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Lilit C Moss*, chemenya@usc.edu, and **William J Gauderman, Juan Pablo Lewinger** and **David V Conti**. *Using Bayes Model Averaging to Leverage Both Gene Main Effects and GxE Interactions to Identify Genomic Regions in Genome-Wide Association Studies.*

Genome-wide association studies (GWAS) typically search for marginal associations between a single nucleotide polymorphism (SNP) and a disease trait while gene-environment (GxE) interactions remain generally unexplored. More powerful methods beyond the simple case-control approach leverage either marginal effects or case-control ascertainment to increase power. However, these potential gains depend on assumptions whose aptness is often unclear a priori. Here, we review GxE methods and use simulations to highlight performance as a function of main and interaction effects and the association of the two factors in the source population. Substantial variation in performance between methods leads to uncertainty as to which approach is most appropriate for any given analysis. Our framework is based on Bayes model averaging, which provides a principled statistical method for incorporating model uncertainty. The resulting method exploits the joint evidence for main and interaction effects while gaining power from a case-only equivalent analysis. Through simulations we demonstrate that our approach detects SNPs within a wide range of scenarios with increased power over current methods. We illustrate the approach on a gene-environment scan in the USC Children's Health Study. (Received August 28, 2018)