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FOLDIT, A VERY SMART APPROACH TO SOLVING THE SECRETS OF VIRUSES

Foldit might be looking complex at first glance, but it actually requires no knowledge of biochemistry, bioinformatics or molecular biology.

The task of the game is to find different patterns of protein placement for researchers then to apply these solutions in reality to eradicate diseases and create biological innovations.

Foldit attempts to apply the human brain's three-dimensional pattern matching and spatial reasoning abilities to help solve the problem of protein structure prediction. 2016 puzzles are based on well-understood proteins. By analysing how humans intuitively approach these puzzles, researchers hope to improve the algorithms used by protein-folding software.

Protein structure prediction is important in several fields of science, including bioinformatics, molecular biology, and medicine. Identifying natural proteins' structural configurations enables scientists to understand them better. This can lead to creating novel proteins by design, advances in treating disease, and solutions for other real-world problems such as invasive species, waste, and pollution.

The process by which living beings create the primary structure of proteins, protein biosynthesis, is reasonably well understood, as is the means by which proteins are encoded as DNA. However, determining how a given protein's primary structure becomes a functioning three-dimensional structure, how the molecule folds, is more difficult. The general process is understood, but predicting a protein's eventual, functioning structure is computationally demanding.

Foldit's developers wanted to attract as many people as possible to the cause of protein folding. So, rather than only building a useful science tool, they used gamification to make Foldit appealing and engaging to the general public.

As a protein structure is modified, a score is calculated based on how well-folded the protein is, and a list of high scores for each puzzle is maintained. Foldit users may create and join groups, and members of groups can share puzzle solutions. Groups have been found to be useful in training new players. A separate list of group high scores is maintained.

Results from Foldit have been included in a number of scientific publications.

Foldit players have been cited collectively as "Foldit players" or "Players, F." in some cases. Individual players have also been listed as authors on at least one paper, and on four related Protein Data Bank depositions.

To maximize your usefulness or if you get bored of folding proteins yourself the creators of Foldit discovered a program to use your computer’s idling time or even background calculating for automatic deduction of folding proteins.

As it can be seen, the experiment of a few talented people from University of Washington is coming to fruition and expanding rapidly, which shows its promising potential and the upcoming benefits of the results.