CONSIDER FOR TALK

8th Annual SEA-PHAGES Symposium Abstract

Washington University in St. Louis

St. Louis MO

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Investigations into the Kibler SD scoring algorithm

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The Kibler scoring algorithm for evaluation of Shine Dalgarno sequences was introduced into DNA Master prior to the spring 2015 *in silico* semester. With the advent of this new scoring metric we wanted to look into scores themselves so as to understand the overall metric. “What is a good score?”, “How are scores distributed?”, “How low can you go?”, were all questions worthy of answers. To that end we created a database of over 500 SEA mycobacteriophages available from Genebank and analyzed the SD scores from those phage. The mean SD score of the called starts across nearly 50,000 genes was -4.2 with a standard deviation of 1.2. The average score varied by cluster from -4.7 for cluster B to -3.8 for cluster C. These and other in depth analysis of SD scores will be presented.