

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

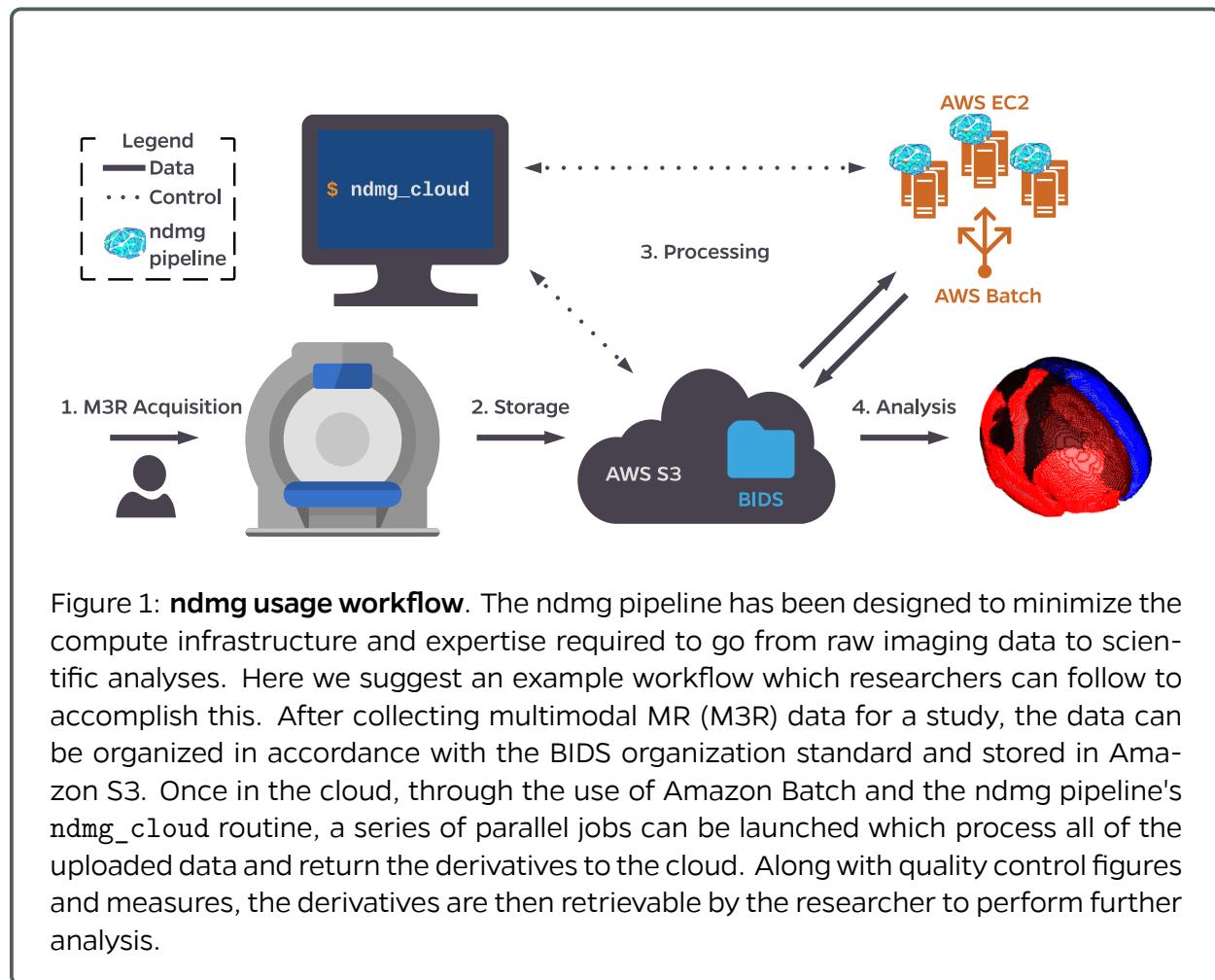
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Abstract

The point of an abstract is kinda abstract...

1 Introduction

2 Methods



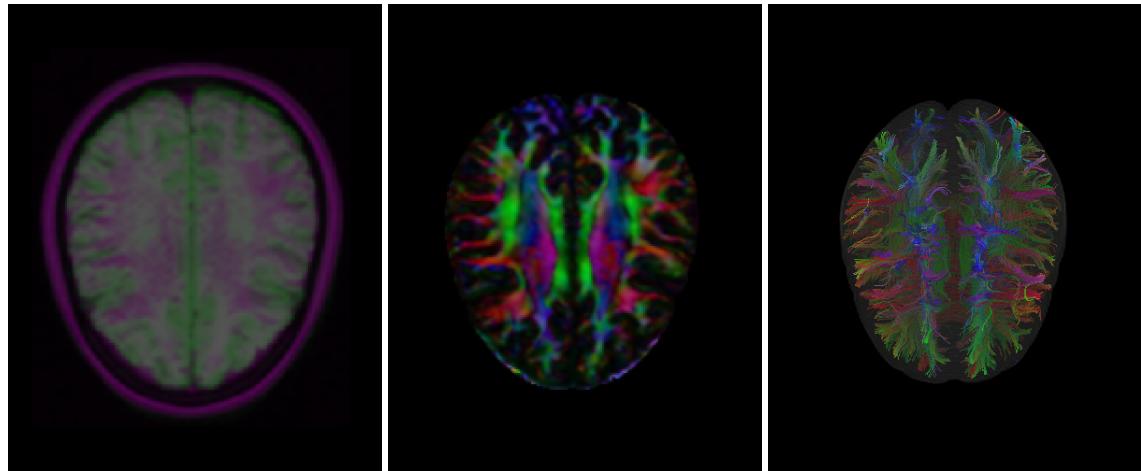


Figure 2: **Intermediate quality assessment outputs from `ndmg`.** Essential when providing a one-click tool was enabling the user to perform their own quality control of the derivatives produced so that they can trust the results. `ndmg` generates registration, tensor, and fiber quality assessment images after each is produced during pipeline operation.

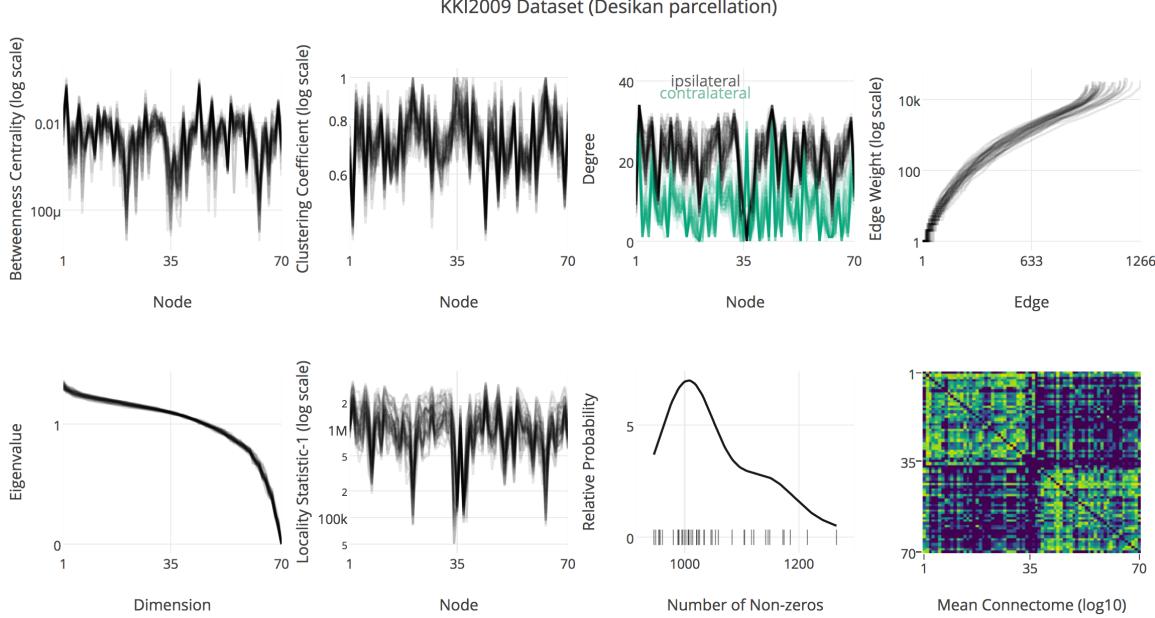


Figure 3: Graph Summary Statistics. Once a collection of sessions is processed through ndmg, group analysis can be performed which plots several summary statistics of the graphs. These features are, clockwise from top left: betweenness centrality, clustering coefficient, hemisphere-separated degree sequence, 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

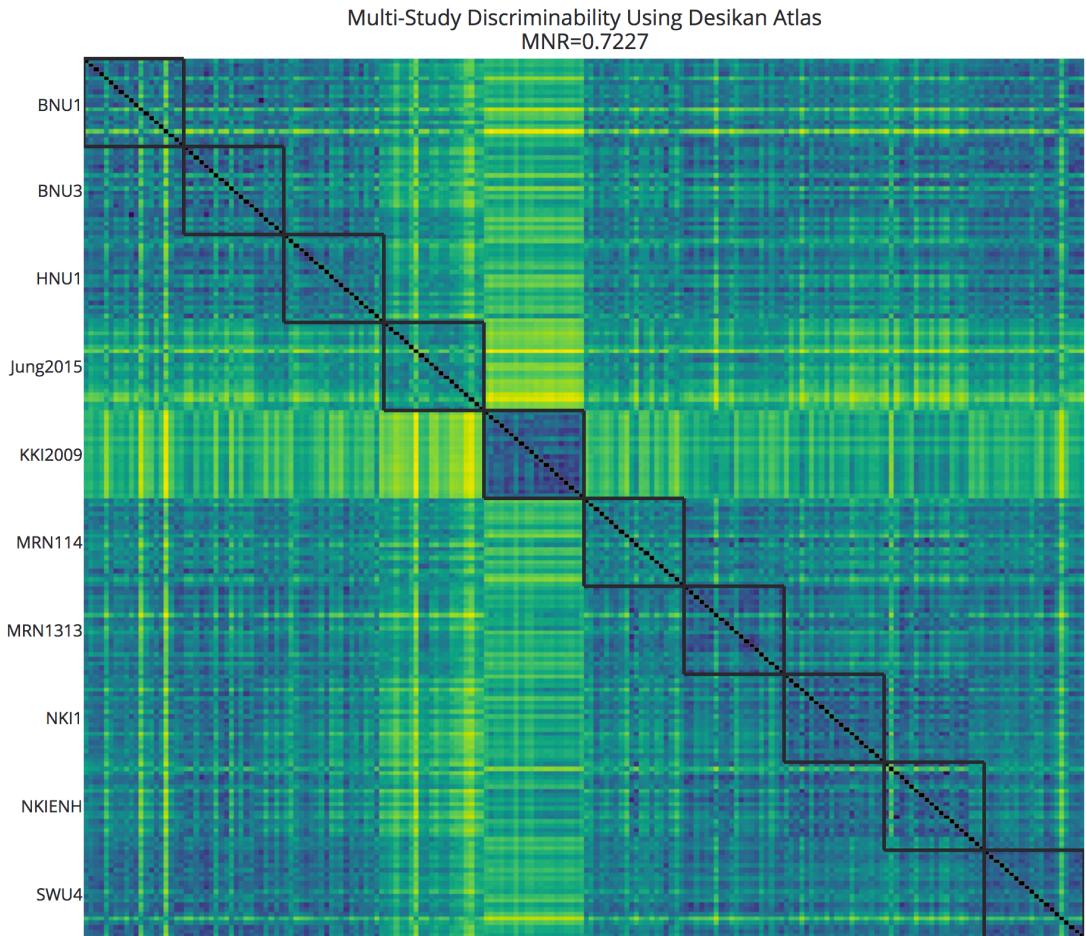
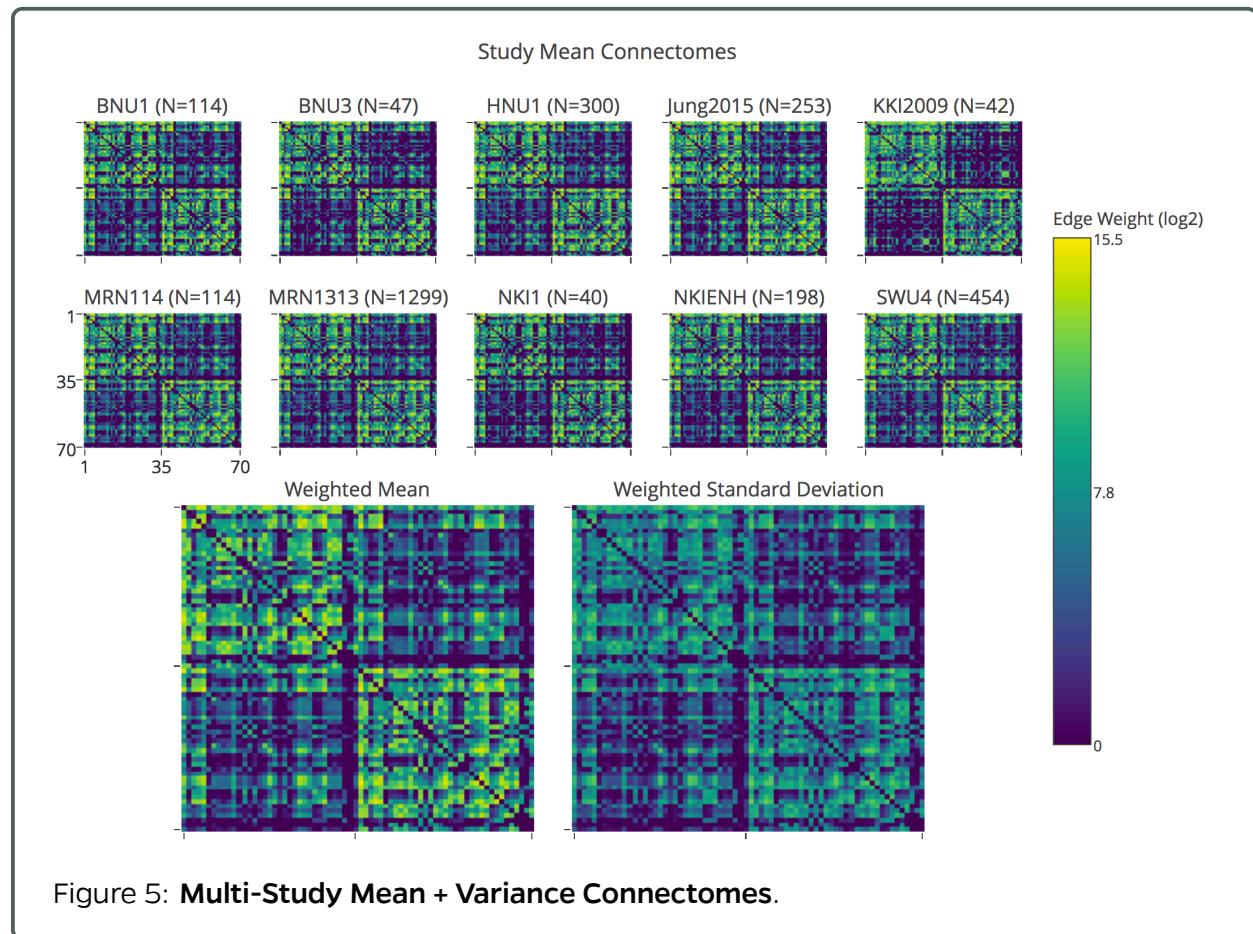


Figure 4: Multi-Study Reliability. Processing test-retest datasets with the ndmg pipeline allows us to evaluate the performance through a metric called discriminability. Discriminability computes the distance between all pairs of observations in the dataset, ranks the distances, and reports the mean of the normalized rank distribution (MNR) which summarizes the probability that graphs from the same subject are more similar to each other than any other graph. We compute this metric on an aggregate of several datasets from different centres and studies. It can be seen that the pipeline has a near perfect discriminability without any outlier removal or data pruning, indicating that ndmg recovers subject-specific signal in the graphs produced.



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

