



CBCB
SEMINAR
09/16/2019

3:30 PM
DELAWARE
BIOTECHNOLOGY
INSTITUTE
Room 102

bioinformatics.udel.edu

BIOINFORMATICS SEMINAR

RIZA LI

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

PREDICTIVE MODELING OF LONG-TERM TYPE 2 DIABETES COMPLICATIONS USING PATIENT DATA IN ELECTRONIC HEALTH RECORDS

Diabetes mellitus (DM) is a chronic condition that affects millions of people. As of 2015 the Centers for Disease Control and Prevention (CDC) estimated 30.3 million people of all ages (~9.4% of the US population) with diabetes. Out of the 30.3 million, 7.2 million (23.8%) were not aware of having diabetes due to the slow progression of the disease. In the long-term, DM gives rise to many health-related complications. Given the increasing number of people living with this disease and the escalating cost of care, the need for personalized care has never been higher. Predictive modeling to assess the risk of DM-related complications is becoming increasingly significant in clinical research. I will discuss the workflow for developing a computational model that will predict the risk of developing complications and experiencing adverse events specifically for patients with Type 2 Diabetes by utilizing electronic health records (EHRs) from Christiana Care. EHRs are a reliable source of longitudinal observations for monitoring the progression of chronic diseases in clinical practice. EHRs also provide large quantities of information regarding a patients' medical history including symptoms, examination findings, test results, prescriptions and procedures.

KELLY MULHOLLAND

PhD Student, Department of Animal and Food Sciences
UNIVERSITY OF DELAWARE

BIOMESEQ: A TOOL FOR THE CHARACTERIZATION OF ANIMAL MICROBIOMES FROM METAGENOMIC DATA

The severity and spread of many human and animal diseases are associated with specific bacterial and viral agents within microbiomes. Recent studies attempting to characterize the respiratory microbiome of poultry have focused primarily on bacteria, however elucidating the complex microbial interactions that result in disease requires the characterization of the viruses, bacteria, bacteriophage and fungi present in the respiratory tract of healthy and diseased flocks. The lack of comprehensive bioinformatics workflows and viral genome databases have limited efforts to characterize the avian virome. To address this, we developed a fully automated bioinformatics workflow along with comprehensive microbial databases to detect and quantify the microbial composition from next-generation sequencing data. The databases include host-specific viral, bacteriophage, bacterial and fungal sequences. The workflow and databases are packaged into a software called BiomeSeq which we utilized to detect and quantify composition of avian microbiomes. In one study, we compared the microbial ecology of the respiratory tract of a healthy commercial broiler flock to a flock clinically diagnosed with avian respiratory disease complex. BiomeSeq is implemented as a user-friendly Docker container that can be employed to facilitate future investigations aimed at characterizing microbiomes of various species.



College of Engineering
CENTER FOR BIOINFORMATICS &
COMPUTATIONAL BIOLOGY