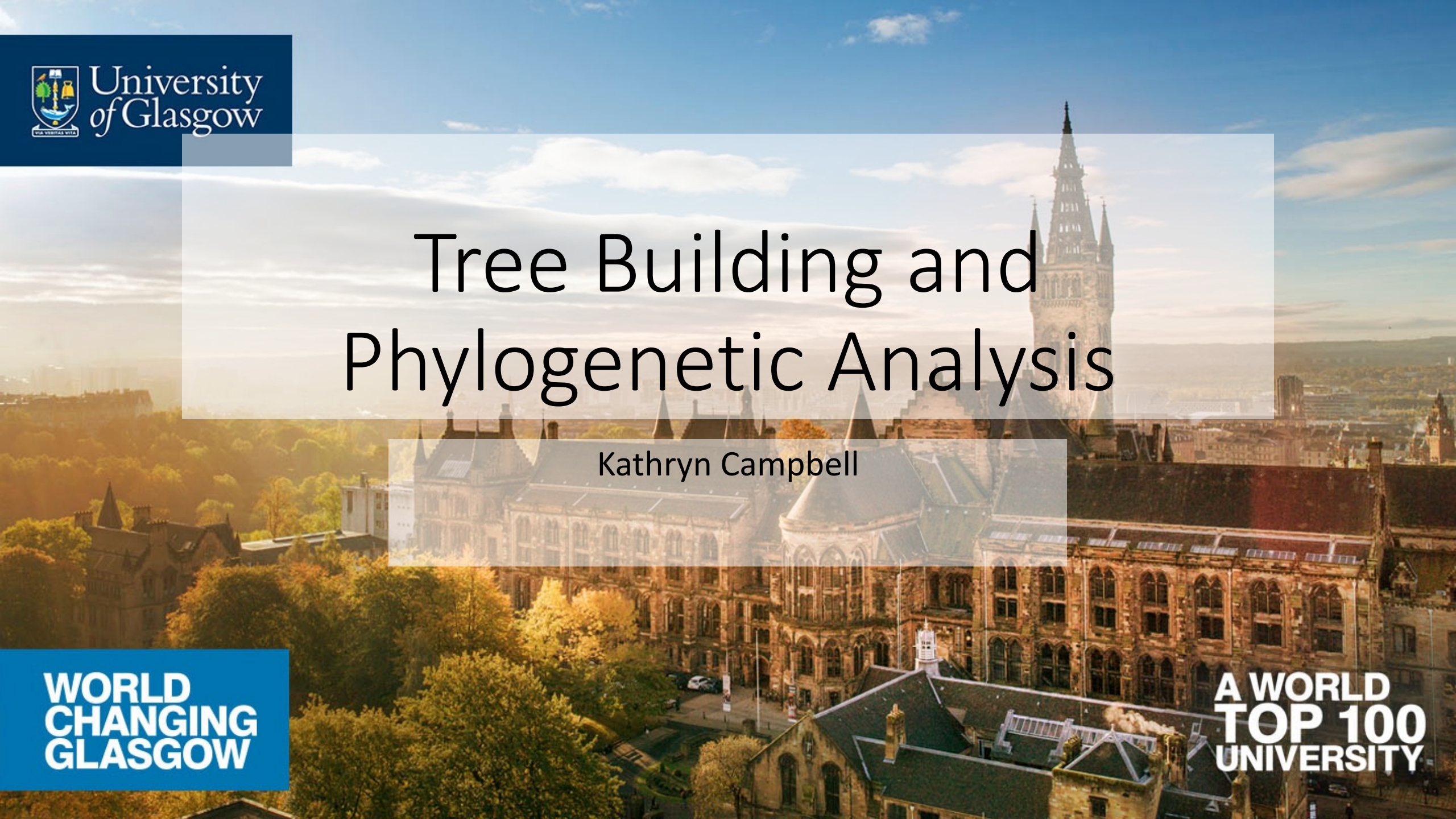


Tree Building and Phylogenetic Analysis

Kathryn Campbell

Schedule

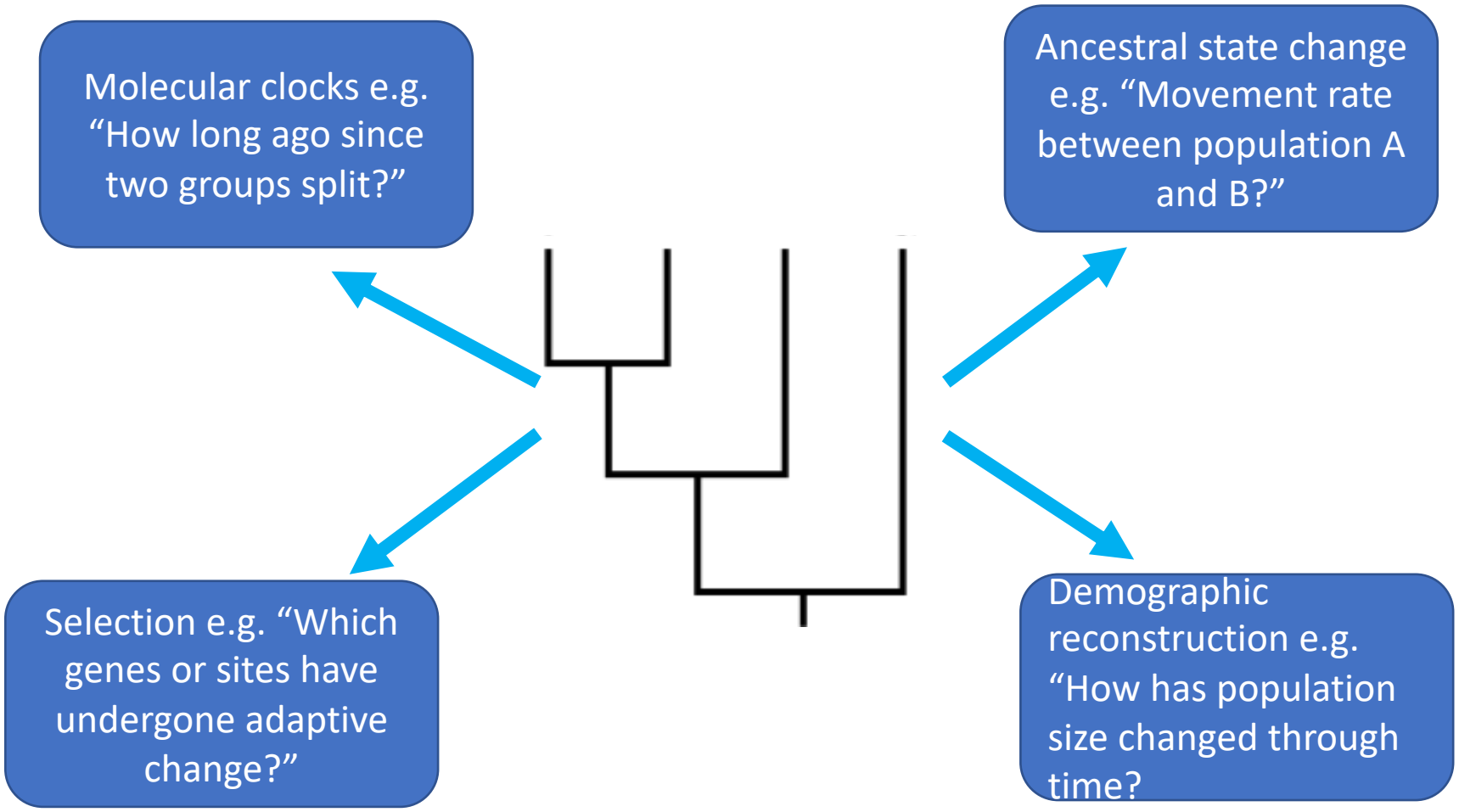
Alignments & Understanding Trees

- Alignments
- **Practical:** Viewing and aligning sequences
- Terminology
- Tree building methods
- **Practical:** Interpreting phylogenetic trees

Tree Building

- Substitution models
- Statistical support (bootstrapping, posterior probabilities)
- **Practical:** Using modeltest and IQTREE2 to find the best substitution model and generate a maximum likelihood tree
- Visualisation using FigTree
- Annotating using metadata
- **Practical:** Preparation of publication ready trees with appropriate annotation and bootstrapping in FigTree

Why use phylogenies?

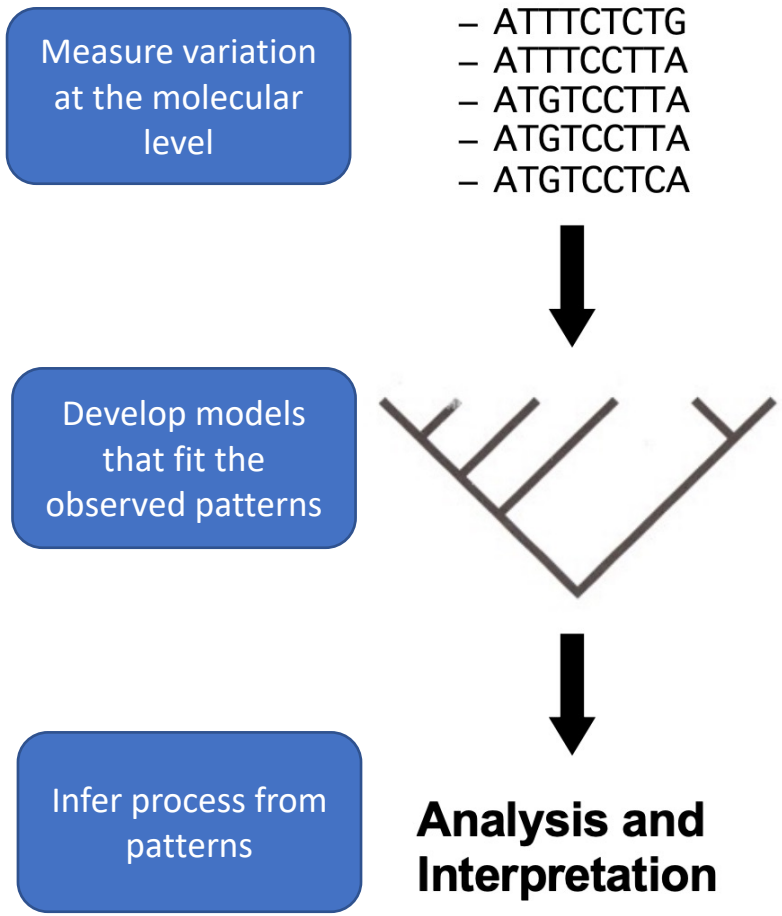


What is phylogenetics?

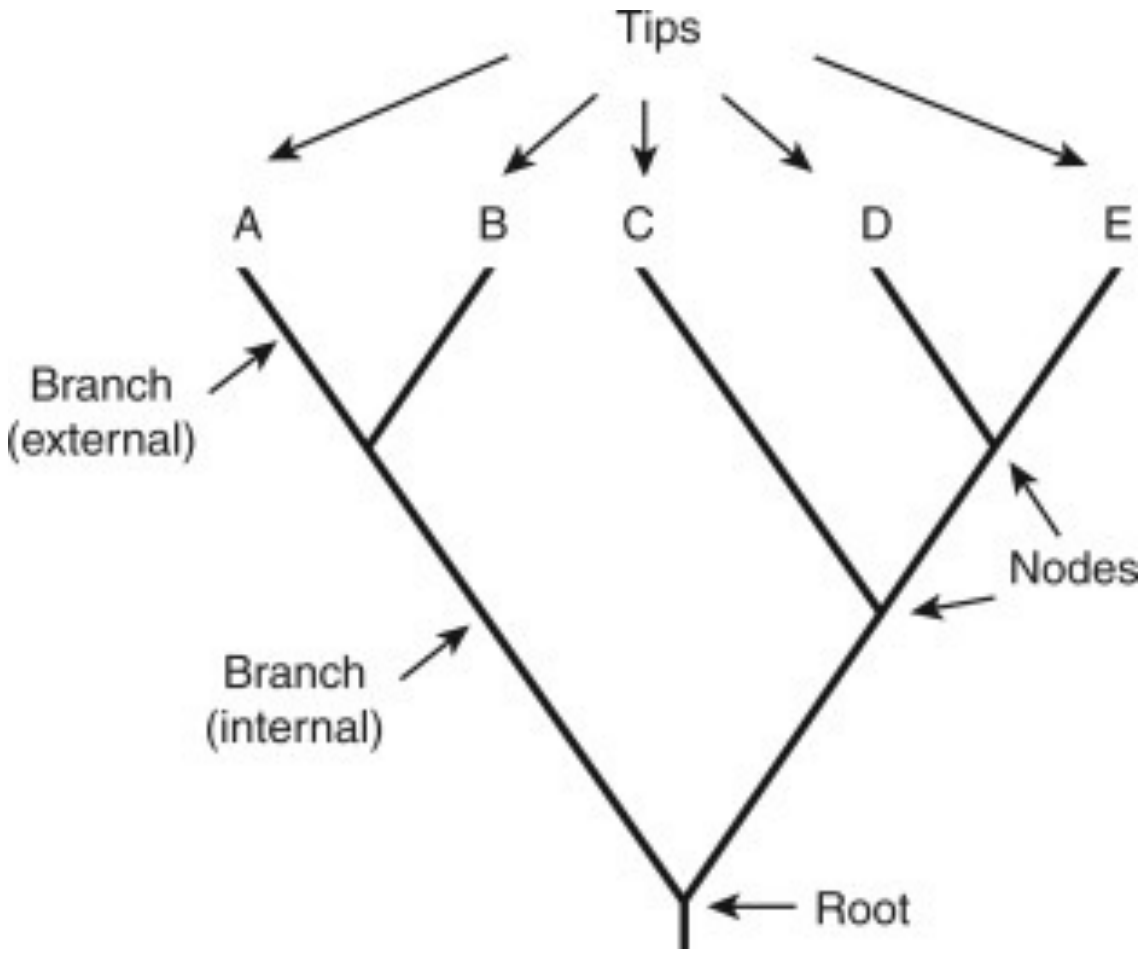
Building trees from genetic sequence data:

- Reconstructing the ancestral relationships among taxa
  - Taxa can be species, individuals or particular genes

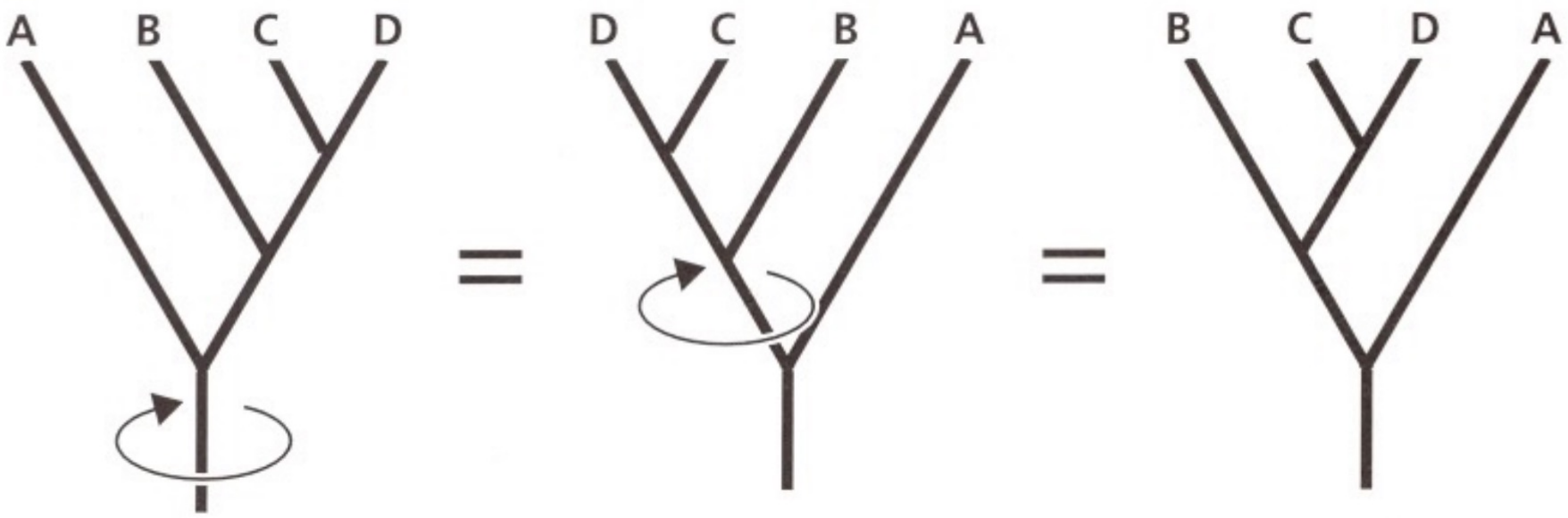
- Tree is only an estimate => “truth” usually unknown



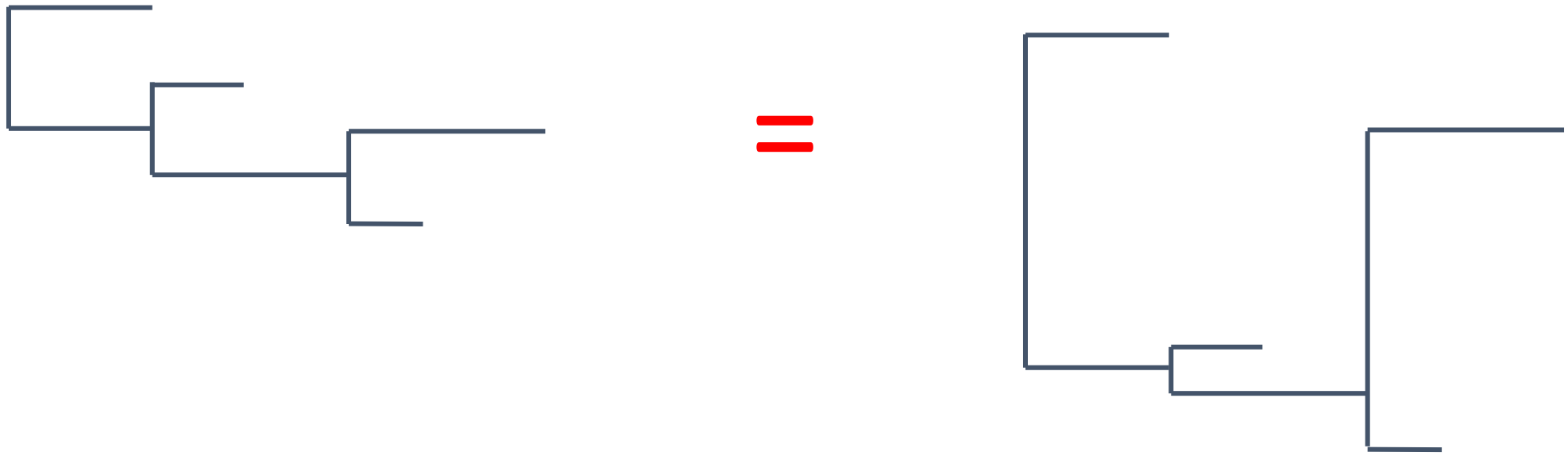
Parts of a phylogenetic tree



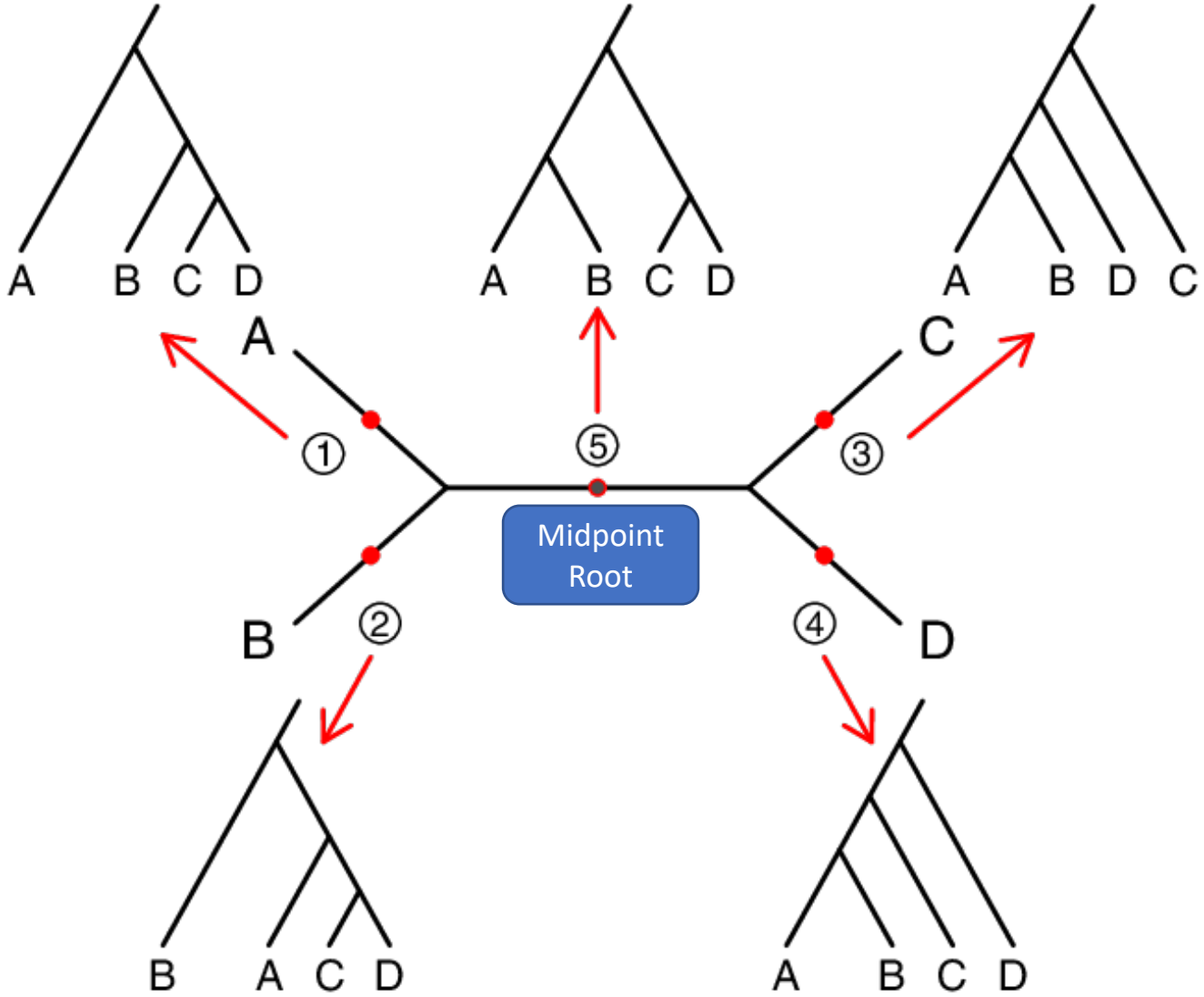
Branches can ‘swivel’



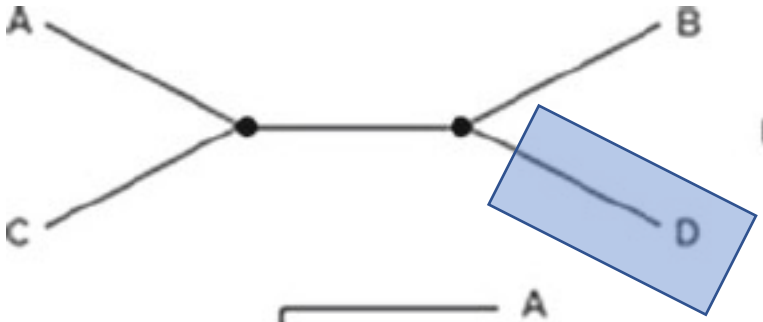
Vertical axis means nothing!



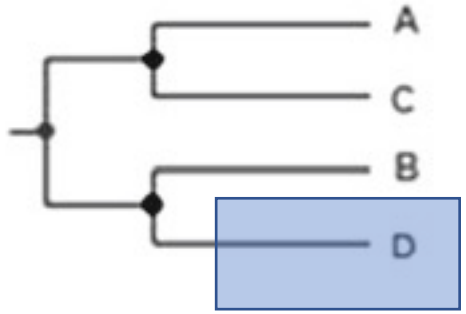
Rooting Trees



Rooting Trees

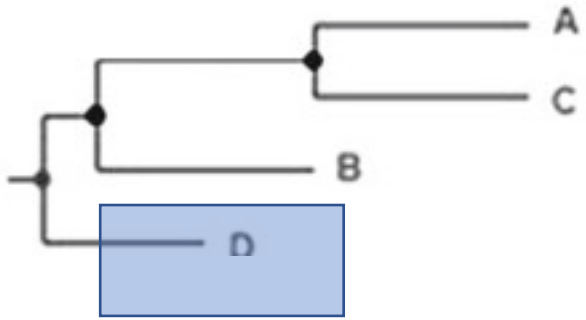


Unrooted Tree



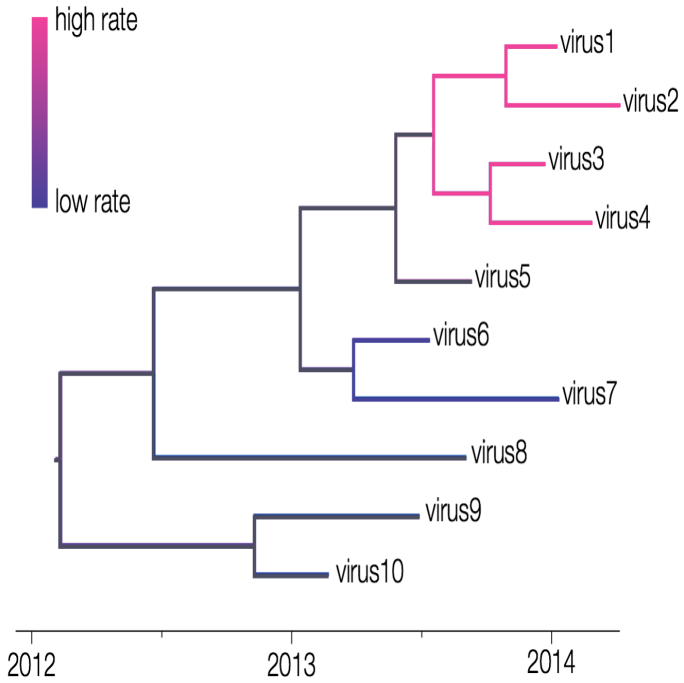
Midpoint rooted Tree

Remember this root could just as easily be put anywhere – it doesn't represent anything!



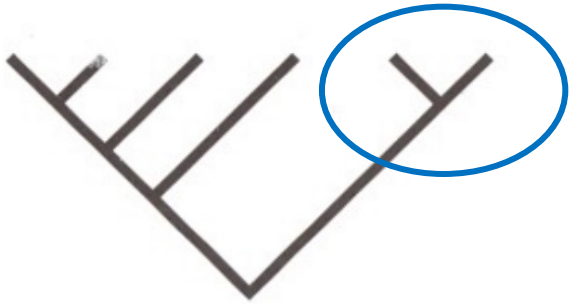
Outgroup rooted Tree

Outgroup – one or more taxa that fall outside the group of interest

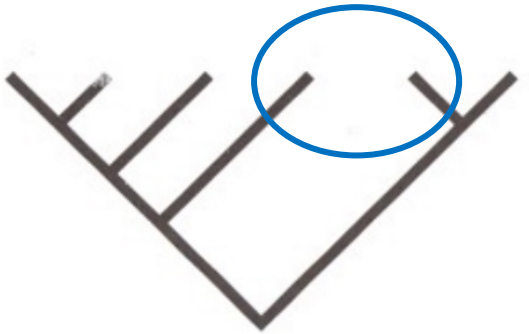


Molecular clock – oriented along an axis of time

Monophyletic



Monophyletic – sharing a single common ancestor



Not monophyletic

Clades, subclades and lineages are monophyletic groups of sequences of increasing levels of resolution

Interpreting phylogenetic trees - Practical

Follow the instructions in

RAGE-workshop-2024/4-command_line/N-tutorial-phylogenetics/day4_tree_visualisation.pdf