UNIVERSITY OF DELAWARE

CENTER FOR BIOINFORMATICS & COMPUTATIONAL BIOLOGY

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BIOINFORMATICS SEMINAR

JIA REN

PhD Student, Department of Computer & Information Sciences
UNIVERSITY OF DELAWARE

IMPROVE LARGE-SCALE AUTOMATIC INFORMATION EXTRACTION FOR BIOMEDICAL KNOWLEDGE DISCOVERY AND CURATION

Numerous efforts have been made for developing text-mining tools to extract information from biomedical text automatically. They have assisted in many biological tasks, such as database curation and hypothesis generation. Text-mining tools are usually different from each other in terms of programming language, system dependency and input/output format. In this talk, I will briefly describe the iTextMine system with an automated workflow to run multiple text-mining tools on large-scale text for knowledge extraction. To improve result quality, the system contains several post-processing steps to filter, evaluate, and aggregate the extracted relations. A confidence module with state-of-art deep learning methods is developed to assign confidence scores for relations extracted by rule-based text-mining tools.

RITA HAYFORD

PhD Student, Department of Computer & Information Sciences
UNIVERSITY OF DELAWARE

USING AN INTEGRATED BIOINFORMATICS APPROACH TO UNDERSTAND THE ROLE OF INTRINSICALLY DISORDERED REGIONS IN CANCER ASSOCIATED PROTEINS

Cancer is the second leading cause of death in the US and worldwide. According to the American Cancer Society Researchers, over 1.7 million new cases are expected to be diagnosed with cancer in the year 2019, and about 606,880 people are likely to die of cancer. There has been a global burden to help to reduce cancer, and understanding the molecular mechanisms underlying it has been challenging. Intrinsically disordered protein regions (IDRs) are protein regions that do not fold into stable secondary or tertiary structure under physiological conditions. IDRs have been implicated in many diseases such as cancer, cardiovascular and neurodegenerative diseases. Given that IDRs provide structural plasticity and functional diversity, we hypothesize that proteins associated with cancer contain disorder regions which play a critical role in regulating their function. The first step for this analysis is data collection. Our goal is to integrate data from relevant resources to help determine the function or regulation of disordered proteins involved in cancer. I will discuss the workflow for collecting IDRs in cancer-related proteins, and workflow to map potential regulatory features such as Post-translational modifications (PTMs) from the individual proteins to the IDRs.

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