

Dockstore:

Enhancing a community platform for sharing cloud-agnostic research tools

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What is Dockstore?

Dockstore is a free and open source platform for sharing scientific tools and workflows. It is a registry of Docker-based resources described using popular workflow languages CWL, WDL, and Nextflow.

- **Portability**
 - Run workflows in any environment that supports Docker
- **Interoperability**
 - Standardize computational analysis through GA4GH APIs
- **Reproducibility**
 - Create, Share, Use
 - Containers + Popular descriptor languages

The screenshot shows the Dockstore website homepage. At the top, there is a navigation bar with icons for Search, Organizations, Docs, and a Login/Register button. Below the navigation is a large banner with the text "Create, Share, Use" and a subtext about Dockstore being developed by the Cancer Genome Collaboratory. A search bar is present, along with a "VIDEO OVERVIEW" button. To the right, there are icons of a ship and a truck, and a sidebar with links for "Sign up to Contribute", "Quick Start", "News and Events", and "Discuss".

Browse Tools | **Browse Workflows**

A tool is a docker container with an associated descriptor describing how to run it.

Name	Author	Format	Project Links	Stars
pancancer/pcawg-dkfz-workflow	Brian O'Connor	CWL	GitHub Quay.io	4★
pancancer/pcawg-sanger-cgp-workflow	Keiran Raine	CWL,WDL	GitHub Quay.io	3★
wtsicgp/dockstore-biobambam2/bamtofastq	Keiran Raine	CWL	GitHub Quay.io	2★

Tweets by @DockstoreOrg

Dockstore Retweeted
Mike Lin (@ONAmIn) [minidi v0.3.0](#) is the first version with independent capability to run DOpenWDL workflows on the local host. Early testing, eager for community to try it out & report interop problems. @WDL_dev @DockstoreOrg @GA4GH @cziscience [github.com/chanzuckerberg...](#)

chanzuckerberg/ml...
A static analysis tool... [github.com](#) Jul 19, 2019

Now on version 1.6.0, first presented version 1.25 at BOSC2017

What is Dockstore?

<https://dockstore.org/>

[dockstore / dockstore](https://github.com/dockstore/dockstore)

Code Issues 460 Pull requests 4 Projects 0 Wiki Security Insights

Our VM/Docker sharing infrastructure and management component <https://dockstore.org/>

dockstore docker cwl wdl containers bioinformatics nextflow workflow

2,158 commits 24 branches 178 releases 1 environment 22 contributors Apache-2.0

Branch: develop New pull request Create new file Upload files Find file Clone or download

NatalieEO Feature/2498/track tos acceptance (#2626) ... Latest commit 8916d3e 5 hours ago

.circleci	Feature/2374/token resource it (#2581)	15 days ago
.github	Feature/dockstore classpath (#342)	3 years ago
THIRD-PARTY-NOTICES	Standardize model boilerplate (#1356)	last year
dockstore-client	[maven-release-plugin] prepare for next development iteration	2 days ago
dockstore-common	[maven-release-plugin] prepare for next development iteration	2 days ago
dockstore-event-consumer	[maven-release-plugin] prepare for next development iteration	2 days ago
dockstore-file-plugin-parent	[maven-release-plugin] prepare for next development iteration	2 days ago
dockstore-integration-testing	[maven-release-plugin] prepare for next development iteration	2 days ago
dockstore-language-plugin-parent	[maven-release-plugin] prepare for next development iteration	2 days ago
dockstore-webservice	Feature/2498/track tos acceptance (#2626)	5 hours ago
openapi-java-client	[maven-release-plugin] prepare for next development iteration	2 days ago
openapi-java-wes-client	[maven-release-plugin] prepare for next development iteration	2 days ago
reports	[maven-release-plugin] prepare for next development iteration	2 days ago

Github: <https://github.com/dockstore/dockstore>

Dockstore API 1.6.0

Base URL: <https://dockstore.org/api/> | <https://dockstore.org/swagger.json>

This describes the dockstore API, a webservice that manages pairs of Docker images and associated metadata such as CWL documents and Dockerfiles used to build those images

Terms of service
Dockstore@ga4gh - Website
Send email to Dockstore@ga4gh
Apache License Version 2.0
Dockstore documentation

Schemes HTTPS Authorize

Filter by tag

entries Interact with entries in Dockstore regardless of whether they are containers or workflows

PUT /entries/{id}/aliases Update the aliases linked to a entry in Dockstore.

GET /entries/{id}/collections Get the collections and organizations that contain the published entry

containers List and register entries in the dockstore (pairs of images + metadata (CWL and Dockerfile))

GET /containers/{containerId} Retrieve a tool.

PUT /containers/{containerId} Update the tool with the given tool.

DELETE /containers/{containerId} Delete a tool.

GET /containers/{containerId}/cwl Get the primary CWL descriptor file on Github.

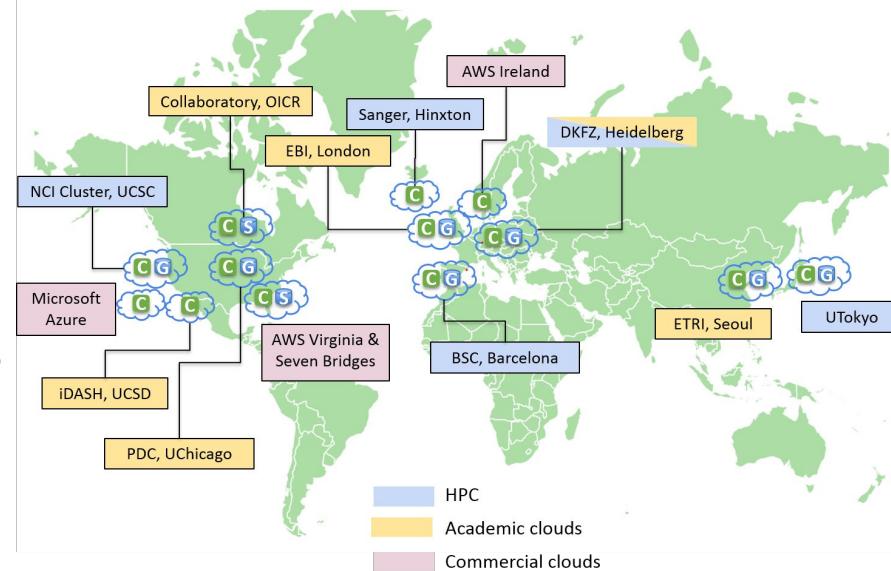
GET /containers/{containerId}/cwl/{relative-path} Get the corresponding CWL descriptor file on Github.

Swagger: <https://dockstore.org/api/static/swagger-ui/index.html#>

Motivations for Dockstore: The Pan Cancer Analysis of Whole Genomes (PCAWG)

Cloud-Based, Distributed Collaboration

- International Cancer Genome Consortium (ICGC)
 - ~5,800 Whole Genomes
 - ~2,800 Cancer Donors
 - 8 sites storing and sharing data via GNOS
 - 300TB -> 900TB
 - 14 Cloud (and HPC) environments
 - 3 Commercial, 7 OpenStack, 4 HPC
 - ~630 VMs, ~15K cores, ~60TB of RAM



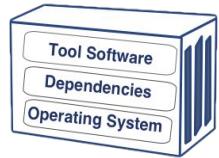
International
Cancer Genome
Consortium



GA4GH Tool Registry Service (TRS) API

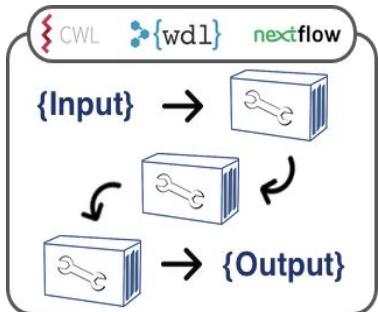
The Global Alliance for Genomics and Health (GA4GH) Tool Registry API standard for listing and describing available tools for exchange, indexing, and searching.

- Stand alone containerized tools
- Workflows with multiple tools wrapped in descriptor languages (Common Workflow Language, Workflow Descriptor Language, Nextflow)



Containerized Tool
+ Descriptor

or

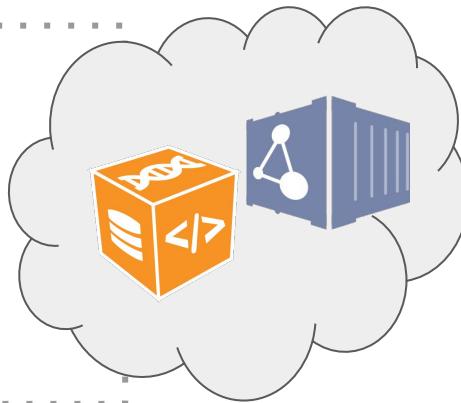


Workflow: Tools + Descriptor

Sharing API

GET /api/ga4gh/v2/tools
/{id}/versions/{version_id}

GET /api/ga4gh/v2/tools

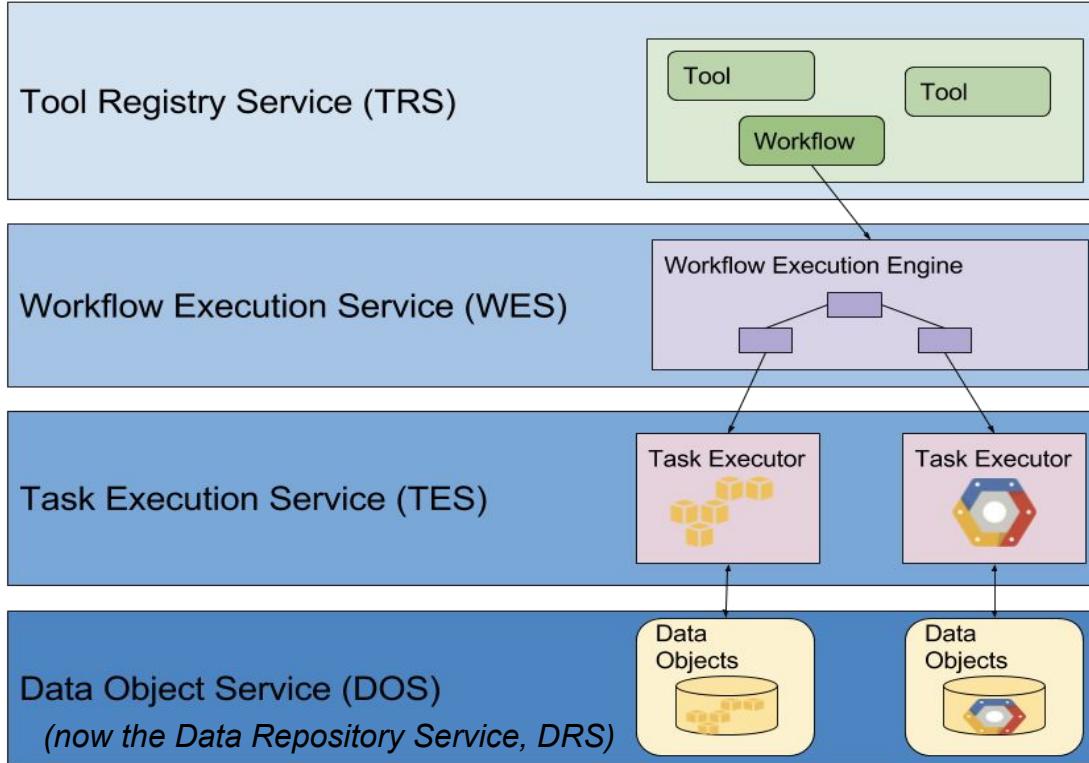


- **GitHub page:** <https://github.com/ga4gh/tool-registry-service-schemas>
- **Latest draft release:** 1.0.0, working on 2.0.0 now



Global Alliance
for Genomics & Health

GA4GH Cloud Work Stream APIs



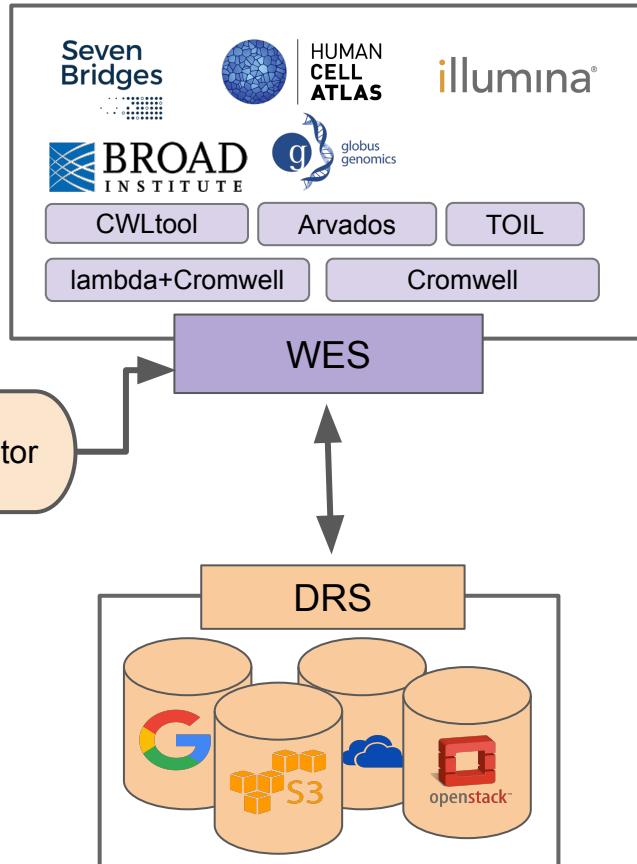
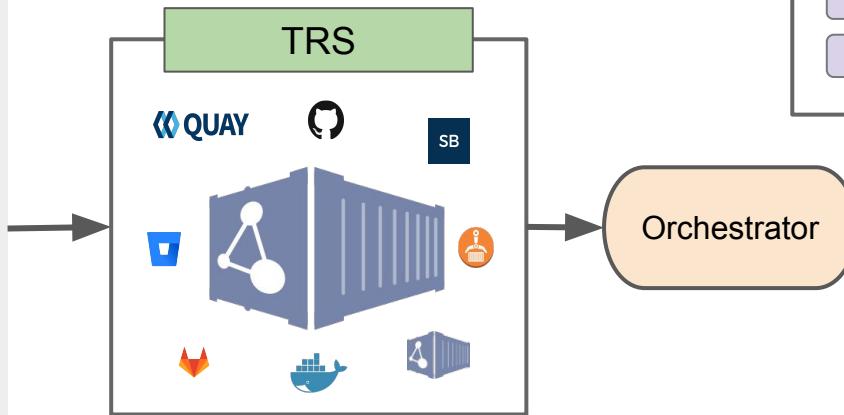
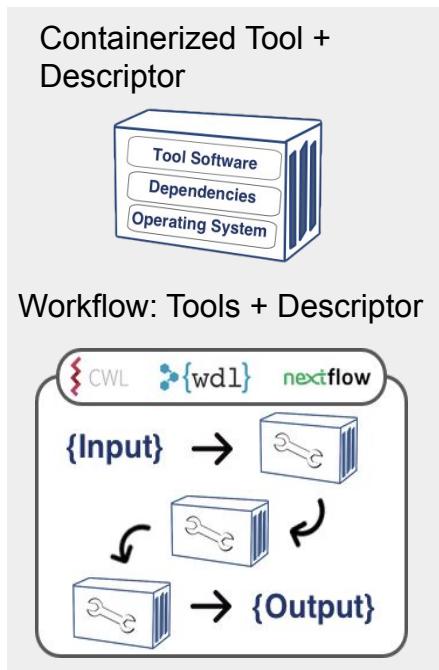
**Sharing Tools
and Workflows**

**Executing
Workflows**

Executing Tasks

Accessing Data

Dockstore & GA4GH Cloud Workstream



Dockstore, going beyond TRS

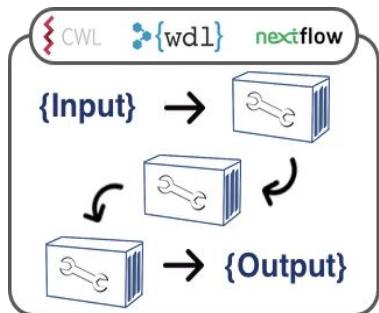
- GA4GH - TRS API
 - Standardized subset of Dockstore and Biocontainers
 - We provide a [validator](#) to help those implementing TRS
- Dockstore API
 - Extends TRS with functionality specific to Dockstore
 - Catalog that brings together multiple external repositories
 - Authenticated access
 - Advanced language support
 - Launch analysis
 - Community and collaboration oriented features
 - Organizations, starring, platform verification

Containers, Descriptors, and Parameter Files

Tool: Container + Descriptor



Workflow: Tool(s) + Descriptor



Descriptor:

The workflow language used to describe how to run your tool or workflow/pipeline.

- Which tools/containers
- What steps and when
- Where I/O parameters
- How to allocate compute requirements
- Can also include metadata information



Parameter File (wdl, cwl):

- Specifies the actual input/output files and where to find them (local, ftp, http, or cloud)
- JSON, YAML

```
{  
    "bam_input": {  
        "class": "File",  
        "format": "http://edamontology.org/format_2572",  
        "path": "/tmp/NA12878.chrom20.ILLUMINA.bwa.CEU.low_coverage.20121211.bam"  
    },  
    "bamstats_report": {  
        "class": "File",  
        "path": "/tmp/bamstats_report.zip"  
    }  
}
```

Dockstore as a Registry

- Searchable and Centralized Catalogue
- Many ways to get your tool or workflow into Dockstore!
 - External Hosting: Github, Bitbucket, Quay.io, Docker Hub
 - Direct Hosting (currently just workflows)



GitHub Account [Login Method](#)

GitHub credentials are used for login purposes as well as for pulling source code from GitHub.
One of GitHub or Google is required.

[GD Link Account](#)

Google Account [Login Method](#)

Google credentials are used for login purposes and integration with FireCloud.
One of GitHub or Google is required.

[GD Link Account](#)

Quay Account

Quay.io credentials are used for pulling information about Docker images and automated builds.

[GD Link Account](#)

Bitbucket Account

Bitbucket credentials are used for pulling source code from Bitbucket.

[GD Link Account](#)

GitLab Account

GitLab credentials are used for pulling source code from GitLab.

[GD Link Account](#)

Ways to Register to Dockstore

My tools

quay.io/lcabansay

Refresh All

My workflows

Refresh All

- github.com/abelhj
- github.com/CancerCollaboratory
- github.com/DataBiosphere
- github.com/dockstore
- github.com/ga4gh
- github.com/Ldcabansay

Through linked account
via supported public
APIs

Register Workflow

1 Workflow storage type

2 Create a workflow

You can write your CWL/WDL and store it on Dockstore.org, or you can register a CWL/WDL/NextFlow from an existing third party repository, such as GitHub, Bitbucket, etc.

Use CWL, WDL or Nextflow from GitHub, Bitbucket, etc.

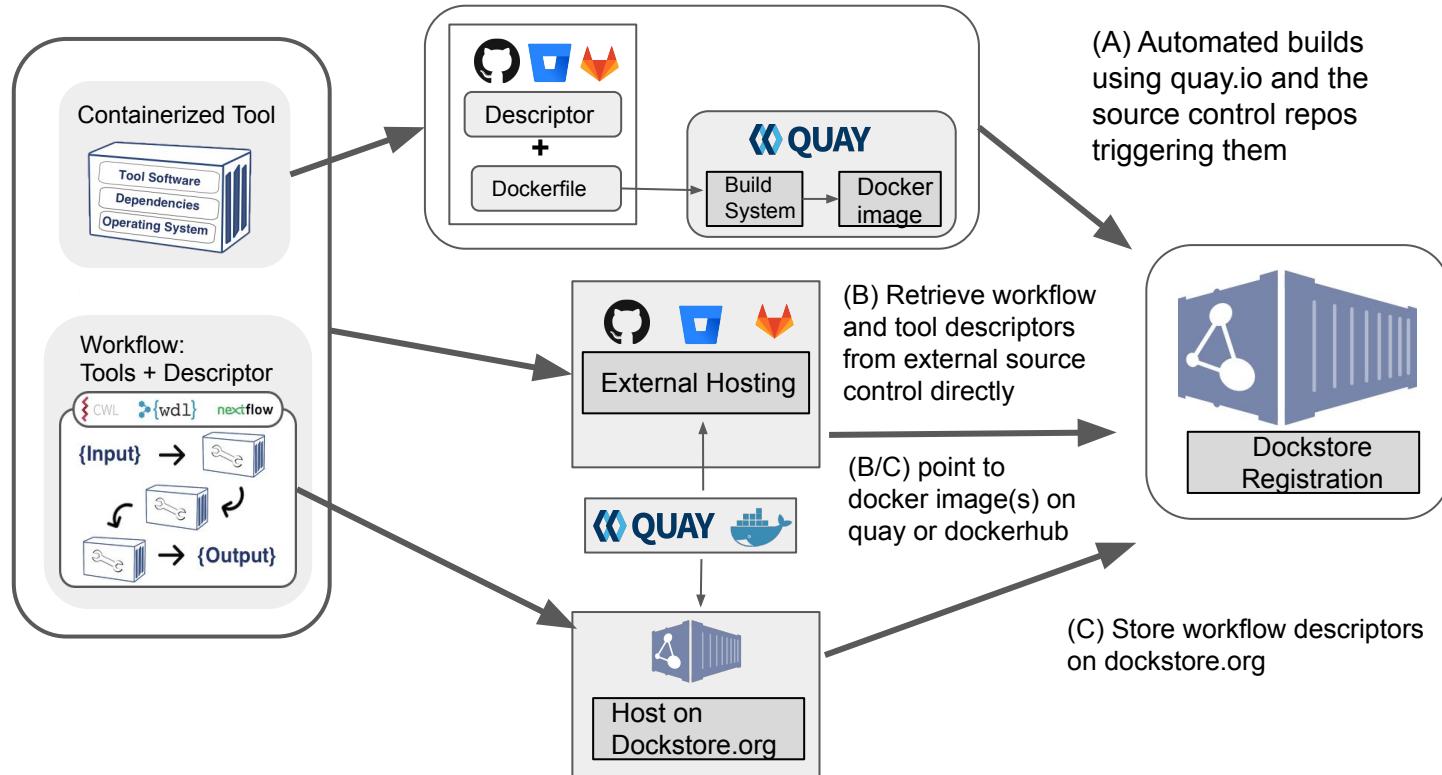
Create and save CWL, WDL, or Nextflow on Dockstore.org

[Close](#)

[Next](#)

OR through manual registration
pointing to external source repo or
directly on Dockstore.org

Ways to Register to Dockstore



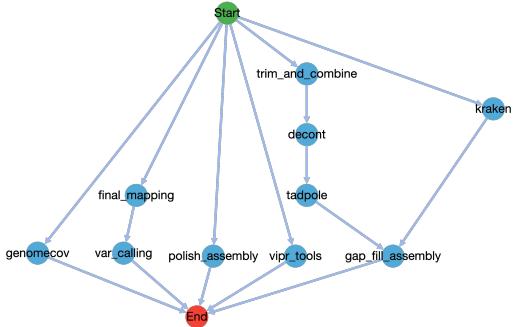
Containers and Descriptor Languages

- Containers
 - Docker
- Descriptor Language Support
 - CWL, WDL, and now Nextflow!
 - Syntax Highlighting, Validation
 - Visualization
 - Including additional visualization options from view.commonwl.org and EPAM WDL Viewer
 - Metadata parsing
 - Authorship, contact info, description
 - Markdown syntax (CWL, WDL)
 - I/O Filetypes (CWL)

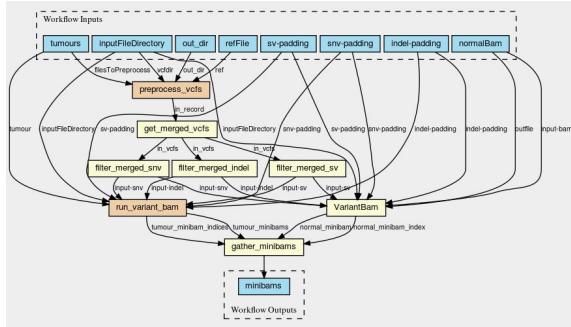


nextflow

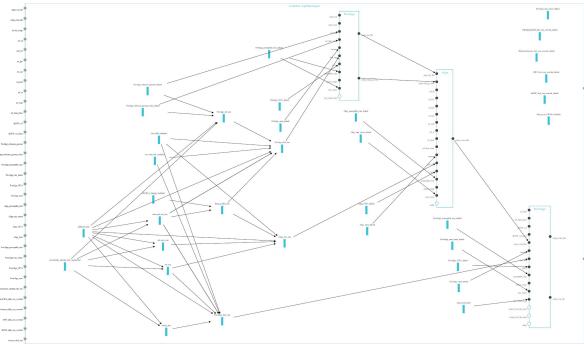
Visualizations



Built-in for CWL, WDL,
and Nextflow (pictured)



view.commonwl.org for
CWL



EPAM Pipeline Builder for WDL

Available Workflows

github.com/DataBiosphere/topmed-workflows/UM_aligner_wdl:1.32.0

Last Modified: 19 days ago

datacommons datastage topmed u-of-michigan

Info Launch Versions Files Tools >

Descriptor Files Test Parameter Files

u_of_michigan_aligner.wdl

```

256 echo "Running pre-alignment"
257
258 samtools view -T ${ref_fasta} -uh -F 0x900 ${input_cram} \
| bam-ext-mem-sort-manager squeeze --in .ubam --keepDups --rmTags AS:i,
| samtools sort -l 1 -@ 1 -T ${pre_output_base}.samtools_sort_tmp - \
| samtools fixmate - - \
| bam-ext-mem-sort-manager bam2fq --in .bam --outBase ${pre_output_b
263
264 }
265 output {
266   File output_list_file = "${pre_output_base}.list"
267   # Capture all the files mentioned in the pre_output_base.list file
268   # So they will be present for the Align task
269   Array[File] output_fastq_gz_files = glob("${pre_output_base}.*")
270 }
271 runtime {
272   maxRetries: max_retries
273   preemptible: preemptible_tries
274   #memory: "6.5 GB"
275   memory: sub(memory, "\\\\"*) + " GB"
276   cpu: sub(CPUs, "\\\\"*)
277   disks: "local-disk" + sub(disk_size, "\\\\"*) + " HDD"
278   zones: "us-central1-a us-central1-b us-east1-d us-central1-c us-central1-f
279   docker: docker_image
280 }
281
283 task Align {
284   File input_list_file
285   Array[File] input_fastq_gz_files
287
288   File ref_alt
289   File ref_bwt
290   File ref_pac
291   File ref_maf
  
```

Recent Versions

- 1.32.0 Mar 11, 2019
- ✓ 1.29.0 Sep 27, 2018
- feature/freeze8-wdl Jun 24, 2019
- master Mar 11, 2019
- develop Mar 11, 2019
- feature/variant-discovery-task Nov 11, 2018
- See all versions

Source Repositories

GitHub

Collections

TOPMed Alignment Pipeline

Launch with

DNAstack »

FireCloud »

DNAexus »

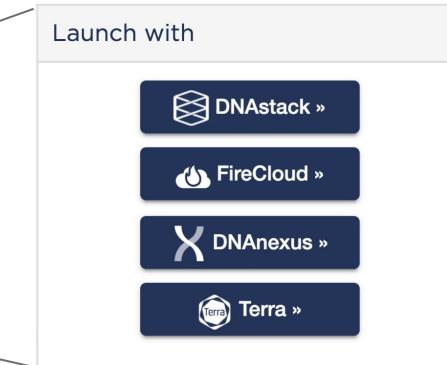
Terra »

Sharing

f t in

Launching Analysis

- GA4GH TRS-WES Orchestrator
 - FireCloud
 - Terra
- Partner Platforms
 - DNAstack
 - DNAexus
 - Terra
 - Local Execution via Dockstore CLI

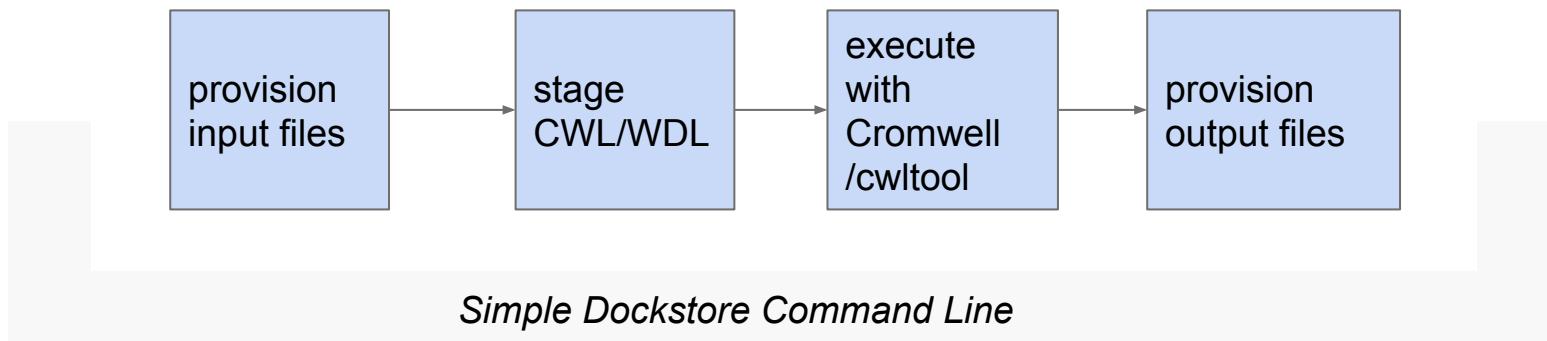


Dockstore CLI

A handy command line resource for developers to play with tools/workflows locally before running them on a cloud

- DRS file provisioning
- WES beta support
- Locally
 - Cromwell
 - Cwltool

Execution with the Dockstore Command Line Interface (CLI)



Organizations and Collections

- Organizations
 - A place for groups, labs, consortiums, etc to showcase their projects, collaborate, and group sets of tools/workflows into ‘collections’
 - Markdown descriptions
 - Membership roles
- Collections
 - Playlist of workflows or tools highlighted by an Organization
 - Markdown descriptions



Human Cell Atlas
To create comprehensive reference maps of all human cells—the fundamental units of life—as a basis for both understanding human health and diagnosing, monitoring, and treating disease.

[✉ hca@humancellatlas.org](mailto:hca@humancellatlas.org) [🔗 https://www.humancellatlas.org/](https://www.humancellatlas.org/)

Collections Members Events

Skylab
Secondary analysis pipelines for the Human Cell Atlas.

+ Create collection



HUMAN CELL ATLAS

ABOUT HUMAN CELL ATLAS

In London on 13 and 14 October, 2016, a collaborative community of world-leading scientists met and discussed how to build a Human Cell Atlas—a collection of maps that will describe and define the cellular basis of health and disease.

Cells are the most fundamental unit of life, yet we know surprisingly little about them. They vary enormously within the body, and express different sets of genes. Without maps of different cell types and where they are located in the body, we cannot describe all their functions and understand the biological networks that direct their activities.

A complete Human Cell Atlas would give us a unique ID card for each cell type, a three-dimensional map of how cell types work together to form tissues, knowledge of how all body systems are connected, and insights into how changes in the map underlie health and disease. It would allow us to identify which genes associated with disease are active in our bodies and where, and analyze the regulatory mechanisms that govern the production of different cell types.

Usability Improvements

- Improved Published Tool/Workflow Interface
 - Labels - improve searchability
 - Metadata and markdown display
 - Authorship, contact info, descriptions
 - Readme like descriptions (CWL, WDL)
 - Versioning: display all tags/versions, set defaults, check validity, verify compatible platforms
 - Link to checker workflow

[github.com/DataBiosphere/topmed-workflows/UM_variant_caller_wdl:1.32.0](https://github.com/DataBiosphere/topmed-workflows/UM_variant_caller_wdl)

Last Modified: 21 days ago

datacommons

datastage

topmed

u-of-michigan

	<	Info	Launch	Versions	Files	Tools	>
Git Reference	◆	Date Modified	↑	Valid	Verified Platforms	Actions	◆
P feature/freeze8-wdl		Jun 24, 2019, 9:12:14 AM	✓	✗		View	
Default P 1.32.0		Mar 11, 2019, 4:10:28 PM	✓	✗		View	
P master		Mar 11, 2019, 4:10:28 PM	✓	✗		View	
P develop		Mar 11, 2019, 3:28:36 PM	✓	✗		View	
P feature/variant-discovery-task		Nov 11, 2018, 8:47:04 PM	✓	✗		View	
P feature/scatter-merge		Nov 11, 2018, 2:09:25 PM	✗	✗		View	
P 1.31.0		Sep 30, 2018, 5:35:11 PM	✓	✗		View	
P 1.30.0		Sep 28, 2018, 5:06:04 PM	✓	✗		View	
P 1.29.0		Sep 27, 2018, 9:46:10 PM	✓	✓	Cromwell	View	
P 1.28.0		Sep 18, 2018, 4:39:53 PM	✓	✗		View	
P feature/scatter-discovery		Sep 13, 2018, 3:30:44 PM	✓	✗		View	

delly dkfz embl nci pcawg sevenbridges

Info Launch Versions Files Tools >

Workflow Information

GitHub: [sbg_dockstore_tools:v1.0.1](#)
TRS: #workflow/github.com/sbg_dockstore_tools/icgc_pcawg_dkfz_embl_sbg_modified
Workflow Path: /pcawg/vc/icgc_pcawg_dkfz_embl_workflow.cwl
Test File Path:
Checker Workflow: n/a
Descriptor Type: CWL

Workflow Version Information

v1.0.1

Author: Seven Bridges
E-mail: support@sbgenomics.com
[Export as ZIP](#)

Description:

The DKFZ/EMBL workflow from the ICGC PanCancer Analysis of Whole Genomes (PCAWG) project.



PCAWG
PanCancer Analysis
OF WHOLE GENOMES

This workflow is a combination of the ICGC PCAWG Seqware Delly Workflow (EMBL workflow) for structural variation and the ICGC PCAWG DKFZ Workflow workflow for SNVs, indels, and copy number variants.

For more information see the PCAWG project page and the GitHub page for the code.

A list of [all inputs and parameters](#) with corresponding descriptions can be found at the bottom of the page.

Common Use Cases

This tool is used to call variants from Tumor/Normal pair of BAM files, previously generated by using the ICGC-PCAWG-Seqware-BWA-Workflow tool available in [Public Apps](#), in the same manner as the VCF files in the ICGC PCAWG dataset. To do this, set:

- Tumor/Normal pair in BAM format, provided via [Input BAM Files](#) port.

Usability Improvements

- **Search Interface**
 - Search name, author, organization, descriptor, etc
 - Filter results using facets
 - Descriptor Language
 - Labels

Advanced Search

Find tools and workflows with files ▾ that have ...

All these words: e.g. bcbio

The exact word or phrase: e.g. cgp

Any of these words: e.g. wxs

None of these words: e.g. wgs

Clear All Advanced Search

Share Search: contains one of "Topmed"

Browse Tools Browse Workflows

Tag Cloud

A workflow is a series of tools strung together, with an associated descriptor describing how to run it.

Name	Author	Format	Project Links	Stars
DataBiosphere/topmed-workflows/UM_variant_caller_wd	Walt Shands	WDL	GitHub	6★
DataBiosphere/topmed-workflows/UM_aligner.wdl	Walt Shands	WDL	GitHub	2★
DataBiosphere/topmed-workflows/CCDG_aligner_functional	Ruchi Munshi	WDL	GitHub	2★
DataBiosphere/topmed-workflows/UM_aligner_cwl	Seven Bridges	CWL	GitHub	1★
DataBiosphere/topmed-workflows/gatk-vcf-comparator	n/a	CWL	GitHub	
DataBiosphere/topmed-workflows/CCDG_aligner_functional	Yilin Xu	CWL	GitHub	
DataBiosphere/topmed-workflows/UM_variant_caller_cwl	Vladimir Obucina	CWL	GitHub	

Items per page: 10 | < > | 1 - 7 of 7

Usability Improvements

- **Lots of new documentation and tutorials!**
- Example Topics:
 - Getting Started With...(Docker, Nextflow, CWL, WDL)
 - Launching Tools and Workflows
 - Writing checker workflows
 - Developing File Provisioning Plugins
 - Creating Organizations
 - And many more!

<https://docs.dockstore.org/>

Developer Tutorial

Go through the process of creating a tool and registering it on Dockstore.

End User Tutorials

Learn how to use Dockstore from the perspective of a user who runs tools and workflows.

Advanced Tutorials

A collection of articles and tutorials regarding advanced Dockstore topics

Documentation / Advanced Developer / Organizations and Collections

Organizations and Collections

Organizations

Organizations are landing pages for collaborations, institutions, consortiums, companies, etc. that allow users to showcase tools and workflows. This is achieved through the creation of collections, which are groupings of related tools and workflows. The users of an organization do not need to own the tools or workflows in any way; the tools and workflows just have to be published. Collections can be thought of as a playlist on a music streaming service where tools and workflows are analogous to individual songs. They can be shared publicly, and the user does not need to own them.

Creating an organization

To create an organization request, go to the organizations page and select [Create Organization Request](#). Any user can request to create an organization by filling out the following form. For now, the request must be approved by a Dockstore curator in order to be public. Until it is approved, you are still able to edit it, add collections, add members, etc.

Create Organization Request

Fill out the form to send an organization request to a Dockstore curator to approve. Once approved, the organization will be publicly visible.

Name *

OICR

The name of the organization

Display Name *

Ontario Institute for Cancer Research

The display name of the organization

Topic *

OICR is a collaborative, not-for-profit research institute accelerating the development of n

A short description of the organization

Organization website

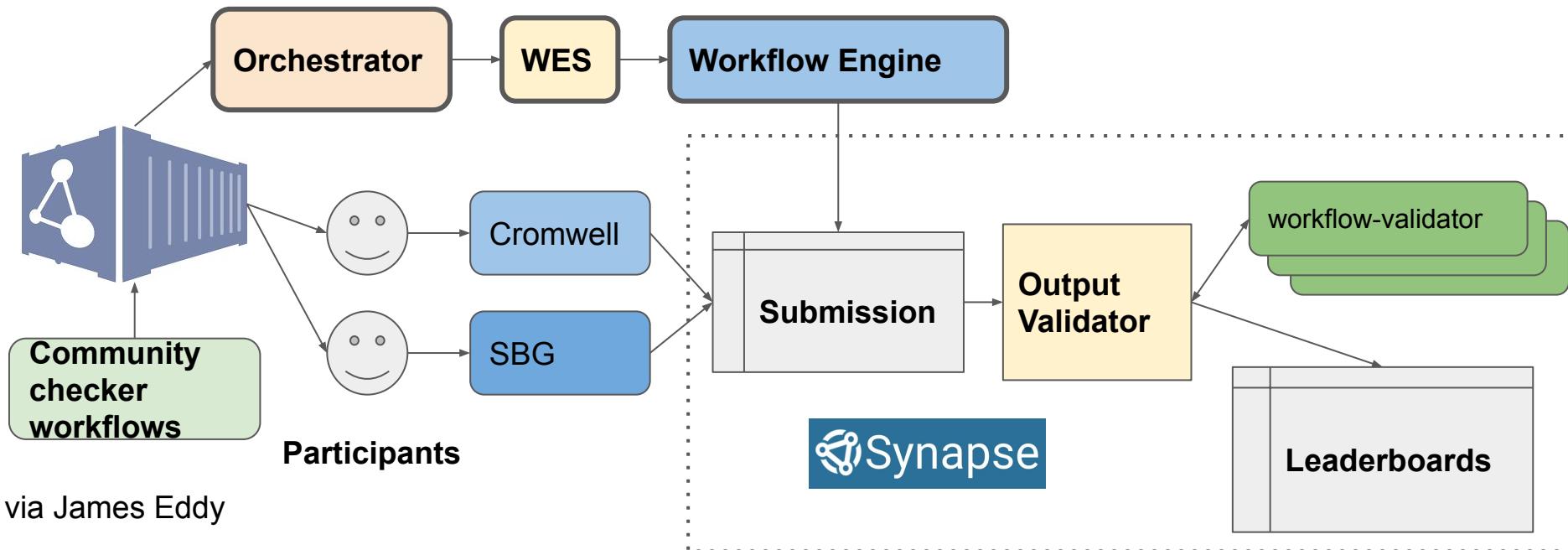
<https://oicr.on.ca/>

Link to organization website

Location

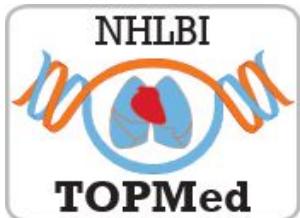
Highlighted Community Content

GA4GH-DREAM Workflow Testbed (2018)



via James Eddy

Collaborations - *The Commons Alliance and Other Projects*



**Da
ta STAGE**

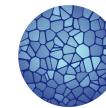
NHLBI Data
STAGE



National Human
Genome Research
Institute



NHGRI
AnVIL



HUMAN
CELL
ATLAS



And Many Others

Dockstore will serve as an official workflow provider for the Commons Alliance, a common infrastructure collaboration to facilitate combining Data + Cloud Compute

Next Release - 1.7.0 (Late August/September)

- Prototype for services/apps
 - Dockerized genome browsers, jupyter notebooks, and reference data providers
 - Playground for Github Apps and automatic update syncing
- Immutable workflow versions
 - DOI issuing via linked Zenodo credentials
- Language support updates
 - WDL draft-3 to 1.0
 - cwltool update (possibly CWL 1.1 support)
- Display of logs from when we test and verify workflows
- Improved security of your data and logging, monitoring of the site
- Summary of changes at <https://docs.dockstore.org/changelog/>

Future Work

- Signing of Entries on Dockstore
 - Verify ownership and integrity of Docker images
- Alternative Containerization Support
 - Singularity and/or uDocker support
- Additional Workflow Languages
- Services/“Apps”
- Testbed Expansion
 - Automated testing for workflows across cloud platforms
- **Open to collaborations with partners for any of these kind of projects!**

The Dockstore Team



Lincoln Stein

Denis Yuen

Andrew Duncan

Gary Luu

Brian O'Connor

Benedict Paten

Cricket Sloan

Charles Overbeck

Walt Shands

David Steinberg

Louise Cabansay

Natalie Perez

Ryan Bautista

Melaina Legaspi

Shreya Radesh

Emily Soth

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Extra Slides

Handy stuff in case of questions



Language Support

Feature	CWL	WDL	Nextflow
Dockstore site			
Tool registration	Yes	Yes	No
Workflow registration	Yes	Yes	Yes
Hosted Workflows	Yes	Yes	Yes
DAG Display	Yes (cwl version=>1.0) ^[0]	Yes (wdl version<=draft-2) ^[1]	Limited support
Tool Tab Display	Yes (cwl version=>1.0)	Yes (wdl version<=draft-2)	Yes
Launch-with Platforms	Not yet!	FireCloud (workflows only) ^[2] DNAnexus (workflows only) DNAstack (workflows only) ^[3] Terra (workflows only)	Not yet!
Metadata Display	Yes	Yes (wdl version<=draft-2)	Yes
Dockstore CLI			
Local workflow engines	cwltool, Cromwell	Cromwell ^[4]	Nextflow
File Provisioning In	Local File System HTTP FTP S3 via plugins Data Object Service	Local File System HTTP FTP S3 via plugins Data Object Service	Local File System HTTP FTP S3
Plugins Support	s3 s3cmd icgc-get Data Object Service	s3 s3cmd icgc-get Data Object Service	No
File Provisioning Out	Local File System HTTP FTP S3 via plugins	Local File System	Local File System S3
Notifications	Yes	Yes	No

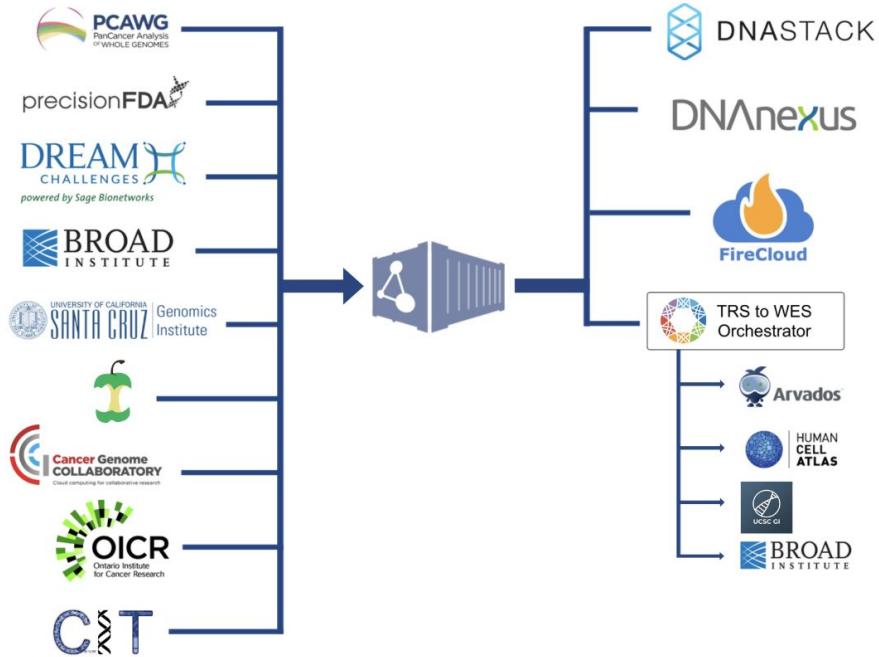
More info:

<https://docs.dockstore.org/docs/user-tutorials/language-support/>

Dockstore Ecosystem

Dockstore is thankful to its many contributors, users, and partners. This community has pulled together a library of over 450 tools and workflows. In the diagram to the right we've highlighted a few select contributors to give a sense of what has been occurring in this space.

Select Contributors and Integrations





BETA

Importing from Dockstore

github.com/DataBiosphere/topmed-workflows/UM_variant_caller_wdl
V. 1.32.0



Please note: Dockstore cannot guarantee that the WDL and Docker image referenced by this Workflow will not change. We advise you to review the WDL before future runs.

```
1 import "https://raw.githubusercontent.com/DataBiosphere/topmed-workflows/UM_variant_caller_wdl"
2
3
4 ## This is the U of Michigan variant caller workflow WDL for the workflow
5 ## https://github.com/statgen/topmed_freeze3_calling
6 ##
7 ## It uses a Docker image built with software tools that can reproduce
8 ## variant calls compatible to TopMed Freeze 3a
9 ##
10 ## NOTE: This workflow assumes that input CRAM files have been built with
11 ## human reference genome. In particular for the TopMed CRAM files the
12 ## reference genome files to use are located here:
13 ## ftp://share.sph.umich.edu/gotcloud/ref/hs38DH-db142-v1.tgz
14 ##
15 ##
16
17 workflow TopMedVariantCaller {
18     Boolean? calculate_DNA_contamination
19     Boolean calculate_contamination = select_first([calculate_DNA_contamin
20
21     Boolean? dynamically_calculate_file_size
22     Boolean dynamically_calculate_disk_requirement = select_first([dynamic
```

Destination Workspace

Select a workspace

IMPORT

Or create a new workspace



Running Dockstore Tools - Launch With FireCloud

FireCloud

Workspaces Data Library Method Repository



broconno@ucsc.edu ▾

Importing github.com/DataBiosphere/topmed-workflows/Functional_Equivalence:1.30.0 from Dockstore

⚠ Please note: Dockstore cannot guarantee that the WDL and Docker image referenced by this Workflow will not change. We advise you to review the WDL before future runs.

Name

Functional_Equivalence

Destination Workspace

Select a workspace ▾

Export

```
1 ## Copyright Broad Institute, 2017
2 ##
3 ## This WDL pipeline implements CCG Pipeline standards to process
4 ## high-throughput sequencing data for downstream processing.
5 ##
6 ## Requirements/expectations :
7 ## - Human whole-genome pair-end sequencing data in unmapped BAM (ubAM) format
8 ## - One or more read groups, one per ubAM file, all belonging to a single sample (SM)
9 ## - Input ubAM files must additionally comply with the following requirements:
10 ##   - filenames all have the same suffix (we use ".unmapped.bam")
11 ##   - files must pass validation by ValidateSamFile
12 ##   - reads are provided in query-sorted order
13 ##   - all reads must have an RG tag
14 ##   - Reference genome must be Hg38 with ALT contigs
15 ##
16 ## Runtime parameters are optimized for Broad's Google Cloud Platform implementation.
17 ## For program versions, see docker containers.
18 ##
19 ## LICENSING :
20 ## This script is released under the WDL source code license (BSD-3) (see LICENSE in
21 ## https://github.com/broadinstitute/wdl). Note however that the programs it calls may
22 ## be subject to different licenses. Users are responsible for checking that they are
23 ## authorized to run all programs before running this script. Please see the docker
24 ## page at https://hub.docker.com/r/broadinstitute/genomes-in-the-cloud/ for detailed
25 ## licensing information pertaining to the included programs.
26
27 # WORKFLOW DEFINITION
28 workflow PairedEndSingleSampleWorkflow {
29
30   File wgs_evaluation_interval_list
31   File wgs_coverage_interval_list
32
33   String sample_name
34   String base_file_name
35   Array[File] flowcell_unmapped_bams
```



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