Educational Modules for Teaching Protein Structure Prediction and Design

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Protein structure determines protein function, and protein interactions are key to almost all cellular processes. Recently developed computational methods can be used to predict protein structure, dock proteins, and even to design proteins. Sidhartha Chaudhury, Sergey Lyskov and Prof. Jeffrey Gray at the Johns Hopkins University have now assembled a book of educational modules to teach protein structure prediction and design. The modules use PyRosetta, a new Python-based interface to the Rosetta package which has a broad range of functionalities. Students can use the tools interactively through the Python shell, or write scripts for more complex protocols including parallel calculations. The modules begin with fundamentals of biomolecular structure and energetics, and then proceed through sampling with discrete and continuous optimization algorithms including backbone fragment assembly, side-chain packing from rotamer libraries, Monte Carlo optimization plus multivariable gradient-based quasi-Newton minimization. Integrated into the modules are applications including de novo folding, structure refinement, protein-protein docking and small-molecule docking, loop building and protein design. PyRosetta enables the creation of methods tailored for particular problems with objects which control the flexibility of the protein and the propagation of conformational changes. Thus, the emphasis is on training students to be able to build custom protocols for particular biomolecular applications. PyRosetta and the modules can be downloaded for free from http://www.pyrosetta.org.