Resource Summary Report

Generated by NIF on May 17, 2025

Bpipe

RRID:SCR_003471
Type: Tool

Proper Citation

Bpipe (RRID:SCR_003471)

Resource Information

URL: https://code.google.com/p/bpipe/

Proper Citation: Bpipe (RRID:SCR_003471)

Description: Software tool for running and managing bioinformatics pipelines. It specializes in enabling users to turn existing pipelines based on shell scripts or command line tools into highly flexible, adaptable and maintainable workflows with a minimum of effort. Bpipe ensures that pipelines execute in a controlled and repeatable fashion and keeps audit trails and logs to ensure that experimental results are reproducible. Requiring only Java as a dependency, it is fully self-contained and cross-platform, making it very easy to adopt and deploy into existing environments.

Abbreviations: Bpipe

Synonyms: bpipe - A tool for running and managing bioinformatics pipelines

Resource Type: software resource

Defining Citation: PMID:22500002

Keywords: genetics, dna, analysis, cluster, workflow, bio.tools

Funding:

Availability: New BSD License, Acknowledgement requested

Resource Name: Bpipe

Resource ID: SCR_003471

Alternate IDs: biotools:bpipe, OMICS_02301

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

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250420T014144+0000

Ratings and Alerts

No rating or validation information has been found for Bpipe.

No alerts have been found for Bpipe.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Kim J, et al. (2023) Cortical thinning in relation to impaired insight into illness in patients with treatment resistant schizophrenia. Schizophrenia (Heidelberg, Germany), 9(1), 27.

Dashnow H, et al. (2022) STRling: a k-mer counting approach that detects short tandem repeat expansions at known and novel loci. Genome biology, 23(1), 257.

Skorska MN, et al. (2021) A Multi-Modal MRI Analysis of Cortical Structure in Relation to Gender Dysphoria, Sexual Orientation, and Age in Adolescents. Journal of clinical medicine, 10(2).

Petrosino G, et al. (2020) Preparation and Analysis of GLOE-Seq Libraries for Genome-Wide Mapping of DNA Replication Patterns, Single-Strand Breaks, and Lesions. STAR protocols, 1(2), 100076.

Sriramachandran AM, et al. (2020) Genome-wide Nucleotide-Resolution Mapping of DNA Replication Patterns, Single-Strand Breaks, and Lesions by GLOE-Seq. Molecular cell, 78(5), 975.

Garcia M, et al. (2020) Sarek: A portable workflow for whole-genome sequencing analysis of germline and somatic variants. F1000Research, 9, 63.

Ramchand J, et al. (2020) Prospective Evaluation of the Utility of Whole Exome Sequencing

in Dilated Cardiomyopathy. Journal of the American Heart Association, 9(2), e013346.

Sadedin SP, et al. (2018) Ximmer: a system for improving accuracy and consistency of CNV calling from exome data. GigaScience, 7(10).

Schmidt BM, et al. (2018) Clinker: visualizing fusion genes detected in RNA-seq data. GigaScience, 7(7).

Dashnow H, et al. (2018) STRetch: detecting and discovering pathogenic short tandem repeat expansions. Genome biology, 19(1), 121.

Causey JL, et al. (2018) DNAp: A Pipeline for DNA-seq Data Analysis. Scientific reports, 8(1), 6793.

Phipson B, et al. (2017) Gene length and detection bias in single cell RNA sequencing protocols. F1000Research, 6, 595.

Cingolani P, et al. (2015) BigDataScript: a scripting language for data pipelines. Bioinformatics (Oxford, England), 31(1), 10.