



BIOINFORMATICS 2015 SPRING 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, March 16, 2015

3:30pm

DBI Room 102

**Beyond single pathogens: how the human microbiome
impacts health and disease.**

Mihai Pop, PhD

Associate Professor

Computer Science Department &

Center for Bioinformatics and Computational Biology

University of Maryland

<http://www.cbcb.umd.edu/~mpop/>

Abstract: Metagenomics studies aim to characterize microbial communities through the direct sequencing of their collective DNA. While initial studies have been focused on simply extending existing approaches developed in microbial genomics, recently scientists have started to explore the potential of metagenomic data to provide biological insights not apparent in isolate genomes. During my talk I will provide an overview of the field and meta-analyses made possible by looking at communities as a whole, and describe some recent results from my lab related to human health.

Bio: Dr. Pop is an associate professor in the Department of Computer Science and the Center for Bioinformatics and Computational Biology at the University of Maryland, College Park (UMCP). Dr. Pop received his Ph.D. in Computer Science at Johns Hopkins University where he focused on algorithms for computer graphics and Geographic Information Systems (GIS) applications. He then joined The Institute for Genomic Research (TIGR) as a Bioinformatics Scientist, where he was responsible for the development of genome assembly algorithms. During this time, Dr. Pop participated in a number of bacterial and eukaryotic genome projects including important human pathogens such as *Bacillus anthracis* and *Entamoeba histolytica*. Since joining the University of Maryland, Dr. Pop has continued to develop novel approaches for genome assembly and analysis, and has developed extensive expertise in the analysis of metagenomic data. His lab has developed a number of widely used open-source software tools, such as the assembly suite AMOS, the NGS aligner Bowtie, the taxonomic classifier Metaphyer, and the metagenomic assembly package MetAMOS. Most recently he co-lead the data analysis working group for the Human Microbiome Project and led the sub-group responsible for the assembly of the data generated in this project.