

Resource Summary Report

Generated by [NIF](#) on Aug 30, 2026

QMSIM

RRID:SCR_013123

Type: Tool

Proper Citation

QMSIM (RRID:SCR_013123)

Resource Information

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

Proper Citation: QMSIM (RRID:SCR_013123)

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: 20260829T183104+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 63 mentions in open access literature.

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

Schrauf MF, et al. (2026) Genomic selection strategies and their potential to maintain rare alleles and de-novo mutations: a long-term assessment. Genetics, selection, evolution : GSE, 58(1).

Zhou L, et al. (2026) Incorporating GO/KEGG Functional Annotations Improves the Accuracy and Stability of Genomic Prediction Across Diverse Beef Cattle Populations. Animals : an open access journal from MDPI, 16(12).

Xue Y, et al. (2026) FSBLUP: a novel strategy of fusion similarity matrix construction via optimally integrating intermediate omics data to enhance genomic prediction. Genome biology, 27(1), 27.

Huang CH, et al. (2026) A modified indirect method for computing inbreeding coefficients. Genetics, selection, evolution : GSE, 58(1).

Nagai R, et al. (2026) Probabilities of two alleles being identity by state at unobserved loci predicted by observed loci in cattle populations. Scientific reports, 16(1).

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 Tierzuchtung 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.

Zhou L, et al. (2025) Comparison of GBLUP and WGBLUP in genomic selection for beef cattle under different LD patterns and mixed multi-population scenarios: a simulation study. BMC genomics, 27(1), 21.

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).

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.

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.