

Presents the Spring 2014 EECS Seminar Series

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“A New Multiple Protein Sequence Alignment Method”
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ABSTRACT

Protein sequence alignment is a basic tool for bioinformatics research and analysis. It has been used essentially in almost all bioinformatics tasks such as protein structure modeling, gene and protein function prediction, DNA motif recognition, and phylogenetic analysis. We designed and developed a new method, MSACompro, to synergistically incorporate predicted secondary structure, relative solvent accessibility, and residue-residue contact information into the currently most accurate posterior probability based MSA methods to improve the accuracy of multiple sequence alignments. To the best of our knowledge, applying predicted relative solvent accessibility and contact map to multiple sequence alignment is novel. The rigorous benchmarking of our method to the standard benchmarks (i.e. BALiBASE, SABmark and OXBENCH) clearly demonstrated that incorporating predicted protein structural information improves the multiple sequence alignment accuracy over the leading multiple protein sequence alignment tools without using this information, such as MSAProbs, ProbCons, Probalign, T-coee, MAFFT and MUSCLE. And the performance of the method is comparable to the state-of-the-art method PROMALS of using structural features and additional homologous sequences by slightly lower scores.

BIOGRAPHY

Dr. Xin Deng is currently a research scientist with LexisNexis Healthcare. She graduated from University of Missouri-Columbia with a Ph.D in computer science, after five plus years research in the field of Bioinformatics. At Mizzou her projects involved designing and applying computational methods and data mining technologies to solve some essential bioinformatics problems, such as protein sequence and profile alignment, fold recognition, protein structure prediction, etc. Today, she is going to share some of her experiences during her PhD study.