



# The University of Manchester

## **CWL Viewer: The Common Workflow Language Viewer**



Mark Robinson<sup>1</sup>, Stian-Soiland-Reyes<sup>1</sup>, Michael Crusoe<sup>2</sup>, Carole Goble<sup>1</sup> <sup>1</sup> The University of Manchester, UK. Email: soiland-reyes@manchester.ac.uk <sup>2</sup> Common Workflow Language project

Project Website: https://view.commonwl.org

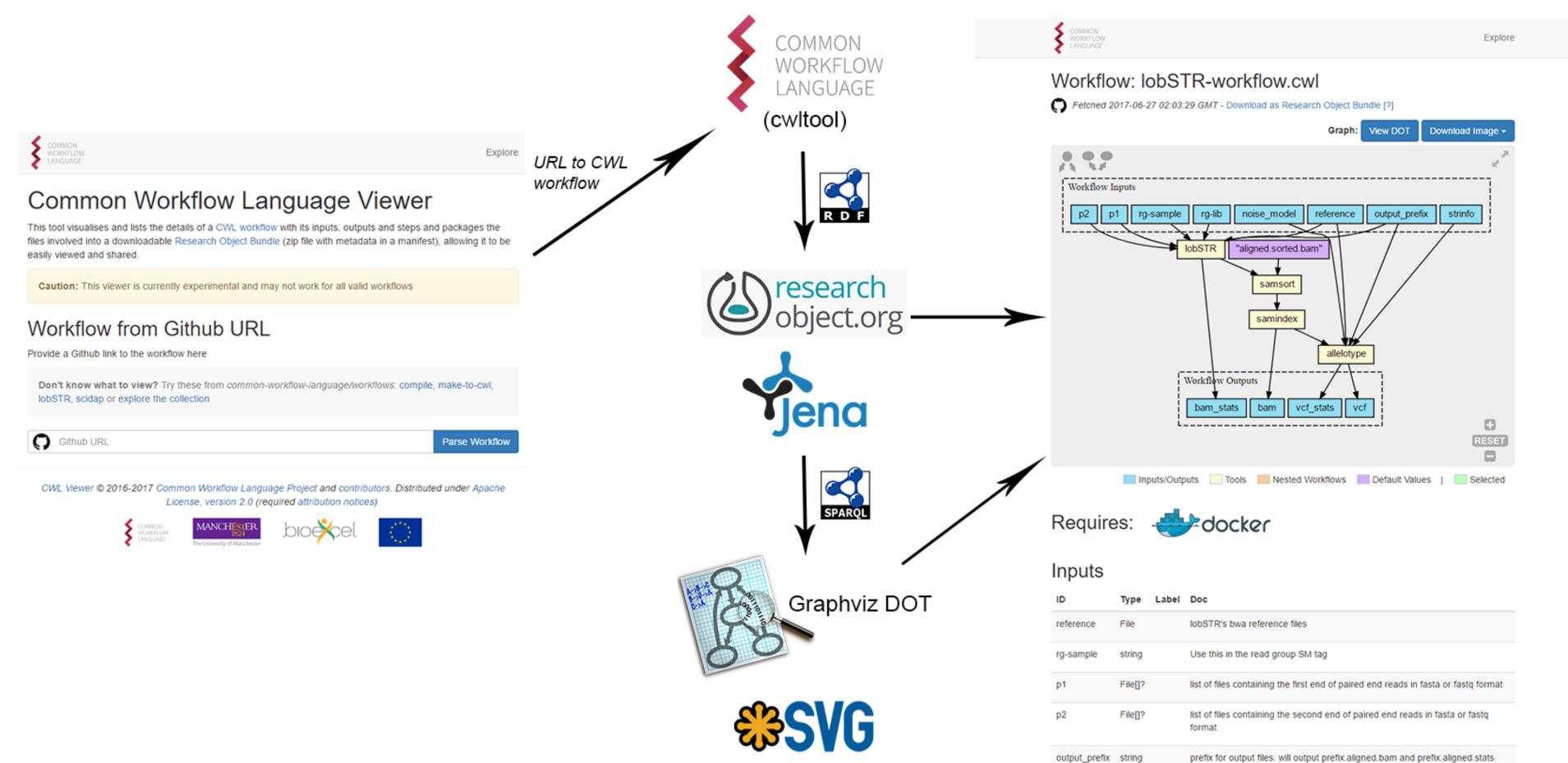
**Source Code:** http://github.com/common-workflow-language/cwlviewer License: CWL Viewer is licensed under the terms of the Apache License, Version 2.0, see https://www.apache.org/licenses/LICENSE-2.0

#### Abstract

Facilitating easy browsing, sharing and understanding of scientific workflows written in the Common Workflow Language

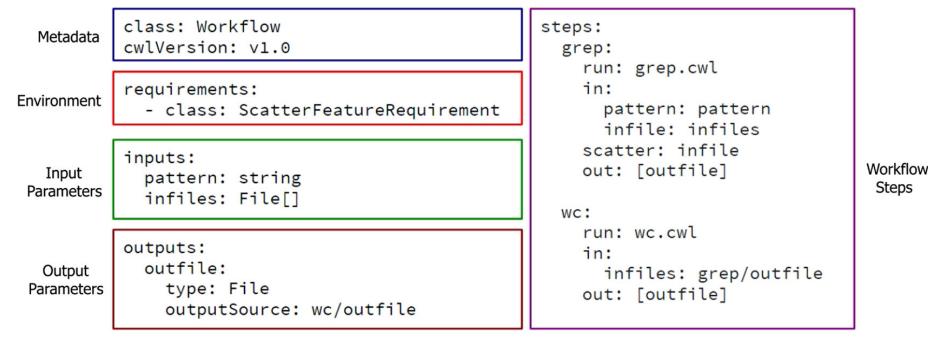
The Common Workflow Language (CWL) project emerged from the BOSC 2014 Codefest as a grassroots, multi-vendor working group to tackle the portability of data analysis workflows. It's specification for describing workflows and command line tools aims to make them portable and scalable across a variety of computing platforms.

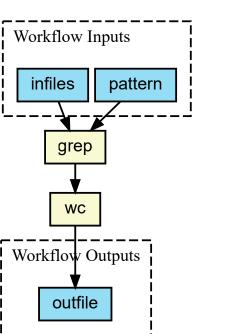
#### **Application Overview**



At its heart CWL is a set of **structured text** files (YAML) with various extensibility points to the format. However, the CWL syntax and multi-file collections are not conducive to workflow browsing, exchange and understanding: for this we need a visualization suite.

#### Example: Grep and Count Workflow





**CWL Viewer** is a richly featured **web visualization suite** which graphically presents and lists the details of CWL workflows with their *inputs*, *outputs* and *steps*. It also packages the CWL files into a downloadable **Research Object** Bundle including attribution, versioning and dependency metadata in the manifest, allowing it to be easily shared.

#### Visualisation

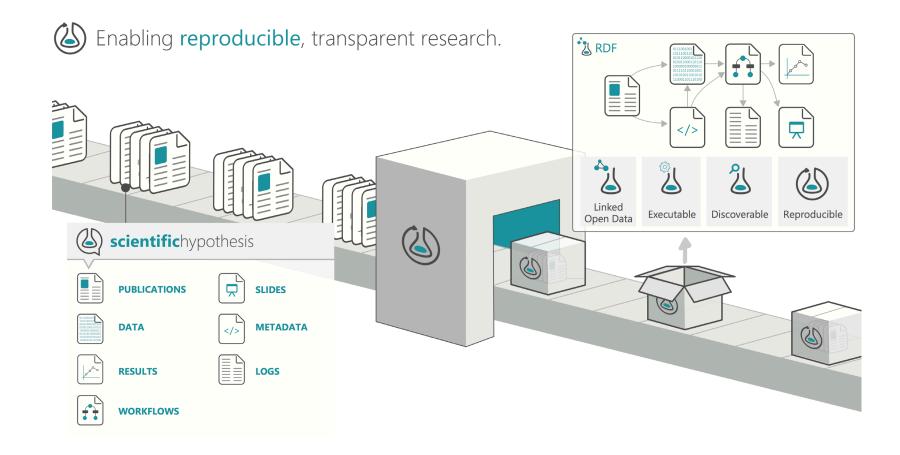
Visualisations allow complex workflows to be understood quickly and easily even without knowledge of the Common **Workflow Language syntax** 

Directed acyclic graphs are created from the workflow descriptions provided using *Graphviz DOT*. The source for this is provided within the application and can be downloaded for use in external applications.

The diagram can be **downloaded** in various formats and included in reports, presentations and external documentation to illustrate and explain their function

#### **Sharing and Research Objects**

**Research Objects** (RO) are an emerging approach to publishing scholarly information on the web and support reuse and **reproducibility**. They consist of a *container* of files with a manifest to provide meaningful information about what the those files are, what they mean, how they relate and provide provenance and versioning information.



The tool operates over **any workflow** held in a GitHub repository. Other features include: path visualization from parent and child nodes; nested workflows support; workflow diagram download in a range of image formats; a gallery of previously submitted workflows; and support for private git repositories and public GitHub including live updates

#### **Permalinks and Archiving**

The workflow pages contain the full Github URL to the workflow within a repository, enabling them to be easily remembered and manipulated within the browser.

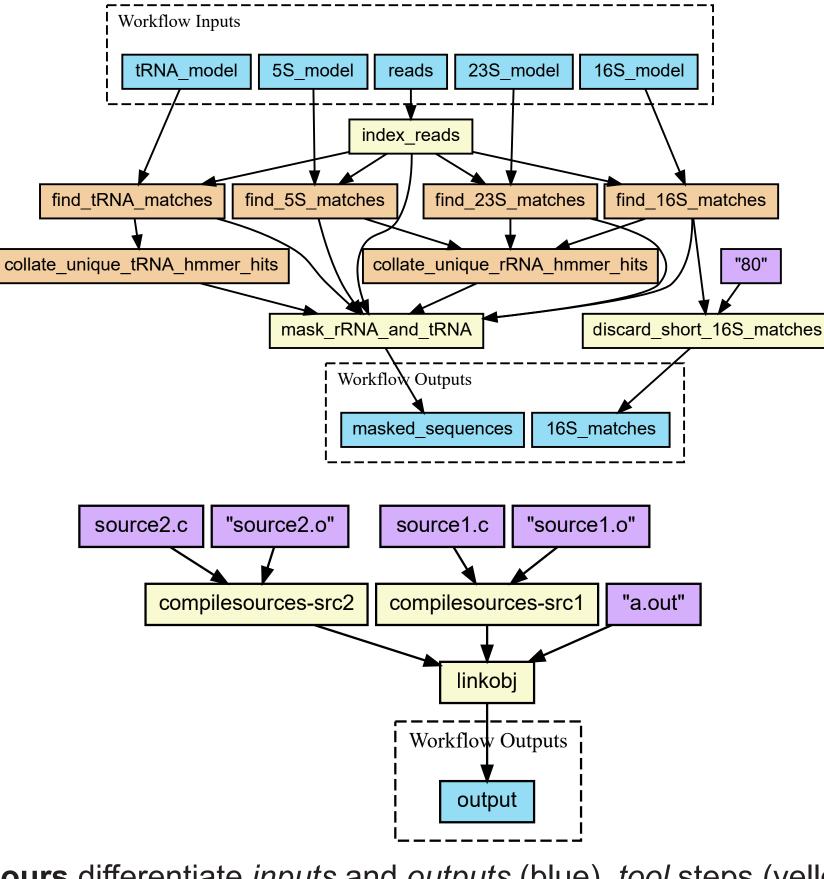
https://view.commonwl.org/workflows/github.com/common-workflow-language/workflows/ blob/master/workflows/lobSTR/lobSTR-workflow.cwl

#### Github URL

If a Git commit ID is used when adding the workflow, the visualisation and download become a "snapshot" of the workflow at a moment in time and exist at that link permanently for sharing.

Otherwise the visualisation will track the *branch* of the Github repository for updates after a cache expires.

### Provenance **Research Object** git commit log

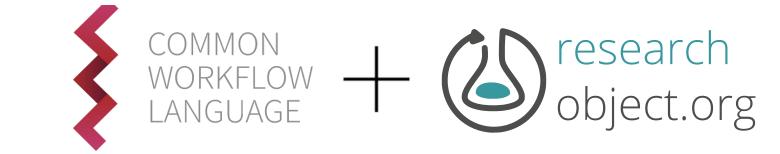


**Colours** differentiate *inputs* and *outputs* (blue), *tool* steps (yellow), nested workflows (orange) and default values (purple).

Labels within the workflow description are included instead of the ID of the element if provided (as well as documentation strings being included in the detailed tables underneath on the page). This encourages best practices when writing CWL workflows.

Within the web application the visualisation can also be panned and **zoomed** to navigate very large workflows.

The Common Workflow Language is not designed to capture detailed Description, provenance and versioning information within a workflow description. However, together the two technologies are a natural combination to provide both the language and packaging elements of execution and produce a self-contained workflow which can easily be run and reasoned about when published online.



CWLViewer produces a download of each workflow added in the form of a **Research Object Bundle** (.zip container) in order to facilitate sharing and reuse. Zenodo can also be used with this to obtain a DOI.

#### Discovery

CWL Viewer also provides a **gallery** of workflows which have been previously viewed using the site. A basic overview of the workflow, where it is from and a **thumbnail** of the visualisation are given.

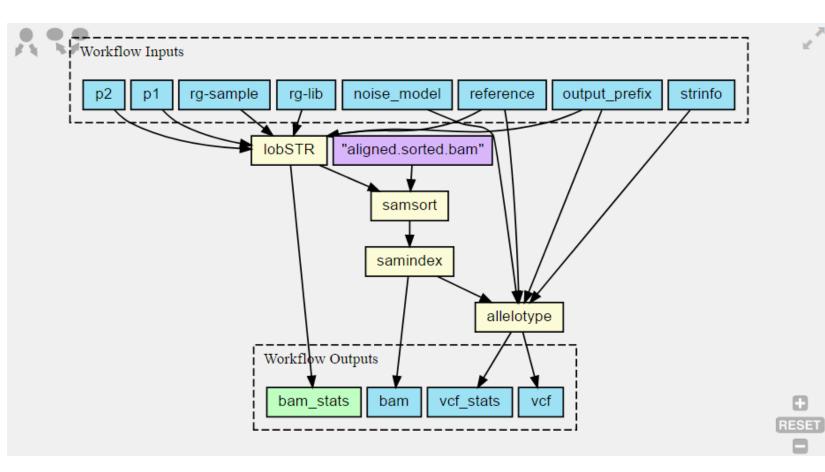
This allows users to locate workflows which are relevant to them and provides a bank of workflows to learn and see helpful techniques being utilised within the Common Workflow Language. It also helps to avoid repetition by the community when developing workflow.



CWL Viewer captures the **git commit** log and converts it to W3C **PROV** RDF statements, which are added to the **Research Object** manifest. This provides authorship and versioned permalinks for each constituent part of the CWL workflow.

Work supported by BioExcel, funded by the European Union Horizon 2020 program under grant agreement 675728

Steps can also be selected in green, which highlights the corresponding row in the table included on the page.



After this, the **selection can be expanded** to *parent* or *child* nodes by clicking the corresponding buttons. This helps to quickly distinguish parts of the workflow contributing to particular elements, eg an output.

	e Workflows		
Graph	rsed workflows here or click here to Name	Retrieved From	Vie
	Trim and reformat reads (single and paired end version)	ProteinsWebTeam/ebi-metagenomics- cwl/workflows/trim_and_reformat_reads.cwl Branch/Commit ID: master	>
	cmsearch-multimodel.cwl	ProteinsWebTeam/ebi-metagenomics- cwl/workflows/cmsearch-multimodel.cwl Branch/Commit ID: 712de5a25d08e359f831f60d1aedd0f3fd1ca32d	>
	texture_emblem.cwl	mr-c/stellaris-emblem- lab/textures/texture_emblem.cwl Branch/Commit ID: cw/	>
	01-qc-pe.cwl ATAC-seq 01 QC - reads: PE	Duke-GCB/GGR-cwl/ATAC-seq_pipeline/01- qc-pe.cwl Branch/Commit ID: <i>master</i>	>
Wetflow topus uthos scinetLbing gradeds	textures.cwl Create emblem textures	mr-c/stellaris-emblem- lab/textures/textures.cwl Branch/Commit ID: <i>cwl</i>	>