

Viral transmission during outbreaks: genomic analysis of Ebola, Zika, and mumps viruses

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Sze Conference room, D1-084

Fred Hutchinson Cancer Research Center

Light refreshments will be served; registration not necessary to attend this event



Abstract: Genomics has emerged as a powerful tool for combating viral outbreaks. In this talk, I will describe how genomic data was used to understand the evolution and spread of three viruses during recent outbreaks. First, I will present our analysis of Ebola virus sequences from the 2014–2016 outbreak in West Africa, and discuss what these genomes tell us about cross-border and individual transmission. I will then describe our efforts to characterize movement of Zika virus throughout the Americas in 2016, focusing on challenges related to low viral content in Zika samples. Finally, I will spend most of the talk discussing our recently submitted study of the 2016–2017 mumps virus outbreak in the United States, and will explain how mumps virus sequences from Massachusetts and several other states informed our understanding of disease spread at several geographic scales. In particular, we found evidence for ongoing mumps transmission in the United States, and show that pairing genomic and detailed epidemiological data reveals detailed transmission within a local community.



Contact: Trevor Bedford (trevor@bedford.io) with questions
<http://www.cidid.org>, [Webcast link](#)