

Time since infection models and applications to contact tracing and waning immunity

Francesca Scarabel

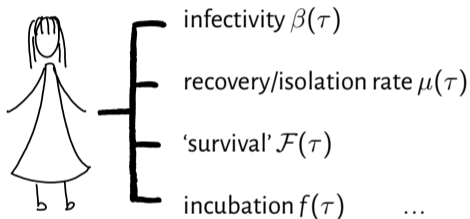
Department of Applied Mathematics, University of Leeds, UK



30 May 2023

Time since infection (deterministic) models

Probabilities and rates depend on time since infection τ

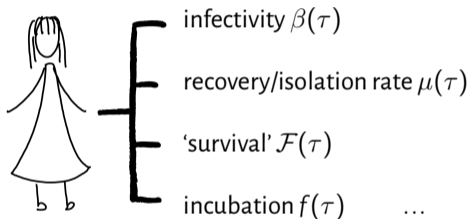


- can be described by **delay equations**
for $b(t) \in \mathbb{R}$ (population birth rate / **incidence**)

$$y(t) = \frac{S(t)}{N} \int_0^\infty \beta(\tau) \mathcal{F}(\tau) y(t - \tau) d\tau$$

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- or, alternatively, as **PDEs**
for $n(t, \cdot) \in L^1$ (population density)

$$\partial_t n(t, \tau) + \partial_\tau n(t, \tau) = -\mu(\tau) n(t, \tau)$$

$$n(t, 0) = \frac{S(t)}{N} \int_0^\infty \beta(\tau) n(t, \tau) d\tau$$

- rarely used in applications due to complexity and lack of software
(ODE compartmental models instead)

Take-home messages

Why should we care? Not just generalisation from Erlang to Gamma!

- more flexibility
- more 'dynamics' → waning immunity
- more modelling power → contact tracing

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Research



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A renewal equation model
to assess roles and
limitations of contact tracing
for disease outbreak control

Francesca Scarabel^{1,2,3}, Lorenzo Pellis^{4,5},
Nicholas H. Ogden⁶ and Jianhong Wu^{1,2}

A modelling example: contact tracing

Aims at stopping as many infection chains as possible, as early as possible, by identifying and isolating individuals among the contacts of one confirmed case.

Forward tracing: search for secondary cases of the index case

A model should account for:

- underlying infection spread
- diagnosis/screening program that can initiate contact tracing
- contacts between individuals and infection transmission
 - contacts are distributed **in the past**
 - infected cases have already progressed through disease stages (and possibly generated infections)

Hard to capture with compartmental ODEs; most often modelled by stochastic agent-based models or branching processes

▶ time-since-infection approach

A SIR time-since-infection epidemic model (1)

The population is divided into three classes:

- **Susceptibles** — no immunity, can contract the infection
- **Infected** — have the disease and can infect others
- **Removed** — recovered and permanently immune or isolated and not infectious

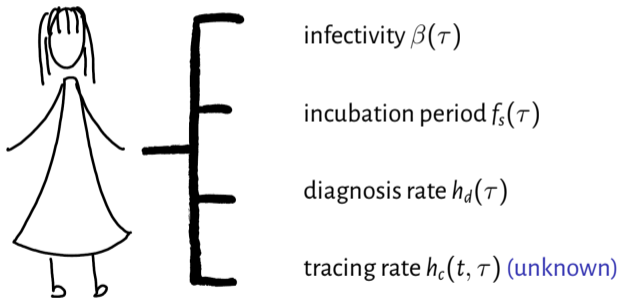
Assuming **homogeneous mixing, identical, independent individuals**.

Three main processes involved:

- 1 infection (and recovery)
- 2 diagnosis from symptoms
- 3 contact tracing

A SIR time-since-infection epidemic model

Individual parameters defined in terms of **time since infection (TSI)** τ :



A renewal equation for the incidence

The equation for the incidence reads

$$y(t) = \frac{S(t)}{N_0} \int_0^\infty \beta(\tau) y(t - \tau) \underbrace{\mathcal{F}(t, \tau)}_{\text{prob not yet isolated}} d\tau$$

where

$\mathcal{F}(t, \tau) =$ prob that an individual **was not isolated** before TSI τ
(defined through the tracing rate h_c , unknown)

Describing forward contact tracing

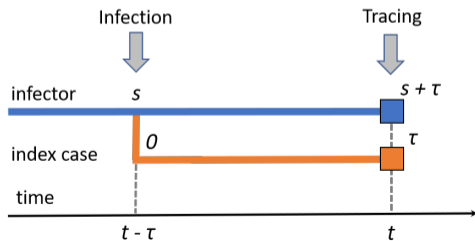
$$\begin{aligned} P(\text{individual traced at time } t) &\propto P(\text{infecter is detected at } t) \\ &= P(\text{infecter is diagnosed or traced at } t) \end{aligned}$$

Describing forward contact tracing

$$P(\text{individual traced at time } t) \propto P(\text{infector is detected at } t)$$

$$= P(\text{infector is diagnosed or traced at } t)$$

break down by time of infection
and by infector's TSI



Integral equation for the contact tracing rate

$$h_c(t, \tau) dt = P(\text{individual traced in } [t, t + dt] \mid \text{infected at } t - \tau)$$

Integral equation for the contact tracing rate

$$\begin{aligned} h_c(t, \tau) dt &= P(\text{individual traced in } [t, t + dt] \mid \text{infected at } t - \tau) \\ &= \varepsilon_c \int_0^\infty P(\text{infector has ASI in } [s, s + ds] \text{ at time } t - \tau) \\ &\quad \times P(\text{infector detected in } [t, t + dt] \mid \text{not detected before } t - \tau, \text{TSI } s) \end{aligned}$$

Integral equation for the contact tracing rate

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The full model: coupled integral equations

(Scarabel, Pellis, Ogden, Wu, *Royal Society Open Science*, 2021)

Putting everything together we get:

$$h_c(t, \tau) = \frac{\varepsilon_c S(t - \tau)}{N_0 y(t - \tau)} \int_0^\infty \beta(s) y(t - \tau - s) \mathcal{F}(t, \tau + s) (h_d(\tau + s) + h_c(t, \tau + s)) ds$$

$$y(t) = \frac{S(t)}{N_0} \int_0^\infty \beta(s) y(t - s) \mathcal{F}(t, s) ds$$

where:

$$\mathcal{F}(t, \tau) = \mathcal{F}_d(\tau) \mathcal{F}_c(t, \tau) = e^{-\int_0^\tau [h_d(\sigma) + h_c(t - \tau + \sigma, \sigma)] d\sigma}$$

$$S(t) = N_0 - \int_0^t y(s) ds$$

- delayed in t and advanced in τ
- can be solved using numerical methods

What about measurable quantities?

h_c is hardly measurable in practice

However, we have all the ingredients to compute concrete quantities of interest:

$$\text{nr individuals diagnosed at time } t = \int_0^{\infty} y(t-s)\mathcal{F}(t,s)h_d(s) ds$$

and

$$\text{nr individuals traced at time } t = \int_0^{\infty} y(t-s)\mathcal{F}(t,s)h_c(t,s) ds$$

Emerging epidemic

In the approximation $S(t) \approx N_0$ (no depletion of susceptibles), we have $y(t) \approx y_0 e^{rt}$, and the system becomes

$$1 = \int_0^{\infty} \beta(s) \mathcal{F}(s) e^{-rs} ds$$

$$h_c(\tau) = \varepsilon_c \int_0^{\infty} \beta(s) e^{-rs} \mathcal{F}(\tau + s) (h_d(\tau + s) + h_c(\tau + s)) ds$$

Note:

- Lotka–Euler type equation for the Malthusian parameter r
- generation time distribution $\beta(s) \mathcal{F}(s)$
- h_c is stationary (independent of t) and satisfies a nonlinear equation

Reproduction numbers

“Average number of secondary infections produced by one typical infected individual in an otherwise susceptible population”

Explicit formulas for the reproduction numbers:

$$R_0 = \int_0^{\infty} \beta(\tau) d\tau \quad \text{unconstrained}$$

$$R_d = \int_0^{\infty} \beta(\tau) \mathcal{F}_d(\tau) d\tau \quad \text{with diagnosis}$$

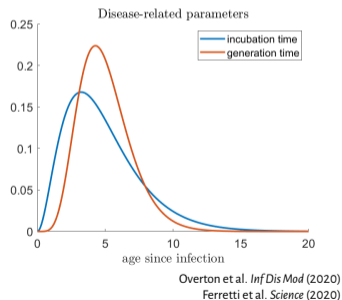
$$R_{d,c} = \int_0^{\infty} \beta(\tau) \mathcal{F}_d(\tau) \mathcal{F}_c(\tau) d\tau \quad \text{with diagnosis \& tracing}$$

General insight: the epidemic is under control if the fraction of transmission occurring before isolation is less than $\frac{1}{R_0}$ (regardless of how isolation is achieved)

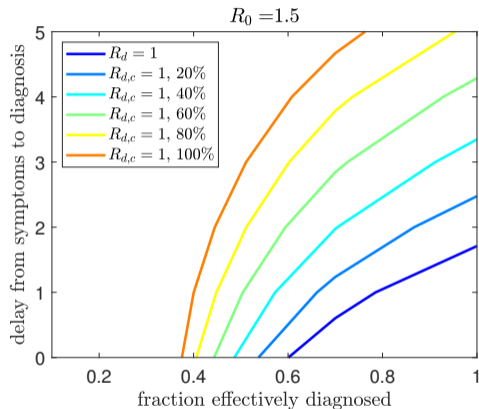
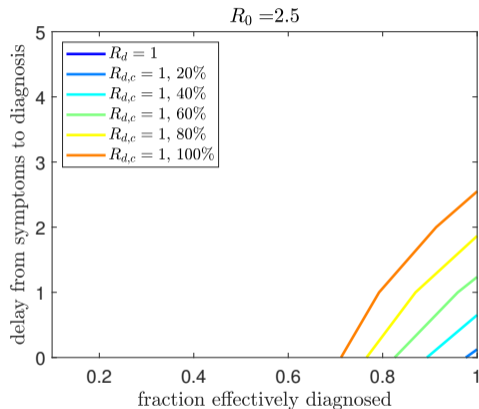
Analyses for COVID-19

We have investigated the impact of:

- diagnosis coverage and delay
- tracing coverage (how many contacts effectively traced?)
- tracing window (how many days back from detection to trace?)
- short-term interruption of contact tracing with limited resources

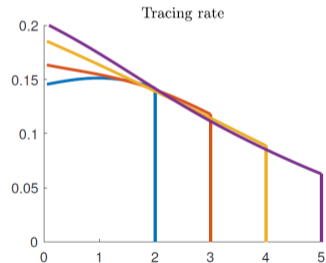
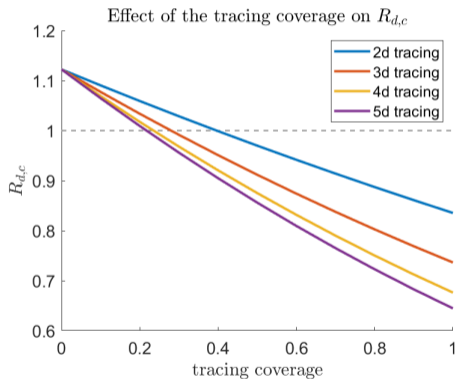


Control of the epidemic with different diagnosis strategies



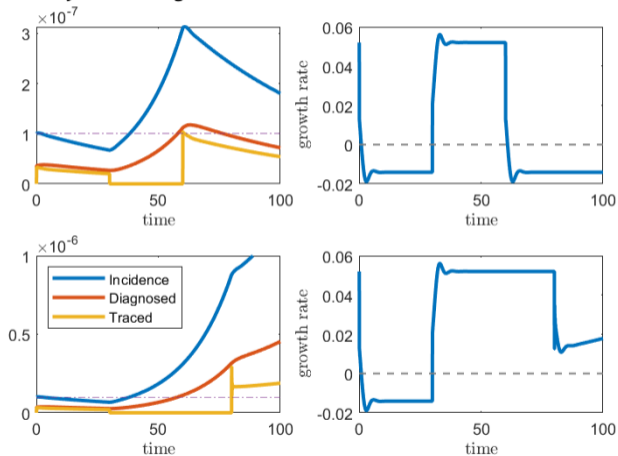
Effect of tracing window ($R_{d,c}$ and computed rate)

$R_0 = 1.5$, 2-day diagnosis delay, 85% diagnosis



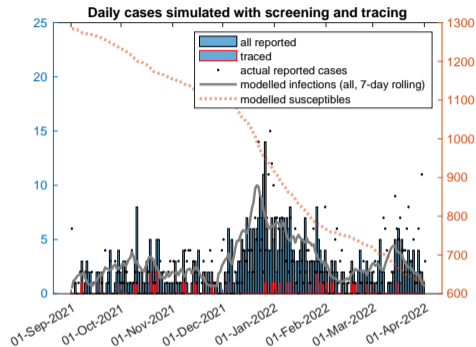
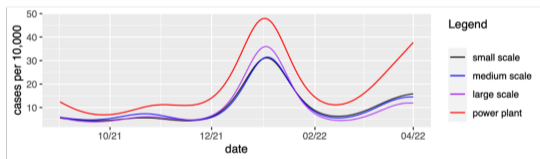
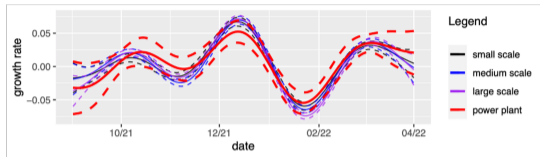
Limit on tracing capacity

$R_0 = 1.5$, 2-day diagnosis delay, 60% diagnosis



Application to workplace transmission (stochastic model)

PROTECT COVID-19 National Core Study on transmission and environment, 'Deep dive into the UK nuclear energy sector'



- similar trends and larger relative size likely due to better surveillance
- relaxing testing results in more infections but less detected cases

Work with: Ian Hall (Manchester), Protect team

Some remarks on the TSI framework for contact tracing

- deterministic:
 - 1) relatively easy and fast to simulate
 - 2) transparent relations between model parameters and output (e.g. R)
- modelling power: first mechanistic model for contact tracing for the full nonlinear epidemic; (and first advanced equation in epidemiology)

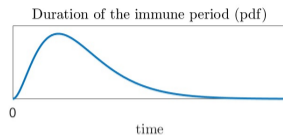
Things I'd like to do

- backward and bidirectional tracing
- correlate infectiousness and incubation period
- comparing with compartmental ODE making simplifying assumptions: is the average outcome similar? do we miss something?
- can we extend to simple network structure?

TSI in the context of waning immunity

$$y(t) = \frac{S(t)}{N} \int_0^{\infty} \beta(\tau)y(t-\tau)\mathcal{F}(\tau) d\tau$$

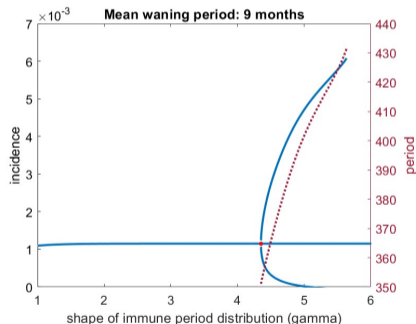
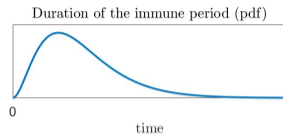
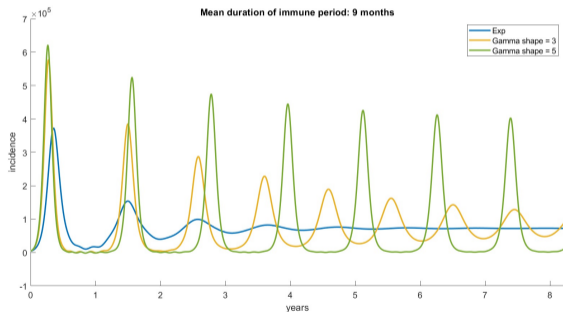
with $\mathcal{F}(\tau)$ 'survival' to reinfection and boosting of immunity



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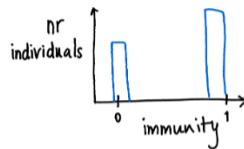
with $\mathcal{F}(\tau)$ 'survival' to reinfection and boosting of immunity



ODEs require a sufficiently large number of compartments (shape of Erlang pdf) to reproduce oscillations

Endemicity, waning immunity and variants

At equilibrium, immunity has a certain stable distribution

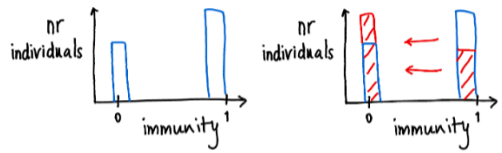


Endemicity, waning immunity and variants

At equilibrium, immunity has a certain stable distribution

A new variant can:

- escape natural and vaccine-induced immunity (hence “shift” the immunity landscape)

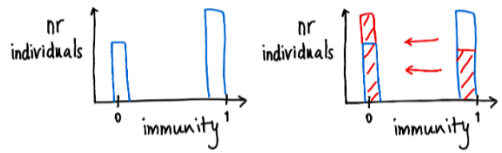


Endemicity, waning immunity and variants

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A new variant can:

- escape natural and vaccine-induced immunity (hence “shift” the immunity landscape)
- have different transmissibility (and/or severity...)

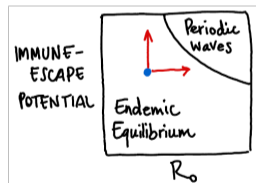
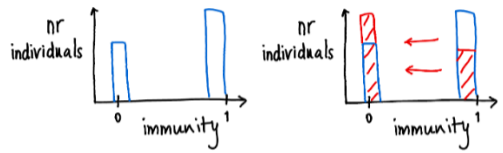


Endemicity, waning immunity and variants

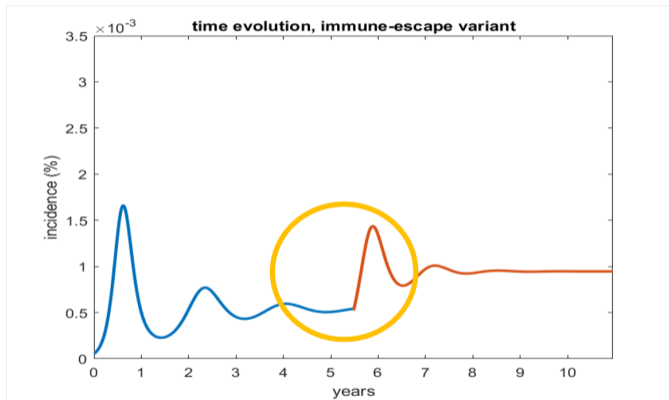
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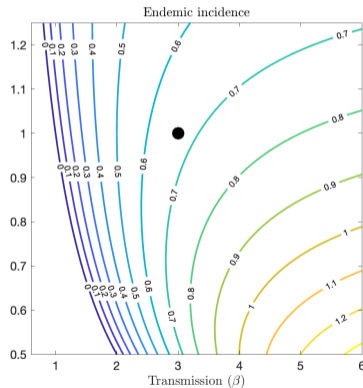
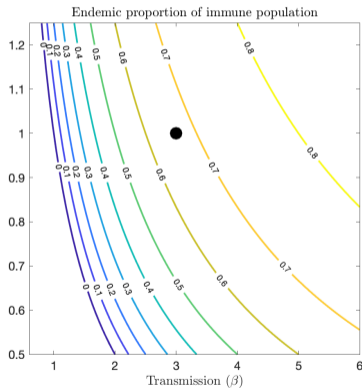
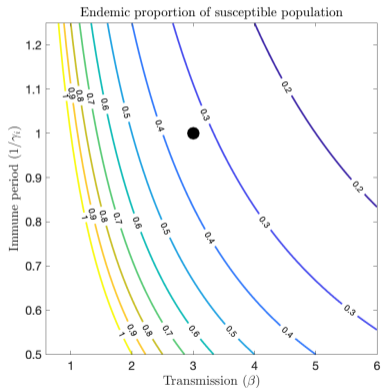
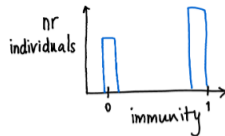
- escape natural and vaccine-induced immunity (hence “shift” the immunity landscape)
- have different transmissibility (and/or severity...)
- affect
 - 1) the endemic equilibrium state;
 - 2) its stability;
 - 3) transient epidemic waves



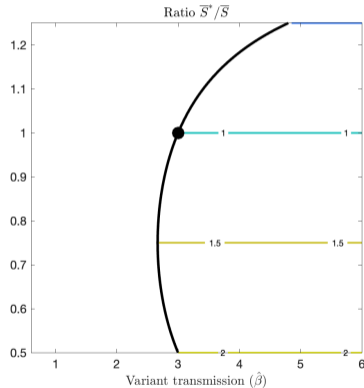
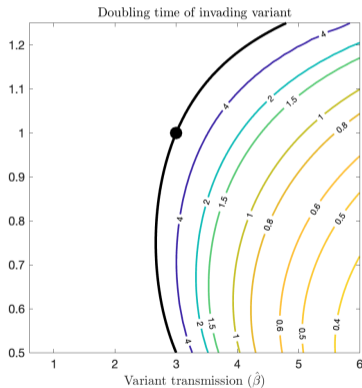
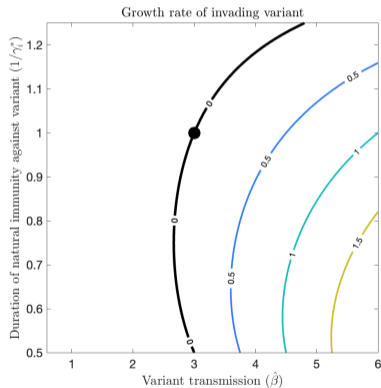
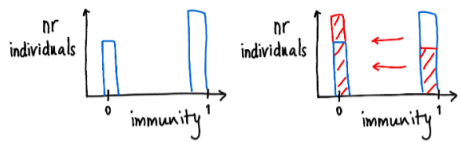
Endemicity, waning immunity and variants



1) Endemic state with waning immunity — SIS

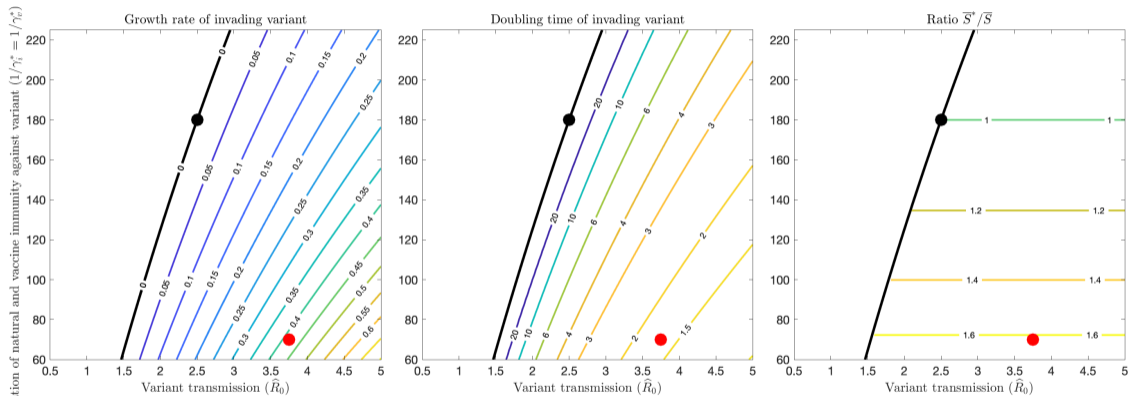


2) Expectations for an invading variant — SIS



In the context of COVID-19: SIRS

in progress



Black: Delta-like; red: Omicron-like

Limitations and things I'd like to do

- preliminary plots are for ODEs
- extend to TSI models (which can account for oscillations)
- can we build 'maps' that help prepare for a next wave in the face of uncertainty?

Numerical methods for delay equations and PSPMs

Work with: Mats Gyllenberg (Helsinki), Odo Diekmann (Utrecht),
Rossana Vermiglio, Dimitri Breda & CDLab (Udine)...

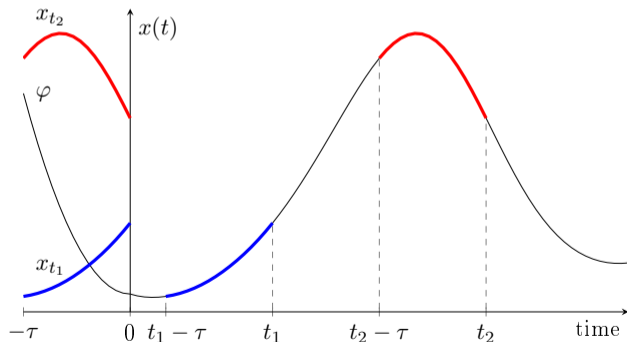


- **Simple** implementation of the approximating ODE system
- **Efficient**: low-dimensional approximation of stability of equilibria and periodic orbits
- **General**: applied to integral, delay differential, partial differential equations

Delay equation: a rule for extending a function given its past

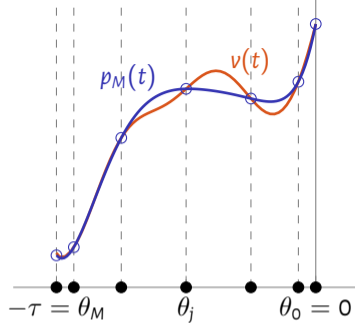
Let $\tau > 0$ be the **maximal delay**. Given a function x , the **history function** is

$$x_t: [-\tau, 0] \rightarrow \mathbb{R}$$
$$x_t(\theta) = x(t + \theta), \quad \theta \in [-\tau, 0]$$



Delay equations and pseudospectral method

$$\begin{aligned} \dot{v}(t) &= \mathcal{A}_0 v(t) + \mathcal{F}(v(t)) \\ &\quad \downarrow \\ \dot{V}_M(t) &= A_M V_M(t) + F_M(V_M(t)) \end{aligned}$$



DDEs $\dot{y}(t) = F(y_t) \rightarrow \begin{cases} \dot{x}_0 = F(p_M) & (x_0 \in \mathbb{R}) \\ \dot{X} = dX_0 + DX & (X \in \mathbb{R}^M) \end{cases}$ with $p_M(t) \approx y_t$

REs $y(t) = F(y_t) \rightarrow \begin{cases} x_0 = 0 \\ \dot{X} = DX + F(p'_M) & (X \in \mathbb{R}^M) \end{cases}$ with $p_M(t) \approx \int_t^{t^+} y_t(s) ds$

for $D \in \mathbb{R}^{M \times M}$, $d \in \mathbb{R}^M$

Final thoughts

- it's not just a matter of having more general parameters (e.g. Gamma instead of Erlang)
- incorporating more detailed micro-scale (within-host) dynamics may be important; we need to think when it's fair to ignore and when not
- numerical methods should be developed and are being developed

More things I'd like to do

- work towards enabling TSI models in public health through development of numerical methods
- further investigate how the within-host dynamics impacts the population scale
- link more closely within- and between-host models and data

CISM Advanced Course (Udine, Italy) "Delays and Structures in Dynamical Systems: Modelling, Analysis and Numerical Methods" November 20–24, 2023

ACADEMIC YEAR 2023
Centre International des Sciences Mécaniques Mécatriques
International Centre for Mechanical Sciences
The Morton Cairns Session

**DELAYS AND STRUCTURES
IN DYNAMICAL SYSTEMS:
MODELING, ANALYSIS AND
NUMERICAL METHODS**

CISM

Advanced School
coordinated by

Dimitri Breda
CDLab - University of Udine
Udine, Italy

Jianhong Wu
LIAM - York University
Toronto, Canada

Udine November 20 - 24 2023

INVITED LECTURERS

Odo Diekmann - Utrecht University, The Netherlands
5 lectures plus discussion on: population dynamics - the notion of state at the individual and at the population level; the notion of environmental condition; the formulation of a size structured model, both in terms of a PDE and in terms of a renewal equation; functional analytic and dynamical systems aspects; density dependence via feedback to the environmental condition; variable maturation delay; biological insights.

Tony Humphries - McGill University, West Montreal, Quebec, Canada
5 lectures plus discussion on: modeling with state-dependent delays; delays defined by threshold conditions; dynamical systems formulation of state-dependent delay equations; linearization and numerical techniques.

Davide Liessi - CDLab, University of Udine, Italy
and **Zachary McCarthy** - LIAM, York University, Toronto, Canada
5 laboratory sessions on: numerical simulation in time of delay equations; computation of equilibria and relevant stability; computation of periodic orbits and relevant stability; numerical continuation; bifurcation analysis from Hopf to chaos - with MATLAB/Octave, Python, MatCont, DDE-Bitool (bring your own laptop).

Stefano Maset - University of Trieste, Italy
and **Rossana Vermiglio** - CDLab, University of Udine, Italy
5 lectures plus discussion on: numerical methods for delay equations; adaptation of continuous methods for ODEs; constrained meshes and superconvergence; functional continuous Runge-Kutta methods; methods for neutral equations; boundary value problems; innovative techniques based on a general abstract formulation; connections to bifurcation analysis.

Shigui Ruan - The University of Miami, Coral Gables, FL, USA
5 lectures plus discussion on: population dynamics models with two structures; relevant semigroup theory and existence of solutions; spectrum theory; eigenvalue problem; stability of steady states; asynchronous exponential growth of solutions (both linear and nonlinear equations will be considered).

Francesca Scarabel - The University of Leeds, UK
5 lectures plus discussion on: examples of mathematical models from ecology and epidemiology; introduction to the dynamical and bifurcation analysis; pseudospectral collocation of nonlinear problems formulated as delay or partial differential equations; stability of equilibria and relevant bifurcations; stability of periodic orbits and relevant bifurcations.

Thank you!
(and questions, comments...?)

Complex behaviour: a model with waning and boosting of immunity

in progress with M.V. Barbarossa, M. Polner and G. Röst

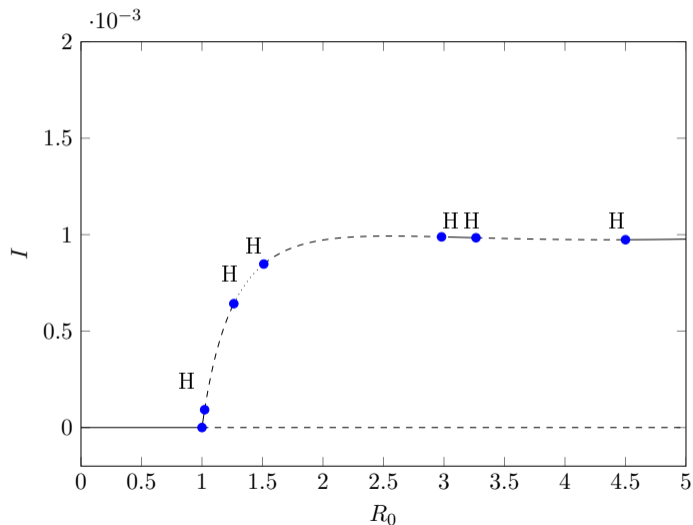
$$\begin{aligned}\frac{dI}{dt} &= \beta SI - (\gamma + d)I \\ \frac{dS}{dt} &= d(1 - S) - \beta SI + I(t - \tau) \underbrace{[\gamma + \nu\beta R(t - \tau)]}_{\text{recovered + boosted}} \underbrace{e^{-d\tau - \nu\beta \int_{t-\tau}^t I(u)du}}_{\text{"survival" in } R \text{ for time } \tau}\end{aligned}$$

- $S + I + R = 1$
- $\beta =$ transmission, $\gamma =$ recovery, $d =$ birth = death
- $\tau =$ maximal duration of immunity unless boosted
- $\nu =$ probability of immunity boosting after contact with infectious individual (boost to the maximal immunity level)

Barbarossa, Polner, Röst, *SIAM. J. Appl. Math.*, 2017

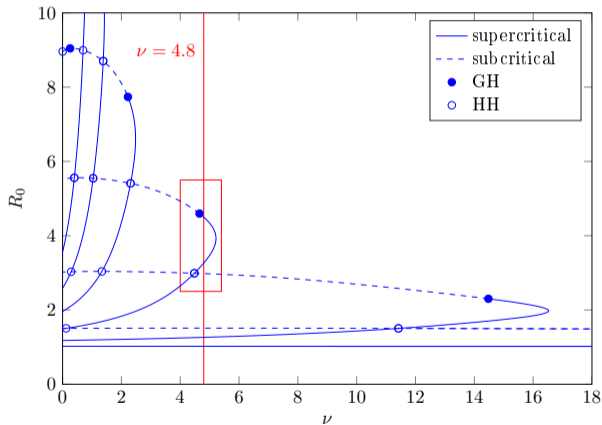
Bifurcations of equilibria

$$d = 0.02, \quad \gamma = 17, \quad \nu = 4.8, \quad \tau = 15, \quad R_0 = \frac{\beta}{d+\gamma} \quad (M = 20)$$

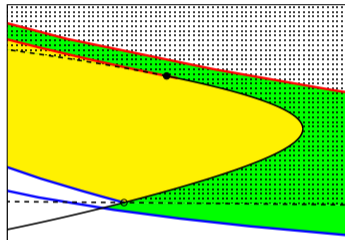


Bifurcations in the plane (ν, R_0)

Hopf bifurcation curves (sub/supercritical)



Zoom



- Dotted: stable positive equilibrium
- Red: fold bifurcation of cycles
- Blue: Neimark-Sacker bifurcations
- Green: (at least) one stable periodic solution
- Yellow: (at least) two stable coexisting periodic solutions