Poster 3960

Functional Stability of the Human Connectome Project Parcellation

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Introduction

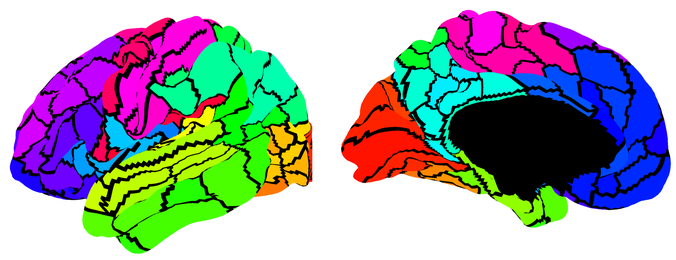
Concerns have recently emerged, when several studies concluded that current rs-fMRI scans are probably not long enough for a good estimation of functional connectivity [6]. The data released by the **Human Connectome Project** (HCP) [1,2] offer an excellent opportunity to investigate this issue. Several studies have already been conducted with the HCP for estimating the time required for a correlation estimation to converge, but the stability of functional parcellations derived from these correlations has not yet been investigated.

In this work, we establish a baseline for the stability of Glasser et al. multimodal HCP parcellation (P360) [3] over the rs-fMRI scans of the hundred unrelated HCP subjects by measuring, with two families of adjusted Rand Index (aRI) [4] estimators, the similarity between segmentations generated by adapting the P360 for fitting random rs-fMRI volumes samplings. We selected an aRI estimator associated with a speedup close to ten, which allowed us to run dozens of millions of parcellation comparisons. Our results suggest that P360 functional stability is moderate without spatial smoothing and improves with scan duration. Individual HCP scans are not long enough for observing a plateau. This result is in agreement with [6].

Methods

for the Human Connectome Project

- parcellation stability measured by comparing parcellations generated from random rs-fMRI scans subsamplings.
- **adjusted Rand Index** (aRI) is used for the comparison, but computational burden needs to be reduced for large number of comparisons
- two approaches for speeding up aRI computation are investigated: **subsampling** and **Locality Sensitive Hashing** (LSH)
- the estimator associated with the best tradeoff is used for establishing HCP parcellation functional stability



multimodal HCP parcellation [3] (left hemisphere)

Data

- minimally processed 100 unrelated HCP subjects [1,2] (MSMall and ICA+FIX denoising)
- bandpass filtering (0.05-0.1 Hz)
- global signal regression

finally

- 4 scans per subject, 1001 volumes per scan

Base Parcellation

Glasser et al. multimodal parcellation [3]

- 180 parcels per hemisphere
- 59412 cortical nodes

Random Parcellations

- random subset of timepoints
- computation of avg. signal for each parcel
- cortical nodes assigned to the most correlated parcel (restriction to neighboring parcels)

adjusted Rand Index (aRI) for Parcellations Comparisons

computed from the mismatch matrix $\mathbf{m}$ between two parcellations X and Y. $\mathbf{m}$ measures the overlap between the parcels of X and Y

$$aRI = \frac{\sum_{k,l}\binom{m_{k,l}}{2} - \left[\sum_k \binom{a_k}{2}\sum_l \binom{b_l}{2}\right]/\binom{N}{2}}{\frac{1}{2}\left[\sum_k \binom{a_k}{2} + \sum_l \binom{b_l}{2}\right] - \left[\sum_k \binom{a_k}{2}\sum_l \binom{b_l}{2}\right]/\binom{N}{2}}$$

where $a_k = \sum_l m_{k,l}$ and $b_y = \sum_k m_{k,l}$

Subsampling

the aRI was estimated for a random subsample of cortical nodes

Locality Sensitive Hashing (LSH)

LSH often used to accelerate the computation of overlap measures, such as Jaccard Coefficient [5]. Extended here for the aRI as follows:

- random sequences of pairs of cortical nodes, measured as concordant (same parcel) or discordant (different parcel) and LSH used to hash this information
- RI estimated as the overlap between two parcellations concordant pairs
- standard aRI adjustment for chance (very fast)

aRI Estimators Validation

- one random sampling per scan retained for measuring or estimating the aRI
- 5 random samplings tested, retaining 100, 250,500,750 or 900 rs-fMRI volumes

HCP Parcellation Stability

- 10 parcellations generated for each subject and scan ; $\binom{4000}{2}$ comparisons total
- parcellation smoothing via nearest neighbor majority voting

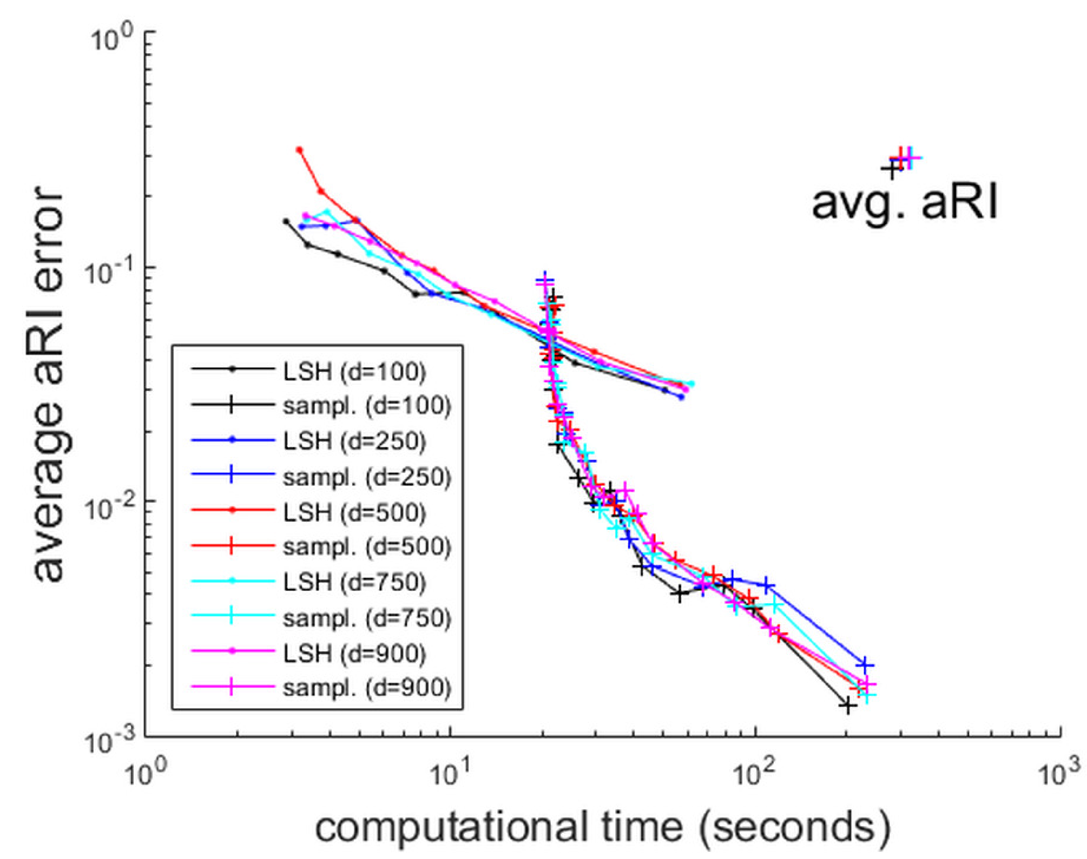


Figure 1. Average estimation error and computational time required for comparing 400 random parcellations, for the five samplings tested keeping respectively 100,250,500,750 or 900 volumes and the two families of estimators, based on LSH[5] and parcellation down sampling (sampl.). Average exact aRI and their computational time are reported for comparison.

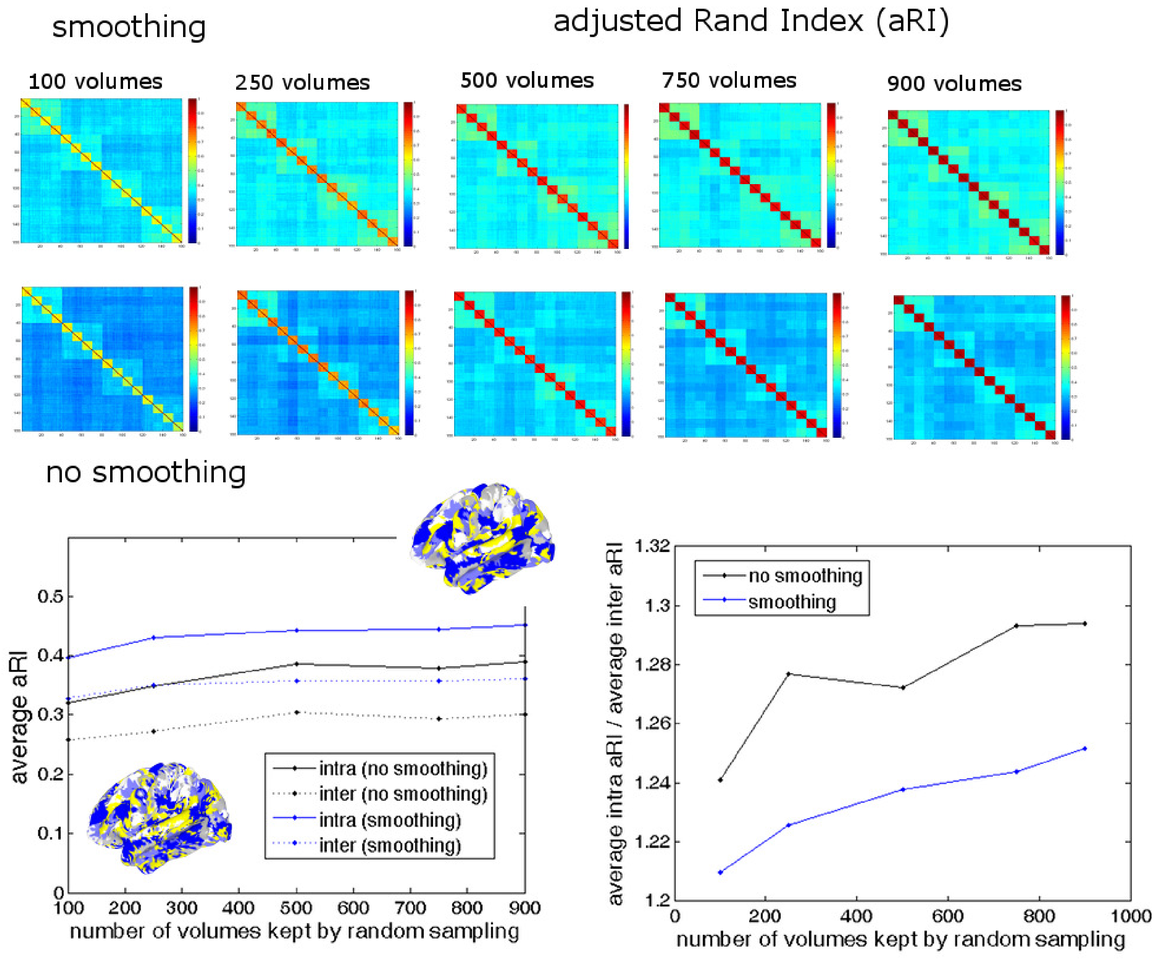


Figure 2. Top: aRI estimated for all samplings when comparing four subjects parcellations, with or without parcellation smoothing. Bottom left: improvement of average intra-subject inter-scan aRI (intra) and inter subject aRI (inter), with and without smoothing, with respect to the number of volumes kept by the random samplings. Bottom right: ratio between intra subject and inter subject aRI. Higher ratios indicate that individual parcellation features are better preserved.

Results

aRI Estimators

- LSH estimator can run faster, but the error is too large for the HCP parcellation
- better tradeoff between speed and error for subsampling (despite limited speedup)
- parcellations downsampling by 50 was selected ($\approx$ 10 times faster, avg. error 1%)

HCP Parcellation Stability

- intra-subject similarity always improves with scan duration and always improves faster than inter-subject similarity
- smoothing significantly improved intra-subject similarity (by 5.7% to 8.1%, p-value$< 10^{-100}$ for all paired T-test)
- parcellation stability plateau was not reached during our experiments

Conclusion

- validation of two aRI estimators. These estimators will speed up the comparison of parcellation methods [7,8]
- we establish baseline parcellation stability for the HCP dataset, that advanced parcellation methods should improve.
- individual HCP scans are too short to observe a convergence
- naive parcellation has a limited stability (aRI below 0.5, even with smoothing) $\Rightarrow$ room for advanced parcellation methods

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