

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

Phenograph

RRID:SCR_016919

Type: Tool

Proper Citation

Phenograph (RRID:SCR_016919)

Resource Information

URL: <https://github.com/dpeerlab/phenograph>

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Description: Software tool as clustering method designed for high dimensional single cell data. Algorithmically defines phenotypes in high dimensional single cell data. Used for large scale analysis of single cell heterogeneity.

Abbreviations: PhenoGraph

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

Defining Citation: [PMID:26095251](#)

Keywords: high, dimension, single, cell, data, phenotype, analysis, heterogeneity

Funding: NIGMS R00 GM104148;
NICHD DP1 HD084071;
NCI R01 CA164729;
NCI U54 CA121852;
NCI R01 CA130826;
NCI U54 CA143907;
US Department of Health and Human Services HHSN272200700038C;
NIH N01 HV00242;
NCI P01 CA034233;
NIAID U19 AI057229;
NCI U54 CA149145;
US FDA HHSF223201210194C;
US DOD W81XWH1210591;
Entertainment Industry Foundation ;
Rachford and Carlota Harris Endowed Professorship ;
CIRM DR1 01477;

CIRM RB201592;
Stand Up To Cancer Phillip A. Sharp Award SU2CAACRPS04;
Packard Fellowship for Science and Engineering ;
NIH Office of the Director DP2 OD002414

Availability: Free, Available for download, Freely available

Resource Name: Phenograph

Resource ID: SCR_016919

Alternate URLs: <https://github.com/JinmiaoChenLab/Rphenograph>

Old URLs: <https://github.com/jacoblevine/PhenoGraph>

License: MIT License

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260808T190038+0000

Ratings and Alerts

No rating or validation information has been found for Phenograph.

No alerts have been found for Phenograph.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 235 mentions in open access literature.

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

Vallelonga V, et al. (2026) PU.1-activated genomic regions define low-risk MDS subsets characterized by immune dysregulation and disease progression. Blood, 147(20), 2358.

Gupta P, et al. (2026) Single-cell spatial atlas of the aging human breast. Nature aging, 6(4), 916.

Marchalot A, et al. (2026) Tumor-infiltrating immature innate lymphoid cells in colorectal cancer are biased toward ILC1/tissue-resident NK cell differentiation. Nature communications, 17(1).

Jiménez-Sánchez A, et al. (2026) Transcriptomic Plasticity Is a Hallmark of Metastatic Pancreatic Cancer. Cancer research, 86(7), 1769.

Hu Y, et al. (2026) Persistent CD8+ T cell-driven immune dysregulation despite normalized CD4+ T cell recovery in ART-treated people living with HIV. *Frontiers in immunology*, 17, 1735779.

Shemonti AS, et al. (2026) CARGO: A Cytometry Analysis framework via Regularized Graph Optimal-transport. *PLoS computational biology*, 22(6), e1014358.

Zhang C, et al. (2026) GNL3 Orchestrates AR Transcriptional Programs to Drive Castration-Resistant Prostate Cancer and Immune Evasion. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(26), e16411.

Lin B, et al. (2026) O-GlcNAcylation of UGDH regulates its activity and remodels the extracellular matrix to facilitate tumor growth. *Cell death and differentiation*, 33(3), 574.

Virgilio T, et al. (2026) Tumor-targeted IL2 promotes specific CD8+ T cells private clonal expansion enhancing lymphoma control. *Journal of experimental & clinical cancer research* : CR, 45(1).

Forjaz A, et al. (2026) Deep Learning Enabled 3D Multi-Omic Analysis Reveals Molecular Signatures of Heterogeneous Response to Chemotherapy in Pancreatic Cancer. *bioRxiv* : the preprint server for biology.

Cowley CJ, et al. (2026) Distinctive DNA sequence features define epigenetic longevity of inflammatory memory. *Science* (New York, N.Y.), 391(6792), eadz6830.

Fehrenbach P, et al. (2026) Beyond the skin barrier: commensal *S. epidermidis* imprint systemic immunity to invasive biofilm infection. *bioRxiv* : the preprint server for biology.

Wang Z, et al. (2026) TGF β induces an atypical EMT to evade immune mechanosurveillance in lung adenocarcinoma dormant metastasis. *Nature cancer*, 7(1), 131.

Näsiaho J, et al. (2026) Spatial single-cell analysis reveals tumor microenvironment signatures predictive of oral cavity cancer outcome. *Cell reports. Medicine*, 7(2), 102615.

Wei L, et al. (2026) A vasculogenic mimicry subtype unveiled by integrated multi-omics predicts prognosis and guides immunotherapy in MIBC. *Frontiers in bioinformatics*, 6, 1796762.

Burgos-Morales O, et al. (2026) Coxsackievirus B escapes antiviral CD8+ T cells but triggers robust CD4+ memory responses. *Science advances*, 12(25), eaef5067.

Belanger K, et al. (2026) Cancer-Associated Fibroblasts Promote Epithelial-Mesenchymal Transition and Classical to Basal Subtype Shift in Pancreatic Cancer. *Cancer research*, 86(14), 3604.

Zhu X, et al. (2026) Ferroptosis-STING co-activation drives GzmB+CD38+CD8+ T-cell expansion to overcome lymphoma immunosuppression. *Biomaterials*, 334, 124250.

Liao G, et al. (2025) Multi-scaled transcriptomics of chronically inflamed nasal epithelium reveals immune-epithelial dynamics and tissue remodeling in nasal polyp formation. *Immunity*, 58(10), 2593.

Okuno N, et al. (2025) Brain macrophages and pial fibroblasts promote inflammation in a hypomyelination model. *Acta neuropathologica communications*, 13(1), 145.