Postdoctoral Position in Biomolecular Simulation – Available Immediately

Join the group of Prof. Daniel M. Zuckerman, which is working to push the limits of statistical-mechanics-based computations for biomolecules and systems biology. Our work focuses on the role of fluctuations in the behavior of proteins and their interactions.

The group is interested in binding and allostery, machine-like behavior of biomolecules, drug design, as well as stochastic modeling of signaling networks. We are therefore attacking key technical problems in the field: simulation methods for equilibrium and non-equilibrium sampling of protein and protein-network dynamics, free-energy/binding-affinity estimation, and flexible docking. The group has a long history of developing new algorithms, software, and databases, including multi-trajectory parallel methods, multi-scale methodology for combining coarse and detailed models, and the Ensemble Protein Database which makes available structure sets with large fluctuations. Further details are on the group website: www.ccbb.pitt.edu/Zuckerman

The Zuckerman group is part of the University of Pittsburgh’s Department of Computational & Systems Biology which offers breadth and depth perhaps unsurpassed in the field, and is integral to a top-ranked medical school.

Start Date: Negotiable.

Salary: Competitive and commensurate with experience. Typically based on NIH guidelines.

Appropriate Background: PhD in Physics, theoretical Chemistry, Chemical Engineering, Biophysics or related field. Must have strong knowledge of statistical mechanics, molecular simulation, and computer programming.

To apply: Email your CV to Prof. Zuckerman: ddmmzz@pitt.edu. In your cover note, indicate the particulars of your background which make you a suitable candidate. Also indicate your primary future research interests. If you have applied before, please write again to indicate you are renewing your application.