- 1 Title: From the micro to the macro to improve human health: Taking
- 2 microorganism ecology and human society seriously in teaching
- 3 Infectious Disease Epidemiology
- 4
- 5 M. Shahmanesh^{1,2} PhD
- 6 G. Harling^{1,2,3,4} ScD
- 7 C. E. M. Coltart¹ PhD
- 8 H. Bailey¹ PhD
- 9 C. King^{1,5} PhD
- 10 R.W. Aldridge⁶ PhD
- 11 J. Gibbs¹ PhD
- 12 J. Seeley^{2,7}, PhD Professor
- 13 A. Phillips¹ , PhD Professor
- 14 C.A. Sabin¹ PhD Professor,
- 15 P. Sonnenberg¹ PhD Professor,
- 16 G.Hart¹ PhD Professor,
- 17 M. Rowson¹ MSc Professor
- 18 D. Pillay^{2,8} PhD Professor,
- 19 A. M. Johnson¹ MD Professor,
- 20 I. Abubakar¹ PhD Professor,
- 21 N Field¹ PhD
- 22 1. Institute for Global Health, University College London, UK
- 23 2. Africa Health Research Institute, South Africa
- 24 3. MRC/Wits Rural Public Health & Health Transitions Research Unit (Agincourt), University
- 25 of the Witwatersrand, South Africa
- Harvard Centre for Population and Development Studies, Harvard T.H. Chan School of
 Public Health, Boston, USA
- 28 5. Department of Public Health Sciences, Karolinska Institutet, Sweden
- 29 6. Institute of Health Informatics, University College London, UK
- 30 7. London School of Hygiene and Tropical Medicine, UK
- 8. Division of infection and immunity, University College London, UK

32 Abstract

Chronic and emergent infectious diseases and antimicrobial resistance remain a substantial global health threat, and our resident microbiota are increasingly recognised to play an important role in health. Infections also have a profound impact beyond health, including on global and local economies.

37

To maximise improvements in human health, the field of infectious disease epidemiology needs to derive learning from ecology and traditional epidemiology. New methodologies and tools are transforming our understanding of these systems, from better understanding of socio-economic, environmental and cultural drivers of infection, to improved methods to detect microorganisms, describe the immunome and understand the role of human microbiota. However, exploiting their potential to improve global health remains elusive.

44

45 We argue that to exploit these advances requires a paradigm shift in the teaching of infectious 46 disease epidemiology to ensure students are well-versed in a breadth of disciplines, whilst 47 maintaining depth in core epidemiological skills. We discuss the following key points 48 illustrated using a series of teaching vignettes: integrated training in classical and novel 49 techniques is needed to develop future scientists and professionals who can work from the 50 micro (interactions between pathogens, their cohabiting microbiota, and host at a molecular 51 and cellular level), with the meso (the affected communities), and to the macro (wider 52 contextual drivers of disease); teach students to use a team-science approach to effectively 53 integrate biological, clinical, epidemiological and social tools for public health impact; and 54 develop the intellectual skills to critically engage with emerging technologies and resolve evolving ethical dilemmas. Finally, students should appreciate that the voices of communities 55 56 affected by infection must be kept at the heart of their work.

58 Introduction

59 Infectious diseases remain a global health threat and continue to lead government risk 60 registers, for example, with the threat of pandemic 2019 novel coronavirus (2019-nCoV) and the development of antimicrobial resistance (AMR).¹ Chronic infectious diseases such as HIV 61 62 and tuberculosis, which together accounted for over 2.1 million deaths globally in 2017, and emerging infections with the potential for rapid expansion, remain a substantial and acute 63 threat to humanity.²⁻⁵ Furthermore, there is growing acceptance that our resident microbes 64 (microbiota) have an important role in non-communicable diseases. The role of single 65 66 pathogens in driving neoplastic disease is well established (e.g. H. pylori, hepatitis B virus, 67 Kaposi's sarcoma-associated herpes virus, and human papillomavirus) whilst the role of the 68 interactions between our microbiota and immune systems in other diseases are under investigation.⁶⁻⁸ Infectious diseases have profound impacts beyond health, including on local 69 and global economies, exacerbating existing socio-economic vulnerabilities.⁹ Moreover, any 70 71 response to these infectious threats needs new drugs, diagnostics and vaccines, for which we 72 are dependent on a pharmaceutical industry, whose vested interest may differ from ours.

73

74 To maximise improvements in human health in the coming decades, we believe that the field 75 of applied infectious disease epidemiology needs to derive learning from both ecology (the 76 branch of biology that deals with the relations of organisms to one another and to their 77 physical surroundings) and traditional epidemiology (the branch of medicine concerned with 78 distributions of disease in time, place, and person, their causes, and control). Infectious 79 organisms thrive when they occupy a permissive ecological niche which enables them to reproduce and evolve.¹⁰ A wide range of interacting and dynamic systems determine whether 80 81 an ecological niche is permissive, including the physical environment, social and cultural 82 context, political and healthcare systems, human behaviours, host and organism genetics, 83 host immune system, and interactions with other microorganisms competing for resources. Perturbations in any of these systems may alter the ecological balance. If we can understand 84 85 the systems and their interactions better, we may identify opportunities to prevent and 86 control infections.

New methodologies are transforming our understanding of these systems, from better 88 89 understanding of socio-economic, environmental and cultural drivers of infection, to 90 improved methods to detect and characterise microorganisms, refined measurement of the immunome at scale, and improved understanding of the role of human microbiota.¹¹⁻¹³ 91 92 Furthermore, our ability to study the genetic evolution of organisms alongside human host genetics and epigenetics brings new insights into disease susceptibility and the immune 93 94 response. These biological insights alongside increasingly powerful bioinformatic methods 95 allow us to reconstruct the evolution of outbreaks by combining molecular data with classical 96 epidemiological and clinical data,¹⁴ and provide powerful new tools to inform disease prevention,¹⁵ including vaccine development.¹⁶ 97

98

99 Working in silos is likely to limit the opportunities for change, but effective integration of these biological, clinical, epidemiological and social tools for public health programmes 100 101 remains in its infancy. Moreover, new technologies bring with them new ethical and moral challenges,¹⁷ which will require ongoing dialogue with communities and individuals affected 102 103 by infectious diseases. We argue that there is an urgent need for education programmes that 104 train a modern cadre of infectious disease epidemiologists who can integrate thinking across 105 fields and methods in order to optimise the prevention of, and response to, infectious disease 106 threats. This means incorporating training in classical and novel techniques to develop 107 scientists and practitioners who can work from the micro, with the meso, and to the macro to improve human health.^{18,19} Here we outline our proposal for a novel approach for training 108 109 of epidemiologists and public health experts specialising in the field of infectious diseases.

110

111 Rethinking infectious disease epidemiology teaching – building on the revolution in

112 teaching social epidemiology?

Societal factors, including the environment, society and health infrastructure (the macro) have long been understood to play a major role in determining the health of individuals and thus populations.²⁰⁻²² This led to the emergence of social epidemiology as a field of enquiry,²³ the adaptation of social ecological models in the field of sociology to public health,²⁴ and the World Health Organization's focus on the social determinants of health.²⁵ Social epidemiology is now extensively taught in traditional epidemiology and public health curricula and has led to increased implementation of structural interventions that have substantially affected
 behaviours and thus health outcomes.²⁶⁻³⁰ Within the field of infectious disease control,
 sanitation, housing, accessible healthcare, and vaccine regulations have substantially reduced
 mortality and morbidity – both historically in young children ^{31,32} and now for adolescents and
 adults.³³

124

125 There is also a better understanding of the dynamic interaction between these wider 126 structural factors and the local community, in infectious disease transmission (the meso level). 127 This has primarily involved locating geographies or occupational communities with higher transmission of infection, for example malaria in particular villages,³⁴ or HIV transmission in 128 settlements next to major transport routes in sub-Saharan Africa,^{35,36} or amongst specific 129 130 occupational communities (fishermen on Lake Victoria in Uganda; miners in sub-Saharan Africa³⁷). However, there is also increasingly understanding about how communities 131 132 (including individuals with their interpersonal relationships, families and households) 133 experience, organise and respond to the threat and reality of disease. Whether through 134 political struggle to secure decent housing and clean water, or advocacy for access to 135 prevention technologies, such as HIV pre-exposure prophylaxis and condoms, and vaccine funding.³⁸⁻⁴⁰ More recently, community mobilisation, community-based healthcare, 136 137 economic empowerment, and gender-based violence reduction strategies are all being seen 138 as integral to controlling the global HIV epidemic.^{41,42} Communities can also be a barrier to effective interventions, such as illustrated in the recent antivaccine movement.^{43,44} Future 139 infectious disease scientists and practitioners need to be trained to listen to the voices of 140 141 those affected, and to include and evaluate community-based solutions to infectious 142 diseases.

143

At the other end of the spectrum (the micro), our appreciation of microorganisms and their hosts at a molecular level has been revolutionised by advances in technology, including the tools to characterise genomes, describe the microbiota, and measure host immunity and inflammation. These advances have generally been technologically driven, often without clear models of future use, with computational biology and data science developments responding to vast increases in the generation of high-density datasets rather than driving health-focused developments.^{12,13} Moreover, the 'omics revolution brings dilemmas. These

151 include the possibility that social and community solutions become side-lined as glamourous 152 molecular innovations attract investment, and unclear clinical and ethical issues associated with the technological advances.¹⁷ It is also vital to apply the same degree of epidemiological 153 caution, particularly regarding inferences about causality, to molecular data.⁴⁵ For example, 154 155 the limited power to study the effect on disease of any one attribute that we measure (e.g. a 156 single nucleotide polymorphisms in the human genome where there is no prior hypothesis of 157 effect) has only recently been more widely appreciated and a lack of replicability remains a concern for these studies⁴⁶ 158

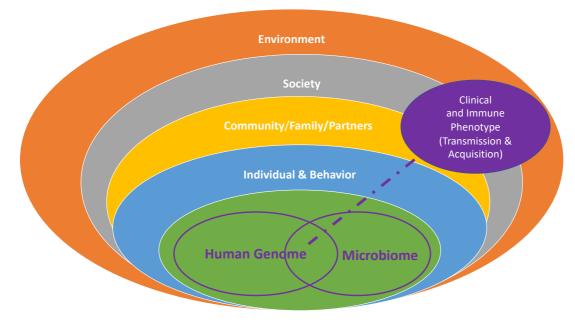
159

160 We argue that teaching current fundamental epidemiological skills will remain key to 161 exploiting scientific and technological advances. Applied infectious disease epidemiologists 162 will need the skills to define the problem, albeit within a socio-ecological-biological 163 framework (figure 1). They will need to know the benefits and limitations of different 164 epidemiological study designs for addressing the problem, their potential for biases (e.g. 165 through informative missing data and measurement bias), the role of chance and (often 166 unmeasured or unknown) confounding, and complex statistical methods, including those for 167 causal inference. They will still need to understand transmission dynamics (air, water, zoonosis, vector-borne, sexual, vertical and parenteral) within and across the life-course. 168 169 Furthermore, they will need to understand how to apply this knowledge to design and 170 evaluate interventions (including cluster randomised trials and quasi experimental methods); 171 and understand how mathematical modelling of transmission can (and generally should) be 172 used to inform scale-up and cost effectiveness.

173

174 However, over and above these concepts, infectious disease epidemiologists will need to 175 understand the way that biologists and social scientists think, i.e. be familiar with pathology 176 and clinical implications as well as the impact of the socio-economic and policy environment. 177 They will need to understand the type of research questions that new methods can answer, 178 their limitations, and how they can be integrated with more traditional approaches. 179 Moreover, they will need to embrace and critically appraise complex data and knowledge 180 from a wide range of sources and learn to include the communities and individuals affected by infection in developing and evaluating solutions^{47,48} and translating findings into policy. 181 182 While no single individual can be expected to have expertise in all of these disciplines, this

- 183 speaks to the importance of training in and rewarding a team science approach bring together
- 184 well-matched inter-disciplinary groups of scientists.^{49,50}
- 185
- 186



187

188 Figure 1: The socio-ecological biological framework to integrate microbiota into human ecology

189 Applying the socio-ecologic-biological framework to infectious disease epidemiology

190 We propose that the next generation of infectious disease epidemiologists must move 191 beyond the dichotomy between communicable and non-communicable diseases and use 192 epidemiological methods at the interface between human population health and 193 microorganisms. Key to this shift will be the expansion from the individual-human level focus 194 of many infectious disease epidemiology programmes to include the microbiota that cohabit 195 with pathogens in the host ecological space (the micro), the expression of this in human 196 communities (the meso), and the wider contextual drivers of disease (the macro) as well as 197 interactions between these. Such shifts are already happening in some training and research 198 programmes, but a systematic approach is vital to ensure all the key factors are included.¹⁸ 199

To assist conceptualisation, we propose an expanded socio-ecological framework that includes the interactions between hosts, pathogens and the wider microbiome as depicted in Figure 1. This socio-ecological-biological framework provides a model to facilitate how we include and critically appraise the range of factors that influence disease. To operationalise
this approach in training the next generation of infectious disease epidemiologists requires
teaching a basic understanding of biological sciences (basic immunology and microbiology),
clinical medicine, social sciences, data science and bioinformatics, engineering, politics and
economics, and public engagement, in relation to health, disease, and transmission.

208

209 Our aim is not a dilution of the discipline of epidemiology and its established methods. Rather 210 we aim to increase students' appreciation of the range of disciplines that contribute to the 211 field of infectious disease epidemiology, and how they can develop their intellectual skills to 212 critically engage across the disciplines. One way we have found to do this is to engage our 213 postgraduate students in inter-disciplinary problem solving through the use of experiential 214 learning techniques, such as vignettes (case studies that illustrate a problem). By using 215 facilitated group work with students simulating "disciplinary" roles, we have found that we 216 can illustrate the practical use of team-science approach, i.e. the need to be an expert in one 217 area, but responsive to and aware of the role of other disciplines in solving complex problems. 218 Furthermore, we ask students to apply the principles of basic immunology, microbiology and 219 pathogenesis to describe micro-organisms' adaptions to transmit (e.g. air-borne, faecal-oral 220 route, sexually transmitted, vector bourne and hospital acquired) as well as the implication 221 for clinical manifestation and thus measurement and case definitions. We present several 222 exemplar teaching vignettes to demonstrate how this integrated socio-ecological-biological 223 framework can be applied in infectious disease epidemiology teaching (Table 1).

224

Table 1: Using vignettes to teach students to use a socio-ecological-biological framework to apply infectious disease epidemiology to improve

human health⁵¹⁻⁵⁵

| Title | Vignette and questions | Interdisciplinarity needed | Key learning points |
|---------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Identifying and explaining an HIV micro-epidemic in a high-prevalence setting. | Phylogenetic analysis of HIV successfully identified the emergence of a new HIV outbreak not picked up through routine surveillance in rural KwaZulu-Natal, South Africa. Why did micro-epidemic occur? What could be done to prevent or control it? | Epidemiological data connected the outbreak to the opening of a new coalmine. Rapid ethnographic methods adapted from anthropology showed how this new industrial development had changed local socioeconomic dynamics by bringing men and money to an area of poverty. Community and public engagement to establish HIV prevention measures prior to the development may have prevented the outbreak. | Whilst the cluster was identified through phylogenetics, traditional epidemiological and social science methods were needed to understand why the outbreak occurred and how it could be controlled. Responsive public health systems may need to layer multiple methods to inform effective and ethical intervention strategies in close to real-time. |
| Causes and control strategies for an Ebola epidemic. | Recent outbreak investigations such as for Ebola in West Africa have used state- of-the art phylogenetic methods to detect and understand clusters of infections. ⁵¹ Why did the outbreaks happen? Why has the national and international response been slow? | Anthropologists, social scientists and health system analysts have been able to describe the role of poor health infrastructure and cultural reasons for health seeking behaviours in fuelling the epidemic. Traditional epidemiology, statistics, computational biology and modelling were used to plan vaccine trials. | The confluence of sociocultural conditions, health systems, and biology underlie the recent Ebola epidemic and all of these disciplines were needed to bring it under control. The effective deployment of a vaccine will require epidemiology, mathematical modelling, public health, and social science understanding of the context and acceptability. |
| The role of early infant microbial colonisation in driving subsequent health outcomes | Observational epidemiological studies have demonstrated associations between early life events (e.g. mode of delivery) and health outcomes such as childhood asthma and obesity. ^{52,53} Other studies have suggested that microbial colonisation is mediated by the same exposures. What is the mechanism for these changes? How might we intervene? | Infectious disease epidemiologists have needed to collaborate effectively with microbiologists, geneticists, lay parents, clinicians, bioinformaticians and statisticians to design longitudinal studies with early-life biobanking and life-long follow-up at sufficient scale to advance understanding of mechanisms and identify modifiable factors that might be subject to intervention. | It is currently unclear what might be a clinically relevant difference at a species level in early life microbial colonisation. Biology epidemiology understanding will be needed to define these differences and translate findings into public health responses. Public engagement will be key to understanding how and when to communicate these complex findings. |

| Establishing an evidence base for the role of digital technologies in controlling infections | The digital revolution is changing social relationships in ways that both impact on infectious disease transmission, e.g. widening social and sexual networks, and provide new opportunities to intervene, e.g. optimising real-time surveillance and revolutionising healthcare delivery. However, many digital health interventions, lack a strong evidence base and may exacerbate social exclusion along the digital divide. <i>Can mHealth deliver effective biomedical HIV care and prevention remote from facilities?</i> <i>Can social and sexual networks deliver this</i> <i>care?</i> <i>What will be the effect on transmission</i> <i>dynamics?</i> | To develop a contextually adapted intervention and safe clinical pathways, bioengineers have worked with human-computer interaction specialists , clinicians , members of the public , and social scientists . Epidemiologists and statisticians use developments in social network analysis and mathematical modellers can measure the impact on transmission dynamics and estimate the cost and cost effectiveness. Scale up and equitable access requires public engagement , economists , geographers , health systems and health policy specialists . | Digital health interventions are complex, requiring iterative theory-based development involving public and user engagement at every stage. We need to be able to evaluate the effectiveness, efficiency, and equity compared to traditional models of care. This can only be achieved through inter-disciplinary working across wide range of disciplines. |
|-------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| The changing transmission dynamics of shigella in high income settings. | Recent shigellosis epidemics driven by transmission between adult men have been observed in the UK, other parts of Europe, Australia and America. Traditional epidemiological studies, including those using male: female ratios and case finding studies with interviews, have demonstrated that these epidemics are linked to sexual behaviours in MSM, including chemsex (sexual activity under the influence of drugs) and social media apps that facilitate sexual networking. <i>How are these outbreaks sustained?</i> <i>How can we move from observation to control?</i> <i>What is the effect on propagation of AMR?</i> | Epidemiologists used surveillance data to monitor shigellosis outbreaks and worked with social scientists to understand the human behaviours. Working with microbiologists , bioinformaticians and comparative biologists has provided an additional layer of understanding by demonstrating that repeated horizontal transfer of a single plasmid containing multiple AMR determinants was associated with successful clonal strains. It seems likely that the shigella epidemics result from a combination of high-risk sexual behaviour, prescribing practices, and the ability of the pathogen to acquire selective evolutionary advantages and exploit a new ecological niche. Integrating advances in social network epidemiology , with phylogenetic analysis can provide further insights into this and other AMR and STI outbreaks. | There are major benefits from joining up thinking between epidemiology, i.e. observing the changing distribution of Shigella, evolutionary microbiology, i.e. identifying antibiotic resistant strain evolution, sexual network analysis i.e. understanding who has sex with who, and health systems, i.e. analysis of clinical policy and prescribing practices across time and space. |

| | · · · · · | | |
|------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Malaria transmission and endemicity in central Myanmar | Myanmar represents an important country for artemisinin resistant malaria and yet few data exist to inform control efforts and realise the WHO malaria elimination target for South East Asia. Internal economic migrants may be important to the ongoing endemicity of malaria in Myanmar, but are also a politically sensitive population What is the prevalence of malaria and artemisinin resistance in central Myanmar? What are the risk factors associated with malaria infection? | Epidemiologists needed to work with in-country clinicians , microbiologists and politicians to access remote and politically sensitive regions with appropriate ethical oversight to design and implement a cross-sectional prevalence survey. ⁵⁴ The blood samples collected were tested for parasites and drug resistance using molecular diagnostics, and for malaria serology. A combination of clinical parasitology , immunological , and biostatistical expertise was needed to interpret the molecular data. Social Science observations on the ground provided insights about the movements of working age men and their involvement in the forestry industry. | The value of molecular data can be substantially enhanced with individual-level clinical, behavioural, and sociodemographic data. Any interpretation (in this case of the finding that seroconversion to <i>P. falciparum</i> was 16-fold higher in men older than 23 years old) needs contextual information about human behaviours and the wider socio-economic and political environment in order to design effective and ethical public health responses. Community engagement and buy-in will be key to sustainable and scalable solutions. |
| Building evidence- based screening policies for tuberculosis in migrants to the UK | In high-income countries an increasing proportion of all tuberculosis cases are detected in migrants. In response to this changing epidemiological pattern, several countries have developed pre-migration tuberculosis screening programmes. Understanding the epidemiology of tuberculosis in migrants to improve the evidence-base of these screening policies is a public health priority. Can probabilistic linkage methods be used to identify migrants across datasets where no standard unique identifier exists? Can molecular strain typing data infer the incidence of active tuberculosis disease in pre- entry screened migrants that is potentially preventable through additional latent tuberculosis infection screening? | Epidemiologists, computer scientists and mathematicians worked together to develop and valid probabilistic methods that could be used to identify non-UK born individuals across separate datasets. These newly validated methods were used to construct a population-based cohort of 519 955 migrants screened before entry to England, Wales, and Northern Ireland. ⁵⁵ Working with molecular epidemiologists and using these newly linked data it was possible to improve our understanding of epidemiology in migrants previously screened for active tuberculosis. This new evidence was then used by Public Health experts and national and international policy makers to improve global screening policies. | This work required a public health data science approach that combined the skills of epidemiologists, computer scientists and mathematicians in order develop and understand new methods and apply these to newly linked datasets that gave new insights and actionable evidence to improve screening for tuberculosis in this population. Public engagement and community advocacy were key to translating the evidence into effective policy and practice. |

230 In conclusion:

231 The field of infectious disease epidemiology is changing rapidly due to improved 232 understanding of disease causation and the role of microbes in a wide range of non-233 communicable as well as communicable diseases. The molecular characterisation of both the 234 pathogen and the host are enabling better understanding of transmission and host networks, 235 however, there are major challenges in bringing these different disciplines together and 236 ensuring critical appraisal in doing so. Moreover, we need to measure and include the 237 environment in disease models if we are to understand complex infectious disease problems. 238 Finally, we need to engage the affected communities, if we are to successfully intervene on 239 complex infectious disease problems at a population level.

240

241 New approaches to teaching need to account for developments in our understanding of 242 infection-related ill health, incorporate emerging technologies, and encourage collaboration 243 across disparate disciplines – including basic science, clinical medicine, statistics and social 244 science. Achieving these goals will require innovative ways of teaching infection disease 245 epidemiology, at the core of which lies the need for familiarity and openness across a range 246 of disciplines, expertise in one or two, and much practice in team-based problem solving. We 247 believe this approach will provide awareness of allied disciplines, and the ability to make 248 connections between fields. Such change is feasible but will require active adaptation and 249 robust evaluation of the outcomes of training programmes.

| Ке | ey messages box: |
|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| • | The field of infectious disease epidemiology is changing rapidly, with: |
| | Better understanding of disease causation and the role of microbes in a wid of disease; |
| | Molecular characterisation of the microbe as well as the host, leading to be understanding of interactions in the ecology of each and translation of this |
| | transmission networks; |
| | Better tools to measure and understand the social and environmental content |
| • | These changes require a response that brings new ways of thinking about teaching |
| | infectious disease epidemiology that includes the macro, meso and micro and: |
| | Connects across basic science, clinical medicine, political and social science, cultural understanding, and population health and statistics in asking and answering the right research questions; |
| | Incorporates emerging technologies to collect and understand complex and dynamic data with a critical approach to the limitations of these methods; |
| | Builds the intellectual skills to critically engage with disparate disciplines an methods, including recognising their strengths and limitations, and new eth dilemmas that may arise. |
| | Keep the voices of the communities affected by infection at the heart of any enquiry |

253 Contributors:

MS and NF conceived the personal view. MS, NF, GHarl, CC, CK were involved in early discussions and mapping the concepts that led to the paper. MS, NF, GHarl, CC, HB, CK, RWA and JG contributed the vignettes, MS, NF, GHarl, and CC wrote the first draft of the manuscript. MS, NF, GHarl, CC, HB, CK, RWA, JG, JS, AP, CAS, PS, GH, MR, DP, AMJ, IA, read and critically revised drafts of the manuscript.

259

260 **Funding:**

MS is in receipt of a National Institutes of Health (NIH) grant 5R01MH114560-03 and her work at the Africa Health Research Institute is supported by a grant from the Wellcome Trust (082384/Z/07/Z). CS is in receipt of a National Institute for Health Research (NIHR) Health Protection Research Unit (HPRU) in Blood-Borne and Sexually Transmitted Infections at UCL in partnership with Public Health England'; and is a co-app on an NIH grant (R01 HL131049); IA has an NIHR senior investigator award (NF-SI-0616-10037). GHarling is supported by a fellowship from the Wellcome Trust and Royal Society (210479/Z/18/Z).

268

.

The views expressed are those of the authors and not necessarily those of the NIHR, the Department of Health and Social Care or Public Health England; Wellcome Trust or NIH. None of our funders played a role in the writing of the manuscript or the decision to submit it for publication.

- 273
- 274 Declaration of Interest:
- 275 We declare that we have no conflicts of interest."
- 276
- 277 Ethics
- 278 Not applicable
- 279

280

281 References

282

Collignon P, Beggs JJ, Walsh TR, Gandra S, Laxminarayan R. Anthropological and
 socioeconomic factors contributing to global antimicrobial resistance: a univariate and
 multivariable analysis. *Lancet Planet Health* 2018; **2**(9): e398-e405.

286 2. Whitmee S, Haines A, Beyrer C, et al. Safeguarding human health in the
287 Anthropocene epoch: report of The Rockefeller Foundation-Lancet Commission on
288 planetary health. *Lancet* 2015; **386**(10007): 1973-2028.

3. Steffen W, Rockstrom J, Richardson K, et al. Trajectories of the Earth System in the
Anthropocene. *Proc Natl Acad Sci U S A* 2018; **115**(33): 8252-9.

4. UNAIDS. Global AIDS Update 2018. Miles to go: closing gaps, breaking barriers,righting injustices, 2018.

Global Burden of Disease Causes of Death Collaborators. Global, regional, and
 national age-sex-specific mortality for 282 causes of death in 195 countries and territories,
 1980-2017: a systematic analysis for the Global Burden of Disease Study 2017. *Lancet* 2018;
 392(10159): 1736-88.

297 6. Cani PD. Human gut microbiome: hopes, threats and promises. *Gut* 2018; 67(9):
298 1716-25.

Flint HJ, Scott KP, Louis P, Duncan SH. The role of the gut microbiota in nutrition and
health. *Nat Rev Gastroenterol Hepatol* 2012; **9**(10): 577-89.

Shanahan F. The gut microbiota-a clinical perspective on lessons learned. *Nat Rev Gastroenterol Hepatol* 2012; **9**(10): 609-14.

9. United Nations Development Programme, International Federation of Red Cross and
 Red Crescent Societies (IFRC). A socio-economic impact assessment of the zika virus in Latin
 America and the Caribbbean: with a focus on Brazil, Colombia and Suriname. Available
 <u>https://www.undp.org/content/undp/en/home/librarypage/hiv-aids/a-socio-economic-</u>
 <u>impact-assessment-of-the-zika-virus-in-latin-am.html</u>, accessed May 2019, 2017.

Calistri P, Iannetti S, Danzetta ML, et al. The components of 'One World - One Health'
approach. *Transbound Emerg Dis* 2013; **60 Suppl 2**: 4-13.

310 11. Khan MM, Ernst O, Manes NP, et al. Multi-Omics Strategies Uncover Host-Pathogen
311 Interactions. ACS Infect Dis 2019; 5(4): 493-505.

312 12. Karczewski KJ, Snyder MP. Integrative omics for health and disease. *Nat Rev Genet*313 2018; **19**(5): 299-310.

Bogyo M, Rudd PM. New technologies and their impact on 'omics' research. *Curr Opin Chem Biol* 2013; **17**(1): 1-3.

Holmes EC, Dudas G, Rambaut A, Andersen KG. The evolution of Ebola virus: Insights
from the 2013-2016 epidemic. *Nature* 2016; **538**(7624): 193-200.

318 15. Wagner M, Lampos V, Cox IJ, Pebody R. The added value of online user-generated
319 content in traditional methods for influenza surveillance. *Sci Rep* 2018; 8(1): 13963.

Hayward AC, Fragaszy EB, Bermingham A, et al. Comparative community burden and
 severity of seasonal and pandemic influenza: results of the Flu Watch cohort study. *Lancet Respir Med* 2014; 2(6): 445-54.

323 17. Coltart CEM, Hoppe A, Parker M, et al. Ethical considerations in global HIV
324 phylogenetic research. *Lancet HIV* 2018; 5(11): e656-e66.

Brownson RC, Samet JM, Chavez GF, et al. Charting a future for epidemiologic
training. *Ann Epidemiol* 2015; **25**(6): 458-65.

327 19. Samet JM, Woodward A. On Being an Epidemiologist. *American Journal of*328 *Epidemiology* 2019; **188**(5): 818-24.

329 20. Virchow RLK, Rather LJ. Collected essays on public health and epidemiology: Science330 History Publications, USA; 1985.

Link BG, Phelan J. Social conditions as fundamental causes of disease. *J Health Soc Behav* 1995; **35**(Extra Issue): 80-94.

333 22. Krieger N. Epidemiology and the People's Health: Theory and Context. New York, NY:334 Oxford University Press; 2011.

335 23. Berkman LF, Kawachi I, Glymour MM. Social epidemiology: Oxford University Press;336 2014.

337 24. Bronfenbrenner U. The Ecology of Human Development: Experiments by Nature and
338 Design. Cambridge, Massachusetts: Harvard University Press; 1979.

339 25. Marmot M, Friel S, Bell R, Houweling TA, Taylor S, Health CoSDo. Closing the gap in a
340 generation: health equity through action on the social determinants of health. *Lancet* 2008;
341 372(9650): 1661-9.

342 26. Asaria P, Chisholm D, Mathers C, Ezzati M, Beaglehole R. Chronic disease prevention:
343 health effects and financial costs of strategies to reduce salt intake and control tobacco use.
344 *Lancet* 2007; **370**(9604): 2044-53.

345 27. Menzies D, Nair A, Williamson PA, et al. Respiratory symptoms, pulmonary function,
346 and markers of inflammation among bar workers before and after a legislative ban on
347 smoking in public places. *JAMA* 2006; **296**(14): 1742-8.

348 28. Sargent RP, Shepard RM, Glantz SA. Reduced incidence of admissions for myocardial
349 infarction associated with public smoking ban: before and after study. *BMJ* 2004; **328**(7446):
350 977-80.

Falbe J, Thompson HR, Becker CM, Rojas N, McCulloch CE, Madsen KA. Impact of the
Berkeley excise tax on sugar-sweetened beverage consumption. *Am J Public Health* 2016; **106**(10): 1865-71.

30. He FJ, MacGregor GA. Effect of modest salt reduction on blood pressure: a metaanalysis of randomized trials. Implications for public health. *J Hum Hypertens* 2002; **16**(11):
761.

357 31. DeBold T, Friedman D. Battling infectious diseases in the 20th century: the impact of
358 vaccines. *Wall Street Journal* 2015.

359 32. Scully T. The age of vaccines. *Nature* 2014; **507**(7490): S2-S3.

360 33. Garland SM, Cornall AM, Brotherton JM, et al. Final analysis of a study assessing
361 genital human papillomavirus genoprevalence in young Australian women, following eight
362 years of a national vaccination program. *Vaccine* 2018; **36**(23): 3221-30.

363 34. Greenwood BM. The microepidemiology of malaria and its importance to malaria 364 control. *Trans R Soc Trop Med Hyg* 1989; **83 Suppl**: 25-9.

365 35. Tanser F, Barnighausen T, Cooke GS, Newell ML. Localized spatial clustering of HIV
366 infections in a widely disseminated rural South African epidemic. *Int J Epidemiol* 2009; **38**(4):
367 1008-16.

368 36. Morris CN, Ferguson AG. Estimation of the sexual transmission of HIV in Kenya and
369 Uganda on the trans-Africa highway: the continuing role for prevention in high risk groups.
370 Sex Transm Infect 2006; 82(5): 368-71.

37. Campbell C. Migrancy, masculine identities and AIDS: the psychosocial context of HIV
372 transmission on the South African gold mines. *Soc Sci Med* 1997; **45**(2): 273-81.

373 38. Terrence Higgins Trust. <u>https://www.iwantprepnow.co.uk</u> Accessed May 2019.

374 39. The International Vaccine Access Centre, <u>https://www.jhsph.edu/ivac/about/</u>
375 Accessed May 2019.

376 40. Gavi, the Vaccine Alliance <u>https://www.gavi.org/about/</u>, Accessed May 2019.

Saul J, Bachman G, Allen S, Toiv NF, Cooney C, Beamon T. The DREAMS core package
of interventions: A comprehensive approach to preventing HIV among adolescent girls and
young women. *PLoS One* 2018; **13**(12): e0208167.

Schaefer R, Gregson S, Fearon E, Hensen B, Hallet TB, Hargreaves JR. HIV prevention
cascades: a unifying framework to replicate the successes of treatment cascades. *The Lancet HIV* 2019; **6**: 60-6.

383 43. Dube E, Vivion M, MacDonald NE. Vaccine hesitancy, vaccine refusal and the anti384 vaccine movement: influence, impact and implications. *Expert Rev Vaccines* 2015; **14**(1): 99385 117.

Kang GJ, Ewing-Nelson SR, Mackey L, et al. Semantic network analysis of vaccine
sentiment in online social media. *Vaccine* 2017; **35**(29): 3621-38.

Little J, Higgins JPT, Ioannidis JPA, Moher D, Gagnon F, et al. STrengthening the
REporting of Genetic Association Studies (STREGA)—An extension of the STROBE Statement. *PLoS Med* (2009); 6(2): e1000022. doi:10.1371/journal.pmed.1000022

391 46. Field N, Cohen T, Struelens MJ, et al. Strengthening the Reporting of Molecular
392 Epidemiology for Infectious Diseases (STROME-ID): an extension of the STROBE
393 statement. *Lancet Infect Dis* 2014; 14(4): 341-52.

47. Concannon D, Herbst K, Manley E. Developing a Data Dashboard Framework for
Population Health Surveillance: Widening Access to Clinical Trial Findings. *JMIR Form Res*2019; **3**(2): e11342.

397 48. Bakker KM, Martinez-Bakker ME, Helm B, Stevenson TJ. Digital epidemiology reveals
398 global childhood disease seasonality and the effects of immunization. *Proc Natl Acad Sci U S*399 A 2016; **113**(24): 6689-94.

49. Bennett LM, Gadlin H. Collaboration and team science: from theory to practice. J
401 Investig Med 2012; 60(5): 768-75.

402 50. The Academy of Medical Sciences. Improving recognition of team science403 contributions in biomedical research careers, 2016.

Gire SK, Goba A, Andersen KG, et al. Genomic surveillance elucidates Ebola virus
origin and transmission during the 2014 outbreak. *Science* 2014; **345**(6202): 1369-72.

- Sandall J, Tribe RM, Avery L, et al. Short-term and long-term effects of caesarean
 section on the health of women and children. *Lancet* 2018; **392**(10155): 1349-57.
- Herd P, Palloni A, Rey F, Dowd JB. Social and population health science approaches
 to understand the human microbiome. *Nature Human Behaviour* 2018; **2**: 808-15.
- 410 54. Ghinai I, Cook J, Hla TT, et al. Malaria epidemiology in central Myanmar:
- 411 identification of a multi-species asymptomatic reservoir of infection. *Malar J* 2017; **16**(1):
- 412 16.

Aldridge RW, Zenner D, White PJ, et al. Tuberculosis in migrants moving from highincidence to low-incidence countries: a population-based cohort study of 519 955 migrants
screened before entry to England, Wales, and Northern Ireland. *Lancet* 2016; **388**(10059):
2510-8.