WHO Blueprint priority pathogen systematic reviews

Anne Cori, Gina Cuomo-Dannenburg, Sabine Van Elsland
On behalf of the Imperial College Priority Pathogen group

MRC Centre for Global Infectious Disease Analysis

WHO Collaborating Centre for Infectious Disease modelling

School of Public Health
Imperial College London

Rationale and overview

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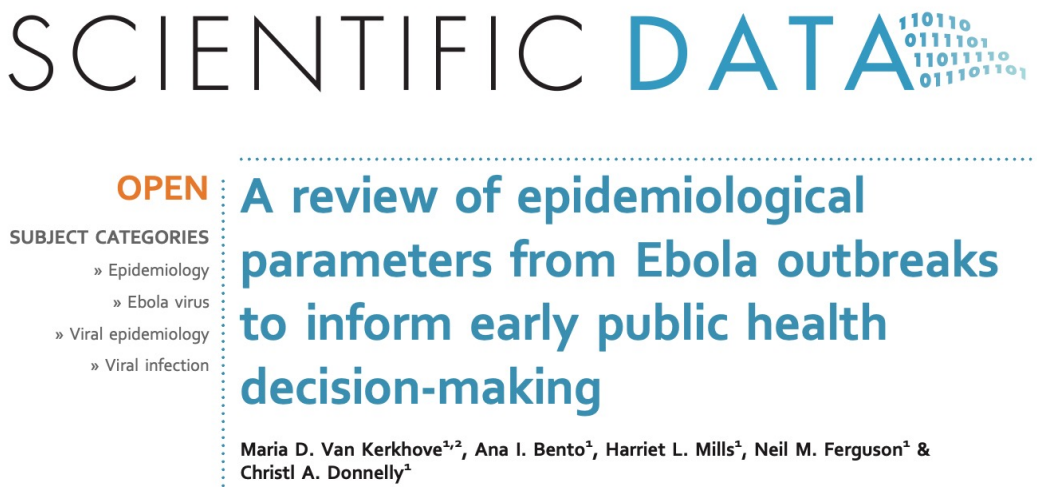
- MRC Centre for Global Infectious Disease Analysis
- WHO collaborating centre for modelling, aiming to provide rapid analysis of urgent infectious disease threats

- Typically designing ID models from early on in epidemics to answer important public health questions

→ Requires rapidly compiling current knowledge on a given pathogen


SCIENTIFIC DATA

OPEN

SUBJECT CATEGORIES
» Epidemiology
» Ebola virus
» Viral epidemiology
» Viral infection

A review of epidemiological parameters from Ebola outbreaks to inform early public health decision-making

Maria D. Van Kerkhove[1,2], Ana I. Bento[1], Harriet L. Mills[1], Neil M. Ferguson[1] & Christl A. Donnelly[1]

→ We often do this in real-time, but we could
  → Be proactive
  → Generate a "live" database of parameter values
  → For "important" pathogens

→ Project started in 2019, using the WHO blueprint priority disease list at the time

→ Paused for the best part of the COVID-19 pandemic

→ Recently re-started

Project Aims

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- To systematically review mathematical models, parameter values, and historical outbreaks for all listed pathogens, excluding disease X:
  - CCHF
  - Ebola
  - Lassa fever
  - Marburg virus disease
  - MERS
  - Nipah and henipaviral diseases
  - Rift valley fever
  - SARS
  - Zika

- To collate information enabling rapid mathematical modelling of these 9 pathogens including:
  - model structures
  - fatality ratios
  - reproduction numbers
  - risk factors (severity & transmission)
  - mutation rates
  - seroprevalence
  - historical outbreaks

Project organization and anticipated outputs

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Who is involved:

- A group of ~20 volunteer researchers interested in outbreaks
- No dedicated funding nor anyone's main project

Anticipated outputs:

- A database storing all the information extracted
  - Which would be designed to be easily updated with any new information (new parameter estimates / new pathogens)
- A series of papers:
  - 9 disease specific papers
  - 1 overview paper comparing the pathogens
    - Archetype pathogens according to their characteristics
    - Facilitating the classification of novel pathogens against these "archetypes"

Search strategy (search performed in 2019)

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- We searched in OVID Medline, Embase and Web of Science:
- **Marburg** *AND (virus OR disease)* AND ((transmission OR epidemiology) OR (model* NOT imag*) OR (“burden” OR “severity” OR “case fatality ratio” OR “CFR”) OR (“serial interval” OR “incubation period” OR “generation time”) OR (“heterogeneity” OR “superspread*”) OR (“reproduction number” OR "reproductive number" OR "R0") OR (“pre-existing immunity” OR “serological” OR “serology” OR “serosurveys”) OR (diagnostic OR diagnosis OR test*) OR ("evolutionary rate" OR "genetic mutation" OR evolution) OR (outbreak OR cluster OR epidemic) OR (“risk factor*”) OR (“case definition”))

- *(adapted with other pathogen names)*
- For Marburg only we added *terms* to exclude Marburg city

Study screening

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	title and abstracts	full text	data extraction
CCHF	1967	656	247
Ebola	9563	1277	420
Lassa	1760	322	102
Marburg	2707	190	42
MERS	10382	623	179
Nipah	959	148	58
RVF	3341	418	149
SARS	11918	800	347
Zika	4518	238	144
total	47115	4672	1688

Marburg: only one published model identified

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OPEN ACCESS Freely available online

PLOS ONE

Transmission Potential and Design of Adequate Control Measures for Marburg Hemorrhagic Fever

Marco Ajelli*, **Stefano Merler**

Bruno Kessler Foundation, Trento, Italy

Abstract

Marburg hemorrhagic fever is rare yet among the most severe diseases affecting humans, with case fatality ratio even higher than 80%. By analyzing the largest documented Marburg hemorrhagic fever epidemic, which occurred in Angola in 2005 and caused 329 deaths, and data on viral load over time in non-human primates, we make an assessment of transmissibility and severity of the disease. We also give insight into the control of new Marburg hemorrhagic fever epidemics to inform appropriate health responses. We estimated the distribution of the generation time to have mean 9 days (95%CI: 8.2–10 days) and standard deviation 5.4 days (95%CI: 3.9–8.6 days), and the basic reproduction number to be $R_0 = 1.59$ (95%CI: 1.53–1.66). Model simulations suggest that a timely isolation of cases, starting no later than 2–3 days after symptoms onset, is sufficient to contain an outbreak. Our analysis reveals that Marburg hemorrhagic fever is characterized by a relatively small reproduction number and by a relatively long generation time. Such factors, along with the extremely high severity and fatality, support the rare occurrence of large epidemics in human populations. Our results also support the effectiveness of social distancing measures - case isolation in particular - to contain or at least to mitigate an emerging outbreak. This work represents an advance in the knowledge required to manage a potential Marburg hemorrhagic fever epidemic.

Citation: Ajelli M, Merler S (2012) Transmission Potential and Design of Adequate Control Measures for Marburg Hemorrhagic Fever. PLoS ONE 7(12): e50948. doi:10.1371/journal.pone.0050948

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* E-mail: ajelli@fbk.eu

- stochastic individual based model
- fitted to data from 2005 Angola epidemic
- examining the impact of social distancing and behaviour changes
- estimated
  - reproduction number,
  - generation time,
  - doubling time

Marburg: overview of parameters retrieved from the literature

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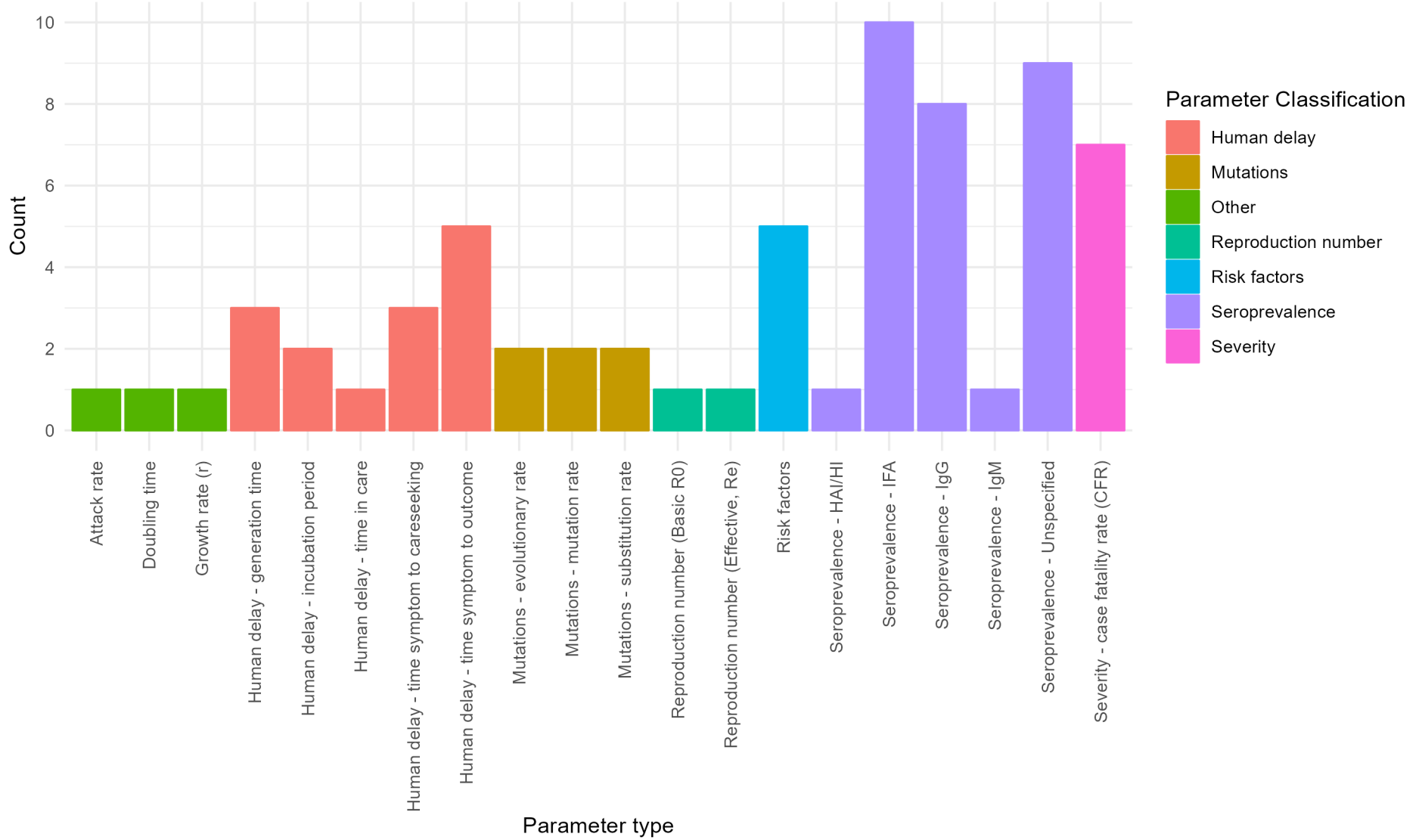

Marburg: overview of reproduction numbers

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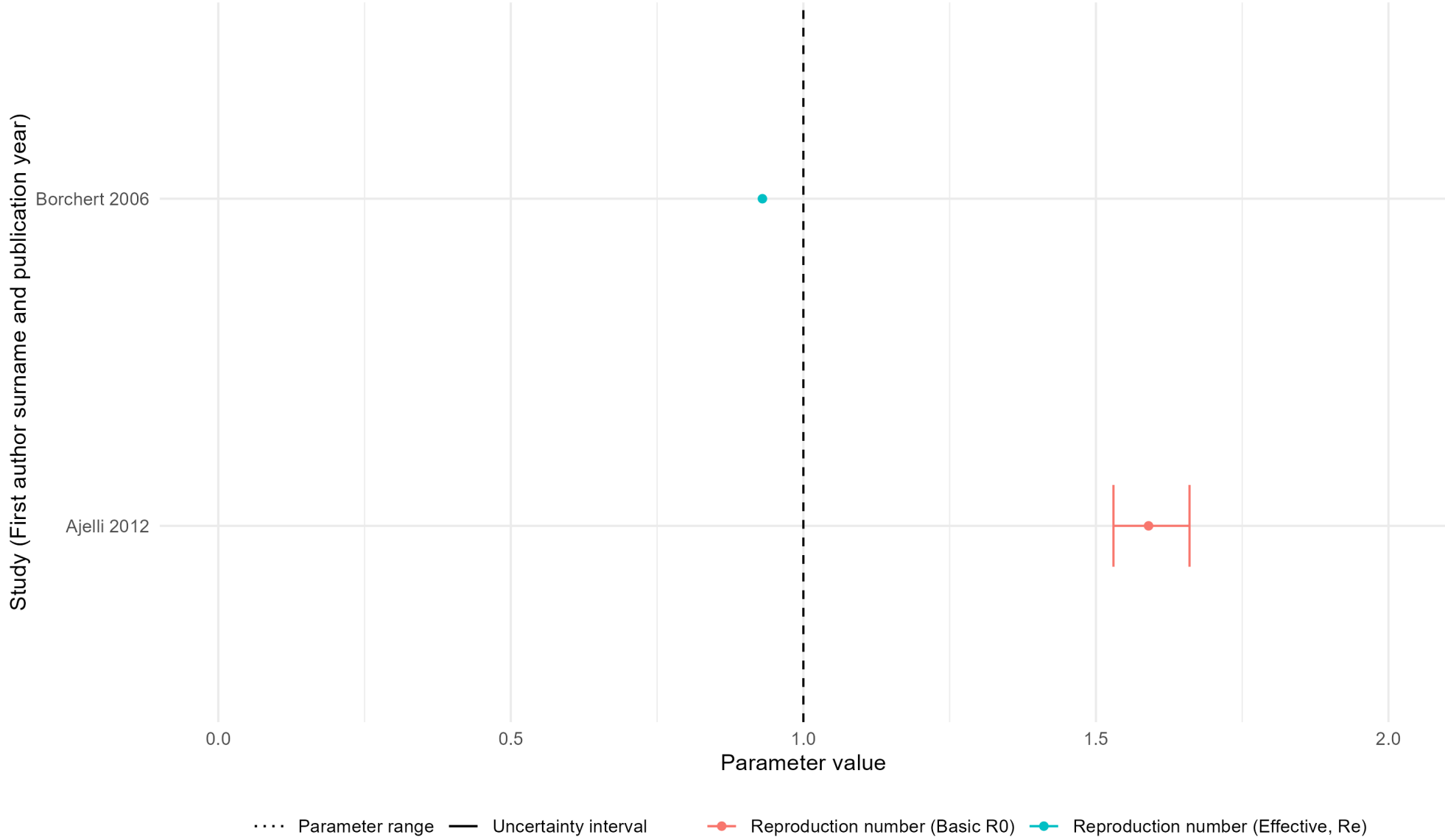

Next steps

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- Finalise extraction
- Repeating the literature search to capture new papers since original search
- Discussion with journals about collection of articles
- Synthesising extracted information
  - Across inconsistent reporting formats (e.g. mean & 95%CrI vs median & IQR)
  - Across different contexts (e.g. different countries, populations, epidemic stages)
  - Accounting for study “quality”
- Constructing a dynamic database
  - Extracted info as a “starting point”
  - What format? How to manage future contributions?
- Expansion to other pathogens / parameters?

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