



# BIOINFORMATICS SEMINAR

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**3:30 PM  
DELAWARE  
BIOTECHNOLOGY  
INSTITUTE**

[bioinformatics.udel.edu](http://bioinformatics.udel.edu)

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### **A Computational Approach to Characterizing Viral Communities of the Microbiome**

Microbiomes are composed of the microorganisms of a particular environment and include bacteria, archaea, fungi, protozoa, viruses and their associated genes. In poultry, several DNA and RNA viruses, interacting within the microbiome, can lead to deficiencies in immune status and overall performance. This may result in poor poultry health, which will negatively impact the poultry industry. By identifying the viral compositions within the avian respiratory tract, we can elucidate the etiology of the diseases to which they contribute. Microbiome studies have traditionally focused on identifying the bacterial component, as well-developed computational methods exist for this analysis. However, viral characterization methods remain underdeveloped. Herein, we present a workflow for identifying viral community abundance within the microbiome with the use of metagenomic next-generation sequencing data and host-specific viral genome databases. This method has been used to successfully identify viral communities in the respiratory microbiome of poultry under various conditions. By implementing this workflow and additional host-specific viral genome databases into a user-friendly interface, this tool may be used to facilitate the rapid characterization of the virome by future investigators.



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