Heritability Estimation and Risk Prediction in Schizophrenia

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Declaration

Acknowledgements

Abbreviations

GWAS Genome Wide Association Study. 7, 8

SCZ Schizophrenia. 11

SNP Single Nucleotide Polymorphism. 7, 8

Contents

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

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 Narrow Sense Heritability

1.4 Risk Prediction

1.5 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

The narrow-sense heritability is defined as

$$h^2 = \frac{var(X)}{var(Y)}$$

where $var(X)$ is the variance of the genotype and $var(Y)$ is the variance of the phenotype. In a Genome Wide Association Study (GWAS), regression were performed between the SNPs and the phenotypes, giving

$$Y = \beta X + \epsilon \tag{2.1}$$

where Y and X are the standardized phenotype and genotype respectively. ϵ is then the error term, accounting for the non-genetic elements contributing to the phenotype (e.g. Environment factors). Based on equation 2.1, one can then have

$$\begin{aligned} var(Y) &= var(\beta X) + var(\epsilon) \\ var(Y) &= \beta^2 var(X) \\ \beta^2 \frac{var(X)}{var(Y)} &= 1 \end{aligned} \tag{2.2}$$

β^2 is then considered as the portion of phenotype variance explained by the variance of genotype. Which can also be considered as the narrow-sense heritability of the phenotype.

It is noted that as both X and Y are standardized, β^2 will be equal to the coefficient of determination (r^2).

A challenge in calculating the heritability from GWAS data is that usually only the test-statistic or p-value were provided and one will not be able to directly calculate the heritability based on equation 2.2. In order to estimation the heritability of a trait from the GWAS test-statistic, we rely on the properties of the Pearson product-moment correlation coefficient:

$$r = \frac{t}{\sqrt{n - 2 + t^2}} \tag{2.3}$$

where t follows the student-t distribution and n is the number of samples. One can then obtain the r^2 by taking the square of 2.3

$$r^2 = \frac{t^2}{n - 2 + t^2} \tag{2.4}$$

It is observed that t^2 will follow the F-distribution and when n is big, t^2 will converge into χ^2 distribution.

As under the null distribution, t^2 should have mean approximately equal to 1, we then define the SNP contribution (f) as:

$$f = \frac{t^2 - 1}{n - 2 + t^2} \tag{2.5}$$

When all the SNPs were independent, the heritability of the phenotype can be simply defined as

$$h^2 = \sum_{1}^{m} f \tag{2.6}$$

where m is the number of SNP.

Considering that one of the main concept in GWAS is to be be able to "tag" the true causal variants using common SNPs based on the linkage disequilibrium between the SNP, it is impractical to assume the SNPs to be independent from each other. When linkage disequilibrium exists between the SNPs, equation 2.6 will provide an over-estimation of the heritability. In order to obtain an unbiased estimation of the heritability of the phenotype, one must take into account of the linkage structure between the SNPs.

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 Exreme 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