

Spread of antimicrobial resistance: genomics and modelling perspectives
Patrick Musicha^{1,2}

¹MORU Health Network, Faculty of Tropical Medicine Mahidol University

²Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine,
University of Oxford.

Abstract

Antimicrobial resistance poses one of the greatest threats to human health globally. While several potential interventions for combating antimicrobial resistance have been proposed, their prioritisation and implementation is being limited by poor understanding of the transmission dynamics of drug resistant bacteria. Classical epidemiology, including involving mathematical/statistical modelling, and whole genome sequencing have both been used to help understand the evolution and spread of antimicrobial resistance within individuals and in populations of both bacteria and humans. However, independently, these methods have their own limitations, which can be minimised if the approaches are integrated. In this talk, I will highlight results from several studies which have employed whole genome sequencing and modelling approaches, first independently and then as an integrated approach, to generate insights into the spread of antimicrobial resistance.