

Resource Summary Report

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Algorithms and Framework for Nonnegative Matrix Factorization

RRID:SCR_023124

Type: Tool

Proper Citation

Algorithms and Framework for Nonnegative Matrix Factorization (RRID:SCR_023124)

Resource Information

URL: <https://cran.r-project.org/package=NMF>

Proper Citation: Algorithms and Framework for Nonnegative Matrix Factorization (RRID:SCR_023124)

Description: Software R package for nonnegative matrix factorization. Implements set of already published algorithms and seeding methods, and provides framework to test, develop and plug new/custom algorithms.

Abbreviations: NMF

Synonyms: Non-negative Matrix Factorization

Resource Type: software resource, software toolkit

Defining Citation: [DOI:10.1186/1471-2105-11-367](https://doi.org/10.1186/1471-2105-11-367)

Keywords: Non-negative Matrix Factorization, nonnegative matrix factorization,

Funding: South-African National Bioinformatics Network ;
Science Foundation Ireland

Availability: Free, Available for download, Freely available

Resource Name: Algorithms and Framework for Nonnegative Matrix Factorization

Resource ID: SCR_023124

Record Creation Time: 20230116T062750+0000

Record Last Update: 20260808T190529+0000

Ratings and Alerts

No rating or validation information has been found for Algorithms and Framework for Nonnegative Matrix Factorization.

No alerts have been found for Algorithms and Framework for Nonnegative Matrix Factorization.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Altendorf L, et al. (2026) Molecular changes during AT/RT progression associated with epithelial-mesenchymal transition and extracellular matrix changes. *Acta neuropathologica*, 152(1).

Shi Y, et al. (2026) Genomic, Clinical, and Spatial Predictors of Durable Response to BRAF/MEK Inhibition in BRAF-Mutant Melanoma. *bioRxiv : the preprint server for biology*.

Gurjao C, et al. (2026) Germline Predisposition to Oncogenic Alkylating Damage in Colorectal Cancer. *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*, 35(3), 420.

Kratz JD, et al. (2025) Subclonal response heterogeneity to define cancer organoid therapeutic sensitivity. *Scientific reports*, 15(1), 12072.

Li Y, et al. (2025) Single-Cell Transcriptomic Landscape Deciphers Intratumoral Heterogeneity and Subtypes of Acral and Mucosal Melanomas. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(12), 2495.

Ren W, et al. (2025) Whole-genome sequencing reveals three follicular lymphoma subtypes with distinct cell of origin and patient outcomes. *Cell reports. Medicine*, 6(8), 102278.

Mauvais FX, et al. (2025) Metallophilic marginal zone macrophages cross-prime CD8+ T??cell-mediated protective immunity against blood-borne tumors. *Immunity*, 58(4), 843.

Zhang J, et al. (2024) Protocol to infer and analyze miRNA sponge modules in heterogeneous data using miRSM 2.0. *STAR protocols*, 5(4), 103317.

Ambeskovic A, et al. (2024) Exon-Skipping-Based Subtyping of Colorectal Cancers. *Gastroenterology*.

Huang C, et al. (2023) Identification of S1PR4 as an immune modulator for favorable prognosis in HNSCC through machine learning. *iScience*, 26(9), 107693.

Berard AR, et al. (2023) Vaginal epithelial dysfunction is mediated by the microbiome, metabolome, and mTOR signaling. *Cell reports*, 42(5), 112474.

Mella L, et al. (2022) SparseSignatures: An R package using LASSO-regularized non-negative matrix factorization to identify mutational signatures from human tumor samples. *STAR protocols*, 3(3), 101513.

Al Mehedi Hasan M, et al. (2022) Identification of key candidate genes for IgA nephropathy using machine learning and statistics based bioinformatics models. *Scientific reports*, 12(1), 13963.