

Supplemental information

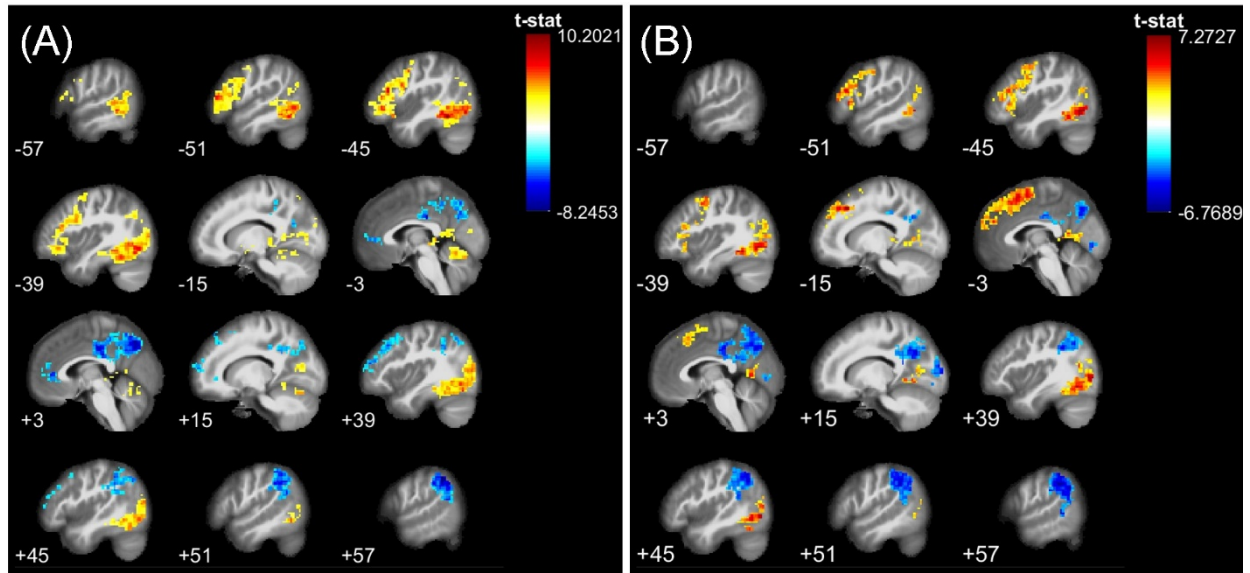


Figure S1. Whole brain analysis for pictures – scrambled pictures within each group. Results from 10,000 permutations of one-sample t-tests at a cluster-defining threshold of  $p < 0.01$ , clusters thresholded at  $p < .05$ , F.W.E. corrected for (A) controls [kcrit extent = 253 voxels] and (B) patients [kcrit extent = 182 voxels]

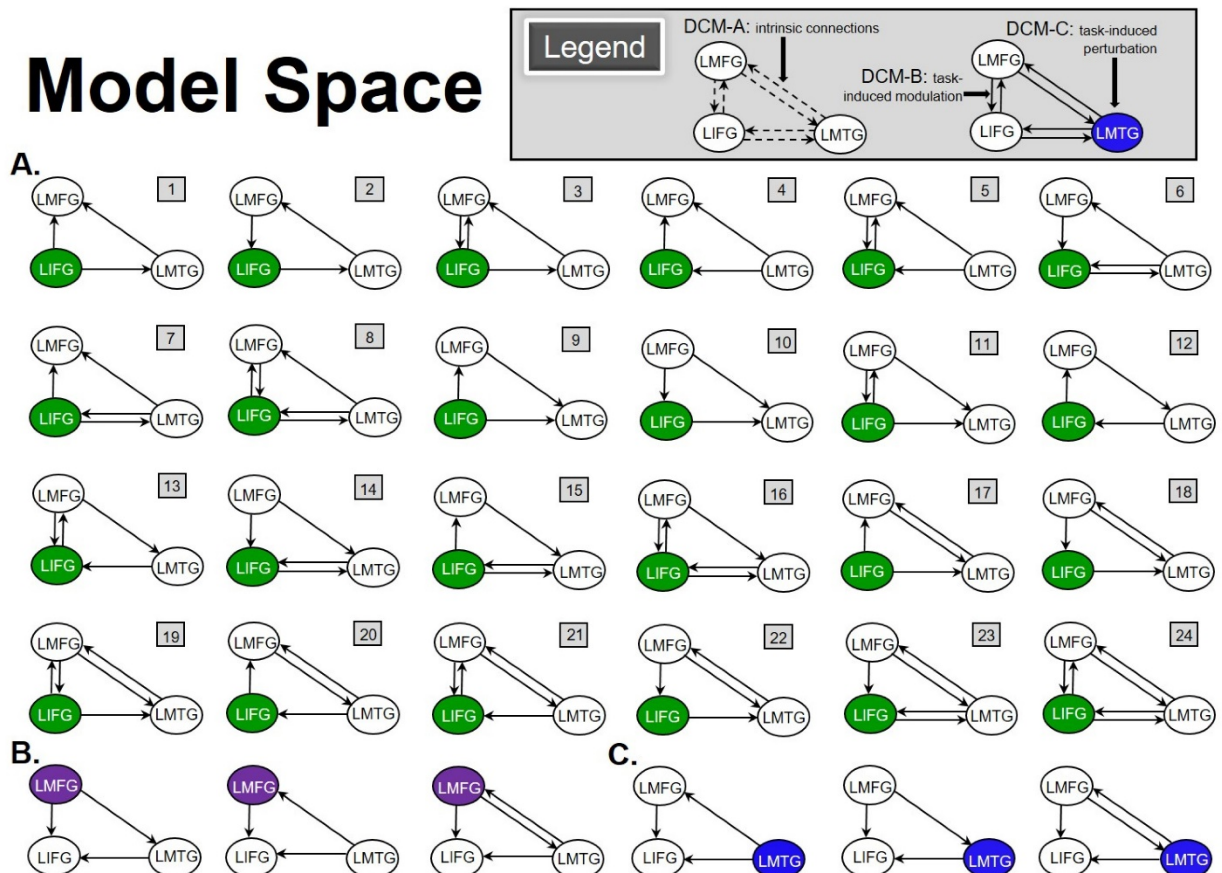


Figure S2. DCM model space from Meier et al. (2016). Full, bidirectional endogenous connections between all regions were modeled (DCM-A). For each model, driving input to only one region was modeled (DCM-C). All possible combinations of uni- and bidirectional task-modulated connections were modeled across the model space. For each model, the input region modulated at least one other region (DCM-B), resulting in 72 unique models. (A) All 24 models in Family 1 are schematized in the figure above. (B) Family 2 included models with the same modulatory connections as Family 1 with three additional models and excluding models #1, #4, and #7 due to lack of modulation from LMFG to the other two regions. (C) Similarly, Family 3 included models with the same modulatory connections as Family 1 with three additional models and excluding models #9, #10, and #11 due to lack of modulation from LMTG to the other two regions.

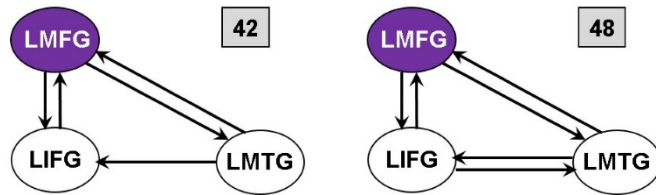


Figure S3. Models #42 and #48 from Family 2: Input to LMFG. Bidirectional modulatory connections (in DCM-B matrix) modeled across all connections in both models, excluding LIFG<sub>tri</sub>→LpMTG in model #42.