CENTER FOR RNA BIOMEDICINE

RNA Innovation Seminar
Monday, October 2nd at 3:00pm
ABC Seminar rooms, Biomedical Research Science Building (BSRB), 109 Zina Pitcher

Maureen Sartor, PhD
Associate Professor of Computational Medicine and Bioinformatics, Medical School Associate Professor of Biostatistics, School of Public Health, Assistant Director for Graduate Education, Computational Medicine and Bioinformatics

Title:

"Using RNA-seq to study HPV-positive tumor subtypes and HPV integration in head and neck cancer"

Abstract:

RNA-seq can be used for many purposes besides differential gene and transcript expression. We have generated RNA-seq and other omics data for human papillomavirus (HPV)-positive and HPV-negative head and neck squamous cell carcinoma patients. We have used this data together with RNA-seq from the Cancer Genome Atlas (TCGA) to study expressed cancer-related mutations, the transcriptional effects of epigenomic differences by HPV-status, cell type signatures, tumor subtypes, and HPV integration. In this presentation, I will focus on how we used the RNA-seq data to identify and characterize two subtypes of HPV-positive tumors, and study HPV integration events in the host genome and their clinically-relevant effects.
The incidence of HPV-related head and neck cancer has greatly increased over the past two decades, and now represents a majority of oropharyngeal cancer cases. Integration of the HPV genome into the host genome is a common event during carcinogenesis that has clinically-relevant effects if the viral early genes are transcribed. Our findings include that HPV integration events are overrepresented in known head and neck, lung, and urogenital cancer genes, often lead to the upregulation of those genes, and that tumors with no detected HPV integration event are characterized by strongly heightened immune signatures and longer survival.