Resource Summary Report

Generated by NIF on May 25, 2025

PurBayes

RRID:SCR_002068
Type: Tool

Proper Citation

PurBayes (RRID:SCR_002068)

Resource Information

URL: http://cran.r-project.org/web/packages/PurBayes/

Proper Citation: PurBayes (RRID:SCR_002068)

Description: An MCMC-based algorithm that uses next-generation sequencing data to estimate tumor purity and clonality for paired tumor-normal data.

Synonyms: PurBayes: Bayesian Estimation of Tumor Purity and Clonality

Resource Type: software resource

Defining Citation: PMID:23749958

Keywords: software package, unix/linux, mac os x, windows, r, bio.tools

Funding:

Availability: GNU General Public License, v2

Resource Name: PurBayes

Resource ID: SCR_002068

Alternate IDs: biotools:purbayes, OMICS_03561

Alternate URLs: https://bio.tools/purbayes

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250525T030650+0000

Ratings and Alerts

No rating or validation information has been found for PurBayes.

No alerts have been found for PurBayes.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Prip F, et al. (2025) Comprehensive genomic characterization of early-stage bladder cancer. Nature genetics, 57(1), 115.

Anurag M, et al. (2024) Multiomics profiling of urothelial carcinoma in situ reveals CIS-specific gene signature and immune characteristics. iScience, 27(3), 109179.

Revkov E, et al. (2023) PUREE: accurate pan-cancer tumor purity estimation from gene expression data. Communications biology, 6(1), 394.

Tang J, et al. (2021) Single-cell exome sequencing reveals multiple subclones in metastatic colorectal carcinoma. Genome medicine, 13(1), 148.

Zhu G, et al. (2021) Tissue-specific cell-free DNA degradation quantifies circulating tumor DNA burden. Nature communications, 12(1), 2229.

Li X, et al. (2021) Whole-genome sequencing of phenotypically distinct inflammatory breast cancers reveals similar genomic alterations to non-inflammatory breast cancers. Genome medicine, 13(1), 70.

Kobayashi H, et al. (2020) Characterization of tumour mutation burden in patients with non-small cell lung cancer and interstitial lung disease. Respirology (Carlton, Vic.), 25(8), 850.

Hatakeyama K, et al. (2019) Mutational burden and signatures in 4000 Japanese cancers provide insights into tumorigenesis and response to therapy. Cancer science, 110(8), 2620.

Árnadóttir SS, et al. (2018) Characterization of genetic intratumor heterogeneity in colorectal cancer and matching patient-derived spheroid cultures. Molecular oncology, 12(1), 132.

Kohli M, et al. (2015) Mutational Landscapes of Sequential Prostate Metastases and Matched Patient Derived Xenografts during Enzalutamide Therapy. PloS one, 10(12), e0145176.