

Wellcome Genome Campus | OC3_2-11_Using_NextStrain_Pangolin

In this video, you'll learn how to analyse the assembled SARS-CoV-2 genome on Nextstrain. From the previous activity, we imported the ARTIC ONT protocol and executed it. On the right panel, click on the medaka consensus output, which is assembled genomes of SARS-CoV-2. Now you can view the output of all files in the fasta format.

Click on Download Collection to download all the samples. This will be a zip file with the assembled genomes. The files are named in the sample name dot fasta format. Now head on to your browser and search for Nextclade. Click on the first results clade.nextstrain.org. This will open the website.

Continue to select SARS-CoV-2 as the pathogen and press Next. Here, you can select your input assembled genome. Click on Select File and select one of the samples. Continue and click on Run. Now you can see the next clade output. The output displays different QC matrix clade to which your sample belongs to and the Pangolin lineage.

In addition to it, it displays a gene and SNPs at various positions in that particular gene. You can also view the highlighted mutations on hovering your mouse over it. In this position, you can see there is an amino acid change from D to R due to nucleotide substitution of C to G. This can be done for different genes and various positions. Thank you.