

Supplementary Figures and Tables for “Fast Effect Size Shrinkage Software of Beta-Binomial Models of Allelic Imbalance”

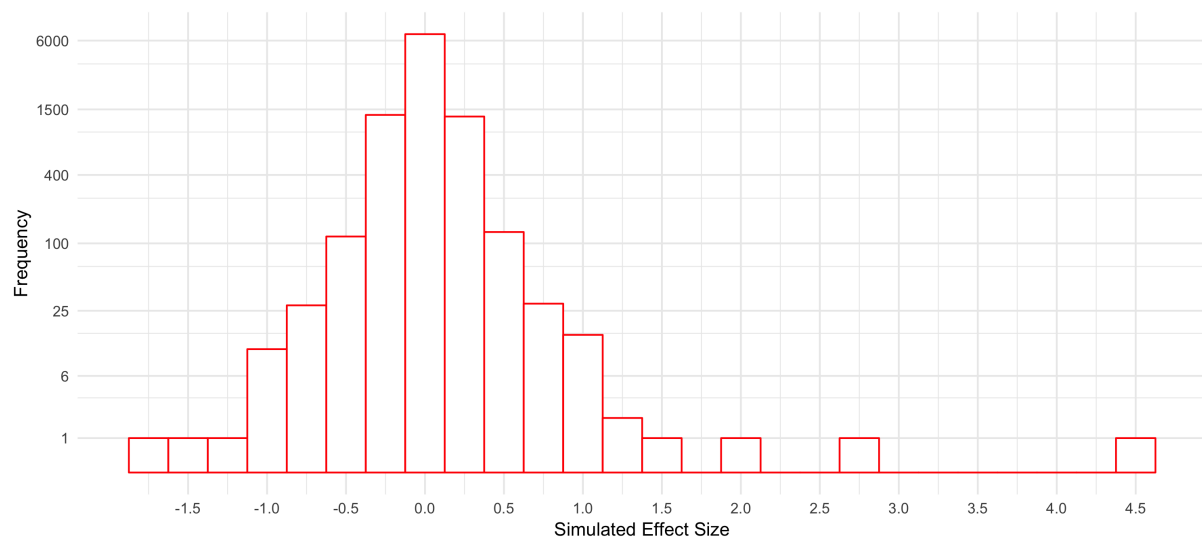


Figure 1: Distribution of Simulated Effect Sizes from Second Simulation

Our sampled distribution gave us mostly very small effect sizes, but with occasional moderate and large effect sizes appearing.

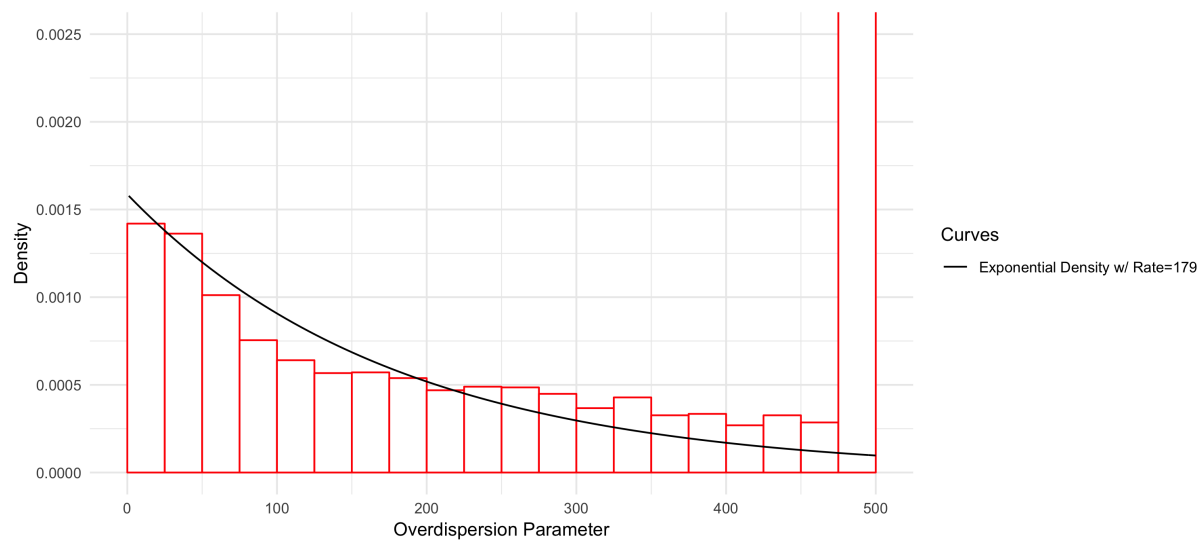


Figure 2: Distribution of Overdispersion Parameter Estimates from Mouse Gene-specific overdispersion parameters were estimated from fitting intercept-only models to each gene in the mouse dataset.

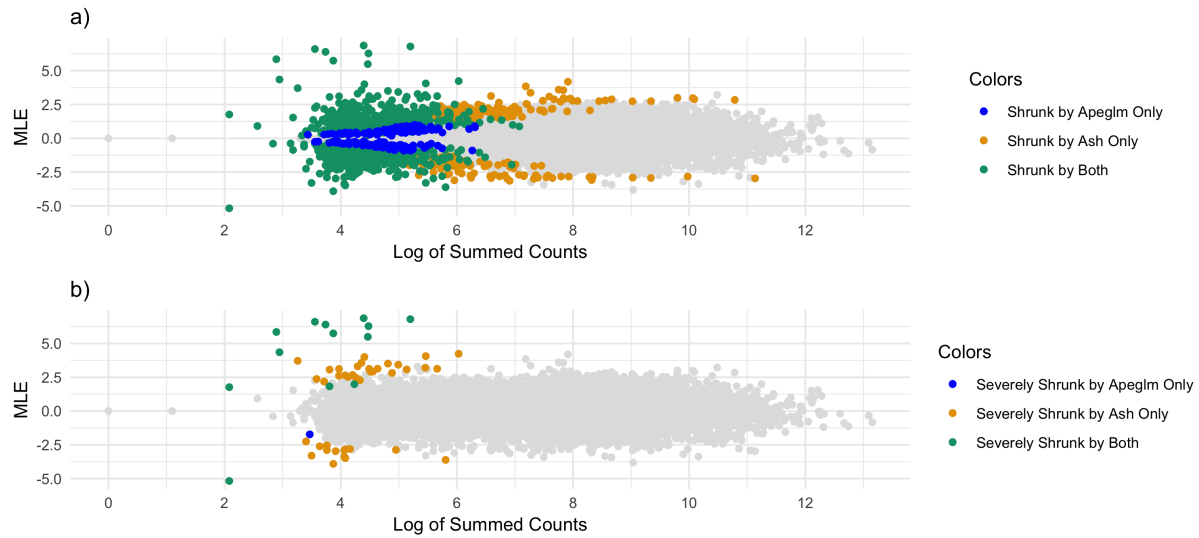


Figure 3: MA Plots for Normal Simulation

Each point is a gene, the x-axis is the logarithm of the gene's summed counts, and the y-axis is the ML estimate for the gene. Points are colored by whether they were shrunk in a) and whether they were severely shrunk in b). Shrunk genes overwhelmingly had low counts, and severely shrink genes universally had low counts.

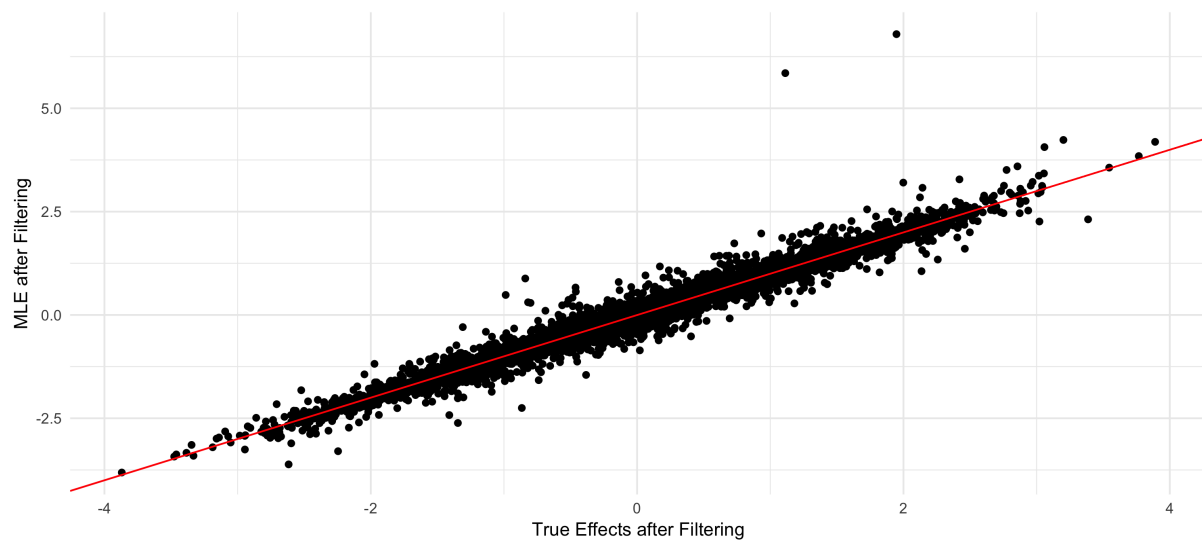


Figure 4: Truth vs. Estimate Plot after Filtering

We can see that most ML estimates that were very far from the truth were removed after filtering out low-count genes using the optimal filtering rule.

Quantiles	50th	75th	90th	95th	97.5th	99th	99.5th	Max	P-value
Apeglm	0.011	0.03	0.106	0.206	0.328	0.467	0.627	5.334	2e-14
Ash	0.009	0.032	0.112	0.225	0.389	0.692	1.054	6.587	

Table 1: Quantiles of Shrinkage Scores for Normal Simulation

Ash had more extreme shrinkage than apegm, as evident by larger shrinkage scores across all quantiles above the 50th. The p-value reported came from a paired t-test between apegm and ash shrinkage scores, with scores paired by gene.

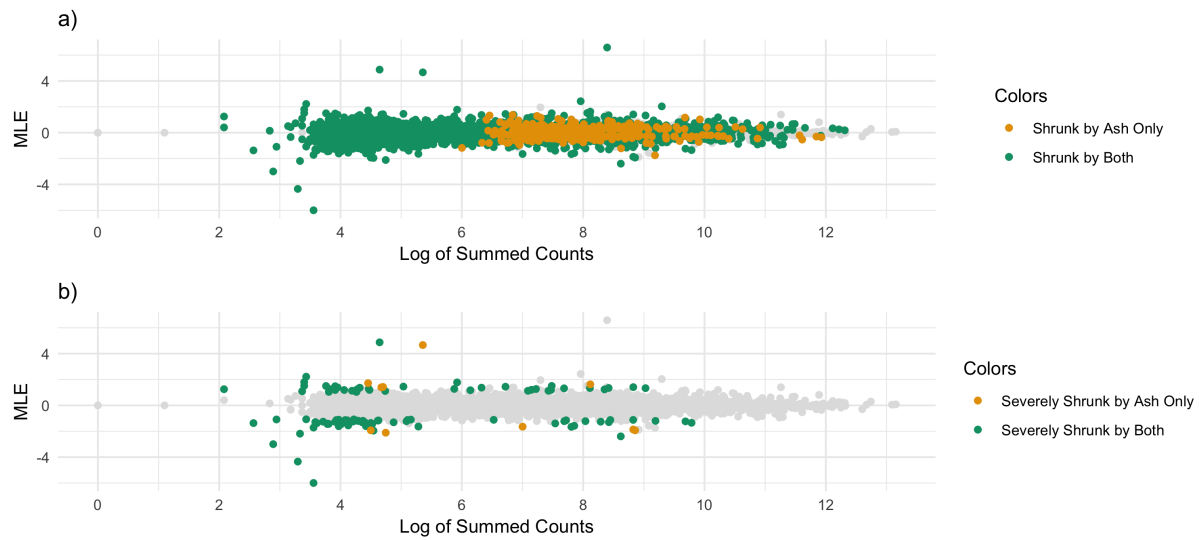


Figure 5: MA Plots for Student's T Simulation

Points are colored by whether they are shrunk in a) and whether they are severely shrunk in b). Any genes noticeably or severely shrunk by `apecglm` were shrunk practically as much or more by `ash`. Unlike in the normal simulation, many noticeably shrunk and severely shrunk genes had moderate or high counts.

Quantiles	50th	75th	90th	95th	97.5th	99th	99.5th	Max	P-value
Apeglm	0.06	0.15	0.338	0.53	0.731	1.033	1.218	5.958	<2e-16
Ash	0.074	0.17	0.355	0.534	0.738	1.025	1.226	5.992	

Table 2: Quantiles of Shrinkage Scores for Student’s t Simulation

Neither method tended to have much more extreme shrinkage than the other in this simulation, though on average ash still shrank more. The p-value reported came from a paired t-test between shrinkage scores, with scores paired by gene.

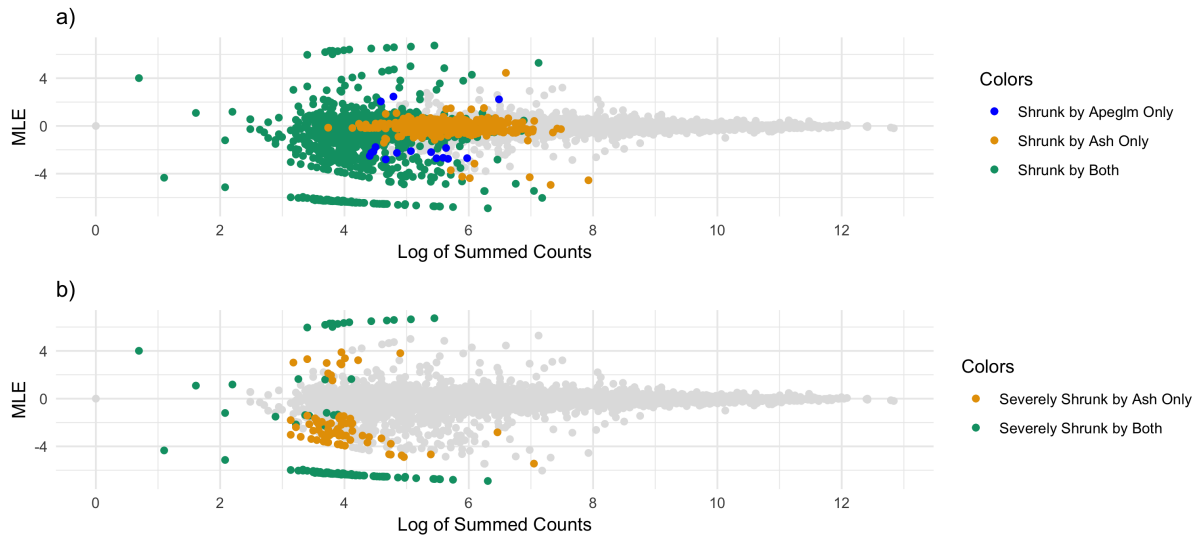


Figure 6: MA Plot from a Random Subsample

The figure comes from one of the 100 random subsamples used in the mouse data benchmarking. Points are colored by whether they were shrunk in a) and whether they were severely shrunk in b). Any genes severely shrunk by apegm were shrunk practically as much or more by ash. Low-count genes had highly variable ML estimates, and overwhelmingly made up the genes that were shrunk or severely shrunk.

Quantiles	50th	75th	90th	95th	97.5th	99th	99.5th	Max	P-value
Apeglm	0.007	0.025	0.11	0.215	0.404	1.31	1.994	2.729	<2e-16
Ash	0.021	0.053	0.164	0.304	0.632	2.628	3.944	5.461	

Table 3: Quantiles of Shrinkage Scores Averaged across Random Subsamples

For each gene, shrinkage scores were averaged across the 100 random subsamples, and quantiles of these averaged shrinkage scores were computed. Ash had more extreme shrinkage than apegm, as evident by larger shrinkage scores across all quantiles above the 50th, and the difference between the methods was greater than in the simulations. The p-value reported came from a paired t-test between shrinkage scores, with scores paired by gene.