"ProteinFlow" v2 - Biocomputational Analysis of Metabolic Pathways to Discover New Carbon Capturing Bacteria

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Climate change poses a significant threat to global ecosystems. Current mitigation strategies are inefficient and costly. Biological solutions, specifically algae, offer a promising alternative. Synechococcus elongatus (SE), has demonstrated remarkable carbon-capturing capabilities relative to its size and the potential to combat climate change. Despite this potential, little research has been conducted to identify other bacteria with similar or superior carbon-capturing abilities. ProteinFlow is a computational workflow that bridges this gap by leveraging key information about the protein pathway in SE and bioinformatics tools to uncover new carbon-capturing bacteria. There are 7 critical proteins in the metabolic pathway that captures carbon in SE, each performing a specific function. ProteinFlow compares the proteins in this metabolic pathway against millions of other organisms. Then, it performs a sequential, phylogenetic, and structural analysis. This 3 faceted approach provides statistical, evolutionary, and functional support when identifying new organisms. ProteinFlow is capable of identifying new organisms with SE's capability, supported statistically. ProteinFlow identified Synechocystis PCC 6803 and Nostoc Punctiforme as bacteria that are capable of capturing carbon. These bacteria have potential to offer increasingly clean and efficient solutions to the climate crisis, even more so than mechanical solutions. Further steps for this study is to quantify these findings in a laboratory setting. ProteinFlow's strength is applicability to any study involving key proteins in a metabolic pathway. It is extensible to finding bacteria that can degrade plastic, and multitudes of other functionalities.

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