

# The Method of Limits and Its Application to The Analysis of Count Data in Genome-Wide Association Studies

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## ABSTRACT

We propose a new method of statistical inference, called the method of limits (MoL), which may be viewed as an extension of the method of moments. This method is motivated by the need to analyze count data for genome wide association studies (GWAS), where the existing methods are hindered in statistical inference due to computational challenges. We establish consistency and asymptotic normality of the MoL estimator of heritability from GWAS data, which is seen as an advantage over the existing PQLseq method. Furthermore, we derived a consistent estimator of the proportion of causal SNPs. MoL also showed an advantage of both statistical and computational efficiency measured by average statistical efficiency (ASE) in our simulation studies compared to PQLseq. We also illustrate the usefulness of MoL through its application to the UK Biobank data to infer the heritability of weekly champagne consumption and week red wine consumption using the count data.

**Keywords:** Asymptotic properties; Big GWAS data; Proportion of causal SNPs; Relative average statistical efficiency

# Weighted Conditional Network Testing for Multiple High-Dimensional Correlated Data Sets

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## ABSTRACT

Gaussian graphical models (GGMs) have been investigated to infer dependence (or network) structure among high-dimensional data by estimating a precision matrix. However, while many estimation methods for GGM have been developed, methods for testing the equality of two precision matrices are still limited. Because testing the equality of the precision matrix depends on other given precision matrices, we develop a weighted conditional network testing for considering other given precision matrices information and also provides theoretical properties. None of the existing methods can be applied to test conditional differences when other networks are conditionally given and different. We demonstrate the advantage of our approach using a simulation study and genetic pathway analysis.

**Keywords:** Conditional Difference; Gaussian Graphical Model; Precision Matrix