



**CBCB
SEMINAR
10/28/2019**

**3:30 PM
DELAWARE
BIOTECHNOLOGY
INSTITUTE
Room 102**

bioinformatics.udel.edu

BIOINFORMATICS SEMINAR SACHIN GAVALI

PhD Student, Department of CIS UNIVERSITY OF DELAWARE

iPTMnet: A CASE STUDY TOWARDS FAIR DATA PRINCIPLES

iPTMnet is an integrated bioinformatics resource for post-translational modification (PTM) network discovery and analysis. It integrates text mining results from eFIP and RLIMS-P, experimentally observed PTMs from a set of curated databases, variants affecting these PTMs from Biomuta and protein as well as proteoform data from Protein Ontology (PRO) to facilitate proper representation, annotation, and comparison of PTMs within and across species. In its present form, the data in iPTMnet is accessible only through the website. This talk will discuss how the latest developments in web technologies such as Docker, Python, and Rust were used to enhance the ability of machines to automatically consume the data from iPTMnet, facilitating easier integration of the data into existing bioinformatics pipelines.

JUNIPER LAKE

PhD Student, Department of AFS UNIVERSITY OF DELAWARE

INCREASED EXPRESSION OF LIPID METABOLISM GENES IN EARLY STAGES OF WOODEN BREAST LINKS MYOPATHY OF BROILERS TO METABOLIC SYNDROME IN HUMANS

Wooden breast is a muscle disorder affecting modern commercial broiler chickens that causes a palpably firm pectoralis major muscle and severe reduction in meat quality. The objective of this study was to identify early molecular signals in the wooden breast transcriptional cascade by performing gene expression analysis on the pectoralis major muscle of two-week-old birds that may later exhibit the wooden breast phenotype by market age at 7 weeks. Biopsy samples of the left pectoralis major muscle were collected from 101 birds at 14 days of age. Birds were subsequently raised to 7 weeks of age to allow sample selection based on the wooden breast phenotype at market age. RNA-sequencing was performed on 5 unaffected and 8 affected female chicken samples, selected based on wooden breast scores (0 to 4) assigned at necropsy. Of the 60 differentially expressed genes that were identified, 26 were previously demonstrated to exhibit altered expression or genetic polymorphisms related to glucose tolerance or diabetes mellitus in mammals. Additionally, 9 genes have functions directly related to lipid metabolism and 11 genes are associated with adiposity traits such as intramuscular fat and body mass index.

ZIDA FAN

MS Student, UNIVERSITY OF DELAWARE

A SCALABLE WEB PORTAL FOR LARGE BIOLOGICAL ONTOLOGY

Ontologies are increasingly being used to define the basic terms and relations in biological domains, often as the foundation for search, integration and exchange of biological data. How to present ontological information and make it easy for users to search and navigate has been a challenge for large and complex ontologies. In this work, we explore building a scalable web portal for large ontologies using the Protein Ontology (PRO) as an example. This work focuses on the development of a new entry page for PRO website using RESTful APIs, SPARQL query and Virtuoso as the backend. Compared to the previous relational database backed PRO entry page, the new entry page displays the hierarchy and basic information about a given PRO term together, thus providing the user with both global and local views simultaneously. In addition, we also give the user freedom to control what additional information to show. The design of new PRO entry page and the user experience learned from this work will be generally applicable to other large ontologies.



College of Engineering
CENTER FOR BIOINFORMATICS &
COMPUTATIONAL BIOLOGY