Infectious Disease Dynamics from the Black Death to COVID-19

David Earn Mathematics & Statistics McMaster University

Outline

- Predicting patterns of epidemic recurrence
- Puzzles presented by plagues of the past
- Forecasting the future: modelling and policy

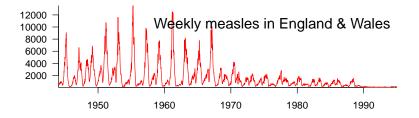
Outline

Predicting patterns of epidemic recurrence

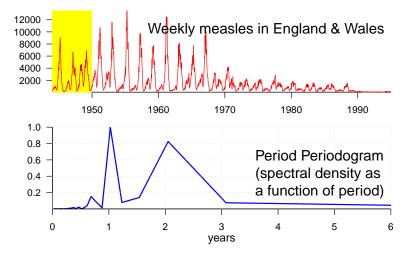
 Puzzles presented by plagues of the past

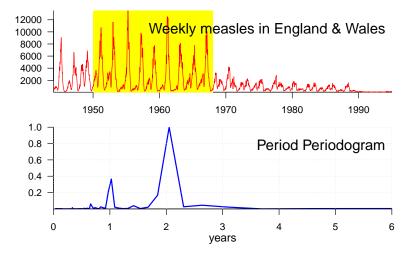
 Forecasting the future: modelling and policy

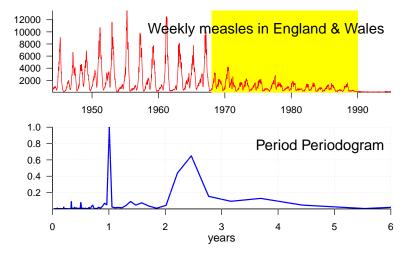
20th century measles dynamics in England and Wales



- Annual epidemics, then biennial, then irregular
- Why is the pattern of epidemic recurrence so complicated?
- What causes changes in frequency content over time?

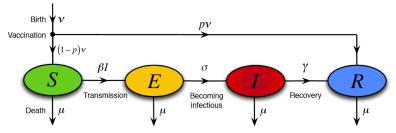








SEIR model



$$\frac{dS}{dt} = \nu(1-p) - \beta SI - \mu S$$

$$\frac{dE}{dt} = \beta SI - \sigma E - \mu E$$

$$\frac{dI}{dt} = \sigma E - \gamma I - \mu I$$

$$\frac{dR}{dt} = \nu p + \gamma I - \mu R$$

- Birth rate (ν for natality)
- Death rate (μ for mortality)
- Proportion vaccinated (p)
- Transmission rate (β)
- Mean latent period ($T_{\rm lat} = 1/\sigma$)
- Mean infectious period $(T_{inf} = 1/\gamma)$

SEIR with vital dynamics and vaccination: Analysis

Two Equilibria

- Disease Free Equilibrium (DFE)
- Endemic Equilibrium (EE)
- Periodic solutions ? Chaos? No.
- Basic reproduction number R₀: expected infections from one infected entering a wholly susceptible population
 - $\begin{array}{ll} \blacktriangleright & \text{Biological derivation: (assuming } \nu = \mu \text{ and } p = 0) \\ \mathcal{R}_0 = \beta \times \frac{\sigma}{\sigma + \mu} \times \frac{1}{\gamma + \mu} & \simeq \beta \gamma^{-1} & \because \frac{1}{\mu} \gg \max\left(\frac{1}{\sigma}, \frac{1}{\gamma}\right) \end{array}$
 - Mathematical derivation:

 *R*₀ = 1 is stability boundary

van den Driessche & Watmough 2002 Mathematical Biosciences <u>180</u>:29–48

- EE is globally asymptotically stable (GAS) if R₀ > 1; DFE is GAS otherwise.
- Approach to EE is typically via *damped oscillations*.
- But observed recurrent epidemics are undamped.

What are we missing?

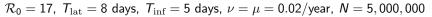


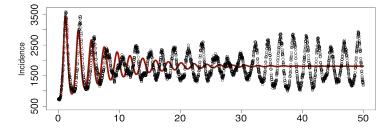
Populations are finite: demographic stochasticity

- ▶ Differential equations describe the expected behaviour in limit that population size $N \rightarrow \infty$
- Re-cast the SEIR model as a stochastic process (continuous time Markov jump process)
- Simulate with standard Gillespie algorithm

Gillespie 1976, J. Comp. Phys. 22, 403-434

Gillespie Simulations: SEIR Results for Measles Parameters





Earn (2009) IAS/Park City Mathematics Series 14:151-186

- Demographic Stochasticity sustains transient behaviour (oscillations do not damp out) (Bartlett 1950's)
- Explains undamped oscillations at a single period
- But, unable to explain changes in interepidemic period, or irregularity, as observed

What are we **STILL** missing?



Contact rates are higher during school terms!



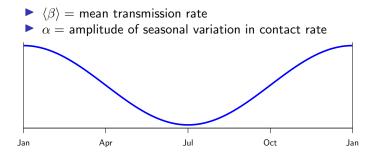
Sinusoidal SEIR Model

Transmission rate β is not constant: high during school terms, low in summer

London WP, Yorke JA, 1973, Am. J. Epidemiol. 98, 453-468

For simplicity, model as a sine wave:

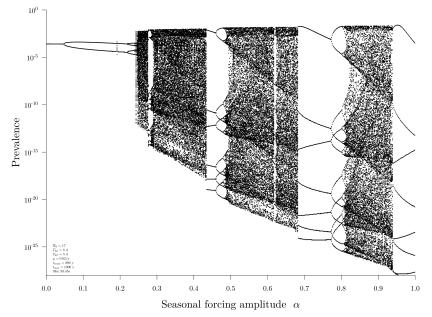
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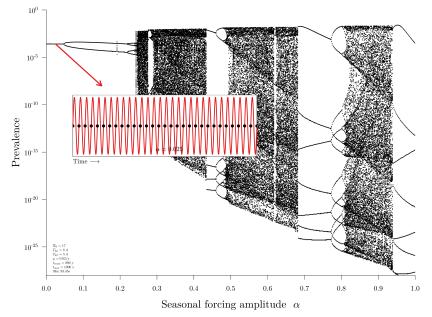


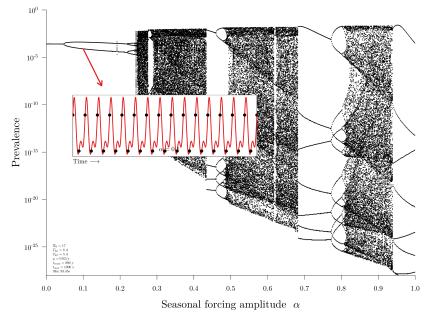
 $\beta(t)$

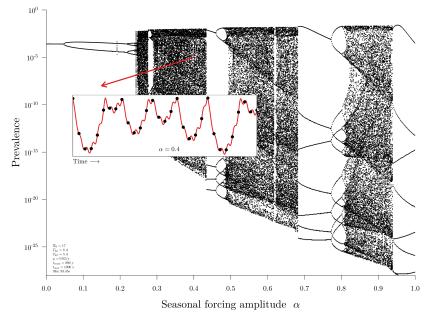
Is this change significant?

- We now have a forced nonlinear system
- Forcing frequency can resonate with the natural timescales of the disease (*e.g.*, period of damped oscillations)
- Very rich dynamical system... (analogy: forced pendulum)









Sinusoidal SEIR Model: Does it explain measles dynamics?

SEIR model with sinusoidal forcing:

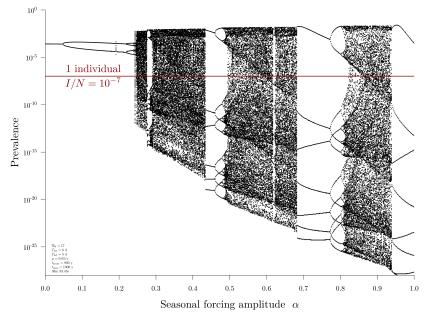
Produces recurrent undamped epidemics of all frequencies observed in measles time series.

Schwartz IB, Smith HL, 1983, J. Math. Biol. 18, 233-253

Produces chaos, which can explain irregular behaviour and transitions from one type of cycle to another

Olsen LF, Schaffer WM, 1990, Science 249, 499-504

- If correct, this implies these transitions are unpredictable.
- BUT... the model also predicts rapid extinction of the virus (not persistence).

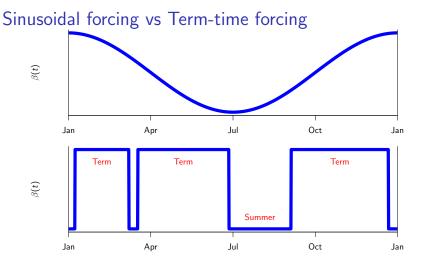


What are we **STILL** missing?



Contact rates are higher during school terms!





<u>Term-time</u> SEIR model *predicts a strictly biennial cycle of measles epidemics, at all times and places.* Is superb agreement with post-war measles dynamics

coincidental???

What **ELSE** might we be missing?



Key Insight

- Suppose \mathcal{R}_0 is estimated when the birth rate is ν .
- If the birth rate changes, v → v', then the dynamical effect is identical to changing R₀ instead:

$$\mathcal{R}_0 \longrightarrow \mathcal{R}_0 rac{
u'}{
u}$$

- More generally, any change in susceptible recruitment rate is equivalent dynamically to a change in R₀.
- A change in birth rate v → v' together with a change in vaccine uptake p → p' is dynamically equivalent to

$$\mathcal{R}_0 \longrightarrow \mathcal{R}_0 rac{
u'(1-p')}{
u(1-p)}$$

Earn et al. (2000) Science 287:667–670 Earn (2009) IAS/Park City Mathematics Series 14:151–186

Predicting Epidemic Transitions

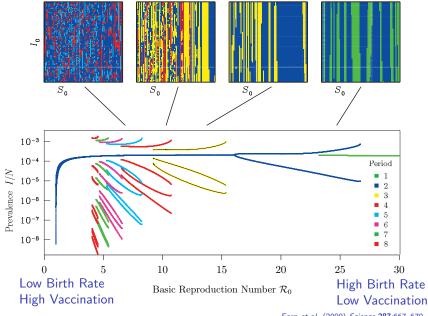
Changes in

- Birth rate (ν)
- Vaccination proportion (p)
- Transmission rate ($\langle \beta \rangle$ or \mathcal{R}_0)

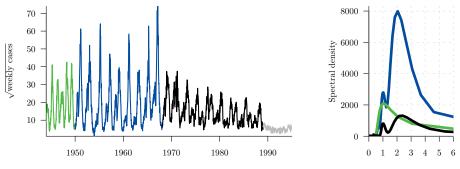
all map onto the same parameter axis.

- ► .:. Summarize possible dynamical changes induced by demographic/behavioural changes with a *one-parameter* (*R*₀) *bifurcation diagram*.
- ... Predict epidemic transitions by mapping observed changes in ν , p or \mathcal{R}_0 onto this diagram.

Measles Bifurcation Diagram (wrt \mathcal{R}_0)



Earn et al. (2000) Science 287:667-670

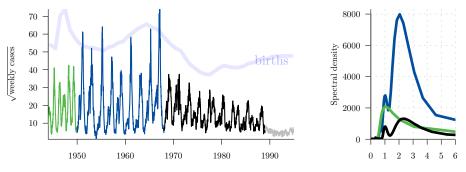


Period (years)

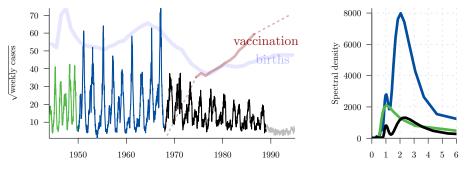
• 1-year cycle

- 2-year cycle
- irregularity; 2.5 year spectral peak

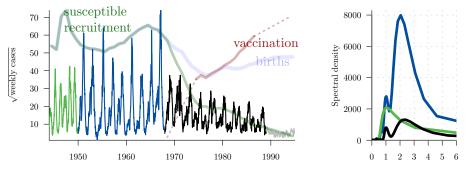
noise only



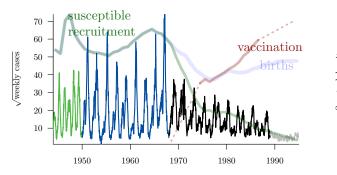
Period (years)

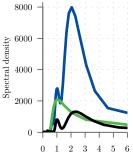


Period (years)



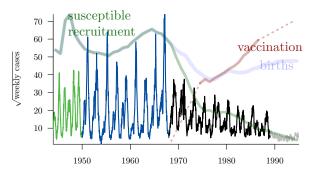
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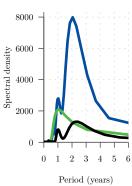


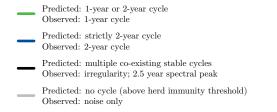


Period (years)



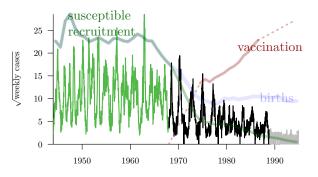


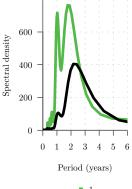


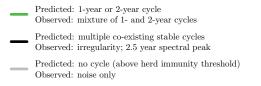




Measles in Liverpool, England

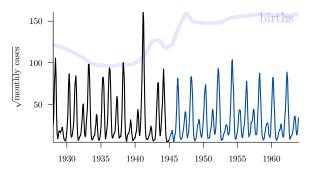


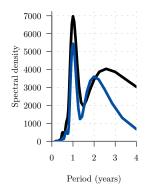






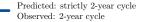
Measles in New York City



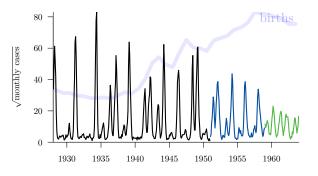




Predicted: multiple co-existing stable cycles Observed: irregularity; 2.8 year spectral peak



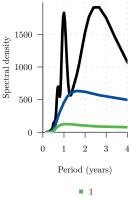
Measles in Baltimore



Predicted: multiple co-existing stable cycles
 Observed: irregularity; 2.8 year spectral peak

Predicted: 1- or 2-year cycle Observed: 2-year cycle

Predicted: 1- or 2-year cycle Observed: 1-year cycle





What about other notifiable childhood infectious diseases?

Does same analysis explain patterns of recurrent epidemics for rubella? chicken pox? whooping cough?

► Alas! No!



- Only attractor of term-time SEIR model for rubella, chicken pox, or whooping cough is annual cycle.
- Yet these diseases show much more complex dynamics!

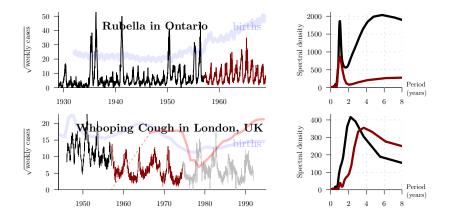
1939 weekly infectious disease notifications in Ontario

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1939 weekly infectious disease notifications in Ontario

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Other Childhood Infections (not measles)



Incidence time series of these diseases show strong spectral peaks at periods not predicted by asymptotic analysis (*i.e.*, **not** displayed by attractors of term-time SEIR model)

Bauch & Earn (2003) Proc. R. Soc. Lond. 270:1573-1578

Argh!

What are we **STILL** missing?



Demographic Stochasticity Comes to the Rescue (Again!)

Sustains transient behaviour

Linear perturbation theory applied to the attractors of the model explains other spectral peaks in data

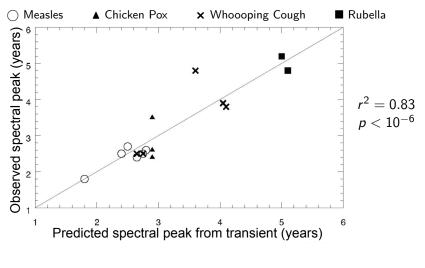
► Whew!

Get More Ambitious!

- Aim to predict all spectral peaks in the data
- Asymptotic analysis —> spectral peaks from attractors
- Perturbation analysis —> spectral peaks from transients

Bauch & Earn (2003) Proc. R. Soc. Lond. **270**:1573–1578 Krylova & Earn (2013) J. R. Soc. Interface **18**(10):20130098 Hempel & Earn (2015) J. R. Soc. Interface **12**(106):20150024

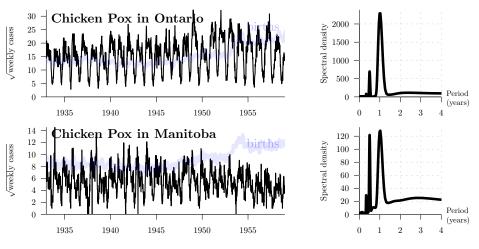
Predicted vs Observed Spectral Peaks from Transients



Bauch & Earn (2003) Proc. R. Soc. Lond. 270:1573-1578

Great! Can we successfully predict even more detail?

Can we predict magnitudes of spectral peaks? *Example:*



Population of MB <
 More demographic stochasticity

Modelling recurrent epidemics: Summary so far

- Good understanding of recurrent epidemic patterns of many infectious diseases in the 20th century (*e.g.*, measles, chicken pox, whooping cough, rubella, ...)
- Perfect prediction of spectral peaks from attractors
- Excellent prediction of spectral peaks from transients
- Population size is key determinant of relative magnitude of peaks from attractors vs. transients (confirmed with stochastic simulations)

Modelling recurrent epidemics: Recent developments

- Extend time series further back in time
 - Does theory still allow us to predict epidemic transitions?
- ▶ Measles in New York City, 1891–1984

Success!

Hempel & Earn (2015) J. R. Soc. Interface 12(106):20150024

Key challenge that had to be overcome: changing patterns of seasonal variation in contact rates

> Papst & Earn (2019) J. R. Soc. Interface 16:20190202 Jagan et al. (2020) PLoS Comp. Biol. 16(9):e1008124

- Smallpox in London, 1664–1930
 - Many observed epidemiological transitions, correlated with policy changes and historical events

Krylova & Earn (2020) PLoS Biology 18(12):e3000506

Dynamical transition analysis in progress

Outline

Predicting patterns of epidemic recurrence

Puzzles presented by plagues of the past

 Forecasting the future: modelling and policy

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Michael Quern

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Sources of mortality data for London, England Wills Parish Registers



since 1258

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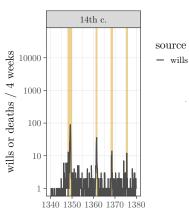
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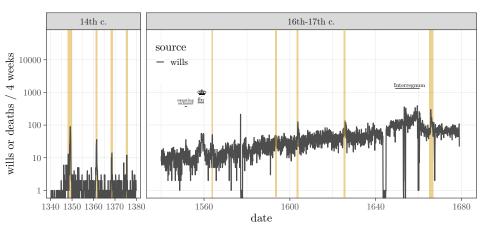
since 1538

since 1563 (continuous since 1661)

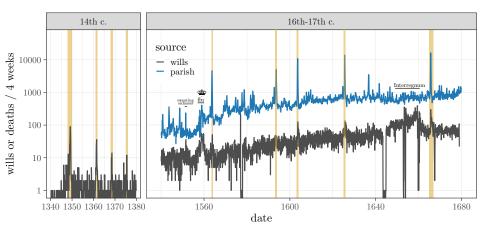
Earn, Ma, Poinar, Dushoff, Bolker (2020) PNAS 117:27703-27711



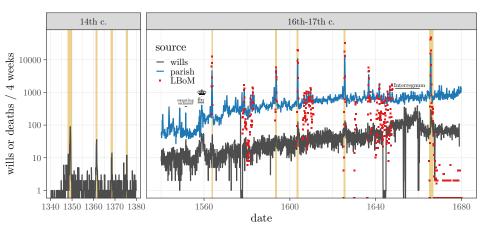
Earn, Ma, Poinar, Dushoff, Bolker (2020) PNAS 117:27703-27711



Earn, Ma, Poinar, Dushoff, Bolker (2020) PNAS 117:27703-27711

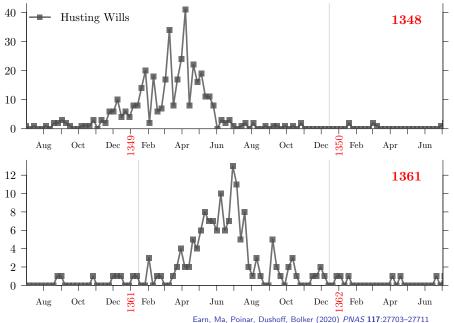


Earn, Ma, Poinar, Dushoff, Bolker (2020) PNAS 117:27703-27711

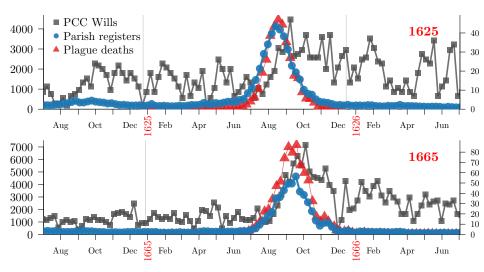


Earn, Ma, Poinar, Dushoff, Bolker (2020) PNAS 117:27703-27711

14th c. plague epidemics in London



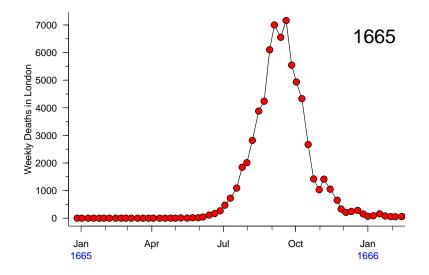
17th c. plague epidemics in London



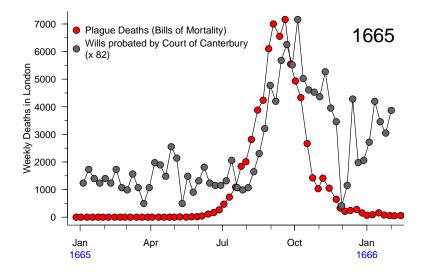
Earn, Ma, Poinar, Dushoff, Bolker (2020) PNAS 117:27703-27711

Is it OK to compare results based on wills with results from mortality data?

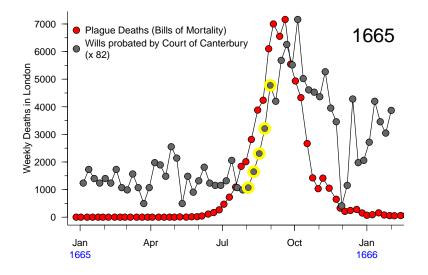
Plague in London



Plague in London



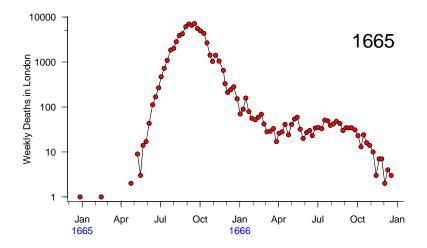
Plague in London



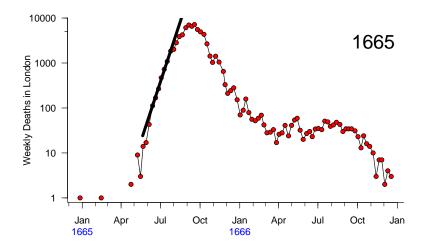
Compare growth rates of plague epidemics in London

- Property of the epidemic curve (the data alone)
- Estimate <u>without</u> assumptions about processes that generated the data (since we don't know the mode of transmission)
 - human-to-human (pneumonic plague)
 - rat-to-flea-to-human (bubonic plague)

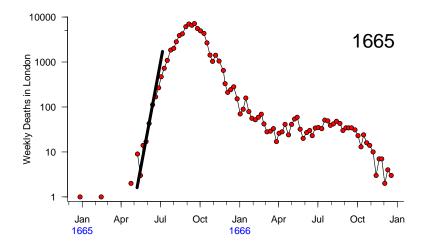
Naïvely, we just fit a straight line to the log of the mortality time series.



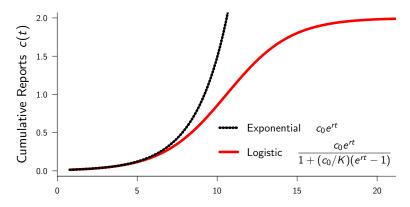
Naïvely, we just fit a straight line to the log of the mortality time series.



Naïvely, we just fit a straight line to the log of the mortality time series.



Instead fit a saturating rather than a purely exponential curve.



- Both curves have same initial exponential growth rate r.
- Test extensively using simulated epidemics for which we know the correct answer.

Initial growth rates for plague in London, 1348–1665

• Later plagues grew $\frac{4 \times \text{ faster}}{4 \times \text{ faster}}$ than early plagues!

Doubling time:

- ▶ In 1348: ~ 45 days
- ► In 1665: ~ 11 days

Why did plague epidemics "accelerate"?

- Evolution of increased infectiousness? longer infectious period?
- Changes in population density? social structure? contact patterns?
- Changes in weather?
- Bubonic *vs.* pneumonic plague?

Earn, Ma, Poinar, Dushoff, Bolker (2020) PNAS 117:27703-27711

Bubonic or pneumonic plague?

Suppose pneumonic plague during second pandemic was exactly like modern pneumonic plague.

Pneumonic in 14th century London? $\implies \sim 20\% \text{ of population infected}$

 $\underline{\mathsf{BUT}}\sim 30{-}50\%$ of total population died in 1348

- \implies early plagues probably <u>not</u> (primarily) pneumonic
- A remarkable inference to be able to make based on counting wills! (and a little mathematical modelling)

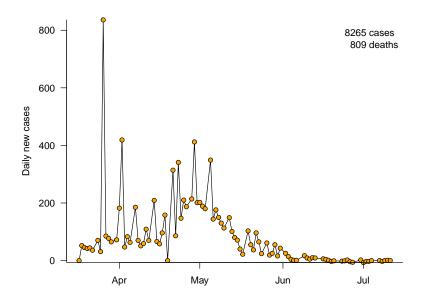
Earn, Ma, Poinar, Dushoff, Bolker (2020) PNAS 117:27703-27711

Outline

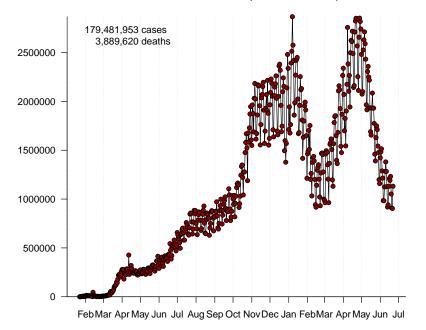
- Predicting patterns of epidemic recurrence
- Puzzles presented by plagues of the past
- Forecasting the future: modelling and policy

SARS

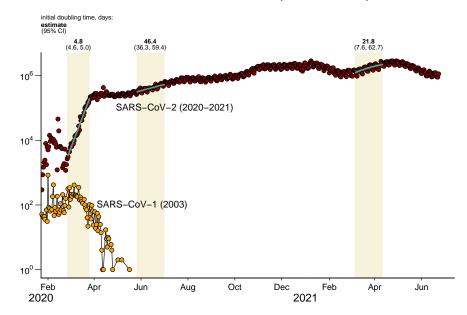
Daily SARS-CoV-1 in 2003 (Worldwide)



Daily SARS-CoV-2 in 2020-2021 (Worldwide)



Daily SARS-CoV-2 vs SARS-CoV-1 (Worldwide)



SARS-CoV-2 in Ontario

COVID-19 cases in Ontario

initial doubling time, days: estimate (95% CI) **3.8** (3.4, 4.2) **10.6** (7.4, 15.1) **40.6** (38.5, 42.8) 12.9 (9.6, 17.2) 5000 -4000 -3000 -2000 -1000 -0 Mar May Jul Sep Nov Jan Mar May Jul 2020 2021

Modelling SARS-CoV-2 / COVID-19

Much richer data (compared with historical epidemics):

- Daily counts of positive tests, hospital occupancy, ICU occupancy, deaths, ...
- Daily vaccine doses administered
- Daily measures of weather, mobility
- Info on policy changes, travel restrictions, new virus variants,

Harder problem:

. . .

Forecast the future!

Modelling SARS-CoV-2 / COVID-19

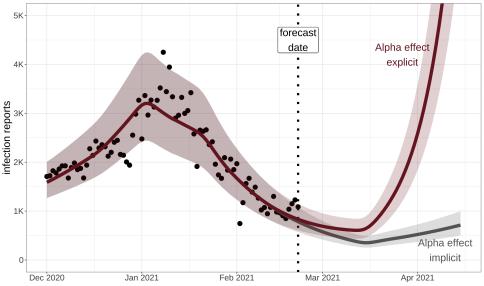
Approach:

- Expand SEIR model to include compartments for cases, deaths, hospital occupancy, etc
- Simultaneously fit model to all the types of data we have
- Predict the future based on various scenarios

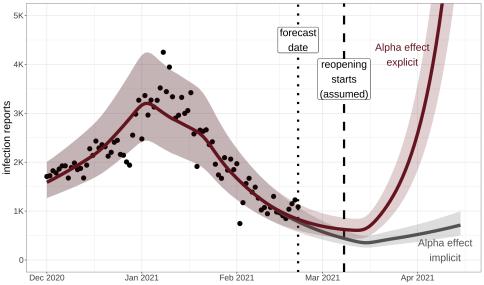
Interpret forecasts with caution:

- Quantify uncertainties we understand (parameter estimates, observation and process noise)
- Be aware that models cannot capture all processes

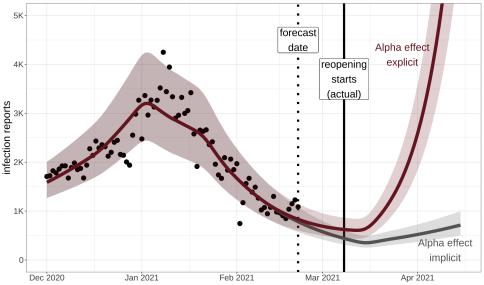
Forecast from 21 Feb 2021



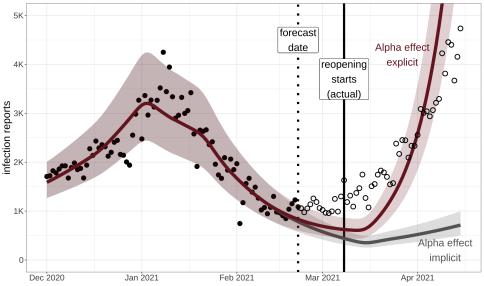
Forecast from 21 Feb 2021



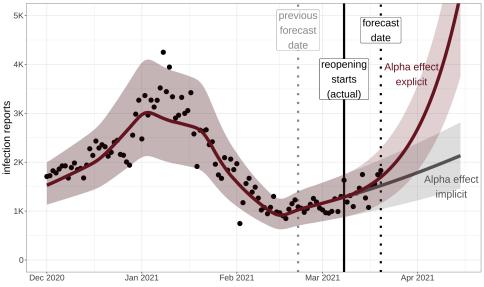
Forecast from 21 Feb 2021



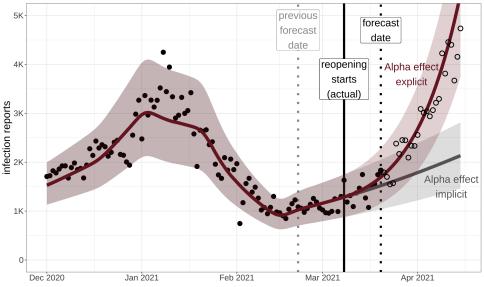
Forecast from 21 Feb 2021



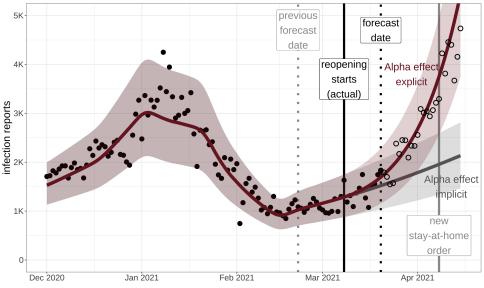
Forecast from 20 Mar 2021



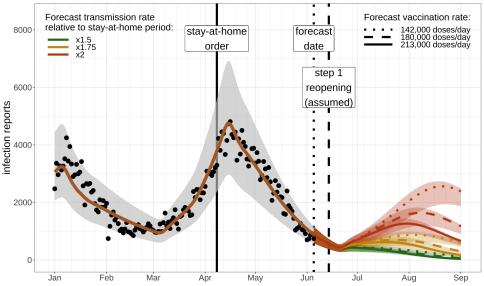
Forecast from 20 Mar 2021



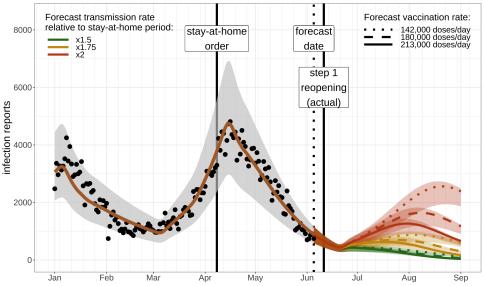
Forecast from 20 Mar 2021



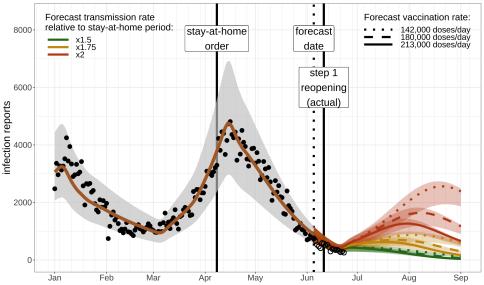
Forecast from 5 Jun 2021



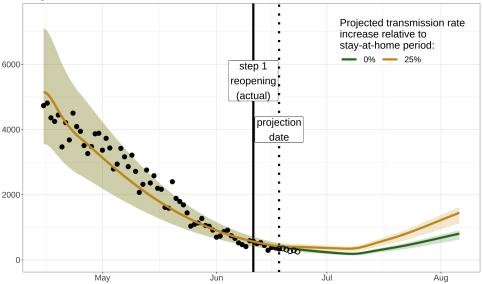
Forecast from 5 Jun 2021



Forecast from 5 Jun 2021



Projections from 18 Jun 2021



Acknowledgements

- McMaster University: Ben Bolker, Jonathan Dushoff, Hendrik Poinar
- University of Victoria: Junling Ma
- University of Alberta: Karsten Hempel
- Public Health Agency of Canada: Michael Li, David Champredon
- University of Waterloo: Mikael Jagan
- Cornell University: Irena Papst
- Canadian Institute for Health Information (CIHI): Olga Krylova

Funders:









Thanks for your interest!

https://davidearn.mcmaster.ca https://mac-theobio.github.io/covid-19/

6 Mechanistic Modelling of Recurrent Epidemics II; \mathcal{R}_0



Mathematics and Statistics $\int_{M} d\omega = \int_{\partial M} \omega$

Mathematics 4MB3/6MB3 Mathematical Biology

Instructor: David Earn

Lecture 6 Mechanistic Modelling of Recurrent Epidemics II Tuesday 8 October 2024

Draft Project Description Document is posted.

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The project is to be submitted as a paper in the style of a research article for publication.

Draft Project Description Document is posted.

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- The project descriptions ask you questions and suggest directions for investigation, but you must construct the final document as a coherent single manuscript, not answers to a bunch of questions.

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- Midterm test:

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- The project descriptions ask you questions and suggest directions for investigation, but you must construct the final document as a coherent single manuscript, not answers to a bunch of questions.

Midterm test:

- Date: Tuesday 5 November 2024
- *Time:* 2:30pm 4:30pm
- Location: in class, HH-102

- Draft Project Description Document is posted.
 - The project is to be submitted as a paper in the style of a research article for publication. It is <u>not</u> just a big assignment.
 - The project descriptions ask you questions and suggest directions for investigation, but you must construct the final document as a coherent single manuscript, not answers to a bunch of questions.

Midterm test:

- Date: Tuesday 5 November 2024
- *Time:* 2:30pm 4:30pm
- Location: in class, HH-102

Assignment 4 is due the day of the midterm.

Draft Project Description Document is posted.

- The project is to be submitted as a paper in the style of a research article for publication. It is *not* just a big assignment.
- The project descriptions ask you questions and suggest directions for investigation, but you must construct the final document as a coherent single manuscript, not answers to a bunch of questions.

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- Location: in class, HH-102
- Assignment 4 is due the day of the midterm. Due Monday 4 November 2019 before class.
 - Make sure you personally can do the question on calculating \mathcal{R}_0 on this assignment *before* the midterm test.

\mathcal{R}_0 : biological definition

The **basic reproduction number** \mathcal{R}_0 is:

the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual

e.g., Anderson and May (1991) "Infectious Diseases of Humans"

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\mathcal{R}_0 : more mathematical definition

The **basic reproduction number** \mathcal{R}_0 is:

the number of new infections produced by a typical infective individual in a population at a disease free equilibrium (DFE)

van den Driessche and Watmough (2002) Mathematical Biosciences 180, 29-48

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\mathcal{R}_0 : most mathematical definition

The **basic reproduction number** \mathcal{R}_0 is:

the spectral radius of the next generation operator at a disease free equilibrium (DFE)

Diekmann, Heesterbeek & Metz (1990) J. Math. Biol. 28, 365-382

Definitions from matrix analysis

Definitions from matrix analysis

Definition (Spectrum of a matrix)

Let M be an $n \times n$ real (or complex) matrix. The *spectrum of* M is

$$\sigma(M) = \{\lambda : Mv = \lambda v \text{ for some non-zero } v \in \mathbb{C}^n\},\$$

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Let M be an $n \times n$ real (or complex) matrix. The *spectral radius* of M is

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i.e., $\rho(M)$ is the maximum modulus of the eigenvalues of M.

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Mathematically, the spectral radius of the next generation operator at the DFE is exactly this quantity. With this definition, it is also true that the disease persists if R₀ > 1 and goes extinct if R₀ < 1.</p>

$$\frac{dS}{dt} = \mu N - \frac{\beta SI}{N} - \mu S$$
$$\frac{dE}{dt} = \frac{\beta SI}{N} - \sigma E - \mu E$$
$$\frac{dI}{dt} = \sigma E - \gamma I - \mu I$$
$$\frac{dR}{dt} = \gamma I - \mu R$$

- Birth and death rate (μ)
- Transmission rate (β)
- Mean latent period $(1/\sigma)$
- Mean infectious period $(1/\gamma)$

Consider flows in and out of the infected compartments

$$\frac{\mathrm{d}}{\mathrm{d}t} \begin{pmatrix} E \\ I \end{pmatrix} = \begin{pmatrix} \beta SI - \sigma E - \mu E \\ \sigma E - \gamma I - \mu I \end{pmatrix}$$

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- Then the *next generation matrix* is FV^{-1}

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- Let F = linearization of F at DFE
- Let V = linearization of \mathcal{V} at DFE
- Then the *next generation matrix* is FV^{-1}
- Analogous to $\beta \gamma^{-1}$ in simple case.

Interpretation of FV^{-1} as next generation matrix

Almost verbatim from p. 33 of van den Driessche and Watmough (2002) Mathematical Biosciences 180, 29-48

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- Hence, the (i, k) entry of the product FV⁻¹ is the expected number of new infections in compartment i produced by the infected individual originally introduced into compartment k.

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- Hence, the (i, k) entry of the product FV⁻¹ is the expected number of new infections in compartment i produced by the infected individual originally introduced into compartment k.
- Following Diekmann et al. (1990), we call FV^{-1} the next generation matrix for the model and set

$$\mathcal{R}_0 = \rho(\mathbf{F} V^{-1}),$$

where $\rho(A)$ denotes the spectral radius of a matrix A.

$$\mathcal{F} = \begin{pmatrix} \beta S I \\ 0 \end{pmatrix}$$

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\mathcal{R}_0 via FV^{-1} for the SEIR model

V

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Note wrt previous slide that the (2, 1) entry of V^{-1} is the average time an individual who enters the *E* compartment spends in the *I* compartment: only a proportion $\sigma/(\sigma + \mu)$ of such individuals make it to the *I* compartment, where the average time spent—by individuals who get there—is $1/(\gamma + \mu)$.

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Computing \mathcal{R}_0 for other compartmental ODE models

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 - **3** The DFE is stable in the absence of new infection (if there is more than one DFE, \mathcal{R}_0 may depend on which one we focus on).
 - 4 The population size *N* is constant (or the model is expressed in terms of proportions in each compartment).

Theorem (van den Driessche and Watmough (2002))

Instructor: David Earn Mathematics 4MB3/6MB3 Mathematical Biology

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Theorem (van den Driessche and Watmough (2002))

If the vector field associated with an ODE infectious disease model satisfies the conditions specified on the previous slide, then

- **1** \mathcal{R}_0 can be computed as $\rho(FV^{-1})$;
- **2** if $\mathcal{R}_0 < 1$ then the disease-free equilibrium (DFE) is locally asymptotically stable (LAS), whereas if $\mathcal{R}_0 > 1$ then there is a LAS endemic equilibrium (EE).

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- If possible, it is best to use both methods to find an expression for \mathcal{R}_0 , and make sure they agree.
- A completely different challenge is to estimate \mathcal{R}_0 for a real epidemic from data...

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 - Estimate β via

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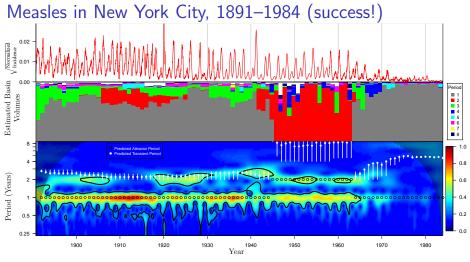
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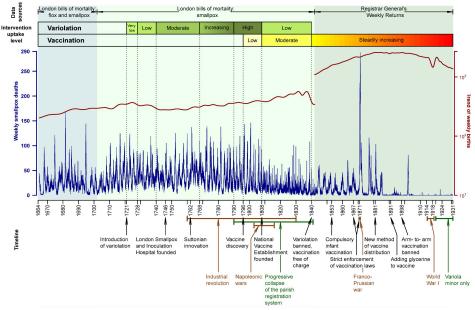


Hempel & Earn (2015) J. R. Soc. Interface 12(106):20150024

Key challenge that had to be overcome: changing patterns of seasonal variation in contact rates

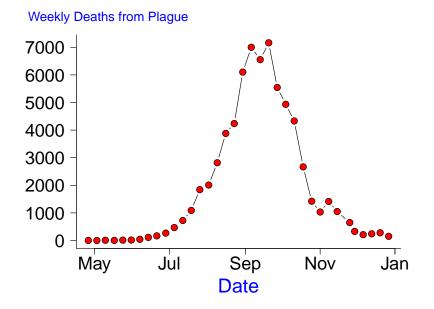
> Papst & Earn (2019) J. R. Soc. Interface 16:20190202 Jagan et al. (2020) PLoS Comp. Biol. 16(9):e1008124

Smallpox in London, 1664–1930 (in progress)



Krylova & Earn (2020) PLoS Biology 18(12):e3000506

The Great Plague of London, 1665



SEIR Model Fit to the Great Plague of London

