Bug Fix Regarding the Generation of Uniform Rotations on the Sphere

Aaron Alexander-Bloch (1), Julien Lefèvre (2), Jakob Seidlitz (3), Haochang Shou (4), Siyuan Liu (3), Theodore D. Satterthwaite (5), David C. Glahn (1, 6), Russell T. Shinohara (4), Simon N. Vandekar (4,7), Armin Raznahan (3)

1. Yale University School of Medicine, Department of Psychiatry

2. Aix-Marseille University, CNRS, INT, Inst Neurosci Timone, Marseille, France

3. Developmental Neurogenomics Unit, Human Genetics Branch, National Institute of Mental Health, Intramural Program

4. University of Pennsylvania Perelman School of Medicine, Department of Biostatistics, Epidemiology, and Informatics

5. University of Pennsylvania School of Medicine, Department of Psychiatry

6. Olin Neuropsychiatric Research Center, Institute of Living, Hartford Hospital

7. Vanderbilt University Medical Center, Department of Biostatistics

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Alexander-Bloch et al. (2018) proposed a spatial permutation testing procedure to perform a randomization test of the correspondence between brain maps, by sampling uniformly from the space of possible rotations of a spherical representation of the cortical surface. The procedure uses a finite number of permutations to compute the distribution of the test statistic. However, the implementation of generating random rotations originally described in our paper — rotating the coordinates of vertices at angles uniformly chosen between zero and 360 degrees about each of the x (left-right), y (anterior-posterior) and z (superior-inferior) axes — introduces a preference towards oversampling certain rotations. The publicly available code has thus been modified to incorporate an approach that samples uniformly from the space of possible rotations. We are grateful to Lefèvre et al. (2018) for bringing this error to our attention. For details about this issue, see Blaser and Fryzlewicz (2016).

Our original procedure, which does not sample uniformly on the surface, was employed in Alexander-Bloch et al. (2018), where we introduced the methodological foundation for the spin test procedure, as well as in another recently published paper (Reardon, Seidlitz, et al., 2018). A natural question is whether the results in these reports stand when the correct procedure is used to generate random rotations uniformly. Here, we demonstrate that the correct implementation of the spin procedure, employed by Lefèvre et al. (2018), which samples from all possible rotations uniformly, reproduces the same substantive findings produced in Alexander-Bloch et al. (2018) and Reardon, Seidlitz, et al. (2018).

**Table 1:** Original p-values for the analyses presented in Reardon, Seidlitz, et al. (2018), compared with p-values calculated using the uniform resampling procedure.

|  |  |  |
| --- | --- | --- |
| Test (continuous, *categorical*) | Original p-value | Uniform p-value |
| NIH vs. PNC | 0 | 0 |
| PNC vs. HCP | 0.002 | 0 |
| NIH vs. HCP | 0.001 | 0 |
| PNC vs. Evo | 0.003 | 0 |
| NIH vs. Evo | 0.003 | 0 |
| PNC vs. Devo | 0.03 | 0.008 |
| NIH vs. Devo | 0.011 | 0.012 |
| PNC vs. ASL | 0 | 0 |
| NIH vs. ASL | 0.063 | 0.02 |
| PNC vs. CMRGlu | 0.023 | 0.003 |
| NIH vs. CMRGlu | 0.052 | 0.011 |
| *PNC von Economo class 3 (+)* | 0.007 | 0.004 |
| *PNC von Economo class 6 (-)* | 0.014 | 0.011 |
| *NIH von Economo class 3 (+)* | 0.034 | 0.041 |
| *NIH von Economo class 6 (-)* | 0 | 0 |
| *PNC Yeo7 DMN (+)* | 0.001 | 0 |
| *PNC Yeo7 Lim (-)* | 0.007 | 0.003 |
| *NIH Yeo7 DMN (+)* | 0.004 | 0.005 |

*Abbreviations as follows: National Institute of Health sample (NIH); Philadelphia Neurodevelopmental Cohort sample (PNC); Human Connectome Project (HCP) sample; Yeo Atlas limbic system (Yeo7 Lim) and default mode network (DMN); evolutionary (evo) and developmental (devo) expansion; arterial spin labeling (ASL); cerebral metabolic rate of glucose (CMRGlu).*

To determine whether this change in implementation affected the results reported in Reardon, Seidlitz, et al. (2018), we reran all the analyses using the updated uniform sampling procedure. Specifically, 18 tests of correlation were performed between morphological scaling calculated using the National Institute of Mental Health (NIH), Philadelphia Neurodevelopmental Cohort (PNC) and Human Connectome Project (HCP) samples, and maps of scaling were compared with previously published maps of brain structure, function, physiology and development (see Table 1). The uniform procedure yielded quantitatively smaller p-values in 15 analyses and larger p-values in 3 analyses, but all results remained statistically significant as reported in the original paper.

To determine whether the change in implementation affected the results reported in Alexander-Bloch et al. (2018), we reran the tests of correlations between 120 Neurosynth meta-analytic maps. Out of 7,140 tests in the original paper, there were 35 significant correlations between maps which comprised 8 functional-anatomical clusters. Out of 7,140 tests in the re-analysis, 34 of the 35 correlations remained significant and formed the same 8 clusters. No new correlations were significant. The single change was within the “movement and motor planning” cluster; specifically, the correlation between the meta-analytic map for “action” and for “representation” did not meet the threshold for significance with the improved implementation.

In summary, statistical inferences based on the test appear to be robust to this change. However, we recommend using the updated code for future work.

Works Cited

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