Generating public health reports

Alt-text Figure 17 - Infection of three different variants of SARS-CoV-2 amongst three wards

Illustration representing viral infection in a hospital. Viral variants are presented by purple, red and green colours. In ward X, there are infection cases with purple and green variants, while in wards Y and Z, there are cases of red only and all three variants, respectively. WGS was used to confirm the presence of the variants in each ward.

Alt-text Figure 18 - Example phylogenetic tree showing similarities and differences between sequenced cases of SARS-CoV-2

Illustration representing an hypothetical phylogenetic tree showing the separate clusters of Alpha (pink), Delta (green) and Omicron (blue) SARS-CoV-2 lineages.

Alt-text Figure 19 - Example of R-markdown reporting of clusters identified using TransCluster

Example image of R-markdown output. On the top of the image is written: "Cohor transmission clustering. To access whether these samples represent a true transmission cluster, the transcluster package in R was used to infer transmission between samples. This takes as an input the number of SNP differences between the likelihood that they are separated from one another by a set number of transmission events (T): Transmission based clusters for T = 1 using region. The image shows a cloud of clustered circles presenting samples. The circles are coloured according to SARS-CoV-2 lineage: mustard = B.   1, green = B.1.1.7 and blue = B.1.620.