

Fast Categorization of Bacteriophage Protein Families using Computer Graphics

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Although there are many bacteriophages, only a small number of the ones existing in our soil have been characterized. In order to be able to use them for phage therapy, there is a need for fast and accurate methods of categorizing them. The Hardies Laboratory chose to compare bacteriophage genes with each other by Secondary Structure Prediction, using SAM and Psipred. In order to accelerate the process of displaying the data in a visual format, I developed programs for taking SAM's and Psipred's output and displaying the aligned predicted secondary structures onto a graphical image, which is made by Gbrowse. The result, is that hypotheses and experiments on secondary structure prediction programs using the same formatting standards have a much faster time to graphical image generation. With that, testing various aspects like accuracy of said secondary structure prediction programs becomes easier, as well as invaluable assistance in solving the hypothesis 'These phage genes are(are not) related.'