Title	Unifying workflow systems with the CWL
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URLs	http://common-workflow-language.github.io/
	https://github.com/common-workflow-language/common-workflow-language/
License	Apache License, Version 2.0

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Bioinformatics workflow platforms provide provenance tracking, execution and data management, repeatability, and a platform for data exploration and visualization. Example F/OSS bioinformatics workflow platforms include Arvados, Galaxy, Rabix, Mobyle, iPlant DiscoveryEnvironment, Apache Taverna and Yabi. Each one presently represent workflows using different vocabularies and formats, and adding new tools requires different procedures for each system.

Neither the description of the *workflows* nor the descriptions of the *tools* that power them are usable outside of the workflow platforms they were written for. This results in duplicated effort, reduced reusability, and impedes collaboration.

Three engineers (Peter Amstutz, John Chilton, and Nebojsa Tijanic) representing leading bioinformatics platform teams (Curoverse, Galaxy Team, and Seven Bridges Genomics) and a tool author (Michael R. Crusoe / khmer project / Michigan State University) started working together at the BOSC 2014 Codefest with an initial focus on developing a portable means of representing, sharing and invoking command line tools; this serves as the basis for portable workflow descriptions. The group placed high value on re-using existing formats and ontologies; they governed themselves with a lazy consensus / do-ocracy approach.

On March 31st, 2015 the group released their second draft of the Common Workflow Language specification. The serialized form is a YAML document that is validated by an Apache Avro schema and can be interpreted as an RDF graph using JSON-LD. The documents are also valid Wf4Ever wfdesc descriptions after a simple transformation. Future drafts will include the use of the EDAM ontology to describe the tools enabling tool discovery via the ELIXIR tool registry.

The organizations behind Curoverse Arvados (Seven Bridges Genomics) and Galaxy have stated intent to implement support for the Common Workflow Language, with interest from other propjects and organizations like Apache Taverna, BioDatomics and the Broad Institute.
Developers on the Galaxy bioinformatics platform are exploring adding CWL tool description support with plans to add support for the CWL workflow descriptions. Tool authors and other community members will benefit as they will only have to describe their tool and workflow interfaces once. This will enable scientists, researchers and other analysts to share their workflows and pipelines in an interoperable and yet human readable manner.