Resource Summary Report

Generated by NIF on May 15, 2025

GNUMAP

RRID:SCR_005482
Type: Tool

Proper Citation

GNUMAP (RRID:SCR_005482)

Resource Information

URL: http://dna.cs.byu.edu/gnumap/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 3rd,2023. A software program designed to accurately map sequence data obtained from next-generation sequencing machines (specifically that of Solexa/Illumina) back to a genome of any size. By using the posterior probability of mapping a given read to a specific genomic loation, we are able to account for repetitive reads by distributing them across several regions in the genome. In addition, the output of the program is created in such a way that it can be easily viewed through other free and readily- available programs. Several benchmark data sets were created with spiked-in duplicate regions, and GNUMAP was able to more accurately account for these duplicate regions.

Abbreviations: GNUMAP

Synonyms: Genomic Next-generation Universal MAPper

Resource Type: software resource

Keywords: next-generation sequencing, genome, bio.tools

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GNUMAP

Resource ID: SCR_005482

Alternate IDs: OMICS_00664, biotools:gnumap

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

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250420T014253+0000

Ratings and Alerts

No rating or validation information has been found for GNUMAP.

No alerts have been found for GNUMAP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Afzal M, et al. (2020) Legume genomics and transcriptomics: From classic breeding to modern technologies. Saudi journal of biological sciences, 27(1), 543.

Han Y, et al. (2016) Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and biology insights, 10, 267.

Whipple JM, et al. (2015) Genome-wide profiling of the C. elegans dsRNAome. RNA (New York, N.Y.), 21(5), 786.

Hong C, et al. (2013) Probabilistic alignment leads to improved accuracy and read coverage for bisulfite sequencing data. BMC bioinformatics, 14, 337.

Francis OE, et al. (2013) Pathoscope: species identification and strain attribution with unassembled sequencing data. Genome research, 23(10), 1721.

Warf MB, et al. (2012) Effects of ADARs on small RNA processing pathways in C. elegans. Genome research, 22(8), 1488.

Rope AF, et al. (2011) Using VAAST to identify an X-linked disorder resulting in lethality in male infants due to N-terminal acetyltransferase deficiency. American journal of human genetics, 89(1), 28.