Resource Summary Report

Generated by dkNET on Apr 17, 2025

GENERECON

RRID:SCR_009195
Type: Tool

Proper Citation

GENERECON (RRID:SCR_009195)

Resource Information

URL: http://www.daimi.au.dk/~mailund/GeneRecon/

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Description: Software application for linkage disequilibrium mapping using coalescent theory. It is based on a Bayesian Markov-chain Monte Carlo (MCMC) method for fine-scale linkage-disequilibrium gene mapping using high-density marker maps. GeneRecon explicitly models the genealogy of a sample of the case chromosomes in the vicinity of a disease locus. Given case and control data in the form of genotype or haplotype information, it estimates a number of parameters, most importantly, the disease position. (entry from Genetic Analysis Software)

Abbreviations: GENERECON

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c++, unix, linux, macos, ms-windows, bio.tools

Funding:

Resource Name: GENERECON

Resource ID: SCR_009195

Alternate IDs: nlx_154338, biotools:generecon

Alternate URLs: https://bio.tools/generecon

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250416T063539+0000

Ratings and Alerts

No rating or validation information has been found for GENERECON.

No alerts have been found for GENERECON.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Bohra A, et al. (2013) Emerging paradigms in genomics-based crop improvement. TheScientificWorldJournal, 2013, 585467.