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AlphaFold Across Conserved Genes in Bacteriophages Skitty, AdaS, GoldDust, and Halloweekend

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Bacteriophages are viruses that infect bacterial cells and lend to useful applications within genetic engineering, biotechnology, and pharmaceutical fields of research. With the unique ability to isolate and lyse bacterial hosts, bacteriophage present opportunity for recombination and a wealth of bioinformatic fascination. Within the Purdue University ABE 226 and 327 workflow, four bacteriophages were isolated with the host *Arthrobacter globiformis* and sequenced: Skitty, AdaS, GoldDust, and Halloweekend. In ABE 327, students utilize AlphaFold 3, an AI tool created to predict the protein folding structures based on a nucleotide fasta sequence. AlphaFold has the capability to structure RNA, DNA, proteins, and hydrophobic interactions. Currently used in a multitude of fields for structure education, AlphaFold has also established value within drug discovery as it predicts not only characteristics of ligands, proteins, and antibodies, but also their interactions within the human body. Students in ABE 327 utilized AlphaFold 3 to research protein sequences to further their bioinformatic literacy, and to cross check the predictions made from auto-annotation programs. In conjunction with auto-annotation programs such as DNA Master and databases such as NCBI GenBank, AlphaFold was used to visually compare four conserved endolysin genes within the selected genomes from ABE 226 in Fall 2024. Mathematical evidence for the proposed function and probabilities of each of these genes were used to draw conclusions about the function of each conserved gene. Due to the gap within bacteriophage and genome annotation databases, further analysis to verify the function and structure of each of these conclusions would involve wet lab procedures such as affinity purifications, mass spectrometry analysis, and protein-protein interaction assays.