**Session 5: Pipe Dreams: Analytical Methods, Bioinformatics Tools, and Pipelines**

**The CDC Domestic Influenza Surveillance System: From Pipe Dream to High Performance Reality**

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CDC’s influenza surveillance program determines and reports disease prevalence and severity indicators based on syndromic and patient case reports and conveys characteristics of circulating viruses such as genetic type and immunologic reactivity. The Influenza Division prioritizes use of clinical specimens for genetic characterization and has recently completed work to create a cloud-based, next generation sequencing (NGS) system for domestic surveillance of influenza viruses. This molecular surveillance system depends upon collaboration between three state public health laboratories that act as National Influenza Reference Centers (Wisconsin State Laboratory of Hygiene, New York State Department of Health-Wadsworth Center and California Department of Public Health) and the CDC Influenza Division. These reference center laboratories use the cloud-based system to produce and curate high quality genetic data in parallel; full genome and minor variant data is often available in as little as 2-3 weeks from date of collection of original clinical specimens. Since becoming fully operational in 2016, the system operates year-round with near 24/7 availability to provide a total of 8,000 fully curated genome sets on average per calendar year, and has provided early awareness of rapidly changing influenza A(H3N2) viruses, type B deletion mutants and zoonotic reassortants. This collaborative surveillance system ensures sustainability of virologic surveillance by providing capacity for fail-over and surge capacity and provides high quality data for integration efforts, faster than ever before. Early merging of epidemiologic indicators with molecular markers for viral antigenicity, pathogenesis, transmission and susceptibility will encourage transformation of influenza surveillance efforts to a more inclusive precision public health approach.