

## **Introduction to phylogenetics: tools and models**

Alt-text Figure 14 - Phylodynamic approaches to the investigation of SARS-CoV-2 transmission

Decorative illustration describing potential models for transmission studies where phylogenetics plays an important role. a) Phylogenetic approaches estimate the rate of international lineage introductions and distinguish introductions from community transmission. b) Genome sequences and phylogenetics support outbreak analyses by identifying or refuting links between local cases; this can lead to the identification of outbreak sources and drivers or assessment of nosocomial transmission. c) Phylodynamic techniques using epidemiological demographic models, such as the susceptible–exposed–infected–recovered (SEIR) model, allow us to compare transmission rates between lineages bearing different key genotypes (for example, variants of concern (VOCs) and pre-existing lineages). d) Relative timing of variant and lineage emergence from the global (or regional) phylogeny, and scattering of case genomes across clades can distinguish persistent from repeat infections in some scenarios.

Alt-text Figure 15 - Different graphic representations of a phylogenetic tree

Three illustrative phylogenetic trees in black, purple and green, respectively. Detailed explanation in the main text.