

Supplement - lrgpr: Interactive linear mixed model analysis of genome-wide association studies with composite hypothesis testing and regression diagnostics in R

Gabriel E. Hoffman, Jason G. Mezey, and Eric E. Schadt

Supplementary Table 1: Comparison of runtimes when the options for optimization of variance components in the linear mixed model are the same across multiple programs. The options are set so that the log-likelihood is maximized with respect to δ , the ratio of variance components, in 100 intervals of δ evenly spaced on a logarithmic scale between -10 and 10. This is the default setting for lrgpr and EMMA and thus results are shown in the main text. Here the options of GEMMA and FaST-LMM were set to be consistent with these settings. These options cannot be set for the other programs.

samples, markers	GEMMA	FaST-LMM
5K, 500K	581m 46s	183m 56s
10K, 1M	2989m 13s	NA ¹

¹Requires more than 64Gb of memory