Resource Summary Report

Generated by RRID on May 20, 2025

myExperiment

RRID:SCR_001795
Type: Tool

Proper Citation

myExperiment (RRID:SCR_001795)

Resource Information

URL: http://www.myexperiment.org/

Proper Citation: myExperiment (RRID:SCR_001795)

Description: Community repository and virtual research environment where scientists can safely publish their workflows and experiment plans, share them with groups and find and use those of others. Workflows, other digital objects and collections (called Packs) can be swapped, sorted and searched. It supports Linked data, has a SPARQL Endpoint and REST API and is based on an open source Ruby on Rails codebase. Scientific workflows in various formats can be uploaded. Specific support is provided for Taverna workflows for which the system displays relevant metadata, components and visual previews, that are retrieved directly from workflow files. Version history for workflows is collected. This feature allows the contributor to keep previous versions of the workflow available, when the latest one is uploaded. This brings additional benefit for the users by allowing them to view the development stages of the workflow towards its latest implementation.

Abbreviations: myExperiment

Synonyms: my experiment

Resource Type: software application, service resource, community building portal, database, workflow software, data processing software, data or information resource, portal, software resource, storage service resource, data repository

Defining Citation: PMID:20501605

Keywords: workflow, pipeline, platform, component, data sharing, publish, digital object, experimental method, workflow management, virtual research environment, collaborative computing, taverna workflow workbench, bioinformatics, web service, bio.tools

Funding: JISC ;
Microsoft Technical Computing Initiative ;
EPSRC

Availability: The community can contribute to this resource, Acknowledgement requested

Resource Name: myExperiment

Resource ID: SCR_001795

Alternate IDs: nif-0000-10309, biotools:myexperiment

Alternate URLs: https://www.force11.org/node/4638, https://bio.tools/myexperiment

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250519T203151+0000

Ratings and Alerts

No rating or validation information has been found for myExperiment.

No alerts have been found for myExperiment.

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 RRID.

Samota EK, et al. (2021) Knowledge and Attitudes Among Life Scientists Toward Reproducibility Within Journal Articles: A Research Survey. Frontiers in research metrics and analytics, 6, 678554.

Thursby SJ, et al. (2020) CandiMeth: Powerful yet simple visualization and quantification of DNA methylation at candidate genes. GigaScience, 9(6).

Türková A, et al. (2019) Integrative Data Mining, Scaffold Analysis, and Sequential Binary

Classification Models for Exploring Ligand Profiles of Hepatic Organic Anion Transporting Polypeptides. Journal of chemical information and modeling, 59(5), 1811.

Carbonell P, et al. (2018) Enzyme Discovery: Enzyme Selection and Pathway Design. Methods in enzymology, 608, 3.

Carissimo G, et al. (2017) Metavisitor, a Suite of Galaxy Tools for Simple and Rapid Detection and Discovery of Viruses in Deep Sequence Data. PloS one, 12(1), e0168397.

Palmblad M, et al. (2017) Spatiotemporal analysis of tropical disease research combining Europe PMC and affiliation mapping web services. Tropical medicine and health, 45, 33.

Jovanovi? J, et al. (2017) Semantic annotation in biomedicine: the current landscape. Journal of biomedical semantics, 8(1), 44.

Zdrazil B, et al. (2016) From linked open data to molecular interaction: studying selectivity trends for ligands of the human serotonin and dopamine transporter. MedChemComm, 7(9), 1819.

Sfakianaki P, et al. (2015) Semantic biomedical resource discovery: a Natural Language Processing framework. BMC medical informatics and decision making, 15, 77.

Velloso H, et al. (2015) BOWS (bioinformatics open web services) to centralize bioinformatics tools in web services. BMC research notes, 8, 206.

Zheng CL, et al. (2015) Use of semantic workflows to enhance transparency and reproducibility in clinical omics. Genome medicine, 7(1), 73.

Dahlö M, et al. (2015) BioImg.org: A Catalog of Virtual Machine Images for the Life Sciences. Bioinformatics and biology insights, 9, 125.

Morrison SS, et al. (2014) Impact of analytic provenance in genome analysis. BMC genomics, 15 Suppl 8(Suppl 8), S1.

Vaughan LK, et al. (2013) Where in the genome are we? A cautionary tale of database use in genomics research. Frontiers in genetics, 4, 38.

Milsted AJ, et al. (2013) LabTrove: a lightweight, web based, laboratory "blog" as a route towards a marked up record of work in a bioscience research laboratory. PloS one, 8(7), e67460.

Toffano-Nioche C, et al. (2013) Detection of non-coding RNA in bacteria and archaea using the DETR'PROK Galaxy pipeline. Methods (San Diego, Calif.), 63(1), 60.

Vasilevsky N, et al. (2012) Research resources: curating the new eagle-i discovery system. Database : the journal of biological databases and curation, 2012, bar067.

Truszkowski A, et al. (2011) New developments on the cheminformatics open workflow environment CDK-Taverna. Journal of cheminformatics, 3, 54.

Oshita K, et al. (2011) KBWS: an EMBOSS associated package for accessing bioinformatics web services. Source code for biology and medicine, 6, 8.

Romano P, et al. (2011) Tools and collaborative environments for bioinformatics research. Briefings in bioinformatics, 12(6), 549.