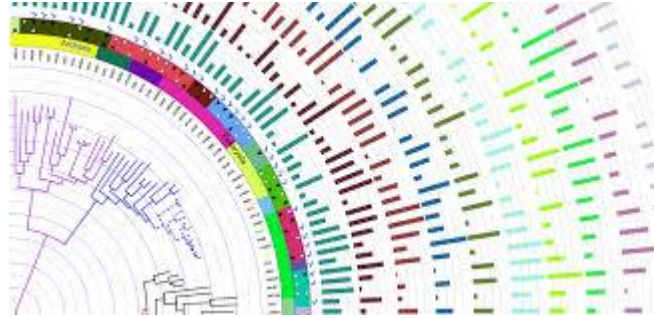


HIGH-PERFORMANCE INTERACTIVE TREE VISUALIZATION

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Background

Phylogenetic trees are a tree data structure that represent the genetic relationship between various organisms. When genomics researchers wish to test hypothesis or do data driven discovery, they often rely on interactive visualizations to explore the data. In this project you will work with genomics data from 50000+ strains of the pathogenic bacteria *M. tuberculosis*, which kills 1.5 million people a year. Currently no methods exist that allow us to interactively explore this data set with corresponding meta-data.



The goal of this proposal is to evaluate how to create an interactive tool for tree exploration with the ability to export publication ready images.

Approach

You will first evaluate existing tree visualization technologies and determine the desired and required properties of the tool. This will be done based on review of recent literature and interviews with scientist working in the field. Next, you will identify suitable software technologies that can deliver the required features. This should culminate in the development and deployment of a stand-alone app. Challenges include the development of new scalable visualizations for trees and the development of graphical encodings to create a rich interactive visualization

Suggested literature

<https://itol.embl.de/>