

BIOENGINEERING SEMINAR SERIES

Thursday, March 29, 2012, 12:00 - 1:00 p.m.

2240 Digital Computer Lab (DCL)

"Understanding the vertebrate microbiome by the use of Next-generation sequencing approaches"

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Abstract: The ecological relationships that have evolved between the animal host and its microbiome are, for the most part mutually beneficial. However, perturbations of the typical taxonomic structure of a microbiome can alter its ecological function leading to numerous negative influences on health and causative links have been made between perturbed microbiomes and numerous diseases and disorders. Advances in genomics and the reduction in costs associated with next-generation sequencing technologies have made it possible to query these microbiomes at an unprecedented depth of sequence. Initial studies have revealed an unanticipated level of microbial diversity in the gastrointestinal tracts of humans, non-human primates and production animals. Much of the current research in this area has focused on the diversity and broader trends that exist within and between host species and their associated microbial ecosystems, and modeling is now being used to query these relationships. Through a multi-omics approach with next-generation sequencing as the underpinning, we are finding evidence that modeling can predict system health.

Biography: Bryan White is currently a Professor of Animal Sciences in the Institute for Genomic Biology, and Director of Microbiome Projects in the Division of Biomedical Sciences at the University of Illinois. He received his Bachelor of Science at Virginia Wesleyan College and his Ph.D. in Microbiology from the Medical College of Virginia, and was a NIH Postdoctoral Fellow in the Department of Oral Biology at the University of Michigan. His major research interests are in using microbial genomics, metagenomics, and microbial ecology to understand host-microbe interactions. He uses human, non-human primates, mice and production animals as models of health and disease.