

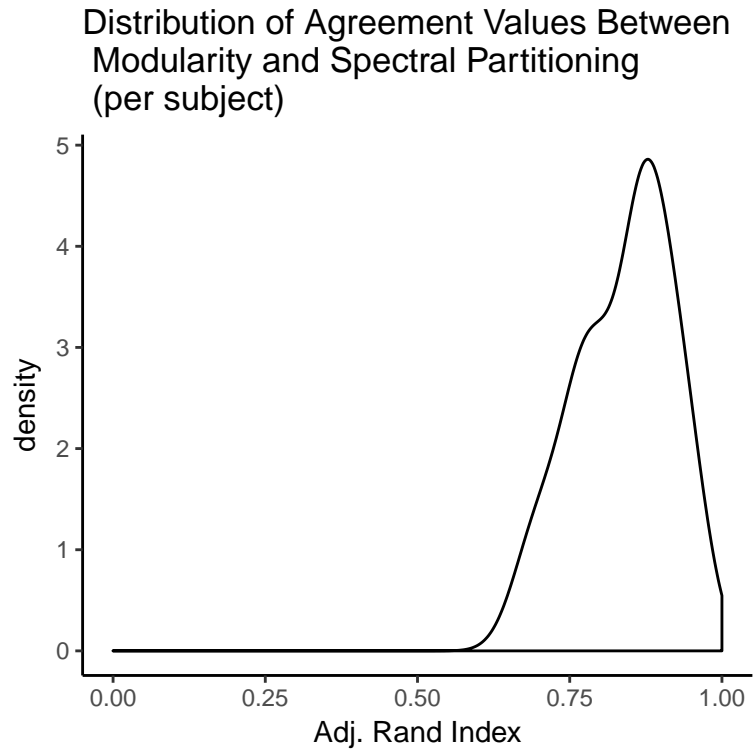
Community_analysis

CTS

7/2/2018

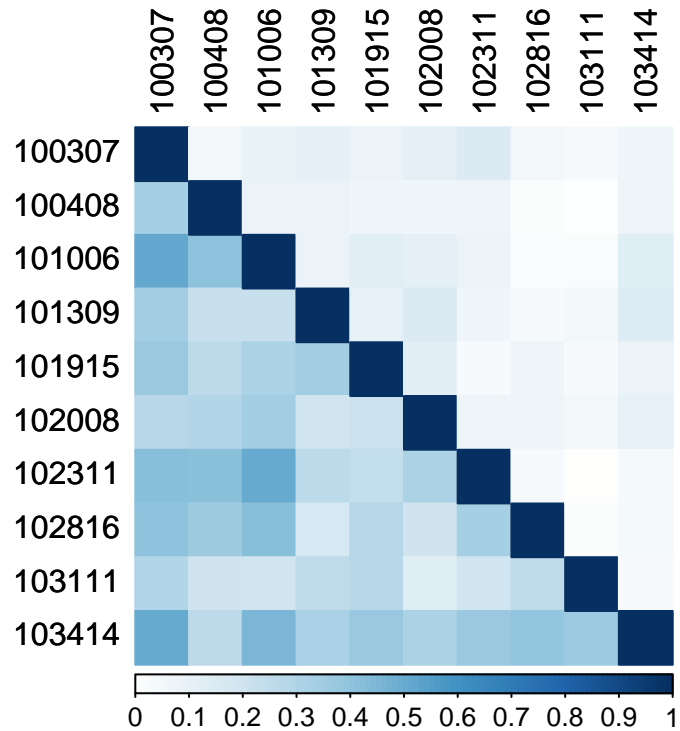
Partition Comparison: All

This just gives an idea of the level of agreement within and between subjects. The first plot shows how well (in approx %) do modularity and spectral partitioning agree in parsing PCC and mPFC.



The second shows every pairwise comparison among all subjects for PCC (lower) and PFC (upper) separately.

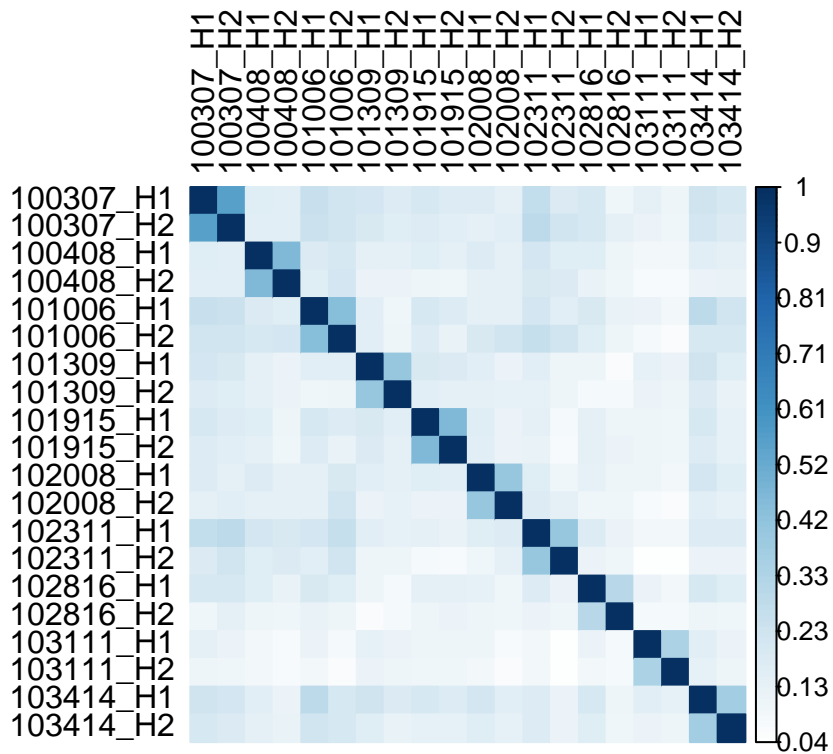
RI-based Agreement of Communities Among Every Pair of Subjects (PCC and PFC)



Partition Comparison: Halves

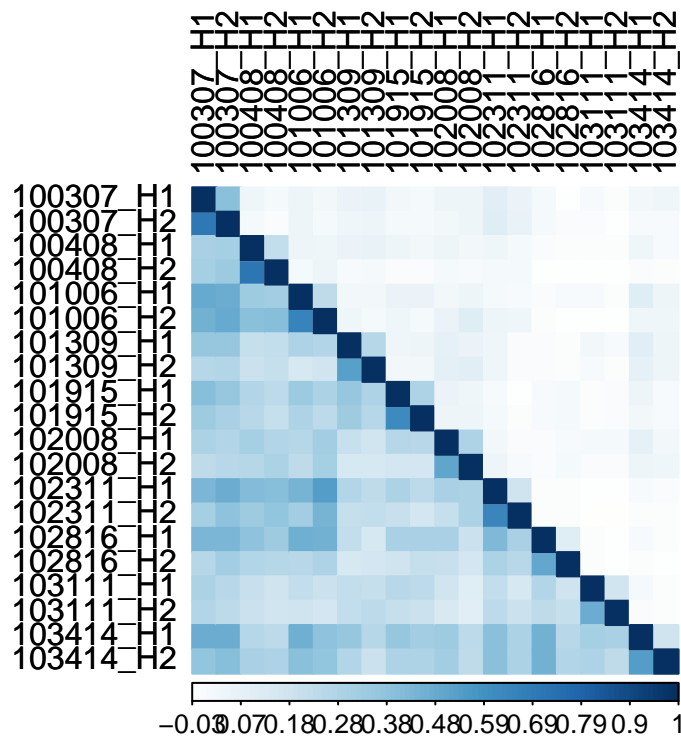
HCP resting state data is separated into 4 runs (2 per day of scanning). This section shows how much agreement there is between partitions taken on each day. The first similarity matrix shows the pairwise level of agreement for the overall data among all subjects.

RI-based Agreement Between Day 1 and Day 2 (Overall)



The second divides this data into PCC and mPFC.

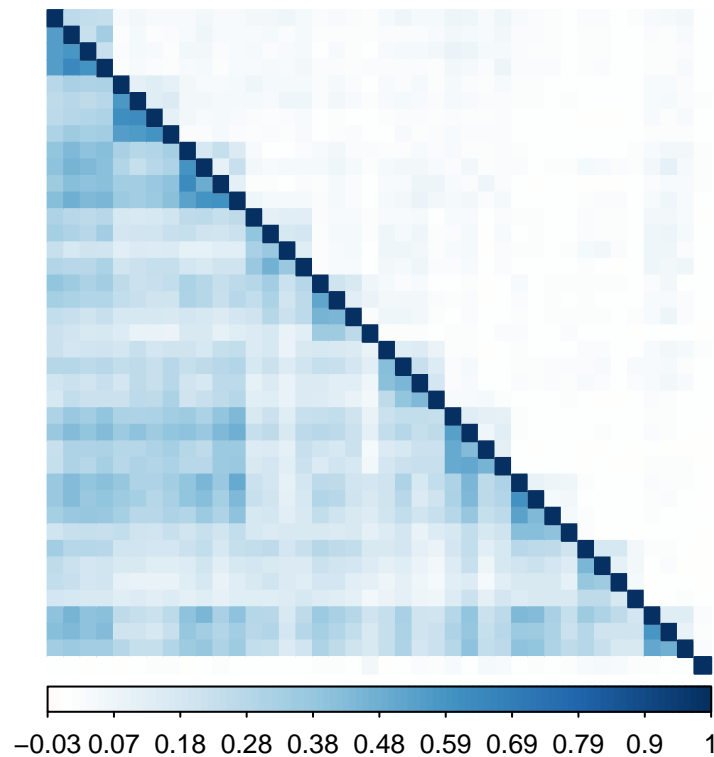
RI-based Agreement Between Day 1 and Day 2: PCC and mPFC



Partition Comparison: Session

Next, each session is evaluated independently. The similarity matrix shows how each session data corresponded within and between subjects for PCC and mPFC separately.

RI Values for PCC and PFC across rsfMRI Sessions



```
##
## Call:
## glm(formula = tempY ~ ., family = "quasibinomial", data = coeffList)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -0.80199  -0.06653   0.00009   0.06392   0.41418
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  5.638428   0.704682   8.001 4.68e-15 ***
## `100307_H1`  0.334117   0.074326   4.495 8.05e-06 ***
## `100307_H2`  0.299024   0.074326   4.023 6.33e-05 ***
## `100408_H1`  0.193402   0.077787   2.486 0.013125 *
## `100408_H2`  0.089628   0.077787   1.152 0.249602
## `101006_H1`  0.174120   0.075987   2.291 0.022214 *
## `101006_H2`  0.202473   0.075987   2.665 0.007875 **
## `101309_H1`  0.050310   0.082053   0.613 0.539972
## `101309_H2` -0.103119   0.082053  -1.257 0.209242
## `101915_H1`  0.127236   0.084462   1.506 0.132376
## `101915_H2` -0.300794   0.084462  -3.561 0.000392 ***
## `102008_H1`  0.025426   0.082791   0.307 0.758846
## `102008_H2` -0.112877   0.082791  -1.363 0.173165
```

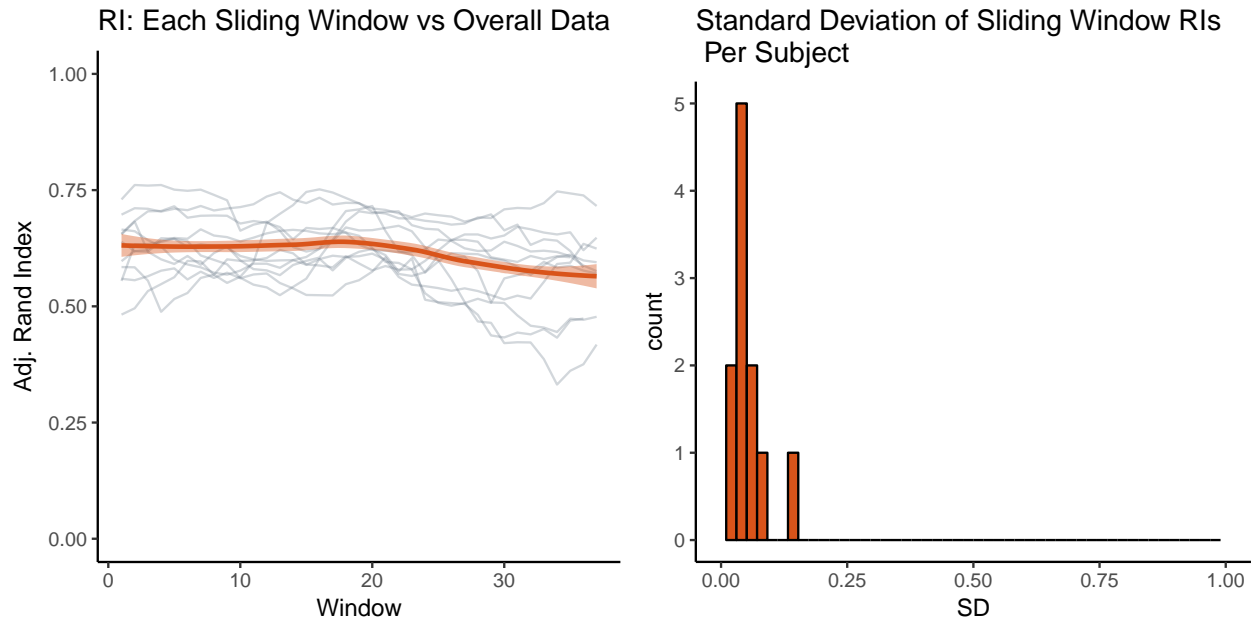
```

## `102311_H1` 0.158890 0.081196 1.957 0.050734 .
## `102311_H2` -0.185457 0.081196 -2.284 0.022647 *
## `102816_H1` 0.024037 0.085776 0.280 0.779375
## `102816_H2` -0.312060 0.085776 -3.638 0.000294 ***
## `103111_H1` -0.009699 0.091002 -0.107 0.915147
## `103111_H2` -0.416542 0.091002 -4.577 5.51e-06 ***
## `103414_H1` 0.013571 0.098092 0.138 0.890003
## `103414_H2` -0.839334 0.098092 -8.557 < 2e-16 ***
## `100307` -0.546236 0.068461 -7.979 5.54e-15 ***
## `100408` -0.679966 0.072175 -9.421 < 2e-16 ***
## `101006` -0.471795 0.070255 -6.715 3.71e-11 ***
## `101309` -0.639538 0.076743 -8.333 3.74e-16 ***
## `101915` -0.689643 0.079306 -8.696 < 2e-16 ***
## `102008` -0.676271 0.077528 -8.723 < 2e-16 ***
## `102311` -0.529071 0.075836 -6.977 6.66e-12 ***
## `102816` -0.543337 0.080710 -6.732 3.33e-11 ***
## `103111` -0.922867 0.086220 -10.704 < 2e-16 ***
## `103414` -0.310013 0.093694 -3.309 0.000982 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 0.01461578)
##
## Null deviance: 36.439 on 779 degrees of freedom
## Residual deviance: 12.663 on 749 degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 5

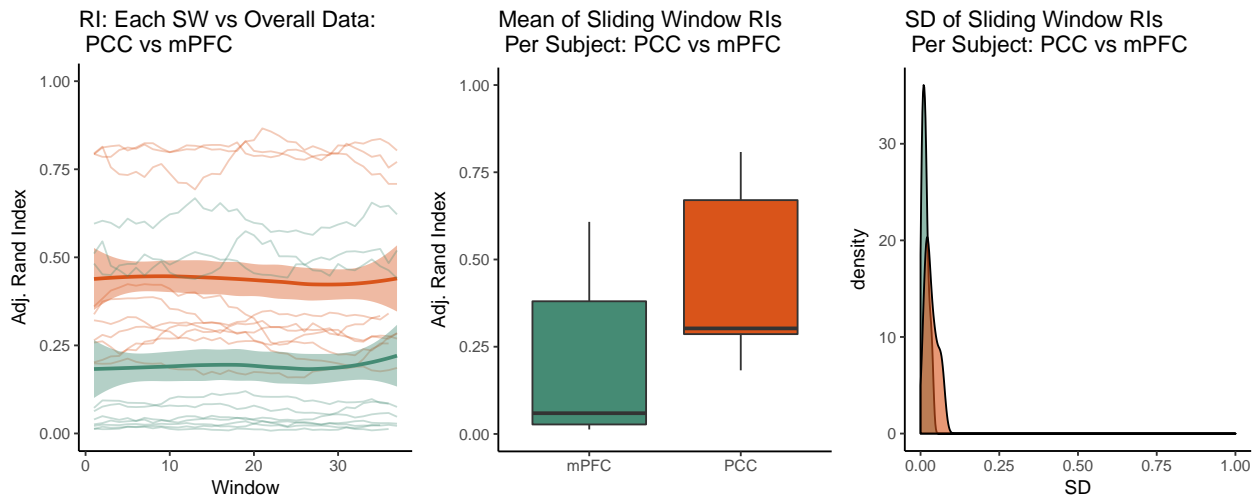
```

Stability per subject

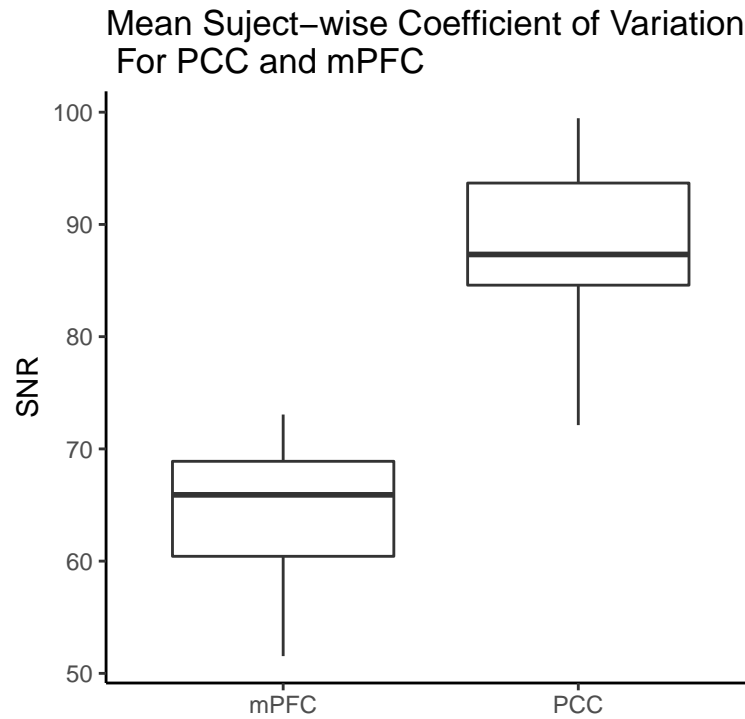
It is also worth considering how stable these measures are, so we performed a sliding window analysis (20 min windows shifting at ~1 min). The first two plots show how well each window's clustering agreed with the partition derived from the whole data, as well as how variable this index was throughout the time series.



The next three show similar data, but for PCC and mPFC separately. The middle plot compares the mean adjusted Rand Index per subject for PCC and mPFC. While mPFC shows an overall significantly lower level of agreement with the overall partition, the variance throughout the time series is small (i.e. stable).



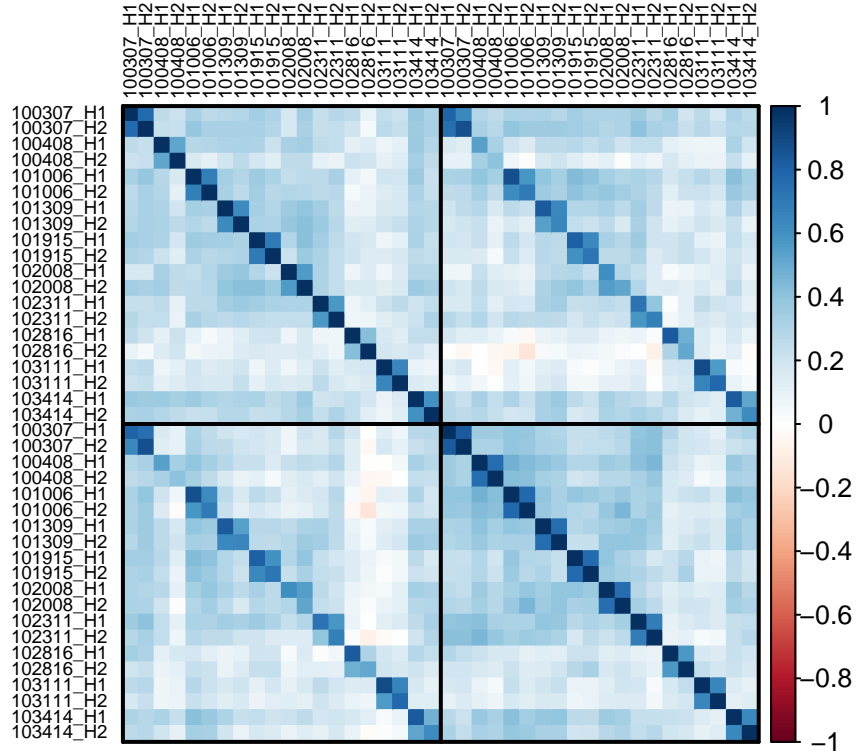
However, the last plot shows that the SNR is lower for mPFC than PCC, which could negatively affect our results.



Correlation vs community detection in mPFC

Finally, it is worth examining what we gain from using graph theoretic approaches over a simple seed-based functional connectivity analysis from PCC. The similarity matrix shows how Day 1 vs Day 2 comparisons for mPFC partitions generated with seed-based correlations (top-left quadrant) vs community detection (bottom-right) across all participants, as well as how much did these methods agree with each other (not much, but enough, which is good).

Comparing All Community and Correlation mPFC Partitions Across All Subjects



The final plot shows the spatial correlation between days for each method across participants. Community detection was significantly more stable across days than a simple correlation, even though mPFC has relatively low signal to noise ratio. Low intra-subject and high inter-subject variability of DMN partitions is in agreement with previous papers (Laumann 2015; Gordon et al., 2017; Braga & Buckner, 2017; Kong... Yeo, 2018). Graph-based community detection might thus be a better way to detect stable functional topologies, since high stability throughout days is a consistent feature of DMN topologies.

mPFC Spatial Correlation Between Day 1 and Day 2
Correlation vs Community Approaches

