UNIVERSITY OF DELAWARE

CENTER FOR BIOINFORMATICS & COMPUTATIONAL BIOLOGY

CBCB SEMINAR 10/5/2020

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BIOINFORMATICS SEMINAR

XIHAN QIN

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CAPTURING MUTATIONS AND THEIR IMPACT IN ALZHEIMER'S DISEASE VIA TEXT MINING METHODS

TextAlzheimer's Disease (AD) is a progressive neurodegenerative disorder characterized typically by memory problems, and different levels of impairment of cognitive skills, among other symptoms. It is one of the leading causes of death in the US. Its underlying molecular mechanism is not yet fully understood, and there is no effective treatment available. With the aim of helping researchers in the field increase their pace of discovery of molecular mechanisms and therapeutics, we are developing a text mining tool to detect mutation and corresponding impact to AD and other neurodegenerative diseases. DiMex is a text mining tool, developed in Dr. Shanker's lab, which extracts gene mutation to cancer associations. We are extending and enhancing DiMex to identify mutation and disease associations in AD. The association of a gene-mutation-disease may be of different nature, the mutation could affect some property of the protein product (e.g., biological process it is involved), could serve a biomarker role, affect disease progression, or drug response, among others. Thus, we are evaluating what aspects of the disease impacted by the mutation are relevant to capture, with the aim of developing text mining methods to automatically detect and extract these from the literature. We will integrate all text mining outputs into iTextMine, an integrative text mining framework to visualize text mining entities and relations relevant to proteins/genes with direct links to the evidence.

JOSE DANIEL CHAZI CAPELO

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WHOLE-GENOME METAGENOMIC ANALYSIS OF THE GUT MICROBIOME IN HORSE KEEPERS

The role of the gut microbiome in health and disease has been growing in recent years. In horses, the gut microbiome has been recently linked to its metabolic status, whose some bacterial communities have been associated with health issues like obesity. Previous techniques such as 16S ribosomal RNA has contributed to reporting these findings. However, this technique based on amplicon sequencing has limitations such as its sequences come from only a single region of the bacterial genome. On the other hand, sequencing broad regions of the genome such as the whole-genome microbial sequencing do, is emerging as an alternative to providing a more detailed analysis of the species present in the microbiome as well as an increased detection of diversity and increased prediction of genes. This additional information can help to understand the impact of these microbial communities on the health and well-being of the horse. Thus, the aim of this research is to identify differences in microbial composition and functional genes in hard, medium, and easy keepers. These differences may lead to identifying important metabolic pathways involved in a horse-related to keeper status.

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