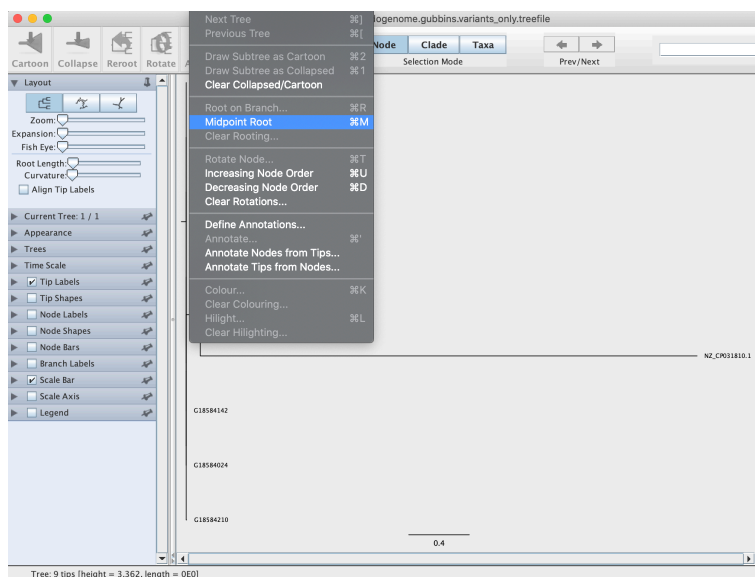


# [10E] Phylogeny

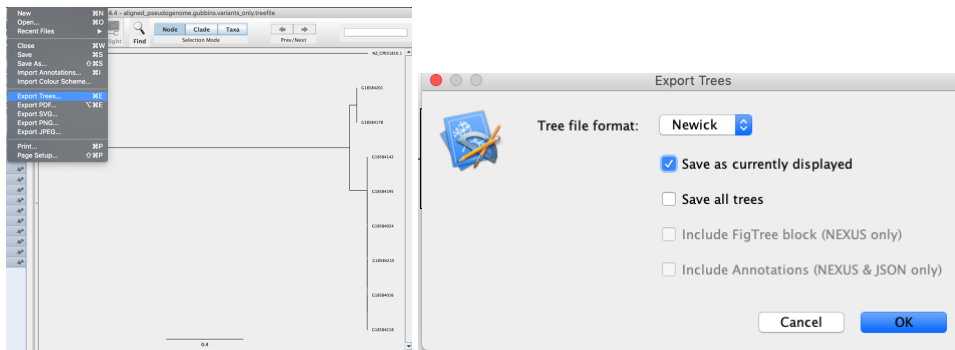
## Tutorial

In this session you will learn how to view phylogenetic trees using [FigTree](#), as well as import tree and metadata into [Microreact](#) (it is advisable to create a new Microreact account).

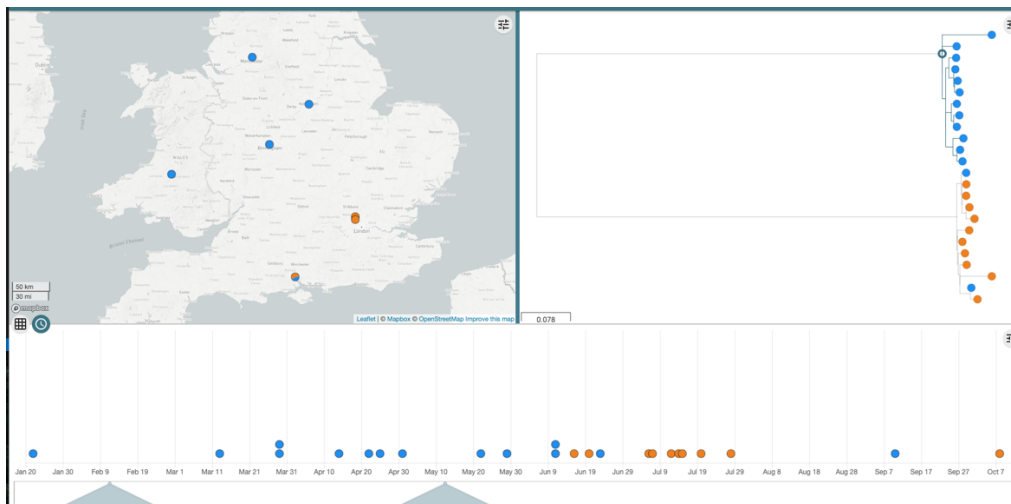
- Install FigTree in your computer:
  - FigTree is designed as a graphical phylogenetic tree viewer. It can be downloaded and run on a Windows/Linux/Mac computer, and can be found [here](#).
- Download the phylogenetic tree and metadata file to your computer:
  - You will be working with a microbial dataset. Phylogenetic tree has been built on your behalf. Metadata has also been prepared on your behalf.
- Open the tree file using FigTree, edit, and export.
  - The tree is in the Newick (.nwk) format. When prompted what to label the node/branches with, leave the default “label” as it is and click “OK”. The tree will initially be unrooted. If an appropriate outgroup is not known (this is often the case) then the tree can be midpoint rooted (using the menu or Ctrl-M (Windows/Linux) CMD-M (Mac) and then re-ordered in descending or ascending order (using the menu or Ctrl-D (Windows/Linux) CMD-D (Mac)).



- To save the tree file as currently displayed, export tree in newick format (which is the format Microreact accepts) by selecting: File → Export Trees → Tree file format (Newick) → Save as currently displayed → add .nwk extension to the filename.



- Visualize saved phylogenetic tree (newick format) and metadata in [Microreact](#).
  - Go to the microreact page using either Google chrome or Firefox
  - Navigate to the folder where you have saved the tree (in .nwk format) and the metadata file (in .csv format). More details on formatting your metadata file can be found [here](#).
  - Select both files and drag and drop the files.
  - Provide a name for your project and a brief description (optional). You may leave the 'project website' section blank and your email is also optional. Select 'create project'.
  - Your project should look like the figure below, with the map panel on the left, the phylogenetic tree on the right panel, and the timeline on the bottom.



- Watch this [video](#) to learn more about microreact.
- Study the FigTree and Microreact visualization, and answer the questions in the following Survey: <https://www.surveymonkey.com/r/10Ephylogeny> (please post any questions for clarification the Slack channel).
  1. How many major clades can you see?
  2. Is there anything unique about the clades? Hint: Look for the places where the samples were isolated. Look at the dates too.
  3. What is the benefit of visualising the metadata together with the phylogenetic tree (Microreact) versus having only the phylogenetic tree (FigTree)?

4. How does having a metadata affect your interpretation of the data? Based on the available metadata, can you identify any possible outbreak isolates? What are your reasons?

The data used for this training was extracted from a training module (<https://training.bactgen.sanger.ac.uk/#/F1/>) organized by the Bentley group at the Wellcome Sanger Institute.