



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 15, 2014
DBI Room 102

What It's Really Like To Be A Google Intern
3:30pm – Yifan Peng
PhD Student
Computer & Information Sciences

ABSTRACT: If you have ever seen "The Devil Wears Prada", you know that sometimes working as an intern means fetching coffee, making copies, and doing the busy work no other full-time employee feels like doing. Other times, you don't. In this talk, I will share my experiences at Google this summer, where internships are highly sought after positions. I will talk about the interview and conversion process, the project I did, the development skills I learned, and of course the perks. Instead of talking about myself, I am more than willing to turn the talk into a conversation and answer as many questions as possible. So if you are interested in the Google internship next year or wish to become a software engineer in the near future, curiosity will be satisfied.

**Mining Metagenomes for Mycological Relevance - Finding Fungal
Functions within Environmental Samples**

4:00pm – Joshua R. Herr, PhD
Department of Microbiology & Molecular Genetics
Michigan State University
<http://joshuaherr.com>

ABSTRACT: It has long been understood that fungi contribute to many key ecosystem processes. Despite their important ecological roles, there is a paucity of information regarding their taxonomic and functional diversity in comparison to other Eukaryotic organisms. This is due largely to the fact that many fungi are unculturable, lack known sexual structures, and are known only by their nucleotide fingerprints. Next-generation sequencing technologies have revolutionized our abilities to use sequence data to address ecological and physiological questions, but identifying both taxonomic and functional diversity of the fungi has been hampered by technical hurdles. In this presentation I will outline recent technical advances in metagenome assembly and how we can use computational algorithms and data analysis strategies to identify the fungal component of environmental samples. By "sifting" through large publically available datasets and identifying fungal nucleotide sequences derived from metagenomes, I provide a framework for taxonomic and functional diversity of the fungi using rDNA amplicon, whole-genome-shotgun, and meta-transcriptomic sequencing data.