

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 application, software resource

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

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: 20260805T044308+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 57 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Zhao Q, et al. (2025) Optimal Combination of Different Selection and Mating Strategies on Exploiting Genetic Diversity and Genetic Gain in Small Pig Conservation Populations. Journal of animal breeding and genetics = Zeitschrift fur Tierzucht und Zuchtungsbiologie, 142(4), 444.

Yang J, et al. (2025) Incorporating information of causal variants in genomic prediction using GBLUP or machine learning models in a simulated livestock population. Journal of animal science and biotechnology, 16(1), 118.

Li W, et al. (2025) Improving multibreed genomic prediction for breeds with small populations by modeling heterogeneous genetic (co)variance blockwise accounting for linkage disequilibrium. Journal of animal science and biotechnology, 16(1), 176.

Manunza A, et al. (2025) Estimating the optimal number of samples to determine the effective population size in livestock. Frontiers in genetics, 16, 1588986.

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).

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.

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).

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.

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.

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.

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.

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.

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