

Resource Summary Report

Generated by [NIF](#) on Aug 27, 2026

Phenograph

RRID:SCR_016919

Type: Tool

Proper Citation

Phenograph (RRID:SCR_016919)

Resource Information

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

Proper Citation: Phenograph (RRID:SCR_016919)

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

Defining Citation: [PMID:26095251](#)

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

Funding: CIRM DR1 01477;
CIRM RB201592;
Entertainment Industry Foundation ;
NCI P01 CA034233;
NCI R01 CA130826;
NCI R01 CA164729;
NCI U54 CA121852;
NCI U54 CA143907;
NCI U54 CA149145;
NIAID U19 AI057229;
NICHD DP1 HD084071;
NIGMS R00 GM104148;
NIH Office of the Director DP2 OD002414;
NIH N01 HV00242;
Packard Fellowship for Science and Engineering ;
Rachford and Carlota Harris Endowed Professorship ;

Stand Up To Cancer Phillip A. Sharp Award SU2CAACRPS04;
US Department of Health and Human Services HHSN272200700038C;
US DOD W81XWH1210591;
US FDA HHSF223201210194C

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: 20260821T194112+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 [NIF](#) .

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.

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.

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.

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.

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.

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.

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

Wang Y, et al. (2025) MuCST: restoring and integrating heterogeneous morphology images and spatial transcriptomics data with contrastive learning. *Genome medicine*, 17(1), 21.