



University  
of Manitoba

## Sojourn time in compartments

MATH 8xyz – Lecture 06

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Winter 20XX

The University of Manitoba campuses are located on original lands of Anishinaabeg, Ininew, Anisininew, Dakota and Dene peoples, and on the National Homeland of the Red River Métis.

We respect the Treaties that were made on these territories, we acknowledge the harms and mistakes of the past, and we dedicate ourselves to move forward in partnership with Indigenous communities in a spirit of Reconciliation and collaboration.

# Outline

Distributions of times to events

Two “extreme” distributions and a nicer one

A simple cohort model with death

Possible fixes to the exponential distribution issue

Sojourn times in an SIS disease transmission model

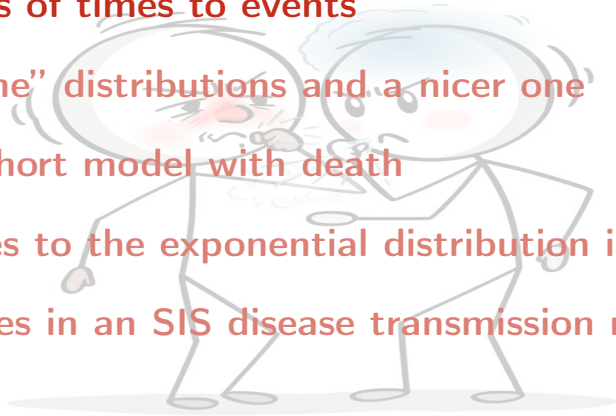
## Distributions of times to events

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See some of the work of Horst Thieme on the subject

If one considers time of sojourn in compartments from a more detailed perspective, one obtains integro-differential models

We use here continuous random variables. See chapters 12 and 13 in [Thieme, 2018] (link) for arbitrary distributions

## Time to events

Suppose that a system can be in two states  $A$  and  $B$

- ▶ At time  $t = 0$ , the system is in state  $A$
- ▶ An event happens at some time  $t = \tau$ , which triggers the switch from state  $A$  to state  $B$

Let  $T$  be the random variable “time spent in state  $A$  before switching into state  $B$ ”

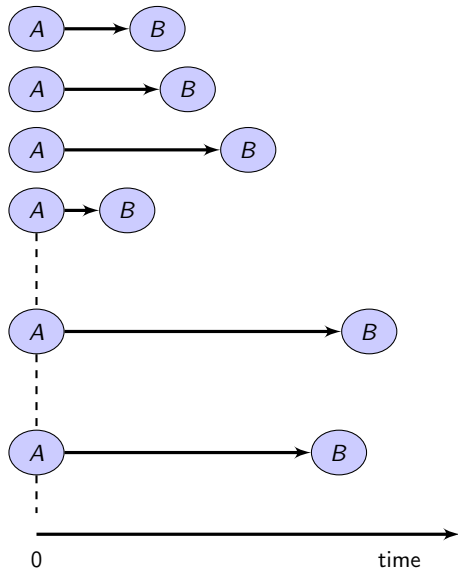
The states can be anything:

- ▶  $A$ : working,  $B$ : broken
- ▶  $A$ : infected,  $B$ : recovered
- ▶  $A$ : alive,  $B$ : dead
- ▶ ...

We take a collection of objects or individuals that are in state  $A$  and want some law for the **distribution** of the times spent in  $A$ , i.e., a law for  $T$

For example, we make light bulbs and would like to tell our customers that on average, our light bulbs last 200 years...

We conduct an **infinite** number of experiments, and observe the time that it takes, in every experiment, to switch from  $A$  to  $B$



# A distribution of probability is a model

From the sequence of experiments, we deduce a model, which in this context is called a **probability distribution**

We assume that  $T$  is a **continuous** random variable



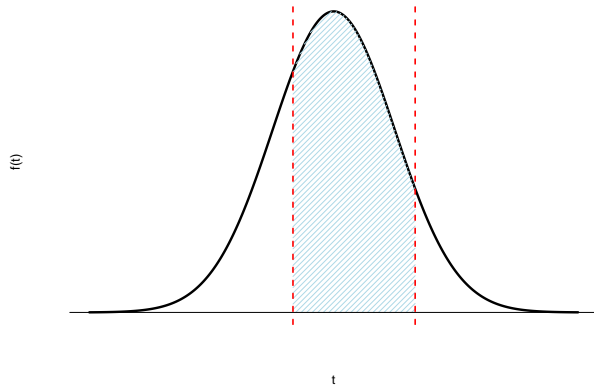
## Probability density function (p.d.f.)

Since  $T$  is continuous, it has a continuous **probability density function**  $f$

►  $f \geq 0$

►  $\int_{-\infty}^{+\infty} f(s)ds = 1$

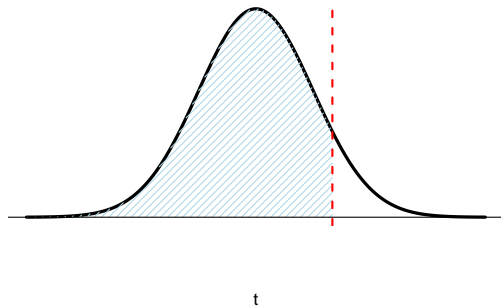
►  $\mathbb{P}(a \leq T \leq b) = \int_a^b f(t)dt$



## Cumulative distribution function (c.d.f.)

The **cumulative distribution function** is a function  $F(t)$  that characterizes the distribution of  $T$ , and defined by

$$F(s) = \mathbb{P}(T \leq s) = \int_{-\infty}^s f(x) dx$$



## Survival function

Another characterization of the distribution of the random variable  $T$  is through the **survival** (or **sojourn**) function

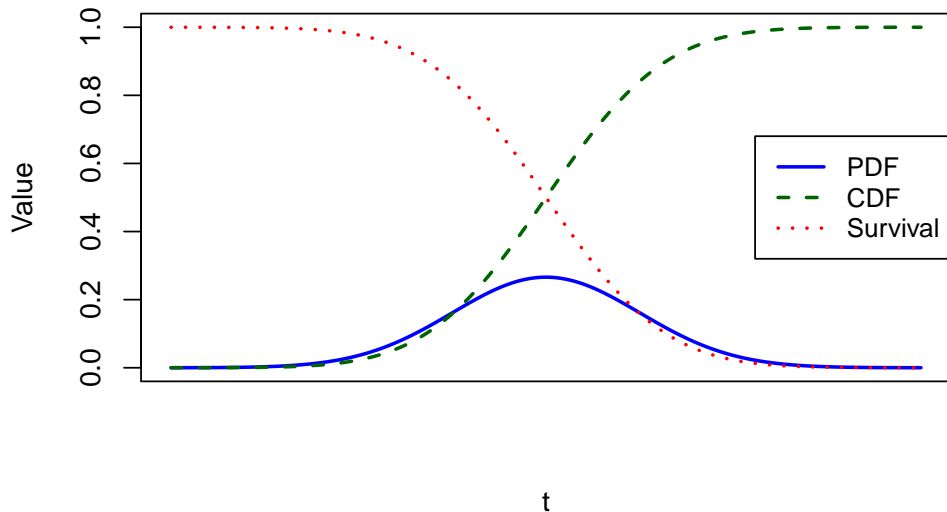
The survival function of state  $A$  is given by

$$S(t) = 1 - F(t) = \mathbb{P}(T > t) \quad (1)$$

This gives a description of the **sojourn time** of a system in a particular state (the time spent in the state)

$S$  is a nonincreasing function (since  $S = 1 - F$  with  $F$  a c.d.f.), and  $S(0) = 1$  (since  $T$  is a nonnegative random variable)

## PD, CD and Survival functions



The **average sojourn time**  $\tau$  in state  $A$  is given by

$$\tau = E(T) = \int_0^{\infty} t f(t) dt$$

Since  $\lim_{t \rightarrow \infty} tS(t) = 0$ , it follows that

$$\tau = \int_0^{\infty} S(t) dt$$

**Expected future lifetime:**

$$\frac{1}{S(t_0)} \int_0^{\infty} t f(t + t_0) dt$$

$$\begin{aligned} S(t) - S(a) &= \mathbb{P} \{ \text{survive during } (a, t) \text{ having survived until } a \} \\ &= \exp \left( - \int_a^t h(u) du \right) \end{aligned}$$

## Hazard rate

The **hazard rate** (or **failure rate**) is

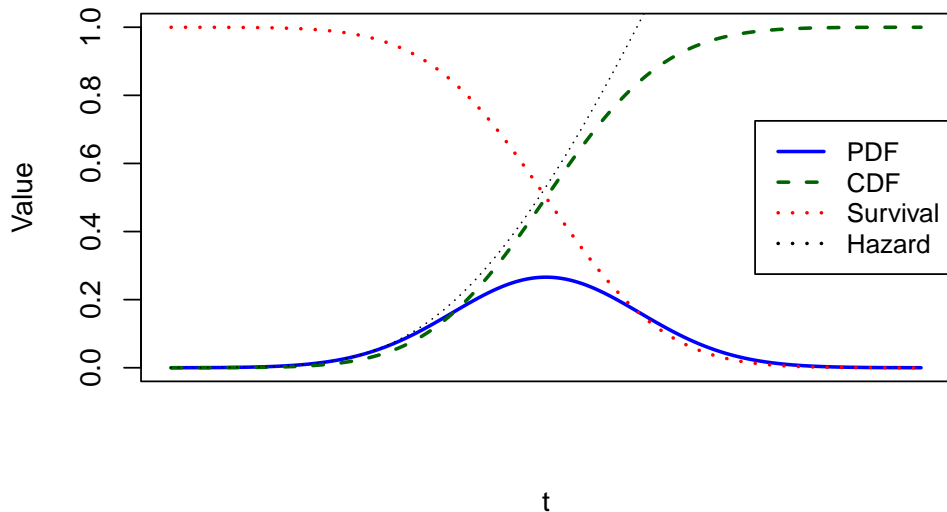
$$\begin{aligned}h(t) &= \lim_{\Delta t \rightarrow 0} \frac{\mathcal{S}(t) - \mathcal{S}(t + \Delta t)}{\Delta t} \\&= \lim_{\Delta t \rightarrow 0} \frac{\mathbb{P}(T < t + \Delta t | T \geq t)}{\Delta t} \\&= \frac{f(t)}{\mathcal{S}(t)}\end{aligned}$$

It gives probability of failure between  $t$  and  $\Delta t$ , given survival to  $t$ .

We have

$$h(t) = -\frac{d}{dt} \ln \mathcal{S}(t)$$

## PD, CD and Survival functions & Hazard rate



## Competing risks

Suppose now that the system starts in state  $A$  at time  $t = 0$  and that depending on which of the two events  $\mathcal{E}_1$  or  $\mathcal{E}_2$  takes place first, it switches to state  $B_1$  or  $B_2$ , respectively

Consider the random variables  $T_A$ , *time spent* in state  $A$  (or sojourn time in  $A$ ),  $T_{AB_1}$ , *time before switch to  $B_1$*  and  $T_{AB_2}$ , *time before switch to  $B_2$*

If we consider state  $A$ , we cannot observe the variables  $T_{AB_1}$  or  $T_{AB_2}$ . What is observable is the sojourn time in  $A$

$$T_A^* = \min(T_{AB_1}, T_{AB_2})$$

(where  $*$  indicates that a quantity is observable)



## Failure rate by type of event

We have two (or more) types of events whose individual failure rates have to be accounted for

$$h_j(t) = \lim_{\Delta t \rightarrow 0} \frac{\mathbb{P}(T < t + \Delta t, S = S_j | T \geq t)}{\Delta t}$$

where  $\mathbb{P}(T < t + \Delta t, S = S_j | T \geq t)$  is the probability of failure due to cause  $S_j$  ( $j = 1, 2$  ici), i.e.,  $S$  is a discrete r.v. representing the event that is taking place

By the law of total probability, since only one of the event can take place, if there are  $n$  risks, then

$$h(t) = \sum_{i=1}^n h_j(t)$$

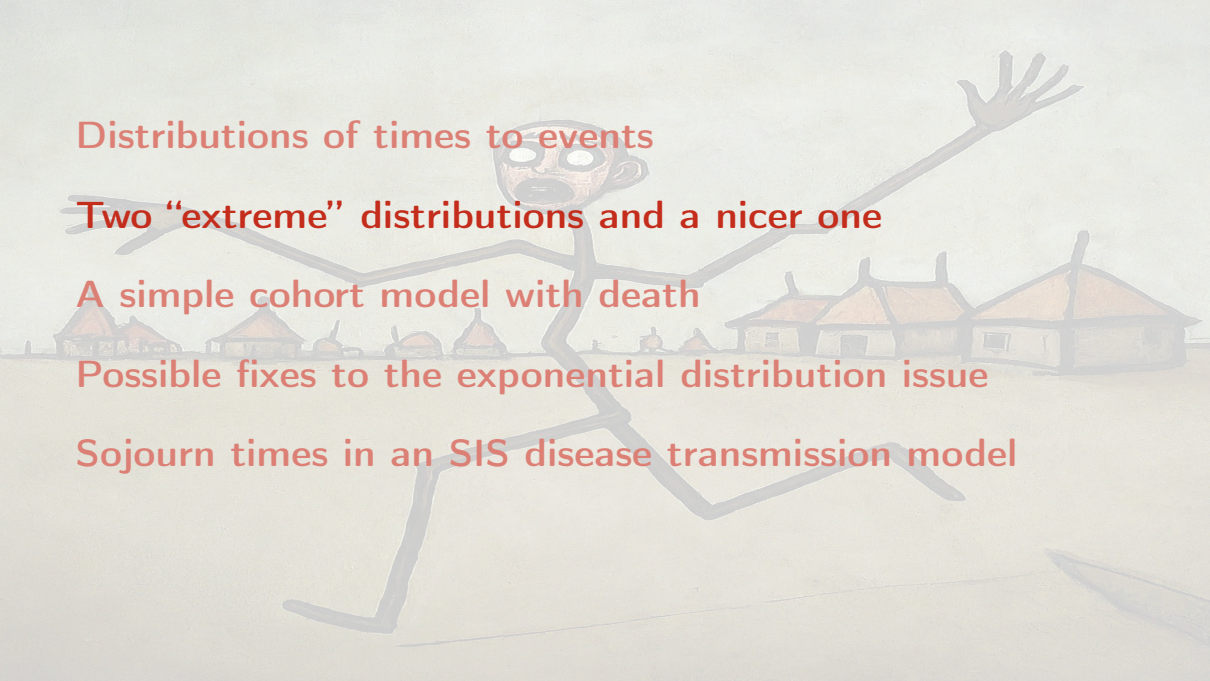
or, identically,

$$\mathcal{S}(t) = \exp \left( - \int_0^t \sum_{j=1}^n h_j(s) \, ds \right)$$

As a consequence, suppose a process is subject to two competing exponential risks with respective distributions with parameters  $\theta_1$  and  $\theta_2$

Then the mean sojourn time in the initial state before being affected by one of the two risks is

$$\frac{1}{\theta_1 + \theta_2}$$



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## The exponential distribution

The random variable  $T$  has an **exponential** distribution if its probability density function takes the form

$$f(t) = \begin{cases} 0 & \text{if } t < 0, \\ \theta e^{-\theta t} & \text{if } t \geq 0, \end{cases} \quad (2)$$

with  $\theta > 0$ . Then the survival function for state  $A$  is of the form  $\mathcal{S}(t) = e^{-\theta t}$ , for  $t \geq 0$ , and the average sojourn time in state  $A$  is

$$\tau = \int_0^{\infty} e^{-\theta t} dt = \frac{1}{\theta}$$

## Particularities of the exponential distribution

The standard deviation of an exponential distribution is also  $1/\theta$ . When estimating  $\theta$ , it is impossible to distinguish the mean and the standard deviation

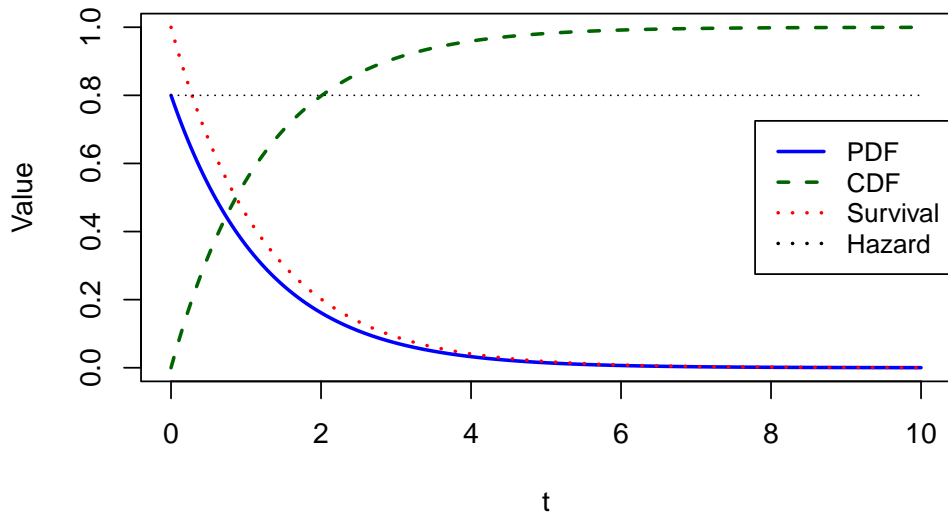
The exponential distribution is **memoryless**: its conditional probability obeys

$$P(T > s + t \mid T > s) = P(T > t), \quad \forall s, t \geq 0$$

The exponential and geometric distributions are the only memoryless probability distributions

The exponential distribution has a constant hazard function  $h(t) \equiv \theta$

## PD, CD and Surv. functions & Hazard rate of exponential



## The Dirac delta distribution

If for some constant  $\omega > 0$ ,

$$\mathcal{S}(t) = \begin{cases} 1, & 0 \leq t \leq \omega \\ 0, & \omega < t \end{cases}$$

meaning that  $T$  has a Dirac delta distribution  $\delta_\omega(t)$ , then the average sojourn time is

$$\tau = \int_0^\omega dt = \omega$$

with standard deviation  $\sigma = 0$



# The Gamma distribution

R.v.  $X$  is **Gamma** distributed ( $X \sim \Gamma(k, \theta)$ ) with **shape parameter**  $k$  and **scale parameter**  $\theta$  (or **rate**  $\beta = 1/\theta$ ) (all positive) if its probability density function takes the form

$$f(x; k, \theta) = \frac{x^{k-1} e^{-\frac{x}{\theta}}}{\Gamma(k) \theta^k} \quad (3)$$

where  $x > 0$  and  $\Gamma$  is the Euler Gamma function, defined for all  $z \in \mathbb{C}$  s.t.  $\operatorname{Re}(z) > 0$  by

$$\Gamma : z \mapsto \int_0^{+\infty} t^{z-1} e^{-t} dt$$

## Properties of the Gamma distribution

Mean  $k\theta$ , variance  $k\theta^2$

Survival function

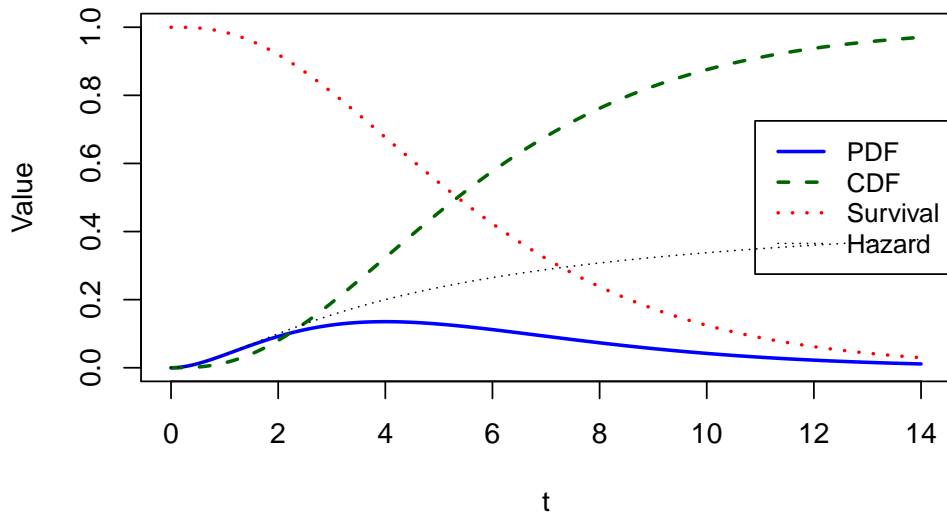
$$\mathcal{S}(t) = 1 - \frac{1}{\Gamma(k)} \gamma\left(k, \frac{t}{\theta}\right) = 1 - \frac{1}{\Gamma(k)} \gamma(k, \beta t)$$

where

$$\gamma(a, x) = \int_0^x t^{a-1} e^{-t} dt$$

is an incomplete Gamma function

## PDF, CDF, Survival & Hazard of Gamma Distribution





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## A model for a cohort with one cause of death

Consider a **cohort** of individuals born at the same time, e.g., the same year

- ▶ At time  $t = 0$ , there are initially  $N_0 > 0$  individuals
- ▶ All causes of death are compounded together
- ▶ The time until death, for a given individual, is a random variable  $T$ , with continuous probability density distribution  $f(t)$  and survival function  $\mathcal{S}(t)$

$N(t)$  the cohort population at time  $t \geq 0$

$$N(t) = N_0 \mathcal{S}(t) \tag{4}$$

$\mathcal{S}(t)$  proportion of initial population still alive at time  $t$ , so  $N_0 \mathcal{S}(t)$  number in the cohort still alive at time  $t$

## Case where $T$ is exponentially distributed

Suppose that  $T$  has an exponential distribution with mean  $1/d$  (or parameter  $d$ ),  $f(t) = de^{-dt}$ . Then the survival function is  $\mathcal{S}(t) = e^{-dt}$ , and (4) takes the form

$$N(t) = N_0 e^{-dt} \quad (5)$$

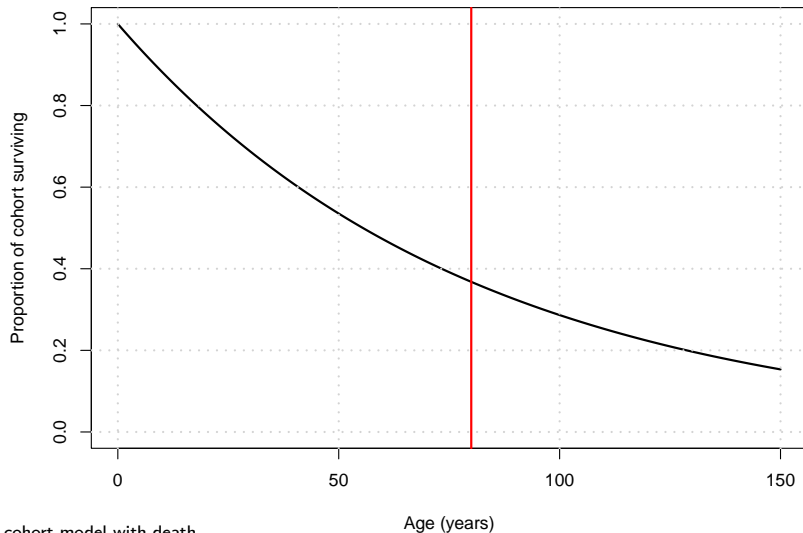
Now note that

$$\begin{aligned} \frac{d}{dt} N(t) &= -dN_0 e^{-dt} \\ &= -dN(t) \end{aligned}$$

with  $N(0) = N_0$ .

⇒ The ODE  $N' = -dN$  makes the assumption that the life expectancy at birth is exponentially distributed

Survival function,  $\mathcal{S}(t) = \mathbb{P}(T > t)$ , for an exponential distribution with mean 80 years



## Case where $T$ has a Dirac delta distribution

Suppose that  $T$  has a Dirac delta distribution at  $t = \omega$ , giving the survival function

$$\mathcal{S}(t) = \begin{cases} 1, & 0 \leq t \leq \omega \\ 0, & t > \omega \end{cases}$$

Then (4) takes the form

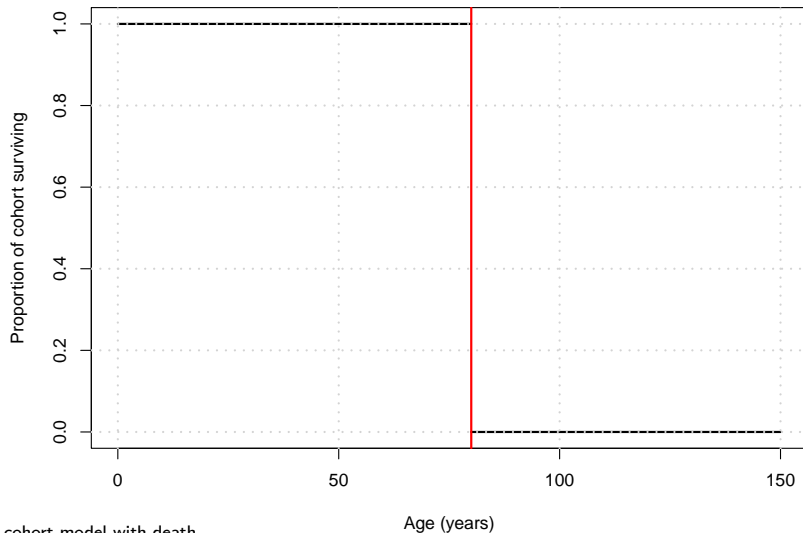
$$N(t) = \begin{cases} N_0, & 0 \leq t \leq \omega \\ 0, & t > \omega \end{cases} \quad (6)$$

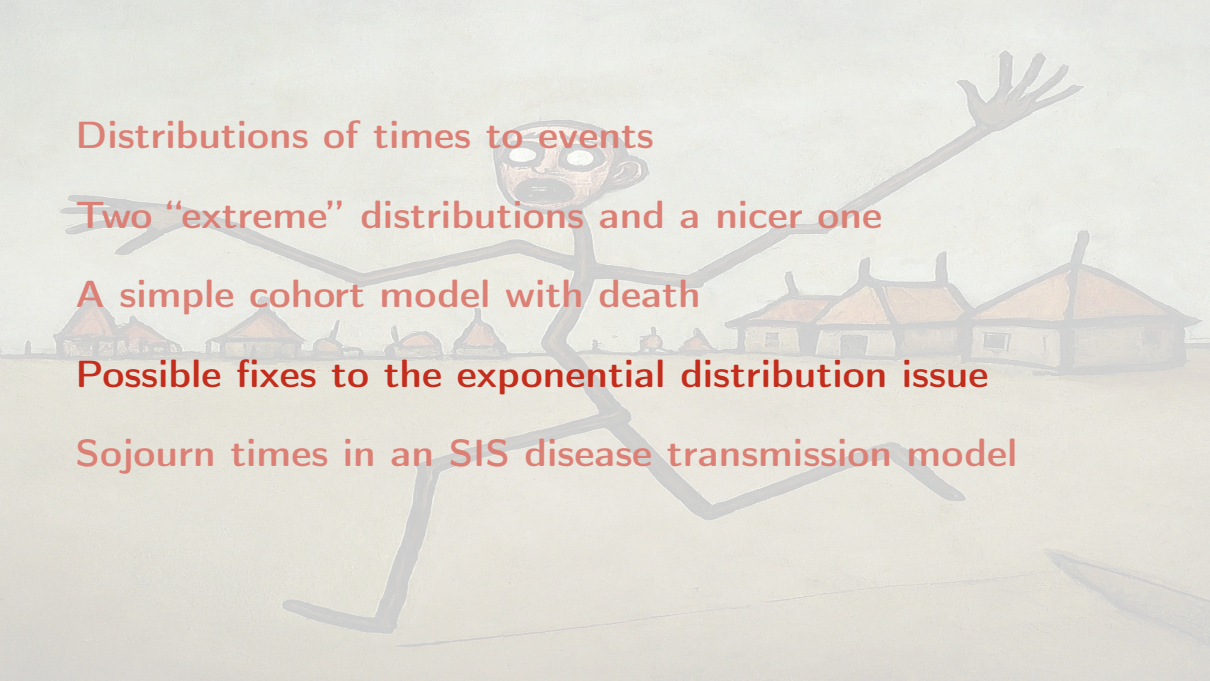
All individuals survive until time  $\omega$ , then they all die at time  $\omega$

Here,  $N' = 0$  everywhere except at  $t = \omega$ , where it is undefined



Survival function,  $\mathcal{S}(t) = \mathbb{P}(T > t)$ , for a Dirac distribution with mean 80 years





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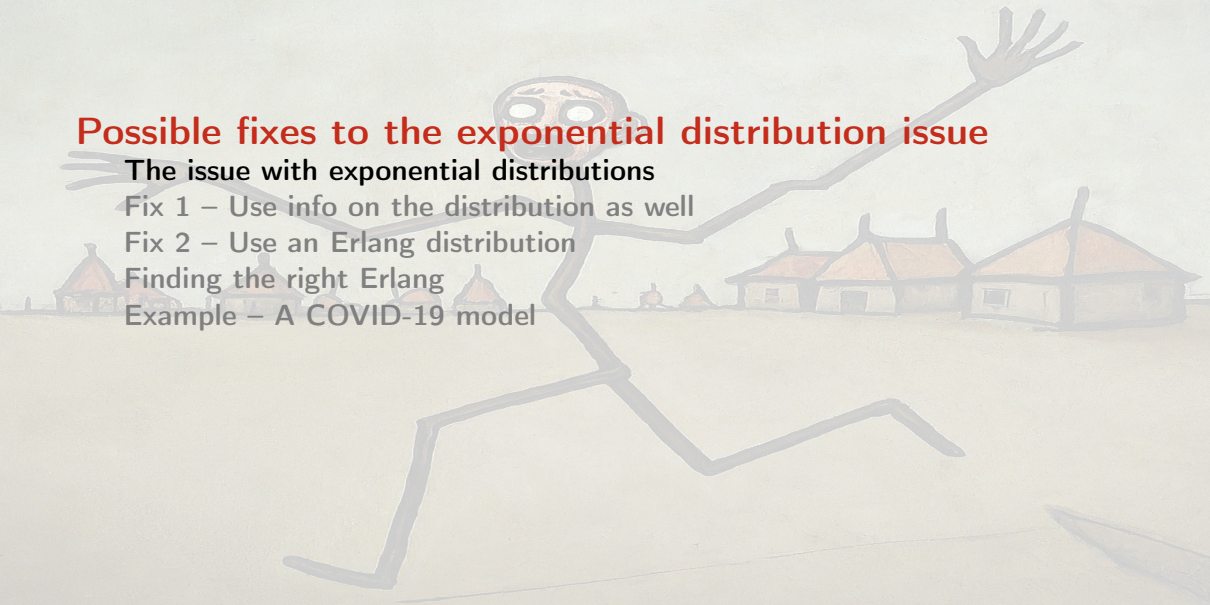
The issue with exponential distributions

Fix 1 – Use info on the distribution as well

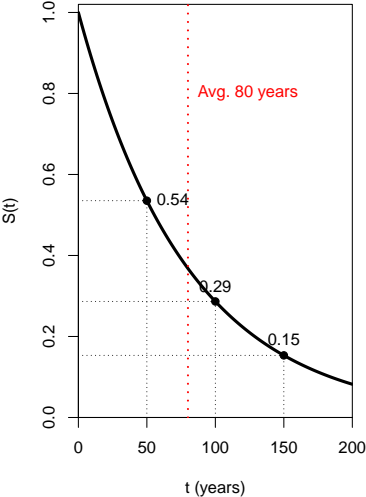
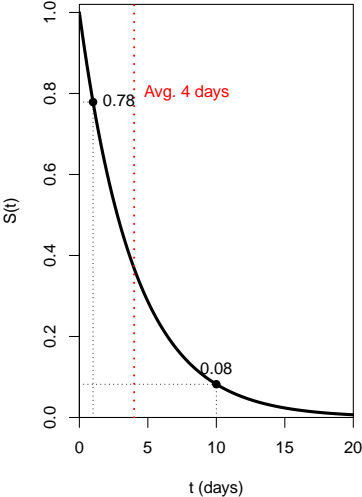
Fix 2 – Use an Erlang distribution

Finding the right Erlang

Example – A COVID-19 model



# Survival for the exponential distribution



## Issues with the exponential distribution

- ▶ Survival drops quickly
- ▶ Survival continues way beyond the mean

Acceptable if what matters is the average duration of sojourn in a compartment (e.g., long term dynamics)

More iffy if one is interested in short-term dynamics

- ▶ Exponential distribution with parameter  $\theta$  has same mean and standard deviation  $1/\theta$ , i.e., a single parameter controls mean and dispersion about the mean

## Possible fixes to the exponential distribution issue

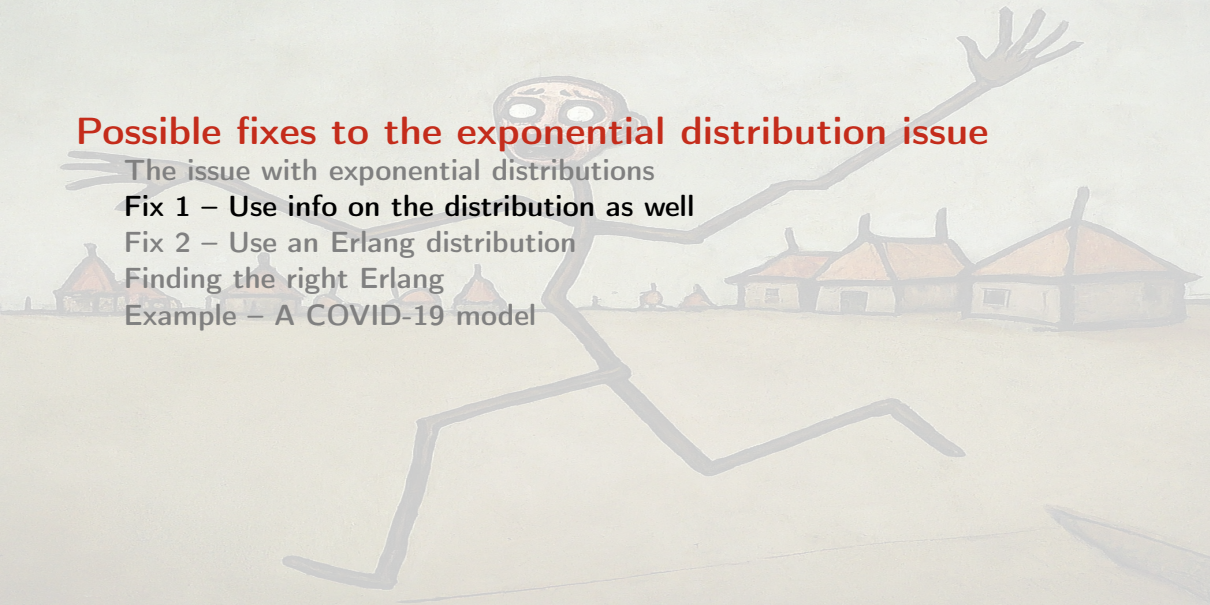
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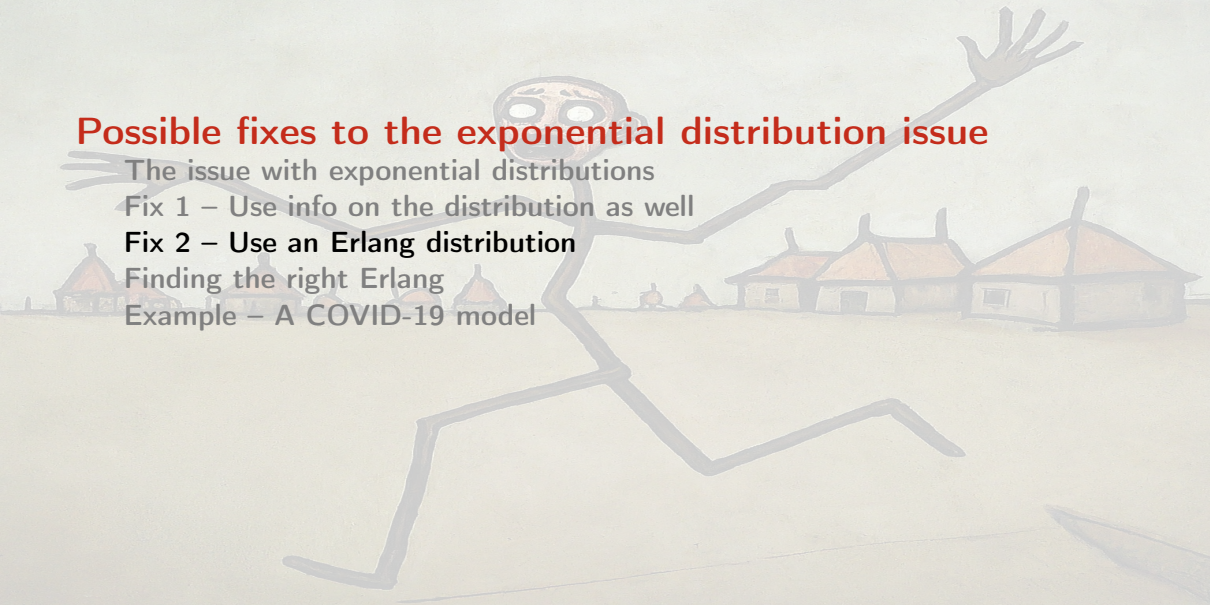
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## Side note – What is a convolution?

- ▶ The *convolution product* is used to find the probability distribution of the *sum of two independent random variables*
- ▶ If  $X$  and  $Y$  are two continuous random variables, and  $Z = X + Y$ , use the convolution to find the p.d.f.  $f_Z(z)$  of  $Z$



## The setting

- ▶ Consider two independent continuous random variables  $X$  and  $Y$  with p.d.f.  $f_X(x)$  and  $f_Y(y)$ , respectively
- ▶ Want to find the p.d.f. of their sum  $Z = X + Y$
- ▶ Simply adding the p.d.f. or multiplying them does not yield the correct distribution for the sum  $Z$
- ▶ Convolution accounts for all possible combinations of  $X$  and  $Y$  that sum to a specific value  $z$

## Deriving the convolution formula

Start with the c.d.f. of  $Z$ :

- ▶  $F_Z(z) = \mathbb{P}(Z \leq z) = \mathbb{P}(X + Y \leq z)$
- ▶ Since  $X$  and  $Y$  are independent, their joint p.d.f. is  $f_{X,Y}(x,y) = f_X(x)f_Y(y)$
- ▶  $\mathbb{P}(X + Y \leq z)$  found by integrating the joint p.d.f. over the region where  $x + y \leq z$

$$F_Z(z) = \iint_{x+y \leq z} f_X(x)f_Y(y) dx dy$$

- ▶ Change the order of integration. For a fixed  $x$ ,  $y$  must be less than or equal to  $z - x$

$$F_Z(z) = \int_{-\infty}^{\infty} \left( \int_{-\infty}^{z-x} f_Y(y) dy \right) f_X(x) dx$$

- ▶ Inner integral is c.d.f. of  $Y$  evaluated at  $z - x$ , i.e.,  $F_Y(z - x)$

$$F_Z(z) = \int_{-\infty}^{\infty} F_Y(z - x)f_X(x) dx$$

## Deriving the convolution formula (2)

To obtain the PDF  $f_Z(z)$ , we differentiate the CDF  $F_Z(z)$  with respect to  $z$

$$\blacktriangleright f_Z(z) = \frac{d}{dz} F_Z(z) = \frac{d}{dz} \int_{-\infty}^{\infty} F_Y(z-x) f_X(x) dx$$

$\blacktriangleright$  Using Leibniz integral rule (differentiating under the integral sign)

$$f_Z(z) = \int_{-\infty}^{\infty} \frac{\partial}{\partial z} F_Y(z-x) f_X(x) dx$$

$\blacktriangleright$  Since  $\frac{d}{du} F_Y(u) = f_Y(u)$ , and here  $u = z - x$ , we have  $\frac{\partial}{\partial z} F_Y(z-x) = f_Y(z-x)$

## The convolution pProduct formula

$$f_Z(z) = \int_{-\infty}^{\infty} f_X(x) f_Y(z - x) dx$$

- ▶ This is the **convolution product** of  $f_X$  and  $f_Y$ , often denoted as  $(f_X * f_Y)(z)$
- ▶ Alternatively, by symmetry

$$f_Z(z) = \int_{-\infty}^{\infty} f_Y(y) f_X(z - y) dy$$

- ▶ **Key condition** – Valid only if  $X$  and  $Y$  are *independent* r.v.

## Exponential distributions are “bad” but also cool

$X_1$  and  $X_2$  2 i.i.d. (independent and identically distributed) exponential r.v. with parametres  $\theta_1$  and  $\theta_2$ . Then the probability density function of the r.v.  $Z = X_1 + X_2$  is given by the convolution

$$\begin{aligned} f_Z(z) &= \int_{-\infty}^{\infty} f_{X_1}(x_1) f_{X_2}(z - x_1) dx_1 \\ &= \int_0^z \theta_1 e^{-\theta_1 x_1} \theta_2 e^{-\theta_2(z-x_1)} dx_1 \\ &= \theta_1 \theta_2 e^{-\theta_2 z} \int_0^z e^{(\theta_2 - \theta_1)x_1} dx_1 \\ &= \begin{cases} \frac{\theta_1 \theta_2}{\theta_2 - \theta_1} (e^{-\theta_1 z} - e^{-\theta_2 z}) & \text{if } \theta_1 \neq \theta_2 \\ \theta^2 z e^{-\theta z} & \text{if } \theta_1 = \theta_2 =: \theta \end{cases} \end{aligned} \tag{7}$$

## The tool we use

### Theorem 1

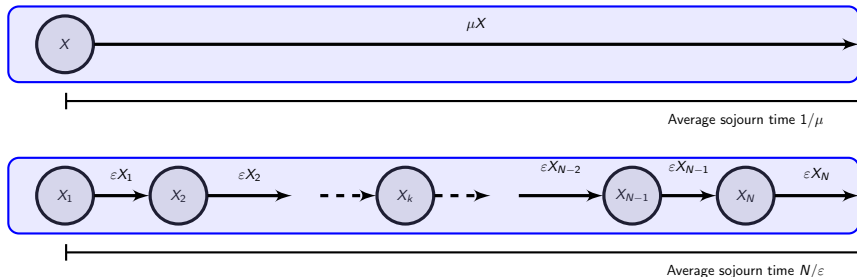
*Let  $X_i$  be independent exponentially distributed random variables with parameter  $\xi$  and  $Y = \sum_{i=1}^n X_i$*

*Then the random variable  $Y \rightsquigarrow E(n, \xi)$ , an Erlang distribution with shape parameter  $n$  and scale parameter  $\xi$*

(Erlang distribution: Gamma distribution with integer shape parameter)

## Consequences for compartmental models

If  $n$  compartments are traversed successively by individuals, with each compartment having an outflow rate of  $1/\xi$  (or a mean sojourn time of  $\xi$ ), then the time of sojourn from entry into the first compartment to exit from the last is Erlang distributed with mean  $E(Y) = n\xi$  and variance  $\text{Var}(Y) = n\xi^2$



I have a Shiny app for this :)

## Possible fixes to the exponential distribution issue

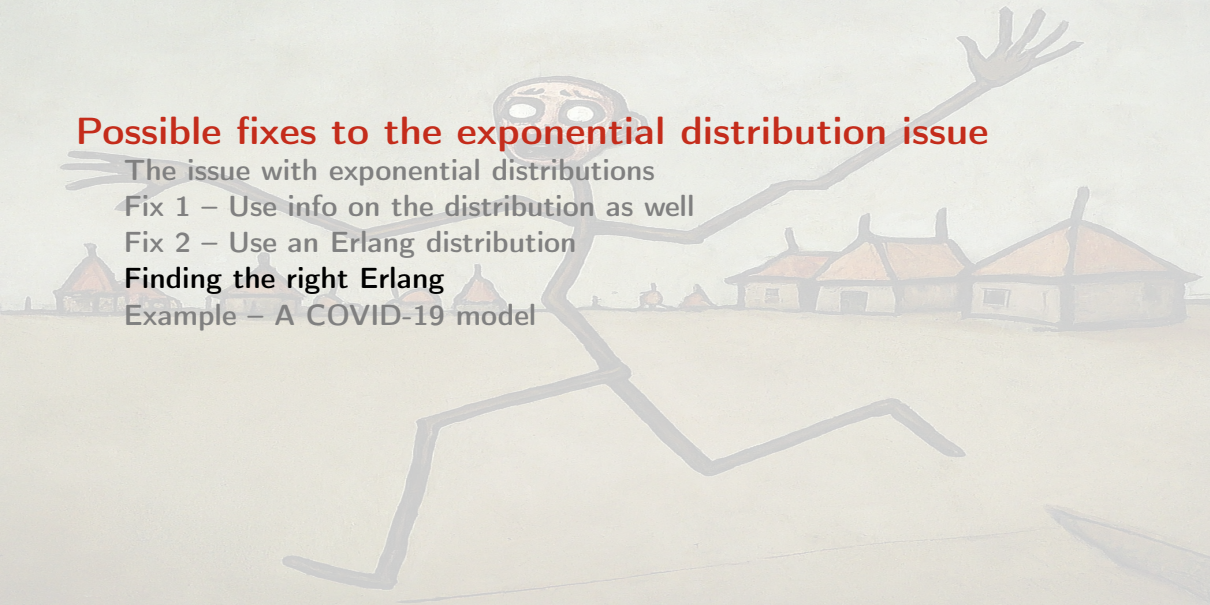
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Fix 1 – Use info on the distribution as well

Fix 2 – Use an Erlang distribution

**Finding the right Erlang**

Example – A COVID-19 model





## Example: EVD incubation periods

During the 2014 Ebola Virus Disease (EVD) crisis in Western Africa, the WHO Ebola Response Team estimated incubation periods in a 2015 paper

Table S2 in the Supplementary Information in that paper gives the best fit for the distribution of incubation periods for EVD as a Gamma distribution with mean 10.3 days and standard deviation 8.2, i.e.,  $n\varepsilon = 10.3$  and  $\varepsilon\sqrt{n} = 8.2$

From this,  $\varepsilon = 8.2^2/10.3 \simeq 6.53$  and  $n = 10.3^2/8.2^2 \simeq 1.57$ . However, that is a Gamma distribution

## Switching to a compartmental model approach

To use multiple compartments to better fit residence times, we need to find the closest possible Erlang distribution to this Gamma distribution

⇒ compute RSS errors between data points generated from the given Gamma distribution and an Erlang

```
error_Gamma <- function(theta,shape,t,data) {  
  test_points <- dgamma(t, shape = shape, scale = theta)  
  ls_error <- sum((data-test_points)^2)  
  return(ls_error)  
}
```



```

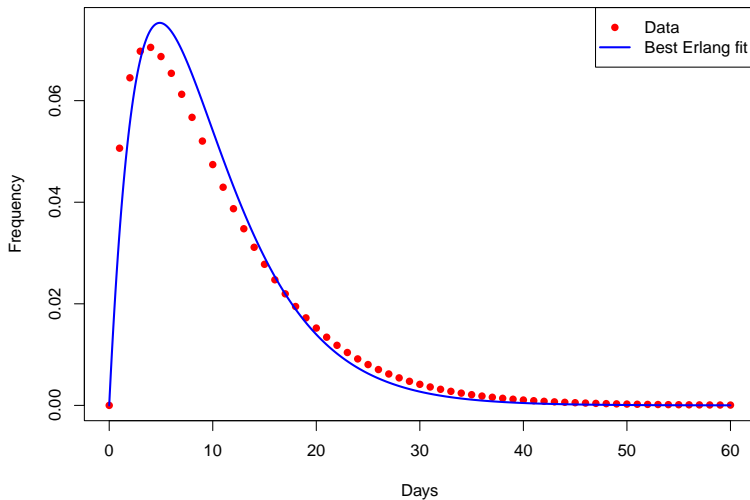
optimize_gamma <- function(t,d) {
  max_shape <- 10
  error_vector <- mat.or.vec(max_shape,1)
  scale_vector <- mat.or.vec(max_shape,1)
  for (i in 1:max_shape) {
    result_optim <- try(optim(par = 3,
                             fn = error_Gamma,
                             lower = 0,
                             method = "L-BFGS-B",
                             shape = i,
                             t = t,
                             data = d),
                        TRUE)

    if (!inherits(result_optim,"try-error")) {
      error_vector[i] <- result_optim$value
      scale_vector[i] <- result_optim$par
    } else {
      error_vector[i] <- NaN
    }
  }
}

```

```
time_points <- seq(0,60)
data_points <- dgamma(time_points, shape = 1.57,
                      scale = 6.53)
# Run the minimization
optim_fits <- optimize_gamma(time_points,data_points)
# Which is the best Erlang to fit the data
idx_best <- which.min(optim_fits$error)
```

We find the best fit below, which is obtained using 2 compartments



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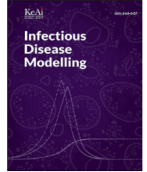
Example – A COVID-19 model



Contents lists available at [ScienceDirect](#)

# Infectious Disease Modelling

journal homepage: [www.keaipublishing.com/idm](http://www.keaipublishing.com/idm)



## A simple model for COVID-19

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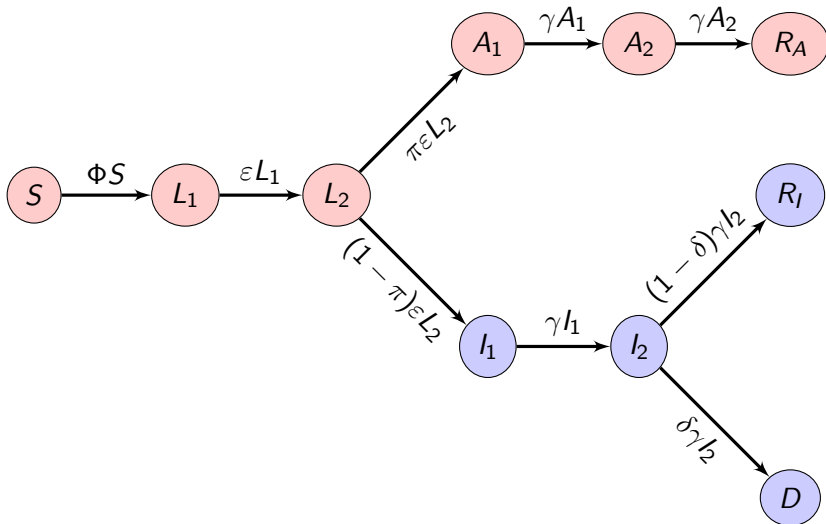
<sup>c</sup> Canadian COVID-19 Mathematical Modelling Task Force, Canada





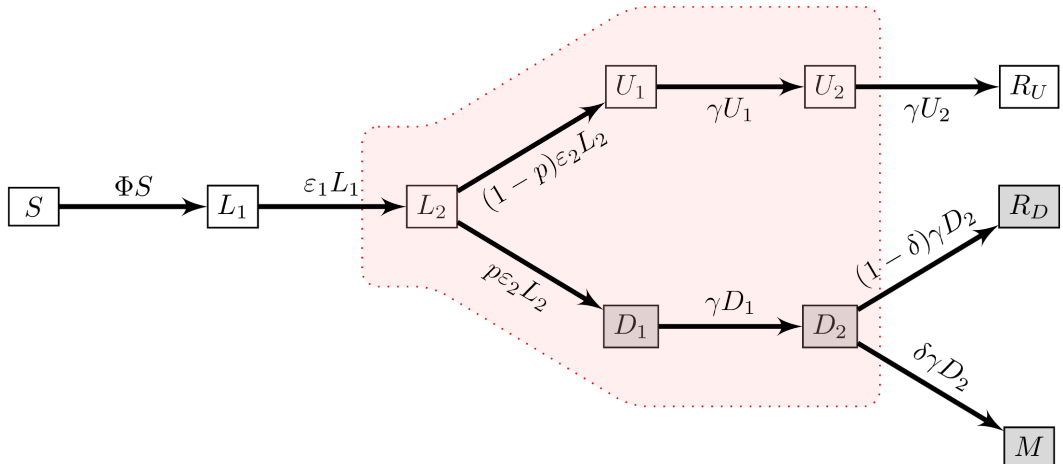
Extends the SLIAR model to take into account non-exponentially distributed stage durations (see lecture 05)

## The original model (well, almost the first one)



## Reinterpreting terms

Here  $D$  stands for *detected*,  $U$  is *undetected*



## Working out when the first COVID-19 case occurred

- ▶ Details of emergence and precise timeline before amplification started unknown
- ▶ Amplification in Wuhan
  - ▶ Cluster of pneumonia cases mostly related to the Huanan Seafood Market
  - ▶ 27 December 2019: first report to local government
  - ▶ 31 December 2019: publication
  - ▶ 8 January 2020: identification of SARS-CoV-2 as causative agent
  - ▶ ~ 23 January 2020: lockdown Wuhan and Hubei province + face mask mandates
- ▶ By 2020-01-29, virus in all provinces of mainland CHN

## Evidence of earlier spread

- ▶ Report to Wuhan authorities on 27 December 2019
  - ▶ First export detections in Thailand and Japan on 13 and 16 January 2020 (with actual importations on 8 and 6 January)
- ⇒ amplification must have been occurring for a while longer
- ▶ France: sample taken from 42-year-old male (last foreign travel to Algeria in August 2019) who presented to ICU on 27 December 2019
  - ▶ Retrospective studies in United Kingdom and Italy also showed undetected COVID-19 cases in pre-pandemic period

## Untangling the first case issue

► Robert, Rossman & Jaric. Dating first cases of COVID-19. *PLoS Pathogens* (2021)  
Find likely timing of first case of COVID-19 in China as November 17 (95% CI October 4)

► Pekar, Worobey, Moshiri, Scheffler & Wertheim. Timing the SARS-CoV-2 index case in Hubei province. *Science* (2021)  
Period between mid-October and mid-November 2019 is plausible interval when the first case of SARS-CoV-2 emerged in Hubei province

Important when trying to understand global spread, so let me illustrate with the model I used, taking into account model evolution since

## Back-calculating the start of spread (example of China)

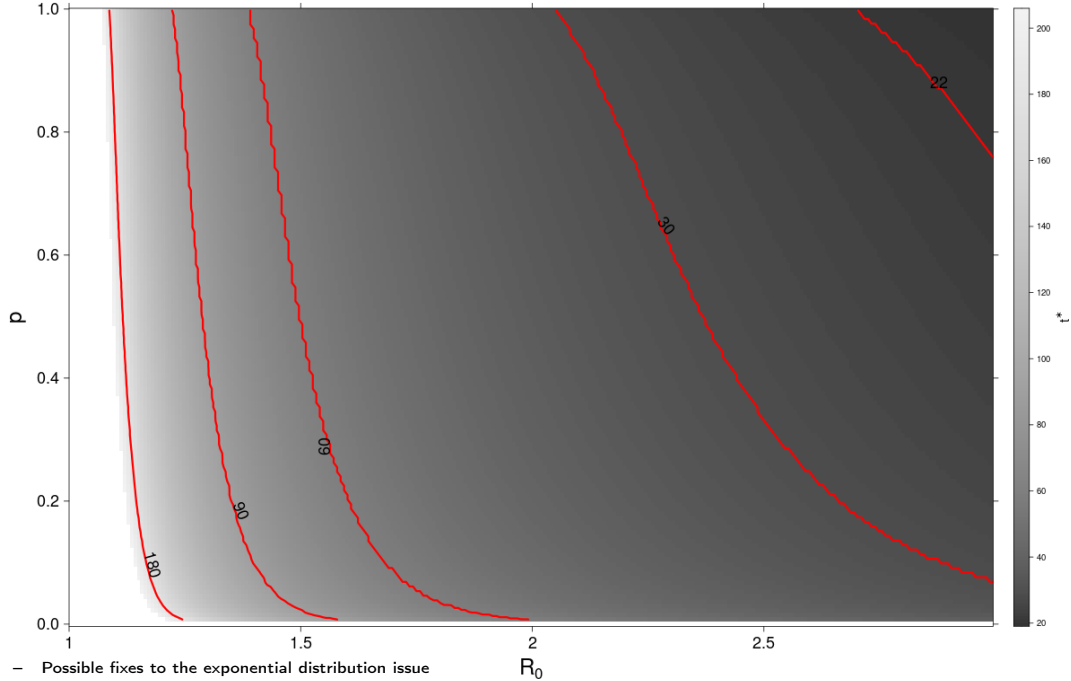
Cumulative confirmed case counts in China as reported to WHO was  $c = 547$  cases on  $t_c = 2020-01-22$

Let  $u$  be a point in parameter space. Solve ODE numerically over  $[0, t]$ , with  $S(0)$  the population of China,  $L_1(0) = 1$  and other state variables 0. This gives a solution  $x(t, t_0 = 0, u)$

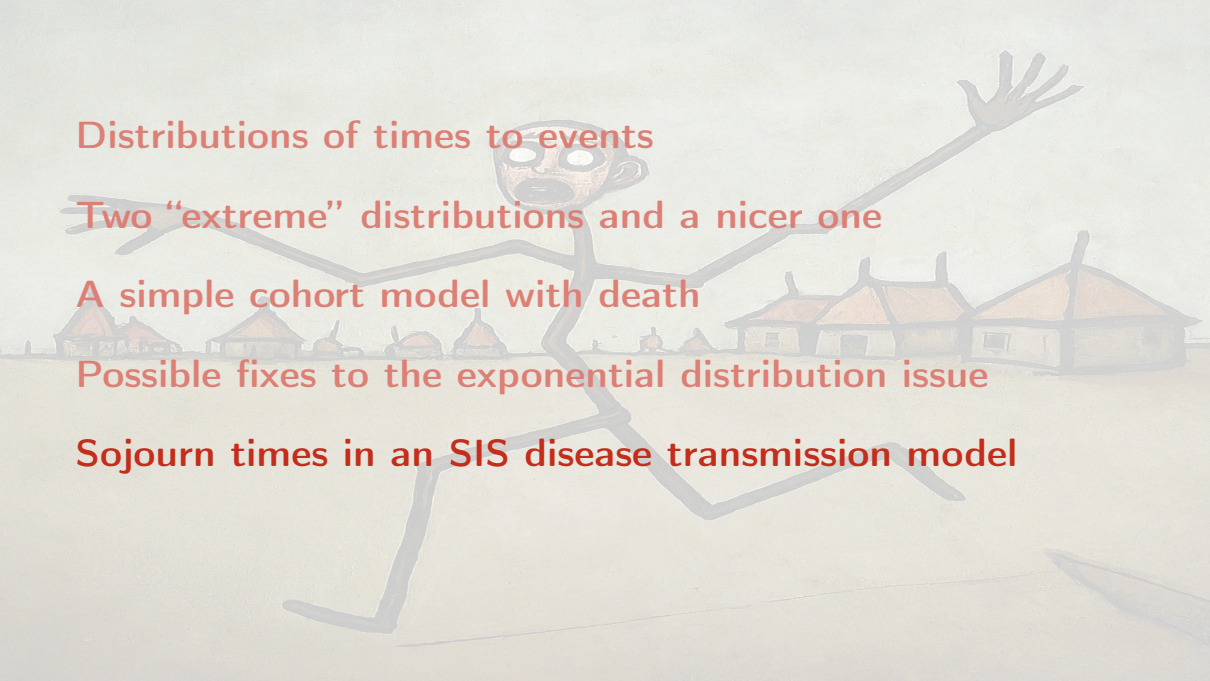
Extracting  $L_2(t, t_0 = 0, u)$  from this solution, obtain cumulative number of new detections as

$$C(t) = \int_{t_0=0}^t p_{\varepsilon_2} L_2(s, t_0, u) \, ds$$

Let  $t^*$  be s.t.  $C(t^*) = 547$ ; then  $t_i = 2020-01-22 - t^*$







Distributions of times to events

Two “extreme” distributions and a nicer one

A simple cohort model with death

Possible fixes to the exponential distribution issue

Sojourn times in an SIS disease transmission model

# An SIS model

## Hypotheses

- ▶ Individuals typically recover from the disease
- ▶ The disease does not confer immunity
- ▶ There is no birth or death (from the disease or natural)  
⇒ Constant total population  $N \equiv N(t) = S(t) + I(t)$
- ▶ Infection is of **standard incidence** type

# Recovery

- ▶ Traditional models suppose that recovery occurs with rate constant  $\gamma$
- ▶ Here, of the individuals that become infective at time  $t_0$ , a fraction  $\mathcal{S}(t - t_0)$  remain infective at time  $t \geq t_0$
- ▶  $\Rightarrow$  For  $t \geq 0$ ,  $\mathcal{S}(t)$  is a survival function. As such, it verifies  $\mathcal{S}(0) = 1$  and  $\mathcal{S}$  is nonnegative and nonincreasing

## Model for infectious individuals

Since  $N$  is constant,  $S(t) = N - I(t)$  and we need only consider the following equation (where  $S$  is used for clarity)

$$I(t) = I_0(t) + \int_0^t \beta \frac{S(u)I(u)}{N} S(t-u) du \quad (8)$$

- ▶  $I_0(t)$  number of individuals who were infective at time  $t = 0$  and still are at time  $t$ 
  - ▶  $I_0(t)$  is nonnegative, nonincreasing, and such that  $\lim_{t \rightarrow \infty} I_0(t) = 0$
- ▶  $S(t-u)$  proportion of individuals who became infective at time  $u$  and who still are at time  $t$

## Expression under the integral

Integral equation for the number of infective individuals:

$$I(t) = I_0(t) + \int_0^t \beta \frac{(N - I(u))I(u)}{N} \mathcal{S}(t - u) du \quad (8)$$

The term

$$\beta \frac{(N - I(u))I(u)}{N} \mathcal{S}(t - u)$$

- ▶  $\beta(N - I(u))I(u)/N$  is the rate at which new infectives are created, at time  $u$
- ▶ multiplying by  $\mathcal{S}(t - u)$  gives the proportion of those who became infectives at time  $u$  and who still are at time  $t$

Summing over  $[0, t]$  gives the number of infective individuals at time  $t$

## Case of an exponentially distributed time to recovery

Suppose  $\mathcal{S}(t)$  such that sojourn time in the infective state has exponential distribution with mean  $1/\gamma$ , i.e.,  $\mathcal{S}(t) = e^{-\gamma t}$

Initial condition function  $I_0(t)$  takes the form

$$I_0(t) = I_0(0)e^{-\gamma t}$$

with  $I_0(0)$  the number of infective individuals at time  $t = 0$ . Obtained by considering the cohort of initially infectious individuals, giving a model such as (4)

Equation (8) becomes

$$I(t) = I_0(0)e^{-\gamma t} + \int_0^t \beta \frac{(N - I(u))I(u)}{N} e^{-\gamma(t-u)} du \quad (9)$$

Taking the time derivative of (9) yields

$$\begin{aligned} I'(t) &= -\gamma I_0(0)e^{-\gamma t} - \gamma \int_0^t \beta \frac{(N - I(u))I(u)}{N} e^{-\gamma(t-u)} du \\ &\quad + \beta \frac{(N - I(t))I(t)}{N} \\ &= -\gamma \left( I_0(0)e^{-\gamma t} + \int_0^t \beta \frac{(N - I(u))I(u)}{N} e^{-\gamma(t-u)} du \right) \\ &\quad + \beta \frac{(N - I(t))I(t)}{N} \\ &= \beta \frac{(N - I(t))I(t)}{N} - \gamma I(t) \end{aligned}$$

This is the classical logistic type ordinary differential equation (ODE) for  $I$  in an SIS model without vital dynamics (no birth or death)

## Case of a step function survival function

Consider case where the time spent infected has survival function

$$\mathcal{S}(t) = \begin{cases} 1, & 0 \leq t \leq \omega, \\ 0, & t > \omega. \end{cases}$$

i.e., the sojourn time in the infective state is a constant  $\omega > 0$

In this case (8) becomes

$$I(t) = I_0(t) + \int_{t-\omega}^t \beta \frac{(N - I(u))I(u)}{N} du. \quad (10)$$

Here, it is more difficult to obtain an expression for  $I_0(t)$ . It is however assumed that  $I_0(t)$  vanishes for  $t > \omega$





When differentiated, (10) gives, for  $t \geq \omega$ ,

$$I'(t) = I'_0(t) + \beta \frac{(N - I(t))I(t)}{N} - \beta \frac{(N - I(t - \omega))I(t - \omega)}{N}.$$

Since  $I_0(t)$  vanishes for  $t > \omega$ , this gives the delay differential equation (DDE)

$$I'(t) = \beta \frac{(N - I(t))I(t)}{N} - \beta \frac{(N - I(t - \omega))I(t - \omega)}{N}.$$

# Bibliography I

-  Arino, J. and Portet, S. (2020). A simple model for COVID-19. *Infectious Disease Modelling*, 5:309–315.
-  Thieme, H. R. (2018). *Mathematics in population biology*. Princeton University Press.