What is FoldIt?

FoldIt is an online game in which people use their problem-solving skills to solve a model of an unfolded protein for its best possible conformation. It has become a useful innovation because usually,the process of using computers alone to solve conformations is very time-consuming. FoldIt takes data of the best-folded proteins from the user database and eventually introduces it to computer programs to help them to learn how to fold proteins more efficiently than ever before.
(The Science Behind Foldit | Foldit, 2019)

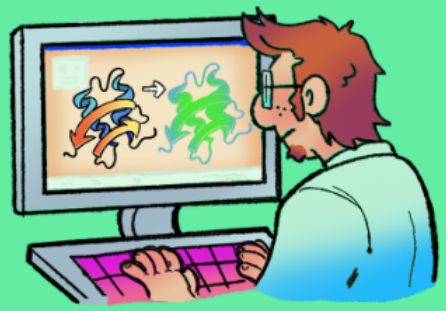
How does it work?

STEP 1:

The process starts when players are given an unfolded model of a protein. These models are digital representations of the tertiary or quaternary strucures of actual proteins, from simple ones to very complex ones. These structures are relatively simplified for the users, but contain depictions of alpha-helicies and beta-sheets with their own side-chains. (Khatib et al., 2019)

STEP 2:

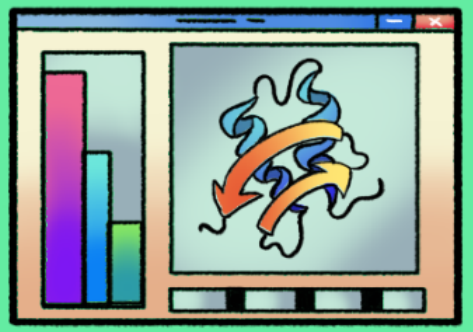
Next, the players will try to get the highest possible score with their protein on FoldIt. This is achieved when the players find the most most stable conformation for the protein. In order to do this, the players must drag different parts of the protein and use their problem-solving skills to clear clashes between amino acid side chains, clear voids between secondary structures, form hydrogen bonds between beta-sheets, and more.
(Khatib et al., 2019)



STEP 3:

Next, FoldIt gathers data from player-folded models. This data is gathered in order to make a comparison between the accuracy of the models that were folded by the players and the accuracy models folded by either an expert in Cryo-EM technology or the current best protein model-building algorithms.

For the comparison, the accuracy of the models folded by the players and the accuracy of the models folded by an expert or by an algorithm are is analyzed by standard electron microscopy validation tools. The quality of each model is measured by factors such as electrostatic properties, number, strength, and position of hydrogen bonds, and torsion angles of side chains and secondary structures. (Khatib et al., 2019)



STEP 4:

After the comparison process, both the validated player data and the problem-solving algorithms generated from it are introduced to computer programs designed for protein folding. This data is introduced to these programs in order to teach them a better, more efficient way of solving protein structures. In addition, it will also help reduce the time and effort needed from experts in solving structures of these proteins themselves. (Khatib et al., 2019)

References for the HONR 399 Ideas Magazine FoldIt informational spread

Khatib, F., Desfosses, A., Players, F., Koepnick, B., Flatten, J., Popović, Z., Baker, D., Cooper, S., Gutsche, I., & Horowitz, S. (2019). Building de novo cryo-electron microscopy structures collaboratively with citizen scientists. *PLoS Biology*, *17*(11). https://doi.org/10.1371/journal.pbio.3000472

The Science Behind Foldit | Foldit. (2019). Fold.it. https://fold.it/portal/info/about