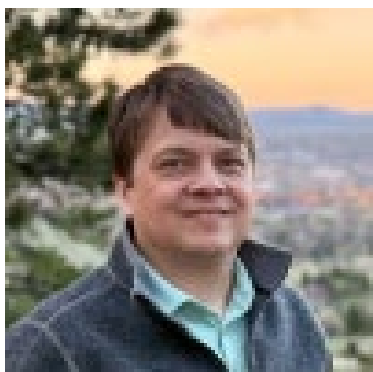


MICHAEL SHIRTS

Professor of Chemical and Biological Engineering
University of Colorado



Thursday, November 13th

10:30 AM – 11:30AM

Steele 006

“Free energy calculations and molecular force fields in modern pharmaceutical design?”

“Why can’t we engineer drugs on a computer yet? And what can be done about it?”

Abstract: The design of airplanes, bridges, chemical plants, and computer chips is aided significantly by modern computational tools. Design of novel molecules, however, is done primarily by trial-and-error. A prime example is the pharmaceutical industry, where the complexity of biomolecular interactions has greatly limited our ability to model and design effective small molecule drugs. This means drug design has remained somewhat of a black art, relying on many ad hoc assumptions and on the intuitive insights of experienced medicinal chemists. What are the barriers that must be overcome in order to model drug-ligand binding affinities, solubilities, partitioning into delivery formulations and polymorph stabilities effectively? Is there a hope to change the process of designing drugs with high efficacy, good bioavailability and a specific mode of action from a trial-and-error art to a nanoscale engineering process using high-quality, reliable modeling?

In my talk, I will discuss the barriers above, some of the successes that are emerging in the field and describe research in the Shirts group on modeling the noncovalent interactions of small molecules with sufficient reliability and efficiency to have a place in the modern pharmaceutical workflow. In particular, I will discuss approaches we are developing to predict binding affinities of small molecules to proteins and develop sufficiently quantitative force fields for these molecules, all of these as part of open science, academic/industry collaborative efforts.

Bio: Dr. Shirts is a Professor of Chemical and Biological Engineering at the University of Colorado Boulder. He works on computational soft matter problems ranging from drug design to membrane separations, with a special emphasis in developing tools to make molecular simulation more robust, predictive, and reliable. He was an undergraduate at Harvard and received a PhD from Stanford, where he was a Fannie and John Hertz Fellow and helped start Folding@Home, the distributed science project for protein biophysics. He also helped found the Open Force Field Initiative, an open science, industry-academic joint effort to design better tools for force field parameterization and is a founder and managing editor of the open-access Living Journal of Computational Molecular Science. He has received awards including the NSF CAREER and the AIChE CoMSEF Impact award.