

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

SamSPECTRAL

RRID:SCR_001858

Type: Tool

Proper Citation

SamSPECTRAL (RRID:SCR_001858)

Resource Information

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

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Description: Software that identifies cell population in flow cytometry data. It demonstrates significant advantages in proper identification of populations with non-elliptical shapes, low density populations close to dense ones, minor subpopulations of a major population and rare populations. It samples large data such that spectral clustering is possible while preserving density information in edge weights. More specifically, given a matrix of coordinates as input, SamSPECTRAL first builds the communities to sample the data points. Then, it builds a graph and after weighting the edges by conductance computation, the graph is passed to a classic spectral clustering algorithm to find the spectral clusters. The last stage of SamSPECTRAL is to combine the spectral clusters. The resulting connected components estimate biological cell populations in the data sample.

Synonyms: SamSPECTRAL - Identifies cell population in flow cytometry data

Resource Type: software resource

Defining Citation: [PMID:20667133](#)

Keywords: software package, mac os x, unix/linux, windows, r, cell biology, clustering, flow cytometry, stem cell, bio.tools

Related Condition: Cancer, HIV

Availability: Free, Available for download, Freely available

Resource Name: SamSPECTRAL

Resource ID: SCR_001858

Alternate IDs: OMICS_05638, biotools:samspectral

Alternate URLs: <https://bio.tools/samspectral>

License: GNU General Public License, v2 or greater

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260905T132440+0000

Ratings and Alerts

No rating or validation information has been found for SamSPECTRAL.

No alerts have been found for SamSPECTRAL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

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

Bhattacharjee A, et al. (2019) Cell type-specific transcriptional programs in mouse prefrontal cortex during adolescence and addiction. Nature communications, 10(1), 4169.

Brink BG, et al. (2018) ddPCRclust: an R package and Shiny app for automated analysis of multiplexed ddPCR data. Bioinformatics (Oxford, England), 34(15), 2687.

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