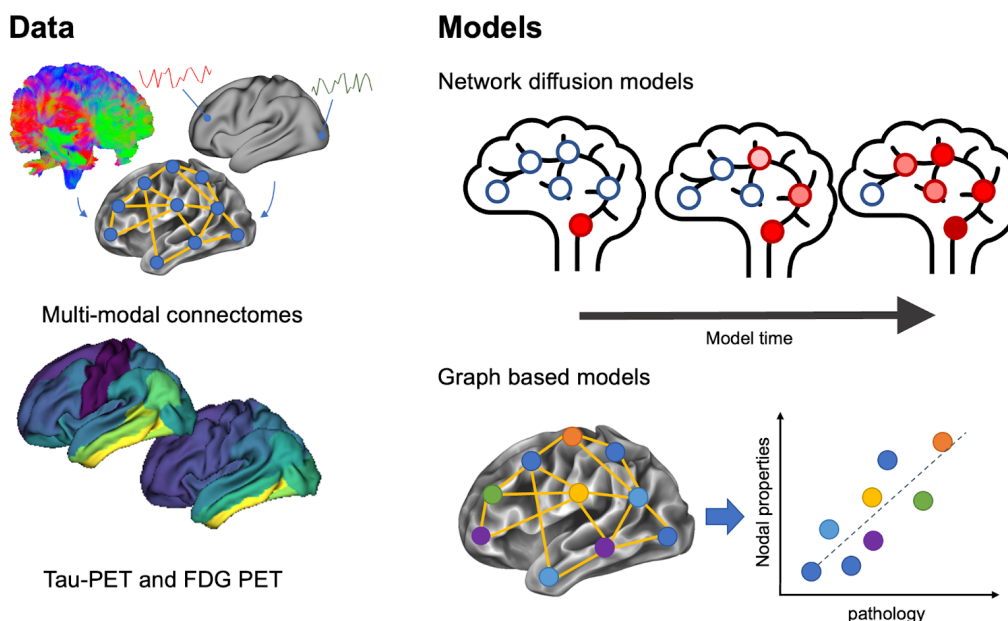


Using Network Spreading Models to Uncover Mechanisms of Alzheimer's Disease Progression

Project background and motivation:

- Connectome-based models are used to probe mechanisms of pathology spread in neurodegenerative disease, and to predict patient-specific outcomes (see [here](#) for a recent review).
- Multiple models have been proposed, but there is no framework available to easily compare them
- Recent work using these models indicates early stages of Alzheimer's disease are dominated by spreading, whereas later stages are dominated by production of tau: [Personalised Regional Modelling Predicts Tau Progression in the Human Brain | bioRxiv](#)



Specific goals:

- Create a toolbox containing different models to allow the user to compare model fits with different models and parameters
- Use the framework to see whether abnormal glucose metabolism (measured by FDG PET) mediates pathology accumulation (measured by tau PET), e.g., spreading vs production

Useful skills/learning areas:

- Python
- Differential equation modelling: numerical integration and parameter estimation
- Building python packages
- Multi-modal imaging data