

PATHOGEN GENOMICS FOR PUBLIC HEALTH: LESSONS FROM ZIKA, COVID-19 AND DENGUE

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Recent advances in pathogen genomics, coupled with developments in data science and mathematical modelling, have transformed our ability to understand and respond to infectious disease outbreaks. During the past decade, genomic surveillance has evolved from a largely research-focused activity into a central component of public health decision-making.

In this lecture, I will discuss how genomic and epidemiological data can be integrated to reconstruct transmission dynamics, identify emerging variants, quantify epidemic spread, and inform public health responses in real time. Using examples from the Zika epidemic in the Americas, the emergence and spread of SARS-CoV-2 variants during the COVID-19 pandemic, and ongoing dengue epidemics across tropical and subtropical regions, I will illustrate how analytical approaches drawn from genomics, statistics, and mathematical modelling can generate actionable insights during rapidly evolving outbreaks.

The lecture will also highlight the growing importance of international surveillance networks, capacity building, and equitable access to sequencing technologies. As infectious disease threats continue to emerge and spread across an increasingly connected world, the integration of genomics, data science, and public health will be essential for strengthening epidemic preparedness and response.