

# A HIGH-THROUGHPUT PIPELINE IDENTIFIES ROBUST CONNECTOMES BUT TROUBLESOME VARIABILITY

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Follow the slides: [ericwb.me/lectures/ohbm/ohbm\\_ndmg.html](https://ericwb.me/lectures/ohbm/ohbm_ndmg.html)

# MULTIMODAL MR IMAGING (M3R) IS COMMONPLACE


- Multimodal MRI (M3R): dMRI, fMRI, sMRI
- Connectome: network of connections in the brain
- Many open-access datasets:
  - Consortium for Reliability and Reproducibility
  - Human Connectome Project
  - Healthy Brain Network
- No brain imaging biomarkers for clinical psychiatry

# PROCESSING AND ANALYSIS OF CONNECTOMES IS CHALLENGING

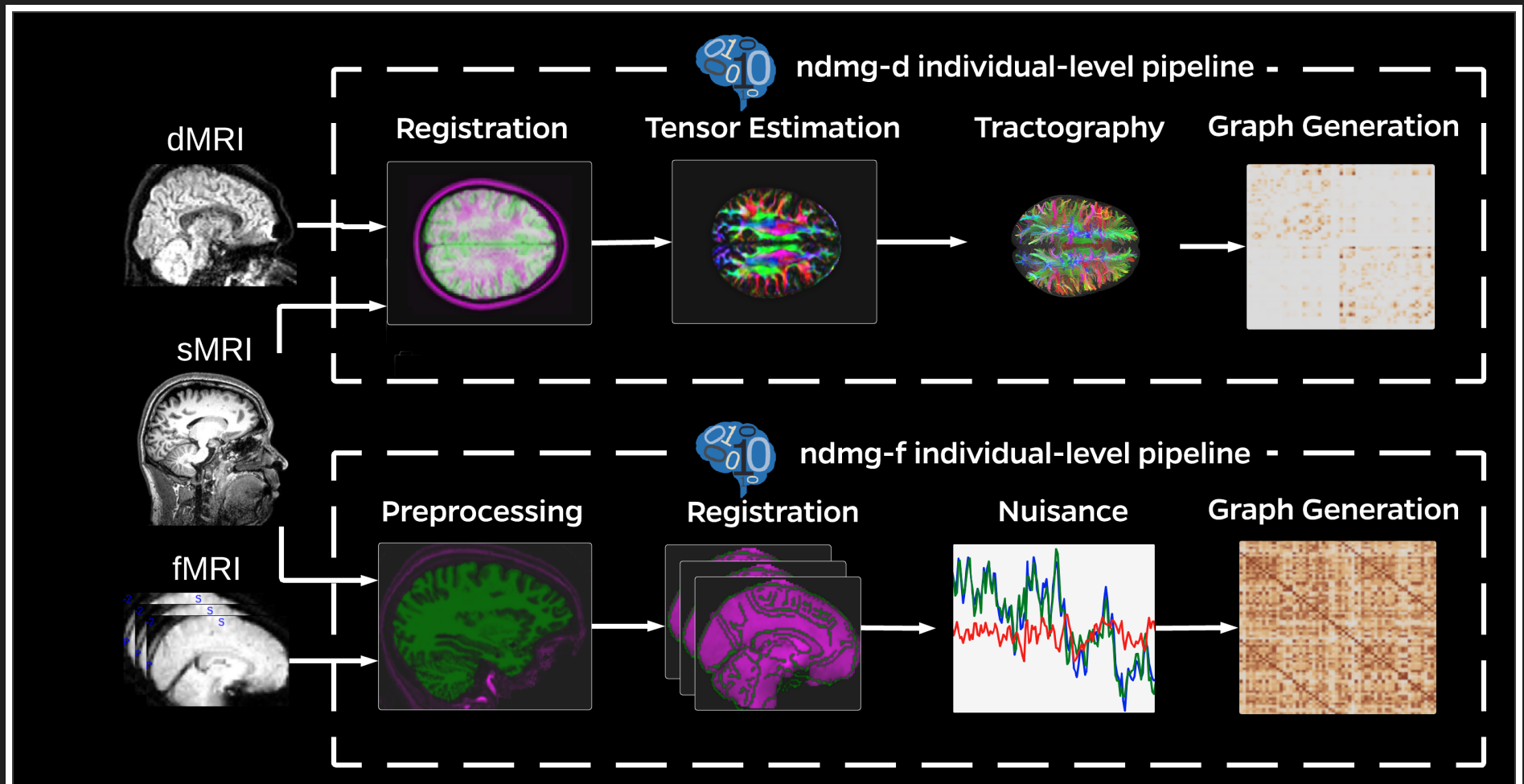
- sample sizes of single studies are relatively small
- data are heterogeneous within and across studies
- existing pipelines are customized per dataset
- lack of generative statistical network models

⇒ many failures to replicate

# A PRINCIPLED APPROACH FOR CONNECTOMICS

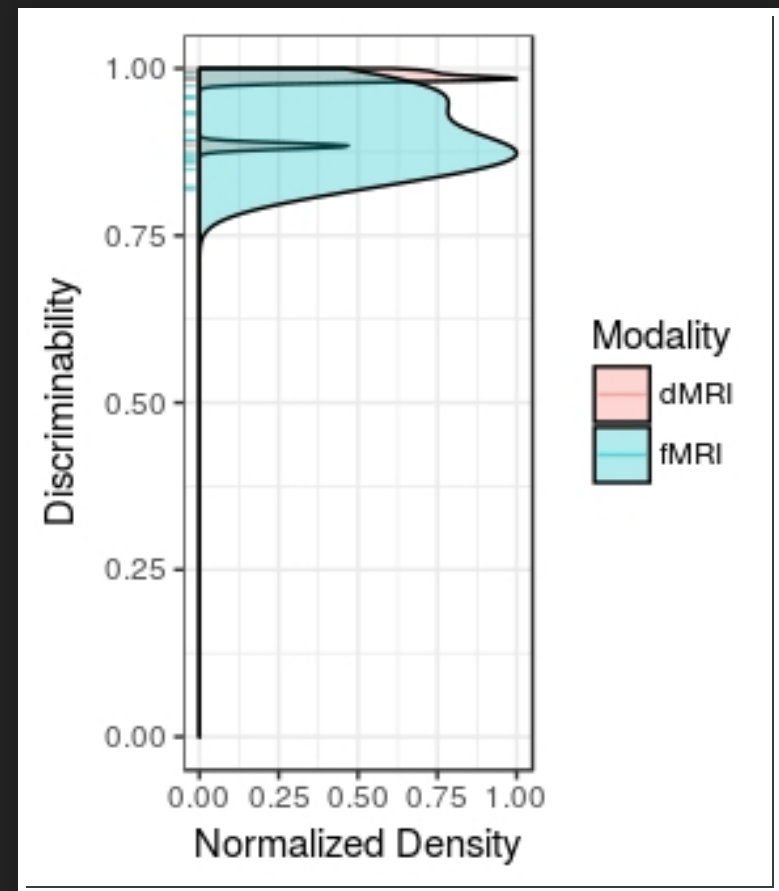
| pipeline   | Statistical Principles |                 |               |                  | Computational Principles |                 |                 |             | Connectome Principles |             |                     |
|--|------------------------|-----------------|---------------|------------------|--------------------------|-----------------|-----------------|-------------|-----------------------|-------------|---------------------|
|  | <i>accurate</i>        | <i>reliable</i> | <i>robust</i> | <i>expedient</i> | <i>scalable</i>          | <i>portable</i> | <i>turn-key</i> | <i>open</i> | <i>dMRI</i>           | <i>fMRI</i> | <i>raw-to-graph</i> |
|  NDMG | ✓                      | ✓               | ✓             | ✓                | ✓                        | ✓               | ✓               | ✓           | ✓                     | ✓           | ✓                   |
| HCP  | ✓                      | ✓               | ✓             | ✓                | ✗                        | ✗               | ✓               | ✓           | ✓                     | ✓           | ✗                   |
| PANDA  | ✓                      | ✓               | ✓             | ✓                | ✓                        | ✓               | ✓               | ✓           | ✓                     | ✗           | ✓                   |
| CMTK   | ✓                      | ✓               | ✓             | ✓                | ✓                        | ✗               | ✗               | ✓           | ✓                     | ✗           | ✓                   |
| CPAC   | ✓                      | ✓               | ✓             | ✓                | ✓                        | ✓               | ✓               | ✓           | ✗                     | ✓           | ✗                   |
| fmriprep   | ✓                      | ✓               | ✓             | ✗                | ✓                        | ✓               | ✓               | ✓           | ✗                     | ✓           | ✗                   |
| NIAK   | ✓                      | ✓               | ✓             | ✓                | ✓                        | ✓               | ✗               | ✓           | ✗                     | ✓           | ✗                   |

# NDMG PROCESSES DMRI & FMRI IN PARALLEL



# DISCRIMINABLE ACROSS 25+ STUDIES AND 6000+ SCANS

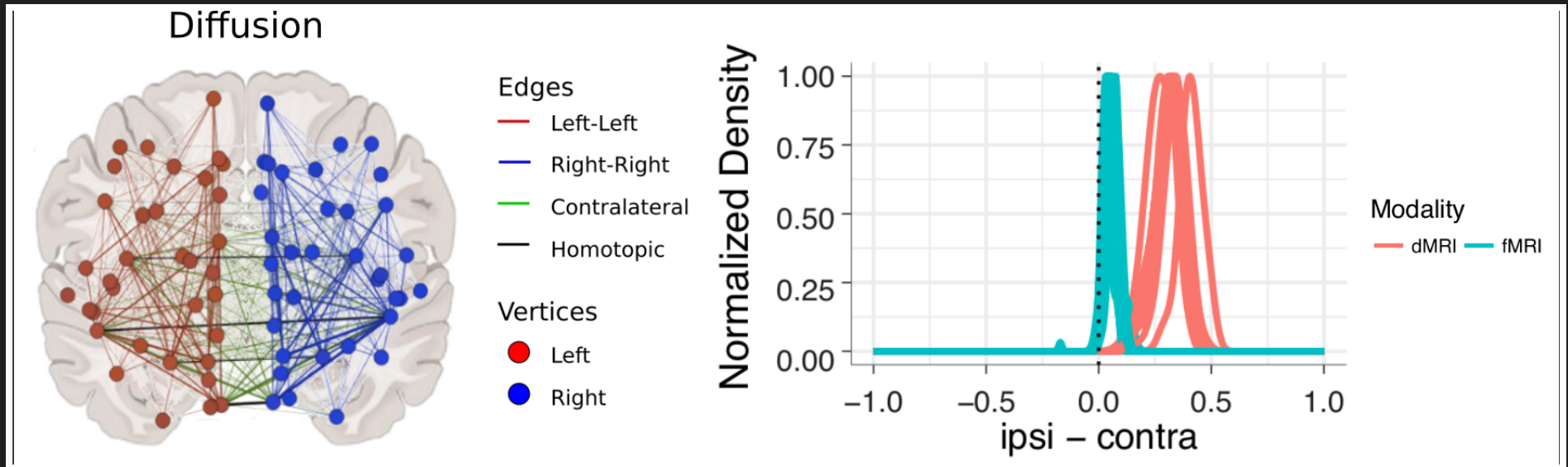
- Discriminability: non-parametric generalization of ICC
- $D = \mathbb{P}(x_{i,i'} < x_{i,j})$
- Are within-subject connectomes more similar than across-subject connectomes?



# WHAT IS MEGA-ANALYSIS?

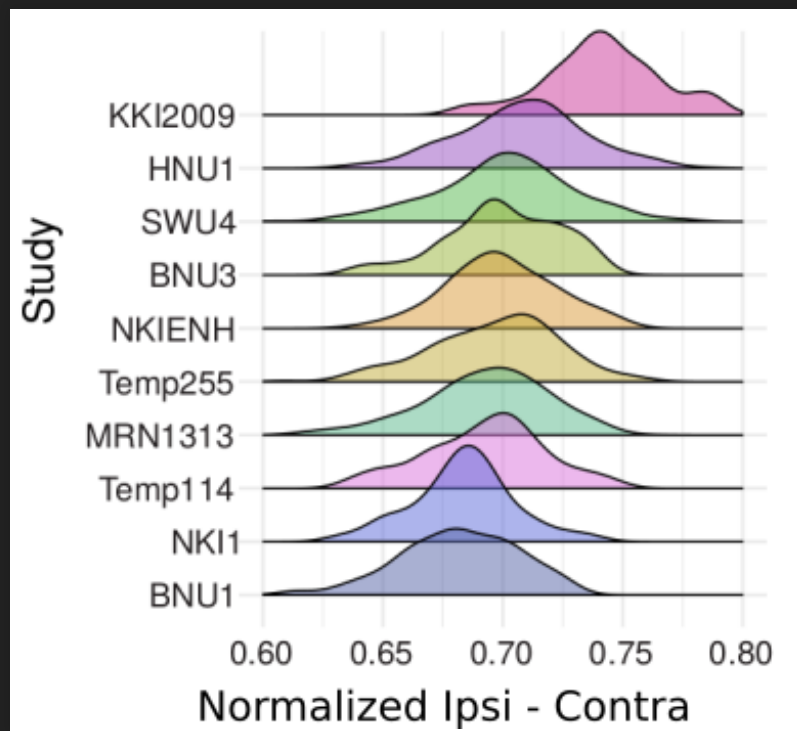
- Multiple Group Level Analysis, or mega-analysis, is when we have several unique groups we want to aggregate data over
- Cohort = 6000+ connectomes across 25+ studies

# IPSILATERAL CONNECTIONS ARE STRONGER THAN CONTRALATERAL IN ALL DIFFUSION CONNECTOMES

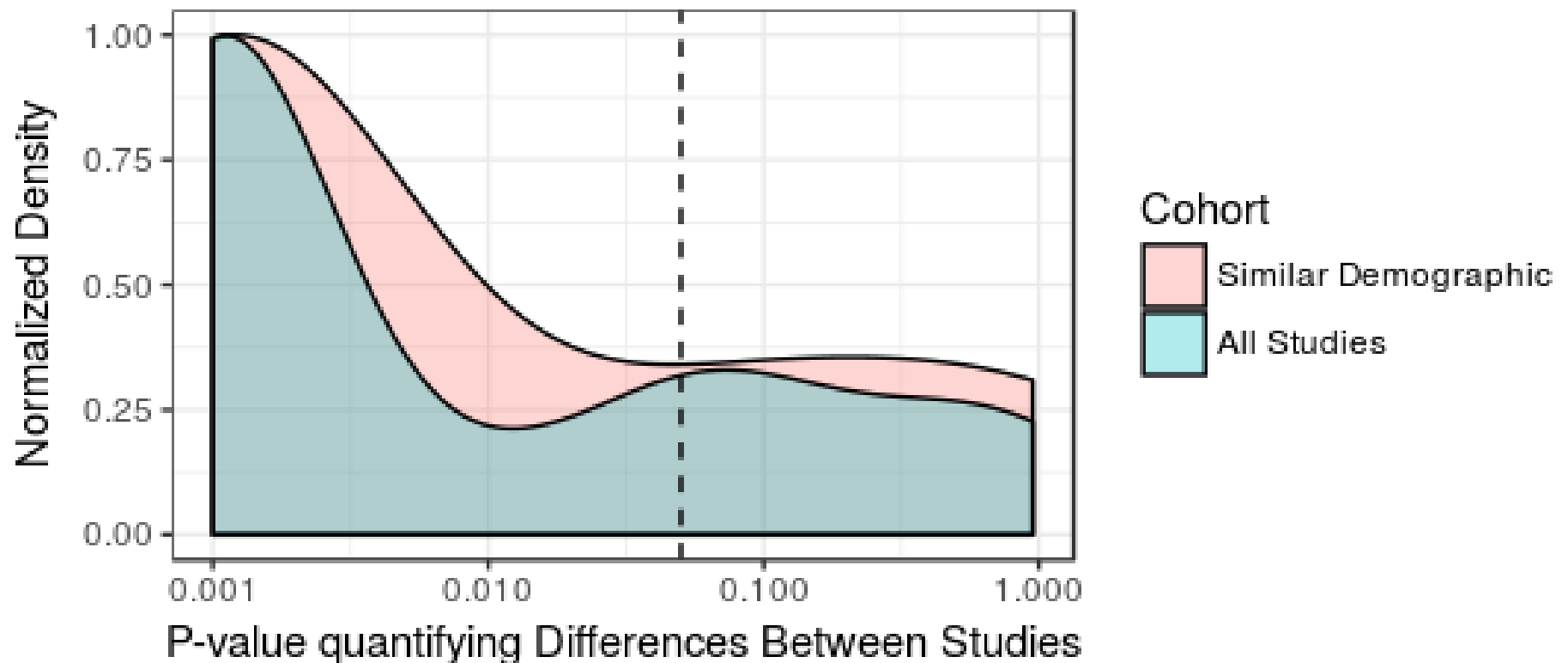




# MAGNITUDES OF EFFECTS EXHIBIT LARGE HETEROGENEITY WITHIN AND ACROSS SITES



# CONDITIONING ON BASIC DEMOGRAPHICS AND STUDY FAILS TO ELIMINATE HETEROGENEITY



# NDMG: AN EFFICIENT PIPELINE FOR SCALABLE CONNECTOMICS

- [ndmg](#) pipeline is open-source, parallel: ~1 hr/scan
- Docker, singularity, BIDS App
- >6000 of connectomes online at [neurodata.io](#)
- extensive QA suite produced with each connectome

# NDMG ESTABLISHES A NEED FOR IMPROVED CROSS-SITE REPLICABILITY

- every dataset is highly discriminable
- certain properties preserved across all scans
- considerable heterogeneity within and across studies
- conditioning on study and demographics fails to mitigate heterogeneity

## POTENTIAL NEXT STEPS

- data analysis improvements
  - probabilistic tractography
  - multiscale atlases
- data acquisition improvements
  - deep phenotyping
  - data acquisition harmonization

# LINKS

- [ndmg paper \(bioarxiv\)](#)
- [neurodata/ndmg \(pipeline on github\)](#)
- [neurodata/ndmg \(docker container\)](#)
- [neurodata/graphstats \(analysis on github\)](#)

# ACKNOWLEDGEMENTS

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# QUESTIONS?