Research Summary of Graduate Student of Hoque-Lab:

Christian Winkler

I am Christian Winkler, a graduate student of Information Technology and Systems Management at Salzburg University of Applied Sciences. During my exchange semester at the University of New Orleans, I am working on my master's thesis in the field of bioinformatics under the supervision of Dr. Hoque.

My research focus aims to improve accuracy of profile-Hidden Markov models in protein family prediction, by extending the scoring-algorithm with predicted secondary structure.

An HMM is a statistical model for joint sequences of internal states and associated emission, both represented by a final set of symbols. HMMs allow for the prediction of the most probable sequence of hidden states given a sequence of emitted symbols. In bioinformatics, they are used for the modelling of sequences of amino acids representing a protein and corresponding HMMs thus represent the typical (most probable) such sequences belonging to a functional family of proteins. While the primary structure of a protein is defined as its raw sequence of amino acids, local spatial formations make up for the so-called secondary structure. As compared to primary, the secondary structure is relatively stable under evolution. This level of information has great importance for the actual composition of the tertiary and quaternary structure of the involved proteins as it is not immediately apparent from their primary structure and thus qualifies for improving solely sequence.

The secondary structure information will help in the non-high-throughput case of protein sequence annotation. In this scenario, the researcher usually has a lot of information about more or less conserved parts in the multiple sequence alignment albeit there might only be weak statistical evidence for solely sequence based scoring. Adding secondary structure in structurally well conserved parts of the alignment is thus expected to improve the performance of the HMM significantly.