Resource Summary Report

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QMSIM

RRID:SCR_013123
Type: Tool

Proper Citation

QMSIM (RRID:SCR_013123)

Resource Information

URL: http://www.aps.uoguelph.ca/~msargol/qmsim/

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Description: Software application designed to simulate a wide range of genetic architectures and population structures in livestock. Large scale genotyping data and complex pedigrees can be efficiently simulated. QMSim is a family based simulator, which can also take into account predefined evolutionary features, such as LD, mutation, bottlenecks and expansions. The simulation is basically carried out in two steps: In the first step, a historical population is simulated to establish mutation-drift equilibrium and, in the second step, recent population structures are generated, which can be complex. QMSim allows for a wide range of parameters to be incorporated in the simulation models in order to produce appropriate simulated data. (entry from Genetic Analysis Software)

Synonyms: Qtl and Marker SIMulator

Resource Type: software resource, software application

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

Funding:

Resource Name: QMSIM

Resource ID: SCR_013123

Alternate IDs: nlx_154560, biotools:qmsim

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

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250416T063637+0000

Ratings and Alerts

No rating or validation information has been found for QMSIM.

No alerts have been found for QMSIM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 53 mentions in open access literature.

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

Barani S, et al. (2024) Optimizing purebred selection to improve crossbred performance. Frontiers in genetics, 15, 1384973.

Eiríksson JH, et al. (2023) Segregation between breeds and local breed proportions in genetic and genomic models for crossbreds. Genetics, selection, evolution : GSE, 55(1), 45.

Wientjes YCJ, et al. (2023) The long-term effects of genomic selection: 2. Changes in allele frequencies of causal loci and new mutations. Genetics, 225(1).

Liu T, et al. (2023) The impact of genotyping strategies and statistical models on accuracy of genomic prediction for survival in pigs. Journal of animal science and biotechnology, 14(1), 1.

Nwogwugwu CP, et al. (2022) Optimal population size to detect quantitative trait loci in Korean native chicken: a simulation study. Animal bioscience, 35(4), 511.

Ling A, et al. (2022) Fuzzy Logic as a Strategy for Combining Marker Statistics to Optimize Preselection of High-Density and Sequence Genotype Data. Genes, 13(11).

Junqueira VS, et al. (2022) Is single-step genomic REML with the algorithm for proven and young more computationally efficient when less generations of data are present? Journal of animal science, 100(5).

Wientjes YCJ, et al. (2022) The long-term effects of genomic selection: 1. Response to selection, additive genetic variance, and genetic architecture. Genetics, selection, evolution : GSE, 54(1), 19.

Khalilisamani N, et al. (2022) Estimating heritability using family-pooled phenotypic and genotypic data: a simulation study applied to aquaculture. Heredity, 128(3), 178.

Marjanovic J, et al. (2021) Factors affecting accuracy of estimated effective number of chromosome segments for numerically small breeds. Journal of animal breeding and genetics = Zeitschrift fur Tierzuchtung und Zuchtungsbiologie, 138(2), 151.

Mancin E, et al. (2021) Accounting for Population Structure and Phenotypes From Relatives in Association Mapping for Farm Animals: A Simulation Study. Frontiers in genetics, 12, 642065.

Ling AS, et al. (2021) Dissection of the impact of prioritized QTL-linked and -unlinked SNP markers on the accuracy of genomic selection1. BMC genomic data, 22(1), 26.

Duenk P, et al. (2021) Predicting the purebred-crossbred genetic correlation from the genetic variance components in the parental lines. Genetics, selection, evolution : GSE, 53(1), 10.

Bermann M, et al. (2021) Validation of single-step GBLUP genomic predictions from threshold models using the linear regression method: An application in chicken mortality. Journal of animal breeding and genetics = Zeitschrift fur Tierzuchtung und Zuchtungsbiologie, 138(1), 4.

Khalilisamani N, et al. (2021) Impact of genotypic errors with equal and unequal family contribution on accuracy of genomic prediction in aquaculture using simulation. Scientific reports, 11(1), 18318.

Esfandyari H, et al. (2020) Effects of Different Strategies for Exploiting Genomic Selection in Perennial Ryegrass Breeding Programs. G3 (Bethesda, Md.), 10(10), 3783.

Wientjes YCJ, et al. (2020) Optimizing genomic reference populations to improve crossbred performance. Genetics, selection, evolution : GSE, 52(1), 65.

Manca E, et al. (2020) Use of the Multivariate Discriminant Analysis for Genome-Wide Association Studies in Cattle. Animals : an open access journal from MDPI, 10(8).

Chen SY, et al. (2020) Genotyping-free parentage assignment using RAD-seq reads. Ecology and evolution, 10(14), 7783.

Duenk P, et al. (2020) The Impact of Non-additive Effects on the Genetic Correlation Between Populations. G3 (Bethesda, Md.), 10(2), 783.