

Resource Summary Report

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flowClust

RRID:SCR_001807

Type: Tool

Proper Citation

flowClust (RRID:SCR_001807)

Resource Information

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

Proper Citation: flowClust (RRID:SCR_001807)

Description: A Bioconductor software package for automated gating of flow cytometry data that implements a robust model-based clustering approach based on multivariate t mixture models with the Box-Cox transformation.

Synonyms: flowClust - Clustering for Flow Cytometry

Resource Type: software resource

Defining Citation: [PMID:19442304](#)

Keywords: software package, mac os x, unix/linux, windows, r, clustering, flow cytometry, visualization

Availability: Artistic License, v2

Resource Name: flowClust

Resource ID: SCR_001807

Alternate IDs: OMICS_05595

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260912T195531+0000

Ratings and Alerts

No rating or validation information has been found for flowClust.

No alerts have been found for flowClust.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Schafer JM, et al. (2025) T cell subsets of urine-derived lymphocytes (UDLs) serve as an indicator of TILs and reflect immunological sex differences in bladder cancer. *Journal for immunotherapy of cancer*, 13(10).

Snyder LF, et al. (2025) Divergence in a eukaryotic transcription factor's co-TF dependence involves multiple intrinsically disordered regions. *Nature communications*, 16(1), 5340.

Alsousli M, et al. (2025) Altered CD4 T cell response in oligometastatic non-small cell lung cancer brain metastasis. *Acta neuropathologica communications*, 13(1), 95.

Siddiq MA, et al. (2024) Plasticity and environment-specific relationships between gene expression and fitness in *Saccharomyces cerevisiae*. *Nature ecology & evolution*, 8(12), 2184.

Chen Y, et al. (2024) Benchmarking digital PCR partition classification methods with empirical and simulated duplex data. *Briefings in bioinformatics*, 25(3).

Snyder LF, et al. (2024) Evolution of a Eukaryotic Transcription Factor's co-TF Dependence Involves Multiple Intrinsically Disordered Regions Affecting Activation and Autoinhibition. *bioRxiv : the preprint server for biology*.

Behle A, et al. (2022) Manipulation of topoisomerase expression inhibits cell division but not growth and reveals a distinctive promoter structure in *Synechocystis*. *Nucleic acids research*, 50(22), 12790.

Lin TC, et al. (2022) Optochemical Control of TET Dioxygenases Enables Kinetic Insights into the Domain-Dependent Interplay of TET1 and MBD1 while Oxidizing and Reading 5-Methylcytosine. *ACS chemical biology*, 17(7), 1844.

López Hernández JF, et al. (2021) Diverse mating phenotypes impact the spread of wtf meiotic drivers in *Schizosaccharomyces pombe*. *eLife*, 10.

Fedorec AJH, et al. (2020) FlopR: An Open Source Software Package for Calibration and Normalization of Plate Reader and Flow Cytometry Data. *ACS synthetic biology*, 9(9), 2258.

Tsai WL, et al. (2020) High throughput pSTAT signaling profiling by fluorescent cell barcoding and computational analysis. *Journal of immunological methods*, 477, 112667.

Lee H, et al. (2019) High-Throughput Analysis of Clinical Flow Cytometry Data by Automated Gating. *Bioinformatics and biology insights*, 13, 1177932219838851.

Rahim A, et al. (2018) High throughput automated analysis of big flow cytometry data. *Methods (San Diego, Calif.)*, 134-135, 164.

Gondois-Rey F, et al. (2017) A Mature NK Profile at the Time of HIV Primary Infection Is Associated with an Early Response to cART. *Frontiers in immunology*, 8, 54.

Éliás S, et al. (2016) TGF- β Affects the Differentiation of Human GM-CSF+ CD4+ T Cells in an Activation- and Sodium-Dependent Manner. *Frontiers in immunology*, 7, 603.