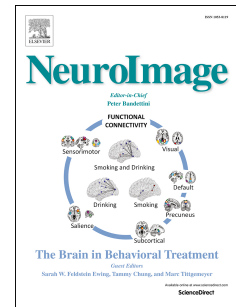


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Improving mass-univariate analysis of neuroimaging data by modelling important unknown covariates: Application to Epigenome-Wide Association Studies

Bryan Guillaume^a, Changqing Wang^a, Joann Poh^{a,f}, Mo Jun Shen^{a,f}, Mei Lyn Ong^f, Pei Fang Tan^f, Neerja Karnani^{c,f}, Michael Meaney^{d,e,f}, Anqi Qiu^{a,b,f}

^a*Department of Biomedical Engineering, National University of Singapore, Singapore*

^b*Clinical Imaging Research Centre, National University of Singapore, Singapore*

^c*Department of Biochemistry, Yong Loo Lin School of Medicine, National University of Singapore, 119228, Singapore*

^d*Ludmer Centre for Neuroinformatics and Mental Health, Douglas Mental Health University Institute, McGill University, Canada*

^e*Sackler Program for Epigenetics and Psychobiology at McGill University, Canada*

^f*Singapore Institute for Clinical Sciences, Agency for Science, Technology, and Research, Singapore*

Abstract

Statistical inference on neuroimaging data is often conducted using a mass-univariate model, equivalent to fitting a linear model at every voxel with a known set of covariates. Due to the large number of linear models, it is challenging to check if the selection of covariates is appropriate and to modify this selection adequately. The use of standard diagnostics, such as residual plotting, is clearly not practical for neuroimaging data. How-

*Anqi Qiu PhD, Department of Biomedical Engineering, National University of Singapore, 4 Engineering Drive 3, Block E4, 04-08, Singapore 117583. Email: bieqa@nus.edu.sg.

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