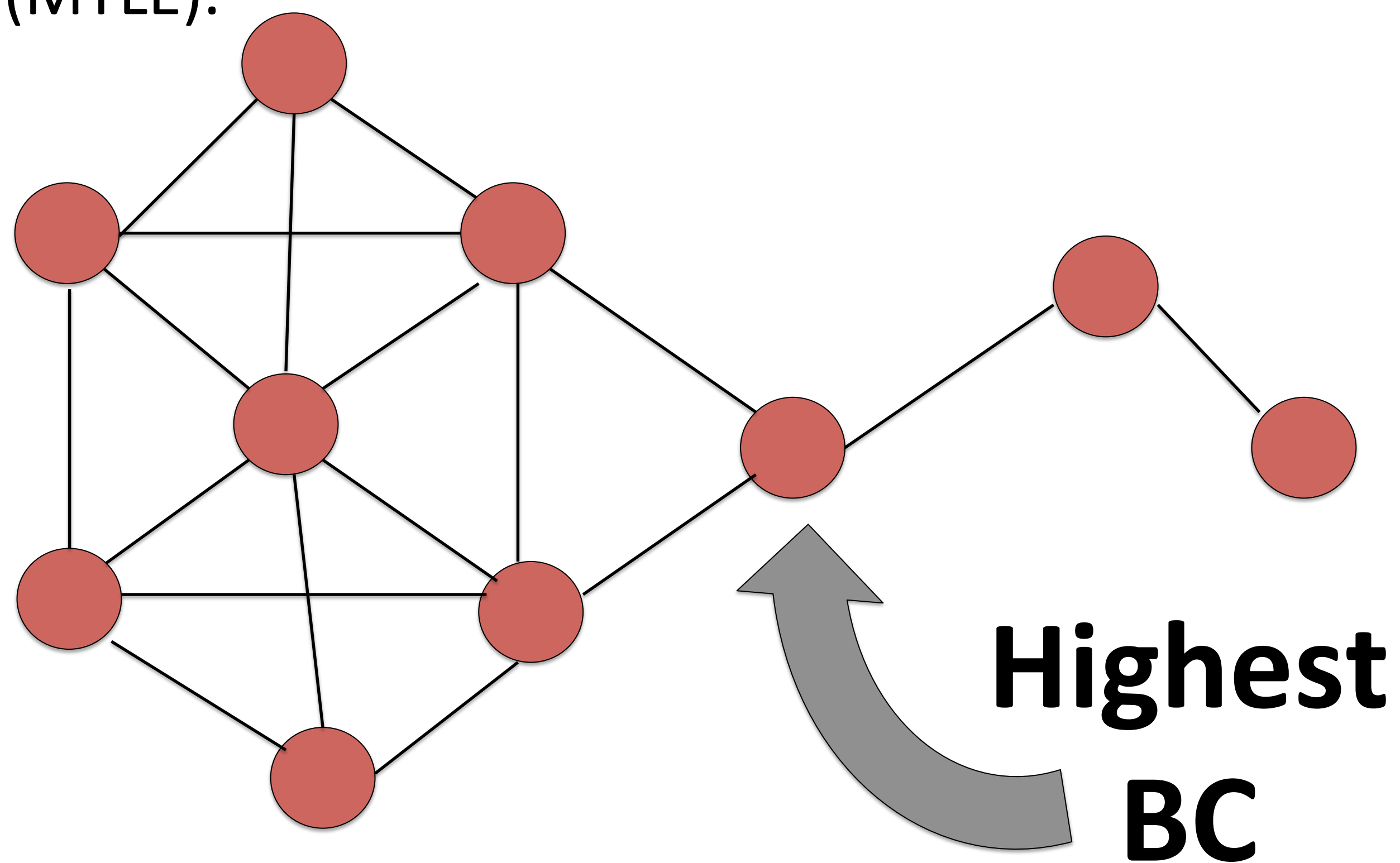


Figure 1. Betweenness centrality is a measure of “hubness” based on communication flow: it is equal to the number of shortest paths from all vertices to all others that pass through a specific node.

Methods & Results

- 50 patients with medication-refractory TLE who underwent anterior temporal lobectomy (ATL)
- Patients were classified as either seizure-free (SF, Engel I, $n = 36$) or non-seizure-free (NSF, Engel II-IV, $n = 14$).
- Individual structural connectomes were reconstructed from their **presurgical** 3T diffusion MRI
- For each patient, we computed the BC of each of the 384 nodes in the network, based on the AICHA atlas, and compared the values between SF and NSF
- Top 10 nodes whose BC most reliably distinguished SF from NSF were entered into a discriminant analysis to determine their ability to classify patients based on their post-surgical outcomes.
- We also performed discriminant analysis on a model with age of onset, seizure frequency and seizure burden, duration of epilepsy, seizure risk factors, presurgical interictal EEG pattern, and age of surgery
- Cross-validation was achieved by means of the leave-one-out approach

Discriminant Analysis Results

BC Model: Wilks’ $\lambda = 0.5$, $\chi^2 = 29.8$, $p = .001$

Clinical Model: Wilks’ $\lambda = 0.9$, $\chi^2 = 1.9$, $p = .98$

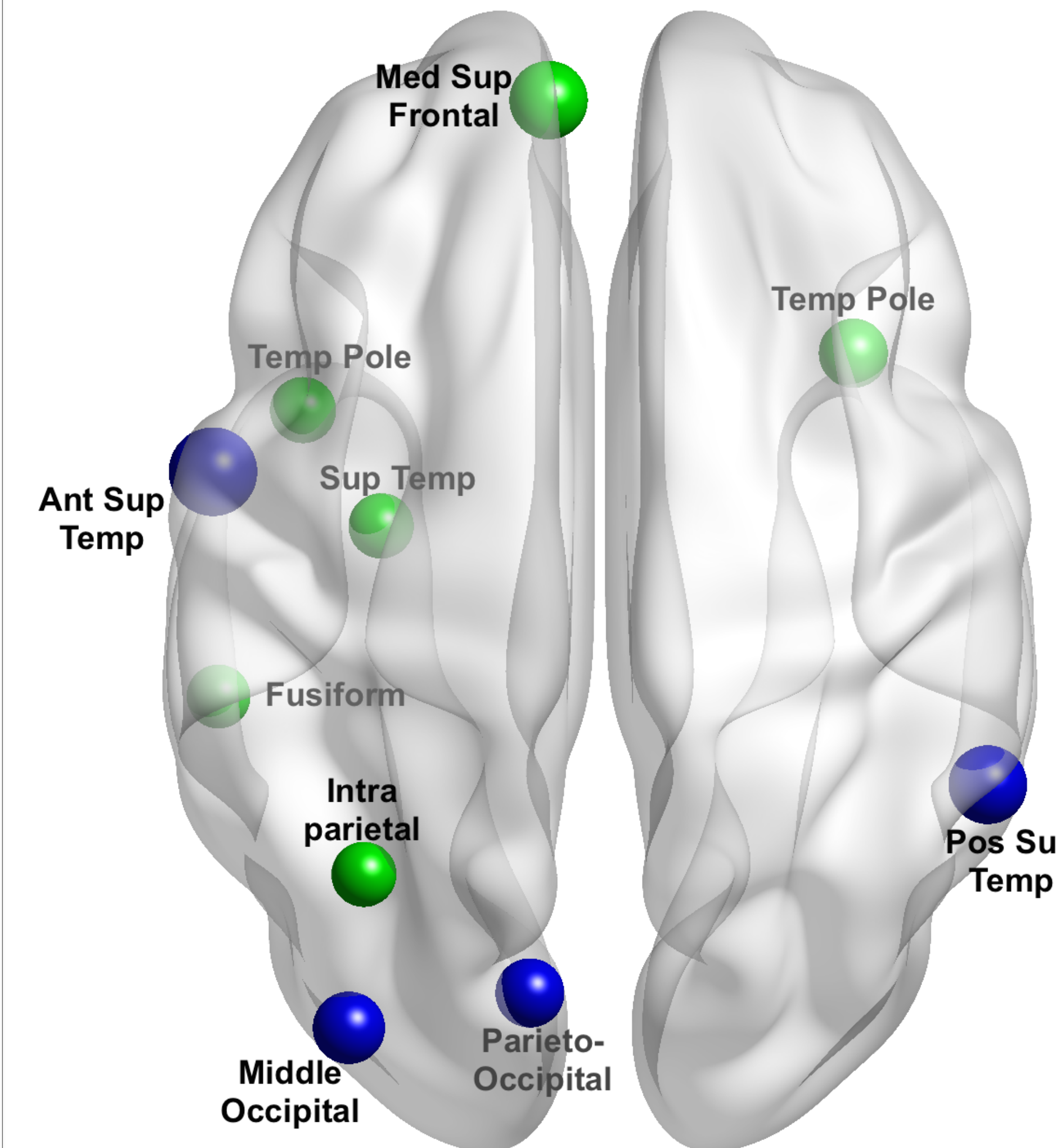


Figure 2. The diagram the left shows the top 10 nodes whose betweenness centrality (BC) value most reliably differentiated seizure-free (SF) from non-seizure free (NSF) patients. Nodes on the left are ipsilateral to seizure onset, while nodes on the right are contralateral. Size of nodes reflects the magnitude of the difference in terms of t values. Blue nodes reflect higher BC values in NSF than SF patients while green nodes represent the reverse pattern.

Table 1. Classification results of discriminant analysis entering the top ten nodes whose betweenness-centrality were most different between seizure-free (SF) and non-seizure-free (NSF) patients.

	Group	Predicted Group Membership		Total
		SF	NSF	
Original	SF ($n = 36$)	35	1	36
	NSF ($n = 14$)	4	10	14
Cross-validated	SF ($n = 36$)	33	3	36
	NSF ($n = 14$)	6	8	14

Conclusions

From the whole-brain connectome of patients with refractory MTLE, we identified regions acting as stronger influencers differently among SF and NSF patients. These nodes correctly identified post-ATL seizure outcomes in 90% of cases and, when cross-validated by means of U-method, reliably classified post-surgical outcome with 82% accuracy. These preliminary findings demonstrate that studying the “hubness” of certain brain regions in the structural connectome of patients with MTLE may help identify biomarkers for prediction of post-surgical seizure outcome.