A ROSETTA STONE FOR PROTEINS

Nearly a million proteins are encoded in the genes recently sequenced by the Human Genome Project. That was a landmark achievement. But, as Ryan notes, the structure and function of more than 95% of the proteins remain unknown. Understanding proteins, the building blocks of life, is crucial to advancements in fields ranging from medicine to nanotechnology. Since it would take a long time to fill in those gaps using traditional wet chemistry, computers will bear the brunt of the job.

There's a hitch, however: Current computational protein-structure-prediction algorithms don't include methods for modeling how proteins are affected by pH, or the level of acidity in various cells in the body. Determining the pH effect on a protein can be essential to evaluating its potential as a new drug, he notes, or as a target for nanotechnology applications such as self-assembling biological devices.

So Ryan developed the first software tool for modeling a protein's pH sensitivity. It's an add-on for Rosetta, a leading algorithm for predicting protein structure. With his program, says Ryan, "a new realm of possibilities opens up." His software not only increases the accuracy of Rosetta but also expands Rosetta's modeling arsenal to include pH-sensitive protein folding, docking, and design.

Prion/antibody blind prediction performed by Michael Daily at Johns Hopkins. The colors represent the prediction (red) and the experimental position (green). Ryan's pH calculations will improve protein docking simulations.

ON THE ISSUES