

5.) How can genomic epidemiology be used to track Covid-19?

Wastewater monitoring



<https://www.biodectiontechnologies.com/programs>

WEDNESDAY, JUNE 29, 2022

TUESDAY, JUNE 28, 2022



3:45 Session Break & Interactive Discussions

Interactive Discussions are informal discussions, allowing participants to exchange ideas and experiences and develop future collaborations around a focused topic. Each discussion will be led by a facilitator who keeps the discussion on track and the group engaged. The format will be in an online networking platform. To get the most out of this format, please come prepared to share examples from your work, be a part of a collective, problem-solving session, and participate in active idea sharing. Please visit the Interactive Discussion page on the conference website for a complete listing of topics and descriptions.

TABLE 1: Automated Biological Identification

Vishaka Santosh, PhD, Postdoctoral Fellow, DEVCOM Chemical Biological Center, Aberdeen Proving Ground

TABLE 2: Using Single-Molecule Sequencing Methods for Routine Bio-surveillance of Pathogens in Wastewater

David Ussery, PhD, Director ArC GEM & Professor, Biomedical Informatics, University of Arkansas for Medical Sciences

TABLE 3: Rapid Biodection Methods for Biopharma and Cellular Ag

Dave Alburty, CEO, InnovaPrep

TABLE 4: Early Warning and Forecast of Infectious Disease Outbreaks: Really or Fiction?

Willy Valdivia-Granda, Founder & CEO, Orion Integrated Biosciences, Inc.

10:00 When Boring Is Good: Limited Mutational Repertoire across Millions of SARS-CoV-2 Genomes
David Ussery, PhD, Director ArC GEM & Professor, Biomedical Informatics, University of Arkansas for Medical Sciences

There are currently more than 11 million SARS-CoV-2 genomes available, with thousands of different COVID-19 Pango lineages, although only a few major clusters. Mutational hot spots along the genome show correlations with RNA structures. We find three major conclusions: this virus has a limited mutation repertoire with few mutations that become fixed; the viral genome undergoes parallel evolution frequently; and finally, we see little genomic recombination.