A Comparison of Neuroimaging Software Procedures and a Contour Inference Method for Group-level Task-fMRI Analysis

by

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Contents

Acknowledgments

Declarations

I, Alexander Bowring, hereby declare that except where specific reference is made to the work of others, the contents of this dissertation are original and have not been submitted in whole or in part for consideration for any other degree or qualification in these, or any other Universities. This dissertation is the result of my own work and includes nothing which is the outcome of work done in collaboration, except where specifically indicated in the text.

- The work presented in Chapter 3 has been published in the *NeuroImage* journal (Bowring et al., 2018). This work was presented at the *Organization for Human Brain Mapping* (OHBM) Annual Meetings in 2017 and 2018. At the OHBM 2018 Annual Meeting, this work was the recipient of an oral presentation and Merit Abstract Award.
- The work presented in Chapter 4 has been published in the *NeuroImage* journal (Bowring et al., 2018). This work was presented at the OHBM Annual Meeting in 2017, where it was the recipient of an oral presentation.
- The work presented in Chapter 5 is based on a pre-printed manuscript.

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Abstract

Over the last three decades, Functional Magnetic Resonance Imaging (fMRI) has rapidly progressed to become the primary tool for human brain mapping. Recently however, considerable attention within the field has been directed towards data-sharing and open science initiatives. This has been driven by a growing apprehension about the reproducibility of findings within the neuroimaging literature, amid concerns that current inference procedures are often misused or misinterpreted causing the overall scientific conclusions to become distorted. With increasing availability to population-size neuroimaging databases, the limitations of such inference methods are also being made apparent: with sufficient statistical power, the null-hypothesis of no activation can be rejected over essentially the entire brain.

One aspect specific to neuroimaging pinpointed as a cause for poor reproducibility is the high flexibility of a typical fMRI analysis workflow. Across the pipeline, researchers can choose from a range of parameters to determine how each analysis step is carried out. In the first part of this thesis, we investigate how the choice of software package used to conduct a statistical analysis can influence the group-level results of a task-fMRI study. We use publicly shared data from three published task-fMRI studies, and reanalyze each study within the three main neuroimaging software packages, AFNI, FSL and SPM, using parameteric and nonparametric inference. All information on how to process, analyze, and model each dataset we obtain from the publications. We use a variety of quantitative and qualitative comparison methods to gauge the scale of variability in our results and assess fundamental difference between each software package. While qualitatively we find broad similarities between packages, we also discover marked differences, such as Dice similarity coefficient

values ranging from 0.000 to 0.743 in comparisons of thresholded statistic maps between software. We discuss the challenges involved in our replication attempt, while also utilizing open science tools in a considerable effort to make our own research reproducible.

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