Resource Summary Report

Generated by dkNET on Apr 18, 2025

MEGASNPHUNTER

RRID:SCR_009287
Type: Tool

Proper Citation

MEGASNPHUNTER (RRID:SCR_009287)

Resource Information

URL: http://bioinformatics.ust.hk/MegaSNPHunter.html

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Description: Software application that takes case-control genotype data as input and produces a ranked list of multi-SNP interactions. In particular, the whole genome is first partitioned into multiple short subgenomes and a boosting tree classifier is built for each subgenomes based on multi-SNP interactions and then used to measure the importance of SNPs. The method keeps relatively more important SNPs from all subgenomes and let them compete with each other in the same way at the next level. The competition terminates when the number of selected SNPs is less than the size of a subgenome. (entry from Genetic Analysis Software)

Abbreviations: MEGASNPHUNTER

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, parkinson, software application

Related Condition: Parkinson's disease, Rheumatoid arthritis

Funding:

Resource Name: MEGASNPHUNTER

Resource ID: SCR_009287

Alternate IDs: nlx_154472

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250416T063542+0000

Ratings and Alerts

No rating or validation information has been found for MEGASNPHUNTER.

No alerts have been found for MEGASNPHUNTER.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Abo Alchamlat S, et al. (2018) Aggregation of experts: an application in the field of "interactomics" (detection of interactions on the basis of genomic data). BMC bioinformatics, 19(1), 445.

Abo Alchamlat S, et al. (2017) KNN-MDR: a learning approach for improving interactions mapping performances in genome wide association studies. BMC bioinformatics, 18(1), 184.

Bougacha-Elleuch N, et al. (2014) A 20 year history of clinical and genetic study of thyroid autoimmunity in a Tunisian multigenerational family: Evidence for gene interaction. Meta gene, 2, 63.