Resource Summary Report

Generated by NIF on Apr 28, 2025

SimRare

RRID:SCR_005226
Type: Tool

Proper Citation

SimRare (RRID:SCR_005226)

Resource Information

URL: https://code.google.com/p/simrare/

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Description: A stand-alone executable software with user-friendly graphical interface implemented in Python/C++ for rare variant association studies. It is designed as a unified simulation framework to provide an unbiased and easy manner to evaluate association methods, including novel methods, under a broad range of choice of biological contexts. It consists of three modules, variant data simulator, genotype/phenotype generator and association method evaluator. SimRare generates variant data for gene regions using forward-time simulation which incorporates realistic population demographic and evolutionary scenarios. For phenotype data it is capable of generating both case-control and quantitative traits. The phenotypic effects of variants can be detrimental, protective or non-causal. SimRare has a graphical user interface which allows for easy entry of genetic and phenotypic parameters. Simulated data can be written into external files in a standard format. For novel association method implemented in R it can be imported into SimRare, which has been equipped built in functions to evaluate performance of new method and visually compare it with currently available ones in an unbiased manner.

Abbreviations: SimRare

Synonyms: SimRare - A program to generate and analyze sequence-based data for rare variant association studies of quantitative and qualitative traits

Resource Type: software resource

Defining Citation: PMID:22914216

Keywords: statistical genetics, simulation framework, gui, association test, sequencing, rare

variant, python, c++, bio.tools

Funding:

Availability: Acknowledgement requested, GNU General Public License, v3

Resource Name: SimRare

Resource ID: SCR_005226

Alternate IDs: OMICS_00257, biotools:simrare

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

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Ratings and Alerts

No rating or validation information has been found for SimRare.

No alerts have been found for SimRare.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Lee S, et al. (2019) Pathway analysis of rare variants for the clustered phenotypes by using hierarchical structured components analysis. BMC medical genomics, 12(Suppl 5), 100.

Lee S, et al. (2018) Pathway-based approach using hierarchical components of rare variants to analyze multiple phenotypes. BMC bioinformatics, 19(Suppl 4), 79.