Identifying networks with common changes in representational similarity over time using jackknife resampling.

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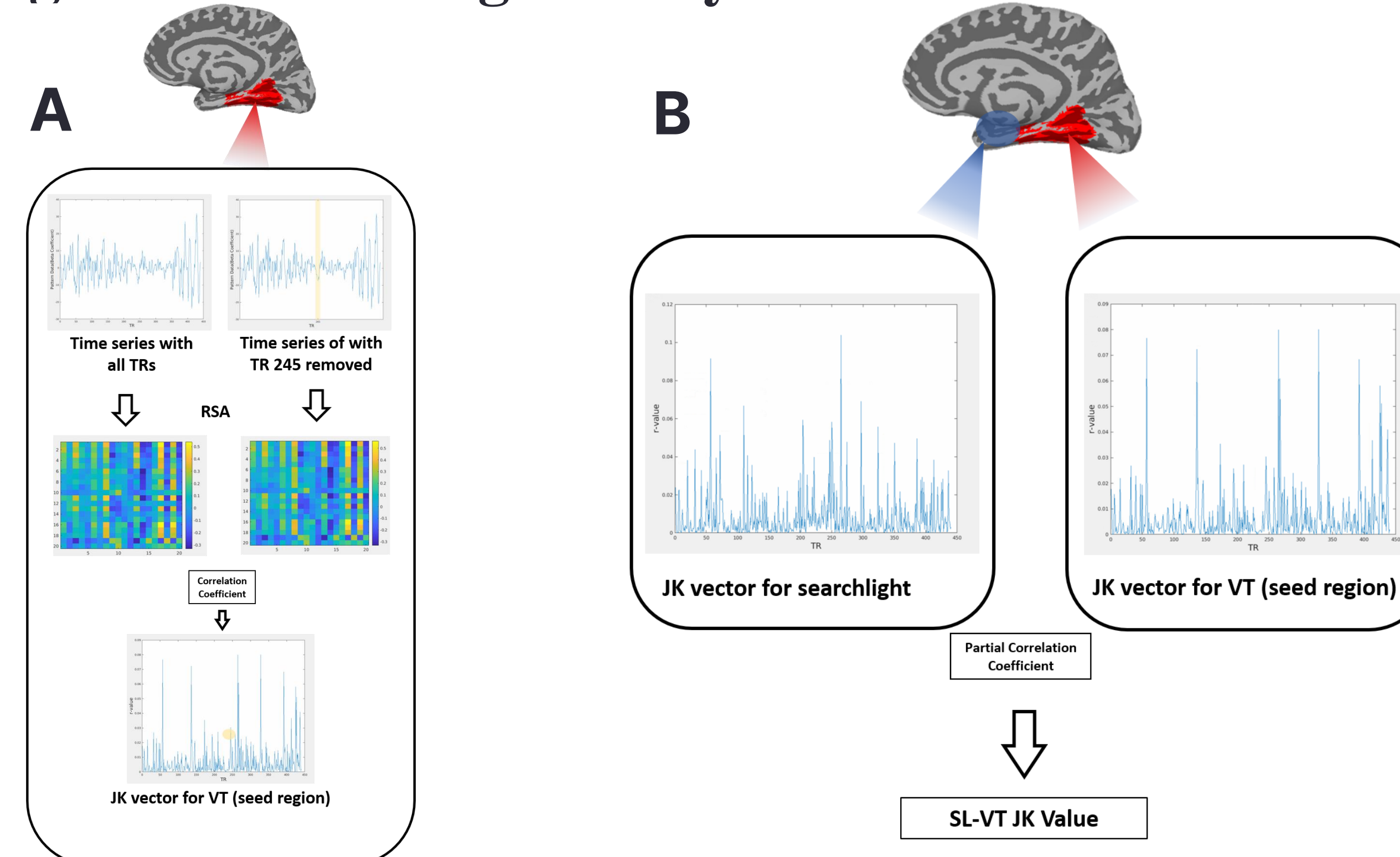[3] Brain Institute, University of Pittsburgh

INTRODUCTION

- Representational Similarity Analysis (RSA) typically collapses data across all TRs in an experiment (Kriegeskorte et al., 2008). Currently, there is no prevalent method for analyzing change over time in RSA.

- Functional Connectivity (FC) (Fair et al., 2006) and Informational Connectivity (IC) analyses (Coutanche & Thompson-Schill, 2013) have illustrated that analyzing the time domain provides information above and beyond what is available from fMRI analyses that collapse across all TRs.

- We propose a novel method of investigating representational connectivity using Jackknife Resampling (JK) to compare fluctuations in representational similarity between regions across time.

- We apply the novel method to a pre-existing dataset from Nastase et al. (2017) using Ventral Temporal (VT) as a seed region.

METHODS

- Dataset from Nastase et al. (2017) contained 12 participants (5 males; mean age = 25.4, standard deviation = 2.6)

- Brain imaging was acquired with a 3T Philips Intera Achieva MRI scanner

- Participants viewed clips of five different animal taxonomies performing each of four behaviors

- Participants were instructed to focus on either the behavior or the taxonomy in each clip and indicate via button press when a taxonomy or behavior was repeated.

- The resampled pattern data corresponding to the TRs of all 20 stimulus clip conditions were organized into a regional 20x20 representational dissimilarity matrix (RDM) representing the activity associated with each condition.

- We correlated the VT seed jackknife RDM with the jackknife RDM of each searchlight (Kriegeskorte, Goebel, & Bandettini, 2006) across the brain. White matter was partialed out of the correlation.

Stimulus pairs of 4 behavior conditions and 5 taxonomy conditions.

METHODS (CONTINUED)

Flow diagram of searchlight analysis with Jackknife resample

A
- Time series with all TRs
- Time series of with TR 245 removed
- RSA
- Correlation Coefficient
- JK vector for VT (seed region)

B
- JK vector for searchlight
- JK vector for VT (seed region)
- Partial Correlation Coefficient
- SL-VT JK Value

RESULTS

Jackknife network for taxonomy at .001 threshold (VT outlined)

left   right

medial

lateral

r value
.562
-.562

Jackknife overlap with FC and second order RSA

Taxonomy 0.005 threshold   Taxonomy 0.001 threshold

JK   FC   JK-FC Overlap

Taxonomy 0.005 threshold   Taxonomy 0.001 threshold

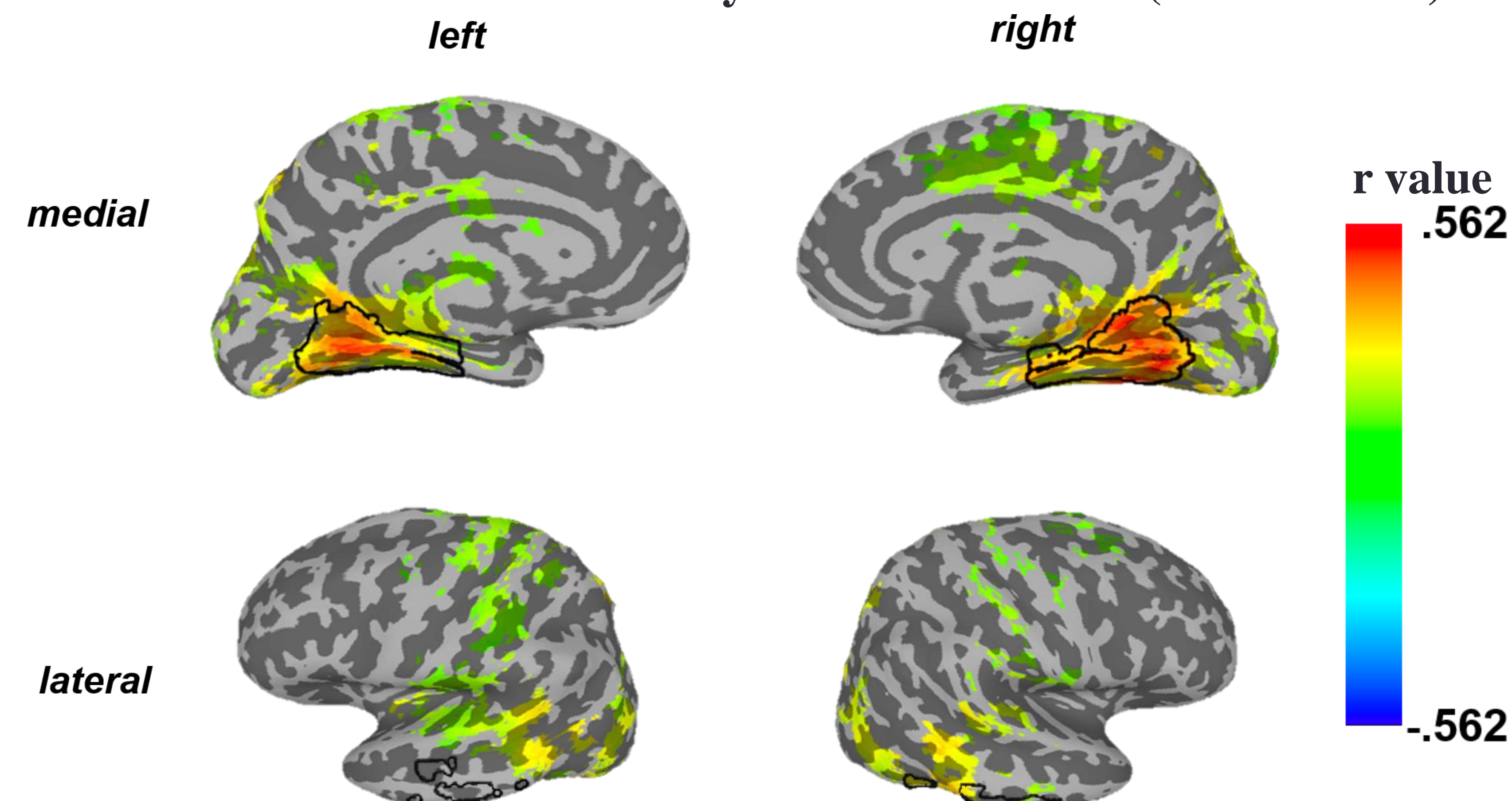JK   RSA   JK-RSA Overlap

CONCLUSIONS

- The JK method successfully identified a network of brain regions in which change in representational strength over time was significantly correlated with similar change in our seed region (VT).

- When compared with networks identified via FC and second-order RSA, the JK method identified both regions of overlap and regions unique to the JK network.

- Results confirm that adding a time dimension to RSA-based multivariate analyses contributes information above and beyond that which is provided by a second-order RSA.

- Incorporating JK analysis into future RSA-based studies will provide an opportunity to analyze novel mechanisms of information representation and a new lens through which to understand the brain on a network level.

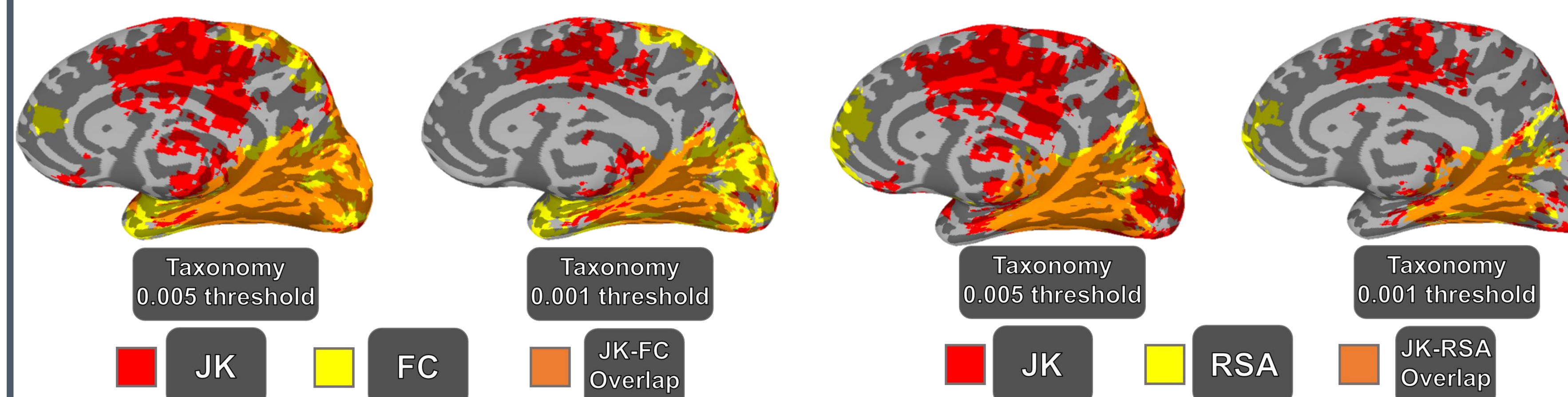## REFERENCES

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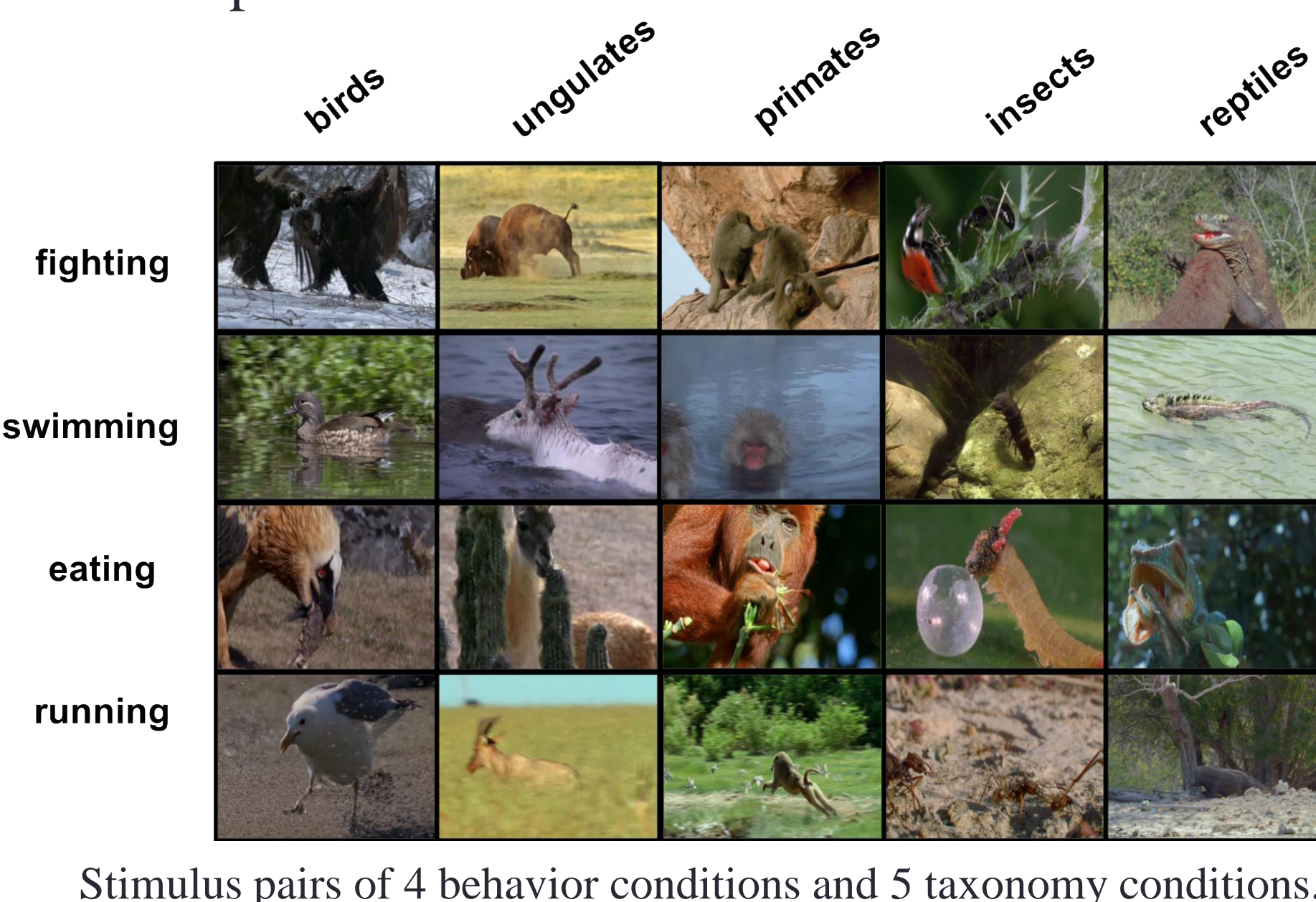
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