# Comparison of phylogenetic trees

Phylogenetic trees are commonly used to analyze the historical evolution of species from a common ancestor. Traditionally phylogenetic tree visualizations were designed for the purpose of browsing and exploring the organization within the tree [1]. Nowadays, with increasing data availability, comparisons between phylogenetic trees are more frequently studied as well. For many biological questions, the comparison of multiple trees is highly relevant. For example, discrepancies in the tree structure can
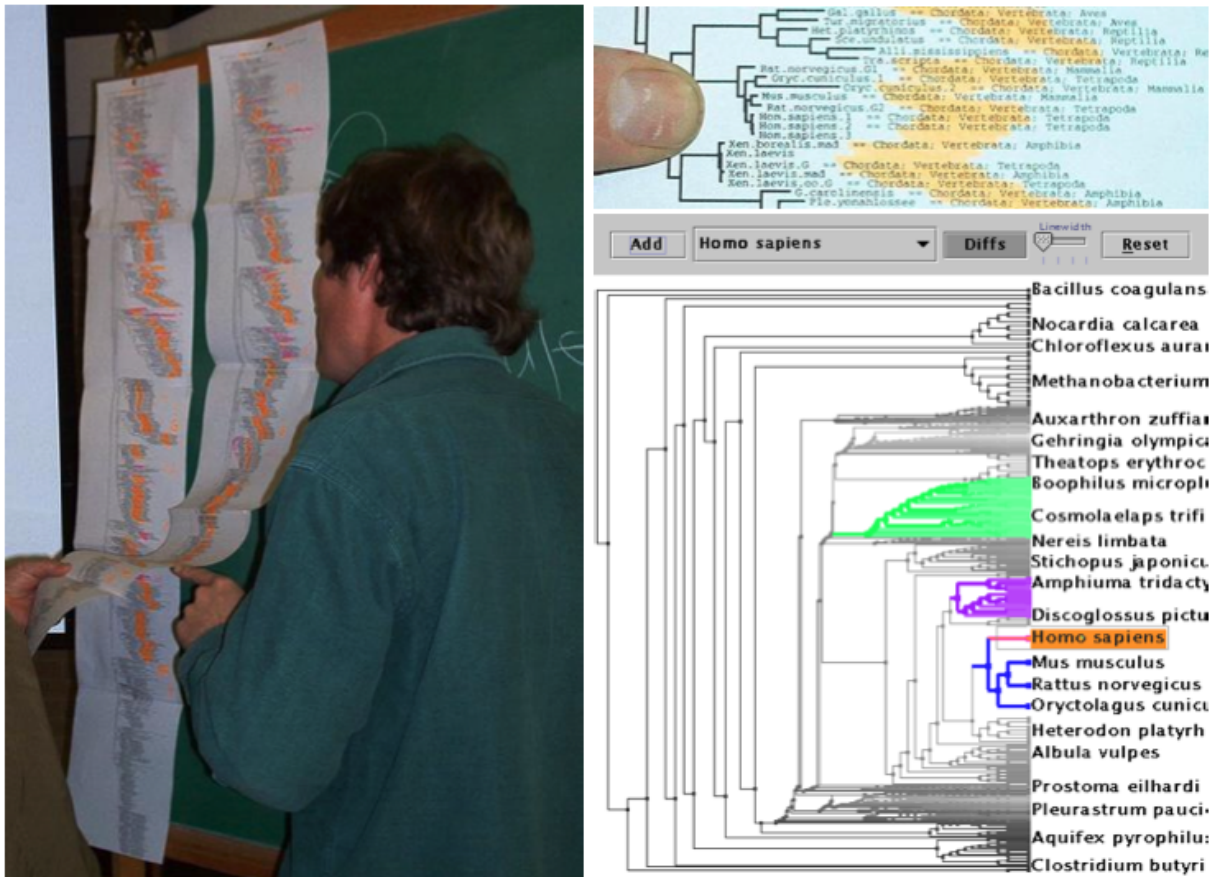
TreeJuxtaposer - Munzner et al. (2006)

hint to biologically meaningful differences. However, with the large amounts of data currently available, trees become very large and scalability of (static) visualizations quickly becomes an issue. Your task in this project is to develop new interactive visual encoding for comparison multiple (large) phylogenetic trees. The new visual encoding should hint to differences in tree structure and organization, such that a biologist can further quickly find and interpret these. It is important to think about navigation in and between these large trees. You can take inspiration from other tree and/or hierarchical visualizations (e.g., [2]). Knowledge about biology is not necessary to do this project.

- Relevant papers:
  - TreeJuxtaposer https://dl.acm.org/doi/10.1145/1201775.882291
  - ADview https://ieeexplore.ieee.org/document/8636969

- Data: the data for this project consists of five phylogenetic trees of Pectobacteria, where each is constructed using a different method. The data structure for the trees is Newick (see more info here), which can be read as a .txt tile.