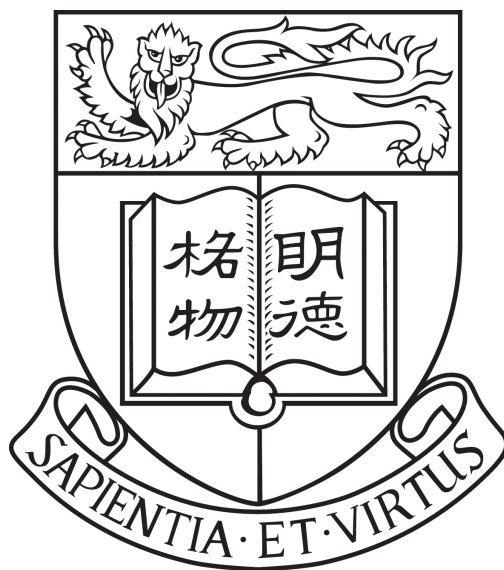


Heritability Estimation and Risk Prediction in Schizophrenia

Choi Shing Wan

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Department of Psychiatry
University of Hong Kong
Hong Kong
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Declaration

Acknowledgements

Abbreviations

SCZ Schizophrenia. 13

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Introduction

Some considerations

1. PRSice requires the phenotype to aid its selection (More information= stronger)
2. It seems like LDSC doesn't necessary perform badly in oligogenic situation. Rather, it is that when the trait is oligogenic, it is more likely for LDSC to behaviour in a strange way.
3. For each condition: extreme phenotype, quantitative trait, case control, we can have a separated review. Discuss on the benefits and challenges of each condition and the method we deal with them. So we can have two chapters (case control, quantitative trait) where extreme phenotype can be a big subsection within quantitative trait.
4. For each chapter, there will be this introduction (review on the method), our methodology (Calculation, implementation and also simulation), result (the simulation result). Then we can have the application (PGC, network)

Chapter 1

Literature Review

1.1 Twin Studies - Delineating Genetic and Environmental Contribution

Should briefly talk about how Twin modeling was used for finding the GE contribution. Should also mention the ACE model. At the end, we can talk about the heritability estimates of SCZ and AD

1.2 Searching for Genetic Variants

1.2.1 Role of Common Variants

Genome Wide Association Study

Should talk about what is GWAS and how it is used. Should also talk about the current GWAS studies in SCZ and AD

1.2.2 Role of Rare Variants

Exome Sequencing

Similar to the GWAS. Talk about the Pros and Cons. Need to briefly mention the Denovo paper and Shaun's paper.

Whole Genome Sequencing

Very very brief description of WGS and the current status.

1.3 Summary

Chapter 2

Heritability Estimation

This chapter should be used in similar way as the general method section in Clara's thesis. Considering that the subsequent chapters all rely on this implementation.

2.1 Introduction

2.2 Methodology

2.2.1 Quantitative Trait

2.2.2 Case Control Studies

2.2.3 Extreme Phenotype Selections

2.3 Simulation

2.3.1 Quantitative Trait

2.3.2 Case Control Studies

2.3.3 Extreme Phenotype Selections

2.4 Result

2.5 Discussion

Chapter 3

Heritability of Schizophrenia

3.1 Introduction

3.2 Heritability Estimation

This will be a very simple section, focused on how to perform the heritability estimation on Schizophrenia (SCZ). Should also tokenize the heritability into subcategories (e.g. immune, neuron, etc)

3.2.1 Methodology

3.2.2 Result

3.3 Brain development and Schizophrenia

Here we will perform the WGCNA and brain development network. Seeing how the whether if any brain development network were enriched with SNPs that explain the variance of phenotype

3.3.1 Methodology

3.3.2 Result

3.4 Discussion

Chapter 4

Heritability of Response to antipsychotic treatment

4.1 Introduction

Here we try to use Beatrice's data and estimate the heritability explained in drug response. Should also repeat the region-wise heritability

4.2 Methodology

4.3 Result

4.4 Discussion

Chapter 5

Risk Prediction

5.1 Methodology

5.1.1 Simulation

5.2 Result

5.3 Discussion

Chapter 6

Conclusion

Appendix