Thanks to WOM, Cromwell can now read both CWL and WDL implicitly.

Cromwell has expanded workflow language support beyond WDL, thanks to a concept we call the Workflow Object Model (WOM). Using a workflow script and WOM types, the Language factory produces a callable WOM bundle. This bundle can then be paired with the workflow script and passed through the language factory again, to produce a WOM executable that Cromwell can read.

As of version 32, Cromwell supports running CWL workflows.

The GA4GH Interoperability Testbed is an effort by the Cloud Workstream to allow driver projects to demonstrate that they have correctly implemented the WES API. Each participating driver project submits the URL of their WES instance, a workflow they run in production, as well as test inputs and a checker tool. Every participant will regularly run all of the workflows from the other projects in order to show interoperability. There are both WDL and CWL workflows in use, requiring the projects to provide a WES endpoint capable of running both. Cromwell is currently the only engine that provides both this capability and a WES implementation.

It’s not just a theory. It really works!

Our goal with Cromwell has always been to provide the same seamless scalability to as many users as possible. We feel it is important that users not be restricted by a language choice. With both CWL and WDL seeing increasing use within the bioinformatics community, we chose to implement support for both in Cromwell.

After many years of an increasingly fractured landscape, the bioinformatics world is now moving towards defining standards that promote interoperability of systems and tools. With efforts such as the Global Alliance For Genomics & Health (GA4GH) and the Open Bioinformatics Foundation as well as large projects such as the Data Biosphere focusing on WDL and CWL, Cromwell can provide them with a single high quality, scalable system which can handle all of their workflow needs.

*"Thanks to the new CWL support, we’re running bcbio validations and analysis workflows using Cromwell. Cromwell’s wide platform support, including clusters with shared filesystems, allows us to continue to transition all our analyses to use CWL since we can now support users in traditional HPC environments.\"* — Brad Chapman, Senior Research Scientist in the Bioinformatics Core at Harvard Chan School

*"We’ve been able to run our latest alignment workflow on a SLURM cluster using Cromwell’s new CWL support. In the past we’ve been limited in our ability to take advantage of parallelism in our workflows, with Cromwell we can now achieve that goal.\"* — Jeremiah Savage, Bioinformatician at the Center for Data Intensive Science, University of Chicago