Computational Molecular Biology 2026, Vol.16, No.3, 159-180
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Appendix A. Checklist for Interpreting SNP-based Heritability Estimates under the GREML Framework

This checklist is intended to standardize the interpretation workflow of SNP-based heritability estimates derived from the GREML framework, emphasizing their dependence on data quality, model specification, and underlying statistical assumptions. Researchers may use this checklist to systematically verify each step of the analysis, thereby improving the transparency and reproducibility of inference.

Table S1 Interpretation of SNP heritability estimates followed a standardized checklist

No.	Check Dimension	Key Items to Check	Completion Status
1	Genotype quality control and variant spectrum	Whether rigorous genotype quality control has been conducted; whether the SNP set adequately covers the allele frequency spectrum, particularly low-frequency and rare variants; and whether limited coverage is expected to result in downward-biased SNP heritability estimates.	☐
2	Phenotype modeling and covariate adjustment	Whether the phenotype distribution has been examined and appropriate transformations applied; whether batch effects, environmental covariates, and other key fixed effects have been included in the model.	☐
3	Repeated measures and multi-environment structure	For phenotypes measured across multiple time points or environments, whether multi-environment or hierarchical mixed models have been adopted to avoid inflation of residual variance.	☐
4	Population structure control	Whether population stratification has been assessed and adjusted for using principal components or equivalent approaches; and whether the estimates are robust to the number of PCs included.	☐
5	Relatedness filtering and kinship threshold setting	Whether criteria for removing close relatives have been clearly defined; and whether the stability of SNP heritability estimates has been evaluated under alternative relatedness thresholds.	☐
6	GRM construction and LD sensitivity	Whether results obtained using the standard GRM have been compared with those from LD-adjusted or partitioned GRM models; and whether sensitivity to linkage disequilibrium assumptions has been assessed.	☐
7	REML convergence and boundary estimates	Whether REML optimization has converged; whether standard errors and confidence intervals have been reported; and whether boundary estimates (e.g., $h^2 = 0$or $h^2 = 1$) are interpreted as indicators of limited information rather than definitive biological conclusions.	☐
8	Estimation stability and sample size adequacy	Whether estimation stability has been evaluated using standard errors; whether resampling approaches such as jackknife or bootstrap have been applied when feasible; and whether the sample size is adequate for reliable variance component estimation.	☐
9	Cross-method validation	Whether GREML-based estimates have been compared with results from summary-statistic methods such as LDSC or SumHer.	☐
10	Integrated interpretation and boundary awareness	Whether SNP heritability estimates are interpreted in the context of marker coverage, model assumptions, and trait biology; and whether SNP heritability is not equated with the trait's "true" heritability.	☐