Making sense of genomic data: COVID-19 web-based bioinformatics

Frequently asked questions

Galaxy questions

Question 1: I cannot change the name of my history in Galaxy.
Please make sure that you are logged on. If you click on the “User” tab at the top, you should see “Logged in as [your_username]”

Question 2: I cannot find the tool you are referring to in Galaxy.
Please make sure that you are logged into the correct Galaxy instance. There are many Galaxy instances such as: https://usegalaxy.eu/, https://usegalaxy.org/, https://africa.usegalaxy.eu, and they do not all have the same tools.

Mapping

Question 1: Is mapping and aligning to a reference genome the same?
They are often used interchangeably because they are often used for the same purpose. But with mapping, we are trying to find the approximate origin/location of a sequence. With alignment, we aim to find the exact differences between two sequences.

Question 2: What is a read?
After sending your DNA/RNA sample to the sequencing facility, your sample gets fragmented into many small fragments so that the sequencing machine can handle it. These fragments are then copied and a camera takes an image of each nucleotide, producing a stretch of letters ACGT/U. This stretch of letters represents the nucleotides that were present in your fragmented piece of DNA. This is also called a read.

Variant calling

Question 1: Is there a difference between variant calling and variant annotation?

Variant calling is simply calling the position where a nucleotide(s) differs from a reference genome. It also tells us how it is different, by telling us which nucleotide was present in the reference genome and how your sample differs. With variant annotation, we show the potential downstream effect of that mutation. For example, if it was an SNP, was it synonymous/non-synonymous. Did a mutation lead to a stop-loss, a frame-shift etc?