

DISSERTATION PRESENTATION AND DEFENSE

Bayesian Variable Selection from Summary Data, with Application to Joint Fine-mapping of Multiple Traits

WHEN

July 15, 2021
2:00 PM, CDT

WHERE

Via ZOOM

ZOOM information will be provided in the email announcement for this seminar.



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Bayesian methods provide attractive approaches to select relevant variables in multiple regression models, particularly in settings with very highly correlated variables. For example, they are popular in genetic fine-mapping problems, aiming to identify the genetic variants that causally affect some phenotypes of interest. However, Bayesian methods are limited by the computational speed and the interpretability of the posterior distribution. Wang et al. (2020) presented a simple and computationally scalable approach to variable selection, the “Sum of Single Effects” (SuSiE) model, which provides a Credible Set for each selection, making the results easy to interpret. The SuSiE model requires access to individual genotypes and phenotypes.

In this dissertation, we provide a method to fit the SuSiE model using summary statistics from univariate regression results. To improve the accuracy and power for variable selection, we further generalize the SuSiE framework to select variables jointly for multiple outcomes and account for complicated effect size heterogeneity among outcomes. We provide multivariate variable selection methods using individual-level data, sufficient statistics, and summary statistics. We illustrate the power and flexibility of our method using realistic numerical simulations and applications to joint fine-mapping UK Biobank blood cell traits.

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