

Resource Summary Report

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Rtsne

RRID:SCR_016900

Type: Tool

Proper Citation

Rtsne (RRID:SCR_016900)

Resource Information

URL: <https://github.com/jkrijthe/Rtsne>

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Description: R wrapper for Van der Maaten's Barnes-Hut implementation of t-Distributed Stochastic Neighbor Embedding.

Abbreviations: t-SNE

Synonyms: R t-distributed stochastic neighbor embedding, R t-Distributed Stochastic Neighbor Embedding

Resource Type: software application, data processing software, software resource, data visualization software

Keywords: wrapper, implementation, t-distributed, stochastic, neighbor, embedding, data, visualization

Funding: Dutch Scientific Organization ;
Google ;
Microsoft

Availability: Free, Available for download, Freely available

Resource Name: Rtsne

Resource ID: SCR_016900

License: BSD licence

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260903T235400+0000

Ratings and Alerts

No rating or validation information has been found for Rtsne.

No alerts have been found for Rtsne.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 85 mentions in open access literature.

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

Duan B, et al. (2023) Widespread epistasis shapes RNA Polymerase II active site function and evolution. *bioRxiv : the preprint server for biology*.

Ajuyah P, et al. (2023) Histone H3-wild type diffuse midline gliomas with H3K27me3 loss are a distinct entity with exclusive EGFR or ACVR1 mutation and differential methylation of homeobox genes. *Scientific reports*, 13(1), 3775.

Nakamura M, et al. (2023) Molecular genetic positioning of small intestine and papilla of Vater carcinomas including clinicopathological classification. *Cancer medicine*.

Hancock SE, et al. (2023) FACS-assisted single-cell lipidome analysis of phosphatidylcholines and sphingomyelins in cells of different lineages. *Journal of lipid research*, 64(3), 100341.

Subkhankulova T, et al. (2023) Zebrafish pigment cells develop directly from persistent highly multipotent progenitors. *Nature communications*, 14(1), 1258.

Ross KE, et al. (2023) Network models of protein phosphorylation, acetylation, and ubiquitination connect metabolic and cell signaling pathways in lung cancer. *PLoS computational biology*, 19(3), e1010690.

Martinek J, et al. (2022) Transcriptional profiling of macrophages in situ in metastatic melanoma reveals localization-dependent phenotypes and function. *Cell reports. Medicine*, 3(5), 100621.

Tu J, et al. (2022) Sensitivity to copy number variation analysis in single cell genomics. *Gene*, 808, 145995.

Angst P, et al. (2022) Genetic Drift Shapes the Evolution of a Highly Dynamic Metapopulation. *Molecular biology and evolution*, 39(12).

Gabay O, et al. (2022) Landscape of adenosine-to-inosine RNA recoding across human tissues. *Nature communications*, 13(1), 1184.

Ebrahimi A, et al. (2022) Pleomorphic xanthoastrocytoma is a heterogeneous entity with pTERT mutations prognosticating shorter survival. *Acta neuropathologica*

communications, 10(1), 5.

Zhang Y, et al. (2022) A novel ferroptosis-related gene signature for overall survival prediction and immune infiltration in patients with breast cancer. *International journal of oncology*, 61(6).

Gill PA, et al. (2022) A randomized dietary intervention to increase colonic and peripheral blood SCFAs modulates the blood B- and T-cell compartments in healthy humans. *The American journal of clinical nutrition*, 116(5), 1354.

Molina L, et al. (2022) Bi-allelic hydroxymethylbilane synthase inactivation defines a homogenous clinico-molecular subtype of hepatocellular carcinoma. *Journal of hepatology*, 77(4), 1038.

Zipper L, et al. (2022) The MicroRNA miR-277 Controls Physiology and Pathology of the Adult *Drosophila* Midgut by Regulating the Expression of Fatty Acid β -Oxidation-Related Genes in Intestinal Stem Cells. *Metabolites*, 12(4).

Williamson D, et al. (2022) Medulloblastoma group 3 and 4 tumors comprise a clinically and biologically significant expression continuum reflecting human cerebellar development. *Cell reports*, 40(5), 111162.

Aramaki M, et al. (2022) Transcriptional control of cone photoreceptor diversity by a thyroid hormone receptor. *Proceedings of the National Academy of Sciences of the United States of America*, 119(49), e2209884119.

Perico CP, et al. (2022) Genomic landscape of the SARS-CoV-2 pandemic in Brazil suggests an external P.1 variant origin. *Frontiers in microbiology*, 13, 1037455.

Li R, et al. (2022) Metabolic incorporation of electron-rich ribonucleosides enhances APEX-seq for profiling spatially restricted nascent transcriptome. *Cell chemical biology*, 29(7), 1218.

Roncalli V, et al. (2021) Post-diapause transcriptomic restarts: insight from a high-latitude copepod. *BMC genomics*, 22(1), 409.