

# Resource Summary Report

Generated by [dkNET](#) on Apr 26, 2025

## SNM

RRID:SCR\_001299

Type: Tool

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### Proper Citation

SNM (RRID:SCR\_001299)

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### Resource Information

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

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**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

**Funding:**

**Availability:** GNU Lesser General Public License

**Resource Name:** SNM

**Resource ID:** SCR\_001299

**Alternate IDs:** OMICS\_02036

**Record Creation Time:** 20220129T080206+0000

**Record Last Update:** 20250420T014025+0000

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## Ratings and Alerts

No rating or validation information has been found for SNM.

No alerts have been found for SNM.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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