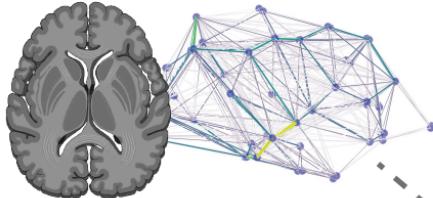
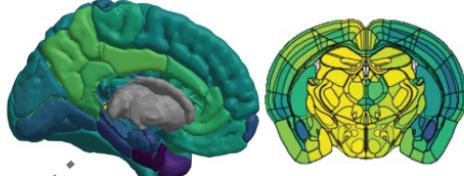


Structural connectivity



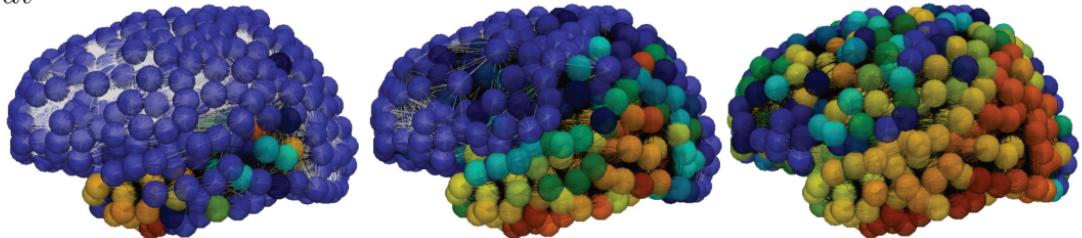
Pathology data (PET, tissue staining)



Progression along
anatomical connections

Find optimal model
parameters

$$\frac{dp_i}{dt} = \mathcal{N}(\mathbf{p}; W, \theta_{\text{spreading}}) + f(p_i; \theta_{\text{aggregation}}, \theta_{\text{clearance}}, \theta_{\text{inflammation}}, \theta_{\text{genes}})$$



Compare model
performance with null
models (i.e. spatial
diffusive spread)

Predict personalized
disease progression
trajectories

Infer the impact of clearance,
inflammation, and gene
expression on progression and
regional vulnerability