Resource Summary Report

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cwltool

RRID:SCR_015528
Type: Tool

Proper Citation

cwltool (RRID:SCR_015528)

Resource Information

URL: https://github.com/common-workflow-language/cwltool

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Description: Reference implementation of the Common Workflow Language standards. It provides complete features and tools and comprehensive validation of CWL. The reference implementation consists of two packages. The cwltool package is the primary Python module containing the reference implementation in the cwltool module and console executable by the same name. The cwlref-runner package is optional and provides an additional entry point under the alias cwl-runner, which is the implementation-agnostic name for the default CWL interpreter installed on a host.

Synonyms: CWLtool, Common Workflow Language Tool

Resource Type: software toolkit, source code, software resource

Defining Citation: DOI:10.6084/m9.figshare.3115156.v2

Keywords: language, reference implementation, python

Funding:

Availability: Available for download

Resource Name: cwltool

Resource ID: SCR_015528

Alternate IDs: OMICS_28977

Alternate URLs: https://sources.debian.org/src/cwltool/

License: Apache 2.0

Record Creation Time: 20220129T080326+0000

Record Last Update: 20250409T061321+0000

Ratings and Alerts

No rating or validation information has been found for cwltool.

No alerts have been found for cwltool.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Haft DH, et al. (2024) RefSeq and the prokaryotic genome annotation pipeline in the age of metagenomes. Nucleic acids research, 52(D1), D762.

Bray S, et al. (2023) The Planemo toolkit for developing, deploying, and executing scientific data analyses in Galaxy and beyond. Genome research, 33(2), 261.

Kale A, et al. (2023) Utility of the Python package Geoweaver_cwl for improving workflow reusability: an illustration with multidisciplinary use cases. Earth science informatics, 16(3), 2955.

Kyritsis KA, et al. (2023) Software pipelines for RNA-Seq, ChIP-Seq and germline variant calling analyses in common workflow language (CWL). Frontiers in bioinformatics, 3, 1275593.

Suetake H, et al. (2022) Sapporo: A workflow execution service that encourages the reuse of workflows in various languages in bioinformatics. F1000Research, 11, 889.

Ciani Y, et al. (2022) Allele-specific genomic data elucidate the role of somatic gain and copy-number neutral loss of heterozygosity in cancer. Cell systems, 13(2), 183.

Raghavan V, et al. (2022) A simple guide to de novo transcriptome assembly and annotation. Briefings in bioinformatics, 23(2).

Surumbayeva A, et al. (2021) Preparation of mouse pancreatic tumor for single-cell RNA sequencing and analysis of the data. STAR protocols, 2(4), 100989.

Lim HG, et al. (2021) Orchestrating an Optimized Next-Generation Sequencing-Based Cloud Workflow for Robust Viral Identification during Pandemics. Biology, 10(10).

Piccolo SR, et al. (2021) Simplifying the development of portable, scalable, and reproducible workflows. eLife, 10.

Chapman M, et al. (2021) Phenoflow: A Microservice Architecture for Portable Workflow-based Phenotype Definitions. AMIA Joint Summits on Translational Science proceedings. AMIA Joint Summits on Translational Science, 2021, 142.

Jackson M, et al. (2021) Using prototyping to choose a bioinformatics workflow management system. PLoS computational biology, 17(2), e1008622.

Vera Alvarez R, et al. (2021) PM4NGS, a project management framework for next-generation sequencing data analysis. GigaScience, 10(1).

Corley M, et al. (2021) fSHAPE, fSHAPE-eCLIP, and SHAPE-eCLIP probe transcript regions that interact with specific proteins. STAR protocols, 2(3), 100762.

Creason A, et al. (2021) A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. Cell systems, 12(8), 827.

Alvarez RV, et al. (2021) Transcriptome annotation in the cloud: complexity, best practices, and cost. GigaScience, 10(2).

Brito JJ, et al. (2020) Recommendations to enhance rigor and reproducibility in biomedical research. GigaScience, 9(6).

Lee S, et al. (2019) Tibanna: software for scalable execution of portable pipelines on the cloud. Bioinformatics (Oxford, England), 35(21), 4424.

Khan FZ, et al. (2019) Sharing interoperable workflow provenance: A review of best practices and their practical application in CWLProv. GigaScience, 8(11).

Andrio P, et al. (2019) BioExcel Building Blocks, a software library for interoperable biomolecular simulation workflows. Scientific data, 6(1), 169.