

Programming exercise

(Phylogenetic protein trees)

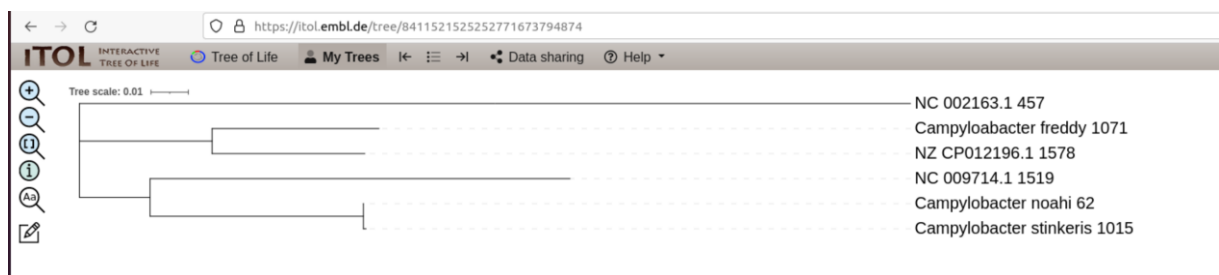
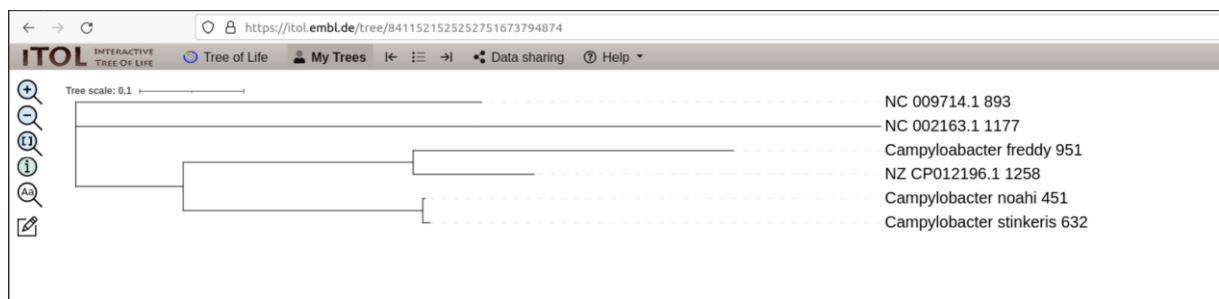
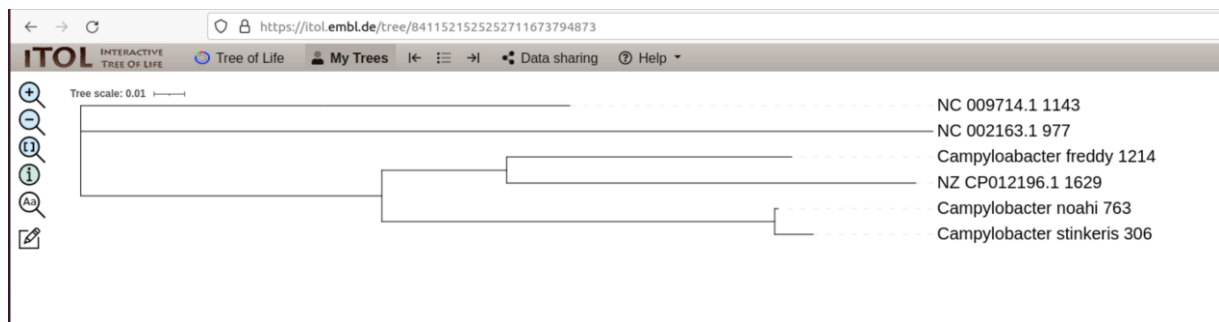
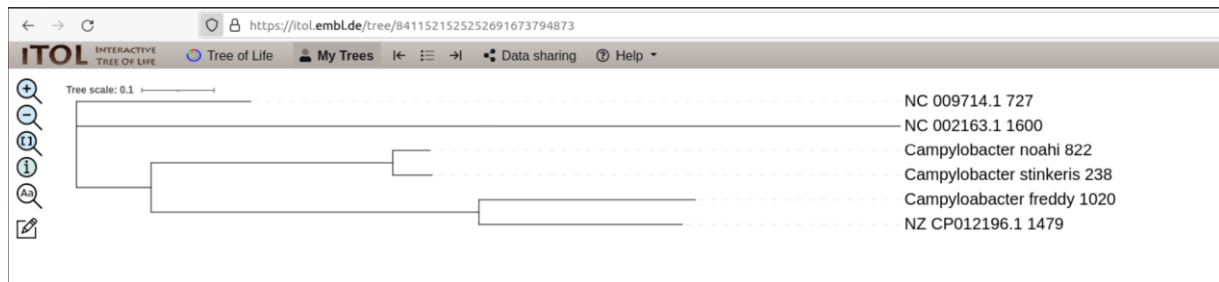
Comparative genomics

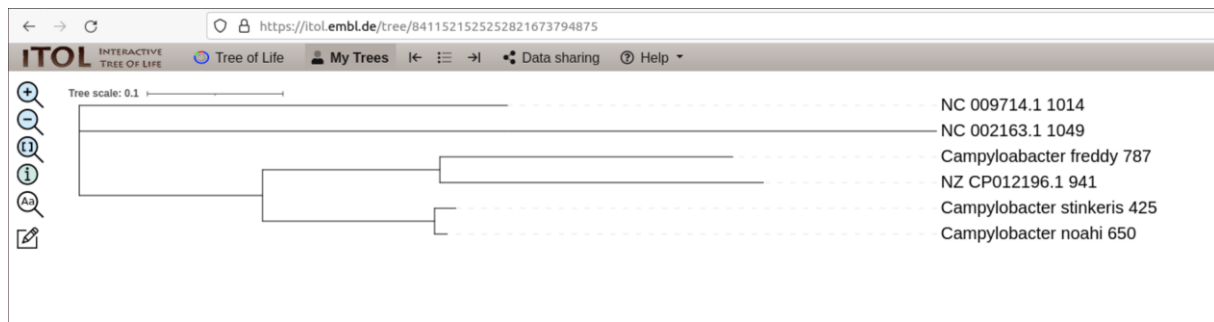
Cameron Strachan

Student: Marjan Aziminezhad

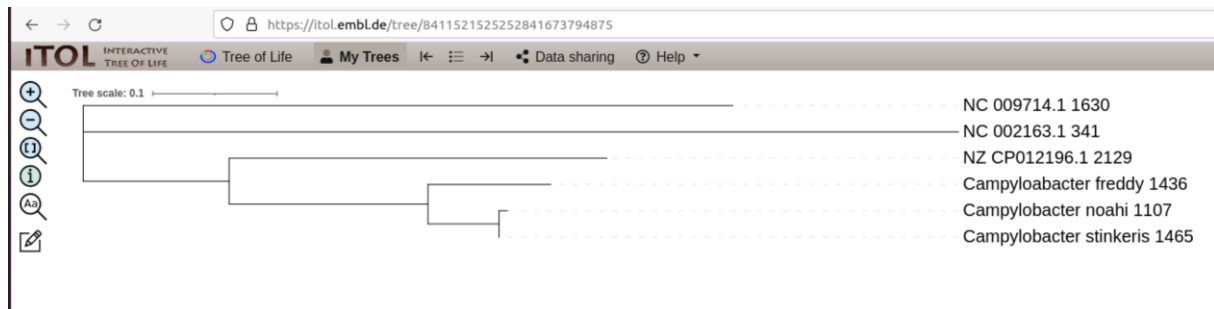
Date: Jan. 2023

Here the result trees visualized by iTOL:





Phylogenetic tree 5: Peptidase



Phylogenetic tree 6: Signal-Peptidase II

Interpretation:

The result could provide us insights into the evolutionary relationships among the bacterial species, as well as the functional and structural relationships of the protein among the different bacteria based on the sequence of the protein being analyzed.

-If the tree shows a clear separation of the different bacterial groups, it could indicate that the protein has diverged significantly over time and the bacteria groups have different functions or environments. Besides, if the tree shows that certain bacterial groups are closely related, it could indicate that the protein has a similar function or structure in those bacteria and that they have diverged relatively recently in evolutionary time.

It's also possible to infer horizontal gene transfer events, where a gene is transferred between organisms that are not closely related in evolutionary terms.

In a protein phylogenetic tree for different bacteria, short branches represent lineages of bacteria that have not diverged much over time in terms of the protein being analyzed, while long branches represent lineages of bacteria that have diverged significantly over time in terms of the protein being analyzed.

Short branches indicate that the bacteria at the tips of the branch have relatively similar sequences for the protein in question and have thus diverged relatively recently in evolutionary time. This could be the result of the protein having a similar function in those bacteria and being subject to similar selective pressures.

Long branches, on the other hand, indicate that the bacteria at the tips of the branch have diverged significantly in the sequence of the protein, and have thus diverged a long time ago in evolutionary time. This could be the result of the protein evolving new functions or adapting to new environments in different bacteria, leading to greater sequence divergence.

It is important to note that the branch length does not indicate the absolute time of divergence, but rather the relative evolutionary distances among the sequences being analyzed.