

Heritability Estimation using Regularized Regression Approach (HERRA)

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Heritability is a concept that summarizes the proportion of phenotypic variance that is due to genetic factors, with broad-sense heritability referring to genetic variation that may include effects due to dominance and epistasis, and narrow-sense heritability referring to additive genetic variation. The popular GCTA software uses the random effects approach to estimate the narrow-sense heritability based on GWAS data of unrelated individuals without identifying causal loci. Many methods have since extended this approach to various situations, e.g., related subjects, explicitly accounting for latent causal loci and uneven linkage disequilibrium between SNPs. However since the proportion of causal loci among the variants is typically very small and GCTA uses all variants to calculate the similarities among individuals, the estimation of heritability may be unstable, resulting in large variance of the estimates. Naturally an approach that filters out irrelevant variants has the potential to improve the accuracy of estimation. In this talk we present a novel narrow-sense heritability estimator using regularized regression approach. Our proposed heritability estimator is a consistent estimator; has a smaller variance compared to the state-of-the-art estimators; and also computationally more efficient. We demonstrate these features by simulation study and a real-data example, and provide the R code for implementing our estimator.

This is a joint work with Li Hsu, Fred Hutchinson Cancer Research Center, Seattle, USA