Risk management in the public health context

The COVID-19 experience of risk-based decision making in Ireland

Philip Nolan

Director General, Science Foundation Ireland
Chair, Irish Epidemiological Modelling Advisory Group

PDA Ireland – PRST TU Dublin Joint Seminar and Workshop **8 September 2022**

Approach

- Pharmaceutical quality systems as *"a framework for delivering quality products to patients"* [1]
- Public health emergency responses as a framework for delivering quality public health interventions in populations
- *"Science and risk-based decisions"* (ICH Q10) require a mutually reinforcing relationship between risk management and knowledge management [1]
- "Knowledge", "science" and "evidence" are dynamic, contested and sometimes unstable

[1] Greene A & Lipa M "Steps Towards Digital Transformation in the Pharmaceutical Manufacturing Landscape Knowledge-Enabled Technology Transfer" *Level 3 17(2)1*

Irish Epidemiological Modelling Advisory Group (IEMAG)

- Ireland had no formal national advanced biostatistics or disease modelling infrastructure
- 8-13 March 2020 – *ad hoc* group mobilized from across university and public health system
  - Monitor and model pandemic in Ireland
  - Irish Epidemiological Modelling Advisory Group (IEMAG)
  - Applied mathematics, statistics, computer science, geospatial science, epidemiology, public health
  - Membership grew dynamically over time – 50 members in 4 working groups
- IEMAG reported to a wider National Public Health Emergency Team (NPHET) which was also a very large group (>40)
- *"Monitor and model the COVID-19 outbreak in Ireland"*
  - Knowledge management: data – information – insight – action
  - Risk assessment

Data infrastructures

PCR testing
NVRL and HSE laboratory systems

Positive tests and contacts
Contact Management Programme (CMP)
COVID Care Tracker (CCT)

Antigen test portal
Contact Management Programme (CMP)

Cases
Health Protection Surveillance Centre (HPSC)
Computerised Infectious Disease Record (CIDR)

Genotyping
NVRL WGS and SGT data

Vaccination
HSE CoVAX

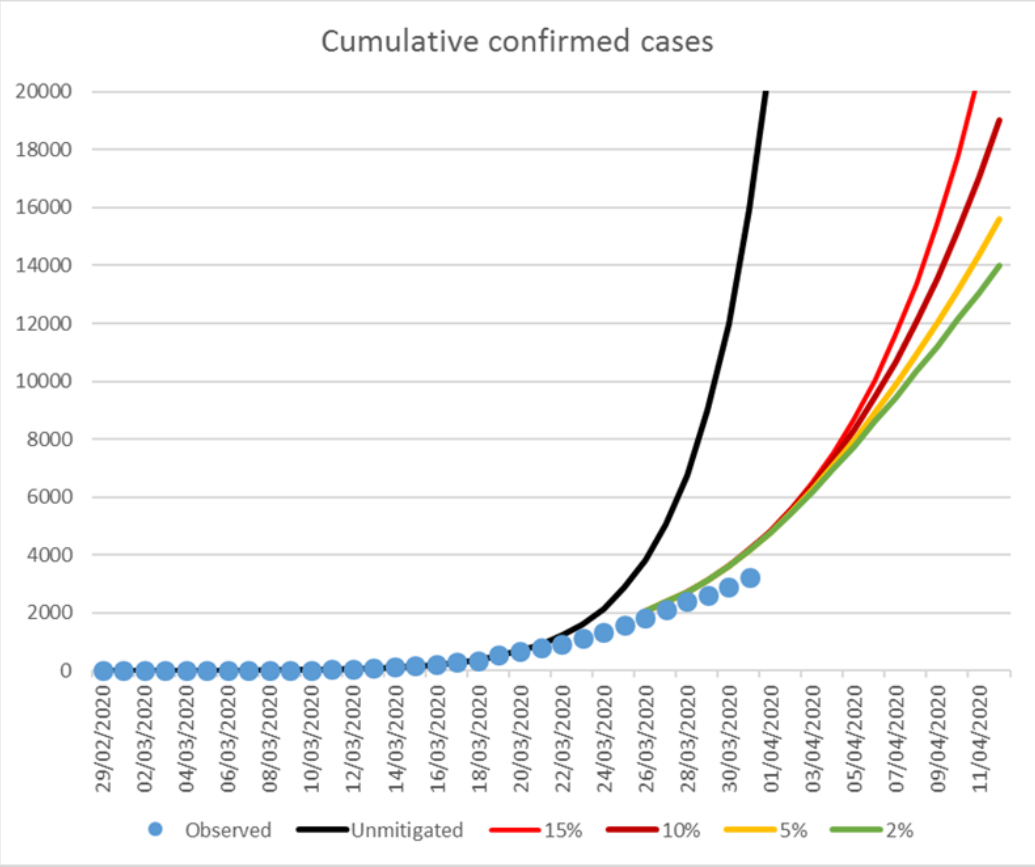
Hospital admissions
HSE-PMIU-SDU daily data
HIPE

ICU admissions
NOCA ICU-BIS

Data incomplete, delayed, unlinked, not geocoded
Slow negotiation of data sharing agreements
Systems not integrated
Failure to implement an individual health identifier and Eircode

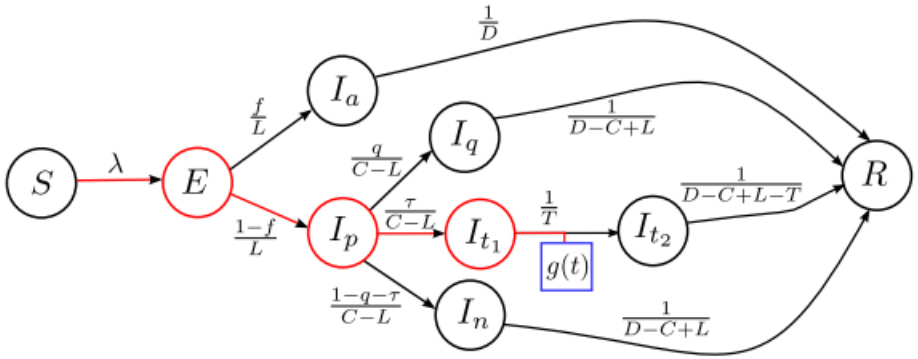
Data governance
Societal questions of privacy, security and trust

Early exponential growth projections



Exponential growth projections from 26 March 2020, at different growth rates

SEIR models



I_a: asymptomatic infected
I_p: presymptomatic infected
I_q: symptomatic infected quarantined
I_t: symptomatic infected quarantined and tested
I_n: symptomatic not quarantined

$$\frac{dS}{dt} = -\lambda S$$

$$\frac{dE}{dt} = \lambda S - \frac{1}{L}E$$

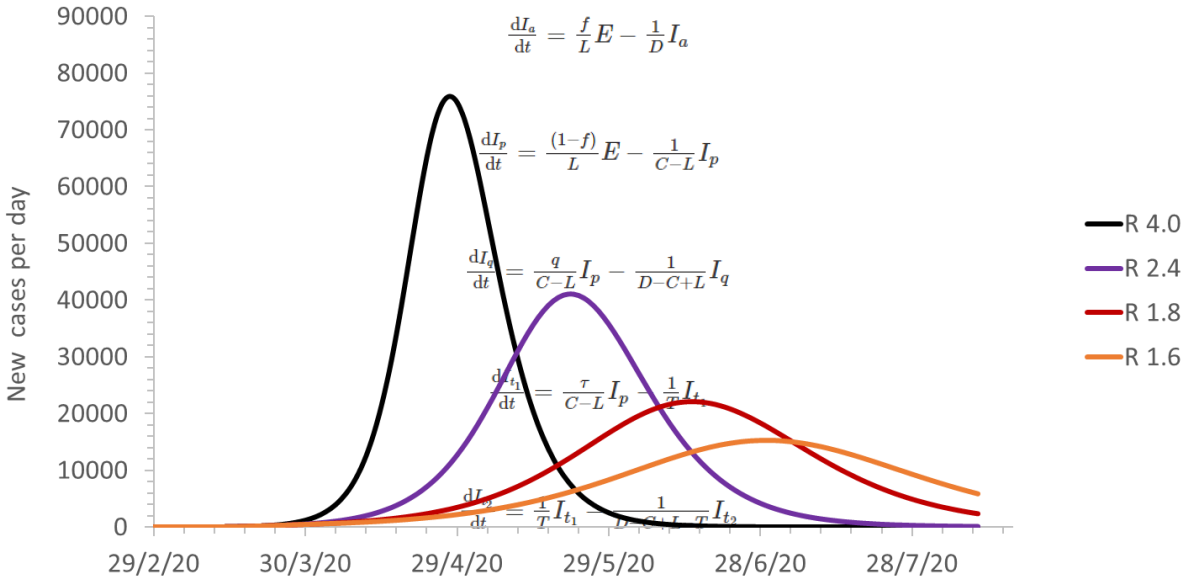
$$\frac{dI_a}{dt} = \frac{f}{L}E - \frac{1}{D}I_a$$

$$\frac{dI_p}{dt} = \frac{(1-f)}{L}E - \frac{1}{C-L}I_p$$

$$\frac{dI_q}{dt} = \frac{q}{C-L}I_p - \frac{1}{D-C+L}I_q$$

$$\frac{dI_{t_1}}{dt} = \frac{\tau}{C-L}I_p - \frac{1}{T}I_{t_1}$$

$$\frac{dI_{t_2}}{dt} = \frac{1}{T}I_{t_1} - \frac{1}{D-C+L-T}I_{t_2}$$



$$\frac{dI_n}{dt} = \frac{(1-q-\tau)}{C-L}I_p - \frac{1}{D-C+L}I_n$$

and $$\frac{dR}{dt} = \frac{1}{D}I_a + \frac{1}{D-C+L}I_q + \frac{1}{D-C+L-T}I_{t_2} + \frac{1}{D-C+L}I_n,$$

UCD CVERA evidence synthesis

Centre for Veterinary Epidemiology and Risk Analysis

Incubation period

Open access Original research

BMJ Open

Incubation period of COVID-19: a rapid systematic review and meta-analysis of observational research

Conor McAloon ,[1] Áine Collins,[2] Kevin Hunt,[3] Ann Barber,[2] Andrew W Byrne ,[4] Francis Butler,[3] Miriam Casey ,[2] John Griffin ,[5] Elizabeth Lane,[6] David McEvoy ,[7] Patrick Wall,[7] Martin Green,[8] Luke O'Grady,[1,8] Simon J More[2]

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For numbered affiliations see end of article.

Correspondence to
Dr Conor McAloon;
conor.mcaloon@ucd.ie

ABSTRACT

Objectives The aim of this study was to conduct a rapid systematic review and meta-analysis of estimates of the incubation period of COVID-19.

Design Rapid systematic review and meta-analysis of observational research.

Setting International studies on incubation period of COVID-19.

Participants Searches were carried out in PubMed, Google Scholar, Embase, Cochrane Library as well as the preprint servers MedRxiv and BioRxiv. Studies were selected for meta-analysis if they reported either the parameters and CIs of the distributions fit to the data, or sufficient information to facilitate calculation of those values. After initial eligibility screening, 24 studies were selected for initial review, nine of these were shortlisted for meta-analysis. Final estimates are from meta-analysis of eight studies.

Primary outcome measures Parameters of a lognormal distribution of incubation periods.

Results The incubation period distribution may be modelled with a lognormal distribution with pooled mu and sigma parameters (95% CIs) of 1.63 (95% CI 1.51 to 1.75) and 0.50 (95% CI 0.46 to 0.55), respectively. The corresponding mean (95% CIs) was 5.8 (95% CI 5.0 to 6.7) days. It should be noted that uncertainty increases towards the tail of the distribution: the pooled parameter estimates (95% CIs) resulted in a median incubation period of 5.1 (95% CI 4.5 to 5.8) days, whereas the 95th percentile was 11.7 (95% CI 9.7 to 14.2) days.

Conclusions The choice of which parameter values are adopted will depend on how the information is used, the associated risks and the perceived consequences of decisions to be taken. These recommendations will need to be revisited once further relevant information becomes available. Accordingly, we present an R Shiny app that facilitates updating these estimates as new data become available.

Strengths and limitations of this study

- This study provides a pooled estimate of the distribution of incubation periods which may be used in subsequent modelling studies or to inform decision-making.
- Several studies used data that were publicly available, therefore there is potential that some of the data may be used for more than one study.
- This estimate will need to be revisited as subsequent data become available. Accordingly, we present an R Shiny app to allow the meta-analysis to be updated with new estimates.

INTRODUCTION

Reliable estimates of the incubation period are important for decision-making around the control of infectious diseases in human populations. Knowledge of the incubation period can be used directly to inform decision-making around infectious disease control. For example, the maximum incubation period can be used to inform the duration of quarantine, or active monitoring periods of people who have been at high risk of exposure. Estimates of the duration of the incubation period, coupled with estimates of the latent period, serial interval or generation times, may help infer the duration of the presymptomatic infectious period, which is important in understanding both the transmission of infection and opportunities for control.[1] Finally, decision-making in the midst of a pandemic often relies on predicted events, such as daily number of new infections, from mathematical models. Such models depend on key input parameters relevant to the transmission of the specific infectious disease. It is important that input parameters into such models are as robust as possible. Given that some models fit data to many parameters, only some of which are specifically of interest but all of which are interdependent, output estimates may be compared with the robust estimates as part of the validation of the model.

Earlier work has shown that for models of respiratory infections, statements regarding

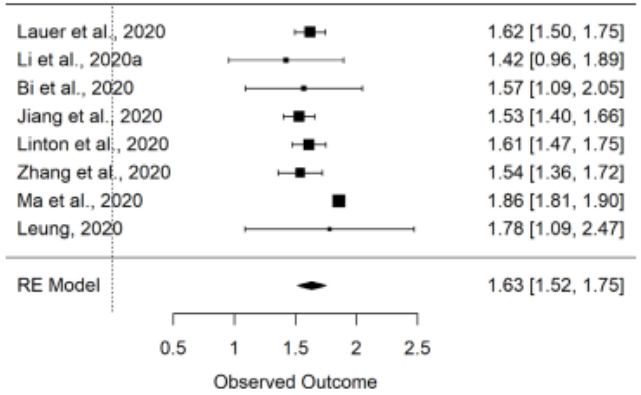

Figure 1 Forest plot of the random effects (RE) meta-analysis of mu parameter of the lognormal distribution of incubation period.

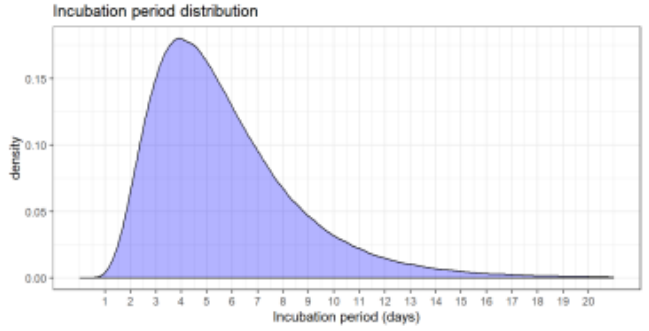

Figure 3 Probability density function of the pooled lognormal distribution of reported incubation period with mu=1.63 and sigma=0.50.

UCD CVERA evidence synthesis

Centre for Veterinary Epidemiology and Risk Analysis

Science Foundation Ireland sfi For what's next

Presymptomatic transmission

Open access Original research

BMJ Open

Presymptomatic transmission of SARS-CoV-2 infection: a secondary analysis using published data

Miriam Casey-Bryars ,[1] John Griffin ,[1] Conor McAloon ,[2] Andrew Byrne ,[3] Jamie Madden,[1] David Mc Evoy ,[4] Áine Collins,[1] Kevin Hunt,[5] Ann Barber,[1] Francis Butler,[5] Elizabeth Ann Lane ,[6] Kirsty O'Brien,[7] Patrick Wall,[8] Kieran Walsh,[7] Simon John More [1]

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For numbered affiliations see end of article.

Correspondence to
Dr Miriam Casey-Bryars; miriam.casey@ucd.ie

ABSTRACT

Objective To estimate the proportion of presymptomatic transmission of SARS-CoV-2 infection that can occur, and the timing of transmission relative to symptom onset.
Setting/design Secondary analysis of international published data.
Data sources Meta-analysis of COVID-19 incubation period and a rapid review of serial interval and generation time, which are published separately.
Participants Data from China, the Islamic Republic of Iran, Italy, Republic of Korea, Singapore and Vietnam from December 2019 to May 2020.
Methods Simulations were generated of incubation period and of serial interval or generation time. From these, transmission times relative to symptom onset, and the proportion of presymptomatic transmission, were estimated.
Outcome measures Transmission time of SARS-CoV-2 relative to symptom onset and proportion of presymptomatic transmission.
Results Based on 18 serial interval/generation time estimates from 15 papers, mean transmission time relative to symptom onset ranged from −2.6 (95% CI −3.0 to −2.1) days before infector symptom onset to 1.4 (95% CI 1.0 to 1.8) days after symptom onset. The proportion of presymptomatic transmission ranged from 45.9% (95% CI 42.9% to 49.0%) to 69.1% (95% CI 66.2% to 71.9%).
Conclusions There is substantial potential for presymptomatic transmission of SARS-CoV-2 across a range of different contexts. This highlights the need for rapid case detection, contact tracing and quarantine. The transmission patterns that we report reflect the combination of biological infectiousness and transmission opportunities which vary according to context.

Strengths and limitations of this study

- We generated estimates of presymptomatic transmission for different countries.
- As this is a secondary analysis of published estimates, we did not analyse data at individual transmission-pair level.
- As control measures such as rapid isolation of symptomatic people may increase the proportion of presymptomatic transmission, we generated estimates based on single locations and did not pool them.

INTRODUCTION

There is currently a pandemic of COVID-19, a recently emerged and rapidly spreading infectious disease that is caused by the novel coronavirus, SARS-CoV-2. There are large direct impacts of COVID-19 among known cases. As of 19 April 2021, the WHO has reported 140, 886 773 confirmed cases and 3 012 251 deaths due to COVID-19.[1] In China, 14% and 5% of cases were classified as severe and critical, respectively.[2] There are also major indirect impacts of COVID-19 and its control measures on other aspects of healthcare[3–5] and on the economy.[6 7]

In addition to vaccination, primary control measures entail reducing transmission from infectious individuals. These include case isolation, contact tracing and quarantine, physical distancing, hygiene and ventilation measures.[8] Infectious people are identified when they report symptoms, and are tested for SARS-CoV-2. Infectious people without symptoms may be identified when an active surveillance programme is in place.

In the absence of active surveillance, infectious people without symptoms may not be quarantined, and therefore may have more contacts with susceptible people resulting in increased SARS-CoV-2 transmission. Therefore, quantifying the transmission potential before or in the absence of symptoms will inform disease control measures and predictions of epidemic progression.

Characteristics of presymptomatic and asymptomatic transmission are potentially different, and separate approaches may be required to understand them. In this paper, we capitalise on the considerable information

Asymptomatic infectiousness

Open access Original research

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Relative infectiousness of asymptomatic SARS-CoV-2 infected persons compared with symptomatic individuals: a rapid scoping review

David McEvoy ,[1] Conor McAloon ,[2] Aine Collins,[3] Kevin Hunt,[4] Francis Butler,[4] Andrew Byrne ,[5] Miriam Casey-Bryars ,[3] Ann Barber ,[3] John Griffin ,[3] Elizabeth Ann Lane ,[3,6] Patrick Wall,[7] Simon John More [3]

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For numbered affiliations see end of article.

Correspondence to
Mr David McEvoy; davidmcevoy20@rcsi.com

ABSTRACT

Objectives The aim of this study was to determine the relative infectiousness of asymptomatic SARS-CoV-2 infected persons compared with symptomatic individuals based on a scoping review of available literature.
Design Rapid scoping review of peer-reviewed literature from 1 January to 5 December 2020 using the LitCovid database and the Cochrane library.
Setting International studies on the infectiousness of individuals infected with SARS-CoV-2.
Participants Studies were selected for inclusion if they defined asymptomatics as a separate cohort distinct from presymptomatics and if they provided a quantitative measure of the infectiousness of asymptomatics relative to symptomatics.
Primary outcome measures PCR result (PCR studies), the rate of infection (mathematical modelling studies) and secondary attack rate (contact tracing studies) - in each case from asymptomatic in comparison with symptomatic individuals.
Results There are only a limited number of published studies that report estimates of relative infectiousness of asymptomatic compared with symptomatic individuals. 12 studies were included after the screening process. Significant differences exist in the definition of infectiousness. PCR studies in general show no difference in shedding levels between symptomatic and asymptomatic individuals; however, the number of study subjects is generally limited. Two modelling studies estimate relative infectiousness to be 0.43 and 0.57, but both of these were more reflective of the infectiousness of undocumented rather than asymptomatic cases. The results from contact tracing studies include estimates of relative infectiousness of 0, but with insufficient evidence to conclude that it is significantly different from 1.
Conclusions There is considerable heterogeneity in estimates of relative infectiousness highlighting the need for further investigation of this important parameter. It is not possible to provide any conclusive estimate of relative infectiousness, as the estimates from the reviewed studies varied between 0 and 1.

Strengths and limitations of this study

- A strength of this study is that it only included peer-reviewed studies.
- This study also had a robust screening process that was used to ensure that the relative infectiousness of asymptomatic compared with symptomatic was defined properly. It ensured that each study properly distinguished asymptomatic and presymptomatic individuals.
- Differences in the definition of infectiousness and the heterogeneity in results between studies negate the potential to provide a pooled quantitative estimate of relative infectiousness.
- The present study highlights the need for additional studies in this area.

INTRODUCTION

The first case of COVID-19 was first reported from Wuhan, China, in December 2019.[1] The outbreak of COVID-19 was declared a Public Health Emergency of International Concern on 30 January 2020 and a pandemic was declared on 11 March 2020.[2] Since then, many countries have sought to contain the spread of the virus through a range of measures aimed at limiting transmission within the population.

At the outset of an epidemic, a key principle of control might be quarantining of individuals with clinical symptoms fitting a particular case definition. However, for many infectious diseases, a proportion of infected individuals may never present with clinical signs (ie, asymptomatic) yet still be infectious to others. The existence of this cohort of SARS-CoV-2 infected individuals is now well recognised.[3]

The transmission potential of such asymptomatic individuals is likely to be different from those who have clinical signs. On the one hand, they might shed lower quantities of the infectious agent; on the other hand, their potential for contacts might be greater. Being unaware that they are infected,

Serial interval/generation time

Open access Original research

BMJ Open

Rapid review of available evidence on the serial interval and generation time of COVID-19

John Griffin ,[1] Miriam Casey ,[1] Áine Collins,[1,2] Kevin Hunt,[3] David McEvoy,[4] Andrew Byrne ,[5] Conor McAloon ,[6] Ann Barber,[1] Elizabeth Ann Lane ,[1,2] Simon More [1]

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For numbered affiliations see end of article.

Correspondence to
John Griffin; johnmgriffin@live.com

ABSTRACT

The serial interval is the time between symptom onsets in an infector–infectee pair. The generation time, also known as the generation interval, is the time between infection events in an infector–infectee pair. The serial interval and the generation time are key parameters for assessing the dynamics of a disease. A number of scientific papers reported information pertaining to the serial interval and/or generation time for COVID-19.
Objective Conduct a review of available evidence to advise on appropriate parameter values for serial interval and generation time in national COVID-19 transmission models for Ireland and on methodological issues relating to those parameters.
Methods We conducted a rapid review of the literature covering the period 1 January 2020 and 21 August 2020, following predefined eligibility criteria. Forty scientific papers met our inclusion criteria and were included in the review.
Results The mean of the serial interval ranged from 3.03 to 7.6 days, based on 38 estimates, and the median from 1.0 to 6.0 days (based on 15 estimates). Only three estimates were provided for the mean of the generation time. These ranged from 3.95 to 5.20 days. One estimate of 5.0 days was provided for the median of the generation time.
Discussion Estimates of the serial interval and the generation time are very dependent on the specific factors that apply at the time that the data are collected, including the level of social contact. Consequently, the estimates may not be entirely relevant to other environments. Therefore, local estimates should be obtained as soon as possible. Careful consideration should be given to the methodology that is used. Real-time estimations of the serial interval/generation time, allowing for variations over time, may provide more accurate estimates of reproduction numbers than using conventionally fixed serial interval/generation time distributions.

Strengths and limitations of this study

- The study provides timely information on serial interval and generation time for those involved in the development of models and in the implementation of control measures against COVID-19.
- This is a rapid review of available evidence in the scientific literature between 1 January 2020 and 21 August 2020 on the serial interval and the generation time and it contains the usual limitations associated with such a review.
- The statistical methods used in the different papers were not analysed in detail.

INTRODUCTION

In response to the COVID-19 outbreak, the Irish Epidemiological Modelling Advisory Group (IEMAG) for COVID-19 was established to assist the Irish National Public Health Emergency Team in their decision-making during the pandemic. A subcommittee from IEMAG was tasked with researching the various parameters, leading to the development of a series of synthesis documents relevant to the parameterisation of a COVID-19 transmission model for Ireland.

The serial interval is the time between symptom onsets in an infector–infectee pair, that is, the interval between the onset of symptoms in an infectee and its presumed infector. This can be a negative number if the onset of symptoms in the infectee occurs prior to the onset of symptoms in the infector. The generation time, also known as the generation interval, is the time between infection events in an infector–infectee pair. The serial interval and the generation time are key parameters for assessing the dynamics of an infectious disease, and the generation time, or its proxy the serial interval, is an essential quantity for estimating the reproduction number.

A number of scientific papers reported information pertaining to the serial interval and/or generation time for COVID-19. In the context of national control efforts in Ireland, our objective was to conduct a rapid review of available evidence to advise the IEMAG on appropriate parameter values for serial interval and generation time in national

HIQA-EAG evidence synthesis

Impact of HRB SPHeRE doctoral training programme

Duration of immunity

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REVIEW

WILEY

Immune response following infection with SARS-CoV-2 and other coronaviruses: A rapid review

Eamon O Murchu[1,2] | Paula Byrne[1] | Kieran A. Walsh[1] | Paul G. Carty[1] | Máire Connolly[3] | Cillian De Gascun[4] | Karen Jordan[1] | Mary Keoghan[5] | Kirsty K. O'Brien[1] | Michelle O'Neill[1] | Susan M. Smith[6] | Conor Teljeur[1] | Máirín Ryan[1,7] | Patricia Harrington[1]

[1]Health Technology Assessment Directorate, Health Information and Quality Authority, Dublin 7, Ireland
[2]The Centre for Health Policy and Management, Trinity College Dublin, Dublin 2, Ireland
[3]School of Medicine, National University of Ireland Galway, Galway, Ireland
[4]UCD National Virus Reference Laboratory, University College Dublin, Dublin 4, Ireland
[5]Department of Clinical Immunology, Beaumont Hospital, Dublin 9, Ireland
[6]Department of General Practice, Health Research Board Centre for Primary Care Research, Royal College of Surgeons in Ireland, Dublin 2, Ireland
[7]Department of Pharmacology & Therapeutics, Trinity Health Sciences, Trinity College Dublin, Dublin 8, Ireland

Correspondence
Eamon O Murchu, Health Information and Quality Authority, George's Court, Dublin 7, Ireland.
Email: eomurchu@hiqa.ie

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Summary

In this review, we systematically searched and summarized the evidence on the immune response and reinfection rate following SARS-CoV-2 infection. We also retrieved studies on SARS-CoV and MERS-CoV to assess the long-term duration of antibody responses. A protocol based on Cochrane rapid review methodology was adhered to and databases were searched from 1/1/2000 until 26/5/2020.

Of 4744 citations retrieved, 102 studies met our inclusion criteria. Seventy-four studies were retrieved on SARS-CoV-2. While the rate and timing of IgM and IgG seroconversion were inconsistent across studies, most seroconverted for IgG within 2 weeks and 100% (N = 62) within 4 weeks. IgG was still detected at the end of follow-up (49-65 days) in all patients (N = 24). Neutralizing antibodies were detected in 92%-100% of patients (up to 53 days). It is not clear if reinfection with SARS-CoV-2 is possible, with studies more suggestive of intermittent detection of residual RNA.

Twenty-five studies were retrieved on SARS-CoV. In general, SARS-CoV-specific IgG was maintained for 1-2 years post-infection and declined thereafter, although one study detected IgG up to 12 years post-infection. Neutralizing antibodies were detected up to 17 years in another study. Three studies on MERS-CoV reported that IgG may be detected up to 2 years.

Abbreviations: CDC, Centers for Disease Control and Prevention; CI, Confidence Interval; Covid-19, Coronavirus disease 2019; HIQA, Health Information and Quality Authority; IgA, Immunoglobulin A; IgG, Immunoglobulin G; IgM, Immunoglobulin M; KCDC, Korea Centers for Disease Control and Prevention; MERS-CoV, Middle East Respiratory Syndrome Coronavirus; N protein, Nucleocapsid protein; RNA, Ribonucleic Acid; RT-PCR, Reverse Transcriptase Polymerase Chain Reaction; S protein, Spike protein; SARS-CoV, Severe Acute Respiratory Syndrome Coronavirus; SARS-CoV-2, Severe Acute Respiratory Syndrome Coronavirus 2; WHO, World Health Organization.

Máirín Ryan and Patricia Harrington are co-senior authors

Duration of infectious period

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journal homepage: www.elsevier.com/locate/jinf

Review

SARS-CoV-2 detection, viral load and infectivity over the course of an infection

Kieran A. Walsh[a,*], Karen Jordan[a], Barbara Clyne[a,b], Daniela Rohde[a], Linda Drummond[a], Paula Byrne[a], Susan Ahern[a], Paul G. Carty[a], Kirsty K. O'Brien[a], Eamon O'Murchu[a], Michelle O'Neill[a], Susan M. Smith[b], Máirín Ryan[a,c,1], Patricia Harrington[a,1]

[a] Health Information and Quality Authority, Smithfield, Dublin 7, Ireland
[b] Health Research Board Centre for Primary Care Research, Department of General Practice, Royal College of Surgeons in Ireland, 123 St Stephens Green, Dublin 2, Ireland
[c] Department of Pharmacology & Therapeutics, Trinity College Dublin, Trinity Health Sciences, James Street, Dublin 8, Ireland

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Review

SUMMARY

Objectives: To summarise the evidence on the detection pattern and viral load of SARS-CoV-2 over the course of an infection (including any asymptomatic or pre-symptomatic phase), and the duration of infectivity.
Methods: A systematic literature search was undertaken in PubMed, Europe PubMed Central and EMBASE from 30 December 2019 to 12 May 2020.
Results: We identified 113 studies conducted in 17 countries. The evidence from upper respiratory tract samples suggests that the viral load of SARS-CoV-2 peaks around symptom onset or a few days thereafter, and becomes undetectable about two weeks after symptom onset; however, viral loads from sputum samples may be higher, peak later and persist for longer. There is evidence of prolonged virus detection in stool samples, with unclear clinical significance.
No study was found that definitively measured the duration of infectivity; however, patients may not be infectious for the entire duration of virus detection, as the presence of viral ribonucleic acid may not represent transmissible live virus.
Conclusion: There is a relatively consistent trajectory of SARS-CoV-2 viral load over the course of COVID-19 from respiratory tract samples, however the duration of infectivity remains uncertain.

Introduction

The Coronavirus Disease 2019 (COVID-19) pandemic is a public health emergency of international concern causing a substantial number of cases and deaths globally.[1,2] COVID-19 presents an unprecedented challenge to governments worldwide due to the transmissibility of the virus, the scale of its impact on morbidity and mortality, the uncertainty regarding the development of long-term immunity in those infected, the current lack of vaccine or treatment options, and the impact on healthcare systems, economies and society.[3,4] Much remains unknown about COVID-19; however, evidence is emerging at a fast pace.[5] Our team at the Health Information and Quality Authority (HIQA) of Ireland has conducted a series of rapid reviews on various public health topics relating to COVID-19. The rapid reviews arose directly from questions posed by policy makers and expert clinicians supporting the Irish National Public Health Emergency Team (NPHET). Hence, the findings of these reviews have informed the national response to the COVID-19 pandemic in Ireland,[6] and have implications for international health policy as well as clinical and public health guidance.

Understanding the trajectory of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and the duration of infectivity is of critical importance to controlling the pandemic.[7] As SARS-CoV-2 is a novel virus in the human population, there is substantial uncertainty regarding virological levels (i.e. detection and viral load) in patients and how this relates to infectivity and disease severity. Information relating to SARS-CoV-2 detection and viral load at different time points of an infection, including in those without any symptoms, will aid with the clinical interpretation of real-time reverse transcriptase polymerase chain reaction (rRT-PCR) test results. Furthermore, information pertaining to the dura-

* Corresponding author at: Health Information and Quality Authority, Unit 1301, City Gate, Mahon T12 Y2XT, Cork, Ireland.
E-mail address: kiwalsh@hiqa.ie (K.A. Walsh).
[1] Both authors are co-senior authors.

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Duration of immunity / risk of reinfection

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REVIEW

WILEY

Quantifying the risk of SARS-CoV-2 reinfection over time

Eamon O Murchu[1,2] | Paula Byrne[1] | Paul G. Carty[1] | Cillian De Gascun[3] | Mary Keogan[4] | Michelle O'Neill[1] | Patricia Harrington[1] | Máirín Ryan[1,5]

[1]Health Information and Quality Authority, George's Court, Dublin, Ireland
[2]Trinity College Dublin, Dublin, Ireland
[3]UCD National Virus Reference Laboratory, Dublin, Ireland
[4]Beaumont Hospital, Dublin, Ireland
[5]Department of Pharmacology & Therapeutics, Trinity College Dublin, Trinity Health Sciences, Dublin, Ireland

Correspondence
Eamon O Murchu, Health Information and Quality Authority, George's Court, Dublin 7, Ireland.
Email: eomurchu@hiqa.ie

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Summary

Despite over 140 million SARS-CoV-2 infections worldwide since the beginning of the pandemic, relatively few confirmed cases of SARS-CoV-2 reinfection have been reported. While immunity from SARS-CoV-2 infection is probable, at least in the short term, few studies have quantified the reinfection risk. To our knowledge, this is the first systematic review to synthesise the evidence on the risk of SARS-CoV-2 reinfection over time. A standardised protocol was employed, based on Cochrane methodology. Electronic databases and preprint servers were searched from 1 January 2020 to 19 February 2021. Eleven large cohort studies were identified that estimated the risk of SARS-CoV-2 reinfection over time, including three that enrolled healthcare workers and two that enrolled residents and staff of elderly care homes. Across studies, the total number of PCR-positive or antibody-positive participants at baseline was 615,777, and the maximum duration of follow-up was more than 10 months in three studies. Reinfection was an uncommon event (absolute rate 0%–1.1%), with no study reporting an increase in the risk of reinfection over time. Only one study estimated the population-level risk of reinfection based on whole genome sequencing in a subset of patients; the estimated risk was low (0.1% [95% CI: 0.08–0.11%]) with no evidence of waning immunity for up to 7 months following primary infection. These data suggest that naturally acquired SARS-CoV-2 immunity does not wane for at least 10 months post-infection. However, the applicability of these studies to new variants or to vaccine-induced immunity remains uncertain.

KEYWORDS
COVID-19, SARS-CoV-2, reinfection

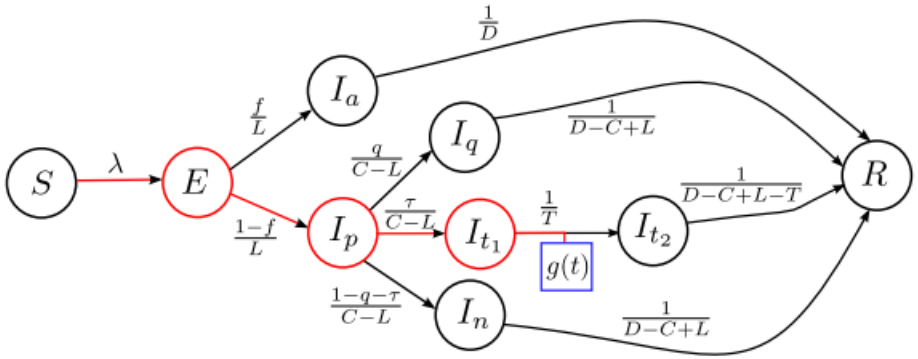
1 | INTRODUCTION

Following the emergence of a novel coronavirus (SARS-CoV-2) in China in December 2019 and the declaration by WHO of a public health emergency of international concern on 30 January 2020, countries worldwide have experienced epidemics of Covid-19. While much is yet unknown about the immune response following infection with SARS-CoV-2, evidence is emerging at a fast pace. The Health Information and Quality Authority (HIQA) of Ireland has conducted a series of rapid reviews on various public health topics relating to

Abbreviations: Covid-19, coronavirus disease 2019; CI, confidence interval; C_t, cycle threshold; HIQA, Health Information and Quality Authority; IgG, immunoglobulin G; NAAT, nucleic acid amplification technology; RNA, ribonucleic Acid; RT-PCR, reverse transcription polymerase chain reaction; SARS-CoV-2, severe acute respiratory syndrome coronavirus type 2; WHO, World Health Organization.

Patricia Harrington and Máirín Ryan are co-senior authors.

SEIR models


S
λ
E
$\frac{f}{L}$
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I_a
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$\frac{1-q-\tau}{C-L}$
$\frac{1}{T}$
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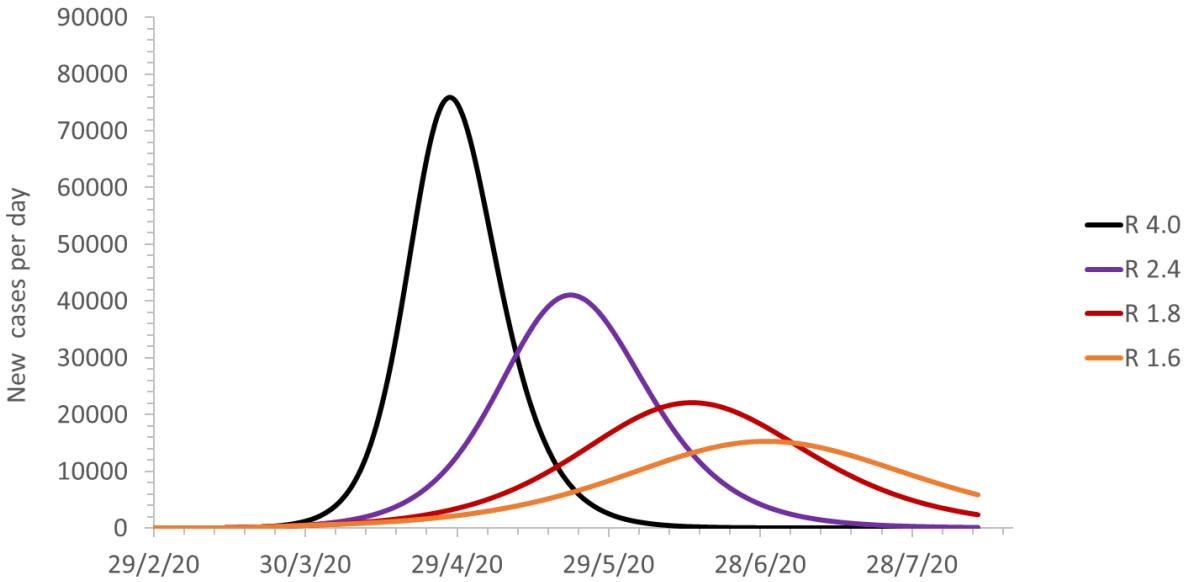
$\frac{1}{D-C+L}$
$\frac{1}{D-C+L-T}$
R


90000
80000
70000
60000
50000
40000
30000
20000
10000
0
New cases per day
29/2/20
30/3/20
29/4/20
29/5/20
28/6/20
28/7/20
R 4.0
R 2.4
R 1.8
R 1.6

Communicating risk and uncertainty

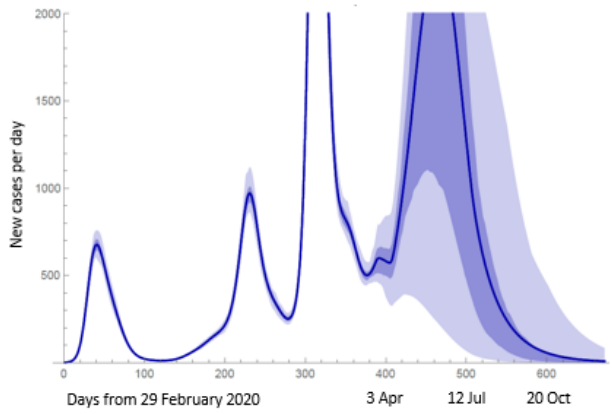
A delay of weeks greatly attenuates any fourth wave

These model runs delay the low additional close contact scenario (initial Reff ≈ 1.5) by four weeks (B1) and eight (B2) weeks, reducing anticipated case numbers and risk by approximately 25% and 50% respectively.

Coronavirus COVID-19 Public Health Advice

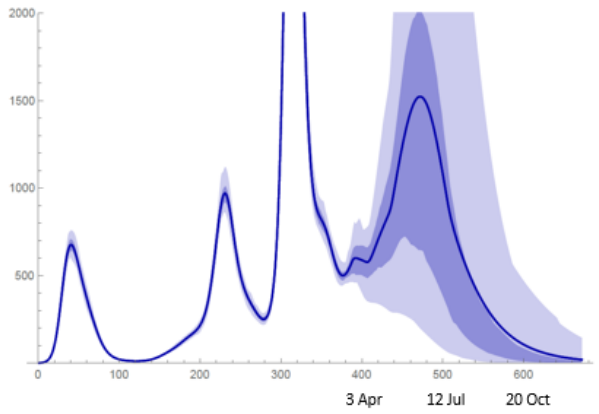
B. 199,000 (95,000-279,000) cases

R_{eff} ≈ 1.5 from 5 Apr 2021



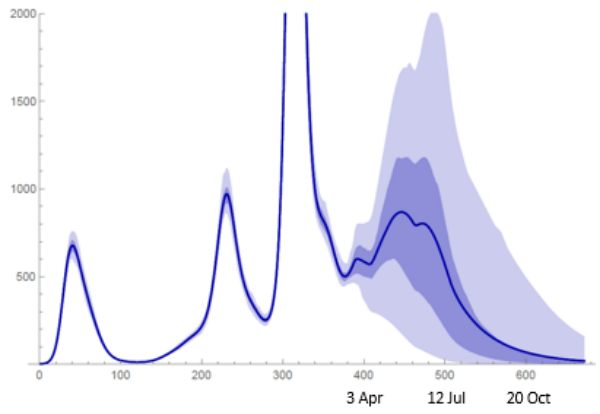
B1. 152,000 (69,000-185,000) cases

R_{eff} ≈ 1.3 from 5 Apr, 1.5 from 3 May



B2. 96,000 (51,000-129,000) cases

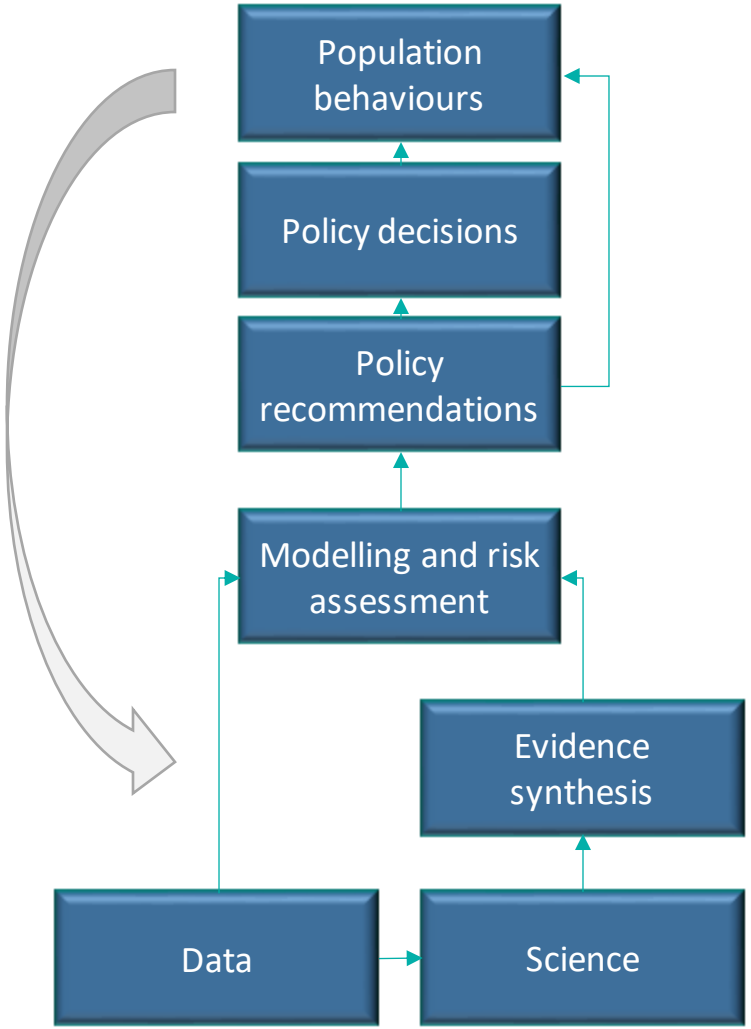
R_{eff} ≈ 1.3 from 5 Apr, 1.5 from 31 May



Homogeneous population SEIR model scenario estimates of new cases per day; credible intervals generated from 1000 runs of the model with different assumptions. The solid line is the ensemble average of all runs, dark ribbon the interquartile range, and the light ribbon the 2.5 and 97.5 percentiles. The effect of vaccination included according to current vaccination plan, with average vaccine effectiveness assumed to be 85% 28 days from first dose and uptake 80-90%. The stated R_{eff} applies on 5 April 2020 – transmissibility is held constant in the model from that point, but measured R_{eff} will decrease as immunity increases; transmissibility is then increased from 3 May or 31 May, and the stated R_{eff} is that which would have applied, for that level of transmissibility, on 5 April 2021. The actual measured R_{eff} will be lower due to increased population immunity

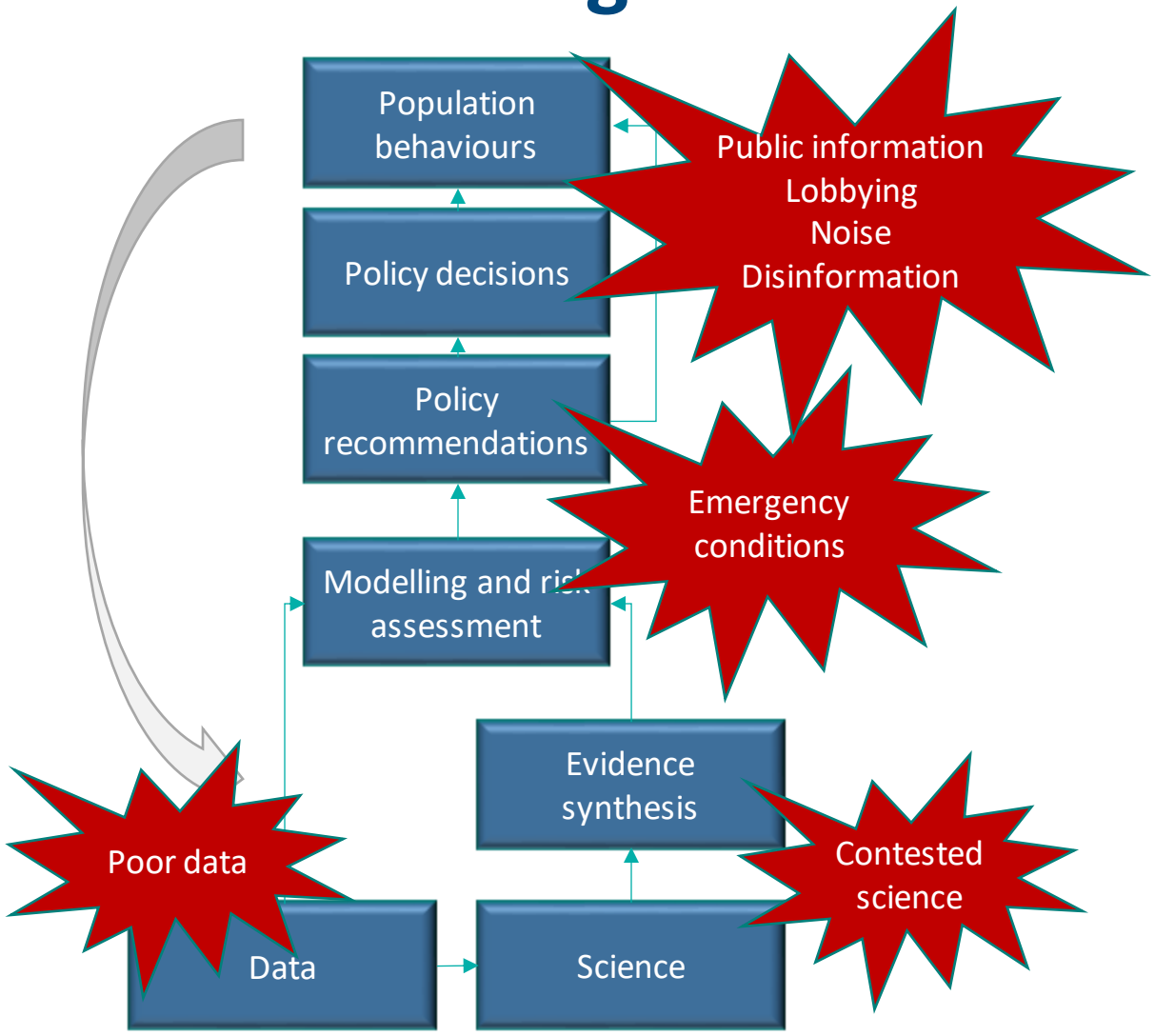
Rialtas na hÉireann Government of Ireland

The challenge of influencing policy



Responsible risk profile	Informed decisions	Risk management
Minimise uncertainty	Maximise understanding	Knowledge management

The challenge of influencing policy



Scope to ease restrictions on golf and children's sport, immunologist claims

Health expert accuses government of 'pandering' to pubs and slams vaccine certs 'catastrophe'

A leading immunology expert has called for an immediate public inquiry into NPHET and the government "while the players are still on the pitch"

Covid-19 antigen tests should be free for everyone in Ireland says immunology expert

"This is Delta and we haven't dealt with Delta in a winter situation before"

Covid boosters should be rolled out to over 40s, immunologist says

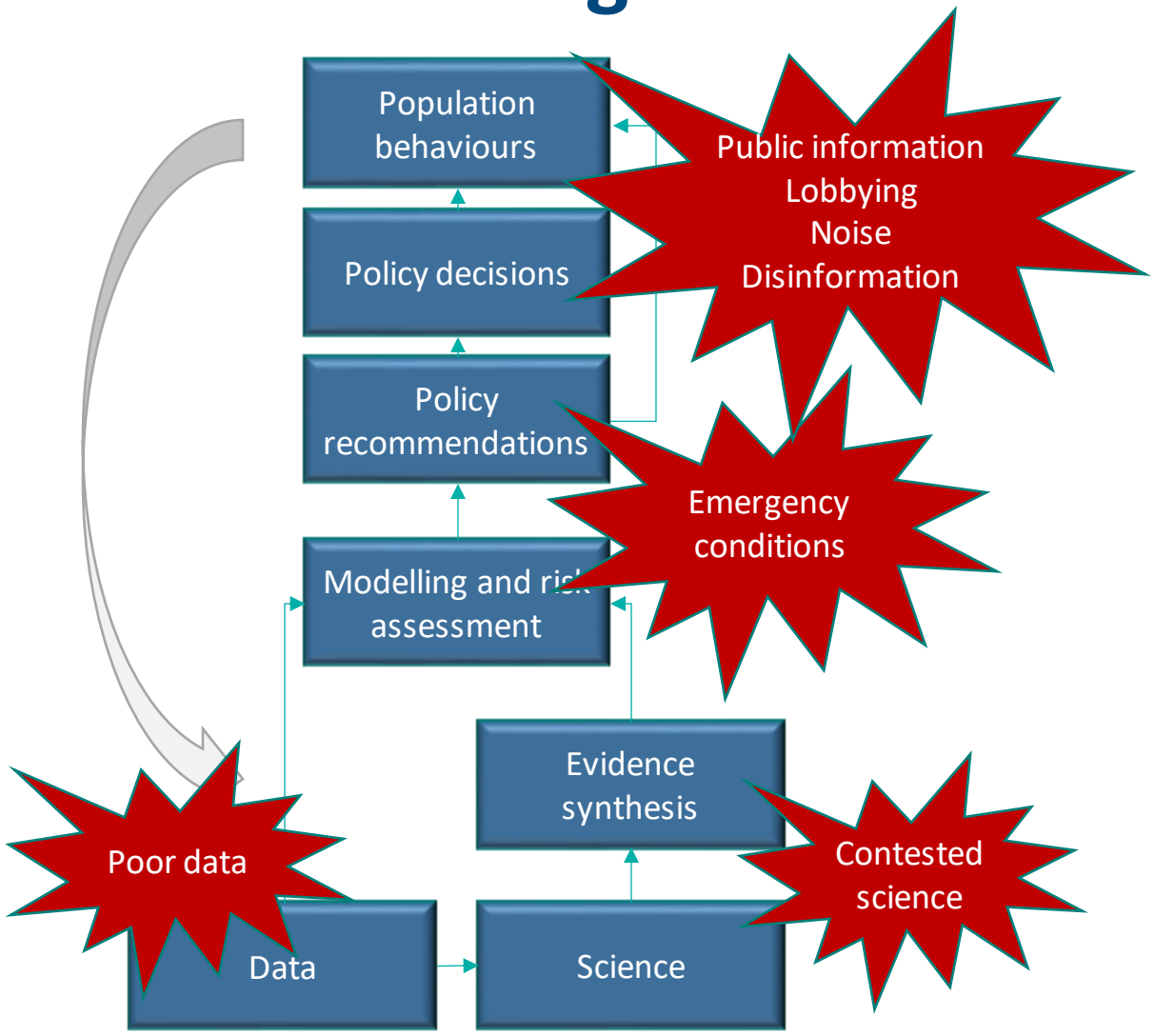
Immunology expert calls for rapid antigen tests for children

Regular Covid-19 vaccines similar to flu jab will be needed - immunologist

The nature of knowledge

- Explicit / scientific knowledge is dynamic, contested and sometimes unstable
- Tacit / experiential knowledge essential, especially with instability or uncertainty
- Knowledge management and evidence synthesis are sophisticated disciplines – ongoing research and training are critical
- Large and diverse expert groups may be useful in achieving *"knowledge and risk-based decisions"*

The challenge of influencing policy



Responsible risk profile | Informed decisions | Risk management

by whom
whose risk

Individuals
Organisations
Government
Population

Minimise uncertainty | Maximise understanding | Knowledge management

by whom
for whom

Lessons and observations

- The need for data infrastructures
  - and a national conversation on governance, privacy, security and trust
- The importance of knowledge management, systematic review and evidence synthesis
- The value of structured PhD programmes for key skills
- The management of population risks (explicit or implicit, direct or indirect) creates particular knowledge and risk management challenges

Lessons and observations

- Science in the media can be confusing for the public
  - “follow the science” versus contested and contingent nature of scientific knowledge
- Independence of a public risk advisory structure is essential
  - but so are humility, empathy, trust, persistence, resilience … and respect for the political system and the democratic mandate
- Difficult questions on governance, ethics and communication where professionals seek to manage risk on behalf of a community or population