## Modeling brain dynamics in brain tumor patients using The Virtual Brain

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Increasingly, computational models of brain activity are applied to investigate the intricate relation between structural and functional brain networks. In addition, biologically interpretable dynamical models may be used as unique predictive tools to investigate the impact of structural connectivity damage on brain dynamics. That is, individually modeled biophysical parameters could inform on alterations in patients' local and large-scale brain dynamics, which are invisible to brain-imaging devices. In this study, we compared biophysical model parameters between brain tumor patients and healthy controls. To this end, we used The Virtual Brain (TVB; Sanz Leon et al. 2013), a neuroinformatics platform that utilizes empirical structural connectivity data to create dynamic models of an individual's brain.

Diffusion and functional MRI data were collected from 11 glioma patients, 14 meningioma patients and 11 healthy partners, on the day before the patient's surgery. Data were preprocessed and converted to a structural and functional connectivity matrix per subject using a modified version of the TVB preprocessing pipeline (Schirner et al. 2015). To simulate neural activity based on the subject's structural connectome, the reduced Wong-Wang model was used (Deco et al., 2014). Two model parameters were individually optimized to investigate possible alterations in brain dynamics in brain tumor patients. The first is the local feedback inhibition control parameter  $J_i$ , that adjusts the connection weights from inhibitory to excitatory neurons within each local subnetwork (Deco et al., 2014). The second is the global scaling factor G, that is multiplied with the structural connectivity weight to interconnect all local subnetworks. Values of G and  $J_i$  yielding optimal correspondence between empirical and modeled functional connectivity were then compared between both brain tumor patient groups and healthy controls and related to cognitive performance and structural network topology.

## References

- Deco, G., Ponce-Alvarez, A., Hagmann, P., Romani, G. L., Martini, D., and Corbetta, M. (2014). 'How local excitation-inhibition ratio impacts the whole brain dynamics', *The Journal of Neuroscience*, **vol. 34**, pp. 7886-7898.
- Sanz Leon, P., Knock, S. A., Woodman, M. M., Domide, L., Mersmann, J., McIntosh, A. R. and Jirsa, V.
  K. (2013). 'The Virtual Brain: A simulator of primate brain network dynamics', *Frontiers in Neuroinformatics*, vol. 7, pp.
- Schirner, M., Rothmeier, S., Jirsa, V. K., McIntosh, A. R. and Ritter, P. (2015). 'An automated pipeline for constructing personalized virtual brains from multimodal neuroimaging data', *NeuroImage*,

**vol. 117**, pp. 343–57.