



181 Longwood Avenue Boston, Massachusetts 02115-5804 **Department of Medicine** *Channing Division of Network Medicine*

Channing Microbiome Seminar

February 16st (Friday), 2018, 1-2pm @ 5th-floor conference room



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Longitudinal Computational Microbiome Methods: Identification, Modeling, and Classification in a Pediatric Lung Transplant Cohort

Complications after lung transplant are common despite advancements in organ preservation, surgical techniques, and allograft surveillance. For children, a vulnerable population, the 5 and 10year survival for lung transplants are only 52% and 29%, respectively. Infections are the most common cause of mortality (>30% of deaths) after transplantation. Understanding the role of the microbiome in transplantation is crucial in improving outcomes. In terms of microbiome characterization, methods achieving high precision can lack sensitivity in some applications, and vice versa. As for longitudinal studies, only identifying differential features between two phenotypes does not provide sufficient information to determine whether a change in the relative abundance is short-term or continuous. However, accurate assessment of how the microbiome changes over time is a powerful approach to classify the contribution of the microbiome to disease states and progression. In this talk, using pediatric lung transplantation as an example, I will discuss computational methods we have developed that help improve on both characterization and longitudinal microbiome analysis approaches. We have been able to (1) classify the microbial sequences with both high precision and high sensitivity using "WEVOTE", (2) identify time intervals of differentially abundant microbial features in longitudinal studies using "MetaLonDA". Using these algorithms, we were able to identify microbiome dynamics that can be suggestive of pediatric lung transplant rejection, insights that can be leveraged to improve lung transplant outcomes. I will also introduce our novel convolutional neural networks (CNN) learning architecture that effectively exploits phylogenetic structure in microbial taxa for phenotype prediction.

Hosted by Kimberly Glass

