

# Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

## 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

**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>

**Record Creation Time:** 20220129T080229+0000

**Record Last Update:** 20260815T182301+0000

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## Ratings and Alerts

No rating or validation information has been found for SimRare.

No alerts have been found for SimRare.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

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.