

Wellcome Genome Campus | OC3_1-20_Using_existing_workflows

Hi. In this video, you will be learning how to import publicly available workflows into your account and execute them. Copy and paste the link given above in your web browser. This is the COVID-19 ARTIC ONT workflow. Here, click on Import Workflow given on the right-hand side top. Click on Start using this workflow.

On the centre panel, you will find the workflow is imported. You can execute the workflow in your account. Once the workflow is loaded, we will require certain inputs for that as provided before upload the data. Choose Files and upload BED file and reference.fasta file. Once both the files are uploaded, you will find it in the History panel.

Once it turns green, we will know that it is uploaded. In the middle panel, the first one, upload the BED file. The second one, upload the reference.fasta file. Next, upload the Nanopore_Runs list that is your collection list. You have to change minimum rate length to 250 and maximum rate length 2,300 as we are using this particular workflow. No other parameters need to be changed. It can be kept default.

Now you can run the workflow. Once successfully the workflow is invoked, the steps and the jobs will be visible in the centre panel, as well as in the History panel. We can see that 24 steps have been completed in which there were 99 jobs. All the reports is visible on your History panel. For an example, let's click on View Data on MultiQC. And you can see all the report mentioned here.