



## Bacterial Phylogenomics

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Besides its classical use to ascertain the evolution of a group of species, phylogenetics has many other applications such as the prediction of the function of a protein and the detection of genes under specific selective constrains. The advent of the genome era has brought about the possibility of extending such analyses to larger sets comprising thousands of sequences from completely sequenced (phylogenomics). To achieve this transition new tools have been developed that allow the large-scale reconstruction of thousands of phylogenetic trees in an automatic way. Here I survey recent progress in the development of automated pipelines to reconstruct and analyze large collections of phylogenetic trees and provide some examples of how such collections have been used to address important biological questions. In particular I will provide two examples of the application of such techniques that involve the use of bacterial genomes. One focuses on the reconstruction of the alpha-proteobacterial ancestor of modern mitochondria and the other deals with the comparison of two *Salinibacter ruber* strains isolated from the same saltern.