Joint Brain Connectivity Estimation from Diffusion and Functional MRI Using a Network Flow Model

Shu-Hsien Chu[1], Keshab K. Parhi[1], and Christophe Lenglet[1]
[1]*University of Minnesota, Minneapolis, Minnesota, United States*

Target audience

Scientists interested in brain connectomics, in particular joint brain networks estimation from diffusion and functional MRI data

Purpose

A novel brain network model for discovering signaling pathways by jointly using diffusion and functional MRI modalities is presented. The proposed method can discover missing and "weak" links that may not be found by only using diffusion MRI (dMRI) data. Moreover, each anatomical subnetwork supporting the functional components can be extracted by the proposed method too.

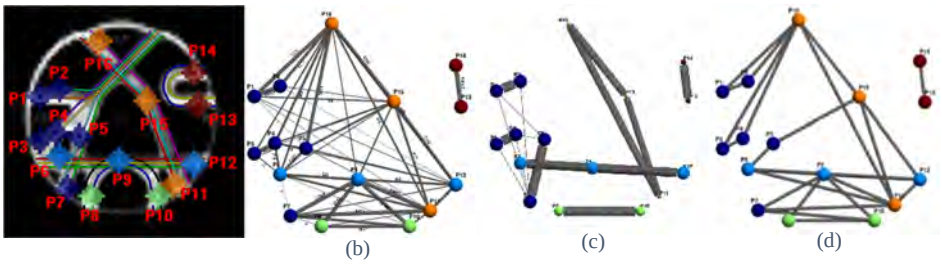

Figure 1 (a) A realistic phantom with the true fiber information know is used for validation. The phantom consists of 16 regions, P1 to P16, which form 5 subnetworks: (P1, P2, P3, P4, P5, and P7), (P6, P9, and P12), (P8 and P10), (P11, P15, and P16), and (P13 and P14); (b) the anatomical network estimated using HARDI model and probabilistic tracking; (c) the supporting anatomical network established by proposed model jointly using dMRI and fMRI; (d) the anatomical network found by the EM approach proposed [4].

Methods

In the proposed model, nodes represent the grey matter regions providing major functionalities and links represent the white matter fiber bundles delivering the electrochemical signal, which we model as a *flow* in the network. The link *capacity* is characterized by the strength of the fiber bundle, e.g. fiber count, based on the dMRI. Since the signal shared through axons triggers neural activities, the gathered signal at each (cortical or subcortical) region corresponding to each functional (temporal-spatial) component must be proportional to brain activity estimated from functional MRI (fMRI) by independent component analysis (ICA)[1]. These two mechanisms form the *link capacity constraint* and the *node demand constraint*, respectively. Additionally, it is assumed that the signal flow originates from an active region and targets a reacting region. Therefore, the flow cannot exceed the observed activity at either of its end nodes, which forms the (last) *feasibility* constraint. The objective function includes two terms which leverages our three constraints. The first term minimizes the message delivery cost which is defined by the reciprocal of link capacity. In other words, the stronger the link, the lower the cost. The second term represents the weighted penalty for adding the compensated capacity for the missing links and the weak links. The weights of the penalty are directly proportional to the link capacity; thus, the optimization finds more missing and "weak" connections for links with less capacity. With the three sets of constraints and the proposed cost functions, solving the linear network optimization problem can be used to identify the brain major signaling pathways.

Results

Performance is first illustrated using a realistic dMRI phantom[2] with synthetic functional MRI time courses generated using the hemodynamic response function and knowledge about connections inferred from the geometry of the phantom (Figure 1). dMRI data was processed with FSL (*bedpostx* and *probtrackx*)[1] to estimate fiber orientations and generate probabilistic tractography maps between regions. fMRI was also processed using FSL (*melodic)* to estimate the functional modes from ICA. Results from the proposed model (Fig 1 c) were compared with results from the method[4] recently proposed (Fig 1 d). The proposed model is able to recover "missing" structural connections by leveraging the information provided by the functional data, while minimizing the number of false positive connections.

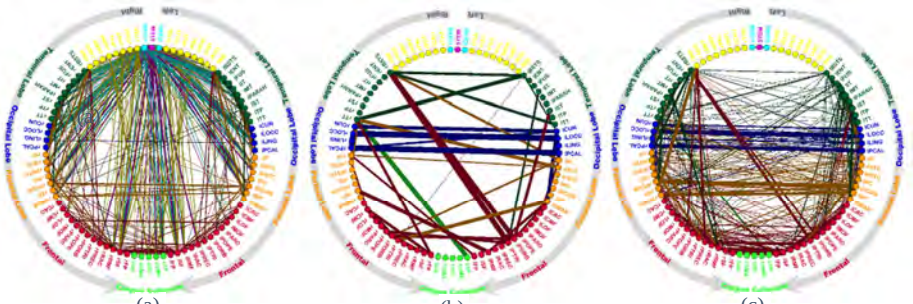

Figure 2. From left to right: (a) the anatomical network estimated by probabilistic fiber tracking, (b) network of missing and "weak" links recovered by the proposed model, and (c) the subnetwork supporting the resting state brain functionality of a healthy subject from the human connectome project (HCP).

Twenty datasets from the HCP database[3] were processed and analyzed through the proposed model. The anatomical network using only diffusion MRI, the missing links recovered by joint modeling, and the supporting anatomical subnetwork, for one representative subject, are presented in Figure 2.

Discussion

As demonstrated by these preliminary results, the proposed model finds the maximum true connections with fewest number of false connections when compared with the connectivity derived from a joint model using the expectation-maximization (EM) algorithm presented in a prior work[4]. This may allow to further improve estimated structural connectivity patterns, as classically obtained using dMRI via HARDI models and tractography. .

Conclusion

The proposed method can be used to extract more accurate anatomical patterns and functional pathways possibly leading to better understanding of brain circuits.

Acknowledgments: Work partly supported by NIH grants P41 EB015894, P30 NS076408, R01 EB008432, and Human Connectome Project (U54 MH091657).

References

1. Jenkinson, M., Beckmann, C. F., Behrens, T. E., Woolrich, M. W., and Smith, S. M., "FSL," Neuroimage 62(2), 782–790 (2012).
2. Fillard, P., Descoteaux, M., Goh, A., Gouttard, S., Jeurissen, B., Malcolm, J., Ramirez-Manzanares, A., Reisert, M., Sakaie, K., Tensaouti, F., et al., "Quantitative evaluation of 10 tractography algorithms on a realistic diffusion mr phantom," Neuroimage 56(1), 220–234 (2011).
3. Van Essen, David C., et al. "The Human Connectome Project: a data acquisition perspective." Neuroimage 62.4 (2012): 2222-2231.
4. Venkataraman, A., Rathi, Y., Kubicki, M., Westin, C.-F., and Golland, P., "Joint modeling of anatomical and functional connectivity for population studies," Medical Imaging, IEEE Transactions on 31(2), 164–182 (2012).