



Research Theme: Biomedical Data Science/Drug Discovery/Machine learning/Computational Biology

MSc Research Project Title: Large-scale analysis of schizophrenia blood-based signatures

Principal Investigator/Supervisor: Wilson Goh

Co-supervisor/ Collaborator(s) (if any): Jimmy Lee

Project Description

a) Background:

The rapidly changing facet of society has imposed strain and pressures amongst young people. This can lead to mental illness, which in turn, imposes social and economic challenges. While therapeutic practices e.g. mindfulness training as implemented in New Zealand, can alleviate these issues, a data-centric approach towards early detection and achieving mechanistic understanding, is desirable.

Mental illnesses have risen rapidly in the rankings from 13 in 1990 to 7 in 2017 as a leading cause of DALYS (Disability-adjusted Life Years). About 75% of mental illnesses have their onset before age 25 and continue to afflict suffering over a prolonged period, causing chronic disability. Mental illnesses rank the second leading cause of years lived with disability (YLD). A young person may be diagnosed as Ultra-High Risk (UHR) for development of mental illness, based on a complex panel of behavioural traits.

While UHR is behavioural in its diagnoses, we hypothesize there is also a molecular signature that is observable. Our early study in blood samples derived from a cohort study suggests that the presence of a reproducible 12-gene signature in peripheral tissue. We currently possess a "pseudo-gold standard" of biospecimens from 194 youths (94 UHR and 100 controls) collected and observed over a 2-year period.

b) Proposed work:

You will work on the bioinformatic analysis of this large-scale one-of-a-kind gene expression dataset. You will combine this early-stage UHR cohort, with analyses and data from chronic schizophrenic cohorts so that we can understand how blood-based signatures change with disease progression.

We will also combine and integrate the gene expression data with proteomic information derived from circulating plasma proteins.

Finally, we will test the prediction accuracy of models developed with pure gene signatures or combinatorial signatures comprised of both gene and protein information.

c) Preferred skills:

Highly motivated candidates with strong computing/mathematical/statistical skills and bioinformatics skills are strongly encouraged to apply.

Supervisor contact:

If you have questions regarding this project, please email the Principal Investigator:

wilsongoh@ntu.edu.sg

SBS contact and how to apply:

Associate Chair-Biological Sciences (Graduate Studies) : AC-SBS-GS@ntu.edu.sg

Please apply at the following:

Application portal:

<https://venus.wis.ntu.edu.sg/GOAL/OnlineApplicationModule/frmOnlineApplication.ASPX>