

M4. MULTI-STATE SURVIVAL ANALYSIS OF MULTI-PsYCHIATRY DISORDERS

Yunpeng Wang¹, Ole Andreassen², Andrew Schork³, Thomas Werge⁴, Wesley Thompson³

¹NORMENT, University of Oslo and Institute of Biological Psychiatry, St. Hans Hospital, Denmark., ²University of Oslo, ³University of California, San Diego, ⁴Institute of Biological Psychiatry, MHC Sct. Hans, Mental Health Services – Copenhagen

Background Psychiatric diseases are complex disorders with sizable portion inheritable component, i.e., heritability. Recent studies have shown that the polygenic genetic architecture fit the observed data, and, multiple types of genetic variants (SNP, CNV, etc.) contribute to the risk of developing the diseases. It has also shown that multiple psychiatric diseases may share common genetic component to some extent. However, very few studies have performed based on the multiple diagnosis of the same subject. Here, we studied the effect of genetic component and other covariates on the transition probabilities among multiple psychiatric disorders.

Methods The iPSYCH project is a case-cohort study which has recorded a comprehensive set diagnosis along with other covariates for ~9 million subjects among which ~80000 subjects have been genotyped. We applied the Multi-State Cox proportional hazards model on the iPSYCH dataset. We investigated the impact multiple types of genetic component (CNV, SNPs based polygenic score) and Gestational Ages on the transition probabilities of developing multiple disorders.

Results The iPSYCH project is a case-cohort study which has recorded a comprehensive set diagnosis along with other covariates for ~9 million subjects among which ~80000 subjects have been genotyped. We applied the Multi-State Cox proportional hazards model on the iPSYCH dataset. We investigated the impact multiple types of genetic component (CNV, SNPs based polygenic score) and Gestational Ages on the transition probabilities of developing multiple disorders.

Discussion Our preliminary findings demonstrate that the iPSYCH project provide the opportunities to investigate the genetic impact on the risk of psychiatric disorders in a more comprehensible manner. The probability of developing multiple diseases and the ordering of diagnoses may also have a unique genetic architecture.

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