



Refining the fingerprints: Optimising connectome fingerprinting for neurodevelopmental applications

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1. Introduction

- Studies using the Intraclass Correlation Coefficient (ICC) show that the *test-retest reliability* of FC measures is moderate, which may explain why biomarker discovery remains a challenge³.
- ICC pits within-subject variance (stability) against between-subject variance (reproducibility), however, and may not represent the best measure for determining how to optimise FC reliability³.
- Connectome fingerprinting* is an alternative approach to investigating FC reliability and determining the factors that influence reliable identification of the individual functional connectome¹⁻².
- Here, our goal is to identify a pipeline that maximises connectome fingerprinting accuracy in developmental populations. The ultimate goal is to leverage this optimised fingerprinting pipeline for the detection of reliable and robust biomarkers of neurodevelopmental conditions.

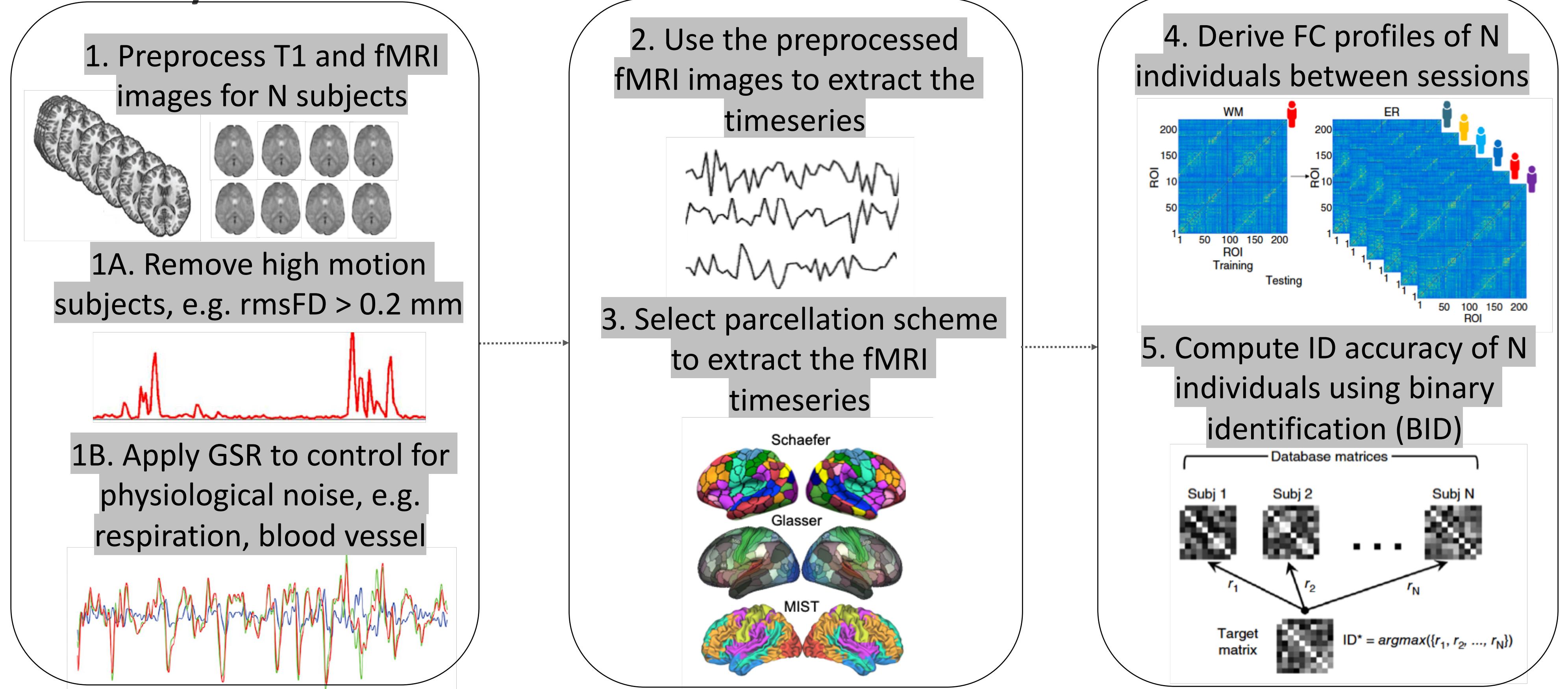
2. Methods

- Five independent fMRI datasets have been obtained from the Consortium for Replicability and Reproducibility (CoRR), spanning children to adulthood⁴.

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 from 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 inaccurately ranked above the true ID, the lower the degree of confusion and lower the RR. Lower RR indicates higher ID accuracy/less confusion. RR is a continuous measure ranging 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 (ID confusion). When high motion subjects are excluded, 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 a role for a developmental influence on SNR (to be investigated). No relationship between age and ID was found.

II. Global Signal Regression (GSR)

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

III. Parcellation Schemes

- ID accuracy varies with parcellation schemes, with higher ID accuracy obtained with higher parcel resolution. GSR boosts ID accuracy even at higher parcel resolutions.

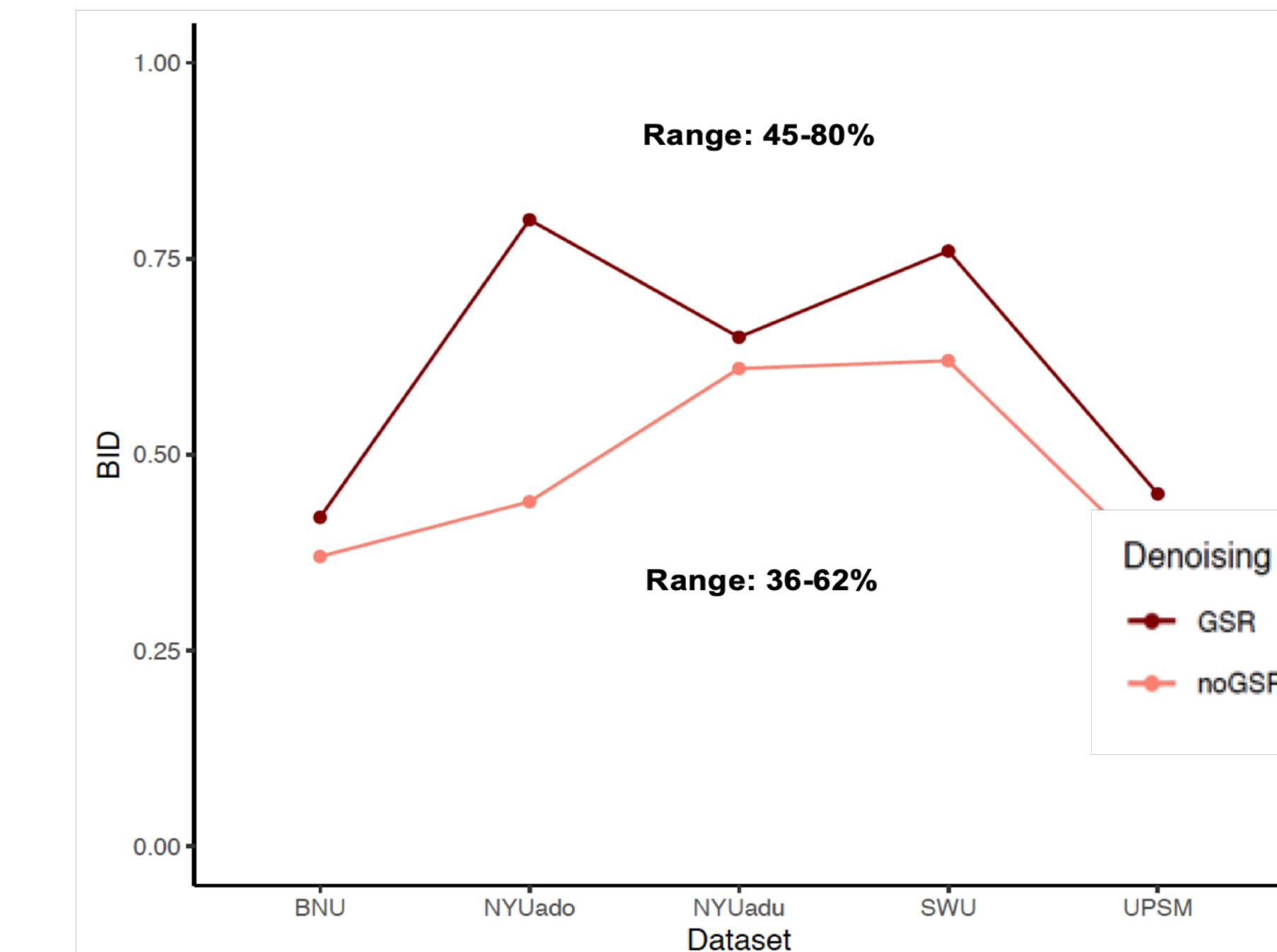


Figure 1. Effects of GSR on ID accuracy derived from BID across the 5 independent datasets using the Shen 268 parcellation scheme.

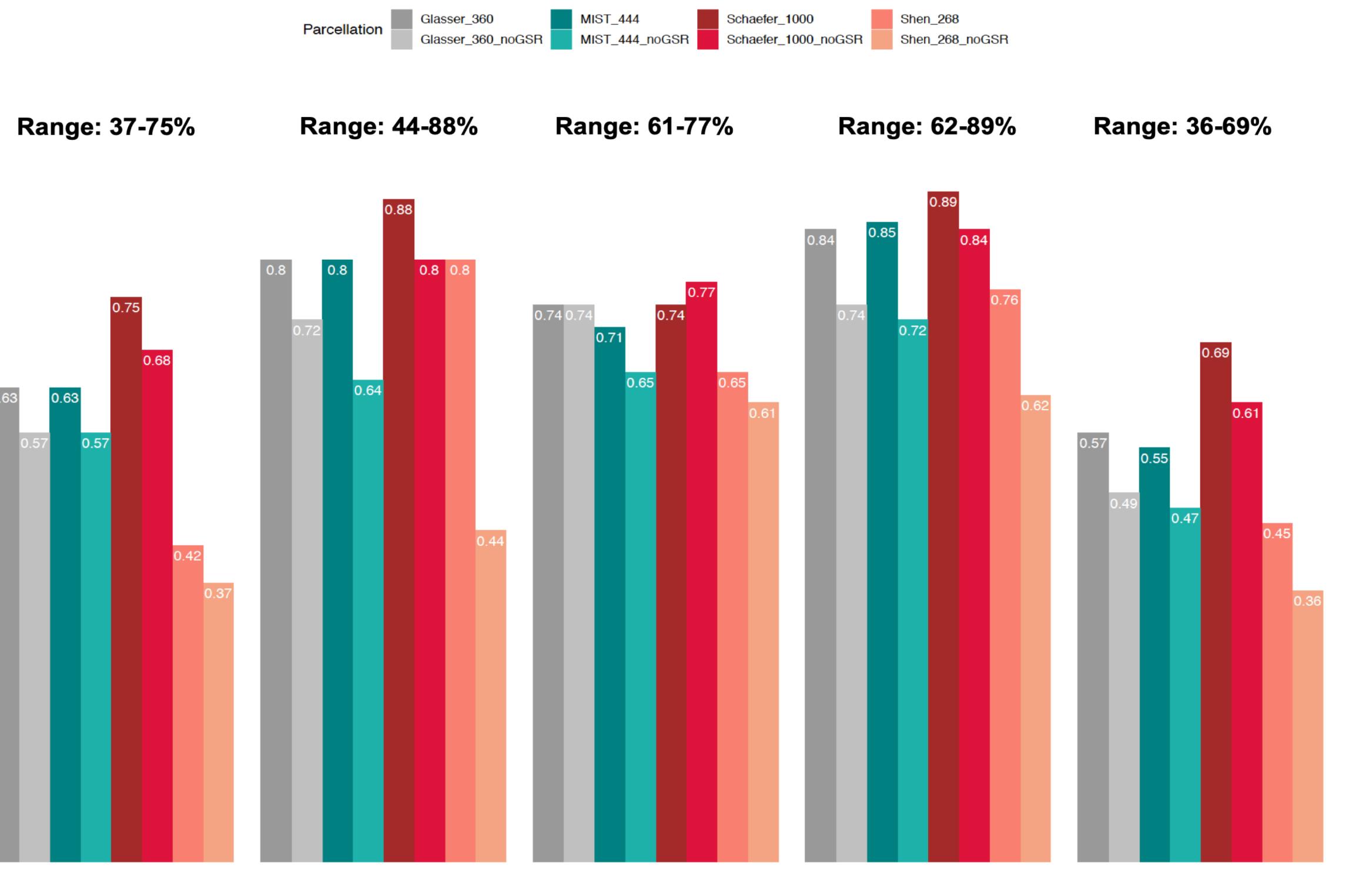


Figure 2. ID accuracy derived from BID across the 5 datasets. The bars show BID values obtained using 4 parcellation schemes such as Shen 268, Glasser 360, MIST 444 and Schaefer 1000-17Networks with/without GSR.

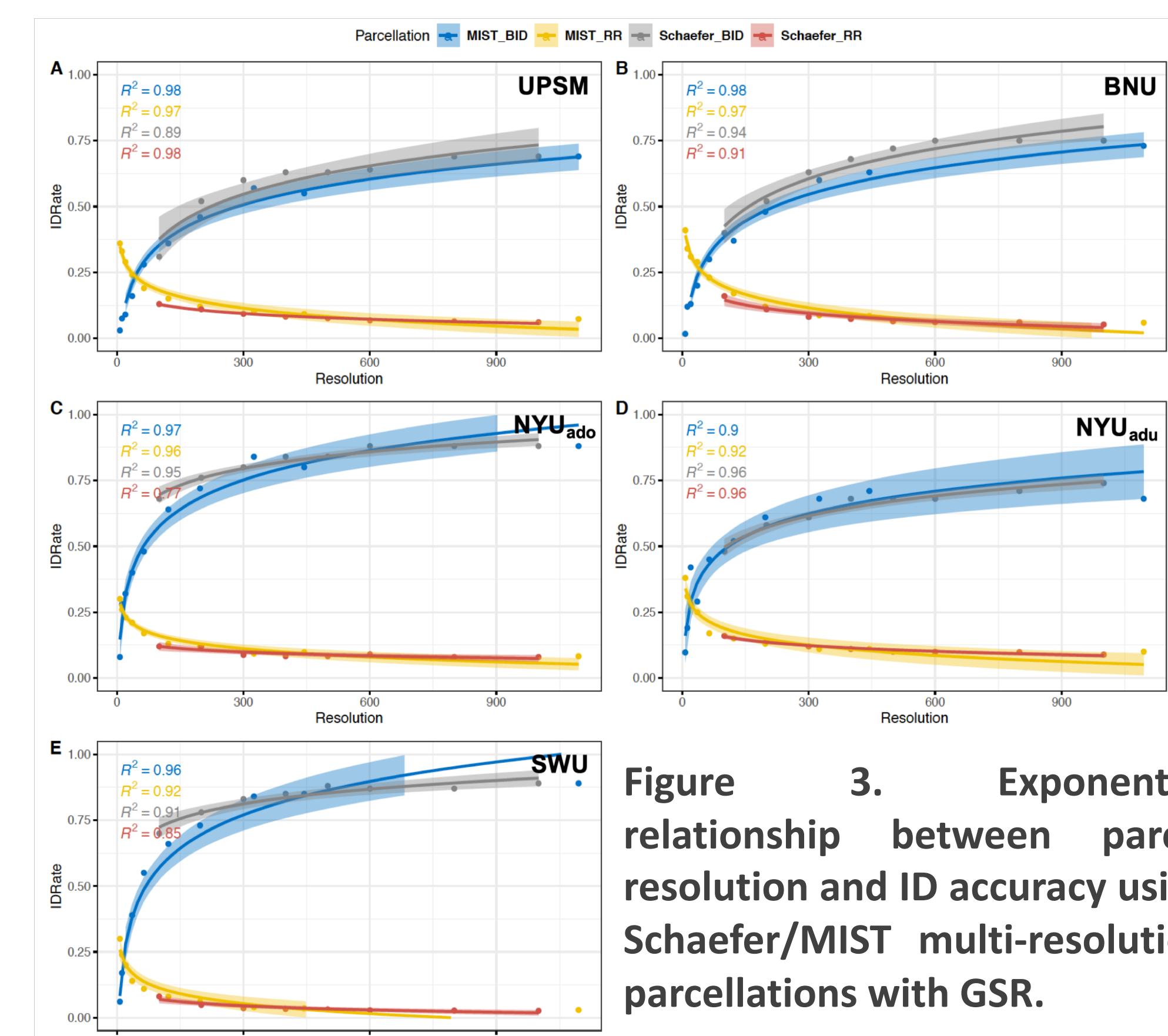


Figure 3. Exponential relationship between parcel resolution and ID accuracy using Schaefer/MIST multi-resolution parcellations with GSR.

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.

5. Conclusions

- GSR and higher parcellation resolutions improve the reliability of the individual functional connectome in developing and non-developing populations. These factors help delineate an optimal FC pipeline for reliable fingerprint ID. Further work will seek to maximize ID, to provide a robust basis for biomarker discovery.

6. References

- Finn, E. (2015). 'Functional connectome fingerprinting: identifying individuals using patterns of brain connectivity', *Nature Neuroscience*, vol. 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*, vol. 203, pp. 116157;
- Zuo, X. (2014). 'An open science resource for establishing reliability and reproducibility in functional connectomics', *Scientific Data*, vol. 1, pp. 140049.