Resource Summary Report

Generated by dkNET on Apr 29, 2025

comrad

RRID:SCR_005101
Type: Tool

Proper Citation

comrad (RRID:SCR_005101)

Resource Information

URL: http://code.google.com/p/comrad/

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Description: A novel algorithmic framework for the integrated analysis of RNA-Seq and Whole Genome Shotgun Sequencing (WGSS) data for the purposes of discovering genomic rearrangements and aberrant transcripts. The Comrad framework leverages the advantages of both RNA-Seq and WGSS data, providing accurate classification of rearrangements as expressed or not expressed and accurate classification of the genomic or non-genomic origin of aberrant transcripts. A major benefit of Comrad is its ability to accurately identify aberrant transcripts and associated rearrangements using low coverage genome data. As a result, a Comrad analysis can be performed at a cost comparable to that of two RNA-Seq experiments, significantly lower than an analysis requiring high coverage genome data.

Abbreviations: comrad

Synonyms: comrad - Discovery of gene fusions using paired end RNA-Seq and WGSS

Resource Type: software resource

Funding:

Availability: Open unspecified license

Resource Name: comrad

Resource ID: SCR_005101

Alternate IDs: OMICS_01344

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250420T014244+0000

Ratings and Alerts

No rating or validation information has been found for comrad.

No alerts have been found for comrad.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Li L, et al. (2024) Preoperative prediction of MGMT promoter methylation in glioblastoma based on multiregional and multi-sequence MRI radiomics analysis. Scientific reports, 14(1), 16031.

Xiao D, et al. (2024) Assessing the transportability of radiomic models for lung cancer diagnosis: commercial vs. open-source feature extractors. Translational lung cancer research, 13(8), 1907.

Grabowski S, et al. (2022) MBGC: Multiple Bacteria Genome Compressor. GigaScience, 11.

Kredens KV, et al. (2020) Vertical lossless genomic data compression tools for assembled genomes: A systematic literature review. PloS one, 15(5), e0232942.

Latysheva NS, et al. (2016) Discovering and understanding oncogenic gene fusions through data intensive computational approaches. Nucleic acids research, 44(10), 4487.

Biji CL, et al. (2015) Compression of Large genomic datasets using COMRAD on Parallel Computing Platform. Bioinformation, 11(5), 267.