Resource Summary Report

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HAPLOPOOL

RRID:SCR_009225
Type: Tool

Proper Citation

HAPLOPOOL (RRID:SCR_009225)

Resource Information

URL: http://haplopool.icsi.berkeley.edu/haplopool/

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Description: Software program for estimating haplotype frequencies either from genotypes of individuals or from genotypes of pooled individuals. The genotypes must be for a block of bi-allelic SNPs (meaning that the SNPs should be in linkage disequilibrium with each other). The program assumes that it is given many genotypes of unrelated diploid individuals in Hardy-Weinberg equilibrium. If the genotypes are from pooled DNA, the program assumes that every pool contains the same number of individuals and the individuals were chosen at random when placed into the pools. For a reasonable running-time, the number of individuals in a pool needs to be between 2 and 4. (entry from Genetic Analysis Software)

Abbreviations: HAPLOPOOL

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, gcc/g++, perl, matlab

Funding:

Resource Name: HAPLOPOOL

Resource ID: SCR_009225

Alternate IDs: nlx_154382

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250420T015751+0000

Ratings and Alerts

No rating or validation information has been found for HAPLOPOOL.

No alerts have been found for HAPLOPOOL.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.