

Bayesian workflow for disease transmission modeling in Stan

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Advanced statistical methods for physicists
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- ▶ Objective: fit simple transmission models in Stan
- ▶ Based on Grinsztajn et al., 2021 ([link](#))
- ▶ Prerequisites:
 - ▶ basic programming with R
 - ▶ general understanding of Bayesian inference
- ▶ All material is available on github ([link](#))

Outline

Models of disease transmission

Bayesian inference with Stan

Fitting a simple SIR

Using simulations to understand the model

Extending from the simple SIR model

Conclusions

Introduction

Models of disease transmission:

- ▶ Interpretability: phenomenological, **mechanistic**
- ▶ Scale: **population-based**, agent-based,
- ▶ Framework: **deterministic**, stochastic
- ▶ Data-generating mechanisms: incubation, contagion, immunity, vaccination, mobility...

Introduction

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- ▶ Scale: **population-based**, agent-based,
- ▶ Framework: **deterministic**, stochastic
- ▶ Data-generating mechanisms: incubation, contagion, immunity, vaccination, mobility...

Mechanistic + population-based + deterministic

→ **ordinary differential equations (ODE)-based compartmental model**

Introduction

ODE-based compartmental model:

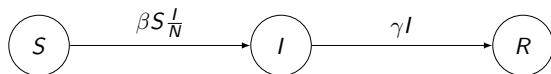
- ▶ Divide the population into homogeneous groups (compartments)
- ▶ Define the flows between compartments with ODEs
- ▶ Define initial conditions (at t_0)
- ▶ Solve for the time-dependent volume in each compartment

Introduction

ODE-based compartmental model:

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- ▶ Define the **flows** between compartments with ODEs
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The **susceptible-infectious-recovered** (SIR) model:

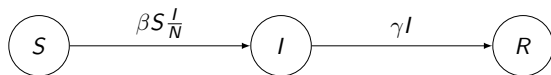


$$\frac{dS}{dt} = -\beta S \frac{I}{N}$$

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

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

The SIR model



$$\frac{dS}{dt} = -\beta S \frac{I}{N}$$

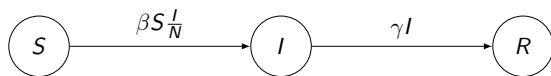
$$\frac{dI}{dt} = \beta S \frac{I}{N} - \gamma I$$

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

Where:

- ▶ $S(t)$ is the number of people **susceptible** to infection
- ▶ $I(t)$ is the number of people **infected** (i.e. the prevalence)
- ▶ $R(t)$ is the number of people **recovered** (lifelong immunity)
- ▶ N is the population size ($S(t) + I(t) + R(t) = N$ for any t)
- ▶ β is the **infectious contact rate** (per day per person)
- ▶ γ is the **recovery rate** (1/infectious period)

The SIR model



$$\frac{dS}{dt} = -\beta S \frac{I}{N}$$

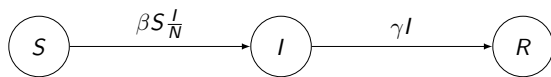
$$\frac{dI}{dt} = \beta S \frac{I}{N} - \gamma I$$

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

Intuition behind the SIR model:

- ▶ $I(t)/N$ is the proportion of infected (and infectious)
- ▶ $\beta I(t)/N$ is the daily number of contacts with infectious people
- ▶ hence each day, $\beta SI(t)/N$ people become infected (the **force of infection**)

The SIR model



$$\frac{dS}{dt} = -\beta S \frac{I}{N}$$

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

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

Assumptions behind the SIR model:

- ▶ homogeneous mixing
- ▶ β and γ constant over time
- ▶ all infections are observed
- ▶ no incubation, exponentially-distributed recovery
- ▶ lifelong immunity
- ▶ stable population

Simulate a SIR in R

- ▶ load library deSolve (and tidyverse)
- ▶ set compartments and differential equations

```
sir = function(t, x, parms, ...) {  
  with(as.list(c(parms, x)), {  
    dS = - beta*S*I/(S+I+R)  
    dI = beta*S*I/(S+I+R) - gamma*I  
    dR = gamma*I  
    list(c(dS, dI, dR))  
  })  
}
```

Simulate a SIR in R

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  })  
}
```

- ▶ set (fixed) values for parameters: $\beta = 0.8$; $\rho = 1/7$

```
pars = c(beta = 0.8, gamma = 1/7)
```

Simulate a SIR in R

- ▶ load library deSolve (and tidyverse)
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sir = function(t, x, parms, ...) {  
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    dR = gamma*I  
    list(c(dS, dI, dR))  
  })  
}
```

- ▶ set (fixed) values for parameters: $\beta = 0.8$; $\rho = 1/7$

```
pars = c(beta = 0.8, gamma = 1/7)
```

- ▶ set (fixed) values for initial values

```
N_0 = 100000  
I_0 = 50  
inits = c(S = N_0 - I_0,  
          I = I_0,  
          R = 0)
```

Simulate a SIR in R

- solve the ODE system numerically (Runge-Kutta 4th order) to obtain unique solutions for $S(t)$, $I(t)$ and $R(t)$

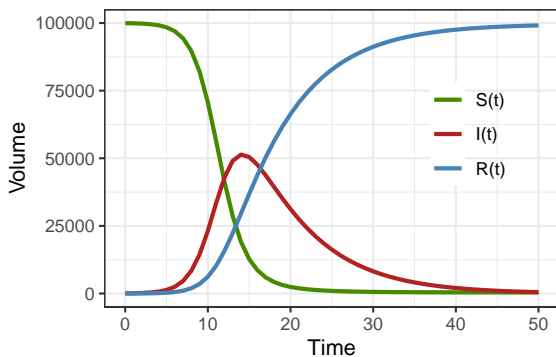
$$f(\beta, \gamma, S_0, I_0, R_0) = \{S(t), I(t), R(t)\}$$

```
times = seq(0,50,by=1)
sim_data = ode(inits, times, sir, pars,method="rk4")
```

```
> tibble(sim_data)
# A tibble: 51 x 1
  sim_data[,"time"] [,"S"] [,"I"] [,"R"]
      <dbl>      <dbl>   <dbl> <dbl>
1           0 99950      50      0
2           1 99894.    96.3   10.1
3           2 99785.   186.    29.5
4           3 99576.   357.    66.9
5           4 99176.   685.   139.
6           5 98415.  1308.   276.
7           6 96984.  2478.   538.
8           7 94350.  4621.  1030.
9           8 89692.  8374.  1934.
10          9 82009. 14457. 3533.
# ... with 41 more rows
```

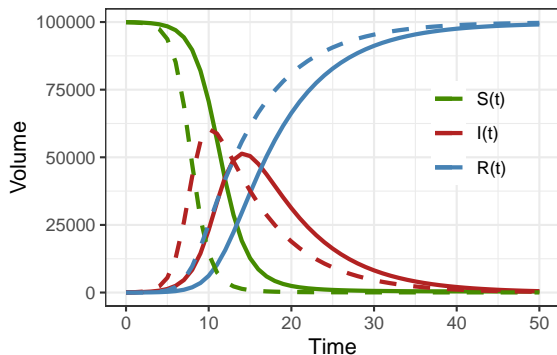
Simulate a SIR in R

with $\beta = 0.8$; $\rho = 1/7$; $S_0 = 100000 - 50$; $I_0 = 50$ and $R_0 = 0$



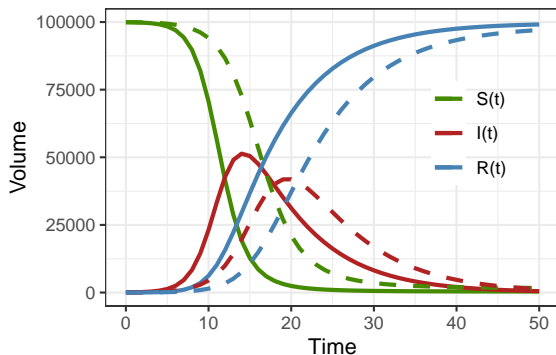
Simulate a SIR in R

with $\beta = 1.1$ instead of 0.8, we get



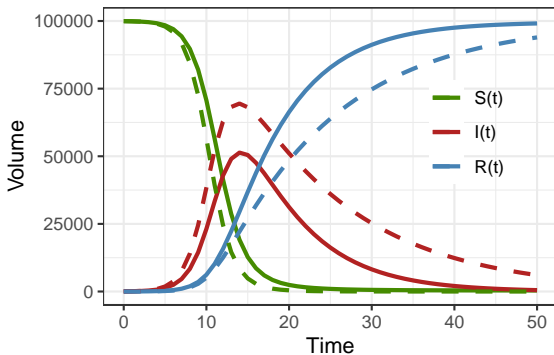
Simulate a SIR in R

with $\beta = 0.6$ instead of 0.8, we get



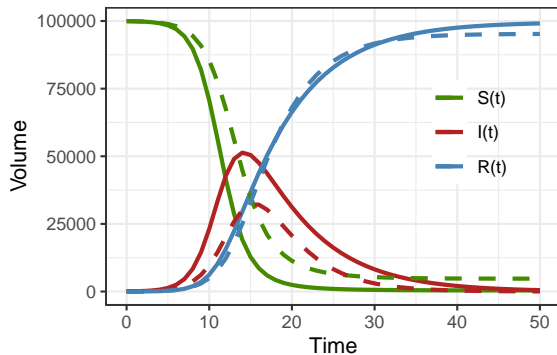
Simulate a SIR in R

with $\gamma = 1/14$ instead of $1/7$, we get



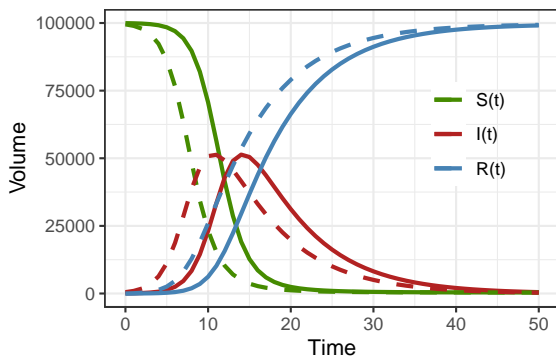
Simulate a SIR in R

with $\gamma = 1/4$ instead of $1/7$, we get



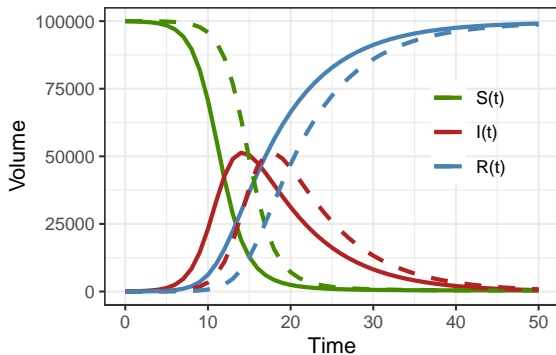
Simulate a SIR in R

with $I(0) = 500$ instead of 50, we get



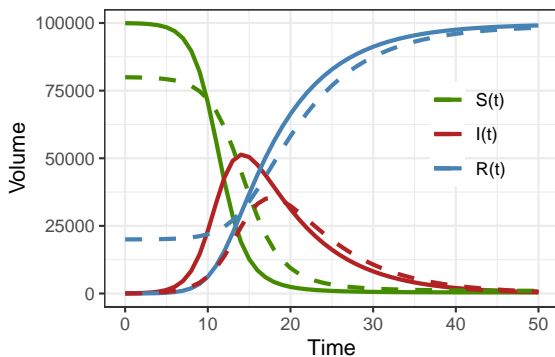
Simulate a SIR in R

with $I(0) = 5$ instead of 50, we get



Simulate a SIR in R

with $R(0) = 20,000$ instead of 0, we get



Applications

Compartmental models have many uses:

- ▶ get **mechanistic insight** about an epidemic (transmissibility levels, drivers of transmission)

$$\mathcal{R}_0 = \frac{\beta}{\gamma}$$

- ▶ formalize and put numerical values on **general concepts** (herd immunity threshold...)

$$V_c = \frac{1}{\mathcal{R}_0}$$

- ▶ produce (short-term) **forecasts** accounting for contagion and immunity

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- ▶ formalize and put numerical values on **general concepts** (herd immunity threshold...)

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- ▶ produce (short-term) **forecasts** accounting for contagion and immunity

→ all these uses are based on **numerical values** for β , ρ and the initial conditions and their **uncertainty**

Enters Bayesian inference:

- ▶ infer parameter values by integrating data and domain knowledge
- ▶ more efficient for complex models (high dimensionality)
- ▶ rigorously quantify and propagate uncertainty in parameter estimates and forecast

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- ▶ infer parameter values by integrating data and domain knowledge
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- ▶ rigorously quantify and propagate uncertainty in parameter estimates and forecast

→ Markov Chain Monte Carlo (MCMC) methods and Stan

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General principle

General principle of Bayesian inference:

- ▶ specify a complete Bayesian model
 - consider data $y = \{y_1, \dots, y_n\}$ and parameter θ
 - specify an **observation model**

$$\Pr(y|\theta) = \prod_n \text{normal}(y_n|\theta, 1)$$

- complete the model with a **prior distribution**

$$\Pr(\theta) = \text{normal}(0, 1)$$

- ▶ sample the **posterior distribution** of the parameter

Stan is a probabilistic programming framework for Bayesian inference

- ▶ it is designed to let the user **focus on modeling** while inference happens under the hood
- ▶ object-oriented language (based on C++) that supports many operations, probability densities and ODE solvers
- ▶ extremely **efficient** MCMC algorithm (Hamiltonian Monte Carlo)
- ▶ **diagnostic tools** to evaluate the inference
- ▶ interfaces in R (package `rstan`), python, julia...

Stan example

Programming in Stan is structured in **blocks**:

- ▶ the data block defines data variables

```
data {  
  int N;  
  real y[N];  
}
```

- ▶ the parameters block defines parameters

```
parameters {  
  real theta;  
}
```

- ▶ the model block defines the **target log probability density function**

```
model {  
  theta ~ normal(0,1);  
  y ~ normal(theta,1);  
}
```

- ▶ save in model_linear.stan

Stan example

We then explore the target with Stan's MCMC **sampler**:

- ▶ load `rstan` package

```
## Setup ----  
library(rstan)  
options(mc.cores = parallel::detectCores())
```

- ▶ simulate $N = 50$ data points with $\theta = 0.7$

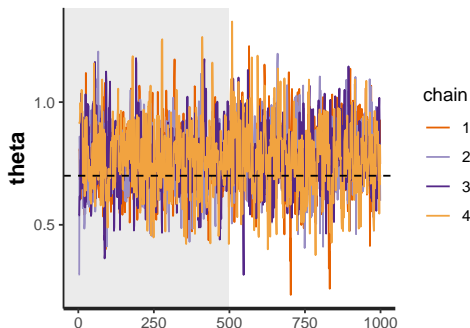
```
## Simulate data ----  
N = 50  
theta = 0.7  
y = rnorm(N,theta,1)  
input_data = list(N=N,y=y)
```

- ▶ run MCMC sampling

```
## Sample ----  
fit = stan(file='model_linear.stan',  
           data=input_data,  
           chains=4,  
           iter=1000)
```

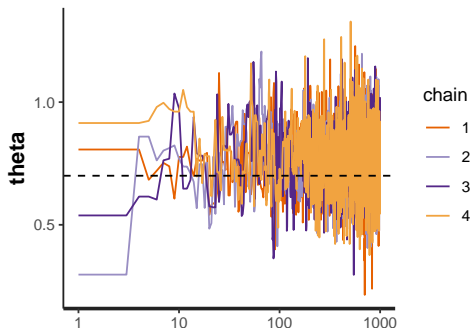
Stan example

We use **multiple chains** that should converge after warm-up



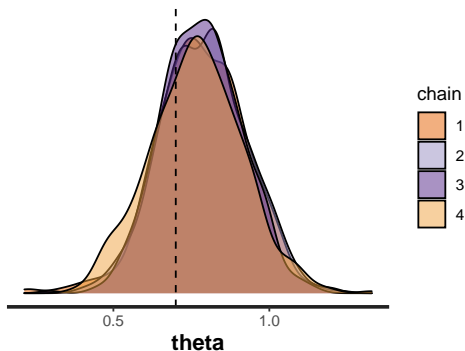
Stan example

We use **multiple chains** that should converge after warm-up



Stan example

The post-warm-up samples of θ approximate its **posterior distribution**



Stan example

We run **basic diagnosis tools**: divergences, tree depth, energy

```
> check_hmc_diagnostics(fit)
```

Divergences:

0 of 2000 iterations ended with a divergence.

Tree depth:

0 of 2000 iterations saturated the maximum tree depth of 10.

Energy:

E-BFMI indicated no pathological behavior.

Stan example

Printing the object gives:

- ▶ **diagnostics**: effective sample size, Gelman-Rubin \hat{R}
- ▶ **inference**: full posterior distribution of θ

```
> print(fit)
Inference for Stan model: model_linear.
4 chains, each with iter=1000; warmup=500; thin=1;
post-warmup draws per chain=500, total post-warmup draws=2000.

      mean se_mean  sd   2.5%   25%   50%   75%  97.5% n_eff Rhat
theta  0.78   0.01 0.14   0.51   0.69   0.78   0.87   1.05   760    1
lp__ -18.30   0.03 0.73 -20.28 -18.44 -18.03 -17.86 -17.81   799    1

Samples were drawn using NUTS(diag_e) at Thu Nov 12 19:15:33 2020.
For each parameter, n_eff is a crude measure of effective sample size,
and Rhat is the potential scale reduction factor on split chains (at
convergence, Rhat=1).
```

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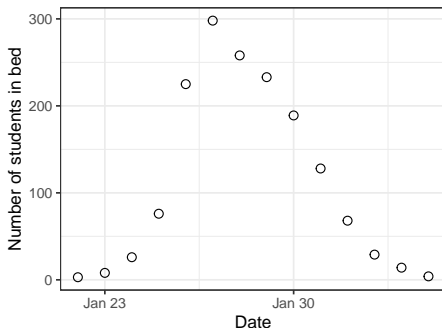
Extending from the simple SIR model

Conclusions

Example dataset

Outbreak of influenza A (H1N1) at a British boarding school in 1978 (available in R package outbreaks)

- ▶ 763 students, 512 had symptoms
- ▶ daily number of students in bed over 14 days (prevalence)



Specify the model

Points to consider:

- ▶ prevalence data: \mathbb{I}_t with $t \in \{1, \dots, 14\}$
- ▶ parameters to estimate: $\theta = \{\beta, \gamma, \phi\}$
- ▶ parameters that will remain fixed: $\{S_0 = 762, I_0 = 1, R_0 = 0\}$
- ▶ map data \mathbb{I}_t to SIR model output $I(t)$ using an observation model with an appropriate **probability distribution**:

$$\Pr(\mathbb{I}|\theta) = \prod_{t=1}^{14} \text{neg-bin}(\mathbb{I}_t|I(t), \phi)$$

- ▶ **prior distributions**

$$\Pr(\beta) = \text{exponential}(1)$$

$$\Pr(1/\gamma) = \text{normal}(2, 0.5)$$

$$\Pr(1/\phi) = \text{exponential}(5)$$

Code the model

We define the ODE system in the function block

```
functions {  
  real[] sir(real t, real[] y, real[] theta, real[] x_r, int[] x_i) {  
  
    real S = y[1];  
    real I = y[2];  
    real R = y[3];  
    real N = x_i[1];  
  
    real beta = theta[1];  
    real gamma = theta[2];  
  
    real dS_dt = -beta * I * S / N;  
    real dI_dt =  beta * I * S / N - gamma * I;  
    real dR_dt =  gamma * I;  
  
    return {dS_dt, dI_dt, dR_dt};  
  }  
}
```

⚠ Be careful of the signature and formats!

Code the model

We declare the data variables in the data block

```
data {  
  int<lower=1> T;  
  real y0[3];  
  real t0;  
  real ts[T];  
  int N;  
  int cases[T];  
}
```

Code the model

We declare the data variables in the data block

```
data {  
  int<lower=1> T;  
  real y0[3];  
  real t0;  
  real ts[T];  
  int N;  
  int cases[T];  
}
```

and define additional data variables in transformed data

```
transformed data {  
  real x_r[0];  
  int x_i[1];  
  x_i[1]=N;  
}
```

Code the model

Similarly, parameters are declared in the `parameters` block

```
parameters {  
  real<lower=0> beta;  
  real<lower=0> recovery_time;  
  real<lower=0> phi_inv;  
}
```

⚠ It sometimes makes more sense to transform some parameters (e.g., recovery rate γ and overdispersion ϕ) to improve interpretability

Code the model

In transformed parameters, we define additional parameters and solve the ODE system

```
transformed parameters{  
  real y[T,3];  
  real phi = 1. / phi_inv;  
  real gamma = 1. / recovery_time;  
  real theta[2];  
  theta[1] = beta;  
  theta[2] = gamma;  
  
  y = integrate_ode_rk45(sir, y0, t0, ts, theta, x_r, x_i);  
}
```

Code the model

```
y = integrate_ode_rk45(sir, y0, t0, ts, theta, x_r, x_i);
```

Two crucial points:

- ▶ be careful about the **formats and signatures**
 - the ODE output y is an array of size $T \times 3$ (number of time steps and number of compartments)
 - `sir` is the name of the function defined in the function block
 - `y0` is an array of size 3 defined in the data block
 - `ts` is an array of size T defined in the data block
 - `theta` is an array of size 2 storing the parameters
 - `x_r` is defined as empty in transformed data, but can be used to store fixed real values
 - `x_i` is an array of size 1 storing the population size N (can also be used to store fixed integer values)

Code the model

```
y = integrate_ode_rk45(sir, y0, t0, ts, theta, x_r, x_i);
```

Two crucial points:

- ▶ two ODE solvers are available:
 - `integrate_ode_rk45` uses the Runge-Kutta method (quicker but non-adapted to stiff systems)
 - `integrate_ode_bdf` uses the backward differentiation method (slower but adapted to stiff systems)

Code the model

In the `model` block, we write the priors and the observation model

```
model {  
  // priors  
  beta ~ exponential(1);  
  recovery_time ~ normal(2,0.5);  
  phi_inv ~ exponential(5);  
  
  // observation model  
  cases ~ neg_binomial_2(col(to_matrix(y),2), phi);  
}
```

⚠ It's important that the chosen distributions correspond with the boundaries set in the parameters block (`<lower=0>`)

⚠ `col(to_matrix(y))` extracts the 2nd column of `y`

Code the model

Last, we add a generated quantities block that does not influence sampling and can be used for “post-processing”:

- ▶ reproduction number $\mathcal{R}_0 = \beta/\gamma$
- ▶ model predictions of prevalence from the negative binomial

```
generated quantities {  
  real R0 = beta/gamma;  
  real pred_cases[T];  
  pred_cases = neg_binomial_2_rng(col(to_matrix(y),2), phi);  
}
```


Code the model

In summary:

- ▶ `functions`: define the ODE system (⚠ signature and formats)
- ▶ `data`: declare data variables that will be provided
- ▶ `transformed data`: additional quantities that can be computed internally or from data variables
- ▶ `parameters`: declare parameters (⚠ boundaries)
- ▶ `transformed parameters`: quantities that can be computed internally or from data or parameters variables, including the ODE output (⚠ signature and format)
- ▶ `model`: priors and observation model
- ▶ `generated quantities`: additional quantities that can be computed without influencing the sampling

Inference

As before, we conduct the inference from R with the package `rstan`:

```
## Format input ----
# prevalence data
cases = influenza_england_1978_school$in_bed
N = 763
n_days = 14
t0 = 0
t = 1:n_days

# initial conditions
i0 = 1
s0 = N - i0
r0 = 0
y0 = c(s0, i0, r0)

# put into list
input_data = list(T = n_days, y0 = y0, t0 = t0, ts = t, N = N, cases = cases)
```

⚠ data is put in a list with names matching the data block in Stan

Inference

Hit the inference button!

```
## Sample ---  
fit = stan(file='sir_negbin.stan',  
           data=input_data,  
           chains=4,  
           iter=1000)
```

Diagnostics

Run basic diagnosis tools:

```
> check_hmc_diagnostics(fit)
```

Divergences:

0 of 2000 iterations ended with a divergence.

Tree depth:

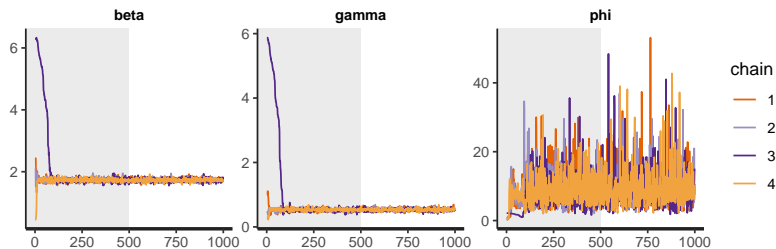
0 of 2000 iterations saturated the maximum tree depth of 10.

Energy:

E-BFMI indicated no pathological behavior.

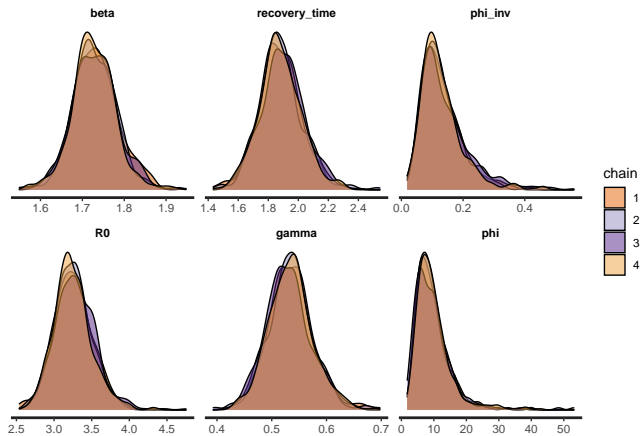
Diagnostics

Examine trace plots:

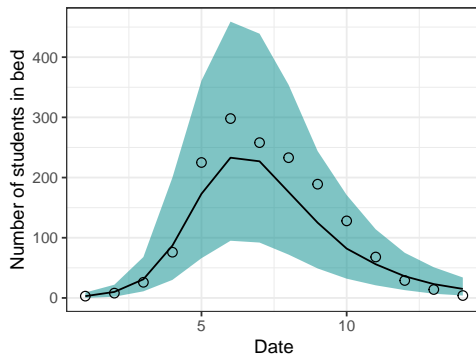


Diagnostics

Examine chain mixing:



Posterior predictive checking:



Results

Print the results:

```
> print(fit,pars=c("beta","gamma","phi","R0","recovery_time"))
Inference for Stan model: sir_negbin.
4 chains, each with iter=1000; warmup=500; thin=1;
post-warmup draws per chain=500, total post-warmup draws=2000.
```

	mean	se_mean	sd	2.5%	25%	50%	75%	97.5%	n_eff	Rhat
beta	1.73	0.00	0.06	1.61	1.70	1.73	1.76	1.85	1049	1
gamma	0.53	0.00	0.04	0.44	0.50	0.53	0.56	0.63	1382	1
phi	9.61	0.22	6.13	2.94	5.72	8.31	11.80	23.40	743	1
R0	3.27	0.01	0.29	2.79	3.09	3.25	3.42	3.96	1403	1
recovery_time	1.89	0.00	0.16	1.59	1.79	1.88	1.98	2.25	1410	1

Samples were drawn using NUTS(diag_e) at Thu Nov 12 19:10:02 2020.
For each parameter, n_eff is a crude measure of effective sample size,
and Rhat is the potential scale reduction factor on split chains (at
convergence, Rhat=1).

- ▶ we estimate \mathcal{R}_0 to 3.3 (95% credible interval: 2.8 to 4.0)
- ▶ this corresponds to the direct estimation from the final size of the epidemic $q = 512/763 = 0.67$

$$\mathcal{R}_0 = 1/(1 - q) = 3.03$$

- ▶ based on **many assumptions**:
 - common to all SIRs (homogeneous mixing, no incubation...)
 - prior distributions (especially on the recovery period)
 - complete ascertainment, no asymptomatics
 - no initial immunity

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Model development

In practice, the situation is often less clear than in the boarding school example:

- incomplete data, insufficient domain knowledge
- uncertainty on **necessary model features**

Fake data can be used to probe the model and better understand its behaviour:

- prior predictive checking
- simulation study

Prior predictive checks

Prior predictive checking consists in simulating data from the priors:

- ▶ visualize priors (especially after transformation)
- ▶ this shows the range of data compatible with the model
- ▶ it helps understand the adequacy of the chosen priors, as it is often easier to elicit expert knowledge on measurable quantities of interest rather than abstract parameter values

Prior predictive checks

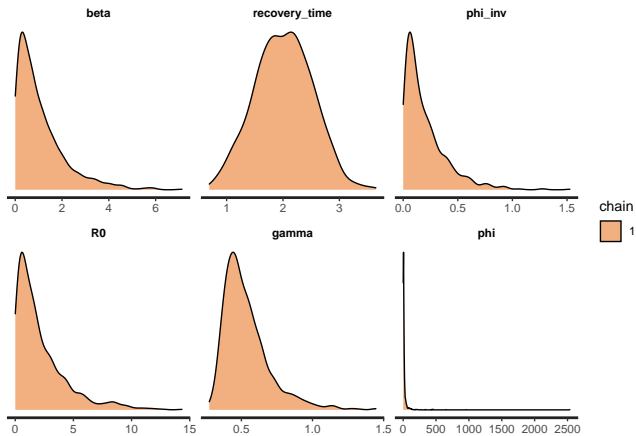
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- ▶ remove (or switch off) the likelihood from the model block

```
// observation model  
if(switch_likelihood==1) cases ~ neg_binomial_2(col(to_matrix(y),2), phi);
```

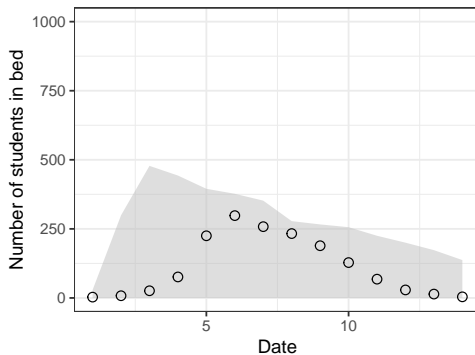
Prior predictive checks

Simulating priors in the boarding school example:



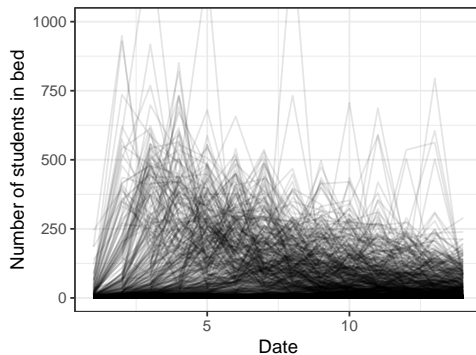
Prior predictive checks

Prior predictive checking: simulating epidemic trajectories



Prior predictive checks

Prior predictive checking: simulating epidemic trajectories



Prior predictive checks

Prior predictive checking brings insight about **non-obvious features**:

- ▶ even if the priors seem weakly informative, there is actually not a lot of leeway
- ▶ **highly constrained** model:
 - if β is high, the epidemic will stop rapidly by lack of susceptibles
 - if β is small, the epidemic will be small
- ▶ the negative binomial might lead to problems in extreme situations, e.g. more cases (>1000) than the overall number of students

Simulation-based checks

A **simulation study** consists in two steps:

- ▶ simulate data with specified parameter values
- ▶ measure the capacity of the model to recover the chosen parameter values

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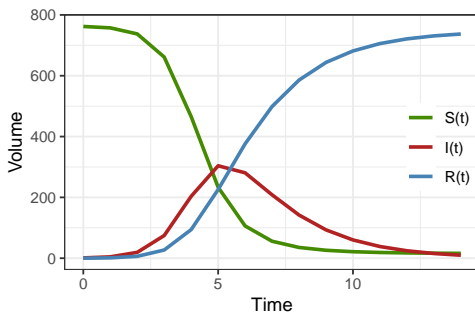
Many advantages:

- ▶ check for bugs and coding mistakes
- ▶ check for **identifiability** issues
- ▶ compare different versions of a model
- ▶ understand in what **situations** a model works or not

Simulation-based checks

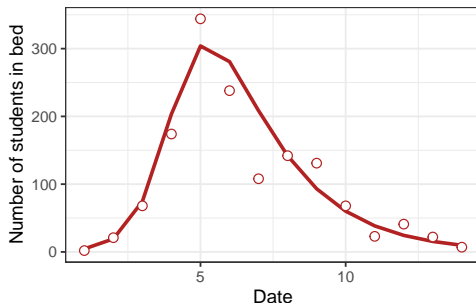
Let's go back to the **simple SIR example** from the beginning:

- ▶ set $\beta = 2$ and $\gamma = 0.5$ (so that $\mathcal{R}_0 = 4$)
- ▶ simulate in a susceptible population of size $N = 763$ with $I_0 = 1$



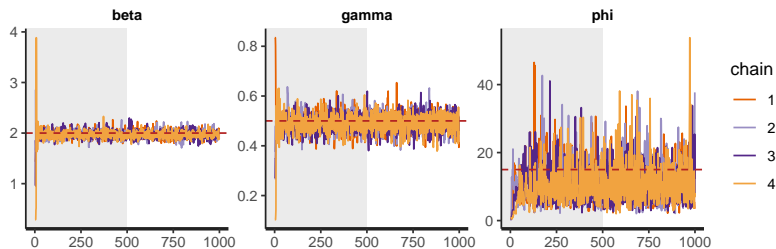
Simulation-based checks

Add noise with a **negative binomial** distribution with $\phi = 15$



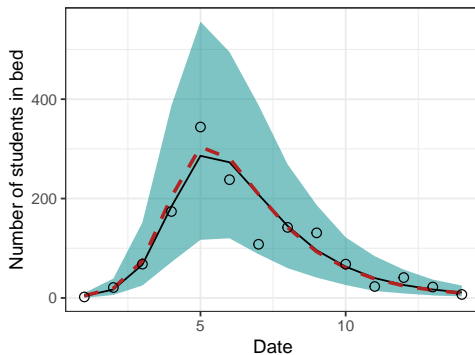
Simulation-based checks

Fit the **same model** as for the boarding school example



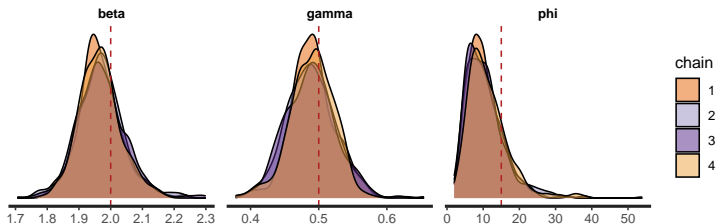
Simulation-based checks

Posterior predictive checking



Simulation-based checks

Compare the posterior distributions of the parameters with the “truth”



- ▶ no identifiability issue
- ▶ β and γ are well estimated, but ϕ is not
- ▶ try with other values to understand when does the model break

Outline

Models of disease transmission

Bayesian inference with Stan

Fitting a simple SIR

Using simulations to understand the model

Extending from the simple SIR model

Conclusions

Limitations to the SIR model

In practice, the boarding school example quickly reaches its **limits**:

- ▶ epidemics are not often observed in such a controlled environment (**under-ascertainment**)
- ▶ epidemics are not always left uncontrolled
- ▶ data generally consist of daily counts of new cases (**incidence**) rather than counts of currently sick people (**prevalence**)
- ▶ most infectious diseases have an **incubation period** (SEIR instead of SIR)
- ▶ transmission is generally not homogeneous in the full population (**stratification** by age, sex...)
- ▶ ...


Example with SARS-CoV-2 from Hauser et al. (2020):

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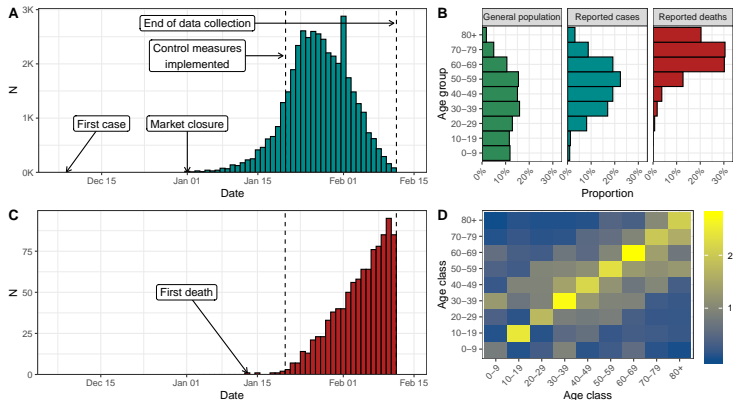
Estimation of SARS-CoV-2 mortality during the early stages of an epidemic: A modeling study in Hubei, China, and six regions in Europe

Anthony Hauser, Michel J. Counotte, Charles C. Margossian, Garyfallos Konstantinoudis, Nicola Low, Christian L. Althaus, Julien Riou 

Published: July 28, 2020 • <https://doi.org/10.1371/journal.pmed.1003189>

Example

In Hubei province (China):



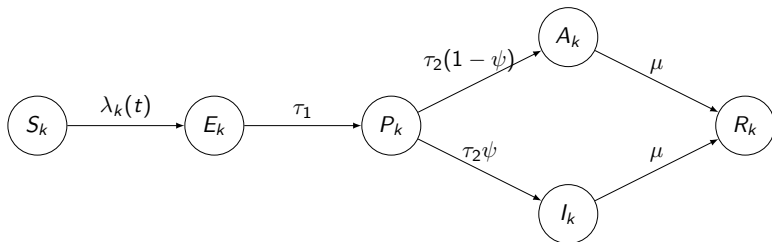
Example

Specific features and natural history of SARS-CoV-2 infection:

- ▶ Incubation period of 5 days (SEIR)
- ▶ Pre-symptomatic transmission accounting for 44-48% (SEPIR)
- ▶ Symptoms in 81% (95%CrI 71%–89%) of cases (SEPIAR)
- ▶ Respiratory virus transmitted through contacts
(age stratification)
- ▶ Effect of control measures (time-dependent force of infection)
- ▶ Mortality is delayed by 20.2 ± 11.6 days (fit to mortality data)

Example

Final model:

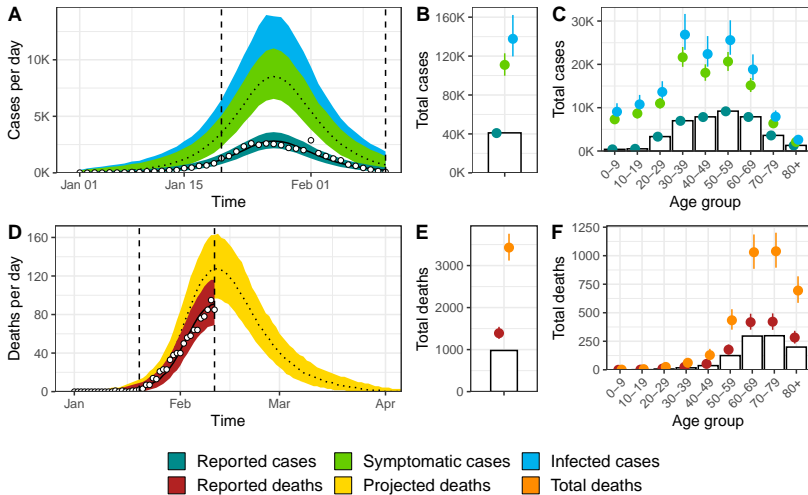


S_k	Susceptible (for age group k)
E_k	Exposed
P_k	Presymptomatic
A_k	Infected asymptomatic
I_k	Infected symptomatic
R_k	Removed

$\lambda_k(t)$	Force of infection (time-dependent)
$1/\tau_1 + 1/\tau_2$	Incubation period (split in two)
ψ	Proportion of symptomatic
$1/\tau_2$	Presymptomatic infectious period
$1/\mu$	Symptomatic infectious period

Example

Posterior predictive check (Hubei):



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General comments:

- ▶ develop models that correspond to the **data-generating mechanisms**
- ▶ use Bayesian inference to **propagate uncertainty** from the data (and priors) into the results (and forecasts)
- ▶ carefully examine the modelling process (Bayesian workflow)
- ▶ be transparent about assumptions (open code)

Acknowledgements & ressources

- ▶ Stan forums
<https://discourse.mc-stan.org/>
- ▶ Michael Betancourt, *Introduction to Stan*
https://betanalpha.github.io/assets/case_studies/stan_intro.html
- ▶ Andrew Gelman et al., *Bayesian workflow*
<https://arxiv.org/abs/2011.01808>
- ▶ Chi Feng, *MCMC interactive gallery*
<https://chi-feng.github.io/mcmc-demo/app.html>
- ▶ Daniel Lee, *ODEs in Stan*
https://youtu.be/hJ34_xJhYeY