

# A Variational Bayesian Approach to Network Modularity Applied to the Structural Connectome of the Human Brain

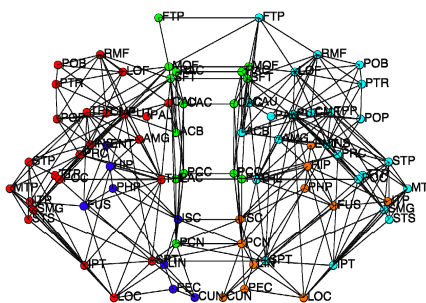
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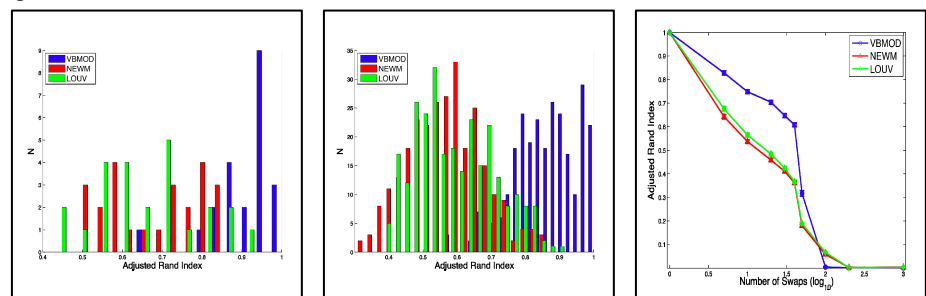
**Purpose:** Data derived from diffusion magnetic resonance imaging (dMRI) can be processed to extract the connectivity of the underlying structural brain network. Numerous graph-theoretic properties have been measured on such networks, including *modularity*. A module is loosely defined as a set of brain regions that are relatively well-connected to each other, and poorly connected to brain regions not included in this set. The most widely used algorithms for identifying modules in a network are based on maximizing the *partition modularity*, although this approach is known to suffer from biases [1]. An alternative approach from the network theory literature poses the problem in the framework of statistical inference, and a recent generalization of this approach, based on Bayesian methods for model selection, has been shown to circumvent such biases [2]. To date this has not been applied to structural brain networks. Here we apply this variational Bayesian technique (VBMOD) to infer module assignments and to identify the optimal number of modules in the structural connectomes of healthy adults. Our results are of interest in particular to researchers in the fields of connectomics and diffusion tractography.

**Methods:** Diffusion MRI (55 directions, b=1000, 1.8-mm voxels) and high-resolution structural MRI were performed on 24 healthy adult volunteers (14 male, 10 female; mean age 26.3±8.6 years, 23 right-handed, one unknown) on a 3T GE EXCITE MR imaging scanner. Construction of the structural networks was performed including (a) data preprocessing removing non-brain tissue [3] and motion and eddy current correction [4]; (b) cortical parcellation into 68 cortical and 14 subcortical regions using FreeSurfer [5]; (c) bedpostx reconstruction and tractography using probtrackx2 [6]; and (d) a standard pipeline for individual and consensus connectome construction [7]. We used the Brain Connectivity Toolbox [8] implementation of two widely-used modularity-detection algorithms which optimize the partition modularity: NEWM [9] and LOUV [10], and freely available source code for implementation of VBMOD [2]. Partitionings were compared using the standard quantity of adjusted rand index (ARI). Robustness was evaluated by iteratively randomizing each individual connectome through swapping edges [11], and then comparing the increasingly randomized version to the original connectome. Scaled-inclusivity was used to quantify the consistency of module assignment of each node [12].

**Results:** We performed modular decomposition of each of the 24 subjects as well as the “consensus” connectome using the three different algorithms. The output of VBMOD consensus network decomposition is shown in Fig 1. The five modules identified are similar to previously published results. VBMOD demonstrates improved accuracy over the NEWM and LOUV methods when comparing the partitionings of each individual network to the consensus connectome partitioning (Fig 2a). VBMOD also demonstrates improved precision over the NEWM and LOUV methods when comparing the partitionings of all of the pairwise individual connectomes (Fig 2b). Finally, when introducing “noise” to each connectome by swapping edges, VBMOD is better able to identify the modular structure compared with the NEWM and LOUV methods (Fig 2c). VBMOD is also better able to identify the correct number of modules (data not shown). The algorithm outputs probabilistic module assignments, which interestingly are correlated with the node-level “consistency” of module assignment.



**Fig 1:** VBMOD partitioning of the consensus connectome.



**Fig 2:** Improved accuracy (a), precision (b), and robustness to noise (c), of the VBMOD algorithm compared with the standard algorithms NEWM and LOUV, which are based on maximizing the partition modularity.

**Discussion:** We demonstrate better precision, accuracy and robustness to noise than the two most widely used current algorithms based on partition modularity optimization. The variational Bayesian approach also offers the advantage of reporting probabilistic module assignments, which can be helpful in cases of uncertain assignment or of nodes belonging to multiple modules. Interestingly, we find that the degree of uncertainty of a node assignment in a single network is related to how consistently the node is assigned across all networks in a group of subjects.

**References:** [1] Newman and Girvan (2004) PRE 69:1-15. [2] Hofman and Wiggins (2008) PRL 100:1-4. [3] Smith (2002) Hum Brain Mapp 17:143-155. [4] Jenkinson et al NeuroImage 17:825-841. [5] Fischl et al (2004) Cereb Cortex 14:11-22. [6] Behrens et al (2007) NeuroImage 34:144-155. [7] Li et al. (2012) Hum Brain Mapp 33:1894-1913. [8] Rubinov and Sporns (2010) NeuroImage 52:1059-1069. [9] Newman (2006) PRE 74,036104. [10] Blondel (2008) J Stat Mech P10008. [11] Wasserman and Faust (1994), Social Network Analysis: Methods and Applications. [12] Steen (2011) Phys Rev E 84:1-13.