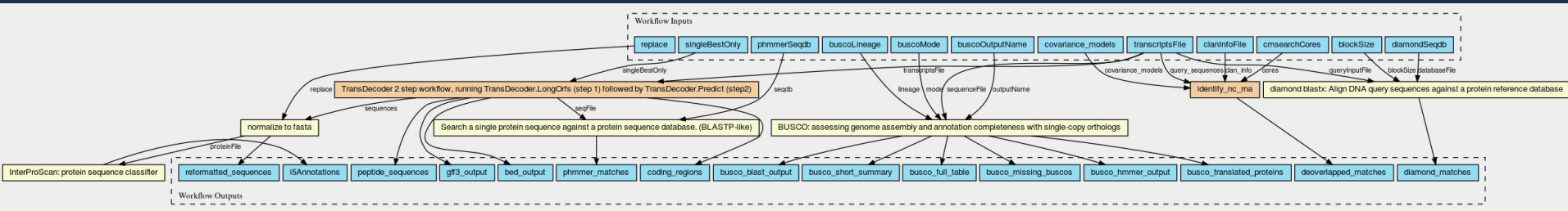


CWL support in Galaxy

Hervé Ménager, John Chilton, Michael Crusoe

<https://www.elixir-europe.org/about-us/implementation-studies/cwl-2018>
<https://github.com/common-workflow-language/galaxy>

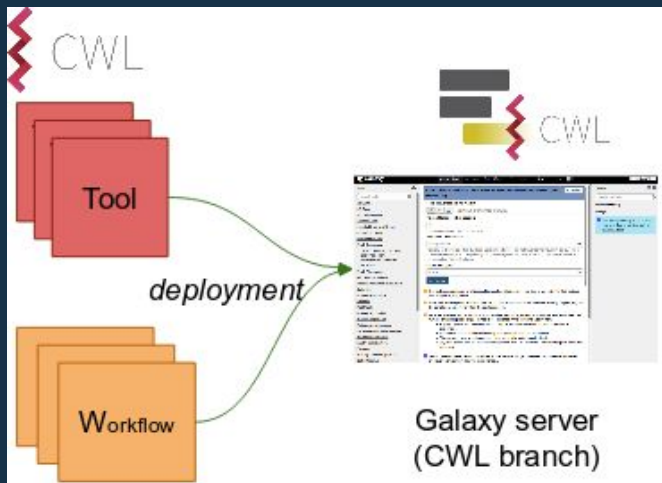
Background



<https://github.com/mscheremetjew/workflow-is-cwl>

- Marine Metagenomics Use Case: annotation pipelines described in CWL.
- “Enabling the reuse, extension, scaling, and reproducibility of scientific workflows”
Implementation Study: demonstrate CWL tool descriptions can be reused, together with additional tool descriptions, to produce extended and new analysis workflows, namely the assembly and functional annotation of transcriptomes from isolated marine eukaryotes.

Background



One of the main goals of this project is portability

- command line environments (Toil, cwlexec)
- cloud environments (GA4GH services)
- graphical workbenches: Galaxy

Galaxy + CWL

<https://github.com/common-workflow-language/galaxy>

CWL support in Galaxy in development since 2015, led by @jmchilton (Penn State University, Galaxy core team developer, CWL founding member)

- **uses the CWL reference implementation (cwltool)**

Motivation for the Biohackathon project

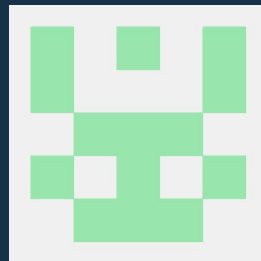
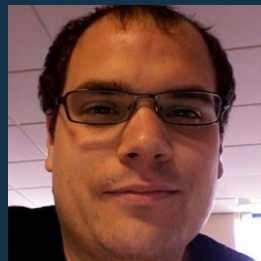
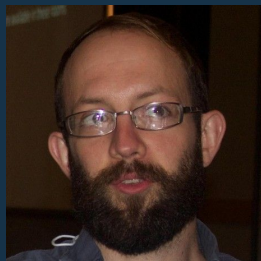
- Partial CWL support is available in Galaxy:
 - Tools
 - Workflows (in progress)
- There are remaining issues, for instance:
 - Data/parameter types are different between Galaxy and CWL
 - CWL workflows and tools references are path based
 - Current solutions to solve frontend issues is “Galactic flavored” CWL, which adds missing and mandatory information for Galaxy in tools.

Goals and Perspectives

- Open meeting, to:
 - synchronize the different codebases, e.g. for Galaxy:
 - galaxyproject/galaxy
 - common-workflow-language/galaxy
 - hmenager/galaxy
 - discuss “open issues”, and resolve them
 - reach out and discuss with all of you!
- CWL support is part of an experimental fork of Galaxy...

Organisation of the hacking project

Duration: 4 hacking days



- Hervé Ménager, Institut Pasteur (<https://github.com/hmenager/>)
 - John Chilton, PSU, Research software developer for @galaxyproject and co-founder of @common-workflow-language (<https://github.com/jmchilton>),
 - Michael Crusoe, CWL Project Lead (<https://github.com/mr-c>),
 - Arnaud Meng, Genoscope (CEA) (<https://github.com/arnaudmeng>)
 - Stian Soiland-Reyes, University of Manchester (<https://github.com/stain>) *starting wednesday*
 - Jérôme Raciazek, Institut Pasteur (<http://github.com/jra001k>) *remote*
- **Call for additional expertise from biohackathon attendees**
 - Python and Javascript developers