BIOF 096: Rosetta for Molecular Modeling and Design

Rosetta is a set of tools used for protein structure prediction and designing. Rosetta is capable of predicting structures either with or without prior knowledge. Apart from large and small molecular docking, Rosetta is also popular for designing novel proteins and peptides.

The course will go over the capabilities of Rosetta, followed by hands-on walk-through for predicting protein structures, docking and protein designing.

Credits: 2
Class Type: Workshop
Program: Bioinformatics and Data Science
Availability Currently Not Available