

# A Bayesian approach to genome-wide genetic association studies with survival time as outcome

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## Abstract

Treatment responses to common diseases, like cancer, often vary greatly, it is of interest to see if genetic variants contribute to the variability and to obtain genetic variants as biomarkers that predict the overall survival or time to progression for a cancer patient given a specific treatment. Conventional approaches that take an agnostic genome-wide association study approach usually perform single SNP analysis with Bonferroni correction, which is too conservative. This practice contributes to the issue of “missing heritability” in the genome-wide genetic approach to disease susceptibility studies. In the context of a survival model, we take a Bayesian approach in which the prior distribution is motivated by classical concept of heritability. This approach helps to assess the heritability in a GWAS approach to survival treatment response. We use Markov Chain Monte Carlo to simulate the posterior distribution for inference. Simulation studies will be provided to indicate the numerical performance of this method and compare it with single SNP analysis method. Illustrations by a real dataset will be included. In particular, we will show that this approach alleviates the issue of missing heritability in GWAS.