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Identification of the elements of models of antimicrobial resistance of bacteria for assessing their usefulness and usability in One Health decision making: a protocol for scoping review

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ABSTRACT

Introduction Antimicrobial resistance (AMR) is a complex problem that requires the One Health approach, that is, a collaboration among various disciplines working in different sectors (animal, human and environment) to resolve it. Mathematical and statistical models have been used to understand AMR development, emergence, dissemination, prediction and forecasting. A review of the published models of AMR will help consolidate our knowledge of the dynamics of AMR and will also facilitate decision-makers and researchers in evaluating the credibility, generalisability and interpretation of the results and aspects of AMR models. The study objective is to identify and synthesise knowledge on mathematical and statistical models of AMR among bacteria in animals, humans and environmental compartments.

Methods and analysis Eligibility criteria: Original research studies reporting mathematical and statistical models of AMR among bacteria in animal, human and environmental compartments that were published until 2022 in English, French and Spanish will be included in this study. Sources of evidence: Database of PubMed, Agricola (Ovid), Centre for Agriculture and Bioscience Direct (CABI), Web of Science (Clarivate), Cumulative Index to Nursing and Allied Health Literature (CINAHL) and MathScinet. Data charting: Metadata of the study, the context of the study, model structure, model process and reporting quality will be extracted. A narrative summary of this information, gaps and recommendations will be prepared and reported in One Health decision-making context.

Ethics and dissemination Research ethics board approval was not obtained for this study as neither human participation nor unpublished human data were used in this study. The study findings will be widely disseminated among the One Health Modelling Network for Emerging Infections network and stakeholders by means of conferences, and publication in open-access peer-reviewed journals.

STRENGTHS AND LIMITATIONS OF THIS STUDY

⇒ Inclusion of both mathematical and statistical models of bacterial antimicrobial resistance (AMR) is one of the strengths of this study.
⇒ The rigorous methodology used in this scoping review will make this study reproducible and can form a basis for a continual update on models of bacterial AMR.
⇒ The study will identify and report elements (features) of bacterial AMR modelling papers that can facilitate decision-makers and researchers in evaluating the modelling papers.
⇒ As a limitation, studies published in English, French and Spanish will only be included in the study.

INTRODUCTION

Rationale

Antimicrobial resistance (AMR) is a global threat with an immense cost to global public health and livelihood. A review chaired by O'Neil estimated that in the absence of a remedial action, the risk could be as high as one death every three seconds and an economic cost of US$100 trillion per year by 2050.[1] Likewise, others have estimated AMR to cause a 2.6%–7.5% annual decline in global livestock production and cost global healthcare between US$300 billion and more than US$1 trillion per annum by 2050.[2]

The global antimicrobial resistome is contributed by the development/selection, transfer and amplification of AMR genes. Anthropogenic antibiotic selection pressure due to the use and misuse of antimicrobials in animals and humans is chiefly responsible for developing and maintaining antimicrobial resistome among bacteria in human, animal and environmental compartments.[3–9] AMR genes, when present in mobile genetic elements like plasmids, transposons and integrons, can be horizontally transferred between commensal, pathogenic and opportunistic bacteria via various mechanisms.[10–12] Both horizontal and vertical transfer of AMR genes among bacteria amplifies the

Table 1 The search terms to be used in this study

Antibiotic resistance	Mathematical model	Statistical model	Language
Antibiotic* resistant, Antibiotic* resistance	Modeling, Modelling,	Stat*	English French Spanish
Antimicrobial resistant	Dynamics	Statistical model	
Antimicrobial resistance	Model	spatial	
Drug resistant, drug resistance	Model based	temporal	
Antibacterial resistant	Computational models	Spatio-temporal	
Antibacterial resistance	Simulations		
Antibacterial drug resistant	Mathematical Model		
Antibacterial drug resistance	Deterministic, stochastic		
Bacterial drug resistance	Ordinary differential equations (ODEs, ODE); partial differential equations (PDE, PDEs); stochastic differential equations (SDEs, SDE)		
multidrug-resistant bacteria, multidrug resistance Bacterial resistance			
Drug resistant bacteria			
Microbial drug resistance			

antimicrobial resistome within each compartment. Likewise, following the transfer of resistant genes between different compartments via various routes,[8 13 14] there is a second amplification of the antimicrobial resistance genes, which leads to an immense global burden of antimicrobial resistome.

AMR is a complex problem traversing human, animal and environment compartments. The understanding and addressing of AMR requires a One Health approach, which is a collaboration between various disciplines working in human, animal and environmental sectors.[15] Mathematical and statistical modelling of diseases has been used to understand the dynamics of various infectious diseases including AMR in a population and to design and evaluate preventive measures.[16 17] While previous reviews have attempted to synthesise the knowledge from various models of AMR in bacteria, their focus was solely on measuring the impact of mathematical models,[18] on AMR due to antimicrobial use only, on antimicrobial resistance in general without a specific focus on bacteria, on a limited number of bacterial genera and species, and on limited types of modelling approaches and settings.[17–24] While these reviews provided important insights in composing our research questions, most of these reviews used non-reproducible and/or less sensitive search strategies, and excluded statistical models, within pathogen/host models, publications in languages other than English, and grey literatures, that is, preprints, thesis, reports and other documents that have not been published in scholarly journals.[17–24] Consequently, previous reviews excluded a wealth of knowledge on AMR models that could enhance our understanding of AMR. Furthermore, such reviews also did not describe the elements/features of modelling processes and approaches used and fundamental elements of model reporting that need to be considered by the end users while using AMR modelling studies to aid in the early detection, and spread of AMR, and evaluation of AMR control measure in the context of One Health.

Table 2 The databases used to search articles

Databases	URLs	Subscription
PubMed	https://pubmed.ncbi.nlm.nih.gov/	Free
Agricola	https://agricola.nal.usda.gov/	Free
Centre for Agriculture and Bioscience (CAB) Direct	https://www.cabdirect.org/	University of Montreal
Web of Science	https://www.webofscience.com/	University of Montreal
Cumulative Index to Nursing and Allied Health Literature (CINAHL)	https://www.ebsco.com/products/research-databases/cinahl-database	University of Montreal
MathSciNet	https://mathscinet.ams.org/mathscinet/	Free

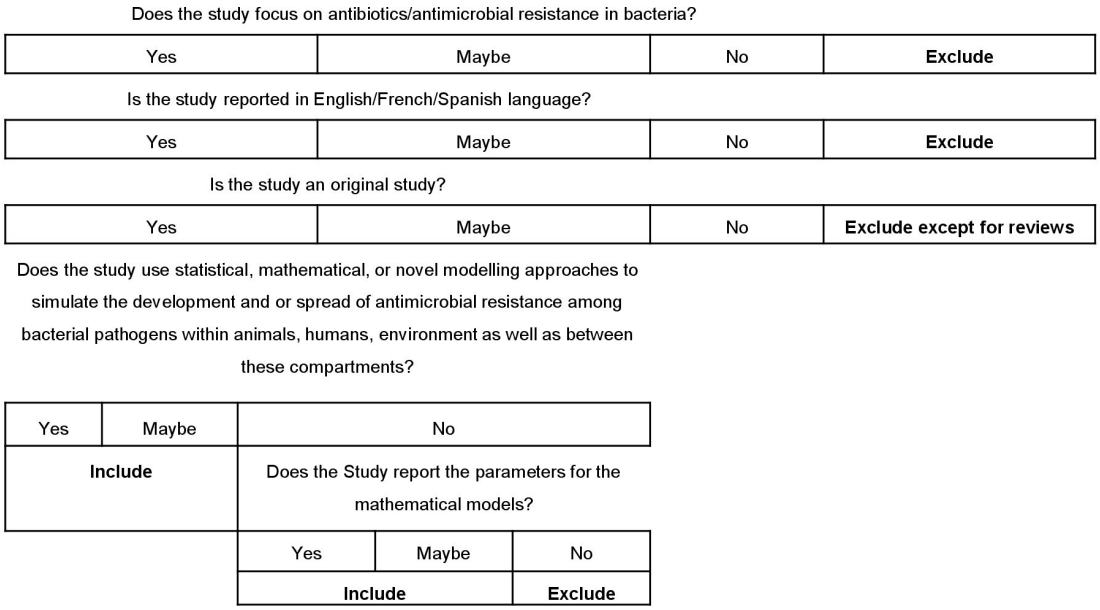

Figure 1 A form that will be used to conduct title and abstract screening of the studies.

Thus, this protocol outlines a reproducible process that can be used to synthesise and update knowledge about statistical and mathematical models of AMR and help identify elements/features of AMR models that aid in the assessment of their usability and usefulness for different purposes. Knowledge generated from this study will not only aid in understanding the development, emergence and dissemination of AMR but also will facilitate decision-makers and researchers in evaluating the credibility, generalisability and interpretation of the results in another context. This approach can also be used to conduct a living systematic review, that is, periodic systematic reviews to continually update new knowledge on mathematical and statistical models of AMR as further information becomes available.[25]

Objectives and research question

The overall objective is to synthesise the knowledge of peer-reviewed statistical and epidemiological models of bacterial AMR.

Specifically, the review will seek answers to the following research questions:

1. What are the most essential elements (features) of bacterial AMR models, like model structure and model process (parameters used, data used, model fitting, model calibration, model validation, forecasting, etc) that should be considered before using them?
2. What are the most essential elements (features) of bacterial AMR model reporting, like research question, study context, model findings, applications and limitations, etc that should be considered before using them?
3. What is a simplest foundational (generic) model to describe the development and dissemination of AMR in different contexts? By simplest foundational model, we mean a model that can be used as a starting point to model the development, emergence and spread of bacterial AMR in different settings.

METHODS AND ANALYSIS

The Preferred Reporting Items for Systematic Review and Meta-Analysis Protocols (PRISMA-P) and its extension for scoping reviews[26 27] were followed to prepare this protocol. All the recommended information outlined in the PRISMA-P checklist for this protocol has been provided. The protocol will be archived on the University of Guelph Atrium (https://atrium.lib.uoguelph.ca/xmlui/handle/10214/10046), and any changes, if made, will also be archived there.

Eligibility criteria

To be eligible for inclusion in this study, the following criteria needed to be fulfilled:

1. Studies should use statistical or mathematical modelling approaches to simulate the development and/or spread of AMR among bacterial pathogens.
2. Studies should focus on the development and/or spread of bacterial AMR within animals, humans and environments as well as between two or more of these compartments. There will not be any restriction regarding the setting of the studies. Studies focusing on within bacteria AMR models will also be considered.
3. Studies should report the parameters (eg, rate of transmission of AMR genes, a force of infection by AMR pathogens, the burden of AMR in different compartments) for the mathematical models.
4. Studies should be reported in English, French and Spanish.
5. Studies will not be restricted based on publication date and geographical settings.
6. Full text of the study should be available.

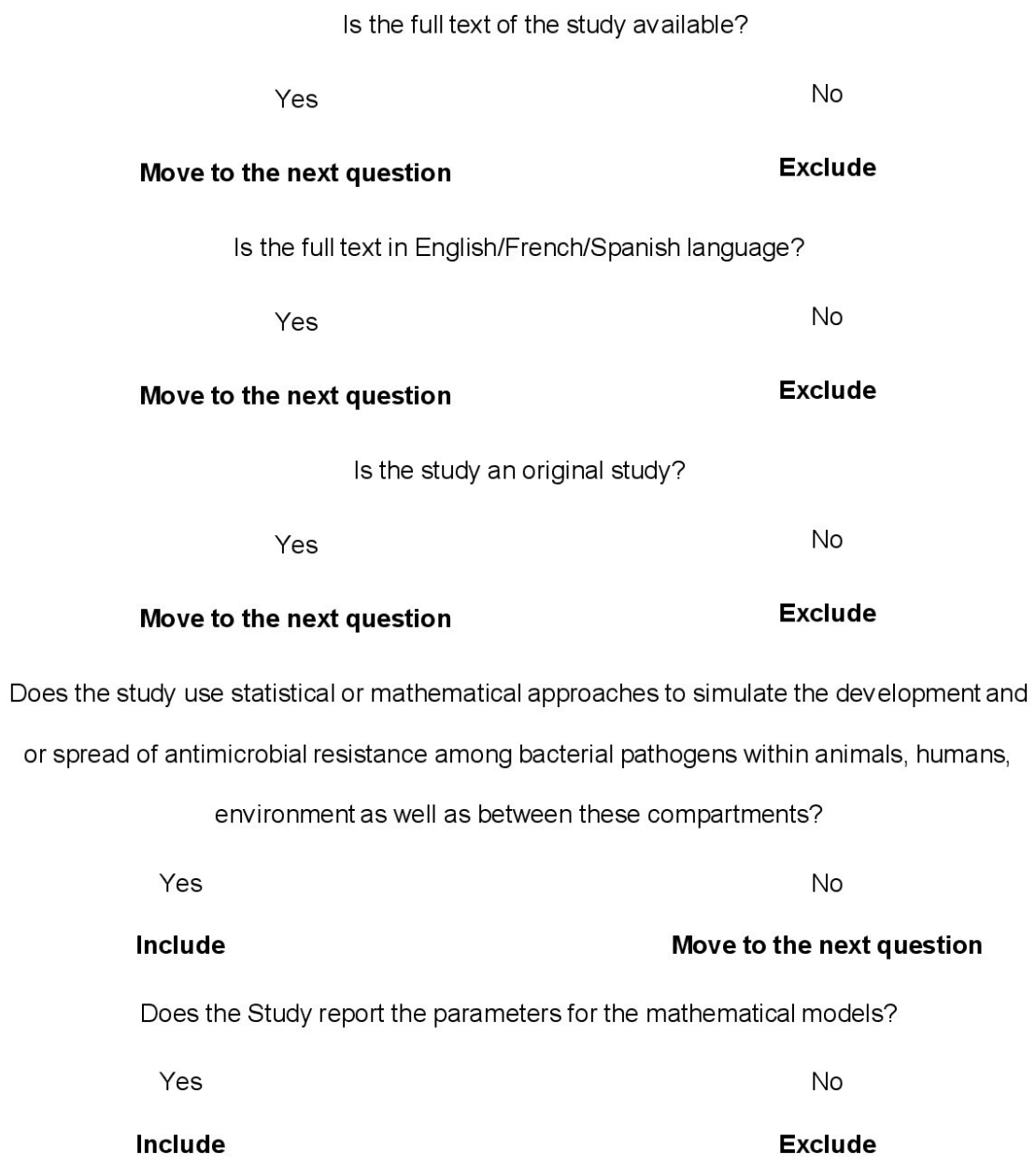

Figure 2 A form that will be used to conduct full-text screening of the studies.

7. Systematic and non-systematic reviews will be retained to identify additional original studies, but these studies will not be further assessed.
8. Preprints will be retained, and if they are printed during the study duration, the published paper will be included in the study.

While most of the studies that will be included in this review will be peer-reviewed studies, some grey literatures are expected to be non-peer-reviewed and will be reported.

Papers describing resistance other than antibacterial resistance, for example, antiviral, antiprotozoal, etc, will be excluded from the study.[18] Similarly, papers that focus on resistance other than antimicrobial/antibiotic resistance, such as, drug resistance in diseases such as diabetes, hypertension, liver diseases and nervous system diseases, will not be included in the study. Likewise, commentary and letters will be excluded unless they report an original model.[18]

Search strategy

A review of published papers was conducted to identify search terms and prepare search strategies for various databases. The search strategy will be tested and refined to ensure its sensitivity and specificity. Previously identified papers will be used to test the effectiveness of the search strategy.[28–42]

The study will focus on the records describing the development and dissemination of bacterial AMR (problem) in all three One Health compartments: humans, animals and environments (context), using mathematical and statistical modelling (interest). Hence, various variants of the keywords (model, bacteria, antibiotics and resistance) will be used (table 1). Understandably, the search result

Table 3 A Data extraction form focusing on model information.

Variables	Description and examples
Year of work	The year the work was conducted or the year of publication. For example, 2019
Geography	Regions. For example, North America
Pathogens	Bacterial species and serotypes. For example, *Escherichia coli* O157: H7
Antibiotics	Name (group). For example, Gentamicin (Aminoglycosides)
Hosts	Animals or humans or environment, for example, Pig
Setting	Hospital, farm, environment, community, etc
Interventions included	Antibiotics restriction, antibiotics cycling, etc
Type of model	Statistical or mathematical
Subtype of model	For example, deterministic, stochastic, etc
Compartments included	Name of the compartments, for example
Parameters and their source	Parameters used in the models. For example, contact rate, rate of transmission of AMR genes, force of infection by AMR pathogens, etc
Validation	Yes/no. If yes, the method used
Sensitivity analysis	Yes/no. If yes, the method used
Major findings	Major findings and conclusions of the study
Application	Application of the study as envisioned
Limitations	Limitations as mentioned
Data availability	Yes/no. If available, details on the data
Code availability	Yes/no. If available, link to the repository

AMR, antimicrobial resistance.

is expected to be less specific and more sensitive. This approach has been adopted to ensure that the search will find most of the modelling papers. The keywords will be modified to suit various databases.

A search conducted in Web of Science on 25 November 2022 using the keywords resulted into 19 241 results (online supplemental table 1). Likewise, a sample search conducted in PubMed on 13 September 2022 using the following keywords resulted in 11 311 results:

(antibiotic* OR antimicrobial* OR antibacterial OR "antibacterial drug" OR "bacterial drug" OR multidrug OR "multi-drug" OR "microbial drug") AND (resistant OR resistance) AND (modeling OR model OR "model-based" OR "computational model*" OR simulat* OR mathematic* OR "mathematic* model*" OR "dynamic model*" OR deterministic OR stochastic OR "deterministic model*" OR "stochastic model*" OR "ordinary differential equation*" OR ODEs OR ODE OR PDE OR PDEs OR, "partial differential equation*" OR SDEs OR SDE OR "stochastic differential equation*" OR SIR OR SEIR OR SVIR OR R0 OR "compartment* model*" OR compartment* OR "epidemic* model*" OR "epidemic*" OR "statistical model*" OR "spatial" OR "temporal" OR "spatio-temporal")

Source of information

Papers will be systematically searched in the major databases like PubMed, Agricola, Centre for Agriculture and Bioscience (CAB) Direct, Web of Science, Cumulative Index to Nursing and Allied Health Literature (CINAHL) and MathScinet. Tables 1 and 2 summarise the tentative keywords to be used, and key database to be searched. The final list of keywords used, and the total number of papers retrieved by the search, will be reported.

Study selection

Two researchers with backgrounds in epidemiology and mathematical modelling will independently screen the deduplicated references in Covidence (Veritas Health Innovation, Melbourne, Australia). Two forms (figures 1 and 2) that will be pretested by the reviewers will be used to conduct two phases of the screening of the papers. In the first stage, the title and abstract of papers will be screened using a form (figure 1) and potential papers for full-text

Table 4 A data extraction form focusing on the metadata of the studies

Authors	Specialisation	Funding	Year of publication	Journal	Citation metrics	Institution of affiliation	Conflict of interest statement

screening will be identified. As indicated in the form (figure 1), if the reviewers are unsure about the inclusion or exclusion of a paper, it will be moved to the full-text screening stage. Inter-rater reliability will be assessed by calculating proportion agreement and Cohen's kappa. In the second stage, full-text screening of the studies will be conducted using a form (figure 2). The researchers will meet virtually to reach a consensus to resolve any conflict in their inclusion/exclusion decisions. When such differences cannot be resolved by agreement, a third reviewer will resolve the dispute. If any additional duplicate studies are encountered during full-text screening, they will be removed manually. The inclusion or exclusion decisions made on the studies at both phases will be visualised as a PRISMA flow diagram, and the rationale for such decisions will also be reported.[43]

Data management

Endnote V.X9 will be used to manage references. The collated citations will be exported to a web-based systemic review management software Covidence (Veritas Health Innovation, Melbourne, Australia; available at www.covidence.org), where the internal algorithm will be applied to deduplication the references before the commencement of the screening of studies.

Data extraction/charting

Data extraction from the papers will be conducted in the Covidence by a single reviewer. A pretest of the charting forms (tables 3 and 4) will be conducted among the reviewers of the study using five selected papers, and the forms will be refined. Apart from the enlisted information, additional information will be collected as deemed necessary by the reviewers to answer the research question. However, the authors of the papers will not be contacted to obtain any additional information or clarification.

Quality assessment

A quality (risk of bias) assessment of the information in the papers will be conducted based on the criteria developed based on previous publications,[44 45] and at least 25 papers will be evaluated based on these criteria.

Synthesis of results

A descriptive analysis of the charted data will be conducted. A narrative summary of the study findings, gaps of the studies and the recommendation for future research will be prepared. Likewise, a summary will be prepared for each group of pathogens by the system involved—enteric infection, respiratory infection, etc. The generic or foundational models on the evolution and spread of AMR will be identified by following the method used previously.[23] Similarly, the papers will be critically evaluated to identify the essential elements (features) of bacterial AMR models and the requirements for reporting AMR modelling papers. The suggestions for this will come from the model structure, model process, interpretation of findings, limitations, recommendations, data availability, data quality, code availability, etc.

Patient and public involvement

No patient and public will be involved in any stage of this study.

ETHICS AND DISSEMINATION

Research ethics board approval was not required for this study as the study does not involve any human participation and does not envision a review of unpublished human data. The findings of this study will be presented within the One Health Modelling Network for Emerging Infections network, conferences and published in open-access, peer-reviewed journals.

Contributors KRA, JPR-L, EJP and BN conceived this study. KRA drafted the manuscript and will conduct the analysis. All the coauthors contributed to the revision of the manuscript and have approved the final manuscript.

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Competing interests None declared.

Patient and public involvement Patients and/or the public were not involved in the design, or conduct, or reporting, or dissemination plans of this research.

Patient consent for publication Not applicable.

Provenance and peer review Not commissioned; externally peer reviewed.

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REFERENCES

1 O'Neill J. Tackling drug-resistant infections globally: final report and recommendations. 2016.
2 World Bank. *Drug-resistant infections*. Washington (DC), March 2017.
3 Stockwell VO, Duffy B. Use of antibiotics in plant agriculture. *Rev Sci Tech OIE* 2012;31:199–210. 10.20506/rst.31.1.2104 Available: http://doc.oie.int:8080/dyn/portal/index.seam?page=alo&aloId=32268
4 McManus PS, Stockwell VO, Sundin GW, *et al*. Antibiotic use in plant agriculture. *Annu Rev Phytopathol* 2002;40:443–65.
5 Larsson DGJ, de Pedro C, Paxeus N. Effluent from drug manufactures contains extremely high levels of pharmaceuticals. *J Hazard Mater* 2007;148:751–5.
6 Ji X, Shen Q, Liu F, *et al*. Antibiotic resistance gene abundances associated with antibiotics and heavy metals in animal manures and agricultural soils adjacent to feedlots in Shanghai; China. *J Hazard Mater* 2012;235–236:178–85.

7 IACG. No time to wait: securing the future from drug-resistant infections. 2019. Available: www.who.int/antimicrobial-resistance/interagency-coordination-group/IACG_final_report_EN.pdf?ua=1 [Accessed 13 Jun 2019].
8 Holmes AH, Moore LSP, Sundsfjord A, *et al*. Understanding the mechanisms and drivers of antimicrobial resistance. *Lancet* 2016;387:176–87.
9 Diwan V, Tamhankar AJ, Khandal RK, *et al*. Antibiotics and antibiotic-resistant bacteria in waters associated with a hospital in ujjain, india. *BMC Public Health* 2010;10:414.
10 Schwarz S, Chaslus-Dancla E. Use of antimicrobials in veterinary medicine and mechanisms of resistance. *Vet Res* 2001;32:201–25.
11 Kelly BG, Vespermann A, Bolton DJ. Gene transfer events and their occurrence in selected environments. *Food Chem Toxicol* 2009;47:978–83.
12 Lorenzo-Díaz F, Fernández-López C, Lurz R, *et al*. Crosstalk between vertical and horizontal gene transfer: plasmid replication control by a conjugative relaxase. *Nucleic Acids Res* 2017;45:7774–85.
13 Price LB, Stegger M, Hasman H, *et al*. Staphylococcus aureus CC398: host adaptation and emergence of methicillin resistance in livestock. *MBio* 2012;3:1–6.
14 Robinson TP, Wertheim HFL, Kakkar M, *et al*. Animal production and antimicrobial resistance in the clinic. *Lancet* 2016;387:e1–3.
15 Mackenzie JS, Jeggo M. The one health approach—why is it so important? *TropicalMed* 2019;4:88.
16 Siettos CI, Russo L. Mathematical modeling of infectious disease dynamics. *Virulence* 2013;4:295–306.
17 Opatowski L, Guillemot D, Boëlle PY, *et al*. Contribution of mathematical modeling to the fight against bacterial antibiotic resistance. *Curr Opin Infect Dis* 2011;24:279–87.
18 Temime L, Hejblum G, Setbon M, *et al*. The rising impact of mathematical modelling in epidemiology: antibiotic resistance research as a case study. *Epidemiol Infect* 2008;136:289–98.
19 Cousins M, Parmley J, Neiterman E, *et al*. A scoping review of existing models of antimicrobial resistance and evidence to parameterize a one health model in a Swedish food system context. *International Journal of Infectious Diseases* 2022;116:S7.
20 Birkegård AC, Halasa T, Toft N, *et al*. Send more data: a systematic review of mathematical models of antimicrobial resistance. *Antimicrob Resist Infect Control* 2018;7:117.
21 Ramsay DE, Invik J, Checkley SL, *et al*. Application of dynamic modelling techniques to the problem of antibacterial use and resistance: a scoping review. *Epidemiol Infect* 2018;146:2014–27.
22 Arepeva M, Kolbin A, Kurylev A, *et al*. What should be considered if you decide to build your own mathematical model for predicting the development of bacterial resistance? recommendations based on a systematic review of the literature. *Front Microbiol* 2015;6:352.
23 Spicknall IH, Foxman B, Marrs CF, *et al*. A modeling framework for the evolution and spread of antibiotic resistance: literature review and model categorization. *Am J Epidemiol* 2013;178:508–20.
24 Niewiadomska AM, Jayabalasingham B, Seidman JC, *et al*. Population-Level mathematical modeling of antimicrobial resistance: a systematic review. *BMC Med* 2019;17:81.
25 Elliott JH, Synnot A, Turner T, *et al*. Living systematic review: 1. introductiondthe why, what, when, and how on behalf of the living systematic review network a. *J Clin Epidemiol* 2017;91:23–30. Available: https://ac.els-cdn.com/S0895435617306364/1-s2.0-S0895435617306364-main.pdf?_tid=ceabbd78-050b-11e8-83b6-00000aab0f01&acdnat=1517241071_db6e1696b30ac07ea690040bab35a165
26 Shamseer L, Moher D, Clarke M, *et al*. Preferred reporting items for systematic review and meta-analysis protocols (prisma-p) 2015: elaboration and explanation. *BMJ* 2015;350:g7647.
27 Tricco AC, Lillie E, Zarin W, *et al*. PRISMA extension for scoping reviews (PRISMA-scr): checklist and explanation. *Ann Intern Med* 2018;169:467–73.
28 Huang QM, Horn MA, Ruan SG. Modeling the effect of antibiotic exposure on the transmission of methicillin-resistant Staphylococcus aureus in hospitals with environmental contamination. *Math Biosci Eng* 2019;16:3641–73.
29 van Bunnik BAD, Woolhouse MEJ. Modelling the impact of curtailing antibiotic usage in food animals on antibiotic resistance in humans. *R Soc Open Sci* 2017;4:161067.
30 D'Agata EMC, Magal P, Olivier D, *et al*. Modeling antibiotic resistance in hospitals: the impact of minimizing treatment duration. *J Theor Biol* 2007;249:487–99.
31 Kim S, Park H, Chandran K. Propensity of activated sludge to amplify or attenuate tetracycline resistance genes and tetracycline resistant bacteria: a mathematical modeling approach. *Chemosphere* 2010;78:1071–7.
32 Bootsma MCJ, van der Horst MA, Guryeva T, *et al*. Modeling non-inherited antibiotic resistance. *Bull Math Biol* 2012;74:1691–705.
33 Arepyeva MA, Kolbin AS, Sidorenko SV, *et al*. A mathematical model for predicting the development of bacterial resistance based on the relationship between the level of antimicrobial resistance and the volume of antibiotic consumption. *J Glob Antimicrob Resist* 2017;8:148–56.
34 Park J, Cho M, Son HS. Simulation model of bacterial resistance to antibiotics using individual-based modeling. *J Comput Biol* 2018;25:1059–70.
35 Austin DJ, Anderson RM. Studies of antibiotic resistance within the patient, hospitals and the community using simple mathematical models. *Philos Trans R Soc Lond B Biol Sci* 1999;354:721–38.
36 Ibargüen-Mondragón E, Romero-Leiton JP, Esteva L, *et al*. Stability and periodic solutions for a model of bacterial resistance to antibiotics caused by mutations and plasmids. *Applied Mathematical Modelling* 2019;76:238–51.
37 Ibargüen-Mondragón E, Mosquera S, Cerón M, *et al*. Mathematical modeling on bacterial resistance to multiple antibiotics caused by spontaneous mutations. *Biosystems* 2014;117:60–7.
38 Daşbaşı B, Öztürk İ. Mathematical modelling of bacterial resistance to multiple antibiotics and immune system response. *Springerplus* 2016;5:408.
39 Alawieh A, Sabra Z, Bizri AR, *et al*. A computational model to monitor and predict trends in bacterial resistance. *J Glob Antimicrob Resist* 2015;3:174–83.
40 Ternent L, Dyson RJ, Krachler AM, *et al*. Bacterial fitness shapes the population dynamics of antibiotic-resistant and -susceptible bacteria in a model of combined antibiotic and anti-virulence treatment. *J Theor Biol* 2015;372:1–11.
41 Hüls A, Frömke C, Ickstadt K, *et al*. Antibiotic resistances in livestock: a comparative approach to identify an appropriate regression model for count data. *Front Vet Sci* 2017;4:71.
42 MacKinnon MC, Pearl DL, Carson CA, *et al*. A comparison of modelling options to assess annual variation in susceptibility of generic escherichia coli isolates to ceftiofur, ampicillin and nalidixic acid from retail chicken meat in canada. *Prev Vet Med* 2018;160:123–35.
43 Moher D, Liberati A, Tetzlaff J, *et al*. Preferred reporting items for systematic reviews and meta-analyses: the PRISMA statement. *J Clin Epidemiol* 2009;62:1006–12.
44 Jaime Caro J, Eddy DM, Kan H, *et al*. Questionnaire to assess relevance and credibility of modeling studies for informing health care decision making: an ISPOR-AMCP-NPC good practice task force report. *Value Health* 2014;17:174–82.
45 Harris RC, Sumner T, Knight GM, *et al*. Systematic review of mathematical models exploring the epidemiological impact of future TB vaccines. *Hum Vaccin Immunother* 2016;12:2813–32.

Supplementary Table 1 The results of literature search on models in bacterial antimicrobial resistance in various databases, without using any restrictions.

Database (date of search)	Search query		Results
Web of Science™ (November 25, 2022)	#1	TI=(("antibiotic* resistan*" OR "antimicrobial* resistan*" OR "antibacterial resistan*" OR "antibacterial drug resistan*" OR "bacterial resistan*" OR "bacterial drug resistan*" OR "multidrug resistan*" OR "multi-drug resistan*" OR "microbial drug resistan*"))	57,059
	#2	TI=((model* OR "model based" OR "computational model*" OR simulat* OR predictive OR mathematic* OR "mathematic* model*" OR "dynamic model*" OR deterministic OR stochastic OR "deterministic model*" OR "stochastic model*" OR "ordinary differential equation*" OR ODEs OR ODE OR PDE OR PDEs OR "partial differential equation*" OR SDEs OR SDE OR "stochastic differential equation*" OR SIR OR SEIR OR SVIR OR R0 OR "compartment* model*" OR "epidemi* model*" OR "statistical model*" OR "spatial" OR "temporal" OR "spatiotemporal" OR “machine learning” OR “artificial intelligence” OR “deep learning” OR "neural networks" OR "cellular automata” OR “time series”))	4,255,205
	#3	#1 AND #2	1,151
	#4	AB =(("antibiotic* resistan*" OR "antimicrobial* resistan*" OR "antibacterial resistan*" OR "antibacterial drug resistan*" OR "bacterial resistan*" OR "bacterial drug resistan*" OR "multidrug resistan*" OR "multi-drug resistan*" OR "microbial drug resistan*"))	131,955
	#5	AB=(model* OR "model based" OR "computational model*" OR simulat* OR predictive OR mathematic* OR "mathematic* model*" OR "dynamic model*" OR deterministic OR stochastic OR "deterministic model*" OR "stochastic model*" OR "ordinary differential equation*" OR ODEs OR ODE OR PDE OR PDEs OR "partial differential equation*" OR SDEs OR SDE OR "stochastic differential equation*" OR SIR OR SEIR OR SVIR OR R0 OR "compartment* model*" OR "epidemi* model*" OR "statistical model*" OR "spatial" OR "temporal" OR "spatiotemporal" OR “machine learning” OR “artificial intelligence” OR “deep learning” OR	12,784,307

		"neural networks" OR "cellular automata" OR "time series")	
	#6	#4 AND #5	18,819
		#3 OR #6	19,241
Pubmed (September 23, 2022)		(antibiotic* OR antimicrobial* OR antibacterial OR "antibacterial drug" OR "bacterial drug" OR multidrug OR "multi-drug" OR "microbial drug") AND (resistant OR resistance) AND (modeling OR model OR "model-based" OR "computational model*" OR simulat* OR mathematic* OR "mathematic* model*" OR "dynamic model*" OR deterministic OR stochastic OR "deterministic model*" OR "stochastic model*" OR "ordinary differential equation*" OR ODEs OR ODE OR PDE OR PDEs OR, "partial differential equation*" OR SDEs OR SDE OR "stochastic differential equation*" OR SIR OR SEIR OR SVIR OR R0 OR "compartment* model*" OR compartment* OR "epidemic* model*" OR "epidemic*" OR "statistical model*" OR "spatial" OR "temporal" OR "spatio-temporal")	11,278
MathSciNet (September 23, 2022)		"Anywhere=(antibiotic* OR antimicrobial* OR antibacterial OR "antibacterial drug" OR "bacterial drug" OR multidrug OR "multi-drug" OR "microbial drug") AND Anywhere=(resistant OR resistance) AND Anywhere=(model* OR "model based" OR "computational model*" OR simulat* OR predictive OR mathematic* OR "mathematic* model*" OR "dynamic model*" OR deterministic OR stochastic OR "deterministic model*" OR "stochastic model*" OR "ordinary differential equation*" OR ODEs OR ODE OR PDE OR PDEs OR "partial differential equation*" OR SDEs OR SDE OR "stochastic differential equation*" OR SIR OR SEIR OR SVIR OR R0 OR "compartment* model*")"	172
Cumulative Index to Nursing and Allied Health Literature (CINAHL) Complete Via EBSCO host (October 14, 2022)		TI = antibiotic* resistan* AND TI = model* OR AB = antibiotic* resistan* AND AB = model*	628