Title: Impact of Brain Connectome and Personality on Cognitive Rehabilitation in Multiple Sclerosis
Statistical analyses will be performed using SPSS 22.0 (IBM Inc., Armonk, NY, USA) and R 3.4.1 (The R Foundation).

[1a] Determine whether low Conscientiousness predicts lesser overall cognitive improvement following cognitive rehabilitation in people with MS. The question of whether Conscientiousness predicts successful intervention will be addressed using baseline measures of trait Conscientiousness and cognitive performance before and after rehabilitation. We will assess linear relationships between baseline trait Conscientiousness and overall magnitude of cognitive improvement using linear regression models. Cognitive improvement will be measured according to differences in cognitive scores between baseline assessment during visit 1 and post-rehabilitation assessment at visit 2. In order to summarize results across all cognitive measures, test scores will be converted to normalized z-scores and averaged together.

[1b] Determine whether the impact of Conscientiousness on cognitive rehabilitation is moderated by executive function and treatment adherence. In order to address the question of whether or not adherence and executive function moderate the impact of Conscientiousness on intervention success, we intend to add interaction parameters to the linear regression analysis described for aim 1a. For instance, we will calculate the interaction variable between Conscientiousness and DKEFS-ST (executive function) and include it in our regression models.

[2] Identify structural and functional brain connectome characteristics which predict successful improvement in sub-domains of cognition following rehabilitation. In order to identify brain connectome characteristics which predict specific responses to sub-domains of cognition following rehabilitation, we intend to employ linear machine/statistical learning techniques, such as partial least squares regression. The correct statistical learning models will be identified at the time of analysis in order to produce the most appropriate predictions. Models will be selected according to the distribution and dimensionality of our connectome variables. Following training of the predictive models, fit of the models will be assessed using k-fold cross validation.