

# From MRI data to the whole-brain dynamical models: a work-flow of The Virtual Brain platform

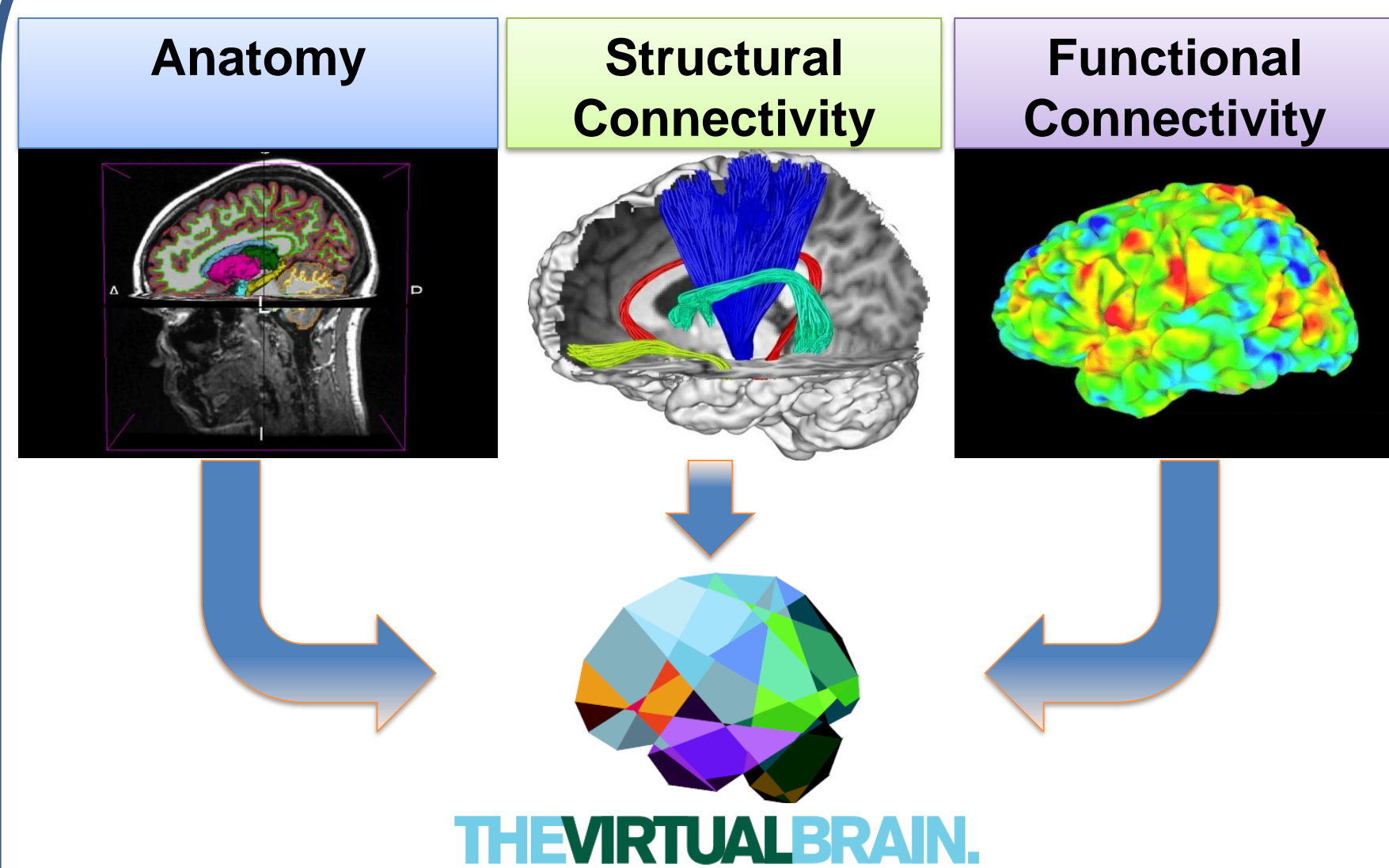
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## The Virtual Brain (TVB) platform



- TVB provides output compatible to clinical brain-scanners.

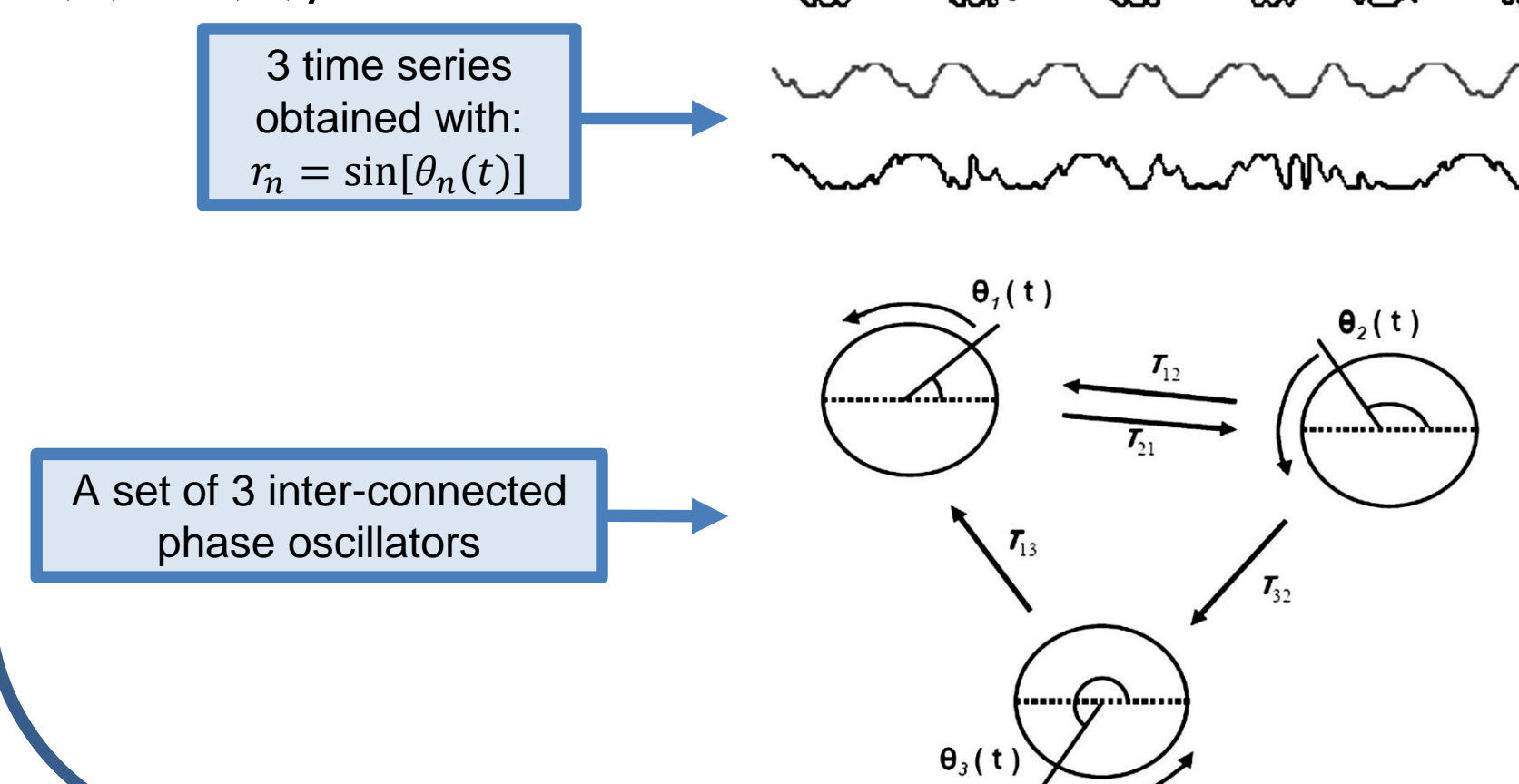
- TVB [1] receives as input commonly measured multimodal data (e.g. EEG, MEG, fMRI).
- TVB uses novel concepts from computational, cognitive and clinical neuroscience, reducing the model's complexity while capturing the most relevant macroscopic activity features.
- The model networks are constructed based on the empirical structural connectivity and the simulation results can be compared with empirical functional data (connectivity).

## The computational model: Kuramoto

We use a computational Kuramoto model of coupled phase oscillators to simulate the dynamics of the resting-state (RS) brain networks [2]. The phase  $\theta_n$  of node  $n$  at time  $t$ , obeys the following dynamical equation [3]:

$$\frac{d\theta_n}{dt} = \omega_n + k \sum_{p=1}^N C_{np} \sin[\theta_p(t - \tau_{np}) - \theta_n(t)] + \eta_n(t), \quad n = 1, \dots, N.$$

$$\langle \tau \rangle = \langle L \rangle / V$$



Model variables	Description
$\theta_n$	phase of node $n$ at time $t$
$k$	global coupling strength
$C_{np}$	relative coupling strength from node $p$ to node $n$
$\tau_{np}$	conduction delay between node $p$ to node $n$
$f_n = \omega_n / 2\pi$	intrinsic frequency of node $n$ on its limit cycle, set at $f = 10$ Hz
$\eta_n(t)$	noise received by the local networks
$\langle \tau \rangle$	mean delay
$\langle L \rangle$	mean fiber length
$V$	conduction speed

## Structural & Diffusion preprocessing

**TVB-recon** structural pipeline [4]:

- Parcellation: Desikan-Killiany brain atlas
- Software method: FreeSurfer
- Motion/eddy correction: ✓
- Intensity normalization: ✓
- Tractography: Probabilistic (MRtrix 3.0)
- SC Metric: Voxel pairs connected with streamline, ROI volume corrected



We used one random subject from the Nathan Kline Institute (NKI) Rockland sample [5] for illustration:

- Name: sub-A00008326, Session: ses-DS2 (Age: 59 years / female)



Magnetic Resonance Imaging Protocol:

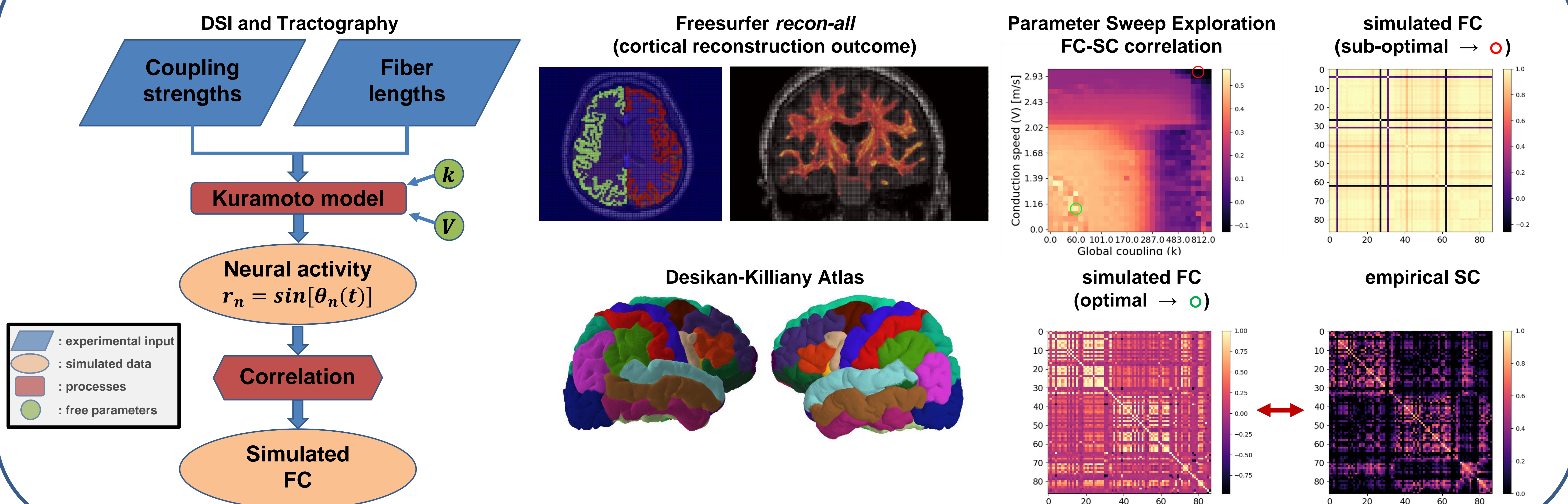
- Anatomical scan: MPRAGE (TR = 1900; voxel size = 1mm isotropic)
- Diffusion Tensor Imaging (137 Directions, voxel size = 2 mm isotropic)

## Parameter Sweep Exploration

- Essential step in order to fit simulations with empirical data.
- Performed using **tvb-hpc** (CUDA) [6].
- TVB model kernels optimized for HPC on hybrid architectures.
- GPU code allows thousands of parameters to be explored in parallel: each parameter is assigned to a thread in the GPU.
- Global coupling ( $k$ ) and conduction speed ( $V$ ) are varied to maximize Functional Connectivity (FC) – Structural Connectivity (SC) correlation.
- Runs are performed on the JURECA GPU partition.



## Preliminary results: numerical simulations



## Summary

- We performed DSI and Tractography.
- We calculated the SC matrix using TVB pipeline.
- We simulated resting-state network dynamics using the Kuramoto model.
- We performed Parameter Sweep Exploration for global coupling and conduction speed to maximize FC to SC correlation.

## Outlook

- Incorporate the Functional processing pipeline → empirical FC matrices.
- Take into account many subjects & evaluate different RS models.
- Run model parameter sweep exploration for optimal tuning and agreement between the static/dynamic empirical FC matrices and the simulated ones.
- Investigate the impact of Anatomical vs Functional Atlases.

## References

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## Acknowledgments

This study was supported by the Deutsche Forschungsgemeinschaft (DFG, EI 816/4-1, LA 3071/3-1), the National Institute of Mental Health (R01-MH074457), the Helmholtz Portfolio Theme "Supercomputing and Modelling for the Human Brain" and the European Union's Horizon 2020 Research and Innovation Programme under Grant Agreement No. 7202070 (HBP SGA1) and No.785907 (HBP SGA2). This project has received funding from the German Federal Ministry of Education and Research project no. 01GQ1504B. Responsibility for the content of this publication belongs to the authors.

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- [6] <https://github.com/the-virtual-brain/tvb-hpc>