

CS Bits & Bytes is a bi-weekly newsletter highlighting innovative computer science research. It is our hope that you will use CS Bits & Bytes to engage in the multi-faceted world of computer science to become not just a user, but a creator of technology. Please visit our website at: <http://www.nsf.gov/cise/csbytes>.

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Crowdsourcing

You have heard the saying, "Two minds are better than one," but what happens when you combine the mind power of an entire crowd? In 2011, players of the online game, Foldit helped to decipher the structure of an enzyme involved in the reproduction of HIV in just ten days. The problem of how to configure the structure had stumped scientists for 15 years!

MUST SEE!



Learn more about Crowdsourcing by watching this Science Behind the News Video: <http://science360.gov/obj/video/ba23cebc-7490-407b-885a-c4fe820a1b7b/science-behind-news-crowdsourcing>.

Crowdsourcing make use of the wisdom of the crowd. Foldit crowdsources by drawing upon the creativity and spatial reasoning of players, and takes advantage of many human minds to accomplish tasks for which computers are ill-suited. As players manipulate the structure of virtual proteins in Foldit, the program calculates how "natural" the configuration is using the laws of physics and chemistry; the more natural the configuration, the higher the score. Imagine a ball rolling down a hill; a "natural" protein configuration is stable, much like a ball that has rolled down a hill and reached the bottom.

Foldit uses networks of human minds to take citizen science to a new level for discovery. Citizen science is the practice of conducting scientific research using crowdsourcing. Through the advancements in technology and computer science, citizens can both collect and analyze data to be used in scientific experiments. For example, by using the citizenry, or the crowd, considerably larger amounts of data may be able to be collected and/or analyzed, resulting in greater accuracy of results. The top players of Foldit have included a 13-year old and a salesman – quite often Foldit players are not scientists. In fact, there is no reason to believe that scientists are better at Foldit than anyone else.



Image of Dr. David Baker.
Credit: University of Washington Medicine.

Who Thinks of this Stuff?! There is a large team of computer scientists, creative experts, and biochemists at the University of Washington who have designed and continue to develop Foldit. The concept was envisioned by Zoran Popović, a computer science professor, and David Baker, a biochemistry professor. They sought to capitalize on the creativity of players to learn new approaches for solving challenging scientific puzzles. In discussing his motivation for undertaking research into protein folding, Professor Baker said, "...what I really like about scientific research is getting to work with fun excited people on discovering new things, and the potential to make the world a



Foldit players use a variety of tools to interactively reshape various regions of proteins. Credit: University of Washington.

better place." When he is not in the research laboratory devising new ways to understand protein folding, Professor Baker likes to climb the nearby mountains.

Links:

For an introductory article including a video on how to play Foldit, see: <http://depth-first.com/articles/2011/10/25/an-introduction-to-foldit/> and to download Foldit go to: <http://fold.it>.

Read the scientific paper about the HIV protein structure that Foldit gamers helped solve at: <http://www.cs.washington.edu/homes/zoran/NSMBfoldit-2011.pdf>.

Learn more about citizen science and find a project to get involved at: <http://www.scientificamerican.com/citizen-science/>.

Activity:

Proteins are cellular machines found in every cell in our body that conduct the tasks essential for maintaining life: metabolism, regulation, growth, reproduction, and more. Proteins are polymers - long, repeating chains of 20 different building blocks called amino acids. These amino acids have different sizes, shapes, and other characteristics that allow proteins to fold into myriad configurations. It is these configurations, as well as the unique characteristics of some amino acids, that make proteins into machines. Think of the engine in a car: it is the form of the engine that determines how it functions. Additionally, protein configurations are typically stable, and because scientists and engineers understand some of the characteristics that make proteins stable, they are able to calculate the stability of a particular protein configuration.

In this activity, students will make a model of a hair protein and show how structural changes in the protein allow a hair curler to change the shape of hair. Give each student or group of students the following materials: pipe cleaners (1 white, 1 green, 5 yellow) – each color represents a different amino acid that makes up a protein, small binder clips, and a paper towel tube. First, twist a loop in the center of each pipe cleaner to represent a functional group. To each loop in the yellow pipe cleaners, attach a binder clip. These represent sulfhydryl groups that can bind together with other sulfhydryl groups. Now attach the amino acids together into a strand by twisting the ends of each pipe cleaner together in the following order: yellow, white, yellow, yellow, yellow, green, and yellow. This represents a hair strand, which is made of keratin protein. Wrap your model around the paper towel tube (a hair curler). Where binder clips (sulfhydryl groups) are in proximity, attach the binder clips together (the heat from the curling iron makes this binding more favorable). Remove the model from the tube and see the curls formed in the protein structure.

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