PhD project #1 in Structural Bioinformatics/ Computational Structural Biology:
Data-driven approaches to explore and target hidden protein states

The Fischer lab at St. Jude Children's Research Hospital is recruiting a computational graduate student for a data-driven project that exploits protein flexibility and hydration for ligand discovery.

The project is driven by the realization that common practices using cryogenic temperature in crystallography can mislead the utility of structural data for ligand discovery.

Your computational skills will help leverage findings from our young interdisciplinary team that uses structural biology (crystallography, NMR), protein biochemistry, and single-molecule methods to characterize dynamic, disease-relevant protein states. By finding ligands against those flexible protein states, and revealing allosteric networks we can explore new ways to modulate protein malfunction in disease.

Our group is part of the Department of Chemical Biology and Therapeutics, and Structural Biology at St. Jude Children's Research Hospital. With ongoing investments into exceptional structural biology, chemical biology and computational facilities, this is an exciting time to join our lab.

This work will provide a solid introduction to current opportunities in structure-based ligand discovery with relevance for both academia and industry. With its excellent core facilities, highly interactive and supportive environment St. Jude Children's Research Hospital is a great place to do research and build a career while living in an affordable city.

Applicants will be enrolled as full-time graduate students earning a PhD degree in Pharmaceutical Sciences from University of Tennessee Health Science Center while working full-time on their dissertation at St. Jude. The applicant will receive a full stipend, and health insurance according to the agreement between the two institutes.

Minimum admission requirements:
- a BS or MS degree in informatics, chemistry, biology, mathematics, engineering, or other appropriate disciplines with a strong focus on computation.
- a minimum Grade Point Average of 3.0
- a combined Graduate Record Examination score (verbal and quantitative) of at least 300
- proof of proficiency in English (e.g. TOEFL)

Specific requirements:
- essential: a strong background in programming using Python, R, and others
- solid understanding of structural biology, especially crystallography
- experience/ interest in molecular dynamics simulations, docking and computational ligand discovery; data analysis using KNIME/ pipeline pilot

Please direct your questions and application package including a cover letter, current CV, and 3 letters of reference to: Dr. Marcus Fischer (marcus.fischer@stjude.org) by January 11th, 2021.

Online application deadline is in March for admission to the Fall Semester starting in August 2021.

Relevant papers include:
• Darby et al. (2019). Water Networks Can Determine the Affinity of Ligand Binding to Proteins. *JACS* 141, 15818-26.
• Balius et al. (2017). Testing inhomogeneous solvation theory in structure-based ligand discovery. *PNAS* E6839-46.
• Fischer et al. (2015). One crystal, two temperatures: cryocooling penalties alter ligand binding to transient protein sites. *Chembiochem* 1560-64.
• Fischer et al. (2014). Incorporation of protein flexibility & conformational energy penalties in docking screens to improve ligand discovery. *Nature Chemistry* 6, 575-83.

More info at: https://www.stjude.org/fischer