

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

SNM

RRID:SCR_001299

Type: Tool

Proper Citation

SNM (RRID:SCR_001299)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/snm.html>

Proper Citation: SNM (RRID:SCR_001299)

Description: Software package that uses a modeling strategy especially designed for normalizing high-throughput genomic data. The premise is that your data is a function of study-specific variables which are either biological variables that represent the target of the statistical analysis, or adjustment variables that represent factors arising from the experimental or biological setting the data is drawn from. The SNM approach aims to simultaneously model all study-specific variables in order to more accurately characterize the biological or clinical variables of interest.

Abbreviations: SNM

Synonyms: Supervised Normalization of Microarrays

Resource Type: software resource

Keywords: differential expression, exon array, gene expression, microarray, multi channel, multiple comparison, one channel, preprocessing, quality control, transcription, two channel

Availability: Free, Available for download, Freely available

Resource Name: SNM

Resource ID: SCR_001299

Alternate IDs: OMICS_02036

License: GNU Lesser General Public License

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260725T190502+0000

Ratings and Alerts

No rating or validation information has been found for SNM.

No alerts have been found for SNM.

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](#) .

Narunsky-Haziza L, et al. (2022) Pan-cancer analyses reveal cancer-type-specific fungal ecologies and bacteriome interactions. Cell, 185(20), 3789.