CBCB SEMINAR 2/10/2020

3:30 PM DELAWARE BIOTECHNOLOGY INSTITUTE Room 102

bioinformatics.udel.edu

BIOINFORMATICS SEMINAR
RYAN MOORE

PhD Student, Department of PLSC UNIVERSITY OF DELAWARE

INTEINFINDER: AUTOMATED INTEIN DETECTION FROM LARGE PROTEIN DATASETS

Inteins are mobile genetic elements found within the coding regions of genes. The protein equivalent of introns, they are transcribed and translated along with their flanking protein fragments (exteins) before splicing out from the precursor protein. Whereas inteins were previously thought to be parasitic genetic elements providing no benefit to the host organism, recent studies suggest that inteins may impact host ecology, providing a selective advantage to the organism in which they reside by exhibiting post-translational control on extein sequences. For example, evidence suggests that inteins in giant virus genomes are involved in exclusion processes during coinfection by related viruses. Inteins can also be used to infer patterns of gene flow within groups of microorganisms. In addition to their ecological interest, inteins are also used in a variety of biotechnology applications including using split inteins to regulate protein function. Given the increased interest in inteins, more studies are focusing on identifying inteins within genomes or other large protein datasets. Though many studies follow a similar workflow (e.g., collecting a reference set of inteins, searching the sequences of interest against this reference set, then validating potential inteins), to date, the process of screening peptide sequences for the presence of inteins has not been consolidated into a single, automated pipeline. To address this problem, we introduce InteinFinder, a standardized, automated pipeline for identifying, cataloging, and removing inteins from peptide sequences. We used InteinFinder to identity inteins in a set of over 125,000 metagenomic viral contigs from a variety of environments. Environments generally considered more extreme (thermal springs, saline and alkaline environments, etc.) were found to harbor proportionally more inteins than marine and freshwater environments, potentially reflecting the intense competition and high rates of horizontal gene transfer typical of extreme habitats. InteinFinder and associated documentation are freely available at https://github.com/mooreryan/InteinFinder.

HEIDI VAN EVERY

PhD Student, Department of AFS UNIVERSITY OF DELAWARE

USE OF HIGH-THROUGHPUT DATA TO CHARACTERIZE POST HATCH HEPATIC DEVELOPMENT IN THE MODERN BROILER CHICKEN

Artificial selection of the modern broiler chicken for production characteristics has led to dramatic changes in phenotype over the last half century, yet the impact of this selection on metabolic and molecular mechanisms is poorly understood. The first three weeks post-hatch represent a critical period of adjustment, during which the yolk lipid is depleted & the birds transition to reliance on a carbohydrate-rich diet. The liver is of prime interest in helping to elucidate the metabolic factors driving phenotypic changes, as the major organ involved in macronutrient metabolism, nutrient allocation, and regulation of many systemic processes. This longitudinal study explores hepatic development over this crucial post-hatch transitional period, from the perspective of the transcriptome and metabolome. For this initial comparison, we focus on Day 4 versus Day 20 post hatch, and integrate the datasets at the pathway level to gain insights into differences in carbohydrate and lipid metabolism.