Resource Summary Report

Generated by NIF on Apr 22, 2025

Patchwork

RRID:SCR_000072
Type: Tool

Proper Citation

Patchwork (RRID:SCR_000072)

Resource Information

URL: http://patchwork.r-forge.r-project.org/

Proper Citation: Patchwork (RRID:SCR_000072)

Description: Software tool for analyzing and visualizing allele-specific copy numbers and loss-of-heterozygosity in cancer genomes. The data input is in the format of whole-genome sequencing data which enables characterization of genomic alterations ranging in size from point mutations to entire chromosomes. High quality results are obtained even if samples have low coverage, ~4x, low tumor cell content or are aneuploid. Patchwork takes BAM files as input whereas PatchworkCG takes input from CompleteGenomics files. TAPS performs the same analysis as Patchwork but for microarray data.

Abbreviations: Patchwork

Resource Type: software resource

Defining Citation: PMID:23531354

Keywords: genome, allele, copy number, bam, unix, r, bio.tools

Related Condition: Cancer, Tumor

Funding:

Availability: Free, Public

Resource Name: Patchwork

Resource ID: SCR_000072

Alternate IDs: biotools:patchwork, OMICS_02118

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

Record Creation Time: 20220129T080159+0000

Record Last Update: 20250420T013927+0000

Ratings and Alerts

No rating or validation information has been found for Patchwork.

No alerts have been found for Patchwork.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Malkani S, et al. (2020) Circulating miRNA Spaceflight Signature Reveals Targets for Countermeasure Development. Cell reports, 33(10), 108448.

Mayrhofer M, et al. (2013) Patchwork: allele-specific copy number analysis of whole-genome sequenced tumor tissue. Genome biology, 14(3), R24.