Resource Summary Report

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CopyKAT

RRID:SCR_024512
Type: Tool

Proper Citation

CopyKAT (RRID:SCR_024512)

Resource Information

URL: https://github.com/navinlabcode/copykat

Proper Citation: CopyKAT (RRID:SCR_024512)

Description: Software R package to estimate genomic copy number profiles at average genomic resolution of 5 Mb from read depth in high throughput single cell RNA sequencing data.Used for inference of genomic copy number and subclonal structure of human tumors from high-throughput single cell RNAseq data.

Synonyms: , Copynumber Karyotyping of Aneuploid Tumors

Resource Type: software resource, software toolkit

Defining Citation: PMID:33462507

Keywords: Inference of genomic copy number and subclonal structure of human tumors, high throughput single cell RNAseq data,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: CopyKAT

Resource ID: SCR_024512

Record Creation Time: 20231002T161337+0000

Record Last Update: 20250416T064011+0000

Ratings and Alerts

No rating or validation information has been found for CopyKAT.

No alerts have been found for CopyKAT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 34 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Deng Y, et al. (2024) Multicellular ecotypes shape progression of lung adenocarcinoma from ground-glass opacity toward advanced stages. Cell reports. Medicine, 5(4), 101489.

Zhang C, et al. (2024) Neoadjuvant sintilimab plus chemotherapy in EGFR-mutant NSCLC: Phase 2 trial interim results (NEOTIDE/CTONG2104). Cell reports. Medicine, 5(7), 101615.

De Zuani M, et al. (2024) Single-cell and spatial transcriptomics analysis of non-small cell lung cancer. Nature communications, 15(1), 4388.

Zhang Q, et al. (2024) Investigating cellular similarities and differences between upper tract urothelial carcinoma and bladder urothelial carcinoma using single-cell sequencing. Frontiers in immunology, 15, 1298087.

Liu B, et al. (2024) Distinctive multicellular immunosuppressive hubs confer different intervention strategies for left- and right-sided colon cancers. Cell reports. Medicine, 5(6), 101589.

Burdett NL, et al. (2024) Timing of whole genome duplication is associated with tumor-specific MHC-II depletion in serous ovarian cancer. Nature communications, 15(1), 6069.

Yang Y, et al. (2024) Reconstitution of the Multiple Myeloma Microenvironment Following Lymphodepletion with BCMA CAR-T Therapy. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(18), 4201.

Yang Z, et al. (2024) Single-cell sequencing reveals immune features of treatment response to neoadjuvant immunochemotherapy in esophageal squamous cell carcinoma. Nature communications, 15(1), 9097.

Wang X, et al. (2024) Single-cell transcriptomics reveals the role of antigen presentation in liver metastatic breast cancer. iScience, 27(2), 108896.

Si Y, et al. (2024) RNA-seq and bulk RNA-seq data analysis of cancer-related fibroblasts (CAF) in LUAD to construct a CAF-based risk signature. Scientific reports, 14(1), 23243.

Ricker CA, et al. (2024) Historical perspective and future directions: computational science in immuno-oncology. Journal for immunotherapy of cancer, 12(1).

Ma J, et al. (2024) Revealing a cancer-associated fibroblast-based risk signature for pancreatic adenocarcinoma through single-cell and bulk RNA-seq analysis. Aging, 16(18), 12525.

He X, et al. (2024) Identification of a senescence-related transcriptional signature to uncover molecular subtypes and key genes in hepatocellular carcinoma. PloS one, 19(10), e0311696.

Bu L, et al. (2024) CHD6 eviction of promoter nucleosomes maintains housekeeping transcriptional program in prostate cancer. Molecular therapy. Nucleic acids, 35(4), 102397.

Liu S, et al. (2024) Single-cell dissection of multifocal bladder cancer reveals malignant and immune cells variation between primary and recurrent tumor lesions. Communications biology, 7(1), 1659.

Kang Z, et al. (2024) Identification macrophage signatures in prostate cancer by single-cell sequencing and machine learning. Cancer immunology, immunotherapy : CII, 73(3), 41.

Liu H, et al. (2024) GJB2 Promotes HCC Progression by Activating Glycolysis Through Cytoplasmic Translocation and Generating a Suppressive Tumor Microenvironment Based on Single Cell RNA Sequencing. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(39), e2402115.

Dong Q, et al. (2023) Mutant RB1 enhances therapeutic efficacy of PARPis in lung adenocarcinoma by triggering the cGAS/STING pathway. JCI insight, 8(21).

Dai Z, et al. (2023) Characterizing ligand-receptor interactions and unveiling the pro-tumorigenic role of CCL16-CCR1 axis in the microenvironment of hepatocellular carcinoma. Frontiers in immunology, 14, 1299953.

De Falco A, et al. (2023) A variational algorithm to detect the clonal copy number substructure of tumors from scRNA-seq data. Nature communications, 14(1), 1074.