

Figure	Data Description	Data Amount
<p>Fig. 2, Figs. S1-3</p>	<p>Data from the 10 sessions were split into two halves of 5 sessions each. One split-half (even numbered sessions) was used to create a “true” best estimate of network variants. The other split-half (odd numbered sessions) was sampled in 5 min. increments up to 100 minutes. For task analyses, data was drawn approximately equally from all 3 task states.</p> <p>Data were consecutively sampled from the beginning of the first session until the full amount of required data was reached or no more data was available. When no more data was available in a given session, the next subsequent session’s data in the split-half was consecutively sampled from the beginning of the scan.</p>	<p>“True” half: Task mean = 109 min. (range = 75.9-123.9 min.) Rest mean = 116 minutes (range = 85.6-144.1 min.)</p> <p>Test half: 5-100 min. per participant <i>(lines stopped early if participants did not have 100 min. in the test half)</i></p>
<p>Figs. 4, 6 Figs. S5-7</p>	<p>Data from the 10 sessions were split into two halves (odd/even numbered sessions) of 5 sessions each.</p> <p>Data was sampled within each split-half to equally match data between participants and task vs. rest states. Data was approximately equally sampled from the 5 sessions within each split-half and (for task data) across the three task states. The same number of data points were sampled from each resting state scan as from the corresponding session’s task scans for each participant. Within these constraints, the data were sampled from consecutive timepoints starting with the beginning of each scan. When enough data was not available for a task (or for rest) in a given session, that remaining data was equally sampled from alternate sessions with enough data (7.2% of task by session combinations).</p>	<p>35.2 min. per split-half (per individual per state)</p>
<p>Figs. 1, 3, 5 Figs. S4, S8-11, S13</p>	<p>Data was matched across participants and between states. Data was approximately equally sampled each session and (for task data) across the three task states. The same number of data points were sampled from each resting state scan as from the corresponding session’s task scans for each participant. Within these constraints, the data were sampled from consecutive timepoints starting with the beginning of each scan. When enough data was not available for a task (or for rest) in a given session, that remaining data was equally sampled from alternate sessions with enough data (9.7% of task by session combinations).</p>	<p>80.6 min. (per individual per state)</p>
<p>Fig. 7 Fig. S12</p>	<p>Data from the 10 sessions were split into two halves (odd/even numbered sessions) of 5 sessions each. Data was sampled within each split-half to equally</p>	<p>11.3 min. (per individual per task)</p>

	<p>match data between participants and the four (3 tasks + rest) states. Data was approximately equally sampled from the 5 sessions within each split-half. The same number of data points were sampled from each resting state scan as from the corresponding session's task scans for each participant. Within these constraints, the data were sampled from consecutive timepoints starting with the beginning of each scan. When enough data was not available for a task (or for rest) in a given session, that remaining data was equally sampled from alternate sessions with enough data (4.1% of task by session combinations).</p>	
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Supplementary Table 1 (S1). The data sampling procedure for the analysis underlying each figure is outlined.

Subject	Rest	Task
MSC01	16	17
MSC02	13	11
MSC03	5	7
MSC04	16	14
MSC05	12	16
MSC06	9	11
MSC07	17	12
MSC09	12	14
MSC10	14	10
Total	114	112

Supplementary Table 2 (S2). The total number of variants is shown for task and rest states for each participant at a 5% threshold. These counts reflect variants that were excluded for being in low signal regions, small size (< 50 vertices), or overlapping more than 50% with the group network template. There were no significant differences in the number of variants across states, $t(8) = .241$, $p = .836$, $d = .08$.

Subject	Rest	Task
MSC01	2192	1975
MSC02	1007	611
MSC03	1050	1332
MSC04	343	938
MSC05	954	567
MSC06	1529	1579
MSC07	927	1128
MSC09	475	532
MSC10	746	604
Total	9233	9266

Supplementary Table 3 (S3). The total number of vertices identified as network variants is shown for task and rest states for each participant at a threshold of $r < .3$. These counts reflect variant vertices that were excluded for being in low signal regions and small contiguous parcels (< 50 vertices). There were no significant differences in the number of vertices composing the network variants between states, $t(8) = .044$, $p = .966$, $d = .01$.

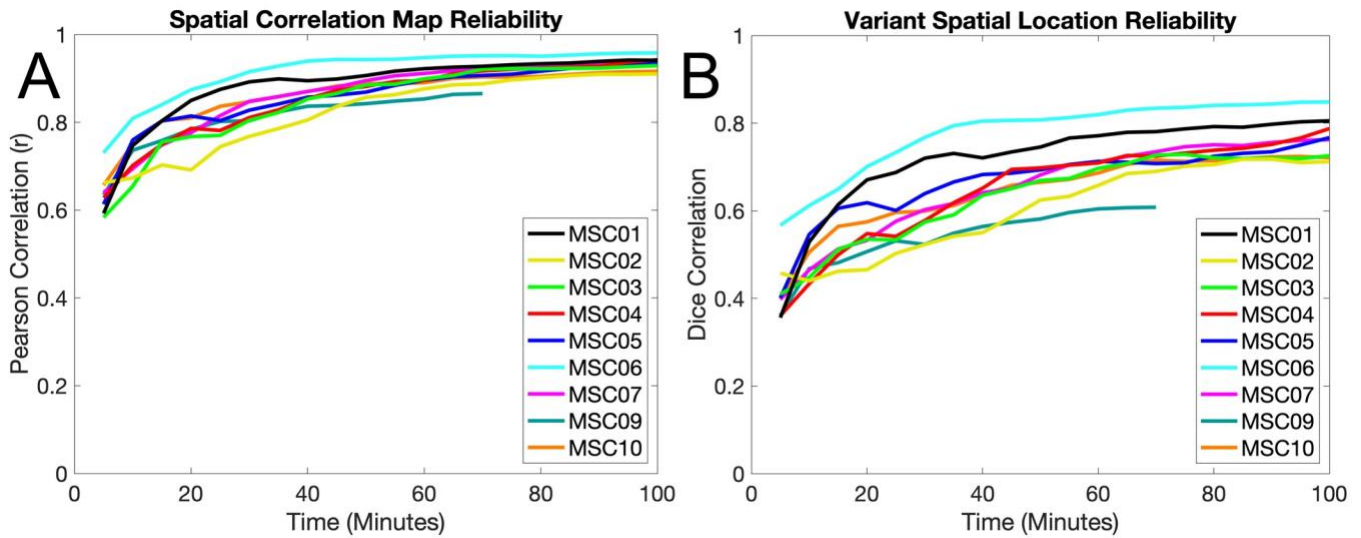


Figure S1. Reliability of network variants in rest data. As for the task data in Figure 2, sessions were split into two halves and compared. All available data was taken from one half and treated as the best estimate of “true” network variants. The other “test” half was sampled in 5 min. increments. (A) Individual-to-group spatial correlation maps were compared using a Pearson correlation. (B) Binarized network variant spatial location maps (the lowest 5% of correlations with the group) were compared using a Dice correlation. Note that MSC09 (70 minutes) did not reach 100 minutes of data in their test half and thus has a shorter line than the rest of the participants.

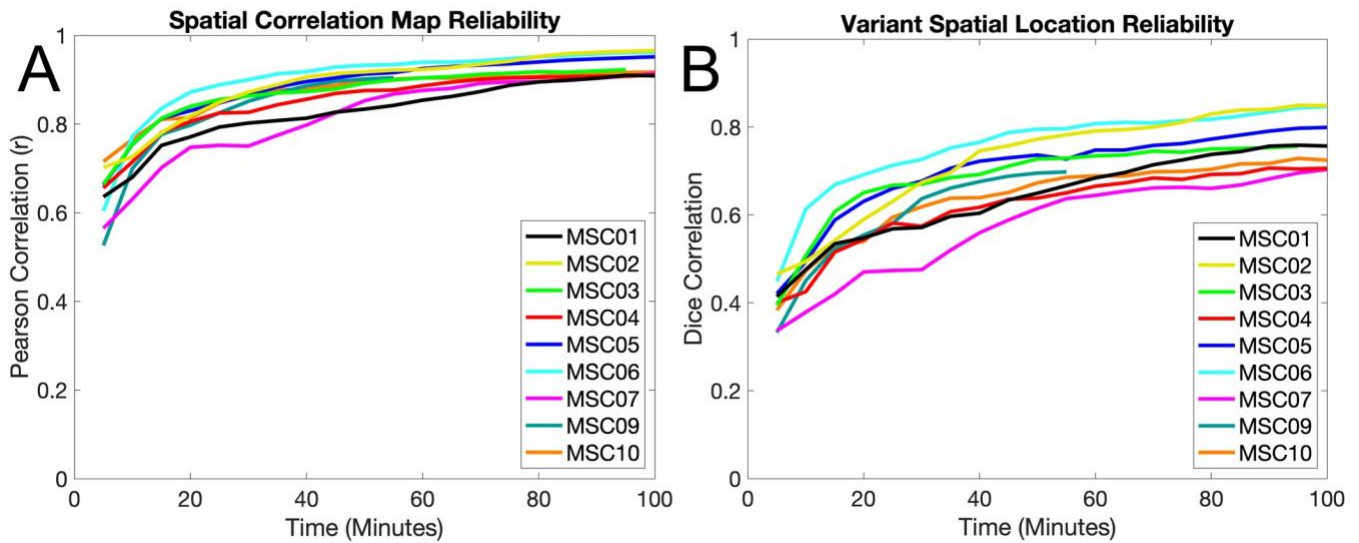


Figure S2. Reliability of non-residualized data (i.e., data without task activations removed), as in Figure 2. Sessions were split into two halves and compared. All available non-residualized data was taken from one half and treated as the best estimate of “true” network variants. The other “test” half of non-residualized data was sampled in 5 min. increments. (A) Individual-to-group spatial correlation maps were compared using a Pearson correlation. (B) Binarized network variant spatial location maps (the lowest 5% of correlations with the group) were compared using a Dice correlation. Note that MSC09 (55 minutes) and MSC03 (95 minutes) did not have 100 minutes of data in their test half, leading to shorter lines. Similar reliability was seen for residualized and non-residualized task data.

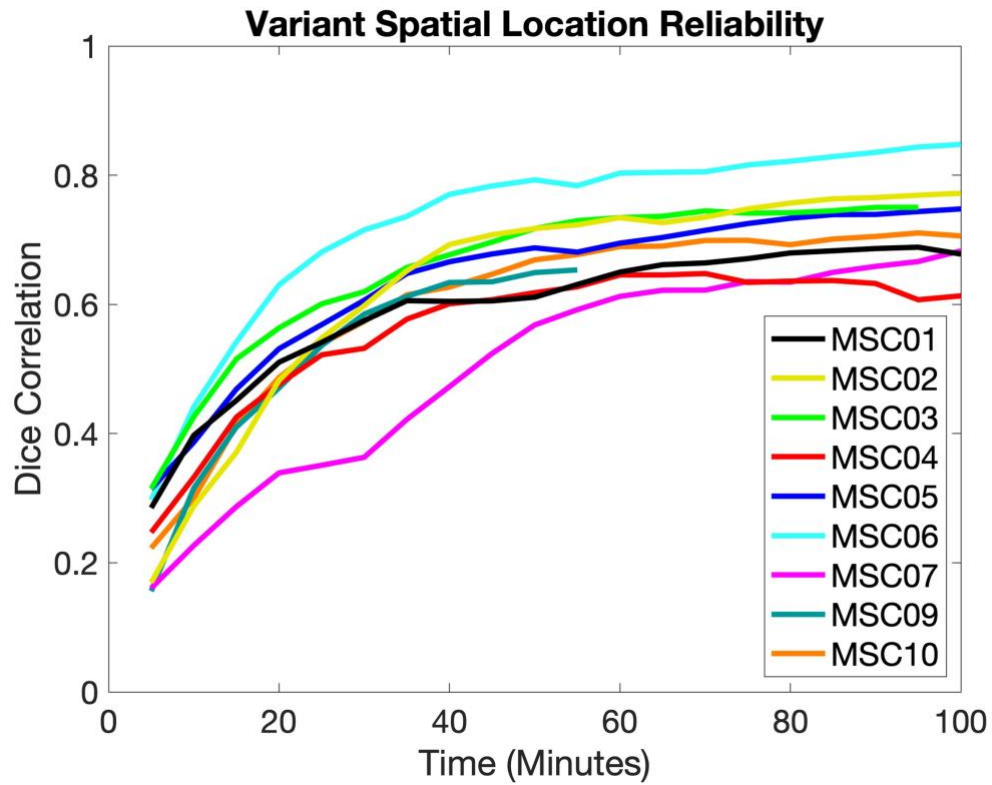
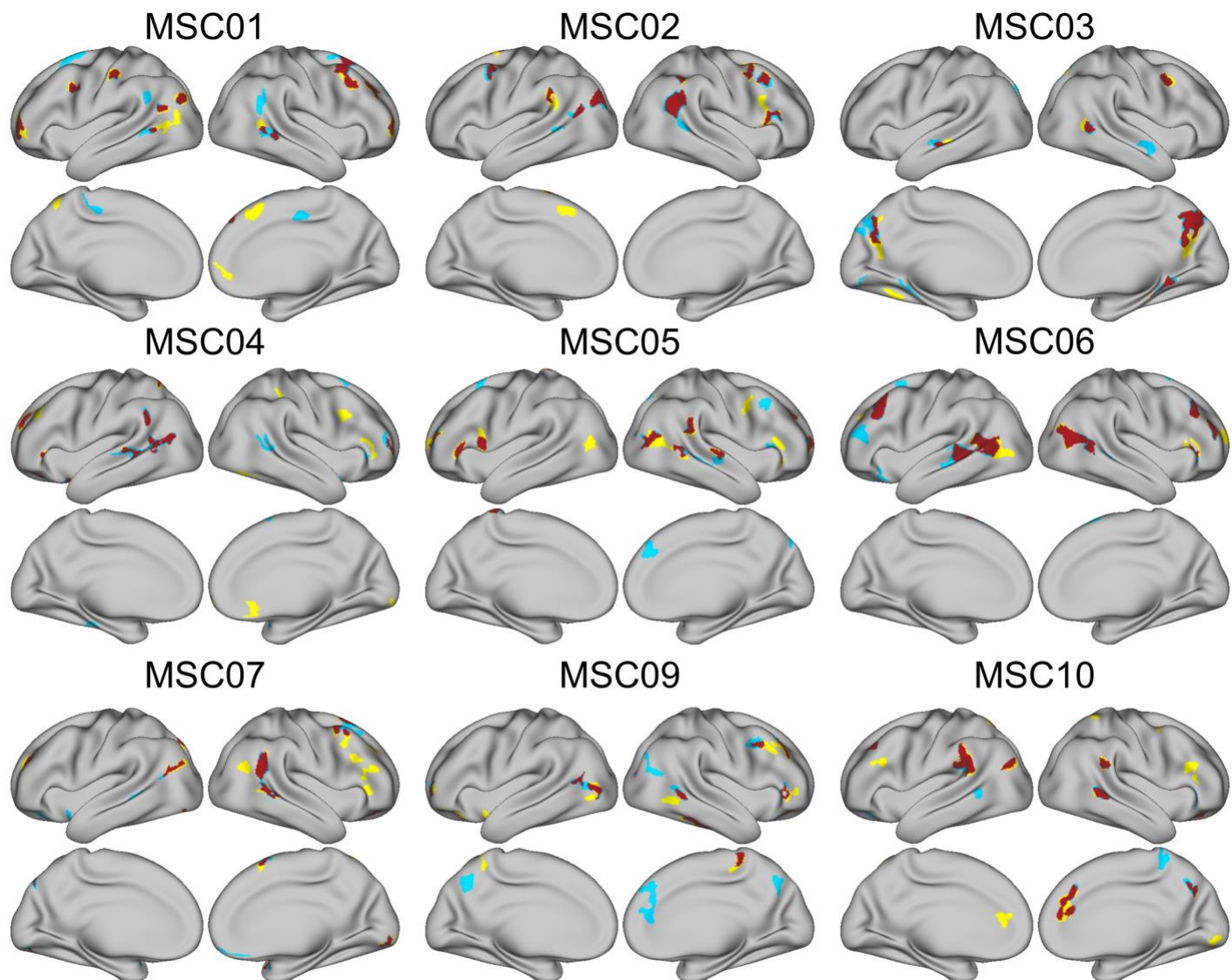


Figure S3. As for the task data in Figure 2, sessions were split into two halves and compared. All available data was taken from one half and treated as the best estimate of “true” network variants. The other “test” half was sampled in 5 min. increments. Binarized network variant spatial location maps ($r < 0.3$ between the individual and group average) were compared using a Dice correlation. Note that MSC09 (70 minutes) did not reach 100 minutes of data in their test half and thus has a shorter line than the other participants.



■ Overlap across states
 ■ Rest variant only
 ■ Task variant only

Figure S4. The overlap in the spatial location of network variants between task and rest states is shown for all included MSC subjects (using a 5% network variant threshold). Areas shaded in yellow represent locations of variants that are only observed during the resting state, areas shaded in blue represent locations of network variants only observed in the task state, and areas shaded in red represent locations where network variants are present in both task and rest states (overlapping).

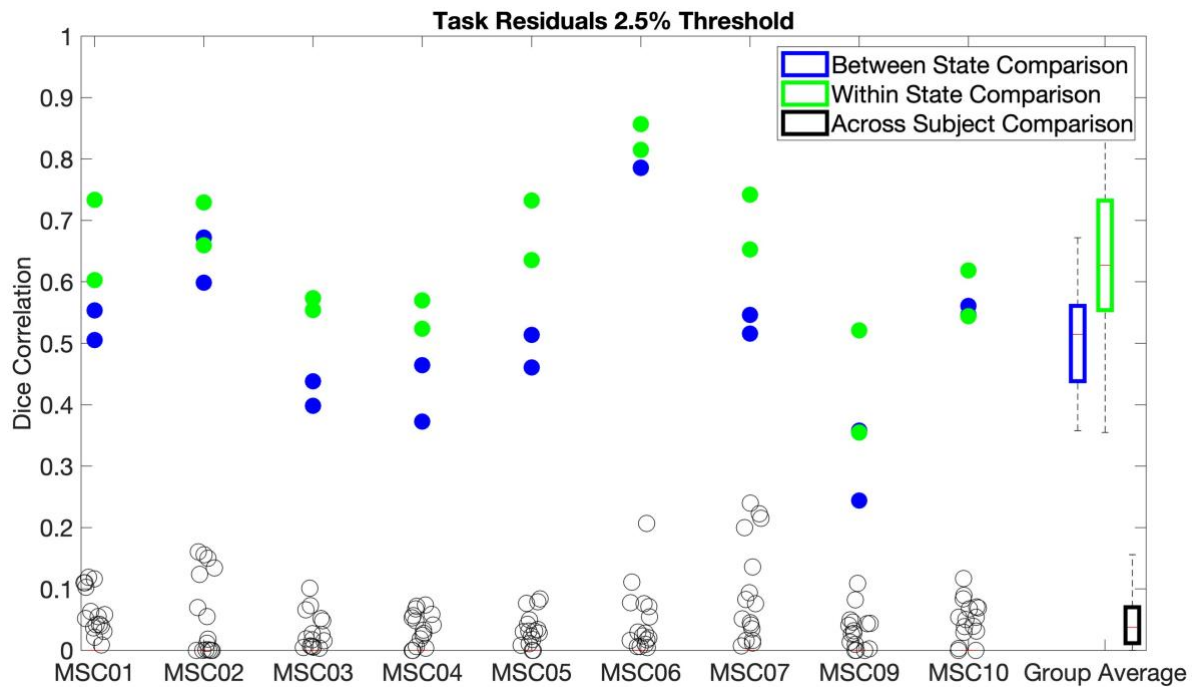


Figure S5. The Dice correlation for the overlap of the spatial locations (vertices) containing network variants between states and within states is plotted for variants thresholded at the 2.5% lowest values of each individual's spatial correlation map. The value for each individual participant is plotted for all of the comparisons, and the value of every across participant comparison is also plotted. Two dots are present for the between and within state comparisons as both pairs of split-halves were used (see sections 2.9.2 and 2.9.3). The results at the 2.5% threshold showed that variant spatial locations were more likely to overlap between states ($M = .518$, $SD = .139$) than across subjects ($M = .049$, $SD = .02$, $t(8) = 10.56$ $p < .0001$, $d = 3.52$). Variant spatial locations were also significantly more likely to overlap within states ($M = .635$, $SD = .115$) than between states ($M = .518$, $SD = .139$, $t(8) = 6.1$, $p = .0003$, $d = 2.03$; see Figure 4). As with the 5% threshold, the magnitude of the difference between states was smaller than the magnitude of the difference across subjects.

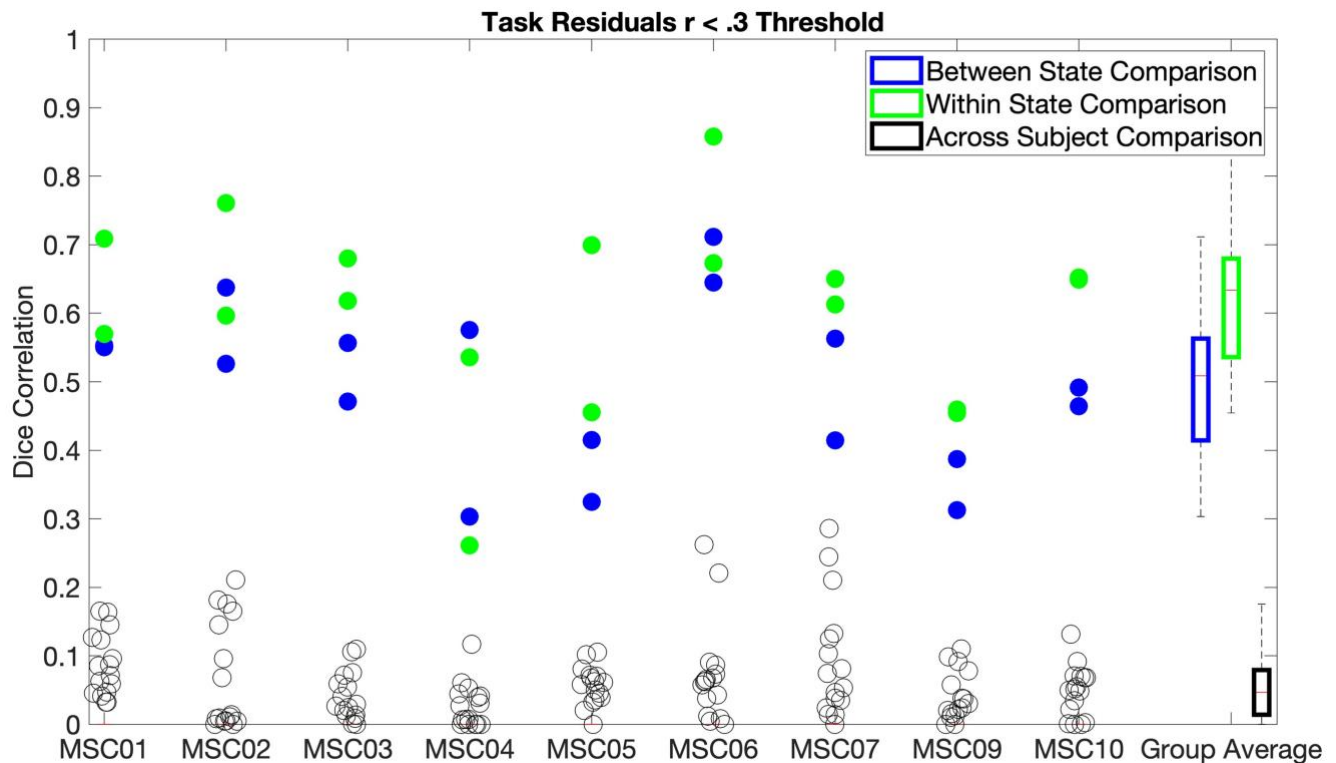


Figure S6. The Dice correlation of the overlap of spatial locations (vertices) containing network variants between states and within states is plotted for variants thresholded at values of $r < .3$ of each individual's spatial correlation map. The value for each individual participant is plotted for all of the comparisons, and the value of every across participant comparison is also plotted. Two dots are present for the between and within state comparisons as both pairs of split-halves were used (see sections 2.9.2 and 2.9.3). The results at the $r < .3$ threshold showed that variant spatial locations were more likely to overlap between states ($M = .495$, $SD = .103$) than across subjects ($M = .059$, $SD = .022$, $t(8) = 13.94$, $p < .0001$, $d = 4.65$). Variant spatial locations were also significantly more likely to overlap within ($M = .605$, $SD = .113$) than between states ($M = .495$, $SD = .103$, $t(8) = 4.75$, $p = .001$, $d = 1.58$; see Figure 4). As with the 5% threshold, the magnitude of the difference between states was smaller than the magnitude of the difference across subjects.

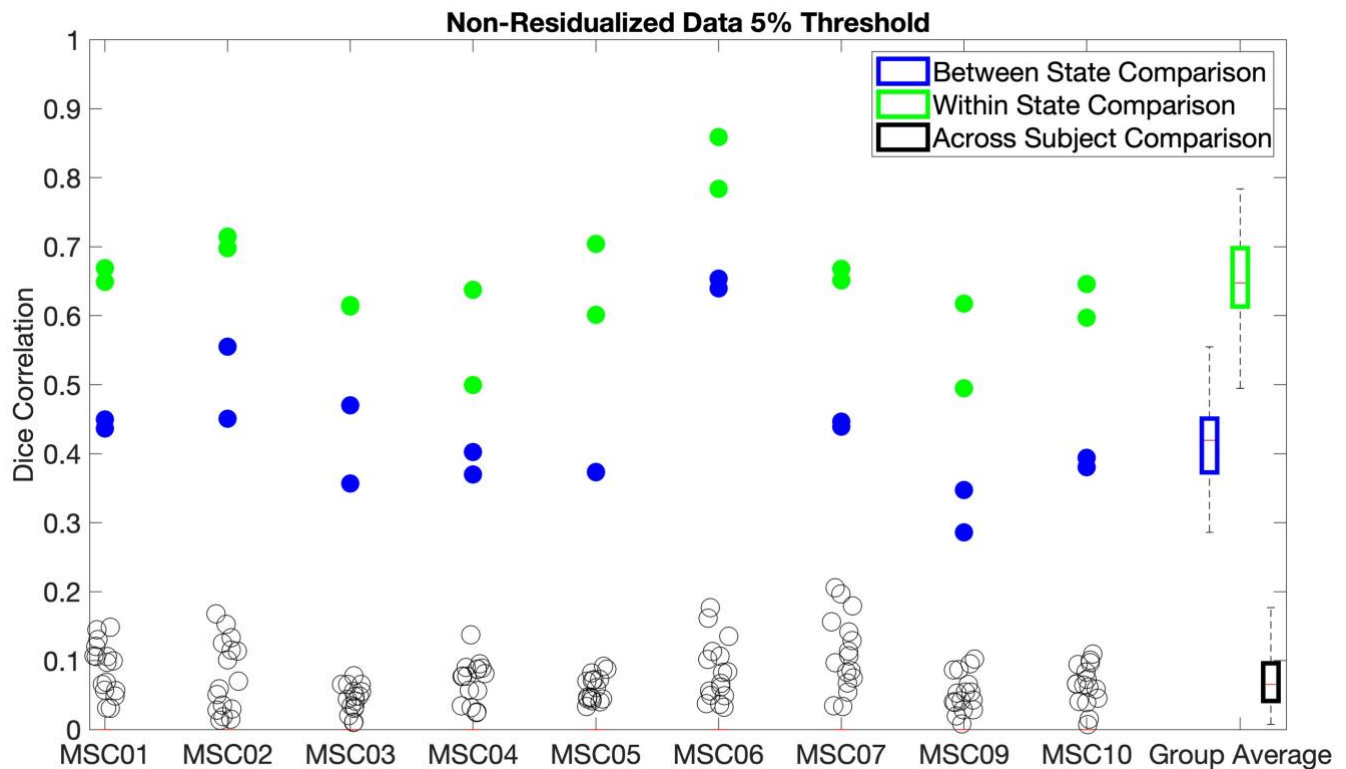


Figure S7. The Dice correlation of the overlap of spatial locations (vertices) containing network variants in non-residualized task data between states and within states is plotted for variants thresholded at the 5% lowest values of each individual's spatial correlation map. The value for each individual participant is plotted for all of the comparisons, and the value of every across participant comparison is also plotted. Two dots are present for the between and within state comparisons as both pairs of split-halves were used (see sections 2.9.2 and 2.9.3). As with the findings from the main manuscript, results for the non-residualized data showed that variant spatial locations were more likely to overlap between states ($M = .435$, $SD = .095$) than across subjects ($M = .072$, $SD = .02$, $t(8) = 12.46$, $p < .0001$, $d = 4.15$). Variant spatial locations were also significantly more likely to overlap within states ($M = .651$, $SD = .079$) than between states ($M = .435$, $SD = .095$, $t(8) = 20.31$, $p < .0001$, $d = 6.77$; see Figure 4). However, direct comparisons showed that variant spatial locations defined using the non-residualized data had significantly lower between-state stability than the residualized data ($p < .0001$, $d = 2.7$). Thus, it appears that removing task activations via regression provides more cross-state stability in defining variant locations than when task activations are left in the data.

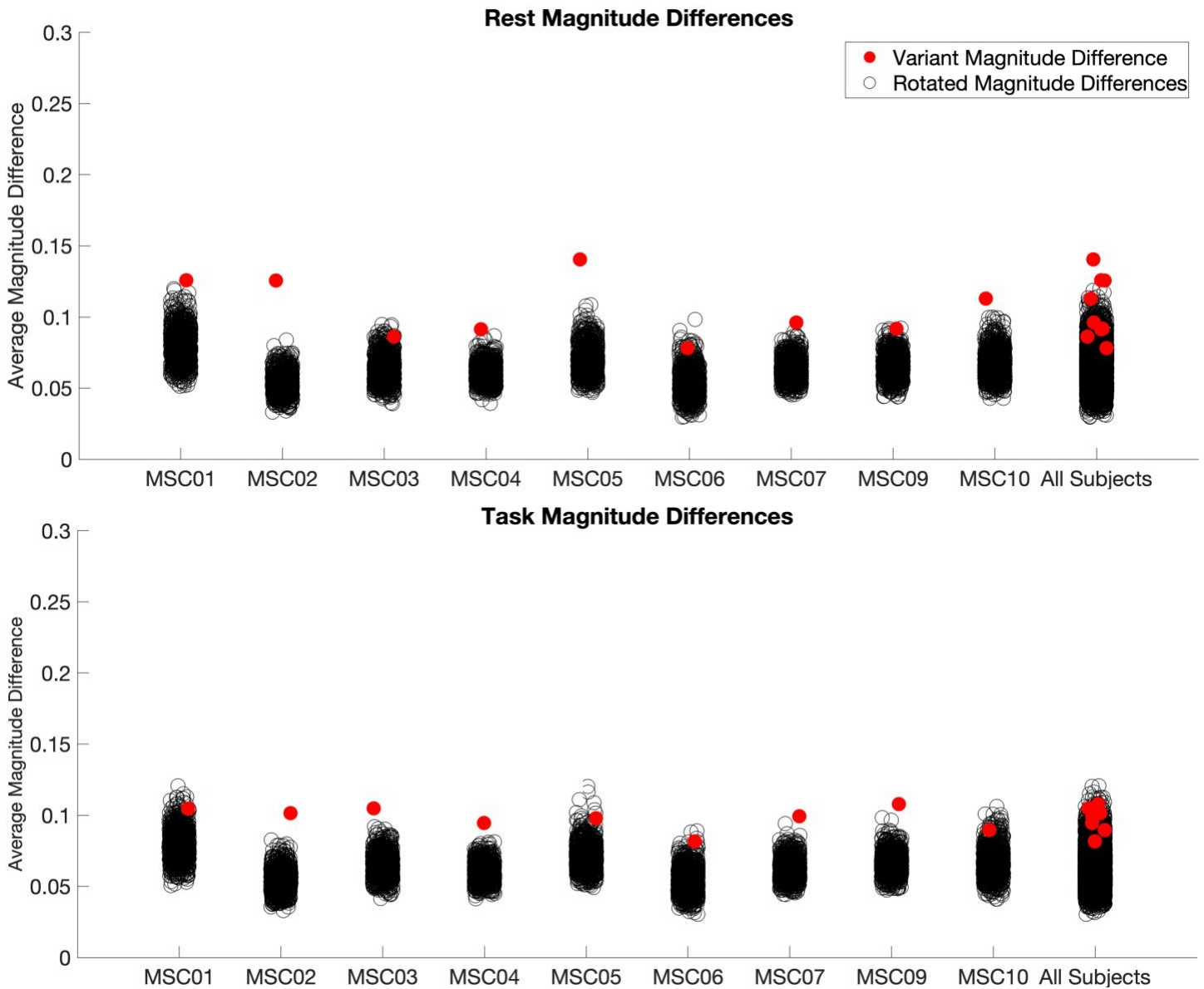


Figure S8. The difference in the magnitude of correlations with the group average spatial correlation map is shown for network variants in rest and task states. In this analysis, the spatial correlations of the vertices identified as network variants during one state were subtracted from the spatial correlations of the same locations during the alternate state. Then the mean of the absolute value of this difference was calculated to obtain a mean difference in magnitude of the correlations between states (see Figure 3C). This magnitude difference is shown separately for variants identified in rest (top) and variants identified in task (bottom). To determine whether these values were different from what would be expected by chance (i.e., relative to other areas of the cortex), the network variants for each participant were rotated 1000 times within each hemisphere. The same operation was then performed for each rotation. Red dots represent the average (absolute) magnitude difference of the observed network variants and the black dots represent the average (absolute) magnitude difference of randomly rotated variants. Network variants showed more variation than would be expected by chance for most participants. As can be seen in Figure 3C, most locations show small deviations (< 0.1), but some locations show larger differences, likely driving this effect.

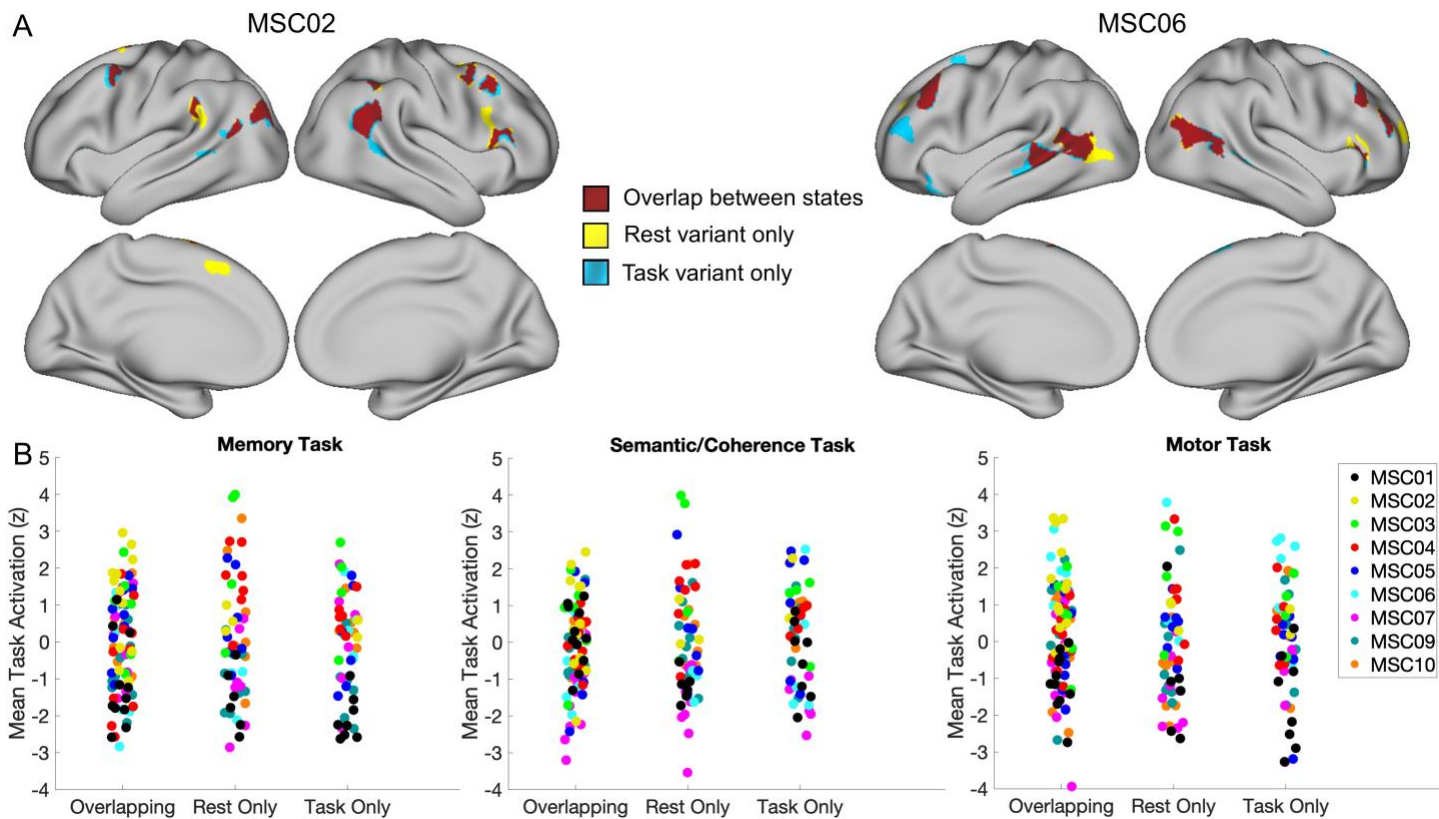


Figure S9. Contribution of task activations to state-dependence in network variants. Variant sub-units that either occur in both states (overlapping; red), only in rest (yellow), or only in task (blue) are shown on the cortical surface for MSC02 and MSC06 (A). For each of these sub-units, the mean task activation was calculated for each variant for each task (B). There were no significant differences in mean task activations across the different sub-units in each task ($p < .05$). Thus, we were unable to find strong evidence that task activations systematically change the underlying connectivity of network variants.

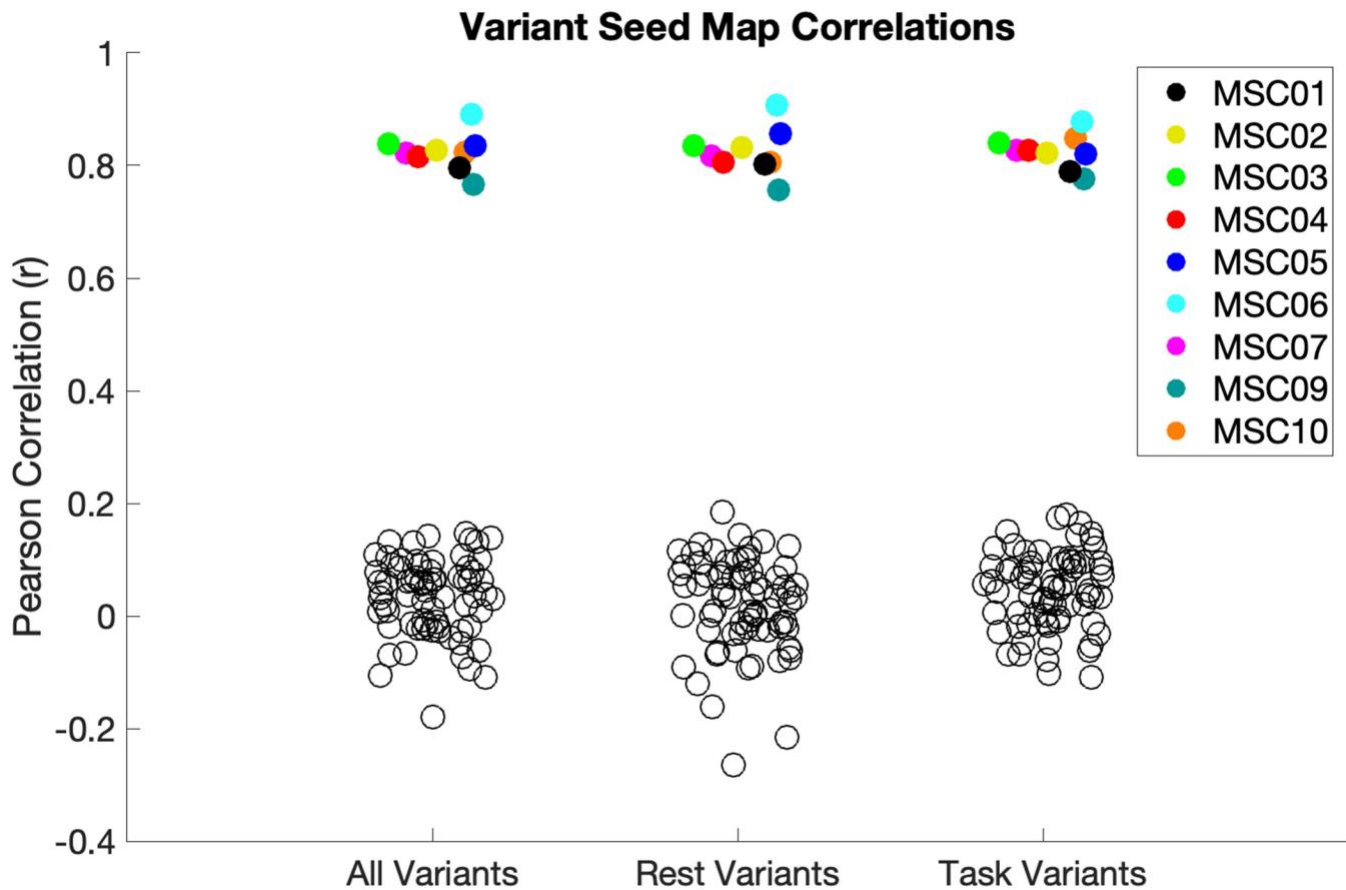


Figure S10. Comparison of seed maps for network variants. For each subject, the averaged seed map of each variant was calculated and correlated with the seed map of the same spatial location in the opposing state. The spatial correlations for the variant seed maps between task and rest states is plotted (averaged within each subject). Plots are shown for all variants (collapsed across states) and for variant estimates made separately during task or rest. Empty black circles show comparisons between network variant seedmaps and the same locations in other subjects. Variant seed maps were quite similar between states ($M = .824$) and much higher than seen across subjects ($M = .034$), $t(8) = 33.07$, $p < .0001$, $d = 11.02$.

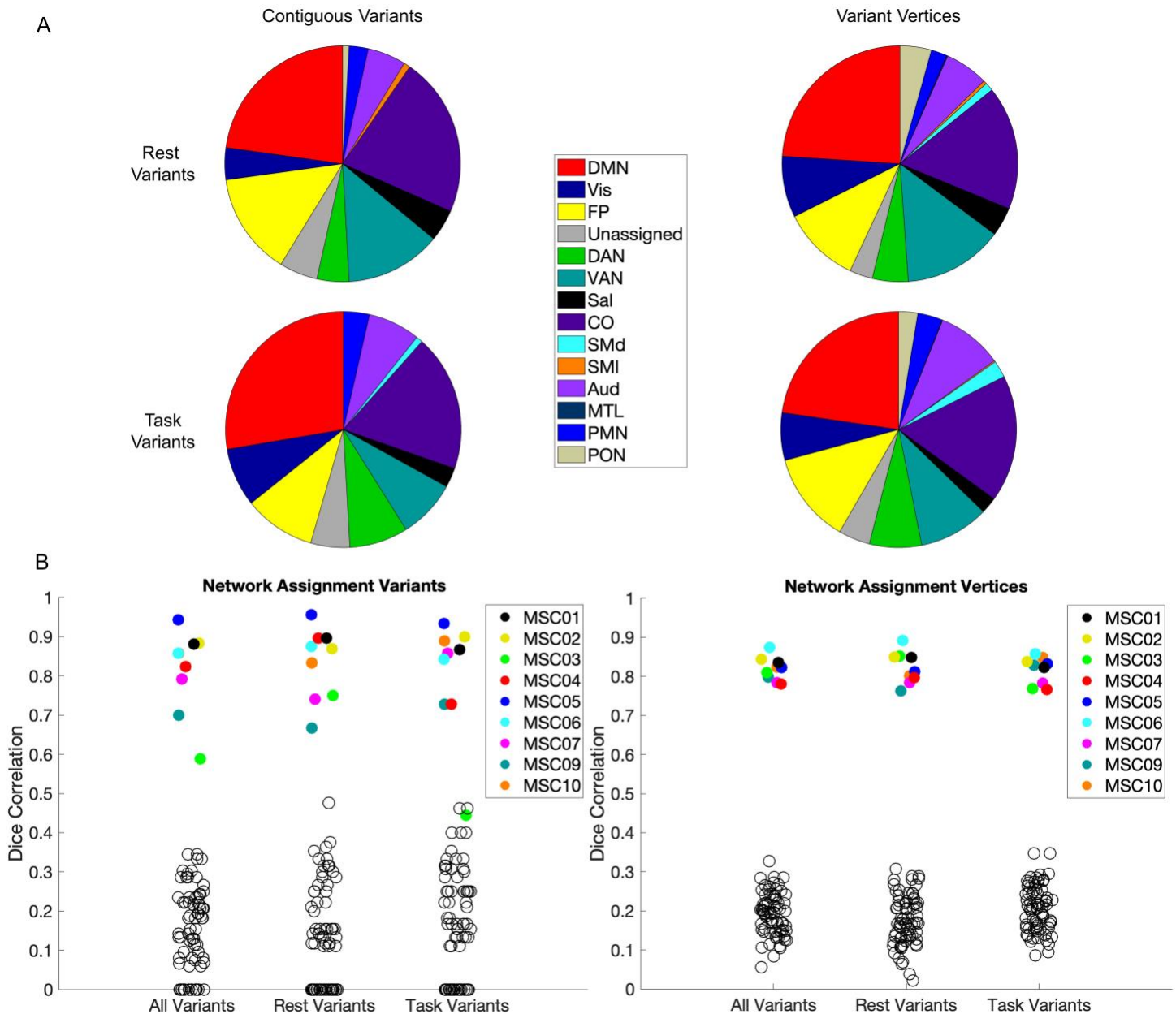


Figure S11. Comparison of network assignments conducted for contiguous variant units (left) or for each vertex composing each variant separately (right). (A) Distribution of network variant assignments during task and rest states. (B) The likelihood network variants are assigned to the same network across states (shown for variant locations identified based on both task and rest states combined as well as broken up by individual states). Empty black circles represent the likelihood of variant locations assigning to the same network in other subjects. As with contiguous variants, vertices were much more likely to assign to the same network between states ($M = .819$, $SD = .03$) than across subjects ($M = .193$, $SD = .028$), $t(8) = 41.69$, $p < .0001$, $d = 13.9$.

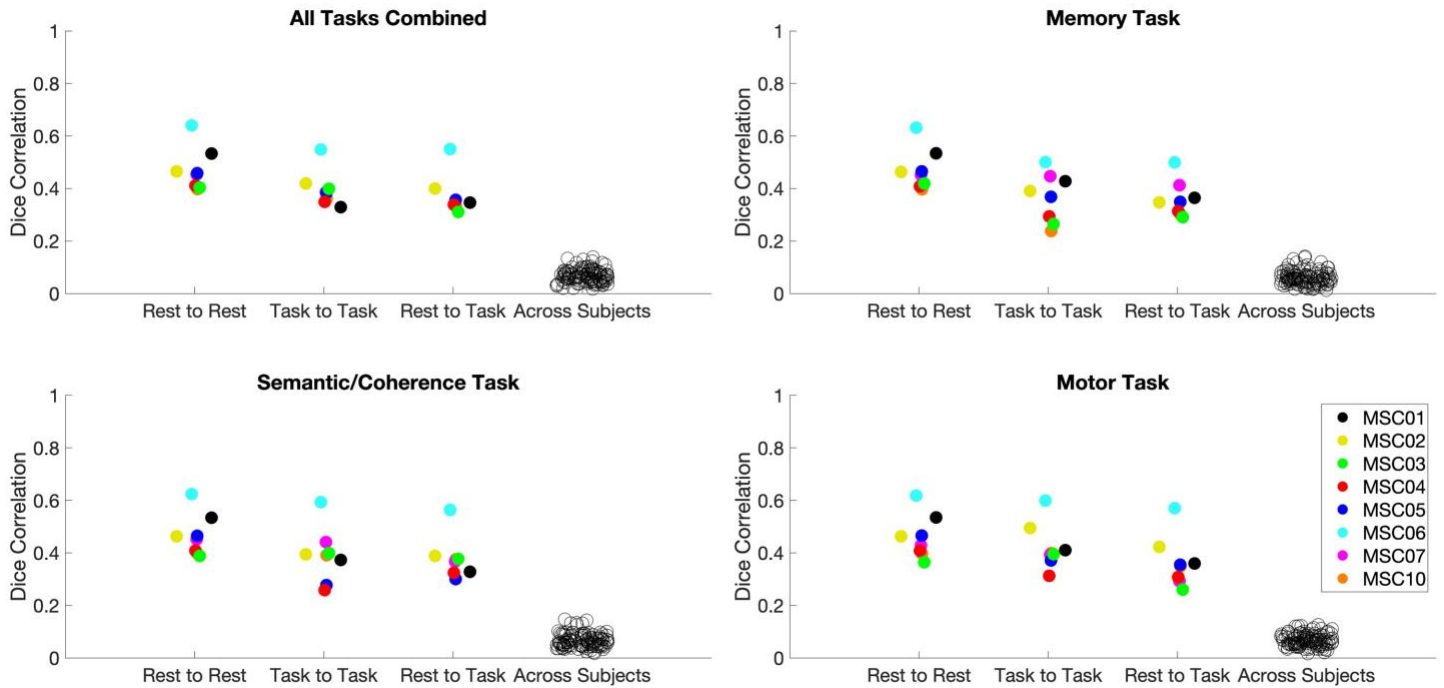


Figure S12. Comparisons for the stability of network variant spatial locations across individual tasks at a 2.5% threshold. Dice correlations for the spatial stability of all 4 tasks are shown using a 2.5% threshold of the lowest correlations with the group average to define network variants. The pattern shown is similar to that observed in Figure 7. As in section 3.5, a within-subject ANOVA was used to test for significant differences in the stability of the spatial location of variants between tasks. A model with one independent variable (Task) was specified for the rest to task comparisons across all 4 tasks. This model was not significant, $F(3,21) = 1.193$, $p = .336$, $d = .83$, indicating that there were no differences in the stability of variant spatial locations between states in any of the four tasks. These results are the same as those observed at the 5% threshold, providing insufficient evidence that there are task-specific effects on the stability of network variants spatial locations between states.

Location and Network Assignment Vertices

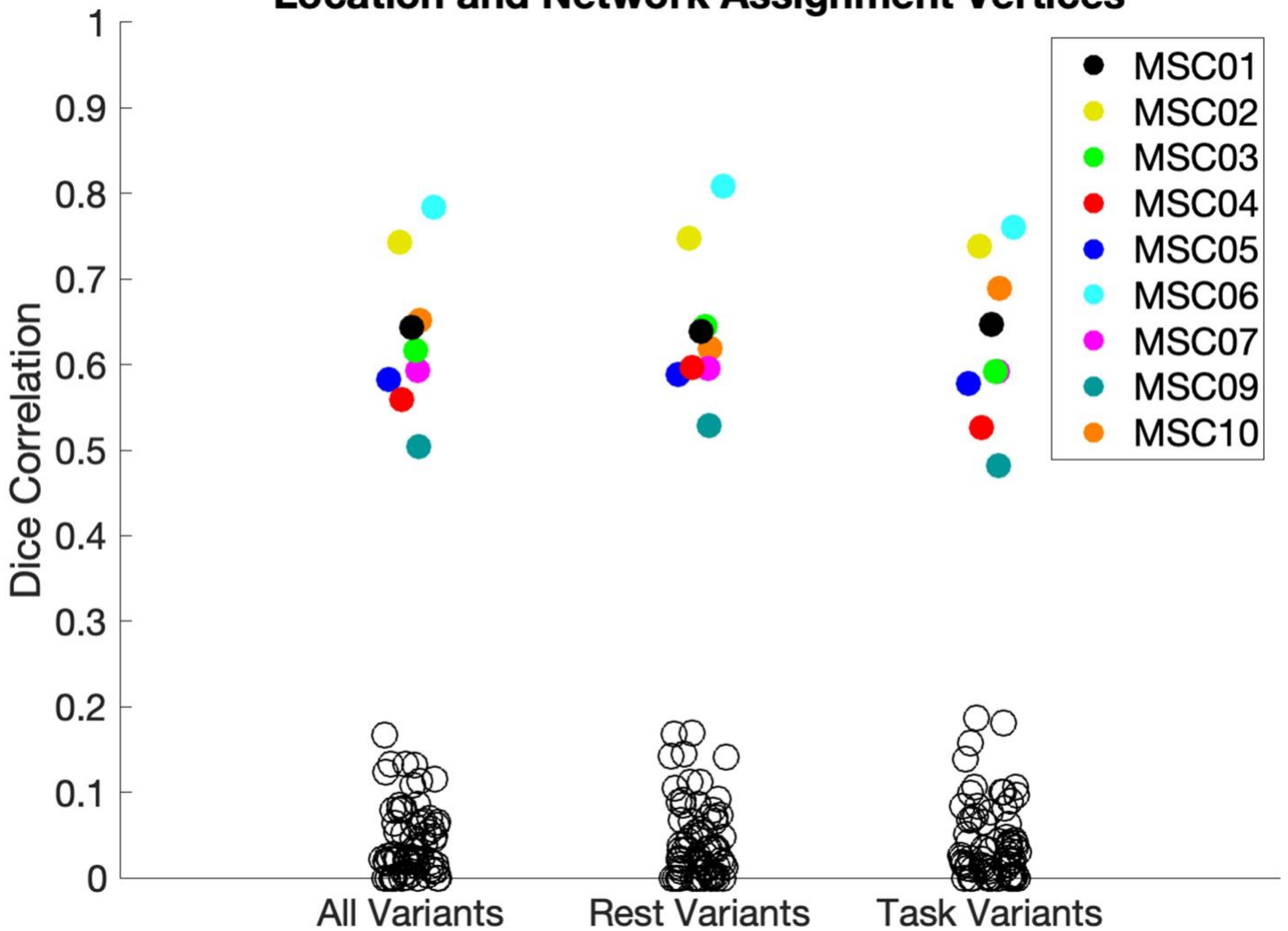


Figure S13. Dice correlations showing the likelihood of each individual vertex composing each network variant both spatially overlapping in their location with another variant (see Figure 4) and their seed map assigning to the same network (see Figure 5) between states. The empty black circles represent the likelihood of these vertices spatially overlapping in their location and assigning to the same network in the opposite state across all subjects. Variant vertices which overlapped with the consensus networks were excluded from analysis and vertices with an assignment lower than the threshold reported in section 2.12.1 were assigned to an “unknown” network. Variants were much more likely to spatially overlap in their location and assign to the same network between states ($M = .631$) than across subjects ($M = .041$), $t(8) = 20.33$, $p < .0001$, $d = 6.78$. Note that this number is higher than the number reported for spatial location overlap alone between states in Figure 4 because this analysis used the same amount of data per subject as Figure 5 (80.6 minutes) versus the amount used in Figure 4 (35.2 minutes) which increased the mean spatial location overlap between states to .769.