Resource Summary Report

Generated by RRID on Apr 19, 2025

Myrna

RRID:SCR_006951

Type: Tool

Proper Citation

Myrna (RRID:SCR_006951)

Resource Information

URL: http://bowtie-bio.sourceforge.net/myrna/index.shtml

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Description: A cloud computing tool for calculating differential gene expression in large RNA-seq datasets. It uses Bowtie for short read alignment and R/Bioconductor for interval calculations, normalization, and statistical testing. These tools are combined in an automatic, parallel pipeline that runs in the cloud (Elastic MapReduce in this case) on a local Hadoop cluster, or on a single computer, exploiting multiple computers and CPUs wherever possible.

Abbreviations: Myrna

Synonyms: Myrna: Cloud-scale differential gene expression for RNA-seq

Resource Type: software resource

Defining Citation: PMID:20701754

Keywords: mapreduce, hadoop, cloud computing, differential expression, gene expression,

rna-seq, bio.tools

Funding:

Availability: Artistic License

Resource Name: Myrna

Resource ID: SCR_006951

Alternate IDs: OMICS_01310, biotools:myrna

Alternate URLs: https://github.com/BenLangmead/myrna, https://bio.tools/myrna

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250410T065503+0000

Ratings and Alerts

No rating or validation information has been found for Myrna.

No alerts have been found for Myrna.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis.

Database: the journal of biological databases and curation, 2015.