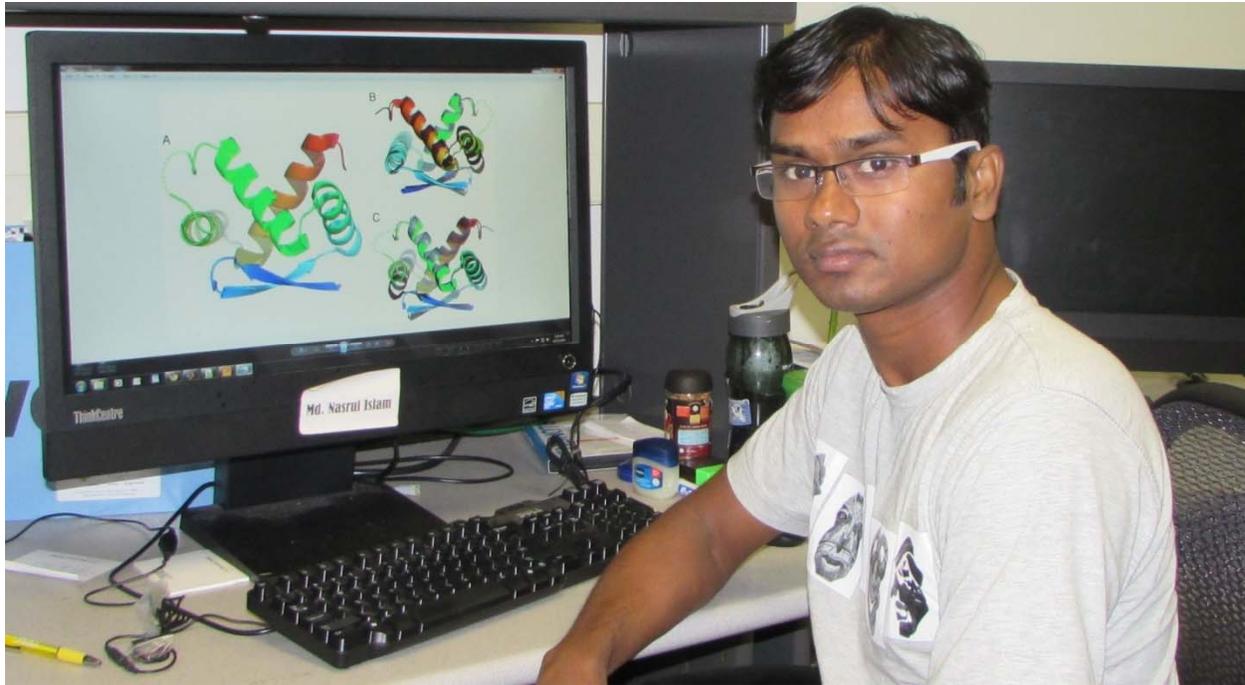


Research Summary of Graduate Student of Hoque-Lab:  
Md Nasrul Islam



I am Md Nasrul Islam, a graduate student of computer science in the University of New Orleans. I am pursuing the MS in Computer Science degree with research option. My research area is Bioinformatics and I am working under the supervision of Dr. Hoque in Hoque lab.

In today's knowledge-based society, Bioinformatics has attained a very crucial position as a research discipline, promising potentials of significantly improving human life facilitating better understanding of biological phenomena. It is a multidisciplinary field where the computer scientists provide biologist critical computational tools to study genomics, proteomics, medicine and many more to mention. Proteomics studies functions and structures of protein. It requires processing and analyzing sea of data. During last several decades' biological data has rapidly increased in a level, reaping the maximum benefits of this data using traditional experimental tools is not possible. Therefore, development of high throughput computational models that may extract useful information from this data within reasonable time becomes increasingly demanding and important. My specific research area is **prediction of secondary structure of protein**. Proteins are the most versatile macromolecules in living organisms and play significant roles essentially in all biological processes. However, the function of protein depends mainly on its 3D structure. This overall 3D structure of protein is a combination of three different local structures, commonly known as secondary structure. Proteins are large biological polymers composed of single or multiple chains of amino acid residues. My research goal is to computationally predict the secondary structure of each amino acid residue from the amino acid sequence. We have taken the challenge to break the current accuracy level of existing secondary structure prediction methods. The current accuracy level has been stuck at around 80% for last five decades. However, protein structure is not rigid, rather it may flex or twist yielding new three dimensional structure. Different structures of same

protein are known as conformation. Such flexibility enables proteins to perform a wide array of functions. I am also working of protein angle fluctuation prediction from sequence. Better angle fluctuation model will help better analysis of protein function.

In my research I use machine learning tools such as neural network, random forest, support vector machine etc. or statistical methods, such as least square, along with highly efficient heuristic approach such as genetic algorithm. Any significant success in my research may help to identify the causes of many critical diseases such as cancer, type2 diabetes, Parkinson's disease, Alzheimer's disease and many more. It will also contribute to the development of current state of machine learning approaches.

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