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### The Workflow Hub

A new registry that is Workflow Management System (WfMS) agnostic.

Workflows may remain in their native repositories in their native forms.

Workflows makers are custodians of their own workflows.

Holds related supplementary information: test and example data, SOPs, presentations etc

Workflows can be crated into collections

Metadata is generated by and harvested from WfMS. Galaxy, Snakemake and Nextflow are working with the Hub to seamlessly support packaging and registration.

Yellow pages

Spaces

Teams

Organizations

People

Assets

Data files

SOPs

Workflows

Publications

Documents

Collections

Activities

Presentations

Events

Samples

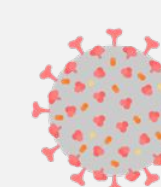
Organisms

Workflows presented as CWL or in native image and form

### A Workflow Zoo...

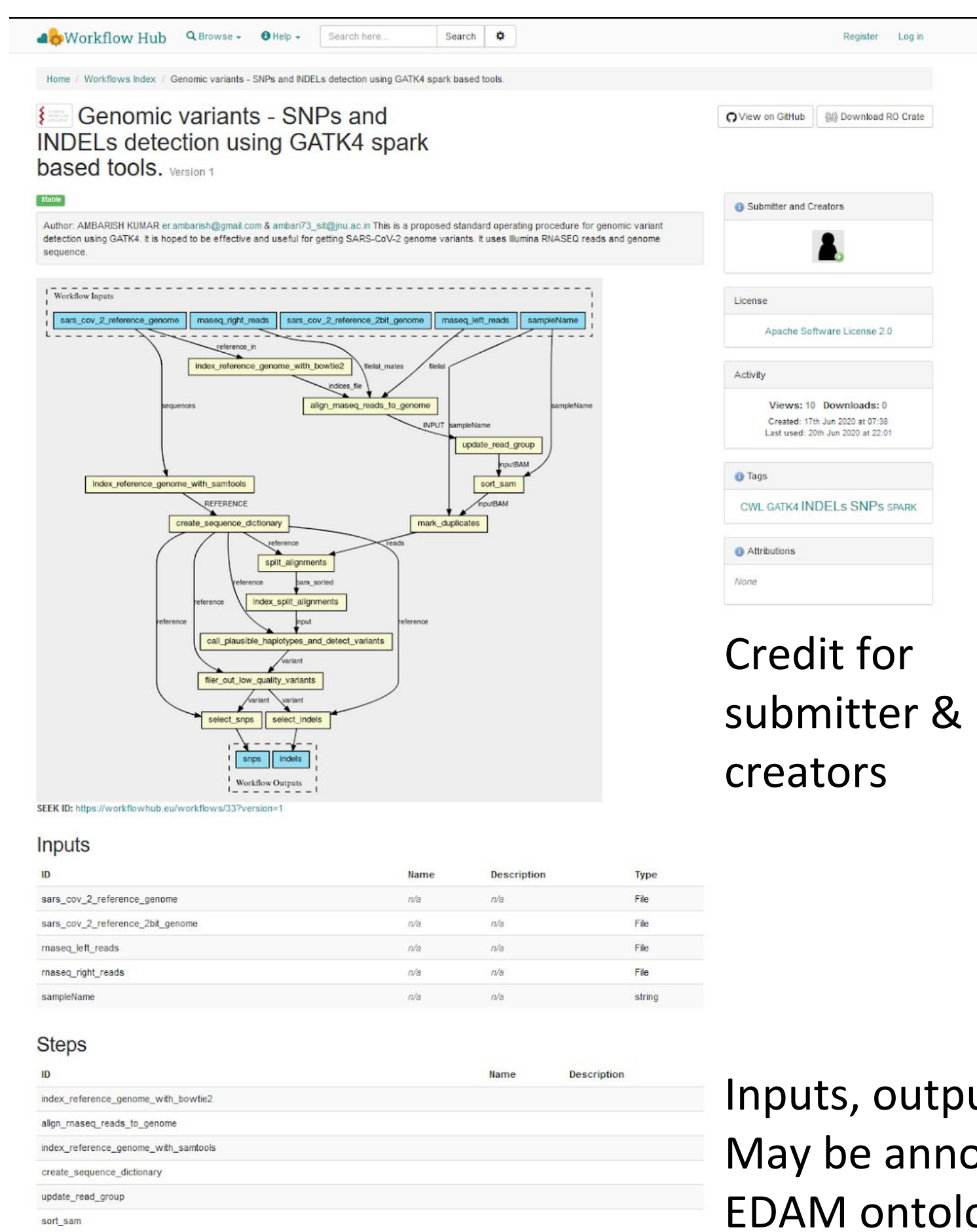
Computational processing using workflows has taken hold in the life sciences. There are 280+ Workflow Management Systems in operation [1]. Workflow registries and repositories typically cater for specific workflow management systems and there is little standardisation of the metadata. But just like data, workflows should be FAIR - Findable, Accessible, Interoperable, Reusable [2].

### Responding to COVID-19



**Workflow Hub**

The Hub is due for Beta release in September 2020. However, the team fast-tracked to open in April 2020 to take COVID-19 workflows. Consequently the Hub is being perpetual developed in the open. So we are rubbing off the rough edges with our users. The Hub is registered on the EU Covid-19 Data Portal (<https://www.covid19dataportal.org/>).



**Genomic variants - SNPs and INDELs detection using GATK4 spark based tools.**

Author: AMBARISH KUMAR & andrew@paul.com & andrew@paul.com This is a proposed standard operating procedure for genomic variant detection using GATK4. It is hoped to be effective and useful for getting SARS-CoV-2 genome variants. It uses Illumina HiSeq2500 reads and genome sequence.

SEEK ID: <https://www.workflowhub.eu/workflows/2/Version-1>

ID	Name	Description	Type
sars_cov_2_reference_genome	n/a	n/a	File
sars_cov_2_reference_204_genome	n/a	n/a	File
masses_left_reads	n/a	n/a	File
masses_right_reads	n/a	n/a	File
sampleName	n/a	n/a	string

ID	Name	Description
index_reference_genome_with_bowtie2		
align_masses_reads_to_genome		
index_reference_genome_with_sambamba		
create_sequence_dictionary		
update_read_group		
sort_reads		



Visit source

Workflows can be viewed at their github or at their source – e.g. Galaxy instance.




Workflows can be uploaded / downloaded as Research Objects

Or registered as collections of files


Credit for submitter & creators

Inputs, outputs and steps  
May be annotated using the EDAM ontology

### Metadata standards

 Bioschemas.org about a workflow

 COMMON WORKFLOW LANGUAGE describe the workflow

 Workflow RO-Crate organise & package the workflow components

The Hub was established during the COVID-19 Virtual Biohackathon April 5-11 2020.

The Hub is an instance of the FAIRDOM-SEEK commons infrastructure [3].

### How do I get involved in Workflow Hub?

- Join the Workflow Hub Club - an open community that works together to develop the Hub.
- Contribute your Workflows – the Hub Club will help you. <https://about.workflowhub.eu/>

### References

- [1] <https://s.apache.org/existing-workflow-systems>
- [2] Goble C et al FAIR computational workflows. Data Intelligence 2(2020), 108–121. doi: 10.1162/dint\_a\_00033
- [3] Wolstencroft K et al SEEK: a systems biology data and model management platform, BMC Systems Biology, 9:33, 2015. doi:10.1186/s12918-015-0174-y.

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