

Individual differences in functional connectivity in neonates

Ursula A. Tooley¹, Ally Dworetzky², Alyssa Labonte¹, Ashley N. Nielsen³, Caterina Gratton², Deanna M. Barch^{1,5,6}, Cynthia E. Rogers^{1,4}, Chris D. Smyser^{3,4,5}, Chad M. Sylvester¹

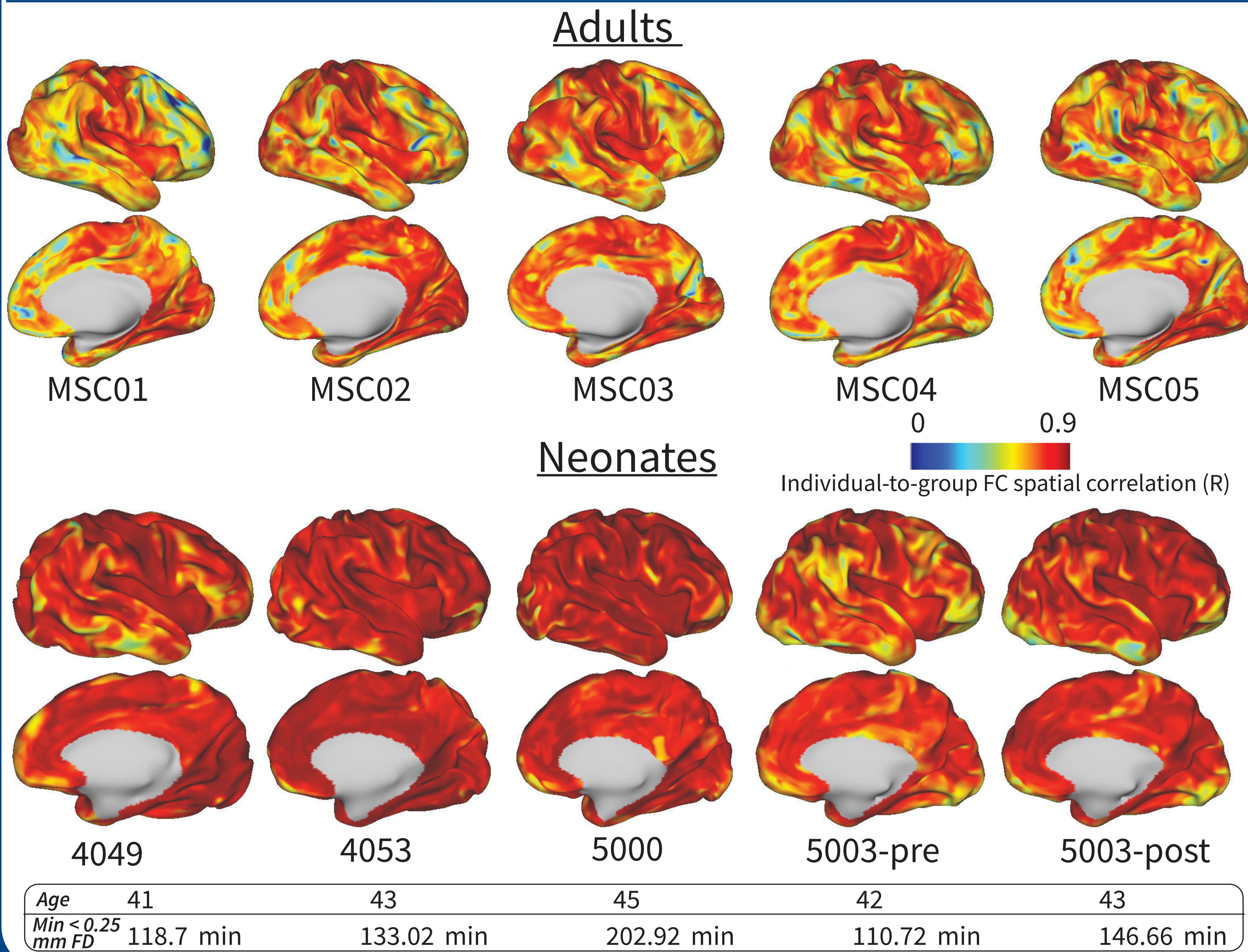
¹Department of Psychiatry, Washington University in Saint Louis ²Department of Psychology, Florida State University ³Department of Neurology, Washington University in Saint Louis ⁴Department of Pediatrics, Washington University in Saint Louis ⁵Department of Radiology, Washington University in Saint Louis ⁶Department of Psychological and Brain Sciences, Washington University in Saint Louis



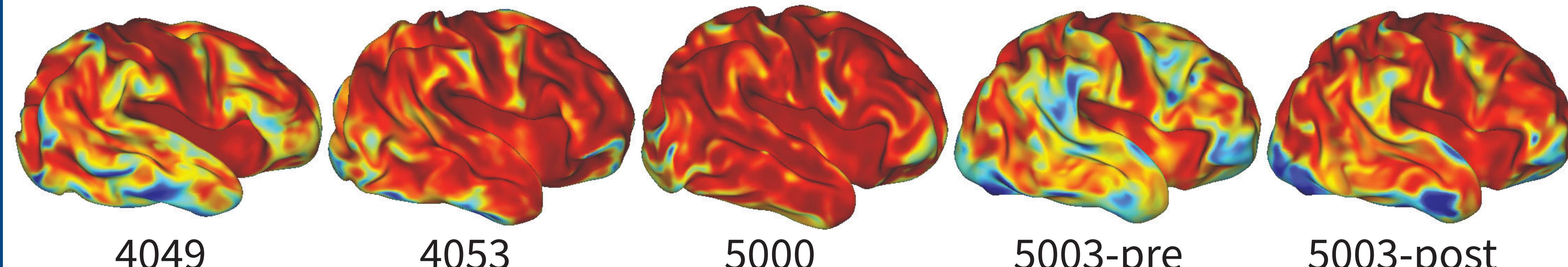
Summary

- Cortical organization varies across individuals. Highly sampled individuals show specific topographic deviations from group-average functional connectivity patterns, deemed “network variants.”
- In adults, network variants show trait-like qualities: they are stable over time, heritable, and predict differences in behavior¹⁻⁴.
- We examined deviations from group-average connectivity patterns in highly sampled neonates, finding that individual variability in connectivity patterns is reduced compared to adults, and this is driven by high interindividual similarity in local connectivity in neonates.**
- Network variants are still detectable in neonates, in similar brain regions as they occur in adults.

Neonates have less individually variable patterns of connectivity than adults



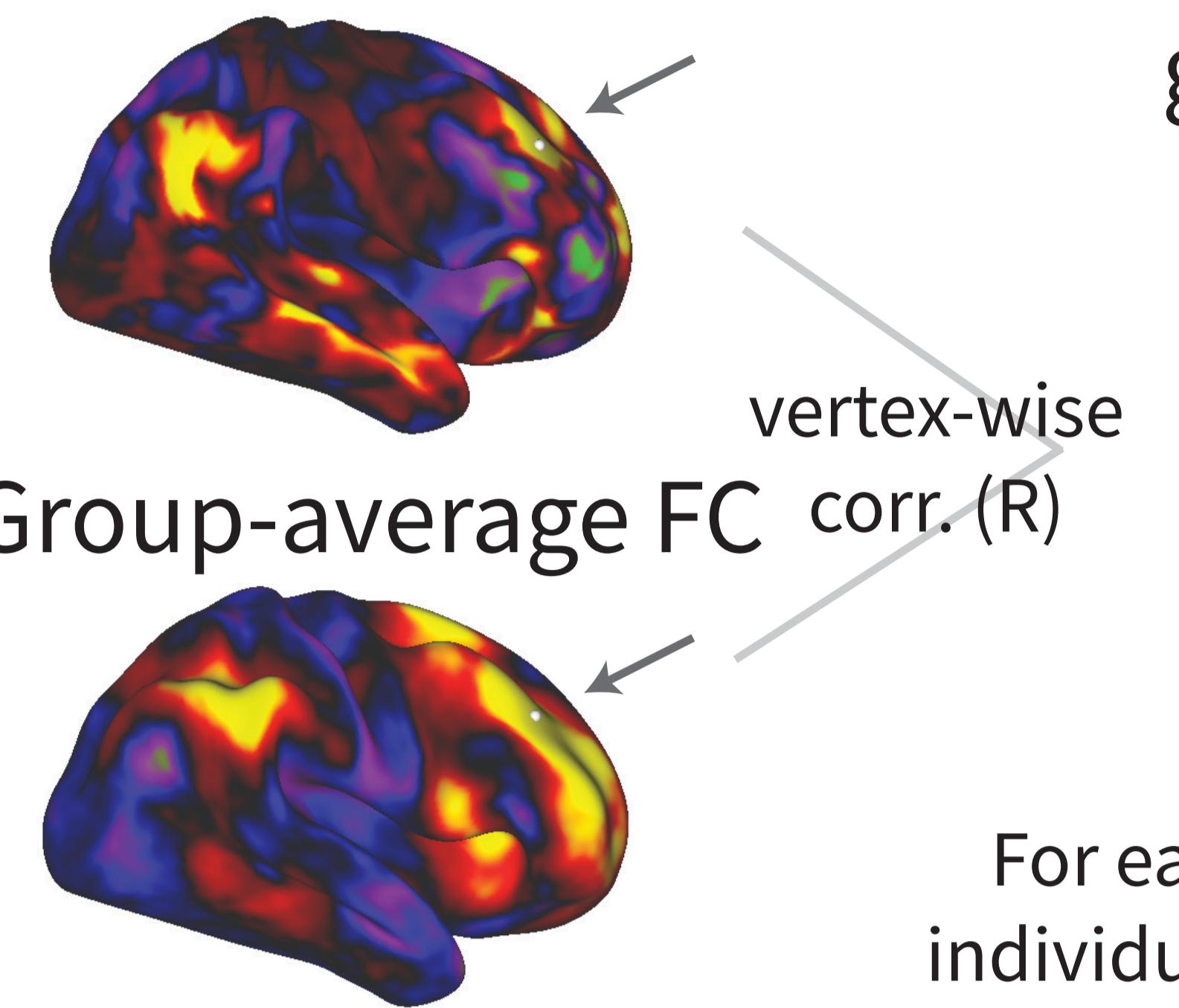
Lower individual variability in neonates is driven to some extent by similarity in local connectivity



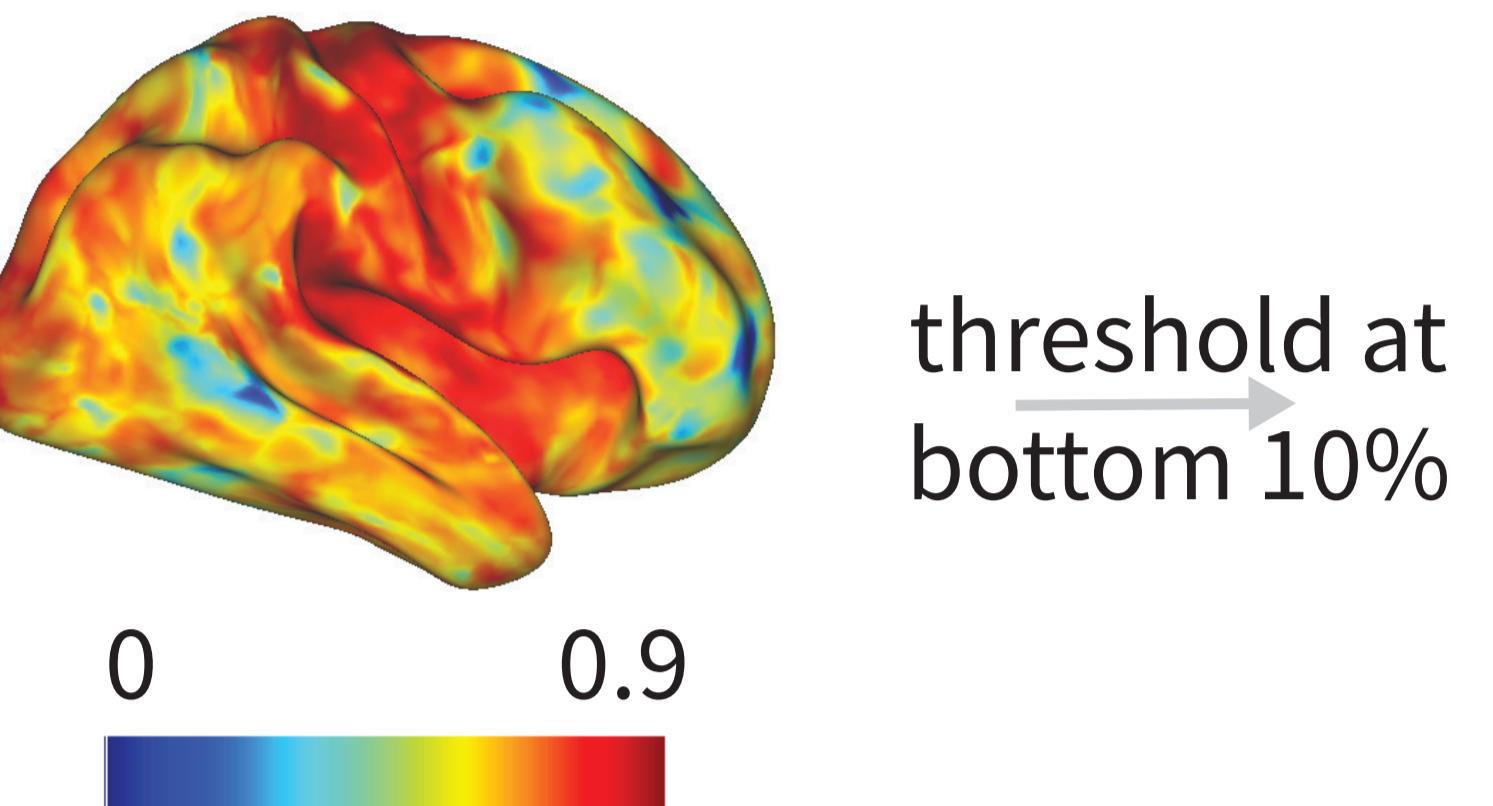
Using a distance exclusion of 49 mm before estimating individual-to-group spatial correlation.

Methods

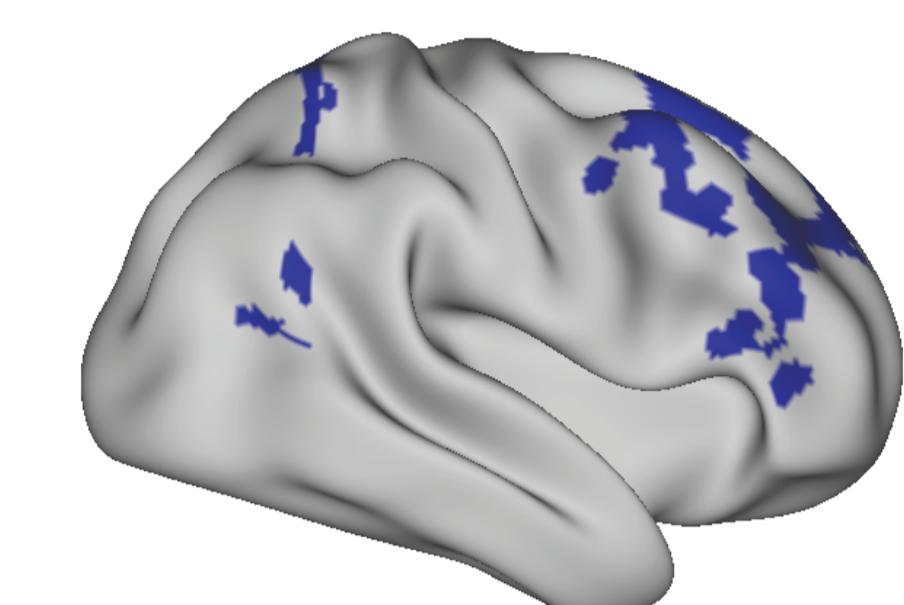
Individual's FC



Individual vs. group-average (R)



Individual's network variants



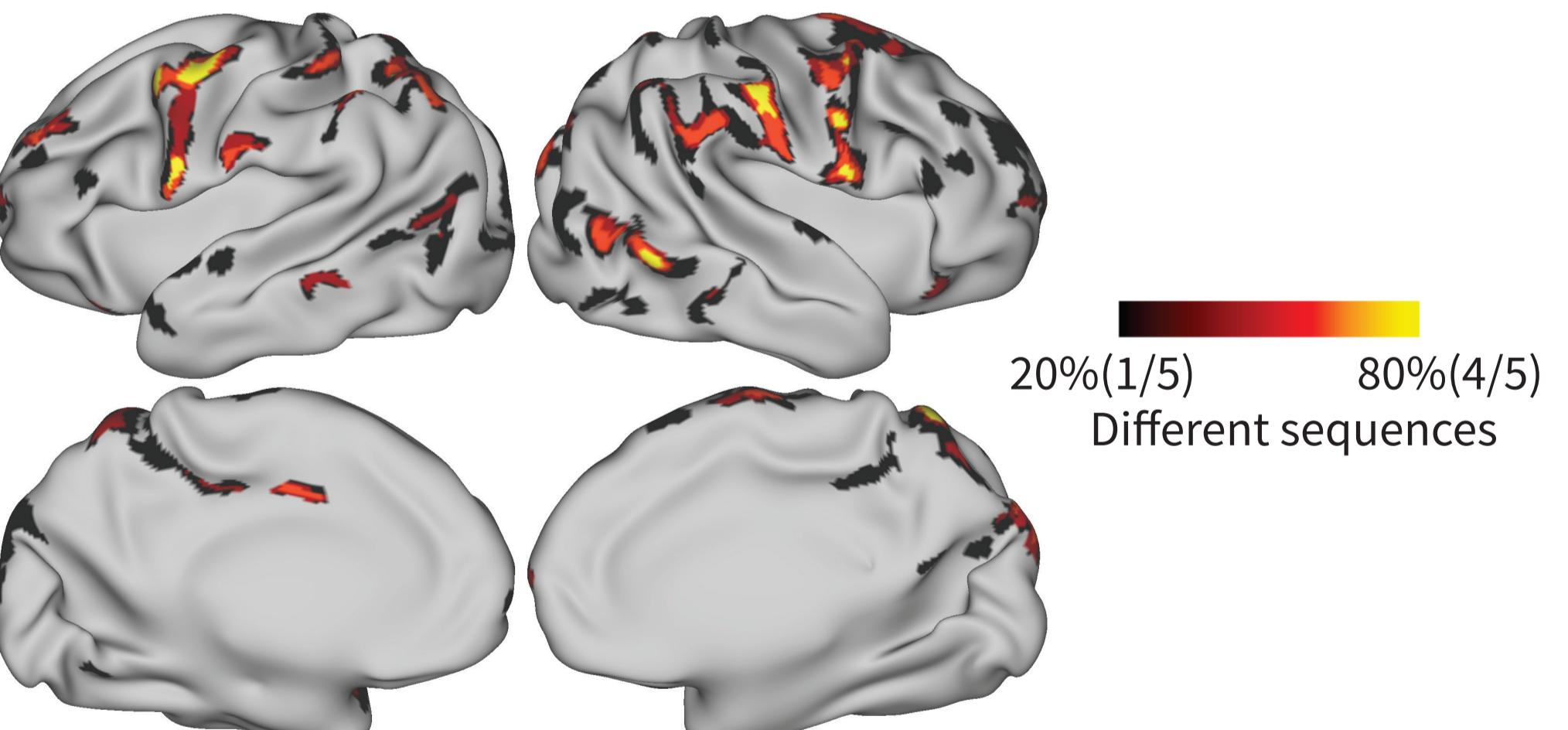
For each subject, localize regions of high individual difference and “network variants”

Precision baby ID	4049 (multi-echo)	4053 (all scans)	5000	5003 pre	5003 post
Gestational age (wks)	40	39	39	39	39
Postmenstrual age at scan (wks)	42	43	45	42	43
Time ex-utero at scan (days)	13	32	37	20	27
Sex at birth	F	F	M	F	F
Sessions	4	4	5	3	3
Total min of fMRI (FD < 0.25 mm)	118.57	133.02	202.92	110.72	146.66

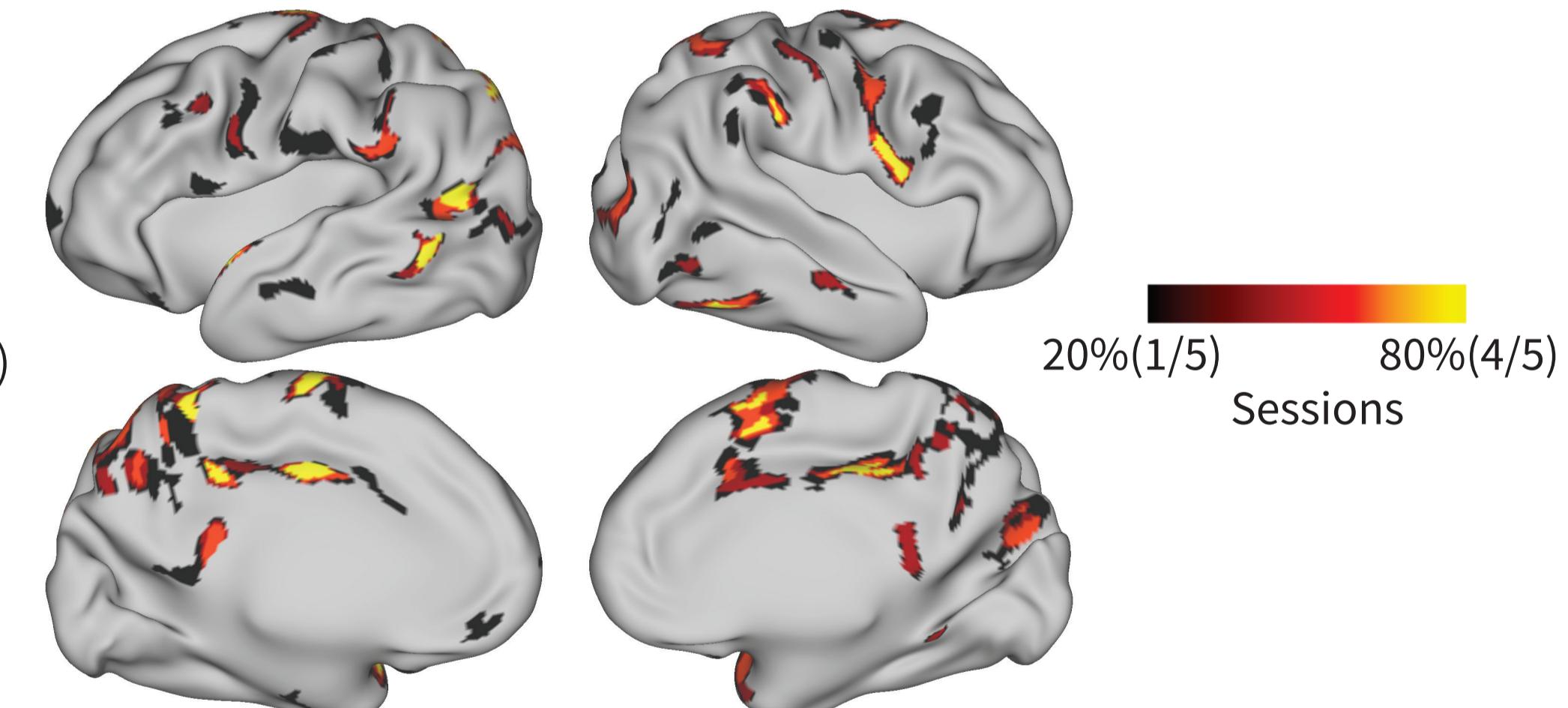
4053 had variation in scan parameters across runs, multi-echo and single-echo, multiband 4/6, voxel size 2.0/2.4mm. 4049 was all collected multi-echo, otherwise scan sequences were single-echo. Group average neonate drawn from a sample of n=319 neonates⁴ (37-45 wks, M = 41 wks, 55% male).

Network variants are robustly detectable and occur in similar areas in babies as in adults

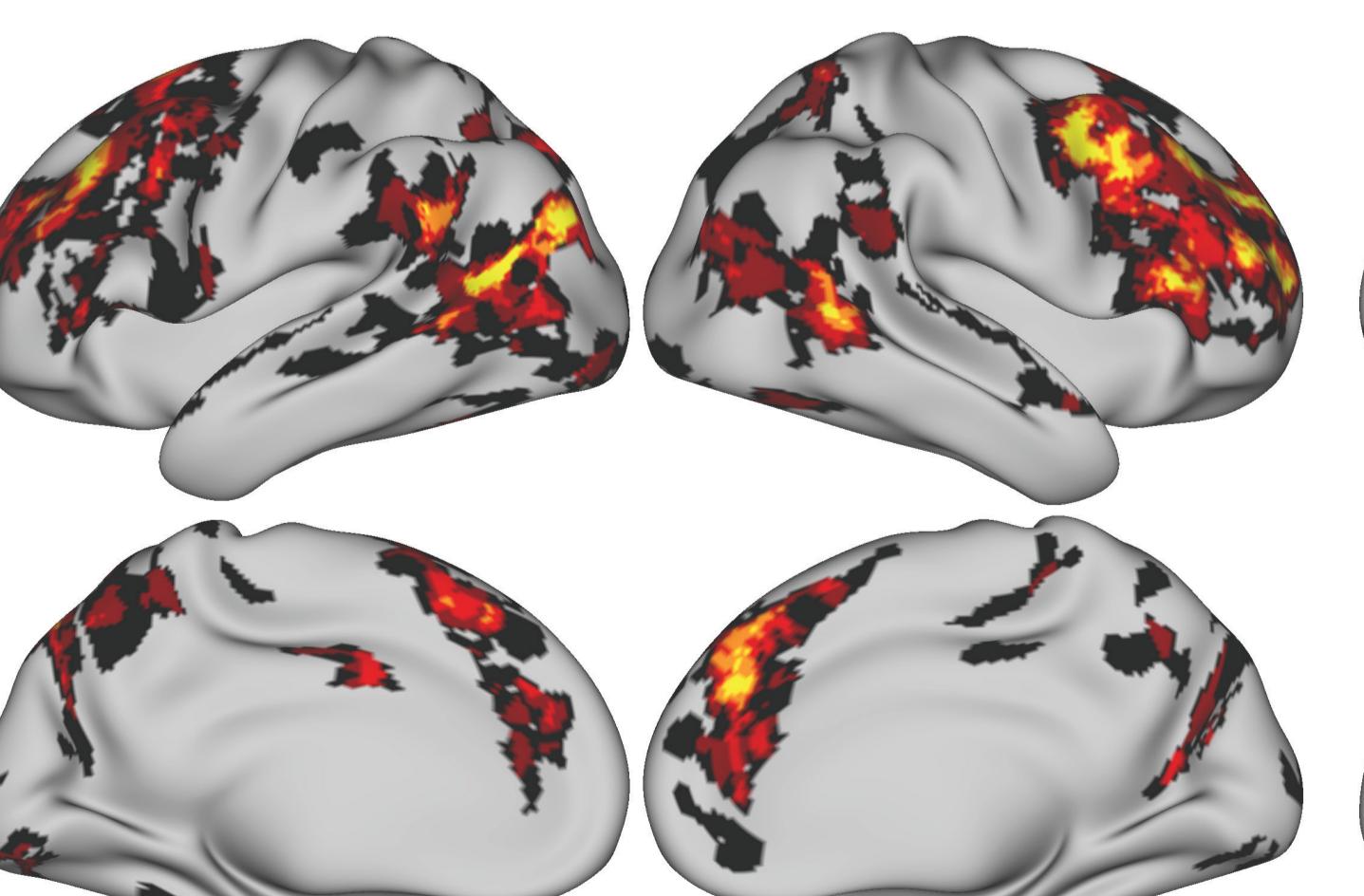
Variant locations within-subject across sequences (4053)



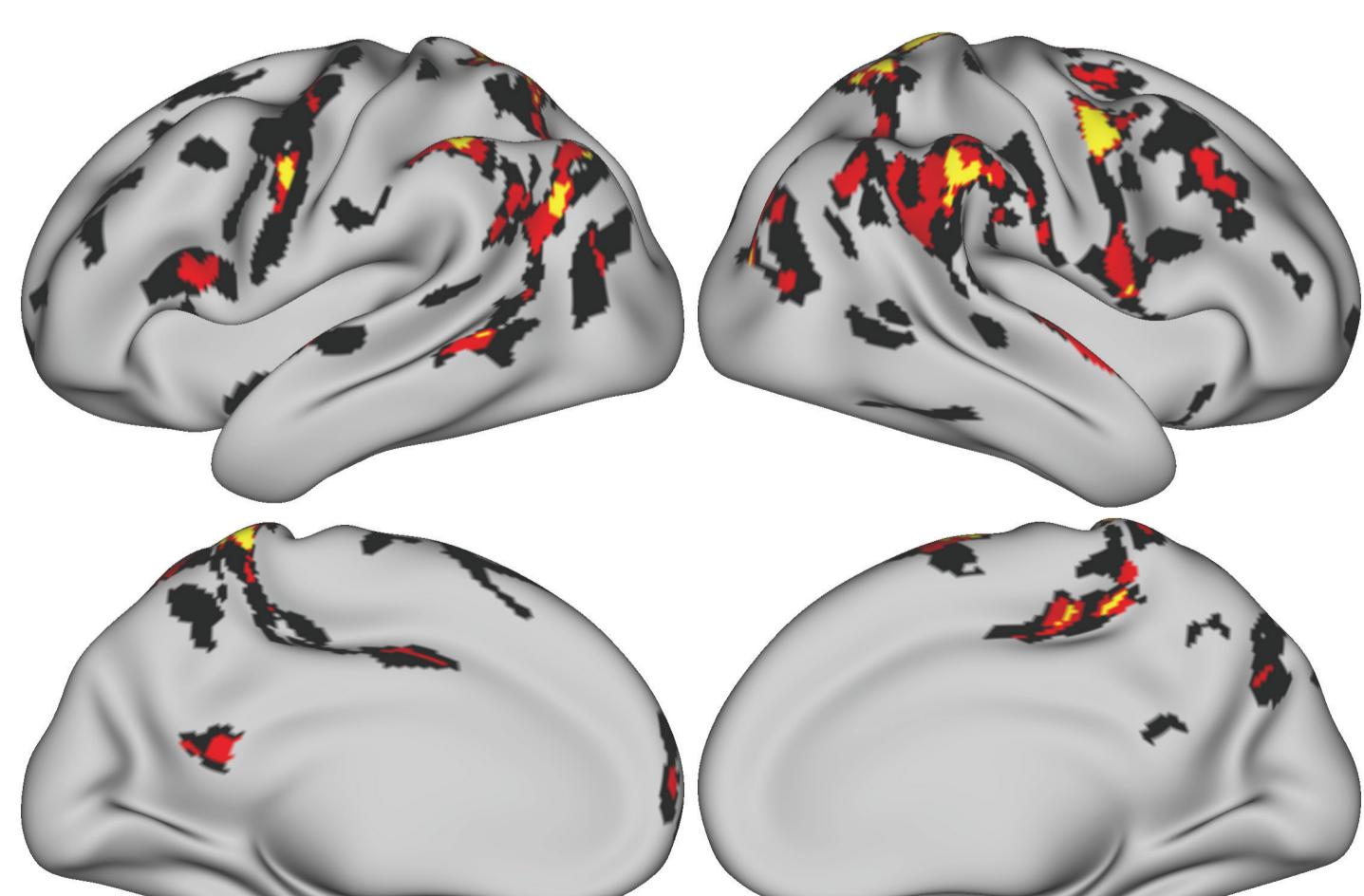
Variant locations within-subject across sessions (5000)



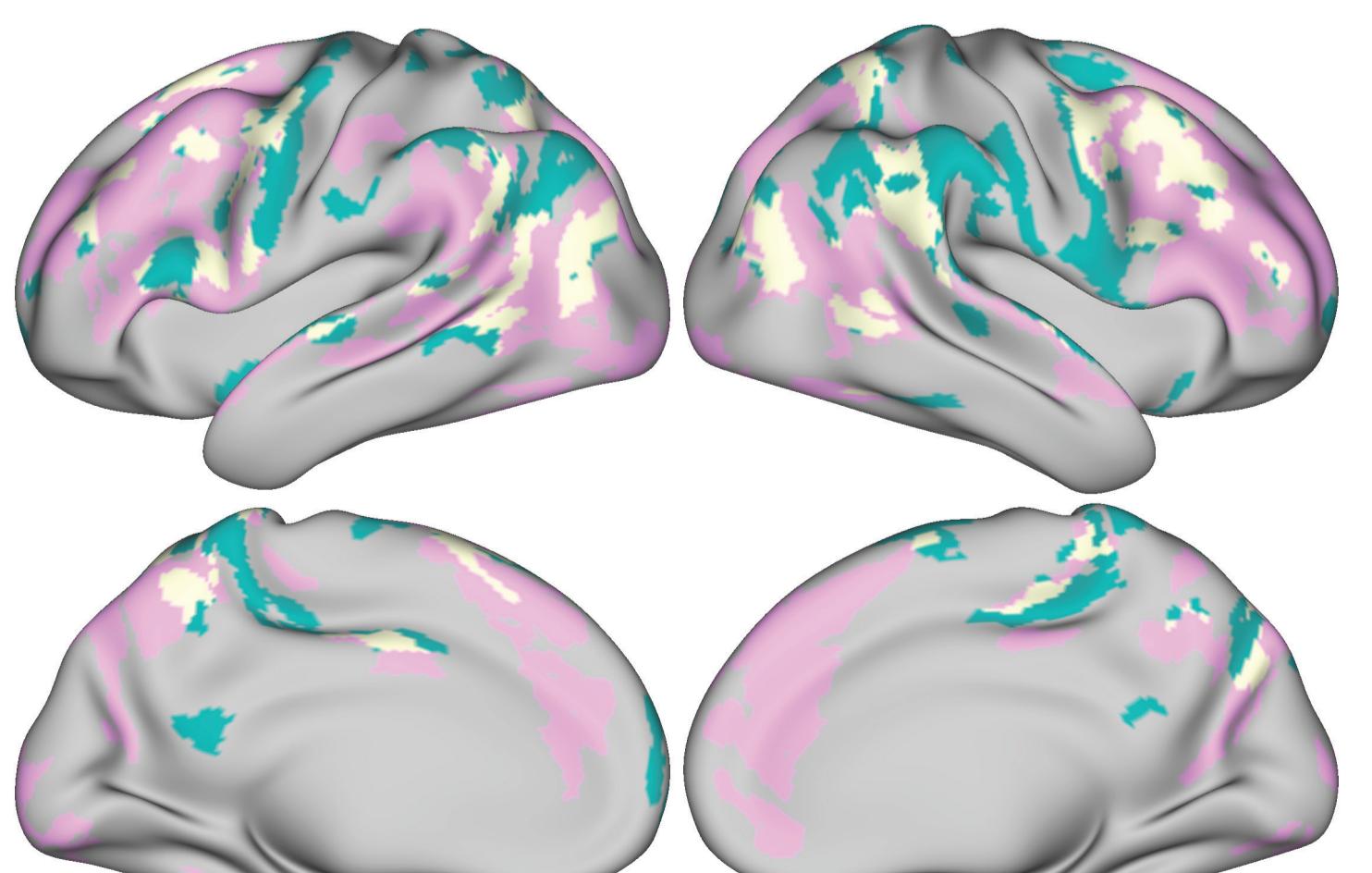
MSC variant locations



Neonatal variant locations



Overlap in variant locations



11% (1/9) Subjects

55% (5/9) Subjects

20% (1/5) Subjects

60% (3/5) Subjects

Adult

Neonatal

Overlap

Sequences for 4053 varied by single-echo/multi-echo, multiband factor, and voxel size. Network variants threshold set to 15% instead of 10% in precision babies.

References

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Acknowledgements

¹Geitzman, et al. (2019). Trait-like variants in human functional brain networks. *Proceedings of the National Academy of Sciences*, 20190292. ²Klaus, et al. (2021). Network variants are similar between task and rest states. *Neuroimage*, 229, 117742. ³Dworetzky, et al. (2023). Two common and distinct forms of variation in human functional brain networks (p. 2021.09.17.469799). bioRxiv. ⁴Perez, et al. (2023). Hemispheric Asymmetries of Individual Differences in Functional Connectivity. *Journal of Cognitive Neuroscience*, 35(2), 200–225. ⁵Luby, et al. (2023). Social disadvantage during pregnancy: Effects on gestational age and birthweight. *Journal of Perinatology*, 43(4), Article 4.