

Meta-analysis of correlated traits using summary statistics from GWAS

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Genome-wide association study (GWAS) is one of the important approaches to detect genetic variants underlying complex traits. Meta-analysis is often conducted to summarize the association evidences from multiple studies. When multiple correlated traits are available, analyses are often performed for each trait separately. For example, researchers often perform analysis for systolic blood pressure, diastolic blood pressure and hypertensive status separately in searching genetic variants underlying hypertension. The Bonferroni correction is used to account for multiple tests. Such analysis procedure may reduce power when the same genetic variants contribute to the variation of correlated traits. Here we propose a novel statistical approach to perform meta-analysis of multiple correlated traits. This method is robust to population structure and correlated samples between different cohorts. Both simulation and real data analysis will be present in this talk.

Key Words: correlated traits, genome wide association study, meta-analysis, multiple tests