RESIST2 :

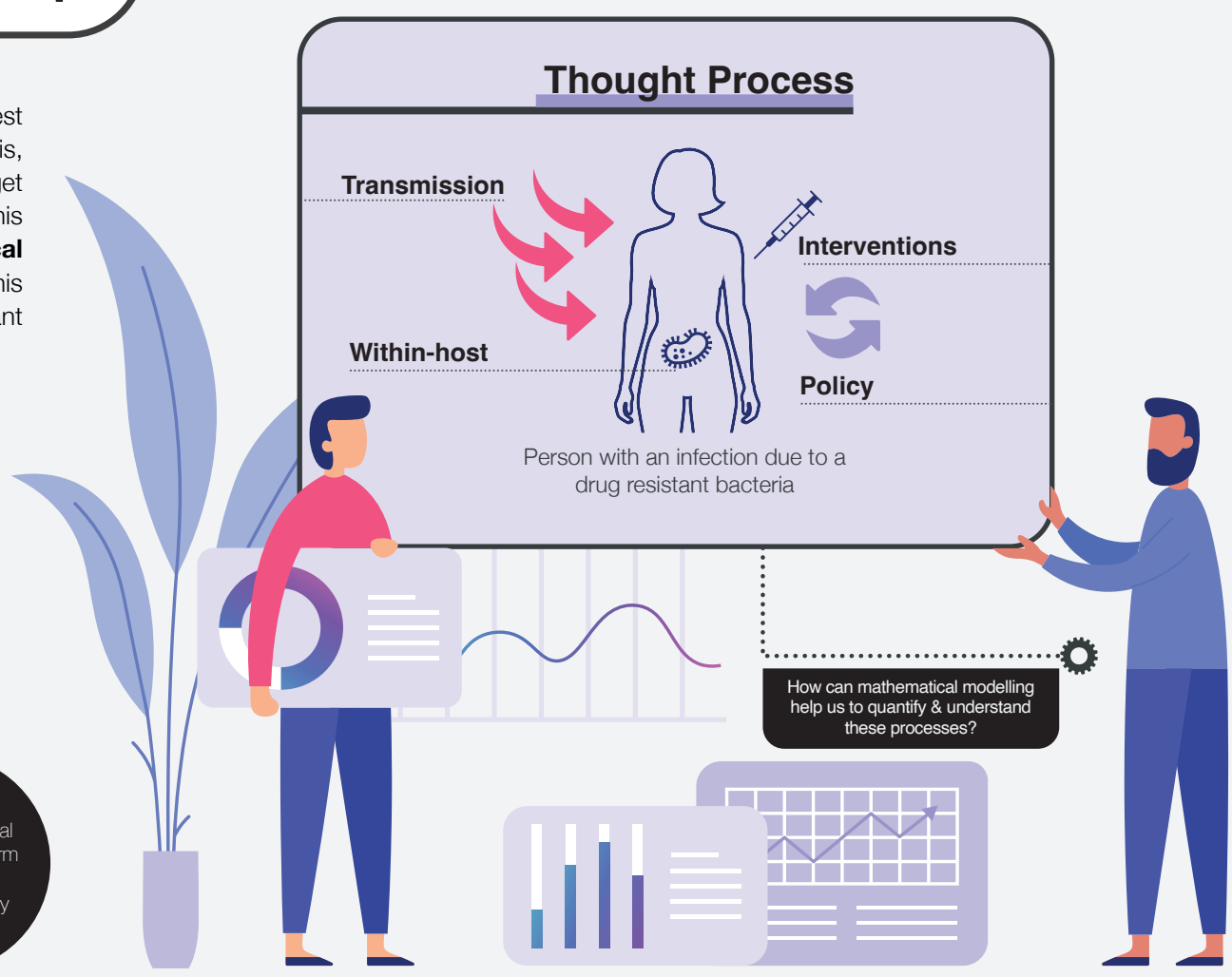
RESIST2 Workshop

Antimicrobial resistance is one of the greatest public health challenges of our time. To tackle this, we need to develop policies that optimally target our resources to reduce the clinical burden. In this workshop we focused on how **mathematical modelling** can reduce the numbers of this endpoint - the patients infected with drug resistant bacteria.

What is Mathematical Modelling?
Mathematical models are increasingly used to understand the transmission of infectious diseases in populations and to evaluate the potential impact of control programmes in reducing morbidity and mortality.

There is a growing demand for mathematical modellers in public health to explain observed disease trends and predict the outcome of interventions, often by synthesising information from different data sources. At the same time, increasing computational power and methodological advances are providing opportunities to fit ever more complex mechanistic models to data.

How can we better use mathematical modelling to inform antimicrobial resistance policy ?



Transmission

How did transmission to this patient happen? Where did the drug resistant bacteria come from? We asked four experts working in a range of environments about different transmission routes:

Resistant bacterial colonization.
Julia Bielicki, MD, PhD, UKBB and SGUL

Changing patterns of hospital-acquired and community-onset infections in the COVID-19 context. Nina J. Zhu, PhD, MPH, MSc, BEng, Imperial College London

MDR-TB Household Contact Management in Children. Finn McQuaid, PhD, LSHTM

Plasmid distributions in human bloodstream-infection-associated and non-human-Enterobacterales in Oxfordshire, UK, demonstrate sharing across reservoirs. Will Matlock, DPhil Student, University of Oxford

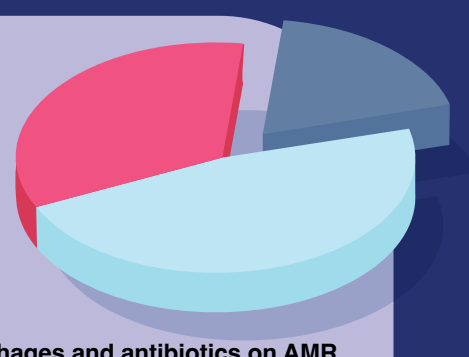
The requirements for mathematical models are not always being integrated in routine data collection.

These requirements could be built into studies from the ground up, especially in the cluster randomised setup that is really powered to look at **transmission**.

There are however challenges around combining the needs for modelling approaches with clinical trials. How can we achieve this balance?

Can we do more to share data that is already available and synthesise different discrete pots of data? We need more platforms that enable this exchange.

Within Host



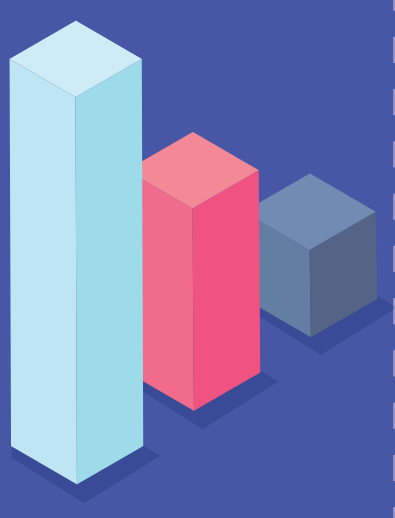
Once an individual is colonised or infected with the bacteria, we ask how resistance arose, what is the competition between that bacteria and other bacteria, or the selective pressures that are happening. We asked 4 experts about evolution and how the bacteria are interacting.

Modelling to reveal the joint effect of bacteriophages and antibiotics on AMR evolution. Quentin Leclerc, PhD student LSHTM, University of London

Within-population dynamics of (multi-)resistance evolution. Danna R Gifford, Independent Research Fellow, MERMan Group, The University of Manchester

How do microbiome-pathogen interactions drive epidemiological dynamics of resistance? David Smith, PhD, Institut Pasteur

Infection modelling - countering resistance and virulence during infection Sara Jabbari, Reader in Mathematical Biology, University of Birmingham



Interventions

How can we reduce mortality and morbidity in a patient with an infection with a drug resistant bacteria? What are the public interventions we can put in place? how can we use modelling to compare between interventions to support this decision making

Emulating a target trial with observational data: an application to estimating mortality of delays in concordant antibiotic treatment for bacteraemia accounting for time-varying confounding and immortal time biases Cherry Lim, Wellcome Trust Training Fellow, DPhil Student, University of Oxford

Interventions to Tackle AMR - how to use modelling to select efficient policies? Nichola Naylor, BEconSc MSc PhD, LSHTM & UKHSA

Antimicrobial Resistance, Modelling x Policy Alison Hill, PhD, Johns Hopkins University

Interventions to Tackle AMR - how to use modelling to select efficient policies? Alice Ledda, PhD, UKHSA

Policy

Modelling can be tailored to provide directly policy related outputs. Have we made progress in understanding and using modelling for AMR policy? COVID-19 has affected AMR in many different ways. Are there lessons to be learnt for modelling AMR?

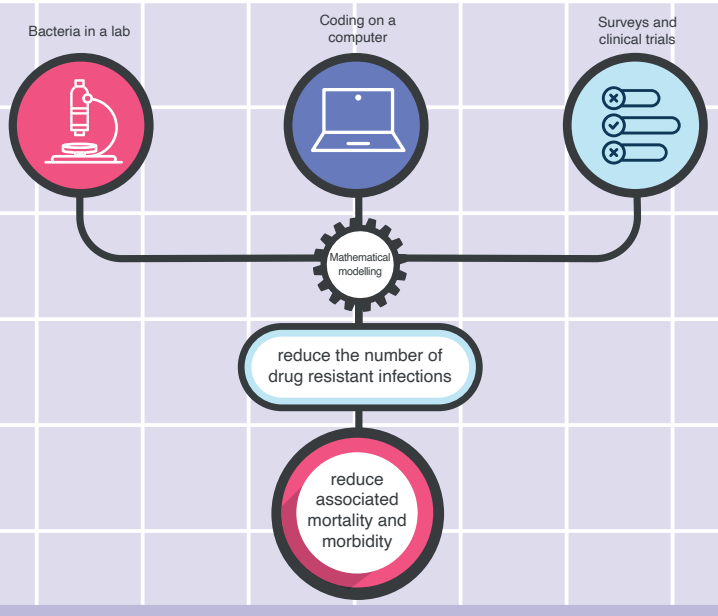
Using modelling for policy: Estimating the global burden of AMR Catrin Moore, PhD, University of Oxford

Antimalarial resistance, modelling to inform policy Alfred Amambua-Ngwa, PhD, LSHTM / Medical Research Council Unit The Gambia

A modeller goes undercover! ...inside a funding organisation Bilal Mateen, BSc MPH MBBS FFCI,Wellcome

Impact of COVID-19: the changing backdrop of antibiotic use and resistance, Julie Robotham, PhD, UKHSA

We brought together interdisciplinary AMR modelling research fields that use mathematical modelling as a tool to answer important questions about AMR. These included clinicians, mathematical modellers, AMR researchers, microbiologists, and policy makers. Whether they are working on bacteria in a lab, coding on a computer or surveys and clinical trials, the end point is the same:



Where next?

Not much progress has been made since RESIST1. How can we better use mathematical modelling to inform AMR policy? Who are the policy makers that we should be interacting with as AMR researchers? **Priorities now include:**

1. Promoting knowledge mobilisation with multiple end users in mind
2. Enablement / encouragement of key stakeholder, policy maker and modelling interaction
3. Innovating funding models to facilitate working with experts across a variety of different fields