Resource Summary Report

Generated by NIF on Apr 18, 2025

Ergatis

RRID:SCR_005377
Type: Tool

Proper Citation

Ergatis (RRID:SCR_005377)

Resource Information

URL: http://ergatis.sourceforge.net/

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Description: A web interface and scalable software system for bioinformatics workflows that is used to create, run, and monitor reusable computational analysis pipelines. It contains pre-built components for common bioinformatics analysis tasks. These components can be arranged graphically to form highly-configurable pipelines. Each analysis component supports multiple output formats, including the Bioinformatic Sequence Markup Language (BSML). The current implementation includes support for data loading into project databases following the CHADO schema, a highly normalized, community-supported schema for storage of biological annotation data. Ergatis uses the Workflow engine to process its work on a compute grid. Workflow provides an XML language and processing engine for specifying the steps of a computational pipeline. It provides detailed execution status and logging for process auditing, facilitates error recovery from point of failure, and is highly scalable with support for distributed computing environments. The XML format employed enables commands to be run serially, in parallel, and in any combination or nesting level.

Abbreviations: Ergatis

Synonyms: ergatis: workflow creation and monitoring interface

Resource Type: software resource

Defining Citation: PMID:20413634

Keywords: workflow, bioinformatics, workflow management, pipeline, computation, genomics, genome, processing

Funding:

Availability: Artistic License

Resource Name: Ergatis

Resource ID: SCR_005377

Alternate IDs: OMICS_01140

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250410T065250+0000

Ratings and Alerts

No rating or validation information has been found for Ergatis.

No alerts have been found for Ergatis.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

D'Mello A, et al. (2019) ReVac: a reverse vaccinology computational pipeline for prioritization of prokaryotic protein vaccine candidates. BMC genomics, 20(1), 981.

Eppinger M, et al. (2014) Genomic epidemiology of the Haitian cholera outbreak: a single introduction followed by rapid, extensive, and continued spread characterized the onset of the epidemic. mBio, 5(6), e01721.