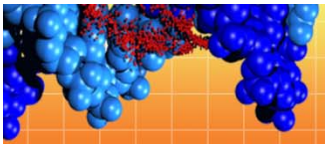


CENTER FOR BIOINFORMATICS & COMPUTATIONAL BIOLOGY

BIOINFORMATICS 2014 FALL SEMINAR SERIES

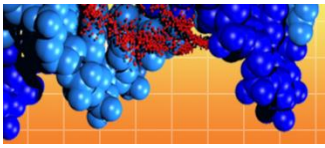
Hosted by: Department of Computer and Information Sciences,
Department of Electrical and Computer Engineering &
Center for Bioinformatics and Computational Biology
http://bioinformatics.udel.edu/seminars

MONDAY, September 22, 2014
DBI Room 102

More than skin deep: Exploring the connection between bacterial community diversity & pathogenic *E. coli* on pre-harvest cattle hides

3:30pm – Ryan Moore
PhD Candidate
Bioinformatics & Systems Biology

ABSTRACT: In the United States, Shiga toxin-producing *Escherichia coli* (STEC) cause over two hundred thousand illnesses and approximately 20 deaths each year. Human infection generally occurs through the ingestion of contaminated beef, causing diarrhea, hemorrhagic colitis, and, in some cases, hemolytic uremic syndrome. It is generally accepted that commensal indigenous microflora mitigate the proliferation of invading pathogens through predation, nutrient competition, antagonism and the excretion of antimicrobial compounds. *Escherichia coli* O157:H7, in particular, has been shown to survive at greater proportion in low diversity conditions. In soil and manure environments, microbial diversity is negatively correlated with the invasion of *E. coli* O157:H7 and *Listeria monocytogenes*. These studies suggest that indigenous microbial populations interact, often negatively, with pathogen populations. However, this phenomenon is widely unexplored on the pre-harvest cattle hide. In order to determine if there was a connection between STEC presence and bacteria diversity, we preformed high throughput 16S rRNA sequencing on hide samples positive and negative for STEC. Preliminary results indicate that STEC presence is associated with slight changes in 16S community profiles, including OTUs specific to infection status. Furthermore, STEC presence appears to be negatively correlated with community richness. These results indicate that STEC presence may have an impact on the diversity of pre-harvest cattle hide. Given these encouraging results, it is possible that microbiome composition may be important to developing better quantitative microbial risk assessment models for STEC within the beef food supply chain.



CENTER FOR BIOINFORMATICS & COMPUTATIONAL BIOLOGY

BIOINFORMATICS 2014 FALL SEMINAR SERIES

Hosted by: Department of Computer and Information Sciences,
Department of Electrical and Computer Engineering &
Center for Bioinformatics and Computational Biology
http://bioinformatics.udel.edu/seminars

MONDAY, September 22, 2014
DBI Room 102

From Metagenomes to Marker Genes: Using Informatics and Genomics to Characterize Phage Populations

4:00pm – Dan Nasko
PhD Candidate
Bioinformatics & Systems Biology

ABSTRACT: You may have heard that there are an estimated 10^{31} viral particles on Earth, but take a moment to consider the magnitude of this number. This is a huge number. More impressive still is the estimated 48-hour turnover rate globally for these particles, meaning ca. 4.6×10^{26} viruses will burst from a cell before you will have finished reading this paragraph.

Cellular microbes dominate marine systems, with viruses playing key role in host mortality and nutrient cycling. These virus-host interactions are critical to the functioning of the Chesapeake Bay, a diverse and anthropogenically impacted estuarine ecosystem. Despite their importance the ecology and diversity of viruses in the environment remains poorly understood. From a metagenomics and informatics perspective bacteriophage (viruses that infect bacteria) present a unique opportunity. With a typical genome size of 100 kilobases or less, it is conceivable to assemble complete phage genomes from environmental shotgun metagenomes.

This project explored the biological potential existing within Chesapeake Bay virioplankton and assessed the utility of deep sequencing (Illumina) and long-read technology (PacBio) for uncovering the biological characteristics of unknown viruses. In doing so we have now sequenced over 18 billion base pairs of shotgun viral DNA (> 6 human genomes worth), requiring tens of thousands of CPU hours to analyze.

An important component of this work was to utilize two genes critical to genome replication, DNA polymerase A and ribonucleotide reductase (RNR, to uncover the morphology and life cycle characteristics within the virioplankton