



Optimising the individual functional connectome for neurodevelopmental and psychiatric disorders

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1. Introduction

- Functional connectivity (FC) measures are largely reproducible across brain states, populations and non-human species. However, the lack of reproducible and reliable FC measures poses a particular challenge to facilitate early biomarker discovery.
- We focused on connectome fingerprinting to identify an individual based on his/her FC profile as an alternative approach to improve the FC reliability and reproducibility in developing populations.

Research Questions

- Which factors influence the reproducibility and reliability of the individual functional connectome?
- Can we optimise the connectome fingerprinting and maximise our ability to detect robust and reliable biomarkers in neurodevelopmental conditions?

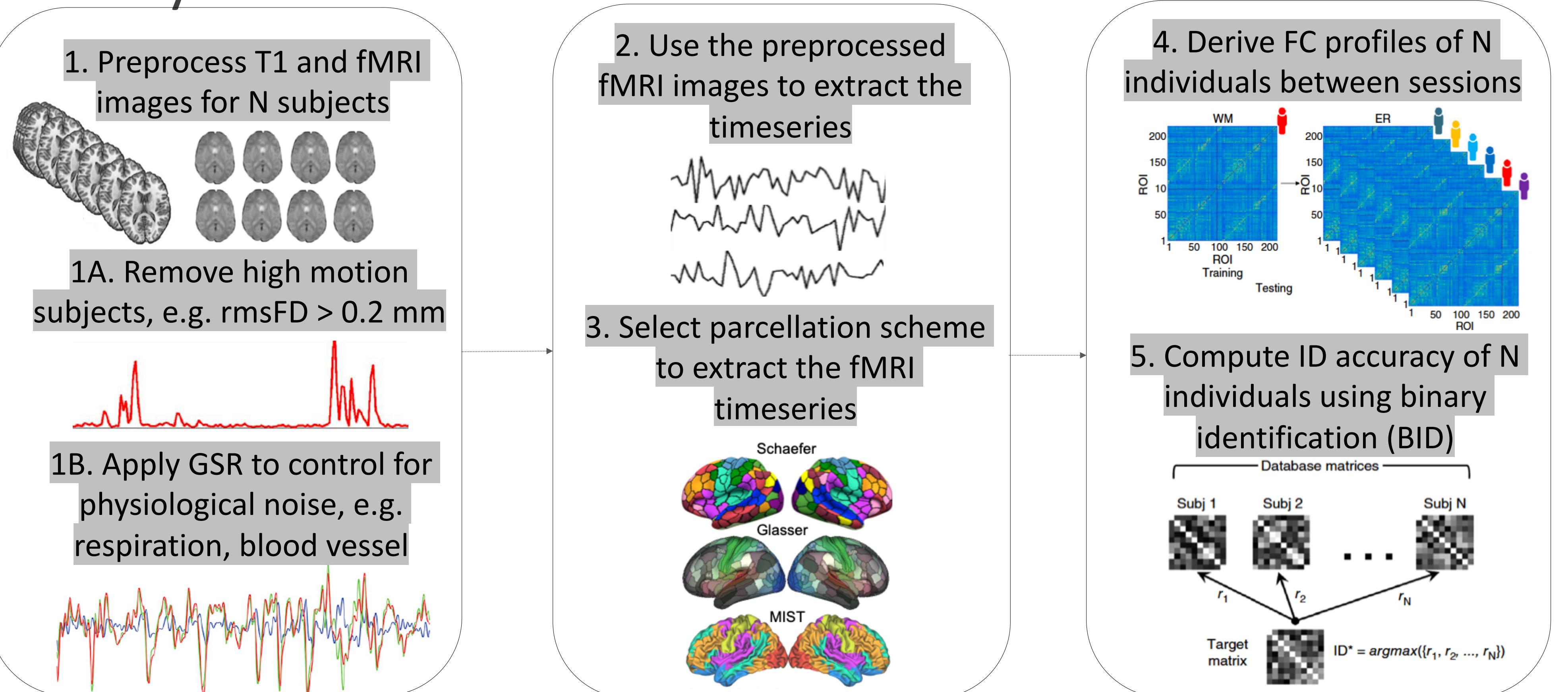
2. Methods

- Five independent fMRI datasets have been obtained from the Consortium for Replicability and Reproducibility (CoRR) to capture children to adulthood including developing populations.

Dataset	Sample Size	Age (Range)	Gender	Scan Duration	Scanner Manufacturer	Field Strength	TR (ms)
NYU _{adu}	31	18-43	M:16 F:15	06:00	Siemens	3.0T	2000
NYU _{ado}	25	7-18	M:15 F:10	06:00	Siemens	3.0T	2000
BNU	60	19-23	M:32 F:28	08:06	Siemens	3.0T	2000
SWU	82	17-27	M:33 F:49	08:06	Siemens	3.0T	2000
UPSM	67	10-19	M:34 F:33	05:06	Siemens	3.0T	1500

- Structural and functional MRI images between two imaging sessions were preprocessed as follows: motion correction, grand-mean scaling, detrending, nuisance signal regression (i.e. motion; WM/CSF; global signal regression (GSR)), spatial smoothing and temporal filtering (0.009-0.1Hz).
- Functional-to-session-average MRI co-registration and standard space transformation were performed. We excluded high motion participants with root-mean-square framewise displacement (rmsFD > 0.2 mm) in either imaging session.

3. Analysis



*ID accuracy is calculated using BID (i.e. if an individual is correctly identified, then ID = 1, otherwise 0) and relative rank (RR; the fewer individuals being inaccurately ranked above their true ID, the lower the degree of confusion and lower the RR. Lower RR indicates higher ID accuracy. RR is a continuous measure which ranges from 0 to 1).

4. Results

I. In-Scanner Motion & Temporal signal-to-noise ratio (tSNR)

- Motion reduces ID accuracy across all datasets and yields significant associations between rmsFD and RR. When high motion subjects are excluded, the ID accuracy increases and there is no associations between motion and RR that achieved statistical significance.
- Only the USPM dataset showed a significant relationship between tSNR and RR ($r = -0.35, p = 0.0068$), suggesting potential developmental characteristics capturing stronger signal intensity (or lower signal variance).

II. Global Signal Regression (GSR)

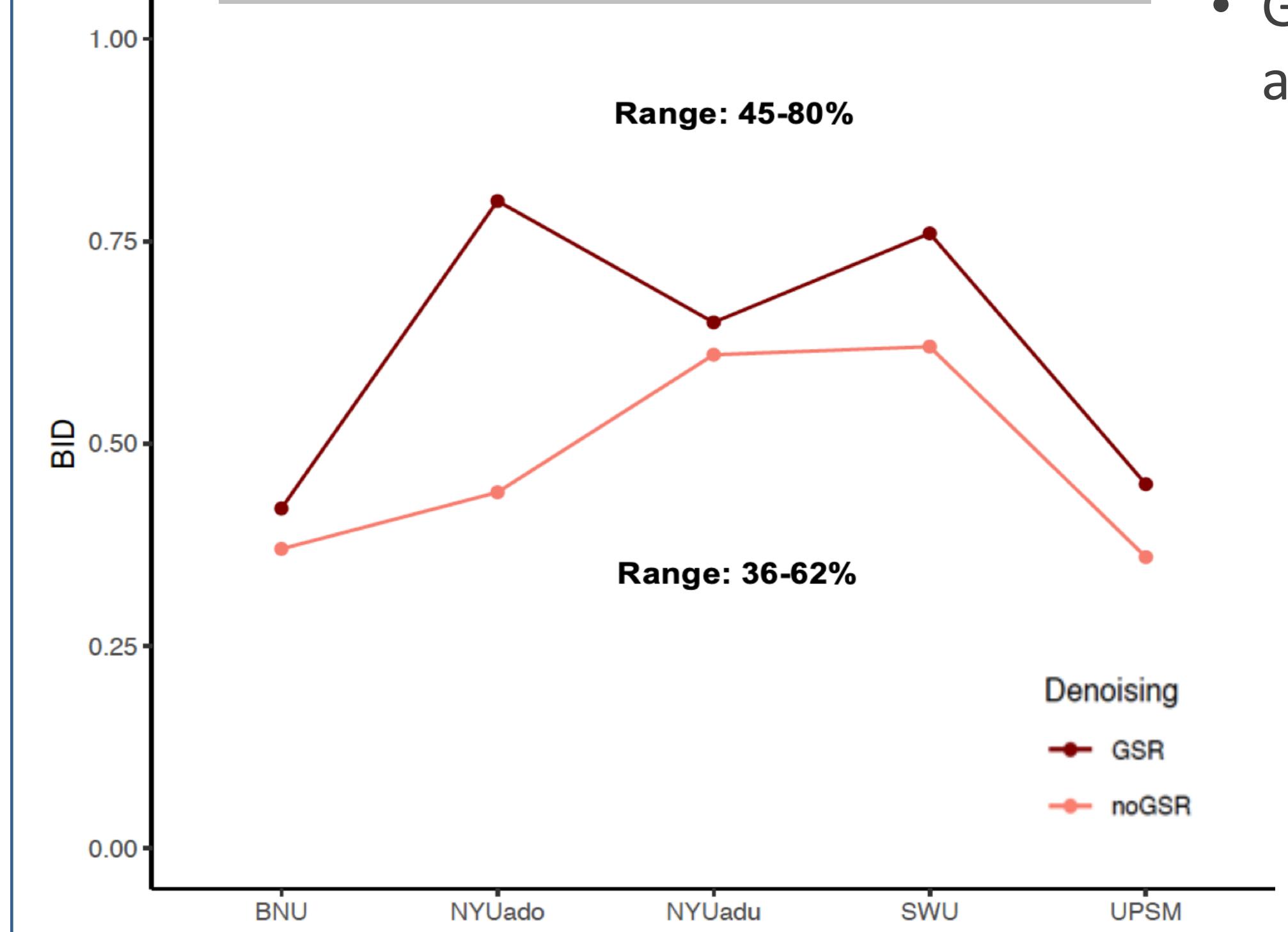


Figure 1. Effects of GSR on ID accuracy derived from BID across the 5 independent datasets using the Shen 268 parcellation scheme.

- GSR improves the ID accuracy and this effect is reproducible across all datasets.

III. Parcellation Schemes

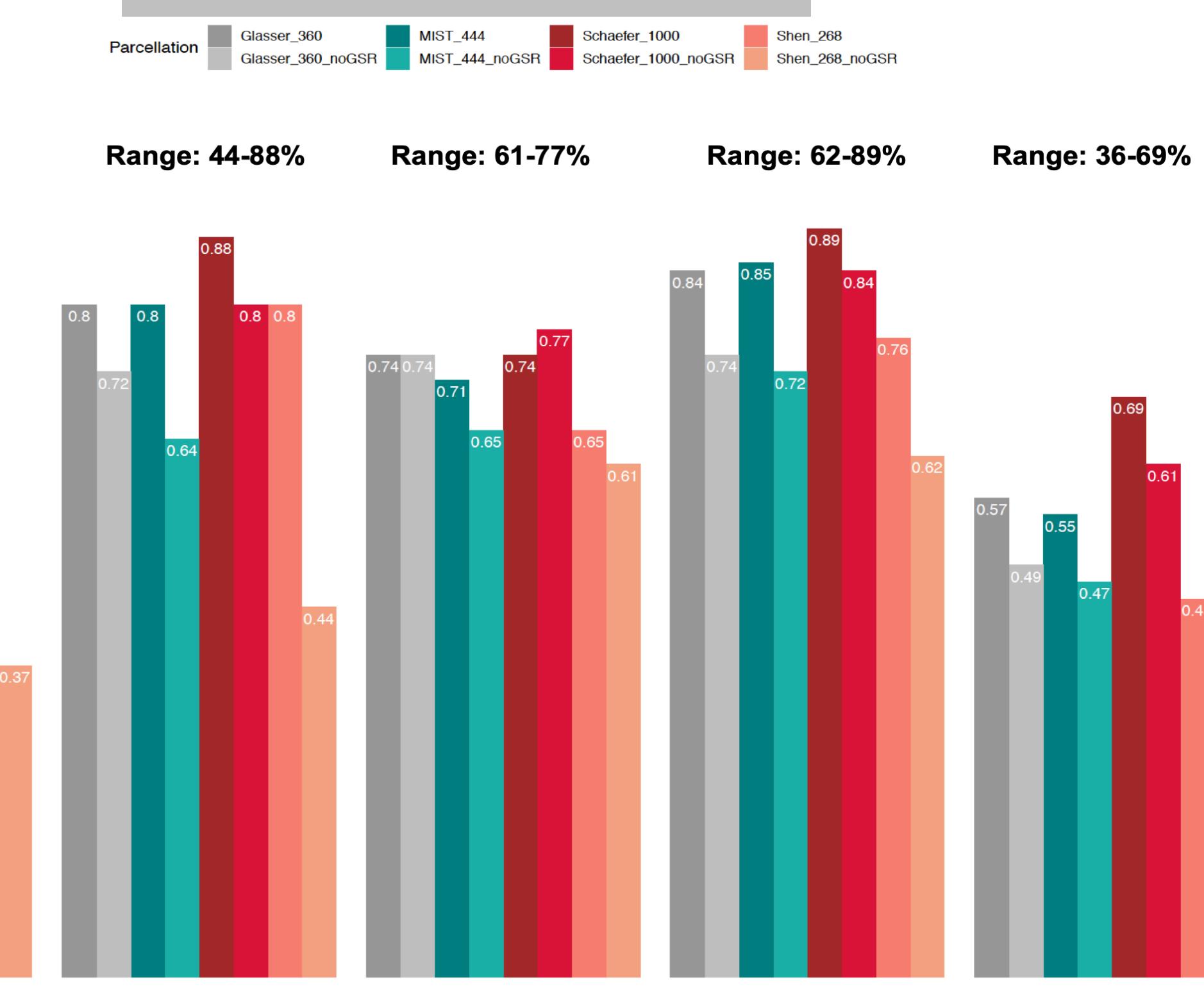


Figure 2. ID accuracy derived from BID across the 5 datasets. The bars show BID values obtained using 4 parcellation schemes such as Shen 268, Glasser 360, MIST 444 and Schaefer 1000-17Networks with and without GSR.

- Parcellation schemes vary the ranges of ID accuracy with higher ID accuracy obtained with higher parcel size. GSR exhibits stronger ID accuracy at higher parcel resolutions.

IV. Parcel Resolution (with GSR)

- There is an exponential relationship between parcel resolution and ID accuracy. Parcel resolution explains 77-98% of the variance in ID accuracy with GSR.
- The exponential relationship persists without GSR and parcel resolution explains 89-99% of variance in ID accuracy.

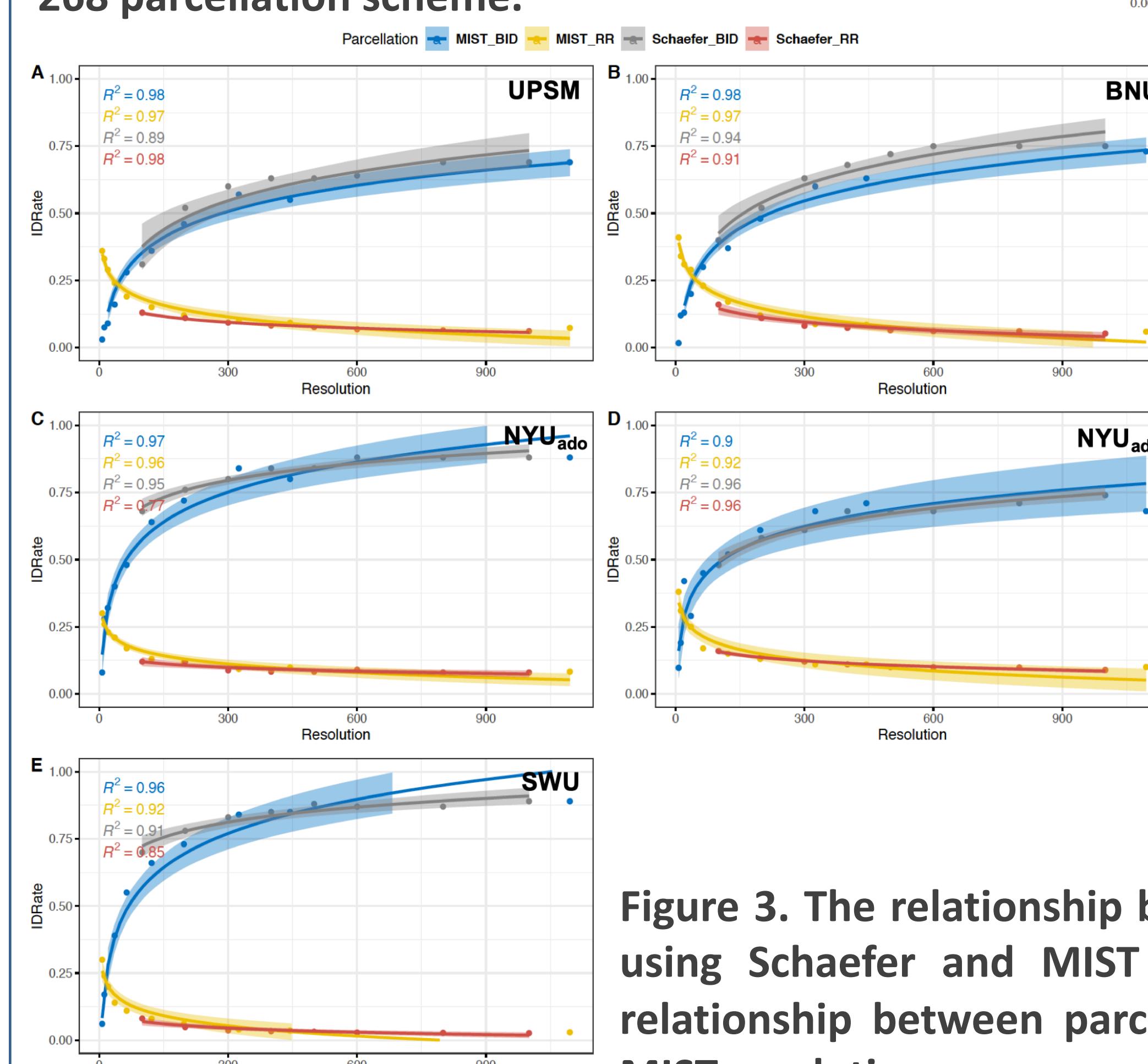


Figure 3. The relationship between parcel resolution and ID accuracy in the 5 datasets obtained using Schaefer and MIST multi-resolution parcellations with GSR. There is an exponential relationship between parcel resolution and ID accuracy across 8 Schaefer resolutions and 10 MIST resolutions.

5. Conclusions

- The functional connectome can be treated as a “fingerprint”.
- GSR, parcellation schemes and their resolutions improve the reliability of the individual functional connectome.
- These factors delineate an optimal FC pipeline to detect sensitive and reliable biomarkers in neurodevelopment.

6. References

- Finn, E. (2015). ‘Functional connectome fingerprinting: identifying individuals using patterns of brain connectivity’, *Nature Neuroscience*, **18**, no. 11, pp.1664-1671; Jalbrzikowski, M. (2019). ‘Cognitive and default mode networks support developmental stability in functional connectome fingerprinting through adolescence’, *bioRxiv* 812719; Noble, S. (2019). ‘A decade of test-retest reliability of functional connectivity: A systematic review and meta-analysis’, *Neuroimage*, **203**, pp. 116157; Zuo, X. (2014). ‘An open science resource for establishing reliability and reproducibility in functional connectomics’, *Scientific Data*, **1**, pp. 140049.