Analyzing the Mechanics of Pollutant Degradation

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As pollution levels rise, the relationship between pollutant degrading proteins across various organisms is vital to create a synthetic microbe that mitigates substance toxicity. To understand this relationship, the programming language R was used to write a program that analyzed trends among proteins involved in toxic substance breakdown. Due to similarity of function across the proteins of various organisms, it was hypothesized that a strong relationship exists between the proteins. In order to analyze how pollutant consumption is related across organisms, a variety of methods from the Bio3D package under the computer language R were employed on eight specific proteins. Once these methods were called, it was found that sets 3, 4, 11, 12, 13, 14, and 17 contained cores, or areas of highly similar protein make-up. Sets 3, 11, and 12 exhibited particularly strong similarities. The normal mode analysis procedure quantified the structural variations between each protein of each set and organized it in a visual plot. These results support the patterns from the core analysis and indicate a level of similarity in both amino acid sequence and structure among various sets of proteins, specifically, between proteins that degrade plastics, toxic chemicals and heavy metals, and hydrocarbons. However, as it is just a visual depiction, further analysis is being explored. These similarities signal the potential to create a synthetic protein that could attack multiple pollutants, specifically, hydrocarbons and plastics or heavy metals, herbicides, and hydrocarbons at once. As the proteins have little variance in structure, a small genetic change that adds the functionality of the other effective proteins is plausible.

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