VISUALIZING EVOLUTIONARY AND FUNCTIONAL RELATIONSHIPS BETWEEN MICROBES FROM A SEQUENCE NETWORK PERSPECTIVE

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The emergence of new molecular techniques has brought a new appreciation for the broad diversity among microorganisms. Comparative sequence analysis, in particular, has exposed both the cultured and uncultured microorganisms to scrutiny like never before. The increasing amounts of sequence data being digested by laboratories have created serious challenges as the sequence analysis becomes the bottleneck of the process. This process has been alleviated by publicly available tools for alignment and tree-parsing, yet it still requires substantial human involvement to prune and move these data along the pipeline. Analyses of the final data in the context of discerning potential evolutionary or functional relatedness between microbes and their communities also require sophisticated methods.

We present an open-source web application which can be installed locally within a laboratory and be used to facilitate the sequence analysis pipeline by automating the process using an intuitive user interface while simultaneously offering a method to visualize a network of potential evolutionary or functional relationships. The automated process follows these general steps: multiple-sequence import, BLASTN is queried from which sequences of interest may be added to the collection, the collection is aligned using CLUSTALW, sequence portions are masked and a phylogenetic tree is constructed using the popular Bayesian or Neighbor-Joining methods. In addition to rendering a phylogenetic tree, the software runs through a series of algorithms to produce numerous reports indicating sequences that are likely to be of interest based on the collection and would be missed without significant manual analysis.
