

# Connectomes for 40,000 UK Biobank participants: A multi-modal, multi-scale dataset for network neuroscience

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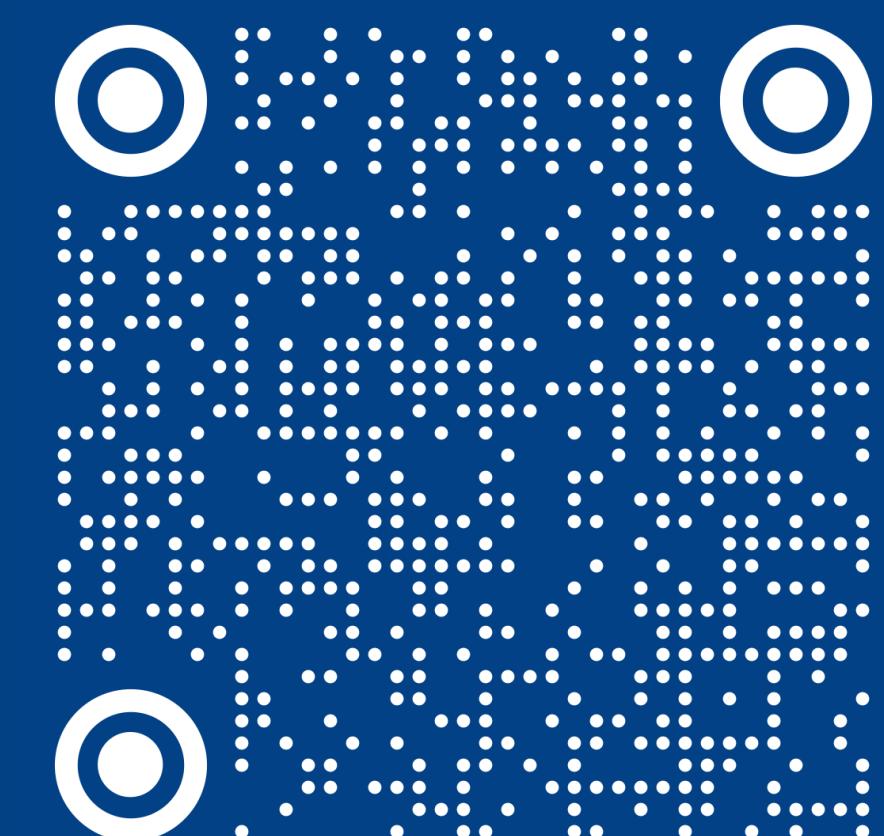
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## Introduction

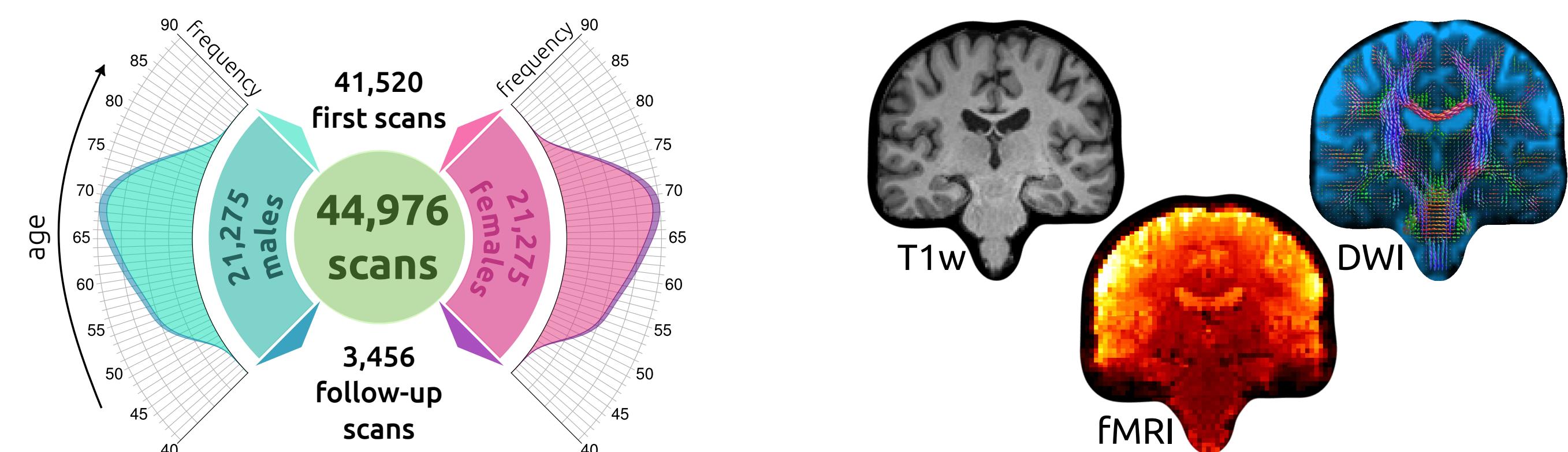
Different aspects of brain connectivity can be quantified using different MRI modalities:

- Diffusion-weighted MRI data → Compute structural brain networks of white-matter connections.
- Functional MRI data → Compute functional connectivity networks describing inter-regional interactions in brain activity.

These network representations of brain connectivity are referred to as connectomes [1,2]. Establishing a large-scale community biobank of structural and functional human connectomes will enable a diverse range of research into brain networks in health and disease.

The UK Biobank (UKB) hosts the world's largest neuroimaging resource [3-5]:

- Bank of ~45,000 brain imaging sessions acquired from ~40,000 participants.
- Tremendous potential for research on early disease prediction and alignment of image-derived phenotypes (IDPs) with cognitive, behavioral, genetic, and medical observations.
- Longitudinal neuroimaging data + constantly updated clinical records enables prospective neuroscientific research at a population scale.

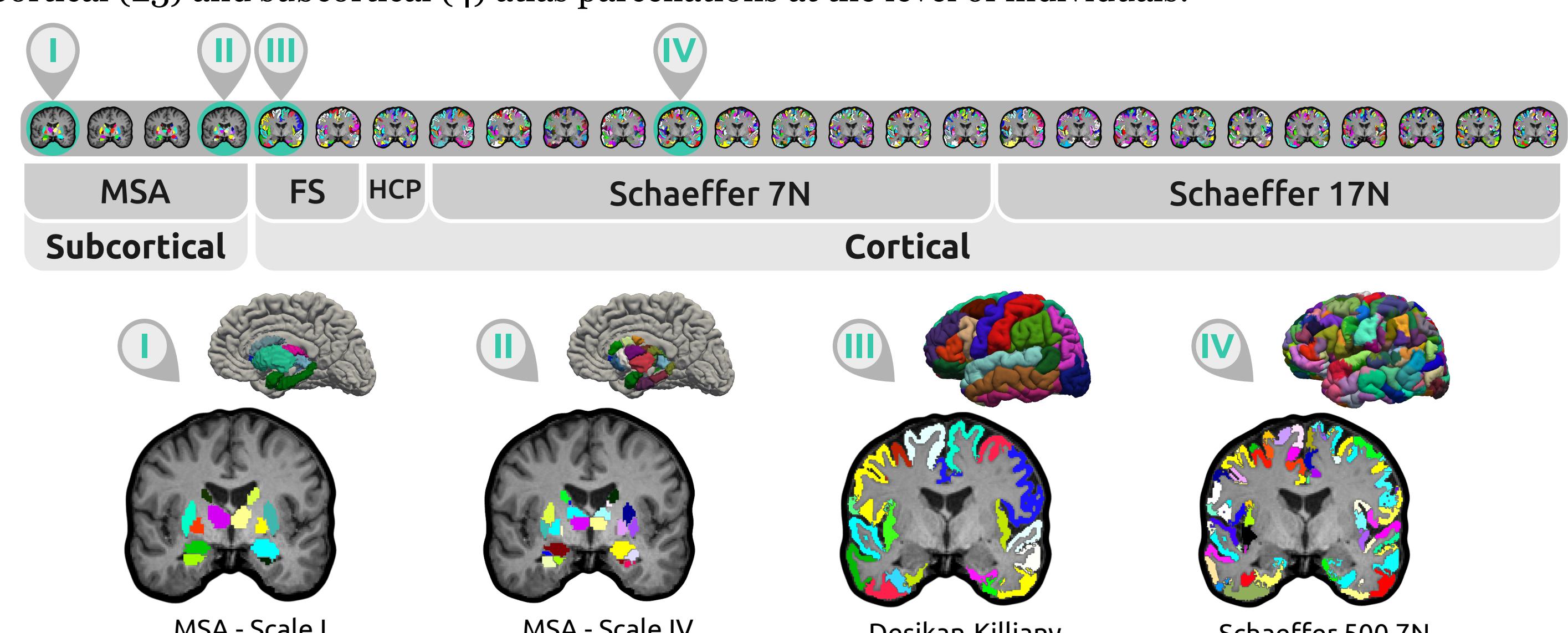


Mapping connectomes from neuroimaging data at scale is computationally burdensome and requires significant technical expertise. Establishing a brain connectivity biobank for the UKB will:

- Ensure rapid access to connectomes for researchers
- Access to connectome without required expertise or computing resources
- Facilitate reproducible neuroscience practices
- Enhance UKB utilization among the research community
- Lead to new discoveries about brain networks.

## Resource: Atlas parcellations

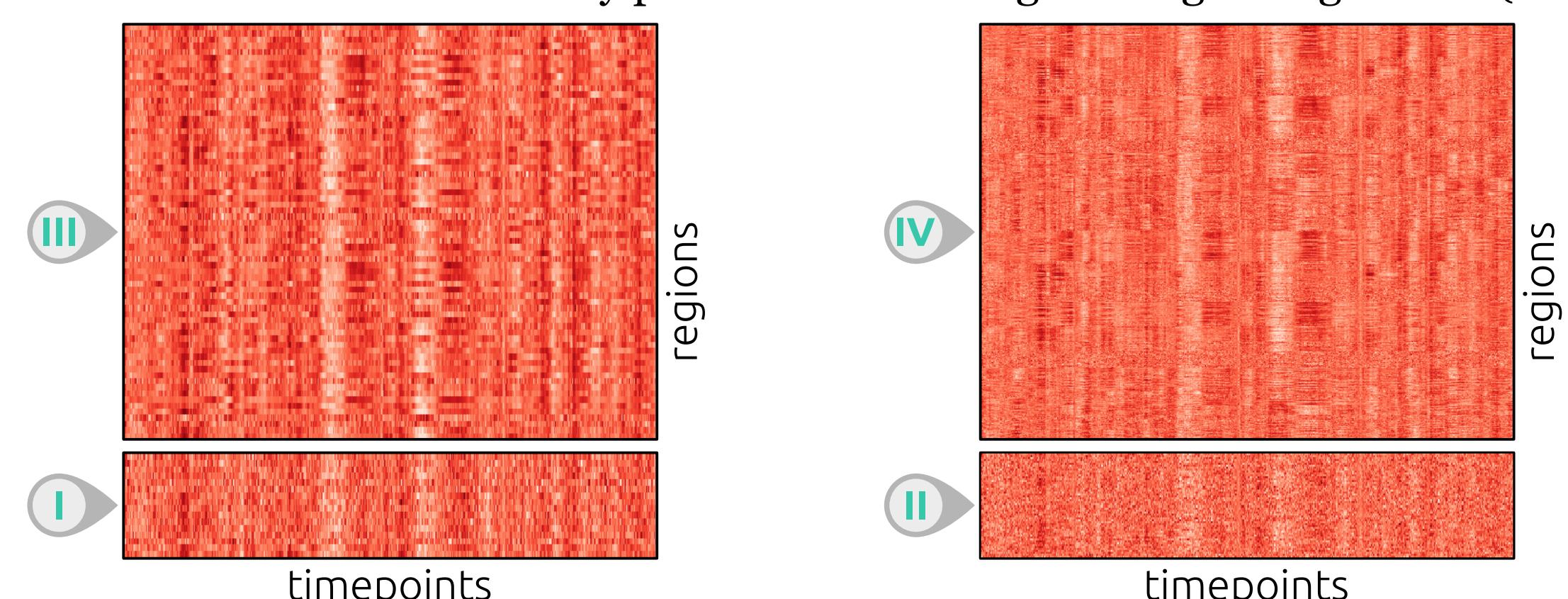
Cortical (23) and subcortical (4) atlas parcellations at the level of individuals:



## Resource: Functional time series

Resting-state functional time series of cortical and subcortical regions were provided.

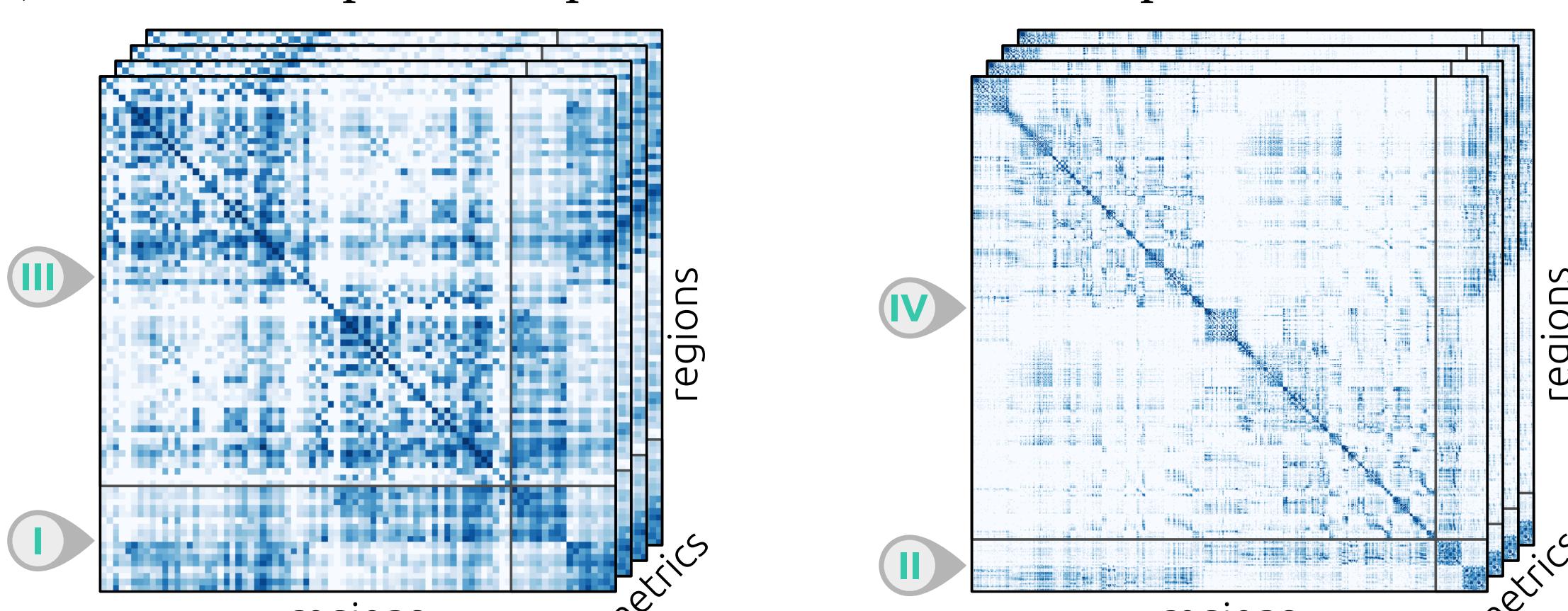
\* Global signal time series was additionally provided to enable global signal regression (GSR)



## Resource: Structural connectomes

White-matter tractography-derived structural connectomes were provided for different atlas combinations and metrics (number of streamlines, fiber bundle capacity, mean length, mean FA).

\* In addition, streamline endpoints and per-streamline metrics were provided.

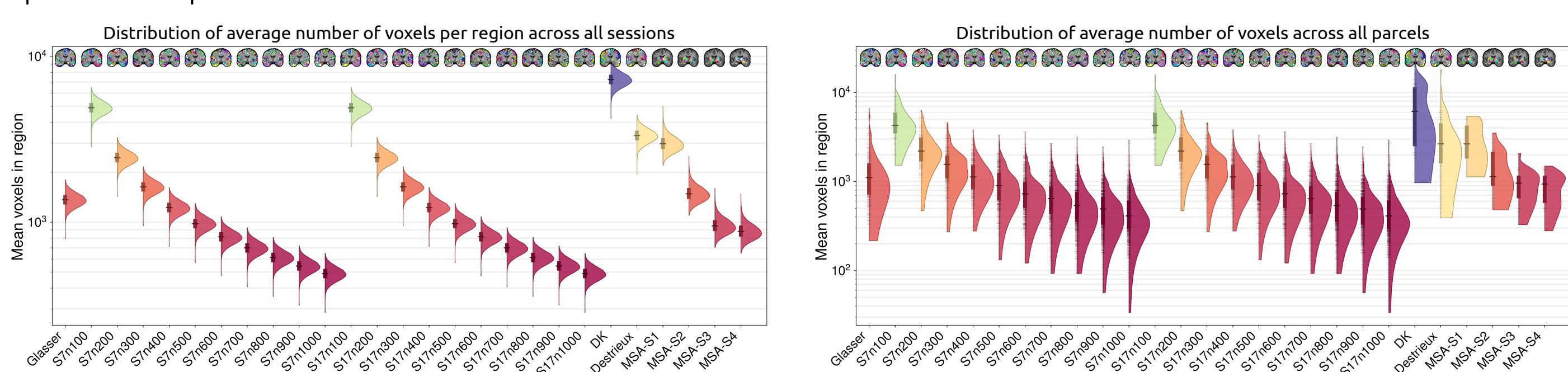


## Quality control

An extensive set of QC measures are provided to complement existing imaging QC efforts by UKB. These measures could be used to exclude low-quality or inaccurate connectomes.

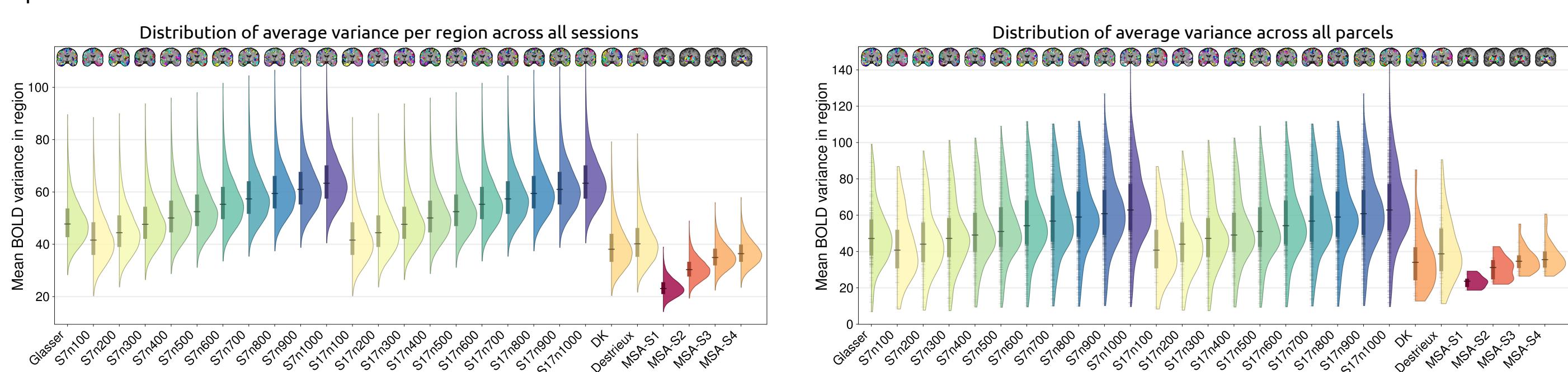
- Regional volumes are provided for atlas parcellations

a | Atlas metrics: parcel sizes



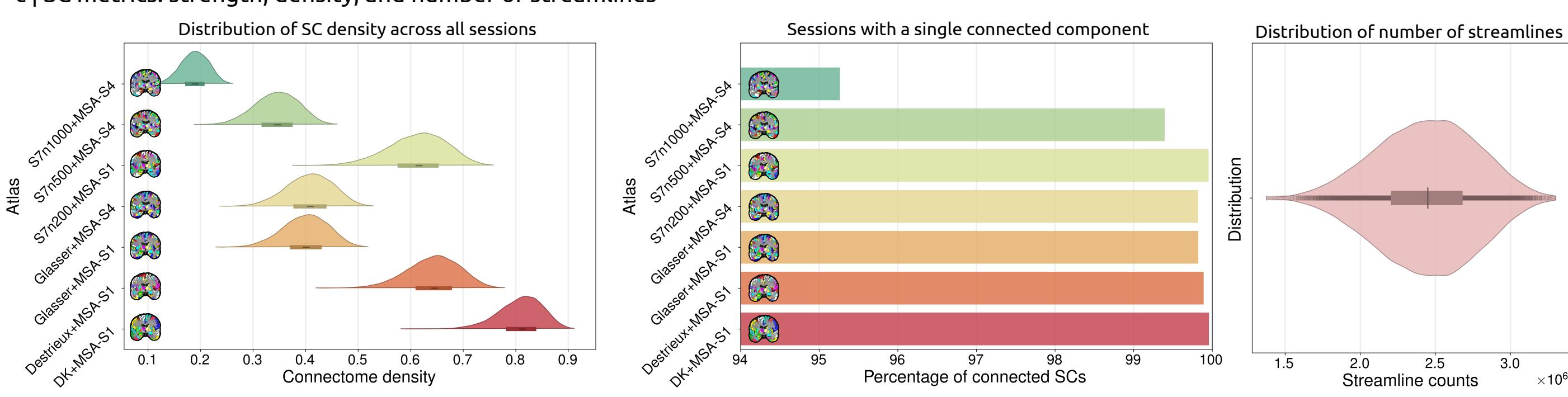
- Variance of regional resting-state signal for functional timeseries

b | FC metrics: BOLD variance



- For SC: density, number of components, total streamlines, and degree distribution

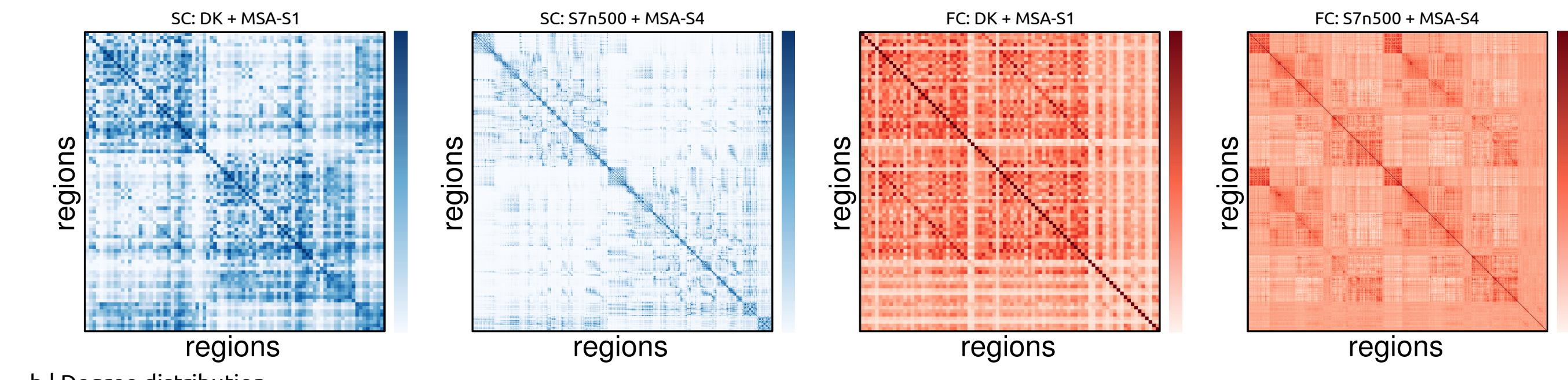
c | SC metrics: strength, density, and number of streamlines



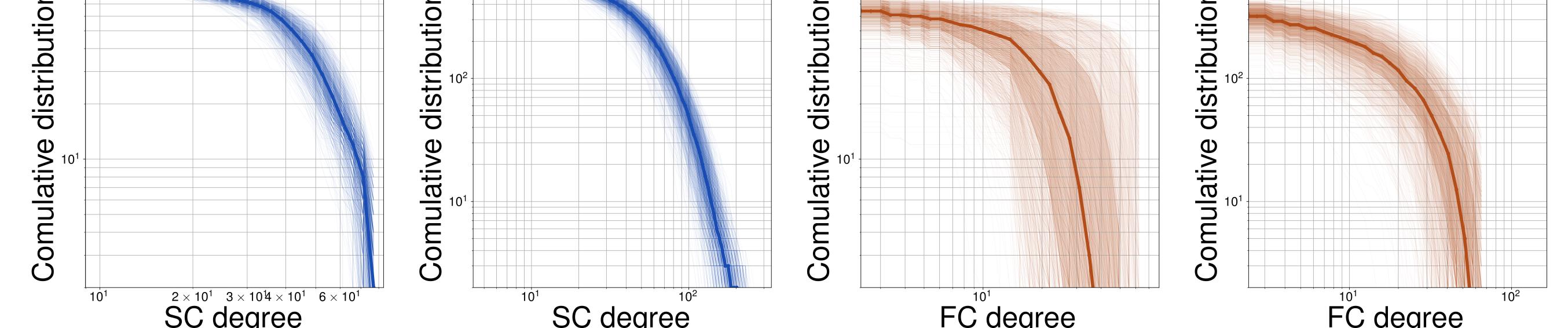
## SC and FC properties

An exploration of SC and FC properties was provided to further demonstrate the utility of this brain connectivity resource:

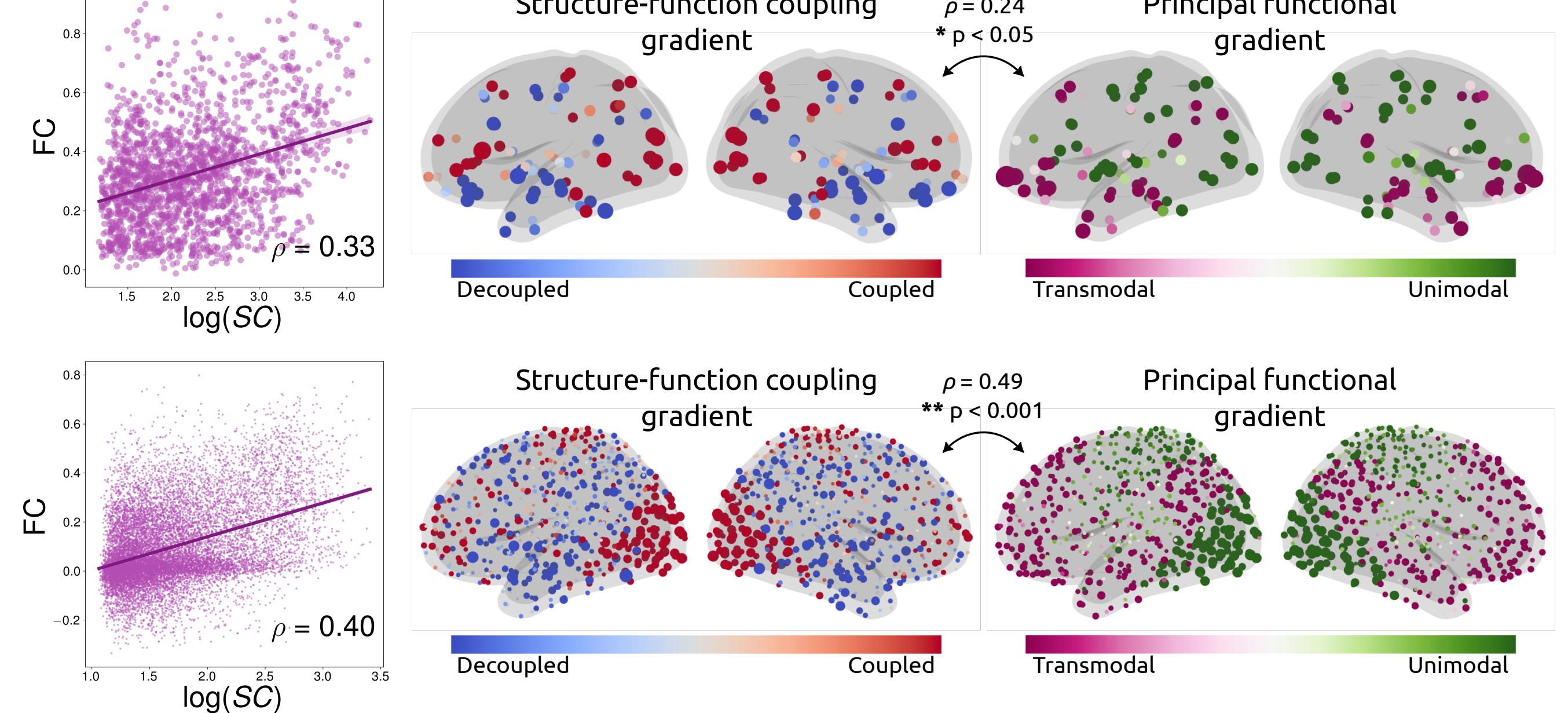
a | Connectivity matrix structure



b | Degree distribution



c | Structure-function coupling



## Concluding remarks

- We provide high-quality functional and structural brain networks for >40,000 UKB participants.
- Alternative out-of-the-box versions of SC and FC provided enables future use flexibility.
- More than 200,000 hours of compute time for the world's largest human connectome resource.
- The resource is accompanied by an extensive set of QC measures.
- All connectomes are available on UKB data sharing platform.
- The connectome mapping pipeline is openly available on Github.
- We envisage this resource will enable studies of human connectomics at an unprecedented scale.