

Faculty of Computer Science 2007–2008 Seminar Series

Applying Combinatorial Rigidity to the Mystery of Protein Allostery

By

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A protein is allosteric if binding a ligand at one site affects how another ligand binds at a different site, and this effect cannot be explained by overlap of the sites or steric collisions between the ligands. Allosteric proteins are "interesting" for several reasons, such as:

• Allostery regulates many functions in the body. For example, allostery is what causes hemoglobin to transfer oxygen from the lungs to other locations.

- Most instances of allostery are not understood.
- Understanding allostery can help drug design.

My interest is piqued by the second reason listed. Whiteley hypothesized that changes in rigidity / flexibility can explain some instances of allostery.

In this talk I will cover a combinatorial technique for exploring rigidity / flexibility of proteins. I will present a model, explain the mathematics behind it (and some of the problems with the math), explain how to convert a protein to this model, and discuss the issues that hydrogen bonds present in this model. I will then illustrate the algorithm used to compute rigidity in this model. Finally, I will explore the interesting topic of finding allosteric effects that are caused by changes in rigidity / flexibility, and computational tricks (both completed and in progress) to do this.

