Final Project Summary -Tyler Locke

Molecular Dynamics Simulation Of Surfactant Protein B Using Amber

Pulmonary Surfactant is a substance composed of mostly lipids and proteins that exists within the lungs. Its primary function is to reduce the surface tension at the air-water interface within the alveoli. Without this reduction, the surface tension would cause alveolar collapse when the lungs fully contract. This is apparent in infants who are born without fully developed surfactant, who will suffer from respiratory distress syndrome, a fatal condition if untreated.

Although surfactant is composed almost entirely of lipids(about 90 percent by mass), its four constituent proteins are vital to its function. Artificial surfactants composed of only lipids have proven to be ineffective and unable to support normal lung function. The four proteins that are present are named surfactant proteins A-D. Proteins A and D are relatively large, have experimental structures, and are mostly engaged in immune response and preventing pathogens from entering the body through this interface. Surfactant proteins B and C are both vital to surfactant function and its structural properties. Although their exact methods of action are not known, these proteins facilitate the rapid restructuring of the surfactant lipid layer that occurs when the lungs expand and contract.

This investigation will focus on surfactant protein B(SP-B). This protein is particularly interesting because it is relatively small and extremely hydrophobic, making it very difficult to isolate and study. As such, there is no experimental structure for SP-B. In order to study this protein, models are created using a combination of experimentally determined fragments(mini-B!) and creating secondary structure based on that of a related protein(homology modelling!). I will be using one of these models to simulate a molecule of SP-B to investigate how its structure differs from the model.

For this I will be using the AMBER and VMD molecular dynamics programs to run and visualize this simulation based on several input files. I will be using bash scripts to run these simulations on the research computing cluster, and python to analyze the data from the output files and create visuals for my paper.

By the end of this project, I would like to have run at least one molecular dynamics simulation to gather some data and get a better idea of the structure of SP-B. This will put me in a good place to continue this project through the summer and hopefully produce some new knowledge.