Supplementary Materials for

Systematic evaluation of fMRI data-processing pipelines for consistent functional connectomics

Luppi *et al.*

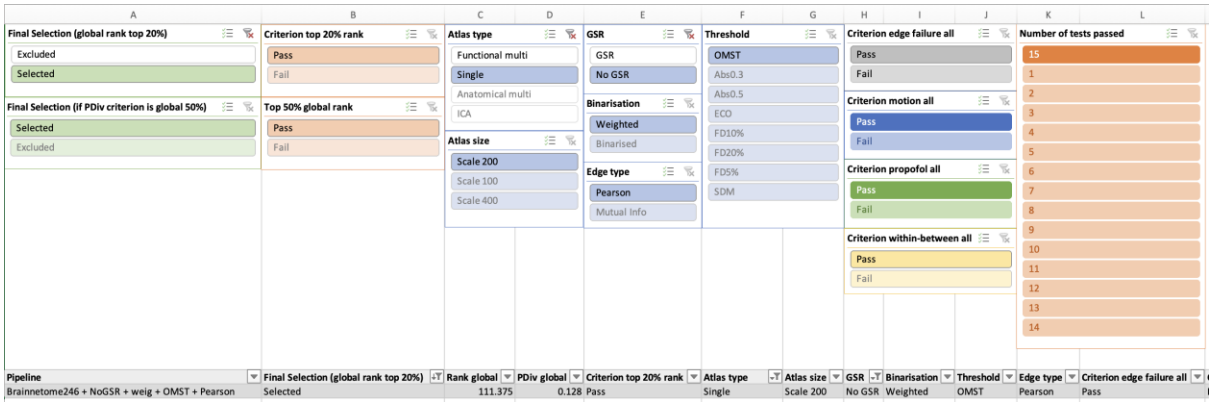
Guide to pipeline selection in the *Pipeline Selection Tool (Supplementary Data 2)*

This document provides a guide for the use of the interactive pipeline selection tool (Supplementary Data 2). The tool is in the form of an Excel file which allows the user to filter pipelines based on specific user-defined criteria. Pipelines can be filtered based on multiple criteria combined to allow the user to specify preferred preconditions for a pipeline choice. The criteria for pipeline selection:

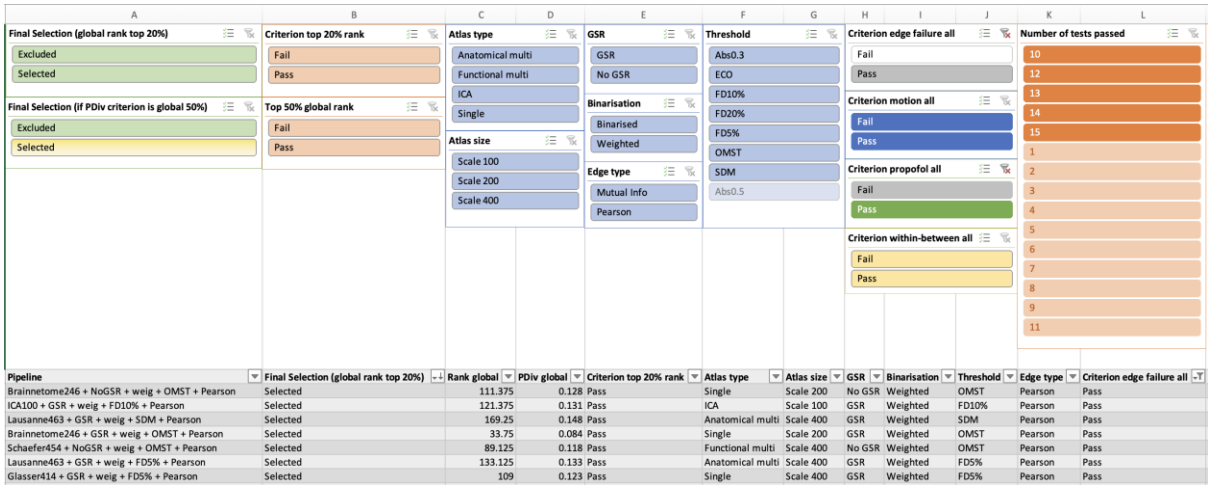
- **Criterion (I):** Avoiding spurious differences ("PDiv ranking"). Since the two networks that we consider are derived from different scans of the same healthy individuals under conditions in which no experimentally meaningful changes in functional network topology are expected, we aim to identify pipelines that minimise test-retest PDiv. We consider pipelines as candidates for optimal if they are in the top 20% in terms of the global PDiv rank calculated across all four test-retest intervals.
- **Criterion (II):** Detecting true experimental differences ("propofol"). Suitable pipelines should detect a significant effect for propofol, in the right direction, in both propofol datasets, i.e., a pipeline is excluded if it fails to detect the expected effect in either of the two propofol datasets.
- **Criterion (III):** Detecting inter-individual differences ("within-between"). A pipeline fails this criterion if the resulting networks are more similar between than within subjects more than 50% of the times, for any of the three test-retest datasets.
- **Criterion (IV):** Avoiding motion-induced differences ("motion"). A pipeline fails this criterion if its PDiv has a significant correlation with differences in head motion in any of the three test-retest datasets.
- **Criterion (V):** Non-empty networks. As a final sanity check, we also exclude any pipelines that remove all connections from a network, in any of the three test-retest datasets.

Column B identifies pipelines that pass all selection criteria (II-V above) and are within the top 20% of average PDiv ranks. The same can be found in Column AX when relaxing the PDiv criterion to 50%. Pipelines that fulfil all of these criteria can be selected by clicking the option "Selected" in the filter.

Combinations of multiple user-defined criteria can be obtained by selecting options in multiple filters at once. For instance, if the user wanted to identify all pipelines which fulfil the above five criteria, used a single scale parcellation type and no global signal regression, this is what the result would look like (showing one pipeline which fulfils these criteria):



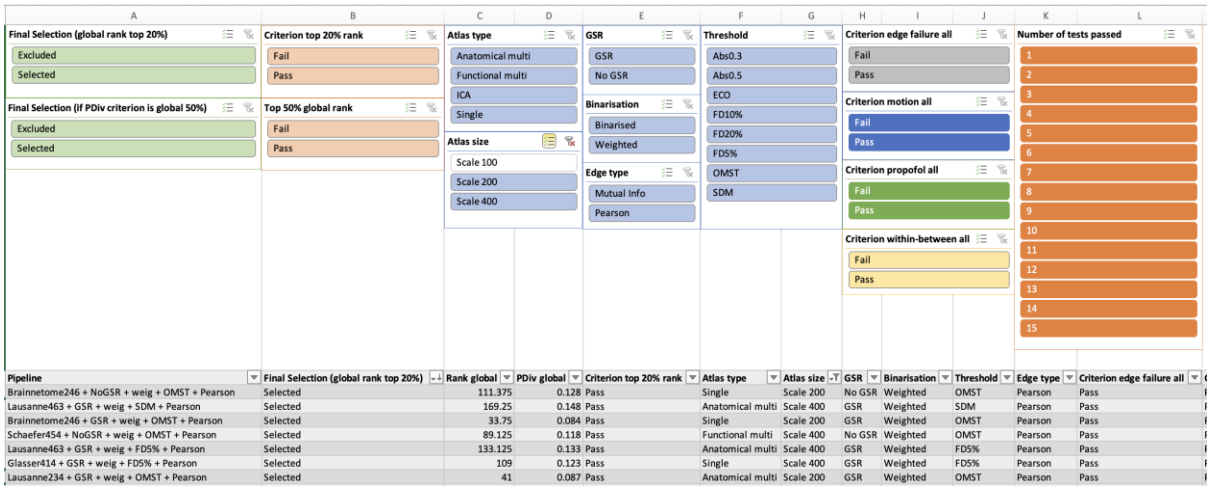
In contrast, if the user only cared about a pipeline passing Criteria II and V above, regardless of portrait divergence or pre-processing choices, the result may look as follows:



In this example, for the threshold slicer, option Abs0.5 can now no longer be selected because no pipelines with this pre-processing choice fulfil the propofol and non-empty network criteria.

A reset can be achieved by clicking on the filter icon with the red cross in the upper right corner of a given filter panel.

If the user wanted to include multiple options in a given filter panel (for instance if all pipelines with parcellation scale 200 and 400 were to be selected), the first option should be selected, followed by a click + command (or right click) on the second option. This would yield the following:



Pipeline	Final Selection (global rank top 20%)	Rank global	PDiv global	Criterion top 20% rank	Atlas type	Atlas size	GSR	Binarisation	Threshold	Edge type	Criterion edge failure all
Brainnetome246 + NoGSR + weig + OMST + Pearson	Selected	111.375	0.128	Pass	Single	Scale 200	No GSR	Weighted	OMST	Pearson	Pass
Lausanne463 + GSR + weig + SDM + Pearson	Selected	169.25	0.148	Pass	Anatomical multi	Scale 400	GSR	Weighted	SDM	Pearson	Pass
Brainnetome246 + GSR + weig + OMST + Pearson	Selected	33.75	0.084	Pass	Single	Scale 200	GSR	Weighted	OMST	Pearson	Pass
Schaefer454 + NoGSR + weig + OMST + Pearson	Selected	89.125	0.118	Pass	Functional multi	Scale 400	No GSR	Weighted	OMST	Pearson	Pass
Lausanne463 + GSR + weig + FD5% + Pearson	Selected	133.125	0.133	Pass	Anatomical multi	Scale 400	GSR	Weighted	FD5%	Pearson	Pass
Glasser414 + GSR + weig + FD5% + Pearson	Selected	109	0.123	Pass	Single	Scale 400	GSR	Weighted	FD5%	Pearson	Pass
Lausanne234 + GSR + weig + OMST + Pearson	Selected	41	0.087	Pass	Anatomical multi	Scale 200	GSR	Weighted	OMST	Pearson	Pass

Alternatively, filtering and sorting of the data based on any column available in the excel sheet can be done by clicking the downward facing arrow next to a column name in row 2.