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Supplementary Information for

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Improved inference of polygenic effects using

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genome-wide association summary statistics

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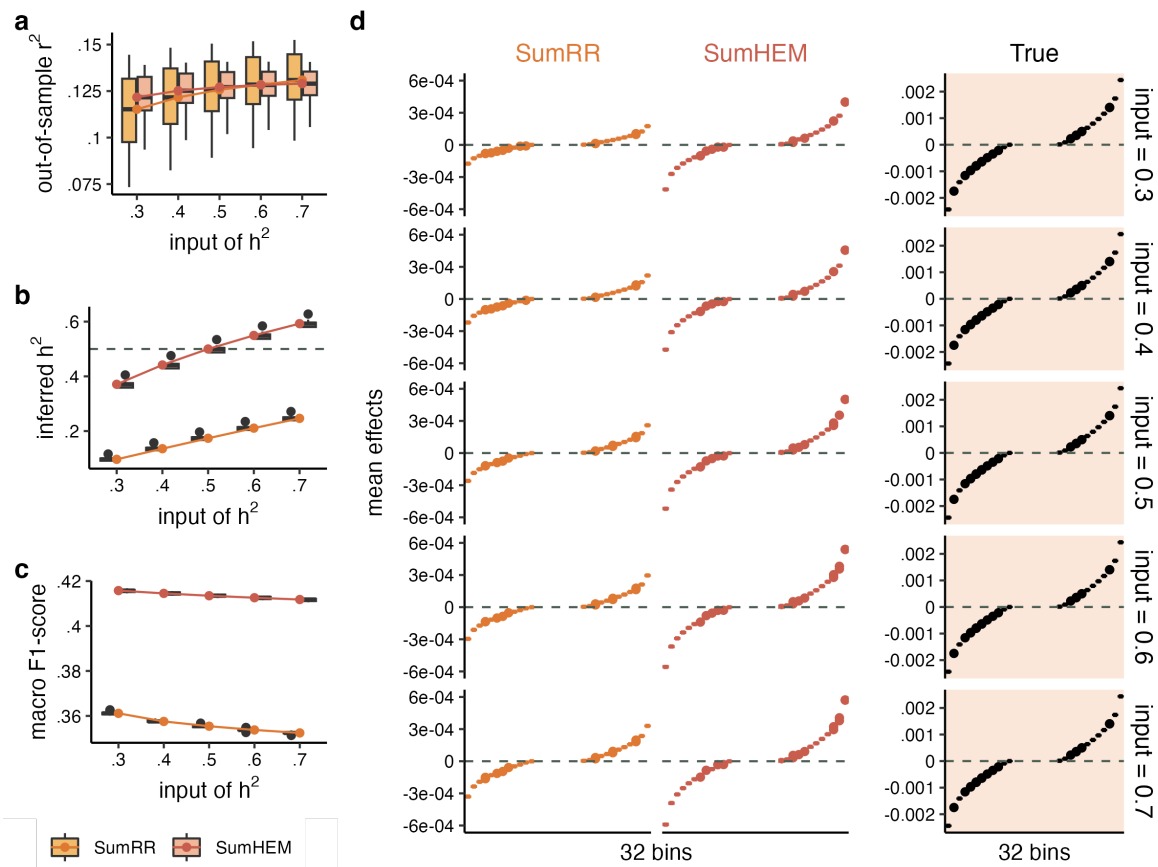
The PDF file includes:

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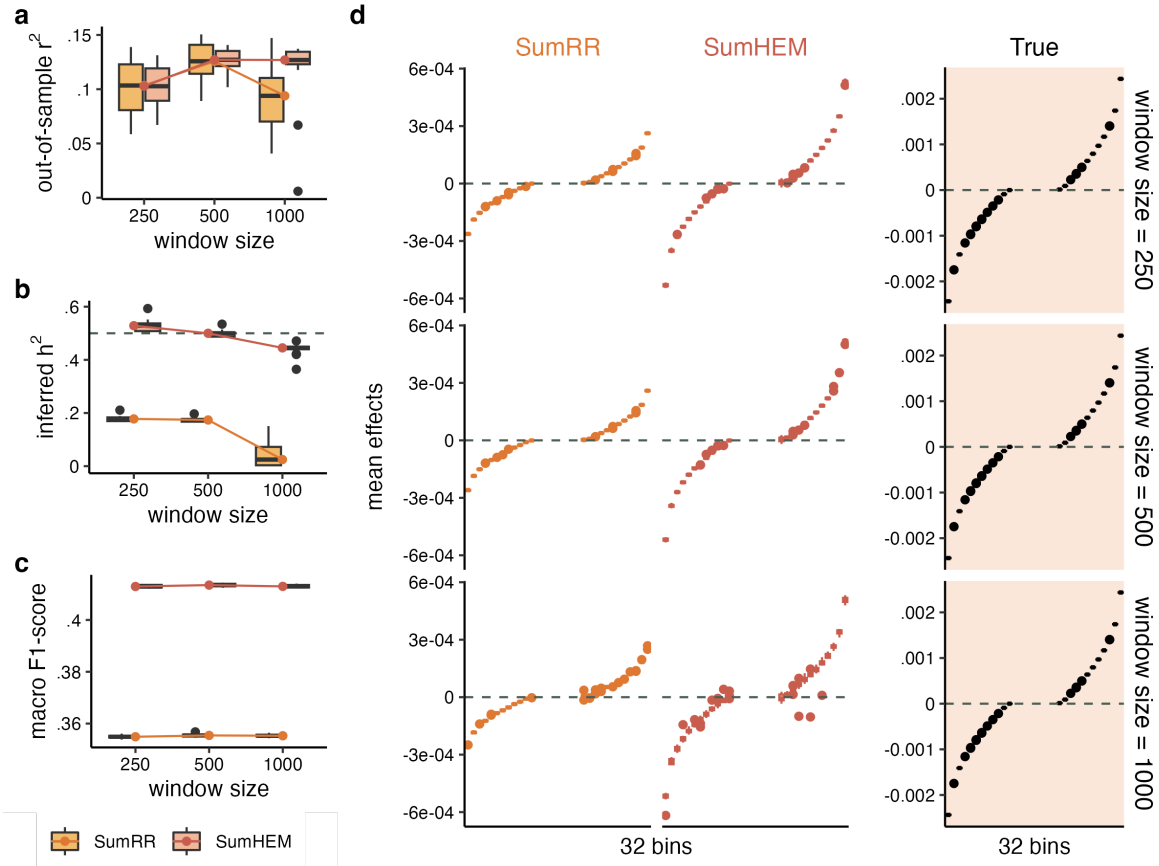
Supplementary Figures 1-3

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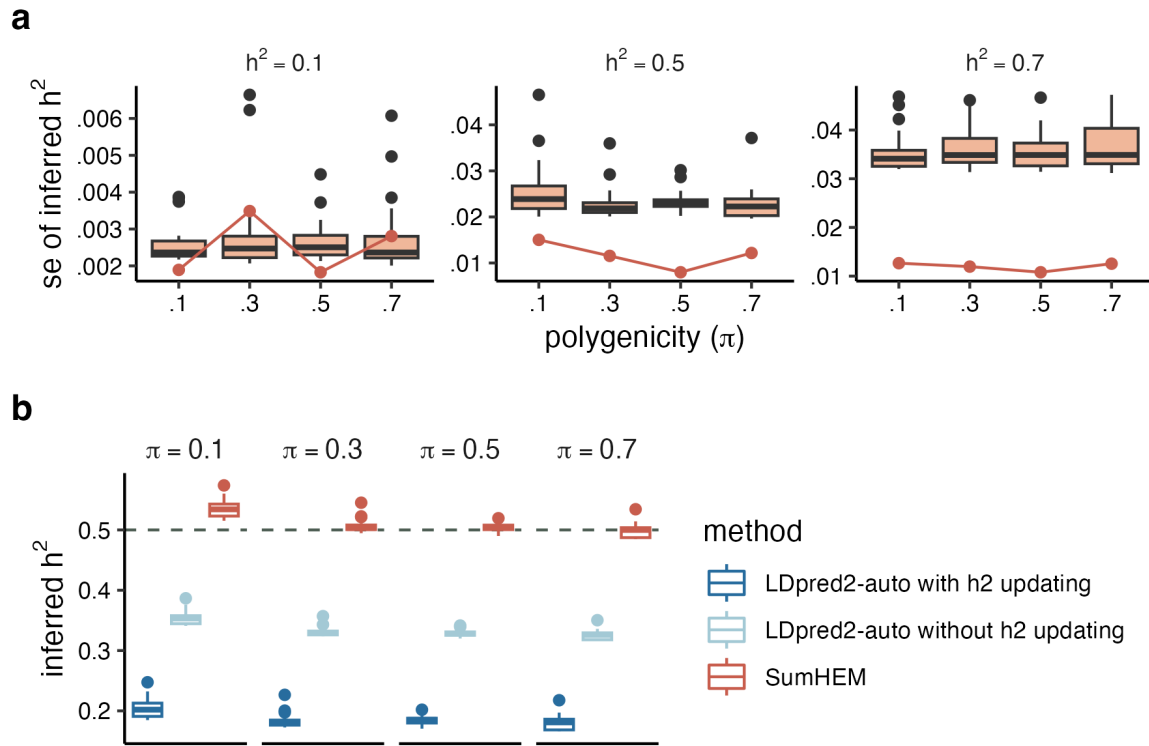
8 Supplementary Figures



Supplementary Figure 1: **Impact of varying input heritability parameters on evaluation metrics in simulations with true heritability of 0.5 and polygenicity of 0.7.** (a-c) Box-plots and mean values of out-of-sample r^2 /inferred heritability/macro F1-score for SumRR and SumHEM across 20 replications. (d) Box-plots of mean genetic effect sizes from SumRR estimates/SumHEM estimates/true values across 32 bins from 20 replications.



Supplementary Figure 2: **Impact of estimation window size on evaluation metrics in simulations with true heritability of 0.5 and polygenicity of 0.7.** (a-c) Box-plots and mean values of out-of-sample r^2 /inferred heritability/macro F1-score for SumRR and SumHEM across 20 replications. (d) Box-plots of mean genetic effect sizes from SumRR estimates/SumHEM estimates/true values across 32 bins from 20 replications.



Supplementary Figure 3: **Standard error of SumHEM-inferred heritability and comparison with LDpred2-auto without h^2 updating.** (a) Estimates of standard error of SumHEM-inferred heritability and standard deviation of SumHEM-inferred heritability across 20 replications. (b) Comparison of inferred heritability among SumHEM, LDpred2-auto and LDpred2-auto without h^2 updating.