Submitter Name: Hae Kyung Im
Submitted email: haky@uchicago.edu

Exploring the mechanism behind drug addiction integrating predicted transcriptomic and radiomic data

Andrew Brown[1], Milton Pividori[2], and Hae Kyung Im[2]

[1]Department of Medicine, University of Dundee; [2]Department of Medicine, The University of Chicago

Genome-wide association studies have discovered tens of thousands of genomic loci robustly associated with a broad set of complex traits. Addiction phenotype loci have been harder to identify but the steady increase in the sample size of the studies is starting to yield new loci and insights into the underlying biology. Advances in statistical methods to integrate multiple sources of phenotypic and omic data open the possibility to extract further knowledge from existing data.

Methods such as PrediXcan have been successful in translating genomic loci into gene level results, which are functionally more informative. However, an analysis solely focused on the genetic component of predicted expression can miss the environmental contribution to disorders.

We hypothesized that brain MRI image derived phenotypes (IDP's, radiomics) can be used to examine both the genetic and environmental contribution to addiction biology.

We obtained brain MRI image derived phenotypes by the UK Biobank and extracted 900 features, covering structural, diffusion, and functional modalities. For each of the IDP's we calculated the correlation with substance abuse, smoking status, coffee intake, and tea intake. We found that a large portion of features correlate significantly with substance abuse, smoking status, and coffee intake. For example, coffee intake was negatively associated with volume of grey matter in various regions.

These results demonstrate the relevance of IDP's in substance-abuse behaviors and we expect that the partitioning of IDPs into genetic and environmental components will provide further insights into the etiology of drug related phenotypes.