

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

## [madsim](#)

RRID:SCR\_014765

Type: Tool

### Proper Citation

madsim (RRID:SCR\_014765)

### Resource Information

**URL:** <https://cran.r-project.org/web/packages/madsim/index.html>

**Proper Citation:** madsim (RRID:SCR\_014765)

**Description:** A function which allows users to generate two biological conditions synthetic microarray datasets. The user provides a subset of parameters, but default parameter settings can be modified.

**Resource Type:** source code, software resource

**Keywords:** source code, r, synthetic microarray, data set, biological condition

**Resource Name:** madsim

**Resource ID:** SCR\_014765

**License:** GPL 3

**Record Creation Time:** 20220129T080322+0000

**Record Last Update:** 20260729T044355+0000

### Ratings and Alerts

No rating or validation information has been found for madsim.

No alerts have been found for madsim.

### Data and Source Information

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

### Usage and Citation Metrics

We found 1 mentions in open access literature.

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

M A Basher AR, et al. (2025) Heterogeneity-preserving discriminative feature selection for disease-specific subtype discovery. Nature communications, 16(1), 3593.