CONSIDER FOR TALK

7th Annual SEA-PHAGES Symposium Abstract

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Functional clustering of Mycobacteriophage proteins using phylogenetic profiles

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Annotating protein functions from genomic sequences is a central aim of the SEA-PHAGES project. One assumption relevant to annotation efforts is that proteins that function together in a pathway or structural complex are likely to evolve in a correlated fashion, and that during evolution, all such functionally linked proteins tend to be either preserved or eliminated in a new species (phage). Phylogenetic profiles describe this property of correlated evolution by characterizing each protein by a string that encodes the presence or absence of a protein in a given genome. The aim of this project was to cluster *Mycobacteriophage* phylogenetic profiles to aid in annotation. Phylogenetic profiling has previously been applied to a variety of systems and shown to identify previously unknown enzymes in metabolic pathways, transcription factors, and explanations for roles of certain mutations in human disease.