

Workflows in **AnVIL**

What are workflows?

For computational biology tasks, workflows help organize a set of connected instructions to process large datasets at once. For example, a simple workflow could involve quality control of raw sequence data followed by alignment using bioinformatics tools.

Consists of

Data and Resources

Example

Exome Sequence Data

WORKFLOWS

Input

General, Automated

Processing

Mapping and Variant Discovery

Specific, Manual

Analysis

Effective Prediction and Variant Load Analysis

Materials and Methods

Sharing

Preprint in bioRxiv

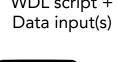
Workflow components





Google Compute Engine runs jobs within a container





Researcher launches workflow



Cromwell execution engine creates individual jobs to run workflow

Workflows In AnVIL



Write your own WDL



Find a docker image that has the tools you need



Write your WDL workflow. Specify the container's image in the WDL:

```
runtime {
docker: 'ubuntu:latest'
```



Submit workflow

on Terra

Specify workflow Inputs

Monitor workflow

and outputs

Images can be used interactively or in a WDL!

```
runtime{
docker: "my_project/do_stuff: 1.2.0"
```

Import workflows

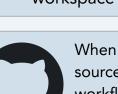
Import a publicly available workflow



Files > Test Parameter Files subtab

On *Dockstore*, you can find a test parameter file (JSON) which you can then upload in Terra after Importing vour workflow

Use a pre-configured workflow in the Terra Repository and import it to a workspace within AnVIL



When exporting from outside sources, note that exporting workflows from these sources is a two-step process!

- 1. Copy the workflow's script to a new method in the Terra Repository or a Dockstore repository
- 2. Export the workflow to an AnVILpowered-by-Terra workspace.

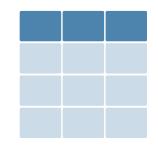




Visualize and analyze outputs using RStudio or Jupyter notebook

Configure Inputs

Workflow inputs can be specified via



Data Tables within the workspace



A JSON file: Upload your own or use a pre-configured one on Terra

Containers for reproducibility

Find existing images containing bioinformatics tools from public registries (e.g., DockerHub, Quay)

push to DockerHub or another registry OR

> Pro tip: Use Github Actions to build and push Docker images! Find more on this Github article.

Build your own and

Public registries with Images:



Additional *Docker* information

- A Docker file defines the container's dependencies, environment variables, file system, and applications.
- A Docker image builds and runs a container, which contains everything defined in the Docker file.

For more information, refer to this AnVIL resource.