CITATION REPORT List of articles citing

Clustering single-cell RNA-seq data with a model-based deep learning approach

DOI: 10.1038/s42256-019-0037-0 Nature Machine Intelligence, 2019, 1, 191-198.

Source: https://exaly.com/paper-pdf/73551737/citation-report.pdf

Version: 2024-04-10

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper IF	Citations
130	DeepImpute: an accurate, fast, and scalable deep neural network method to impute single-cell RNA-seq data. 2019 , 20, 211	85
129	Opportunities for Artificial Intelligence in Advancing Precision Medicine. 2019 , 7, 208-213	23
128	Single-cell RNA-Seq: a next generation sequencing tool for a high-resolution view of the individual cell. 2020 , 38, 3730-3735	O
127	Deep learning of pharmacogenomics resources: moving towards precision oncology. 2020 , 21, 2066-2083	19
126	Model-based autoencoders for imputing discrete single-cell RNA-seq data. 2021 , 192, 112-119	O
125	AAE-SC: A scRNA-Seq Clustering Framework Based on Adversarial Autoencoder. 2020 , 8, 178962-178975	1
124	Imputing missing RNA-sequencing data from DNA methylation by using a transfer learning-based neural network. 2020 , 9,	8
123	LAK: Lasso and K-Means Based Single-Cell RNA-Seq Data Clustering Analysis. 2020, 8, 129679-129688	6
122	Deep soft -means clustering with self-training for single-cell RNA sequence data. 2020 , 2, lqaa039	9
121	scAIDE: clustering of large-scale single-cell RNA-seq data reveals putative and rare cell types. 2020 , 2, lqaa082	1
120	Computational Methods for Single-Cell RNA Sequencing. 2020 , 3, 339-364	35
119	MethylNet: an automated and modular deep learning approach for DNA methylation analysis. 2020 , 21, 108	23
118	Single-Cell Transcriptome Data Clustering via Multinomial Modeling and Adaptive Fuzzy K-Means Algorithm. 2020 , 11, 295	7
117	A Single-Neuron: Current Trends and Future Prospects. 2020 , 9,	14
116	Boosting Tree-Assisted Multitask Deep Learning for Small Scientific Datasets. 2020 , 60, 1235-1244	23
115	Deep learning in next-generation sequencing. 2021 , 26, 173-180	7
114	Single-cell RNA-seq data semi-supervised clustering and annotation via structural regularized domain adaptation. 2021 , 37, 775-784	8

(2021-2021)

113	scRAE: Deterministic Regularized Autoencoders with Flexible Priors for Clustering Single-cell Gene Expression Data. 2021 , PP,	1
112	Cell Subtype Classification via Representation Learning Based on a Denoising Autoencoder for Single-Cell RNA Sequencing. 2021 , 9, 14540-14548	1
111	NMFLRR: Clustering scRNA-seq data by integrating non-negative matrix factorization with low rank representation. 2021 , PP,	2
110	ScSSC: Semi-supervised Single Cell Clustering Based on 2D Embedding. 2021 , 478-489	
109	SUSCC: Secondary Construction of Feature Space based on UMAP for Rapid and Accurate Clustering Large-scale Single Cell RNA-seq Data. 2021 , 13, 83-90	1
108	Cell Type Assignments for Spatial Transcriptomics Data.	3
107	scGAE: topology-preserving dimensionality reduction for single-cell RNA-seq data using graph autoencoder.	1
106	Genome-wide prediction and integrative functional characterization of Alzheimer disease-associated genes.	О
105	Advancing Drug Discovery for Neurological Disorders Using iPSC-Derived Neural Organoids. 2021 , 22,	9
104	Model-based deep embedding for constrained clustering analysis of single cell RNA-seq data. 2021 , 1873	7
103	A hitchhiker's guide to single-cell transcriptomics and data analysis pipelines. 2021 , 113, 606-619	7
102	Deep embedded clustering with multiple objectives on scRNA-seq data. 2021 , 22,	2
101	Elucidating transcriptomic profiles from single-cell RNA sequencing data using nature-inspired compressed sensing. 2021 , 22,	4
100	SAREV: A review on statistical analytics of single-cell RNA sequencing data. e1558	
99	Contrastive self-supervised clustering of scRNA-seq data. 2021 , 22, 280	7
98	A joint deep learning model enables simultaneous batch effect correction, denoising, and clustering in single-cell transcriptomics. 2021 , 31, 1753-1766	6
97	Breast Cancer Case Identification Based on Deep Learning and Bioinformatics Analysis. 2021 , 12, 628136	2
96	DeepOMe: A Web Server for the Prediction of 2'-O-Me Sites Based on the Hybrid CNN and BLSTM Architecture. 2021 , 9, 686894	2

95	REBET: a method to determine the number of cell clusters based on batch effect removal. 2021, 22,	1
94	Integrative Analysis of Next-Generation Sequencing for Next-Generation Cancer Research toward Artificial Intelligence. 2021 , 13,	2
93	An active learning approach for clustering single-cell RNA-seq data. 2021,	1
92	CALLR: a semi-supervised cell-type annotation method for single-cell RNA sequencing data. 2021 , 37, i51-i58	1
91	A deep embedded refined clustering approach for breast cancer distinction based on DNA methylation. 1	2
90	SCDRHA: A scRNA-Seq Data Dimensionality Reduction Algorithm Based on Hierarchical Autoencoder. 2021 , 12, 733906	O
89	ScCAEs: deep clustering of single-cell RNA-seq via convolutional autoencoder embedding and soft K-means. 2021 ,	2
88	A comparison of deep learning-based pre-processing and clustering approaches for single-cell RNA sequencing data. 2021 ,	1
87	Clustering single cell CITE-seq data with a canonical correlation based deep learning method.	
86	UICPC: Centrality-based clustering for scRNA-seq data analysis without user input. 2021 , 137, 104820	3
85	A survey on computational methods in discovering protein inhibitors of SARS-CoV-2. 2021,	1
84	Identification of H3N2 NA and PB1-F2 genetic variants and their association with disease symptoms during the 2014-15 influenza season. 2021 , 7, veab047	1
83	SMILE: Mutual Information Learning for Integration of Single Cell Omics Data.	0
82	DeepCNV: a deep learning approach for authenticating copy number variations. 2021 , 22,	1
81	Unsupervised Cluster Analysis and Gene Marker Extraction of scRNA-seq Data based on Non-negative Matrix Factorization. 2021 , PP,	6
80	Identification of H3N2 NA and PB1-F2 genetic variants and their association with disease symptoms during the 2014-15 influenza season.	1
79	A Joint Deep Learning Model for Simultaneous Batch Effect Correction, Denoising and Clustering in Single-Cell Transcriptomics.	5
78	Imputing missing RNA-seq data from DNA methylation by using transfer learning based neural network.	2

77	Deep learning-based advances and applications for single-cell RNA-sequencing data analysis. 2021,	2
76	Clustering Spatial Transcriptomics Data. 2021 ,	3
75	A topology-preserving dimensionality reduction method for single-cell RNA-seq data using graph autoencoder. 2021 , 11, 20028	1
74	MethylNet: An Automated and Modular Deep Learning Approach for DNA Methylation Analysis.	
73	Graph Convolutional Network-based Method for Clustering Single-cell RNA-seq Data.	2
72	GNN-based embedding for clustering scRNA-seq data. 2021,	O
71	RDAClone: Deciphering Tumor Heterozygosity through Single-Cell Genomics Data Analysis with Robust Deep Autoencoder 2021 , 12,	О
70	Explainability methods for differential gene analysis of single cell RNA-seq clustering models.	
69	Deep learning applications in single-cell omics data analysis.	О
68	Effectively Clustering Single Cell RNA Sequencing Data by Sparse Representation. 2021, PP,	1
67	scCDG: A Method based on DAE and GCN for scRNA-seq data Analysis. 2021, PP,	O
66	ScDA: A Denoising AutoEncoder Based Dimensionality Reduction for Single-cell RNA-seq Data. 2021 , 534-545	
65	Immunotherapy of cancer in single-cell RNA sequencing era: A precision medicine perspective 2021 , 146, 112558	1
64	Dissecting Cellular Heterogeneity Based on Network Denoising of scRNA-seq Using Local Scaling Self-Diffusion 2021 , 12, 811043	
63	scNAME: Neighborhood contrastive clustering with ancillary mask estimation for scRNA-seq data 2022 ,	2
62	Integrating pathway knowledge with deep neural networks to reduce the dimensionality in single-cell RNA-seq data 2022 , 15, 1	1
61	Deep structural clustering for single-cell RNA-seq data jointly through autoencoder and graph neural network 2022 ,	1
60	scHFC: a hybrid fuzzy clustering method for single-cell RNA-seq data optimized by natural computation 2022 ,	O

59	Learning deep features and topological structure of cells for clustering of scRNA-sequencing data 2022 ,	3
58	Cell type annotation of single-cell chromatin accessibility data via supervised Bayesian embedding. Nature Machine Intelligence,	22.5 1
57	scGAC: a graph attentional architecture for clustering single-cell RNA-seq data 2022,	O
56	SCOTCluster: Deep Clustering with Optimal Transport for Large-scale Single-cell RNA-seq Data. 2021 ,	
55	Deep learning tackles single-cell analysis-a survey of deep learning for scRNA-seq analysis 2021,	О
54	Single-cell RNA sequencing data clustering using graph convolutional networks. 2021,	O
53	A Parameter-free Deep Embedded Clustering Method for Single-cell RNA-seq Data.	
52	DeepCI: a deep learning based clustering method for single cell RNA-seq data. 2021,	O
51	GMHCC: High-throughput Analysis of Biomolecular Data using Graph-based Multiple Hierarchical Consensus Clustering 2022 ,	O
50	A parameter-free deep embedded clustering method for single-cell RNA-seq data 2022,	O
49	OUP accepted manuscript.	
48	Data_Sheet_1.pdf. 2020 ,	
47	Imputing DNA Methylation by Transferred Learning Based Neural Network. 2022, 37, 320-329	О
46	UIPBC: An effective clustering for scRNA-seq data analysis without user input. 2022 , 248, 108767	
45	Disease classification for whole blood DNA methylation: meta-analysis, missing values imputation, and XAI.	
44	scDeepC3: scRNA-seq Deep Clustering by A Skip AutoEncoder Network with Clustering Consistency.	
43	De novo reconstruction of cell interaction landscapes from single-cell spatial transcriptome data with DeepLinc. 2022 , 23,	О
42	Dissecting cell fate dynamics in pediatric glioblastoma through the lens of complex systems and cellular cybernetics.	

41	scCNC: A method based on Capsule Network for Clustering scRNA-seq Data.	2
40	scCAN: single-cell clustering using autoencoder and network fusion. 2022 , 12,	O
39	Feature-scML: an open-source Python package for the feature importance visualization of single-cell omics with machine learning. 2022 , 17,	
38	A convolutional neural network model for survival prediction based on prognosis-related cascaded Wx feature selection.	1
37	Dimensionality Reduction of Single-Cell RNA Sequencing Data by Combining Entropy and Denoising AutoEncoder.	0
36	Application of deep learning methods: From molecular modelling to patient classification. 2022 , 418, 113278	
35	A deep matrix factorization based approach for single-cell RNA-seq data clustering. 2022, 205, 114-122	0
34	Predicting the Reprogrammability of Human Cells Based on Transcriptome Data and SGD Classifier with Elastic-Net Regularization.	
33	Contrastive learning enables rapid mapping to multimodal single-cell atlas of multimillion scale.	O
32	Learning discriminative and structural samples for rare cell types with deep generative model.	O
31	scWMC: Weighted Matrix Completion-based Imputation of scRNA-seq Data via Prior Subspace Information.	О
30	DEMOC: a deep embedded multi-omics learning approach for clustering single-cell CITE-seq data. 2022 , 23,	O
29	Decoding brain memory formation by single-cell RNA sequencing.	0
28	A Meta-learning based Graph-Hierarchical Clustering Method for Single Cell RNA-Seq Data.	O
27	Disease classification for whole-blood DNA methylation: Meta-analysis, missing values imputation, and XAI. 2022 , 11,	0
26	DANCE: A Deep Learning Library and Benchmark for Single-Cell Analysis.	O
25	GLAE: A Graph-learnable Auto-encoder for Single-cell RNA-seq Analysis. 2022,	О
24	Introduction. 2022, 1-24	O

23	Changes in tourist mobility after COVID-19 outbreaks. 2023 , 98, 103522	0
22	Machine Learning for Lung Cancer Diagnosis, Treatment, and Prognosis. 2022,	Ο
21	Network-Guided Sparse Subspace Clustering on Single-Cell Data.	0
20	Clustering of single-cell multi-omics data with a multimodal deep learning method. 2022 , 13,	1
19	scDSSC: Deep Sparse Subspace Clustering for scRNA-seq Data. 2022 , 18, e1010772	О
18	Secuer: Ultrafast, scalable and accurate clustering of single-cell RNA-seq data. 2022 , 18, e1010753	O
17	Single-cell RNA-seq data analysis using graph autoencoders and graph attention networks. 13,	О
16	scDCCA: deep contrastive clustering for single-cell RNA-seq data based on auto-encoder network.	O
15	scGMAAE: Gaussian mixture adversarial autoencoders for diversification analysis of scRNA-seq data.	0
14	scMODD: A model-driven algorithm for doublet identification in single-cell RNA-sequencing data. 2,	Ο
13	Graph embedding and Gaussian mixture variational autoencoder network for end-to-end analysis of single-cell RNA sequencing data. 2023 , 100382	1
12	A Meta-learning based Graph-Hierarchical Clustering Method for Single Cell RNA-Seq Data. 2022 ,	Ο
11	G3DC: a Gene-Graph-Guided selective Deep Clustering method for single cell RNA-seq data.	Ο
10	Denoising adaptive deep clustering with self-attention mechanism on single-cell sequencing data.	Ο
9	Topological identification and interpretation for single-cell gene regulation elucidation across multiple platforms using scMGCA. 2023 , 14,	1
8	Artificial Intelligence, Bioinformatics, and Pathology. 2023 ,	Ο
7	Clustering ensemble in scRNA-seq data analysis: Methods, applications and challenges. 2023 , 106939	0
6	Class Discovery, Comparison, and Prediction Methods for RNA-Seq Data. 2022 , 2060-2084	0

CITATION REPORT

5	scBGEDA: deep single-cell clustering analysis via a dual denoising autoencoder with bipartite graph ensemble clustering. 2023 , 39,	Ο
4	Single-cell RNA-seq data analysis based on directed graph neural network. 2023 , 211, 48-60	O
3	Complex hierarchical structures in single-cell genomics data unveiled by deep hyperbolic manifold learning. 2023 , 33, 232-246	O
2	TripletCell: a deep metric learning framework for accurate annotation of cell types at the single-cell level.	O
1	A pattern-recognition-based clustering method for non-invasive diagnosis and classification of various gastric conditions. 146906672311743	O