

ndmg: a reliable one-click pipeline for M3R connectome estimation

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Abstract

The point of an abstract is kinda abstract...

1 Introduction

2 Methods

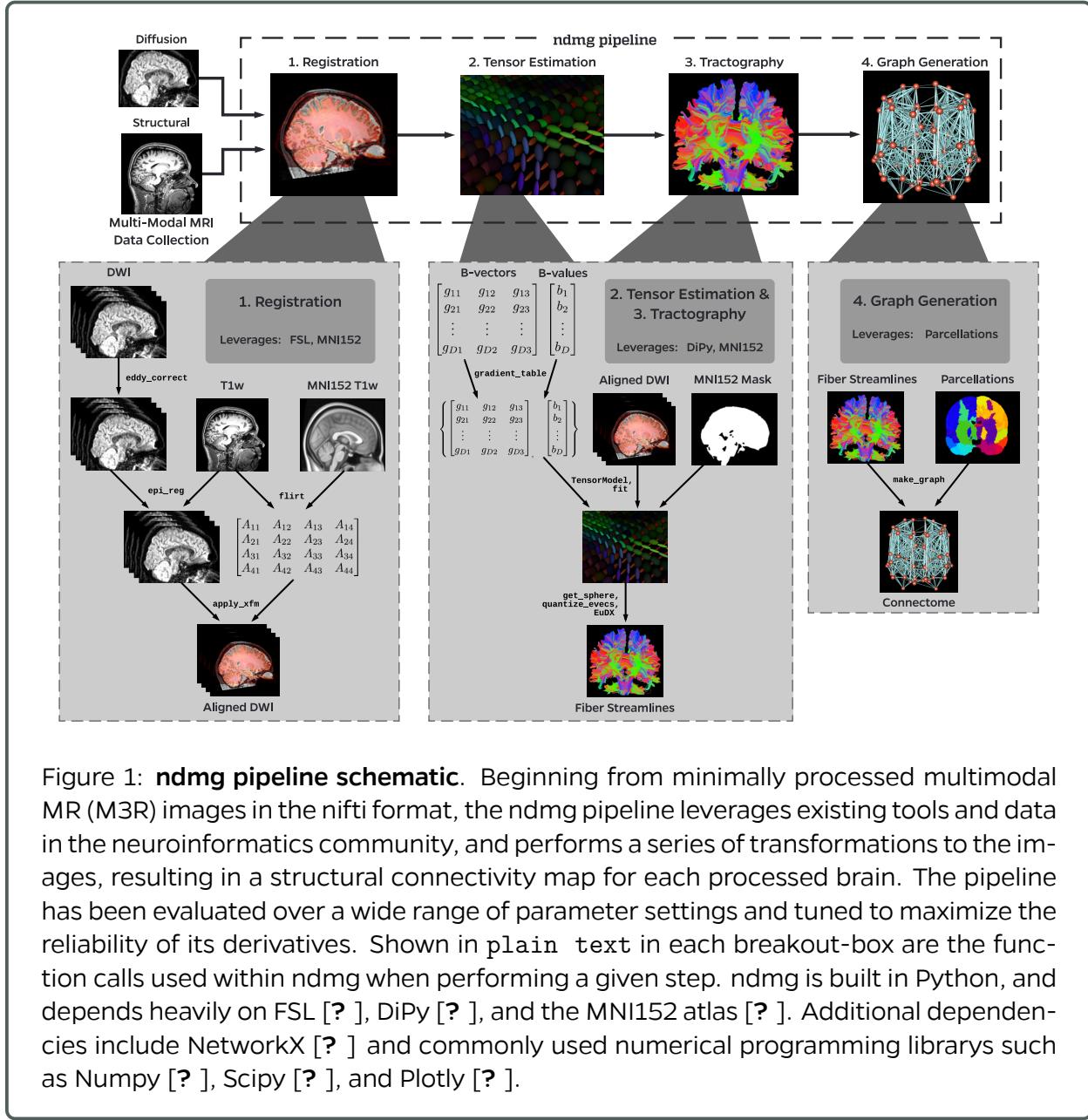


Figure 1: ndmg pipeline schematic. Beginning from minimally processed multimodal MR (M3R) images in the nifti format, the ndmg pipeline leverages existing tools and data in the neuroinformatics community, and performs a series of transformations to the images, resulting in a structural connectivity map for each processed brain. The pipeline has been evaluated over a wide range of parameter settings and tuned to maximize the reliability of its derivatives. Shown in plain text in each breakout-box are the function calls used within ndmg when performing a given step. ndmg is built in Python, and depends heavily on FSL [?], DiPy [?], and the MNI152 atlas [?]. Additional dependencies include NetworkX [?], and commonly used numerical programming libraries such as Numpy [?], Scipy [?], and Plotly [?].

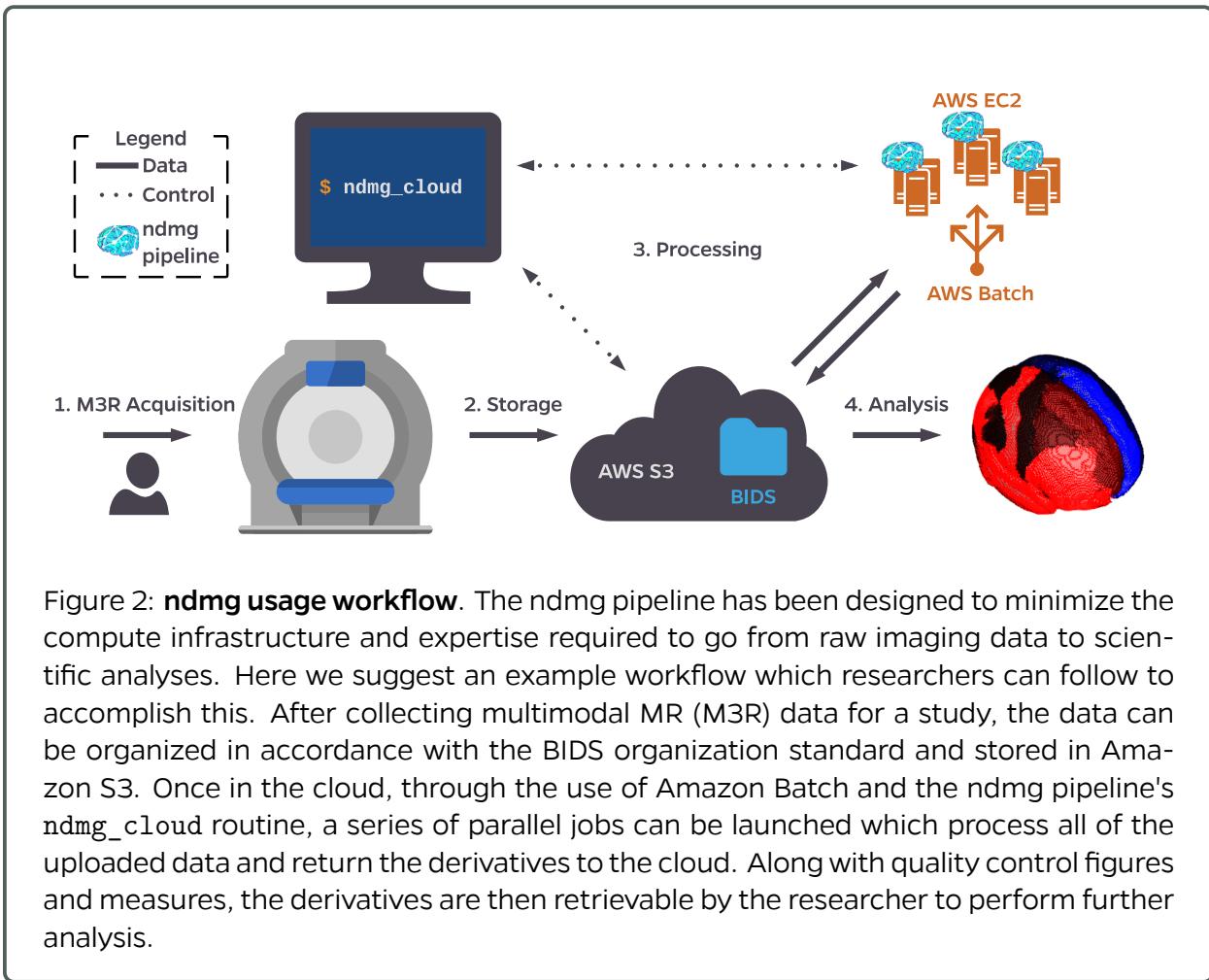


Figure 2: *ndmg* usage workflow. The *ndmg* pipeline has been designed to minimize the compute infrastructure and expertise required to go from raw imaging data to scientific analyses. Here we suggest an example workflow which researchers can follow to accomplish this. After collecting multimodal MR (M3R) data for a study, the data can be organized in accordance with the BIDS organization standard and stored in Amazon S3. Once in the cloud, through the use of Amazon Batch and the *ndmg* pipeline's *ndmg_cloud* routine, a series of parallel jobs can be launched which process all of the uploaded data and return the derivatives to the cloud. Along with quality control figures and measures, the derivatives are then retrievable by the researcher to perform further analysis.

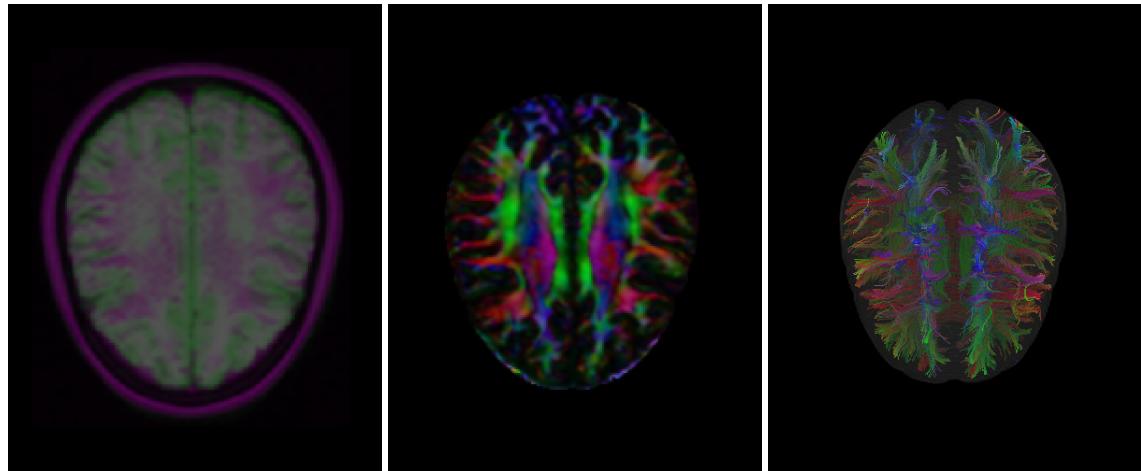


Figure 3: **Intermediate quality assessment outputs from `ndmg`.** Essential when providing a one-click tool was enabling the user to perform their own quality control of the derivatives produced so that they can trust the results. `ndmg` generates registration, tensor, and fiber quality assessment images after each is produced during pipeline operation.

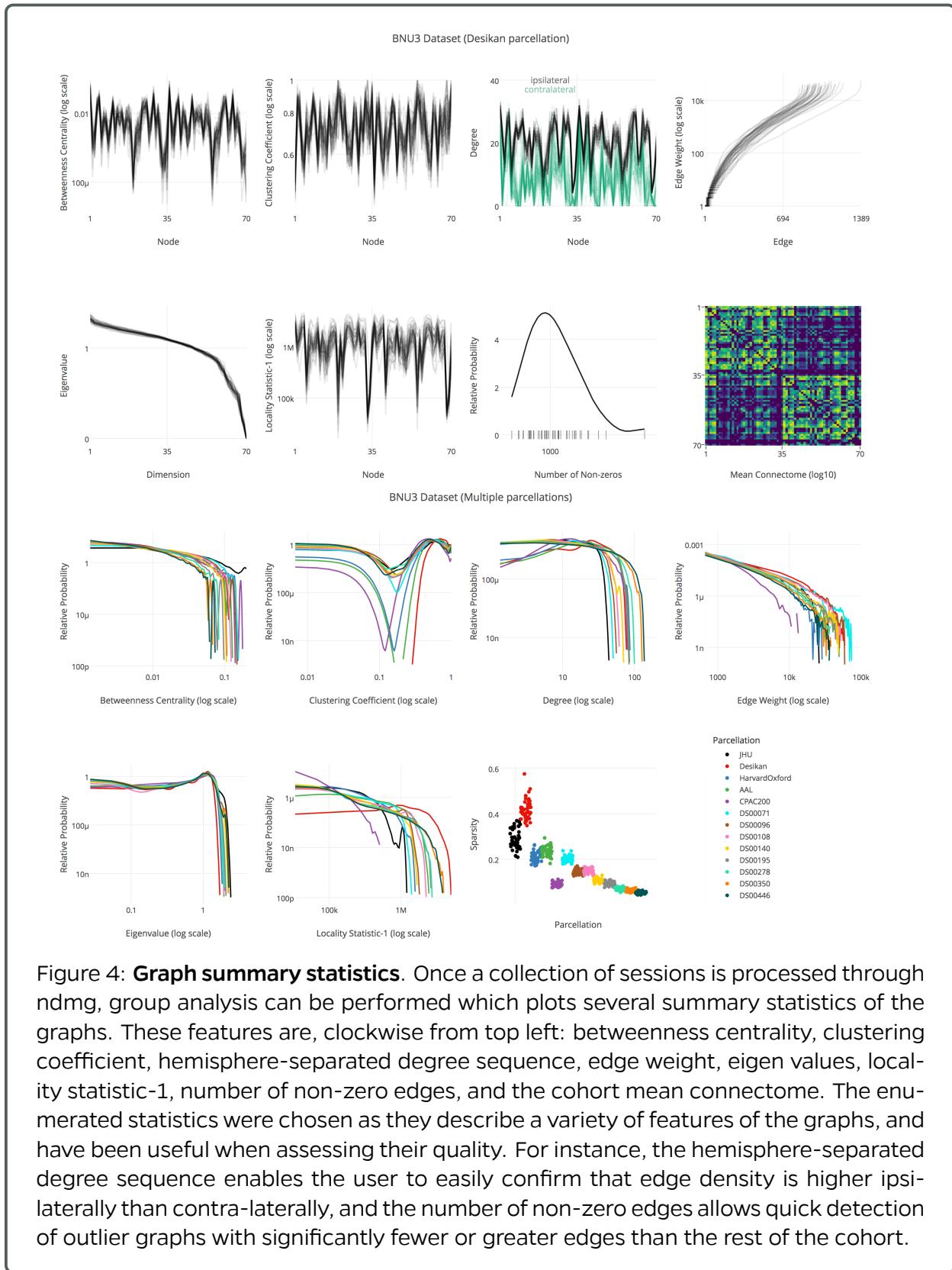


Figure 4: Graph summary statistics. Once a collection of sessions is processed through ndmg, group analysis can be performed which plots several summary statistics of the graphs. These features are, clockwise from top left: betweenness centrality, clustering coefficient, hemisphere-separated degree sequence, edge weight, eigen values, locality statistic-1, number of non-zero edges, and the cohort mean connectome. The enumerated statistics were chosen as they describe a variety of features of the graphs, and have been useful when assessing their quality. For instance, the hemisphere-separated degree sequence enables the user to easily confirm that edge density is higher ipsilaterally than contra-laterally, and the number of non-zero edges allows quick detection of outlier graphs with significantly fewer or greater edges than the rest of the cohort.

3 Results

Table 1: Processed public M3R datasets.

Dataset	Subjects	Scans Per Subject	Total Scans Processed
BNU1 [1]	57	2	114
BNU3 [1]	48	1	47
HNU1 [1]	30	10	300
Jung2015	255	1	253
KKI2009 [2]	21	2	42
MRN114	114	1	114
MRN1313	1313	1	1299
NKI1 [1]	24	2	40
NKI-ENH [3]	198	1	198
SWU4 [1]	235	2	454
Total	2295		2861

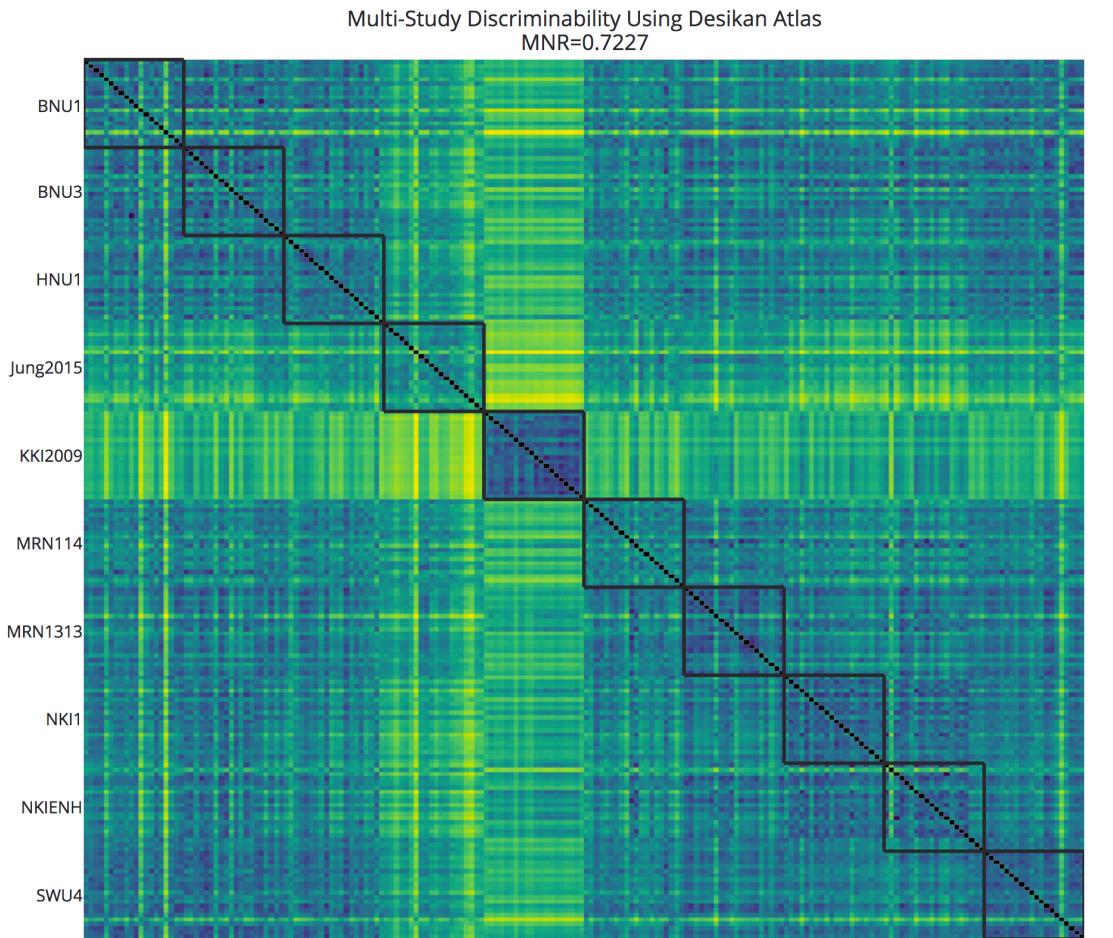
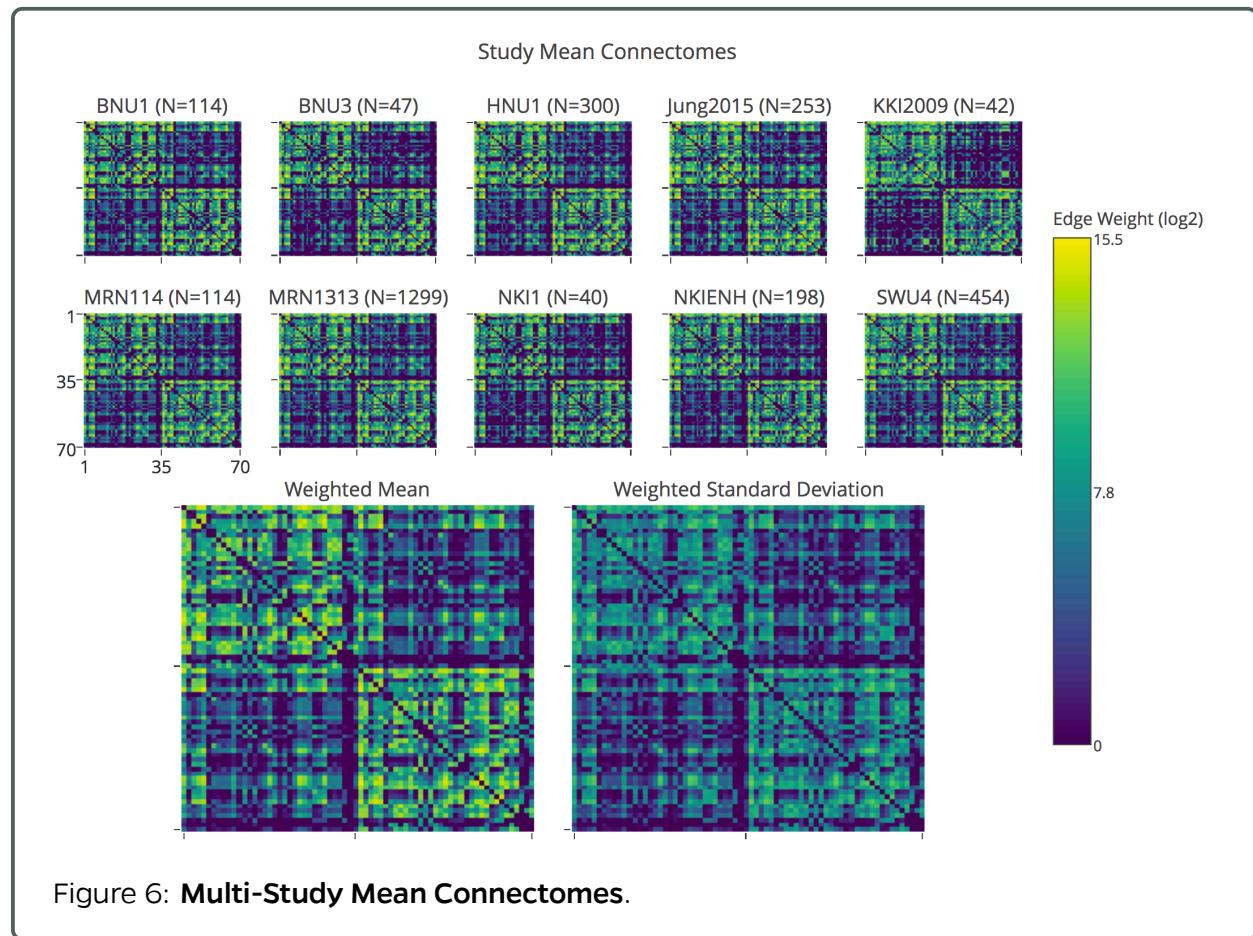


Figure 5: Prevalence of batch effects. Discriminability is a statistical tool which allows the quantification of the reliability of results. In the context of test-retest datasets this can be used to compare connectomes produced by different scans of the same subject, and enables direct evaluation of the graphs produced by the pipeline. A score of 1 indicates perfect reliability, and the worst possible score is 0. Here, we have processed 10 datasets with ndmg pipeline and compute discriminability across dataset rather than subject. Selecting a random subset of sessions from each dataset and eliminating all subjects with multiple sessions, we can quantify the prevalence of batch effects in diffusion MRI. If no batch effect were present, we would expect the discriminability to be at chance as no dataset-specific signal would make a graph more like another from the same dataset as opposed to that from another. With chance here being 0.1, we calculated a discriminability score of 0.7227, suggesting batch effects are present in this data, and there is dataset-specific signal in the graphs.



4 Discussion

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Declarations

Competing Interests The authors declare no competing interests in this manuscript.

References

- [1] X.-N. Zuo, J. S. Anderson, P. Bellec, R. M. Birn, B. B. Biswal, J. Blautzik, J. C. Breitner, R. L. Buckner, V. D. Calhoun, F. X. Castellanos et al., ``An open science resource for establishing reliability and reproducibility in functional connectomics," *Scientific data*, vol. 1, p. 140049, 2014.
- [2] B. A. Landman, A. J. Huang, A. Gifford, D. S. Vikram, I. A. L. Lim, J. A. Farrell, J. A. Bogovic, J. Hua, M. Chen, S. Jarso et al., ``Multi-parametric neuroimaging reproducibility: a 3-t resource study," *Neuroimage*, vol. 54, no. 4, pp. 2854--2866, 2011.
- [3] K. B. Noonan, S. Colcombe, R. Tobe, M. Mennes, M. Benedict, A. Moreno, L. Panek, S. Brown, S. Zavitz, Q. Li et al., ``The nki-rockland sample: a model for accelerating the pace of discovery science in psychiatry," *Frontiers in neuroscience*, vol. 6, p. 152, 2012.

Appendix A Pipeline process