Model parameterization

MATHEMATICAL MODELING FOR INFECTIOUS DISEASE PLANNING IN AFRICA

(30 minutes)

RATE PARAMETERS

- Every rate (arrow) needs to be parameterized, the more rates, the more parameters (and complexity) you are adding to the model
- Are the rates well-known in the literature? How relevant/robust are parameters from the literature to your population?
- Are the parameters from literature based on primary data or rates from other models?
- What are the sources of uncertainty in your parameters?

STATE VARIABLES

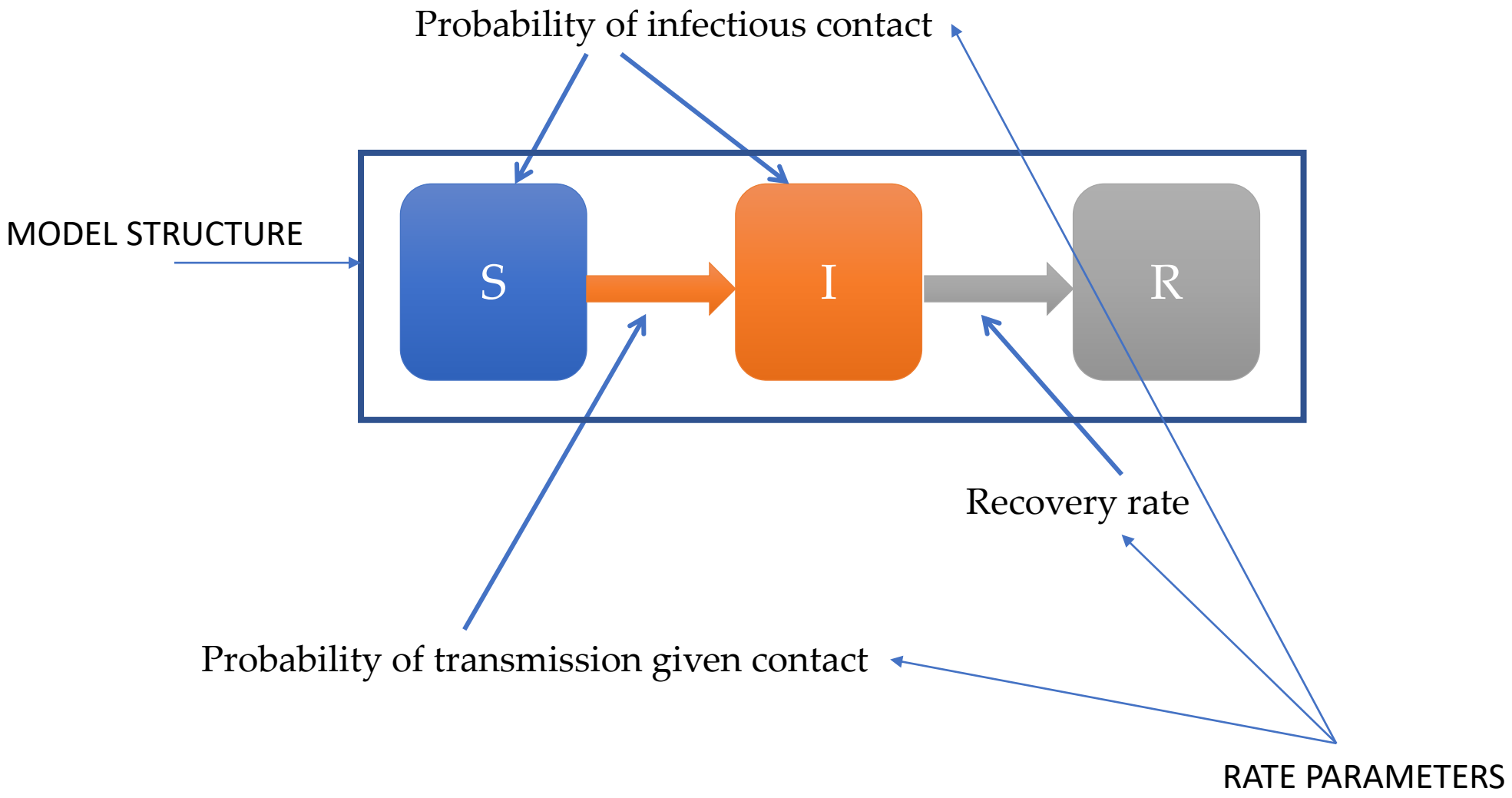
- What data are you using to determine the initial conditions of your model or the current number of susceptible/infected/recovered people?
- How reliable is this data? Where are the sources of uncertainty (e.g. reporting rates, asymptomatic infections)
- Is epidemiological surveillance data for your disease reliable, timely, and complete?
- ***Model fitting is a whole thing…***

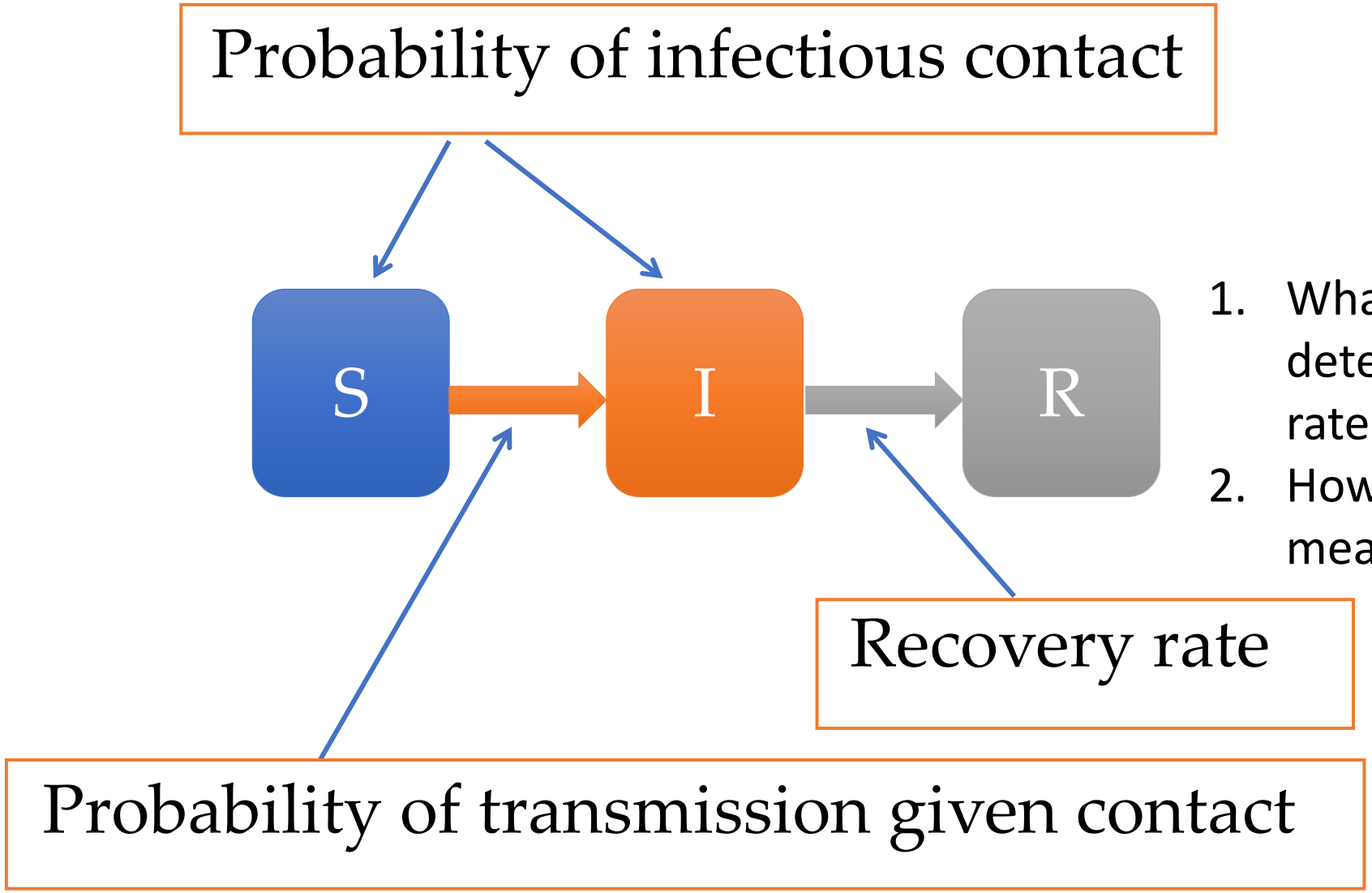
Qualitative versus quantitative models

***2 principle sources of uncertainty:**

-model structure uncertainty (have you got your boxes and arrows right?)

-parameter uncertainty (do we know these rates and how variable are they?)

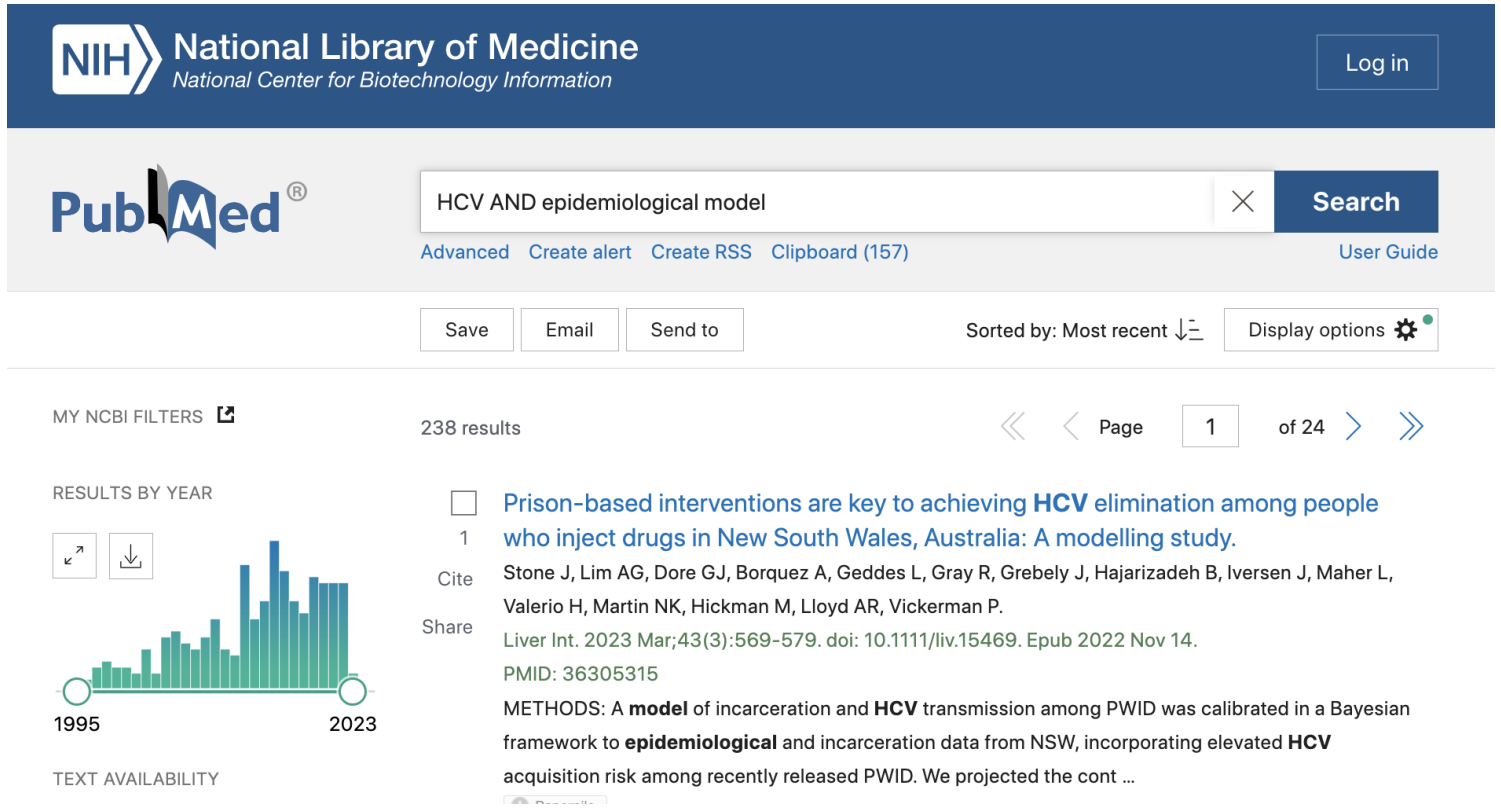




1. What will determine this rate?
2. How would you measure it?

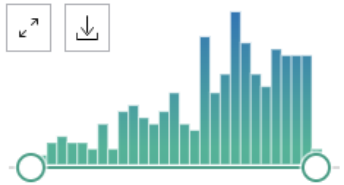
Searching for parameters in the literature

- Google scholar, PubMed etc are good places to start



MY NCBI FILTERS

RESULTS BY YEAR



TEXT AVAILABILITY

- [ ] Abstract
- [ ] Free full text
- [ ] Full text

ARTICLE ATTRIBUTE

- [ ] Associated data

ARTICLE TYPE

- [ ] Books and Documents
- [ ] Clinical Trial
- [ ] Meta-Analysis
- [ ] Randomized Controlled Trial
- [ ] Review
- [ ] Systematic Review

PUBLICATION DATE

- ( ) 1 year
- ( ) 5 years
- ( ) 10 years
- ( ) Custom Range

238 results

Page 1 of 24

1 Cite Share

Prison-based interventions are key to achieving **HCV** elimination among people who inject drugs in New South Wales, Australia: A modelling study.

Stone J, Lim AG, Dore GJ, Borquez A, Geddes L, Gray R, Grebely J, Hajarizadeh B, Iversen J, Maher L, Valerio H, Martin NK, Hickman M, Lloyd AR, Vickerman P.

Liver Int. 2023 Mar;43(3):569-579. doi: 10.1111/liv.15469. Epub 2022 Nov 14.

PMID: 36305315

METHODS: A **model** of incarceration and **HCV** transmission among PWID was calibrated in a Bayesian framework to **epidemiological** and incarceration data from NSW, incorporating elevated **HCV** acquisition risk among recently released PWID. We projected the cont ...

Paperpile

2 Cite Share

Elite controllers long-term non progressors present improved survival and slower disease progression.

Capa L, Ayala-Suárez R, De La Torre-Tarazona HE, González-García J, Del Romero J, Alcamí J, Díaz Fuertes F.

Sci Rep. 2022 Sep 29;12(1):16356. doi: 10.1038/s41598-022-19970-3.

PMID: 36175445 Free PMC article.

The combination of both phenotypes is even less frequent and studied despite being considered as **models** of HIV-1 functional cure. A multicenter, prospective study in retrospect including clinical and **epidemiological** data collected from 313 LTNP of 21 Spanish hospita ...

Paperpile

3 Cite Share

Persistent Transmission of **HCV** among Men Who Have Sex with Men despite Widespread Screening and Treatment with Direct-Acting Antivirals.

Popping S, Cuypers L, Claassen MAA, van den Berk GE, De Weggheleire A, Arends JE, Boerekamps A, Molenkamp R, Koopmans MPG, Verbon A, Boucher CAB, Rijnders B, van de Vijver DAMC.

Viruses. 2022 Sep 2;14(9):1953. doi: 10.3390/v14091953.

PMID: 36146760 Free PMC article.

To develop strategies that can further reduce the spread of **HCV**, it is important to understand the transmission dynamics of **HCV**. ...Importantly, despite an **HCV** incidence reduction after high DAA uptake and continuously monitoring, **HCV** transmission pers ...

Paperpile

4 Cite Share

Syphilis and Co-Infections with HIV-1, HBV, and **HCV** among People Who Use Crack-Cocaine in Northern Brazil.

Baia KLN, Cordeiro ACC, Frade PCR, Gouveia AGN, Resque RL, Pinheiro LML, Fonseca RRS, Machado LFA, Martins LC, Kupek E, Fischer B, Oliveira-Filho AB.

Pathogens. 2022 Sep 16;11(9):1055. doi: 10.3390/pathogens11091055.

Full text

ARTICLE ATTRIBUTE

Associated data

ARTICLE TYPE

Books and Documents

Clinical Trial

Meta-Analysis

Randomized Controlled Trial

Review

Systematic Review

PUBLICATION DATE

1 year

5 years

10 years

Custom Range

Additional filters

Reset all filters

Cite

Share

Fuertes F.

Sci Rep. 2022 Sep 29;12(1):16356. doi: 10.1038/s41598-022-19970-3.

PMID: 36175445 **Free PMC article.**

The combination of both phenotypes is even less frequent and studied despite being considered as **models** of HIV-1 functional cure. A multicenter, prospective study in retrospect including clinical and **epidemiological** data collected from 313 LTNP of 21 Spanish hospita ...

Paperpile

3

Persistent Transmission of **HCV** among Men Who Have Sex with Men despite Widespread Screening and Treatment with Direct-Acting Antivirals.

Cite

Share

Popping S, Cuypers L, Claassen MAA, van den Berk GE, De Weggheleire A, Arends JE, Boerekamps A, Molenkamp R, Koopmans MPG, Verbon A, Boucher CAB, Rijnders B, van de Vijver DAMC.

Viruses. 2022 Sep 2;14(9):1953. doi: 10.3390/v14091953.

PMID: 36146760 **Free PMC article.**

To develop strategies that can further reduce the spread of **HCV**, it is important to understand the transmission dynamics of **HCV**. ...Importantly, despite an **HCV** incidence reduction after high DAA uptake and continuously monitoring, **HCV** transmission pers ...

Paperpile

4

Syphilis and Co-Infections with HIV-1, HBV, and **HCV** among People Who Use Crack-Cocaine in Northern Brazil.

Cite

Share

Baia KLN, Cordeiro ACC, Frade PCR, Gouveia AGN, Resque RL, Pinheiro LML, Fonseca RRS, Machado LFA, Martins LC, Kupek E, Fischer B, Oliveira-Filho AB.

Pathogens. 2022 Sep 16;11(9):1055. doi: 10.3390/pathogens11091055.

PMID: 36145487 **Free PMC article.**

Reactive samples by RQT were used to assess the presence of HBV, **HCV**, and HIV-1 using Enzyme Immunoassay (EIA) and Polymerase Chain Reaction (PCR). Logistic regression **models** were used to determine the association of variables assessed with syphilis. ...

Paperpile

5

Compartmental **model** describing the physiological basis for the HepQuant SHUNT test.

Cite

Share

McRae MP, Helmke SM, Burton JR Jr, Everson GT.

Transl Res. 2023 Feb;252:53-63. doi: 10.1016/j.trsl.2022.08.002. Epub 2022 Aug 7.

PMID: 35948199

Previously, a noncompartmental analysis method, called the minimal **model** (MM), demonstrated reproducible and reliable measures of liver function (Translational Research 2021). The aim of this study was to compare the reproducibility and reliability of a new physiologically ...

Paperpile

6

Probing a Stochastic Epidemic Hepatitis C Virus **Model** with a Chronically Infected Treated Population.

Cite

Rajasekar SP, Pitchaimani M, Zhu Q.

> Acta Math Sci. 2022;42(5):2087-2112. doi: 10.1007/s10473-022-0521-1. Epub 2022 Jul 25.

Probing a Stochastic Epidemic Hepatitis C Virus Model with a Chronically Infected Treated Population

S P Rajasekar [1] [2], M Pitchaimani [1], Quanxin Zhu [3]

Affiliations + expand

PMID: 35911571 PMCID: PMC9310688 DOI: 10.1007/s10473-022-0521-1 Paperpile

Free PMC article

Abstract

The hepatitis C virus is hitherto a tremendous threat to human beings, but many researchers have analyzed mathematical models for hepatitis C virus transmission dynamics only in the deterministic case. Stochasticity plays an immense role in pathology and epidemiology. Hence, the main theme of this article is to investigate a stochastic epidemic hepatitis C virus model with five states of epidemiological classification: susceptible, acutely infected, chronically infected, recovered or removed and chronically infected, and treated. The stochastic hepatitis C virus model in epidemiology is established based on the environmental influence on individuals, is manifested by stochastic perturbations, and is proportional to each state. We assert that the stochastic HCV model has a unique global positive solution and attains sufficient conditions for the extinction of the hepatotropic RNA virus. Furthermore, by constructing a suitable Lyapunov function, we obtain sufficient conditions for the existence of an ergodic stationary distribution of the solutions to the stochastic HCV model. Moreover, this article confirms that using numerical simulations, the six parameters of the stochastic HCV model can have a high impact over the disease transmission dynamics, specifically the disease transmission rate, the rate of chronically infected population, the rate of progression to chronic infection, the treatment failure rate of chronically infected population, the recovery rate from chronic infection and the treatment rate of the chronically infected population. Eventually, numerical simulations validate the effectiveness of our theoretical conclusions.

[6] Shi R Q, Cui Y T. Global analysis of a mathematical model for Hepatitis C virus transmissions. Virus Research, 2016, 217: 8–17

[16] Elbasha E H. Model for hepatitis C virus transmissions. Mathematical Biosciences and Engineering, 2013, 10: 1045–1065

[17] Nazari F, Gumel A B, Elbasha E H. Differential characteristics of primary infection and re-infection can cause backward bifurcation in HCV transmission dynamics. Mathematical Biosciences, 2015, 263: 51–69

$$
\begin{aligned}
S' &= \Lambda - \Phi S - \mu S + \gamma R, \\
I' &= \Phi S + \vartheta \Phi R - (\mu + \zeta + \eta + \varphi) I, \\
P' &= \eta I + \rho T - (\mu + \delta + \upsilon) P, \\
R' &= \zeta I + \delta P + \alpha T - \vartheta \Phi R - (\mu + \gamma) R, \\
T' &= \upsilon P - (\mu + \rho + \alpha) T.
\end{aligned}
$$

Table 2 List of parameters

Parameters	Interpretation	Values	Reference
Λ	Recruitment rate of population	39600 year^{-1}	[6, 16, 17]
β	Disease transmission rate	2.1×10^{-7} year^{-1}	[6]
π	Rate of chronically infected population	0.01	[6, 16, 17]
λ	Rate of treated population	0.5	[6, 16, 17]
μ	Natural mortality rate of population	0.09 year^{-1}	[6, 16, 17]
γ	Rate of subsiding immunity	0.025 year^{-1}	[6, 16, 17]
ϑ	Relative susceptibility of recovered population	0.5	[6, 16, 17]
ζ	Recovery rate of acute infected population	0.5 year^{-1}	[6, 17]
η	Rate of progression to chronic infection	1.5 year^{-1}	[6, 16, 17]
φ	Death from acute infection	0.035 year^{-1}	[6]
ρ	Treatment failure rate of chronically infected population	0.82 year^{-1}	[6, 16, 17]
δ	Recovery rate from chronic infection	0.002 year^{-1}	[6, 16, 17]
υ	Treatment rate of chronically infected population	0.04 year^{-1}	[6, 16, 17]
α	Curing rate by treatment	0.67 year^{-1}	[6, 16, 17]

Global analysis of a mathematical model for Hepatitis C virus transmissions

Ruiqing Shi, Yunting Cui

$$\begin{cases} S' = \Lambda - \lambda S - \mu S + \gamma R, \\ I' = \lambda S - (\mu + \sigma + \varepsilon + d)I, \\ P' = \varepsilon I + \rho T - (\mu + \delta + \tau)P, \\ R' = \sigma I + \delta P + \alpha\sigma V + \eta\delta W + \theta T + \theta Q - \psi\lambda R - (\mu + \gamma)R, \\ V' = \psi\lambda R - (\mu + \alpha\sigma + \kappa\varepsilon + d)V, \\ W' = \kappa\varepsilon V + \zeta Q - (\mu + \eta\delta + \phi)W, \\ T' = \tau P - (\mu + \rho + \theta)T, \\ Q' = \phi W - (\mu + \zeta + \theta)Q, \end{cases} \tag{1}$$

where

$$\lambda = \beta(I + \pi P + \nu V + \omega\pi W + \chi\pi T + \chi\pi Q), N = S + I + P + R + V + W + T + Q$$
.

The biological meanings of all variables and the values for the parameters are given in Table 1.

Table 1. Description of variables and parameters, and the parameters values except β, are from Ref. Elbasha (2013). The value of β is estimated as $(0, 3]\text{year}^{-1}$.

E.H. Elbasha
Model for hepatitis C virus transmissions
Math. Biosci. Eng., 10 (2013), pp. 1045-1065
View in Scopus ↗ Google Scholar ↗

View in article

4.1. **Parameters values.** The baseline parameter estimates are summarized in Table 1. The baseline values were derived as follows. The removal rate μ consists of natural death and cessation of high-risk activity (e.g., injecting drug use). We set the natural death to 0.02 per year, implying that the average life expectancy of this population is 50 years. Estimates of the duration of injecting drug use vary, ranging from 8 to 41 years [29]. We assume that it is 14 years [15]. Thus, $\mu = 0.09$ $(= 0.02 + 0.07)$ per year.

According to data from the National Household Survey on Drug Abuse an estimated 440,000 persons reported IDU within the past year during the period 1979–2002 [6]. Assuming a steady state, this implies $\Lambda = 39,600$ per year.

The rate of recovery from acute infection σ is estimated at 0.5 per year and the rate of progression to chronic infection ε at 1.5 per year, which is equivalent to a mean duration of acute infection of 6 months and an overall rate of clearance of 25% [51]. The rate of recovery from chronic infection δ is estimated at 0.002 per year [8].

Reinfection occurs in approximately 50% of IDU who previously spontaneously controlled primary HCV infection, suggesting a ψ value of 0.5 [42]. Another study found that the odds of developing infection among persons previously cleared HCV infection compared with those infected for the first time is 0.23 (confidence interval, 0.10–0.51) [25]. Also, rates of viral clearance among reinfected patients are approximately 3.3 times faster than rates of clearance of primary infections [42]. Thus, we can assume $\alpha = \eta = 3.3$, and $\kappa = 1/3.3$.

Rate of antibody loss is low. One study estimated it at 0.6 per 100 person-years whereas another study found that antibodies were undetectable in 50% of patients 18–20 years after recovery [1, 46]. Thus, γ can range from 0.006 to 0.035. We choose the average of the two estimates and assume the average life span of antibodies is four decades ($\gamma = 0.025$).

Mainly because of lack of diagnosis and follow up, only a minority of chronically infected patients receive treatment. Estimates of annual treatment rates among IDUs in the US are as low as <1% [37]. Other estimates from other US populations

E.H. Elbasha

Model for hepatitis C virus transmissions

Math. Biosci. Eng., 10 (2013), pp. 1045-1065

View in Scopus ↗ Google Scholar ↗

View in article

predict the probability of viral transmission from a single transfusion given viral load of the donor [49]. Here we make simple assumptions regarding the relative infectivity of persons in classes I, P, W, V, T, and Q. According to data from animal experiments, chronic phase plasma may be 75- to 100-fold less infectious than acute phase plasma [31]. Thus , we assume $\pi = 0.01$. Experimental data from reinfection of chimpanzees that have cleared HCV suggest that viremia levels are six to seven log fold lower compared with viremia levels during primary infection [33]. Thus, we assume $\nu = \omega = 1/6.5$. Because about half of patients on treatment with pegylated interferon alfa and ribavirin have undetectable HCV-RNA, we assume that they are 50% less infectious compared with untreated patients in the chronic phase. Thus, $\chi = 0.5$.

Estimates of the contact rate β can be inferred from data on incidence and seroprevalence of HCV among IDUs in the absence of widespread treatment. Estimates of HCV seroprevalence in the US vary widely, ranging from 18% to 90% [2]. Also,

Parameter uncertainty

- Sometimes there’s no data but our model results don’t rely on that parameter
- Sometimes there is literature from other settings, but it’s likely to be generalizable so we can use the parameters “safely”
- Sometimes the data might be available freely online in various forms (or proxies for our variables)
- Sometimes we have data from our own programs to estimate these parameters

Introducing sensitivity analysis

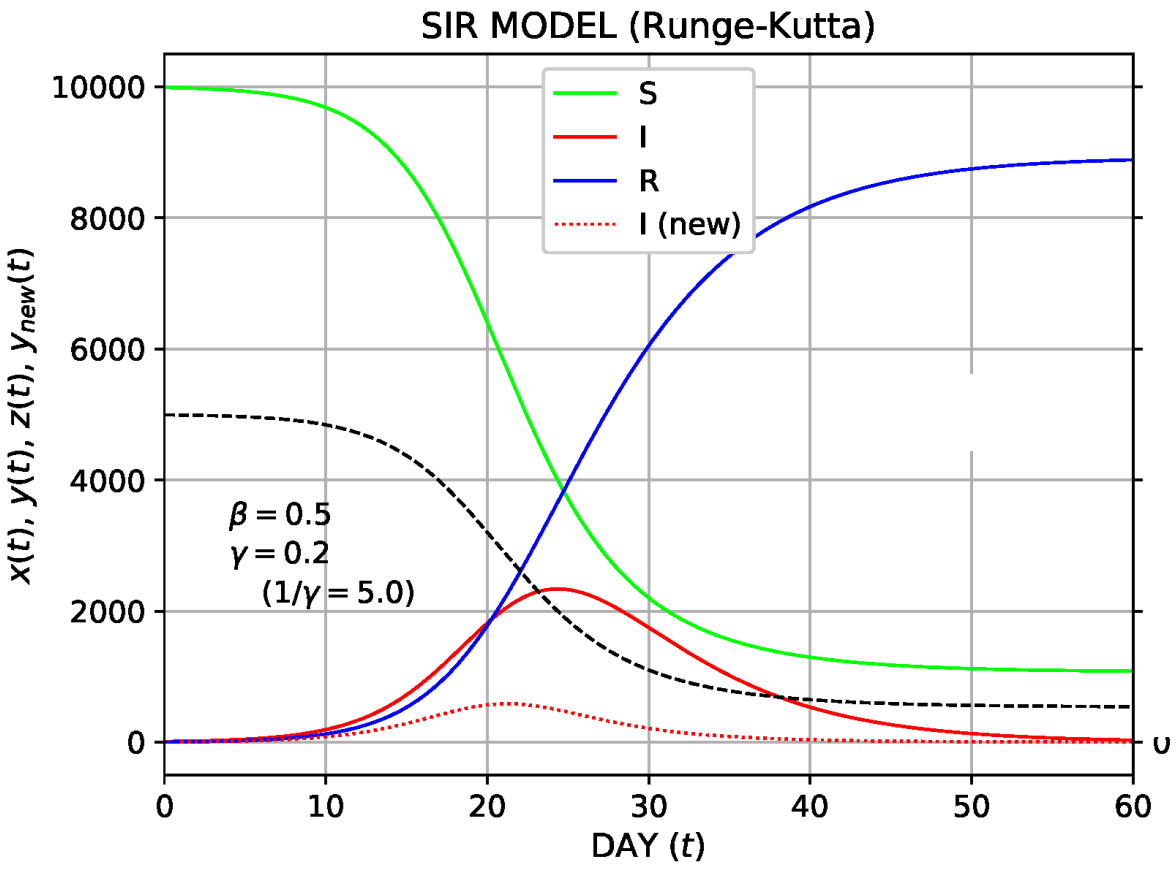
- Sensitivity analyses are one way to manage uncertainty across a range of parameter rates: **we want to check how sensitive our model results are to parameter uncertainty**
- It is also *answering the question itself sometimes*
- A sensitivity analysis may involve varying parameters across their ranges
- Another type of sensitivity of model results could be to initial conditions in the state variables (the number of S, I, and R people)
- “Robust” means that the dynamics don’t change substantially, or qualitatively.

$$\frac{dS}{dt} = \frac{-\beta SI}{N},$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I,$$

$$\frac{dR}{dt} = \gamma I,$$

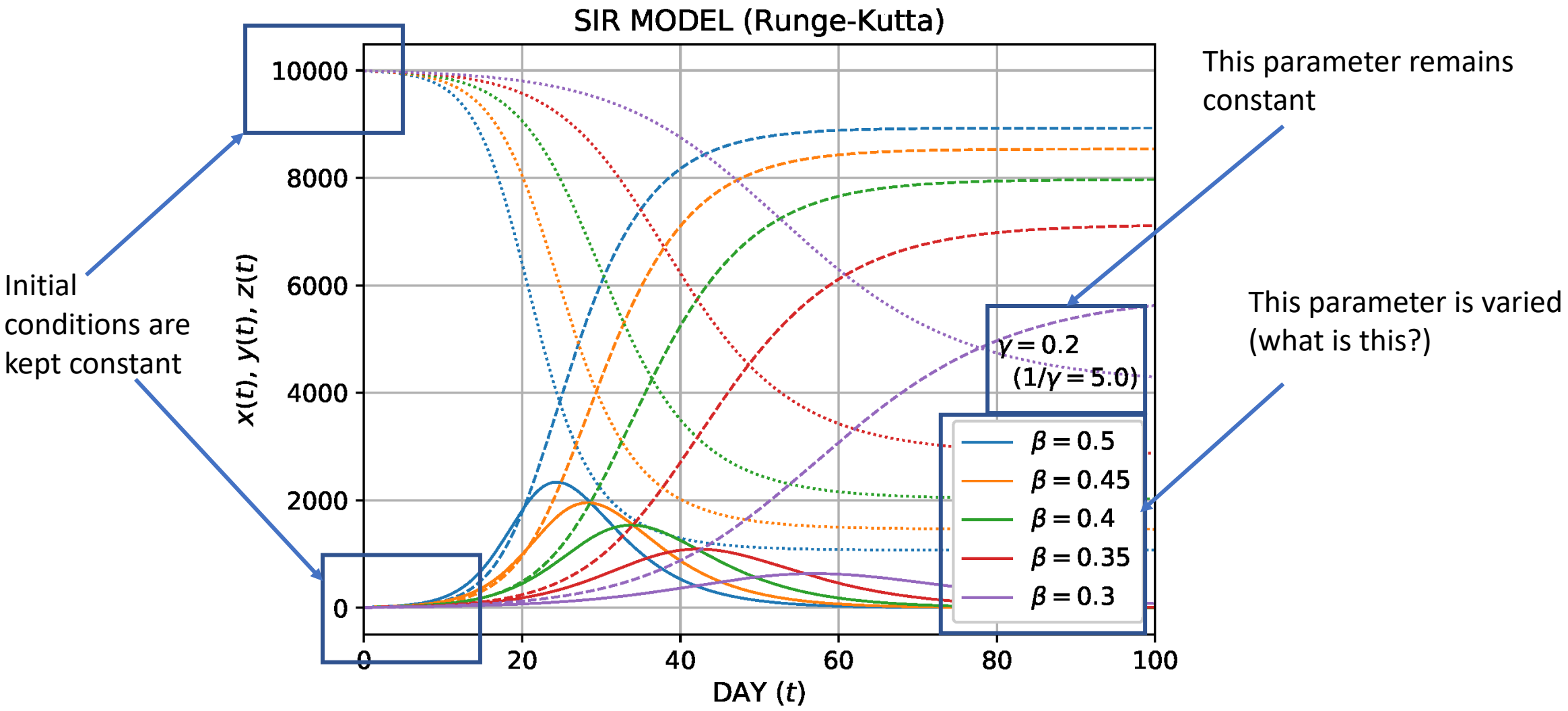
$$N = S + I + R.$$



A Mathematical Model of Epidemics—A Tutorial for Students

by Yutaka Okabe * and Akira Shudo

Hold everything constant, and vary one (or a few) parameters



These parameters remain constant (what are these?)

This parameter is varied (what is this?)

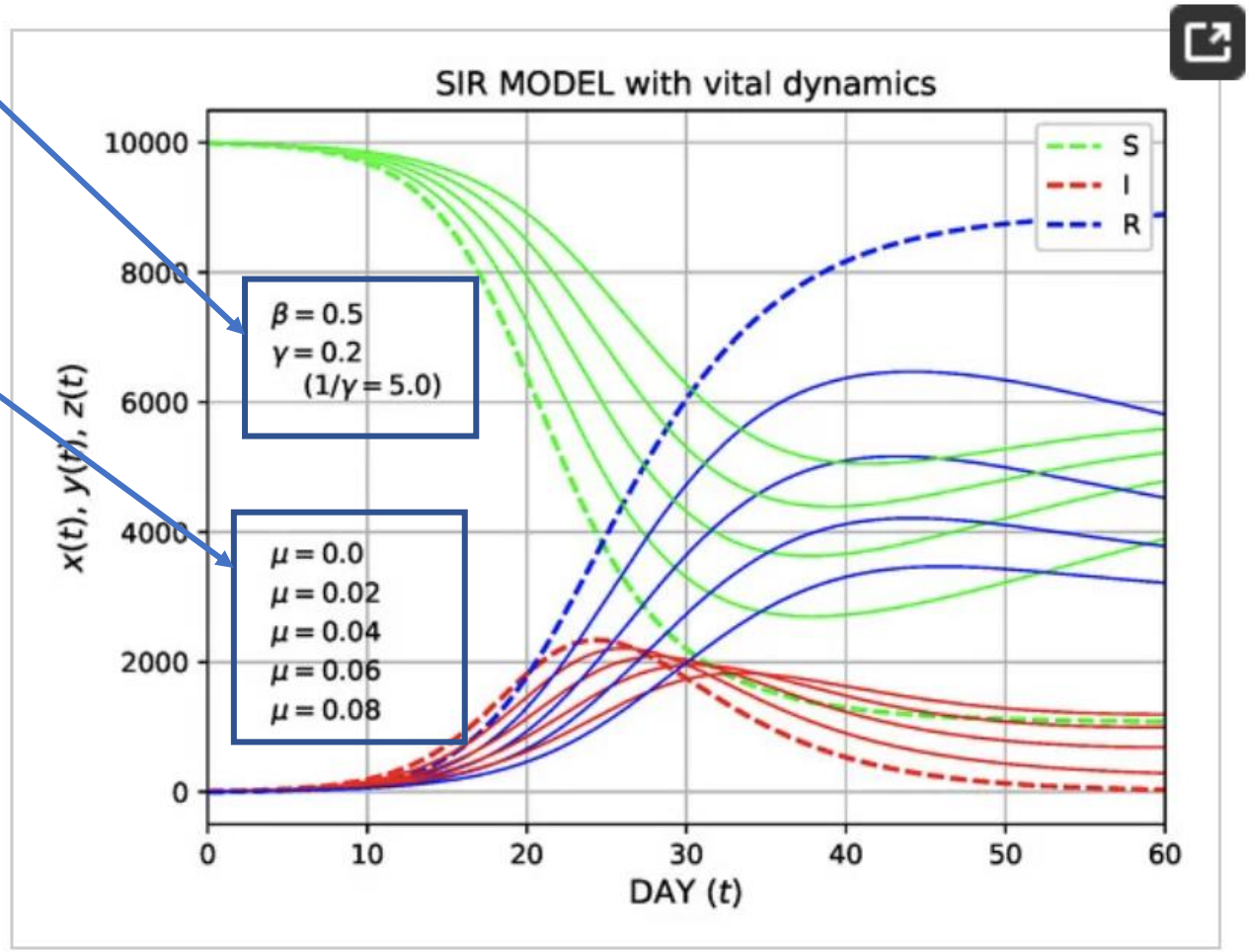


Figure 7. The solution of the SIR model with vital dynamics. The parameter μ is varied as 0.0, 0.02, 0.04, 0.06, and 0.08, and the data of $\mu = 0.0$ are shown by thick dashed curves.

- Sometimes an exhaustive search of all of parameter space is prohibitive, so we might use techniques for efficiently sampling from that space…
- Models are often useful for bounding expectations, so we may want to communicate our results in relation to parameters of interest
- **Sensitivity to parameters is key to understanding the mechanistic behavior of your model!**