RS-fMRI Processing Pipeline

Primary codes are denoted in red

Secondary codes are denoted in green

Image Preprocessing (Registration, Segmentation, Filtering, Parcellation, Normalization, Decomposition)
Code: construct_connectome_main.m
Calls: construct_connectome_helper.m
parcellation_generator.m
glmfitResidOnly.m
(also calls auxiliary functions ceemdan.m, eemd.m and emd.m for mode decomposition and narrowband mode estimation)

↓

Narrowband signal (mode) characteristic frequency and amplitude
calculate_mode_characteristics.m
Calls: save_modeInfo.m
(also calls auxiliary function crossing.m for estimation of zero-crossings based on which mode frequency is estimated)

↓

Mode parameter threshold estimation; Denoising through Mode Elimination; Mode Classification; Denoised Connectome Synthesis
Code: modes_classification_and_connectome_reduction.m
Calls: calculate_mode_thresh.m
save_reduced_connectomes.m

↓

Computes connectivity matrices for both reduced raw data and specific frequency bands of data using any of the following measures: peak cross correlation, peak coherence, and mutual information
Code: process_connectivity_matrix.m

↓

Computes statistical thresholds for median, 75th percentile, moderate outlier, and extreme outlier connectivities across all subjects for both raw and mode-specific data using bootstrapping
Codes: compute_raw_connectivity_thresholds.m
compute_mode_connectivity_thresholds.m
Calls: most_common_mode_bands.m

↓

Calculates network properties such as modularity, small-worldness, etc for the four statistical thresholds
Code: calculate_network_properties.m
Calls: calculate_network_properties_helper.m