Examensarbete

Computational modeling of the type III secrection system

Many biological processes are controlled by large multi-component protein assemblies, the size and complexity of which typically precludes the determination of their highresolution structures. Yet, for these systems ample non-structural data is typically available providing a wealth of lower resolution information. Our goal is to use high-resolution structural modeling techniques guided by constraints taken from lower resolution experimental data to aenerate models of structural important biological protein assemblies for which high resolution structural determination is unfeasible.



In this project you will work on modeling a large protein system from pathogenic bacteria, the type III secretion system.

Modeling the type III secretion system assembly

Our goal is to determine the molecular architecture of the type III secretion system (T3SS), T3SS is an essential component for the virulence of pathogenic Gram-negative bacteria, such as Salmonella and Chlamydia. This macromolecular assembly comprises more than 20 conserved proteins that form a series of ring-like structures and a needle-shaped protrusion, which allows the transport of proteins into a host cell. Our goal is to generate a high-resolution model of the structural foundation of the T3SS by modeling its homo-oligomeric rings and filaments. Such a model would provide an unprecedented view of the molecular architecture of T3SS by visualizing the placement of its components within the assembly as well as interactions between these components.

In this thesis project you will develop a computational method to generate a highresolution model one of the components of the type III secretion system. In this master thesis project you will learn:

- I) State-of-the-art structural modeling using computational tools
- II) Computer programming and how to use unix based operating system in research.
- III) Computational modeling of constraints from experimental data.

Don't hesitate to contact me, <u>ingemar.andre@biochemistry.lu.se</u>, for further information about the project!