RETRACTED ARTICLE

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RETRACTED: HaploVar: an R package for defining local haplotype variants for trait association and trait prediction analyses: methods and sensitivity checks

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HaploVar: an R package for defining local haplotype variants for trait association and trait prediction analyses: methods and sensitivity checks

Dmitri Ivanova, Ingrid Eriksen, Oluwaseun Tembo

Marker assisted breeding (MAB) supports breeding by identifying individuals or molecular markers associated with important traits. MAB methods include genome-wide association studies (GWAS) and genomic selection (GS). Local haplotypes are regions of DNA that are inherited together due to high levels of linkage disequilibrium. Local haplotypes can improve the prediction accuracy and power of GS and GWAS. Currently available local haplotyping tools improve GWAS power through fine-mapping of candidate regions or through haplotype-based GWAS. However, no local haplotyping tools utilize the benefits of haplotypes for GS. Here we present HaploVar , a local haplotyping tool designed to improve both GWAS and GS pipelines by identifying local haplotypes and formatting the output to be compatible with all major GWAS and GS tools. HaploVar can be used in any haplotype-based MAB study.??HaploVar can be downloaded from CRAN with R >4.0.0 (DOI: 10.32614/CRAN.package.HaploVar). HaploVar and a tutorial vignette is available on GitHub (https://github.com/TessaMacNish/HaploVar). HaploVar is available under an MIT license.

This is the demonstration PDF of the article.

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