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2024 SEA Faculty Meeting Abstract

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The inner workings and alternative uses for Starterator

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Starterator is a python 2.7 program originally written in the Hatfull lab by Marissa Pacey led by Dan Russell. It is designed to characterize the evolutionary context of possible start codons among a collection of orthologous genes. By using multiple sequence alignments of genes from all members of a pham the level of conservation and position of annotated start codons is visualized and the results can be used as evidence for start codon annotations of new pham member genes. This poster will present a view of the inner workings of Starterator including the underlying algorithms, it will also discuss how these results are presented in the graphical and textual output, discuss methods to help interpret the results, and discuss the benefits and disadvantages of using whole phage reports vs. whole pham reports. Requests for user input is always welcome.