Preprocessing of imaging data

The fMRI data were first preprocessed using the minimal preprocessing Human Connectome Project pipeline to remove noise and enhances the signal in the images. The functional images were realigned with the mean of all of the volumes, and slice-time corrected with 55 number of slices, 2 second TRs, and around 1.964 TA. The functional images were next coregistered to the T1-weighted structural images, segmented with bias images, normalized to the standard brain, further refined using nonlinear registration in SPM 12 software, and smoothed. Next, brain images were parceled into XXX regions of interest (ROIs) using the Automated Anatomical Labeling (AAL) atlas. The time series of averaged BOLD signals on ROIs were extracted. BOLD functional activation was recorded when subjects were watching a movie. The task-associated BOLD activations were regressed out from the time series before connectivity analysis. We constructed functional connectivity (FC) networks by creating matrices where each row and column represent an ROI and the value of the (i,j) then try of the matrix is the correlation coefficient between the i-th and j-th brain region from the time series of the averaged BOLD signals.