Combi Seminar

Wednesday, 2.22.23 | Foege Auditorium | 1:30
remote viewing option: https://depts.washington.edu/gsrestrc/remote.htm

Dr. Frank DiMaio

University of Washington

"Machine-learning guided protein structure prediction and cryoEM map interpretation"

Dr. Frank Dimaio is an Associate Professor at the Institute for Protein Design. His research is focused on protein structure determination from sparse and noisy experimental data. By combining ideas from protein structure prediction with data-guided conformational sampling, we may uniquely determine a protein's structure to atomic accuracy in cases where neither data nor prediction alone is sufficient. The methods Frank has developed include tools for solving difficult molecular replacement problems, elucidating more than a dozen structures previously unsolved in the laboratories of expert crystallographers. He has also developed a new approach for low-resolution crystal refinement; this method outperforms state-of-the-art refinement packages, making it possible to infer detailed atomic interactions from low-resolution crystal data . Frank is further interested in developing tools for de novo structure determination from low-resolution data, as well as extending these approaches to other sources of data. Additionally, he is more generally interested in structure prediction, developing methods for improving conformational sampling, protein forcefield development, and modeling (and design) of symmetric protein assemblies. Improvements to structure prediction – both sampling methods and forcefields – are critical to designing proteins with novel function.

Questions? Contact Brian Giebel at bgiebel@uw.edu or visit the Combi website at http://www.gs.washington.edu/news/combi.htm