

Revisiting the early stage of the 1720 plague epidemic in Gévaudan

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1 Preamble

In this report, we revisit some of the key elements of the early stages of the bubonic Plague epidemic in Gévaudan, which started in 1720 in the village of Correjac, soon followed by the town of La Canourgue. Historical data suggest that the epidemic was initiated by a convict who travelled from Marseille to Saint-Laurent-d'Olt, where he infected Jean Quintin, who then seeded the epidemic which would first affect his village before spreading to the rest of Gévaudan.

We re-analyse this scenario by combining historical data on the dates of deaths of the first few cases, alongside published estimates of the incubation time or infectious period distributions. A branching process model with augmented data is used for jointly estimating the effective reproduction number and the rate of zoonotic introductions in the early stages of the epidemic.

2 Estimates of key epidemiological features

2.1 Delay distributions

2.1.1 Incubation period

The incubation period is described in multiple papers but a general consensus seems to be around 2-6 days [1–7].

We build a discretized log-normal distribution compatible with these observations:

```
library(distcrete)
library(tidyverse)

incub <- distcrete(
  "lnorm",
  meanlog = log(3.5),
  sdlog = log(1.5),
  interval = 1,
  w = 1
)

incub_dat <- tibble(
  Day = 0:15,
  p = incub$d(0:15)
)

incub_dat %>%
  ggplot(aes(x = Day, y = p)) +
  geom_col(fill = 4) +
  theme_bw() +
  labs(
    x = "Time from infection to symptom onset (days)",
    y = "Probability"
  )
```

2.2 Some stats based upon 1 million draws

```
summary(incub$r(1e6))
```

2.2.1 Infectious period

The infectious period distribution is built similarly to match data from the literature, where for historical outbreaks death is reported to take place within 3 to 5 days post-symptom onset [1,6,8,9].

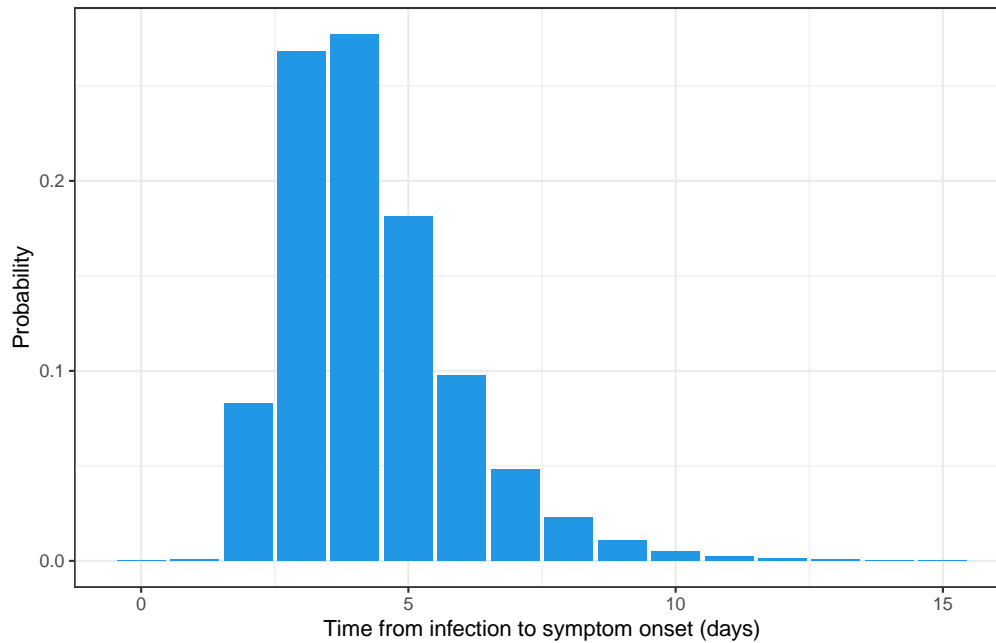


Figure 1: Incubation time distribution of bubonic plague

Note that because this form had near 100% CFR, this is also the distribution of the time from onset of symptoms to death.

```

infece <- discrete(
  "lnorm",
  meanlog = log(3),
  sdlog = log(1.4),
  interval = 1,
  w = 1
)

infece_dat <- tibble(
  Day = 0:15,
  p = infece$d(0:15)
)

## Some stats based upon 10 million draws
summary(infece$r(1e6))

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      1.000   3.000   4.000   3.676   4.000  17.000

infece_dat %>%
  ggplot(aes(x = Day, y = p)) +
  geom_col(fill = 2) +
  theme_bw() +
  labs(
    x = "Time from symptom onset to death (days)",
    y = "Probability"
  )

```

We note that the distribution is well in line with the mean duration of fatal, untreated bubonic plague of 3.6

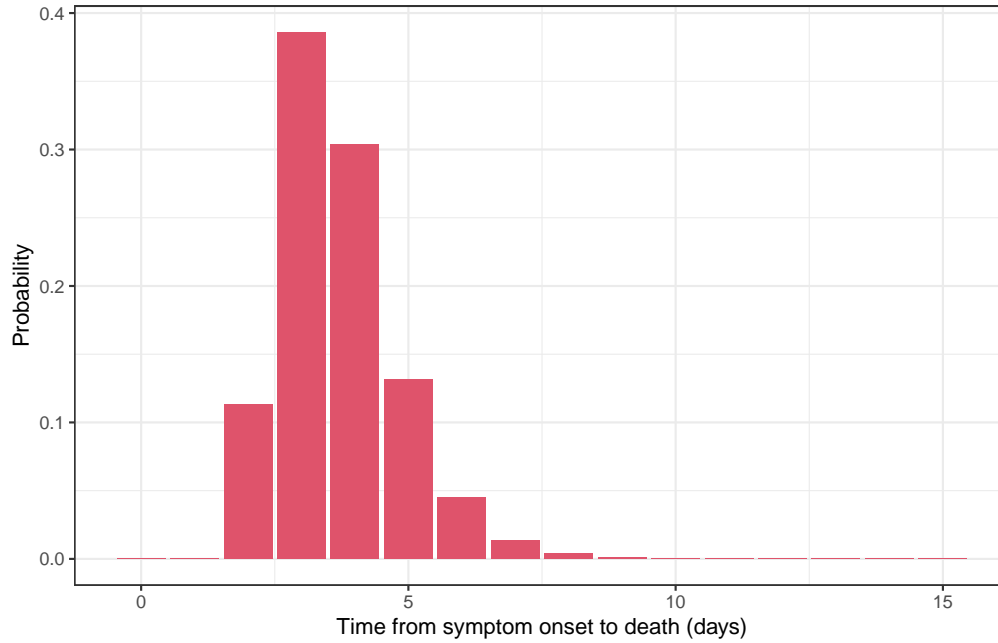


Figure 2: Infectious period distribution of bubonic plague

days [1].

```
## mean of 1 000 000 values from the distribution:
```

```
mean(infec$r(1e6))
```

```
## [1] 3.673125
```

3 Patient zero: the convict from Marseille

The theory of the convict walking all the way from Marseille with an infected bundle of wool to eventually infect Jean Quintin in Saint Laurent d'Olt is suspicious: the man would have had to not get infected during his entire trip, to then infect JQ after a fairly brief encounter.

The trip by foot via current roads is 273 km, and would have likely been longer using roads at the time. Especially since patrols were restricting movement in the area, and would have demanded some extra time to be avoided.

We will explore 3 scenarios, with varying durations for the trip, which we posit was at least about 300 km:

- 10 days (optimistic, 30 km per day)
- 15 days (~ 20km per day)
- 20 days (~ 15 km per day)

We do not know what the daily rate of infection λ from the wool bundle was, but we can derive a likelihood profile for each scenario, using:

$$\mathcal{L}(\lambda) = p(T|\lambda) = (e^{-\lambda})^T (1 - e^{-\lambda})$$

where T is the number of days the trip took, and $(1 - e^{-\lambda})$ is the daily probability of infection from the infected bundle.

Let us look at these profiles, ensuring we re-standardise both densities to 1 to make them comparable, as they rely on datasets of different sizes:

```

like_trip <- function(lambda, T) {
  p <- 1 - exp(-lambda)
  (1 - p)^T * p
}

lambda_res <- tibble(
  val = seq(0, 1.2, length = 1000),
  "10 days" = like_trip(val, 10),
  "15 days" = like_trip(val, 15),
  "20 days" = like_trip(val, 20)
) %>%
  mutate_at(
    vars(contains("days")),
    function(x) x / sum(x)
  )

lambda_res_long <- lambda_res %>%
  pivot_longer(-1, names_to = "scenario", values_to = "likelihood") %>%
  mutate(scenario = factor(scenario, levels = paste(c(10, 15, 20), "days")))

lambda_res_mle <- lambda_res_long %>%
  group_by(scenario) %>%
  summarise(MLE = val[which.max(likelihood)])

lambda_res_mle

```

```

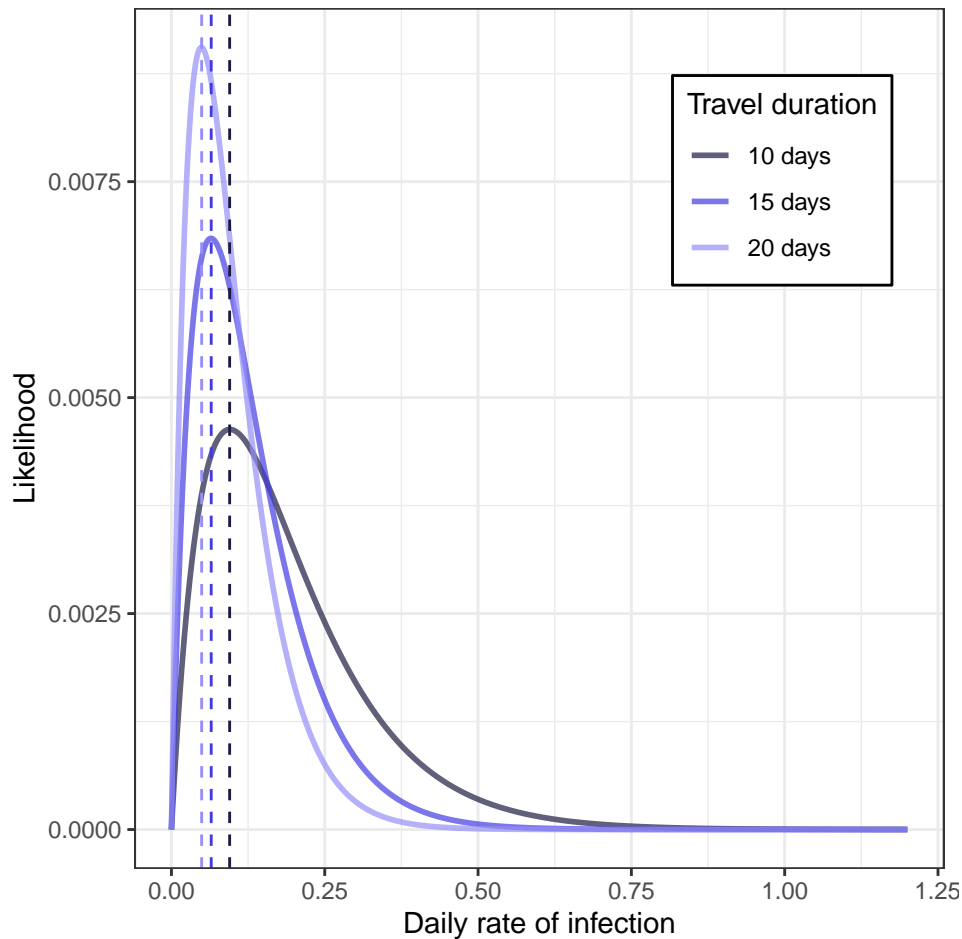
## # A tibble: 3 x 2
##   scenario    MLE
##   <fct>      <dbl>
## 1 10 days  0.0949
## 2 15 days  0.0649
## 3 20 days  0.0492

```

```

lambda_res_long %>%
  ggplot(aes(x = val, y = likelihood, color = scenario)) +
  geom_line(linewidth = 1, alpha = 0.7) +
  geom_vline(data = lambda_res_mle, aes(xintercept = MLE, color = scenario), linetype = 2, show.legend = FALSE) +
  theme_bw() +
  scale_color_manual(
    "Travel duration",
    values = c(
      `10 days` = "#1c1b42",
      `15 days` = "#413ae2",
      `20 days` = "#948ff9")
  ) +
  labs(
    x = "Daily rate of infection",
    y = "Likelihood"
  ) +
  theme(legend.position = c(.8, .8),
        legend.background = element_rect(linetype = 1, color = 1)
  )

```



We find some more likely values than others, and this leans towards fairly low rates ranging from 0.0492 to 0.0949. We calculate the corresponding probabilities that these events occurred using the MLE:

```
lambda_res_mle <- lambda_res_mle %>%
  mutate(
    days = as.integer(sub(" days", "", scenario)),
    proba = like_trip(lambda = MLE, T = days)
  )
lambda_res_mle
```

```
## # A tibble: 3 x 4
##   scenario    MLE  days  proba
##   <fct>      <dbl> <int> <dbl>
## 1 10 days  0.0949     10 0.0350
## 2 15 days  0.0649     15 0.0237
## 3 20 days  0.0492     20 0.0179
```

The resulting probabilities are quite low, ranging from 1.8% chances for a trip of 20 days, to 3.5% for 10 days.

To assess the overall plausibility of these scenari, questions remain: how many such trips where made by people carrying the infection from Marseille at the time? And were such trips indeed possible in the first place, given the containment measures in place?

4 The first case after Jean

Jean Quintin showed symptoms on the 23rd November, and died 3 days later on the 26th. The first case in his household died on the 18th December. We can assess how likely this delay is by looking at the delay distributions for Bubonic plague, integrating over the possible dates of infection (24th, 25th, 26th November), and convolving the incubation period, and the duration of the symptomatic period.

We also consider, as a sensitivity study, the possibility of a transmission after Jean's death from contaminated clothes or bedsheets, where *Y. pestis* can survive up to 5 days [10].

```
## calculate possible delays from infection to death
child_delay <- as.integer(as.Date("1720-12-18") - as.Date("1720-11-24") + 0:2)
child_delay

## [1] 24 25 26

## convolve using 1e7 draws from distributions
sim_delay_inf_death <- incub$r(1e7) + infec$r(1e7)
sim_delay_inf_death_q <- data.frame(
  q = quantile(sim_delay_inf_death,
    seq(0, 1, by = 0.1))
)

## calculate p-values
child_delay_pval <- sapply(child_delay, function(x) mean(sim_delay_inf_death >= x))
child_delay_pval

## [1] 1.3e-05 6.8e-06 4.4e-06

mean(child_delay_pval)

## [1] 8.066667e-06

data.frame(sim_delay_inf_death) %>%
  ggplot(aes(x = sim_delay_inf_death)) +
  geom_histogram(
    binwidth = 1,
    aes(y=..count../sum(..count..)) +
  geom_rug(data = sim_delay_inf_death_q, aes(x = q)) +
  theme_bw() +
  geom_vline(xintercept = child_delay, color = "#6a5ce2", linetype = 2) +
  geom_vline(xintercept = child_delay - 5, color = "#c70039", linetype = 2) +
  labs(
    x = "Days from infection to death",
    y = "Frequency"
  )
)
```

It is very unlikely that the first secondary case was directly infected by Jean Quintin .

```
child_delay_pval_alt <- sapply(child_delay - 5, function(x) mean(sim_delay_inf_death >= x))
child_delay_pval_alt

## [1] 0.0003954 0.0002002 0.0001047

mean(child_delay_pval_alt)

## [1] 0.0002334333
```

It seems we can rule out the hypothesis of a direct transmission of bubonic plague. Possible alternatives are:

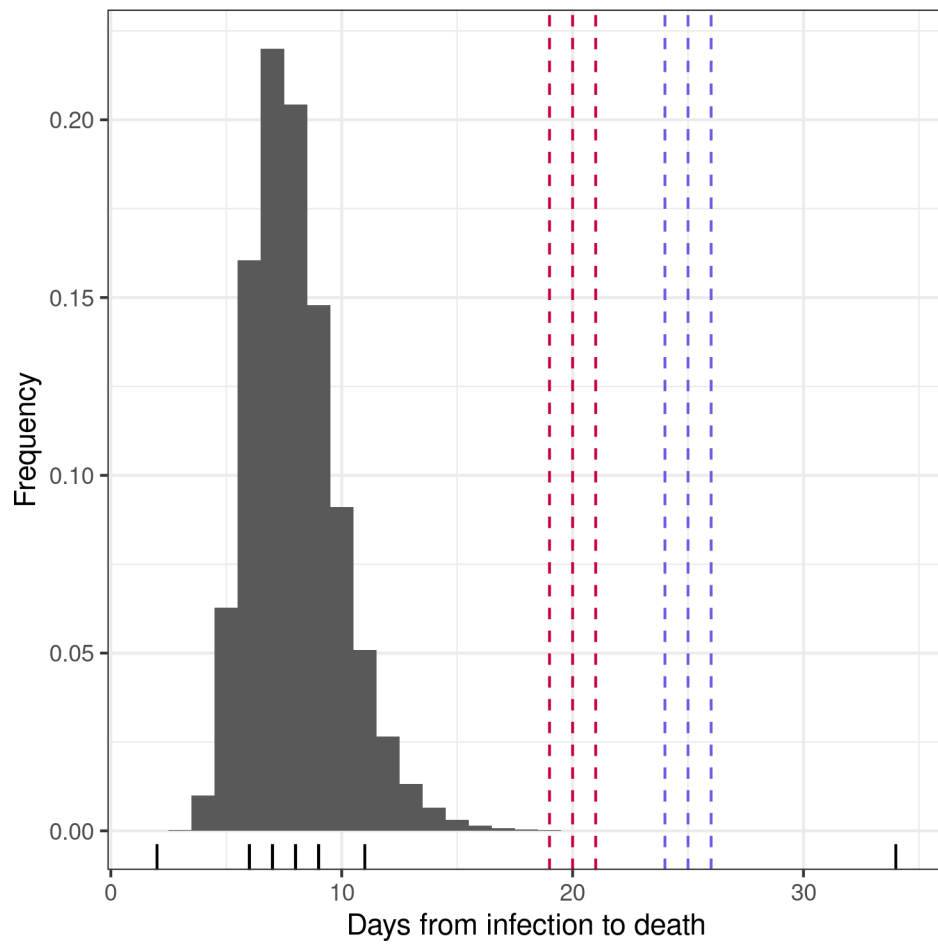


Figure 3: Delays from infection to death for the first transmission

- it was a bubonic plague, with a long duration of illness in the kid; might be unlikely seeing that patients seem to die very quickly - TBC
- the kid was **not** infected by his dad, but from a zoonotic source

5 Modelling the early epidemic

5.1 Epidemic curve

Here we analyse the linelist of the first few cases in Corrégjac, followed by La Canourgue.

```
file_path <- here::here("data", "early_linelist.ods")
x <- rio::import(file_path, sheet = "linelist") %>%
  tibble() %>%
  mutate(date_of_death = as.Date(date_of_death, format = "%d/%m/%Y"))
x
```

```
## # A tibble: 52 x 4
##   name                date_of_death location family
##   <chr>                <date>         <chr>   <chr>
## 1 QUINTIN Jean        1720-11-26   Corrégjac Quintin
## 2 QUINTIN Ambroise    1720-12-18   Corrégjac Quintin
## 3 CASSANHES Marguerite 1720-12-25   Corrégjac Quintin
## 4 QUINTIN enfant 1    1720-12-25   Corrégjac Quintin
## 5 QUINTIN enfant 2    1720-12-25   Corrégjac Quintin
## 6 NOGARET Pierre      1721-01-04   Corrégjac Nogaret
## 7 DEROUCH Jean       1721-01-09   Corrégjac Quintin
## 8 MALAVIALE Marguerite 1721-01-28   Corrégjac Malaviale
## 9 POURCHIER Antoine   1721-02-02   Corrégjac Pourchier
## 10 DEROUCH Jean fils  1721-02-22   Corrégjac Quintin
## # i 42 more rows
```

```
dim(x)
```

```
## [1] 52  4
```

```
table(x$location)
```

```
##
##   Corrégjac La Canourgue
##         43             9
```

```
range(x$date_of_death)
```

```
## [1] "1720-11-26" "1721-08-04"
```

We build a simple epidemic curve for Corrégjac, and for both locations together:

```
library(incidence2)
x_cor <- x %>%
  filter(location == "Corrégjac")
dim(x_cor)
```

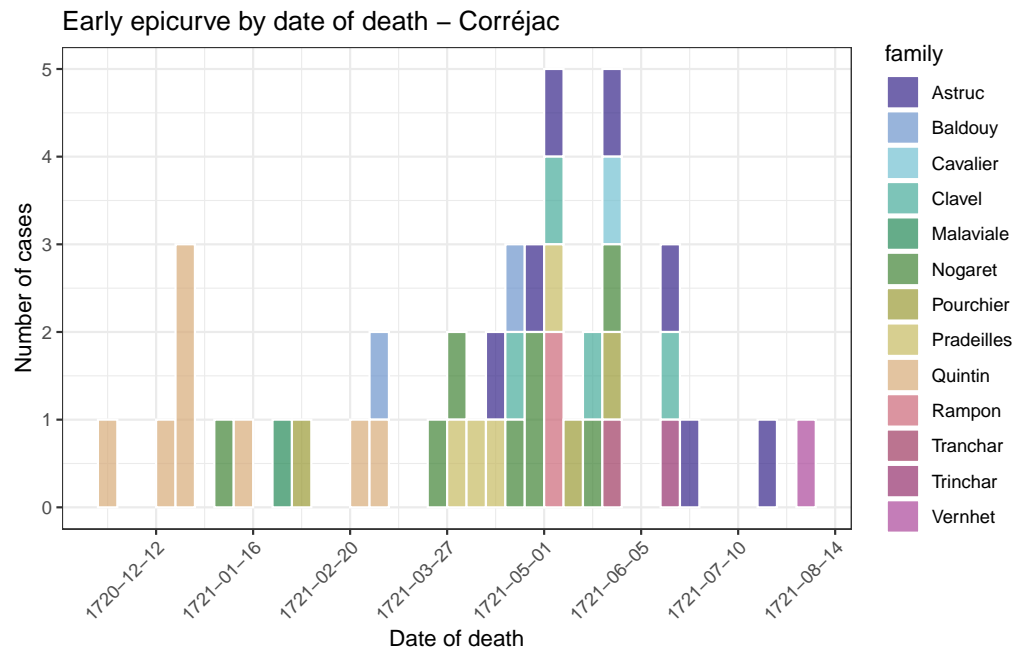
```
## [1] 43  4
```

```
x_cor %>%
  incidence("date_of_death", groups = "family", interval = 7) %>%
  plot(fill = "family", colour_palette = muted, angle = 45, border = "white") +
  labs(
```

```

title = "Early epicurve by date of death - Corrèjac",
x = "Date of death",
y = "Number of cases"
)

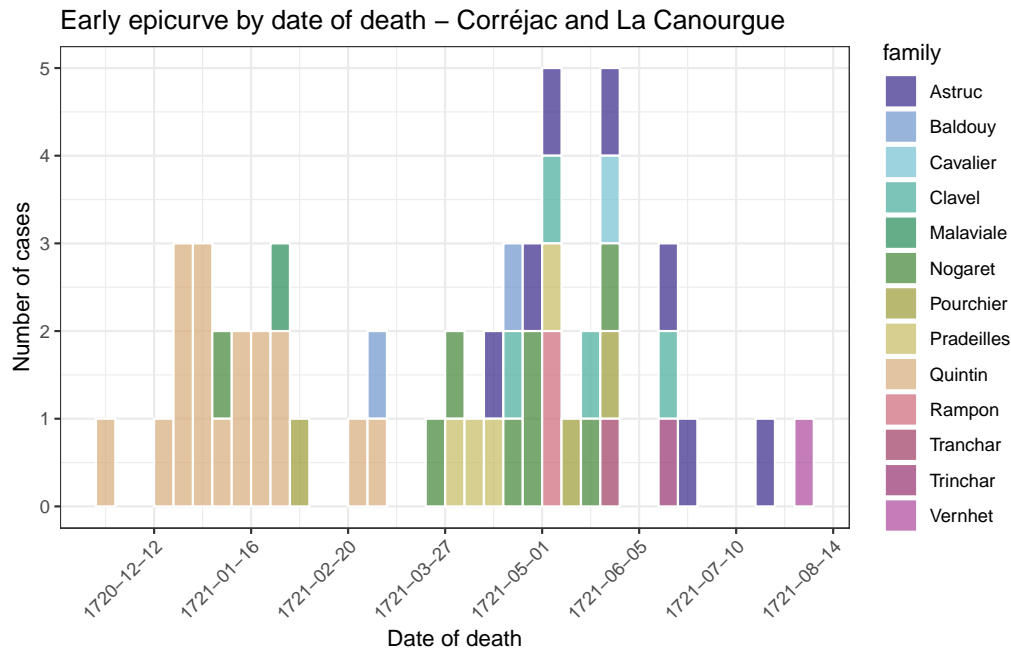
```



```

x %>%
  incidence("date_of_death", groups = "family", interval = 7) %>%
  plot(fill = "family", colour_palette = muted, angle = 45, border = "white") +
  labs(
    title = "Early epicurve by date of death - Corrèjac and La Canourgue",
    x = "Date of death",
    y = "Number of cases"
  )

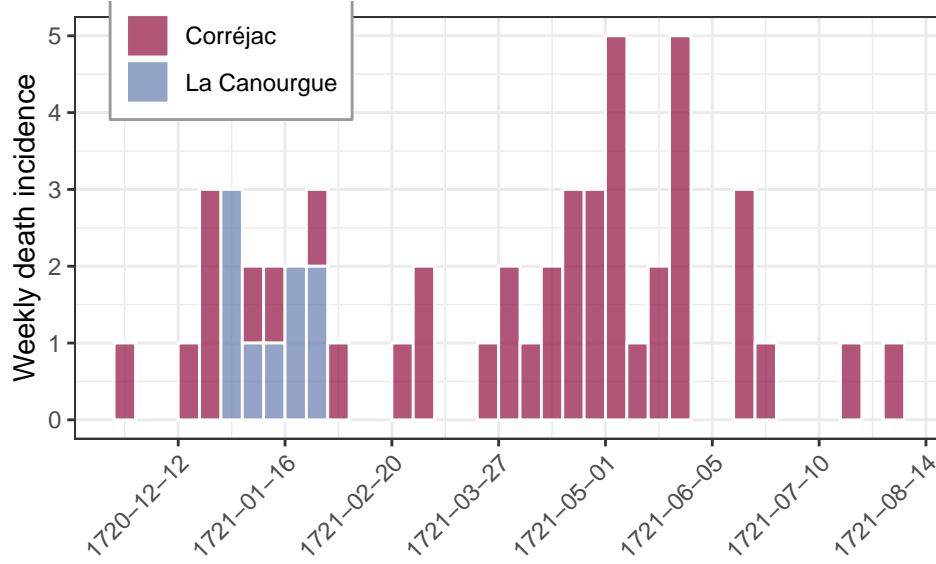
```



We make a figure for the paper:

```
figure_1 <- x %>%
  incidence("date_of_death", groups = "location", interval = 7) %>%
  plot(fill = "location", colour_palette = muted, angle = 45, border = "white") +
  labs(
    title = NULL,
    x = NULL,
    y = "Weekly death incidence"
  ) +
  scale_fill_manual("", values = c("Corrégjac" = "#900c3f", "La Canourgue" = "#647bac")) +
  theme(legend.position = c(0.18, 0.9),
        legend.background = element_rect(
          fill = "white", color = grey(0.6)),
        legend.title = element_blank())

figure_1
```



There is one key question here: do we assume Corréjac and La Canourgue were disconnected at the time, or do we treat these as a single location.

5.2 A transmission model for bubonic plague

A branching process will likely be best at capturing small fluctuations in case incidence over time, whilst neglecting the impact of the depletion of susceptible individuals. However we need to allow for a background rate of zoonotic introduction in addition to the classical person-to-person transmission [11]. As such, we will be using a Hawkes process [12] to model the case incidence over time, using augmented data to make up for the lack of precise information on dates of symptom onset and infection.

5.2.1 Notations

5.2.1.1 Data and augmented data

- $i = 1, \dots, n$: index of individuals
- $t = 1, \dots, T$: time index
- d_i : date of death of case i (data)
- O_i : date of symptom onset of case i (augmented data)
- I_i : date of infection of case i (augmented data)
- Y_t : incidence of new infections at time t (augmented data, derived from I_i)
- S_t : the number of susceptible (*i.e.* non-infected) individuals at time t
- N : the total number of individuals (infected and non-infected) in the area considered

5.2.1.2 Distributions

- \mathcal{F} : probability mass function (pmf) of the infectious/symptomatic period distribution
- \mathcal{G} : pmf of the incubation period distribution
- \mathcal{H} : pmf of the generation time distribution, obtained from the convolution $\mathcal{F} * \mathcal{G} = \mathcal{H}$

5.2.1.3 Parameters

- λ_z : the rate of zoonotic introduction, assumed constant over time
- R_0 : the basic reproduction number

5.2.2 The model

We use a classical Bayesian framework where the posterior distribution is defined for parameters θ and data (x) as:

$$p(\theta|x) \propto p(x|\theta)p(\theta) \quad (1)$$

where $p(x|\theta)$ is the likelihood function and $p(\theta)$ the prior distributions.

The likelihood can be written as:

$$p(x|\theta) = p(d, O, I|\lambda_z, R_0) \quad (2)$$

$$= p(d|O)p(O|I)p(I|\lambda_z, R_0) \quad (3)$$

$$= \left(\prod_i p(d_i|O_i) \prod_i p(O_i|I_i) \right) p(I|\lambda_z, R_0) \quad (4)$$

$$= \left(\prod_i \mathcal{F}(d_i - O_i) \mathcal{G}(O_i - I_i) \right) p(I|\lambda_z, R_0) \quad (5)$$

The calculation of $p(I|\lambda_z, R_0)$ is defined by the Hawkes process for the incidence Y :

$$p(I|\lambda_z, R_0) = p(Y|\lambda_z, R_0) \quad (6)$$

$$= \prod_t p(Y_t|Y_1, \dots, Y_{t-1}, \lambda_z, R_0) \quad (7)$$

The incidence Y_t is governed by:

$$Y_t \sim \mathcal{P}(\lambda_t) \quad (8)$$

where $\mathcal{P}(\cdot)$ is the Poisson distribution, and with:

$$\lambda_t = \lambda_z + \sum_{s=1}^{t-1} R_0 \frac{S_t}{N} Y_s \mathcal{H}(t-s) \quad (9)$$

Finally, we assume independent priors for λ_z and R_0 such that:

$$p(\theta) = p(\lambda_z, R_0) = p(\lambda_z)p(R_0) \quad (10)$$

5.2.3 Estimation process

We can sample from the posterior distribution using the Metropolis algorithm with augmented data with the following process:

1. draw augmented data O using $d_i - O_i \sim \mathcal{F}$
2. draw augmented data I using $O_i - I_i \sim \mathcal{G}$
3. propose (using symmetric proposal distributions) new values for θ^* and accept/reject these values with probability: $\min(1, \frac{p(\theta^*|x)}{p(\theta|x)})$, where θ represents the previous parameter state; in practice, separate movements are used for λ_z and R_0 , using Normal proposal distributions with standard deviations manually tailored to reach about 30-40% acceptance rates
4. go back to 1 until desired number of iterations reached

5.3 Distributions

5.3.1 Generation time

The generation time distribution \mathcal{H} is estimated using the following procedure:

1. Sample a large number n of incubation periods X
2. Sample a large number n of infectious period durations Y
3. Sample n delays from onset to infections Z , uniformly distributed between 0 and Y
4. Derive the empirical distribution of \mathcal{H} from $X + Z$

We note that this can be done using two alternative approaches:

- a. sampling from the discretized distributions for steps 1-3
- b. sampling from continuous distributions for steps 1-3, then discretizing

We will try both approaches out of curiosity (planting the seed of a new MRes project?) but will retain option **b** as the correct one.

We start with approach A, basing estimates on 10 million draws:

```
## RNG for delay from onset to infection
onset_to_inf_r_a <- function(n) {
  floor(runif(n, 0, infec$r(n) + 1))
}

## PMF for delays of 0, 1, ...
gentime_dat_a <- incub$r(1e7) + onset_to_inf_r_a(1e7)
range(gentime_dat_a)

## [1] 1 34

gentime_freq_a <- sapply(
  seq(0, max(gentime_dat_a), by = 1L),
  function(i) sum(i == gentime_dat_a)
)
gentime_pmf_a <- gentime_freq_a
gentime_pmf_a <- gentime_pmf_a / sum(gentime_pmf_a) # superfluous

## emulate density function
gentime_d_a <- function(x, log = FALSE) {
  ## make sure we don't get out of bounds
  x <- as.integer(x)
  max_x <- max(gentime_dat_a)
  x[x < 0] <- 0
  x[x > max_x] <- 0
  out <- gentime_pmf_a[x+1]
  if (log) {
    out <- log(out)
  }
  out
}

## emulate rng function
gentime_r_a <- function(n) {
  sample(gentime_dat_a, size = n, replace = TRUE)
}

gentime_a <- list(d = gentime_d_a, r = gentime_r_a)
```

```

gt_dat_a <- tibble(
  Day = 0:25,
  p = gentime_a$d(0:25)
)

## Summary stats of the GT - approach A
summary(gentime_dat_a)

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      1.000   5.000   6.000   6.137   7.000  34.000

gt_dat_a %>%
  ggplot(aes(x = Day, y = p)) +
  geom_col(fill = 2) +
  theme_bw() +
  labs(
    x = "Time from primary to secondary infection",
    y = "Probability"
  )

```

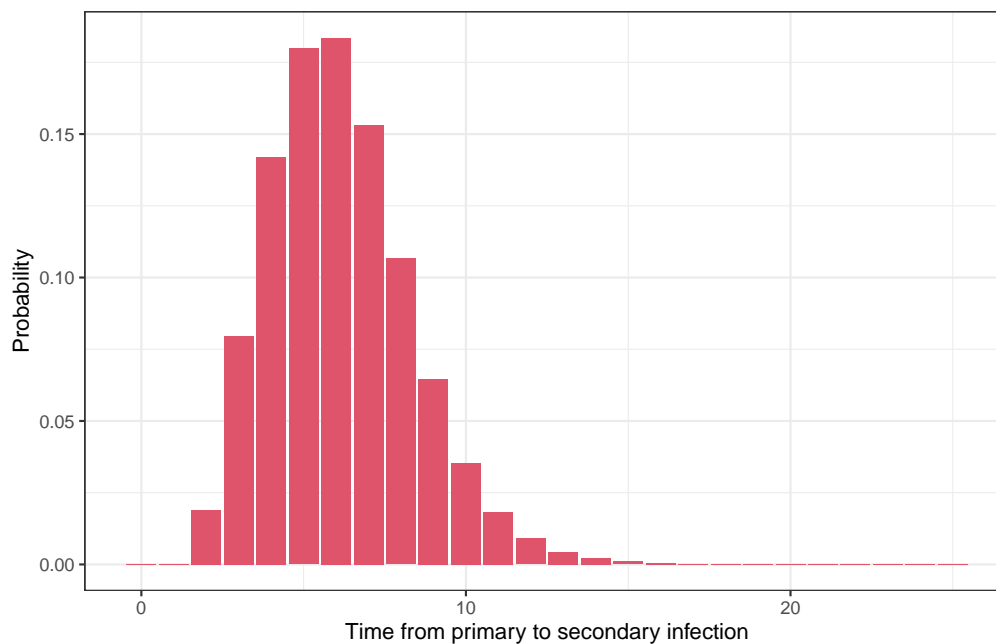


Figure 4: Generation time distribution of bubonic plague (drawing from discrete distributions)

Let's now try the alternative approach 'B':

```

## Continuous version of the incubation and infectious period distributions
incub_cont_r <- function(n) rlnorm(n,
                                   meanlog = log(3.5),
                                   sdlog = log(1.5)
                                   )

infec_cont_r <- function(n) rlnorm(n,
                                   meanlog = log(3),

```

```

sdlog = log(1.4)
)

## RNG for delay from onset to infection
onset_to_inf_r_b <- function(n) {
  runif(n, 0, infec_cont_r(n))
}

## PMF for delays of 0, 1, ...
gentime_dat_b <- floor(incub_cont_r(1e7) + onset_to_inf_r_b(1e7))
range(gentime_dat_b)

## [1] 0 30

gentime_freq_b <- sapply(
  seq(0, max(gentime_dat_b), by = 1L),
  function(i) sum(i == gentime_dat_b)
)
gentime_pmf_b <- gentime_freq_b
gentime_pmf_b[1] <- 0 # force  $p(0) = 0$ 
gentime_pmf_b <- gentime_pmf_b / sum(gentime_pmf_b) # superfluous

## emulate density function
gentime_d_b <- function(x, log = FALSE) {
  ## make sure we don't get out of bounds
  x <- as.integer(x)
  max_x <- max(gentime_dat_b)
  x[x < 0] <- 0
  x[x > max_x] <- 0
  out <- gentime_pmf_b[x+1]
  if (log) {
    out <- log(out)
  }
  out
}

## emulate rng function
gentime_r_b <- function(n) {
  sample(gentime_dat_b, size = n, replace = TRUE)
}

gentime_b <- list(d = gentime_d_b, r = gentime_r_b)

gt_dat_b <- tibble(
  Day = 0:25,
  p = gentime_b$d(0:25)
)

gt_dat_b %>%
  ggplot(aes(x = Day, y = p)) +
  geom_col(fill = 4) +
  theme_bw() +
  labs(
    x = "Time from primary to secondary infection",

```



```
y = "Probability"
)
```

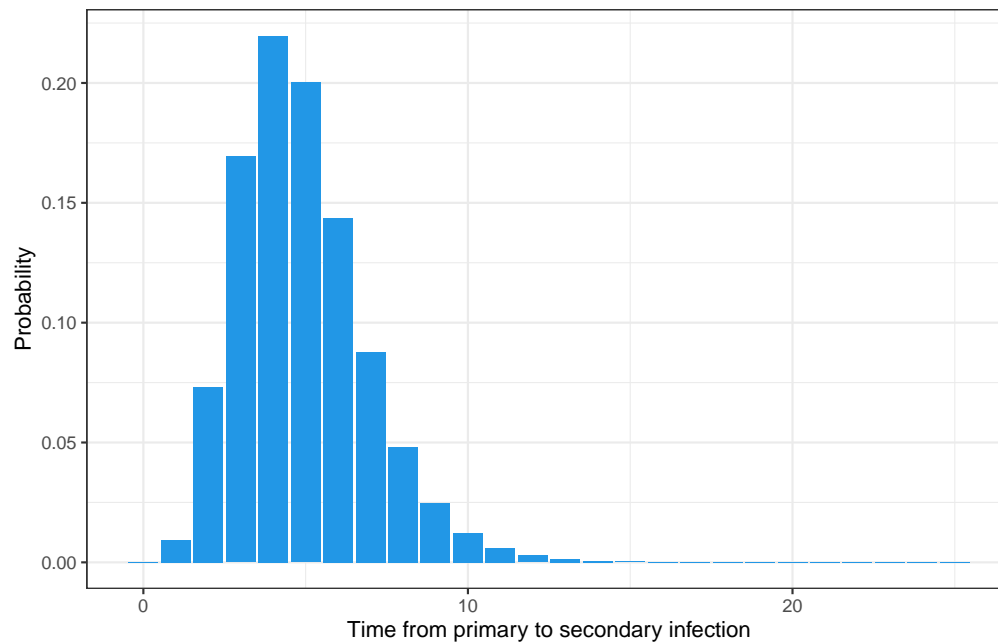


Figure 5: Generation time distribution of bubonic plague (drawing from continuous distributions

```
## Summary stats of the GT - approach B
summary(gentime_dat_b)
```

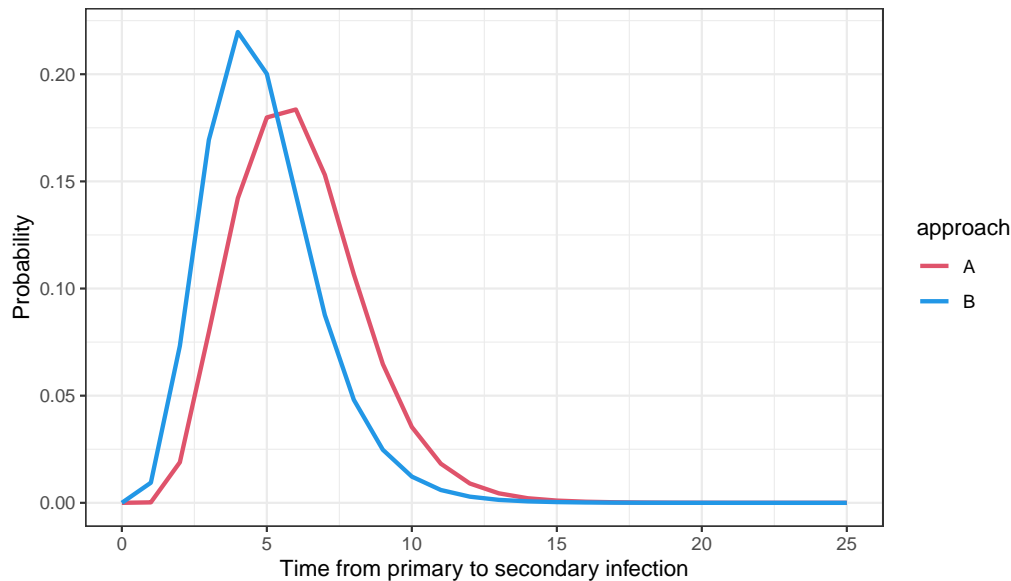
```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.000   3.000   5.000   4.889   6.000   30.000
```

Comparison of the two approaches:

```
gentime_dat_comp <- bind_rows(
  cbind(gt_dat_a, approach = "A"),
  cbind(gt_dat_b, approach = "B")
)
gentime_dat_comp %>%
  ggplot(aes(x = Day, y = p, color = approach)) +
  geom_line(linewidth = 1) +
  scale_color_manual(values = c(A = 2, B = 4)) +
  theme_bw() +
  labs(
    x = "Time from primary to secondary infection",
    y = "Probability",
    title = "Generation time distribution - bubonic plague",
    subtitle = "Comparing approaches"
  )
```

Generation time distribution – bubonic plague

Comparing approaches



```
## stats of the two distributions
```

```
summary(gentime_dat_a)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      1.000   5.000   6.000   6.137   7.000  34.000
```

```
summary(gentime_dat_b)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      0.000   3.000   5.000   4.889   6.000  30.000
```

```
## differences in infectious periods discretized/continuous
```

```
summary(infec$r(1e6)) # discrete
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      1.000   3.000   4.000   3.675   4.000  16.000
```

```
summary(infec_cont_r(1e6)) # continuous
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##      0.5684  2.3920  2.9988  3.1750  3.7643 15.9895
```

We choose the 2nd approach:

```
gentime <- gentime_b
gentime_mean <- mean(gentime$r(1e7))
gentime_mean
```

```
## [1] 4.889306
```

```
gentime_sd <- sd(gentime$r(1e7))
gentime_sd
```

```
## [1] 1.978936
```

5.3.2 Priors

We use a prior for R derived from [8] as a lognormal distribution with mean 1.6 and standard deviation 1.3:

```
prior_R <- function(x, log = FALSE) dlnorm(x, log(1.6), log(1.3), log = log)
prior_R_dat <- tibble(
  x = seq(0, 3, length.out = 1000),
  d = prior_R(seq(0, 3, length.out = 1000))
)

ggplot(prior_R_dat, aes(x = x, y = d)) +
  geom_line() +
  theme_bw() +
  labs(
    x = "R0",
    y = "Density"
  )
)
```

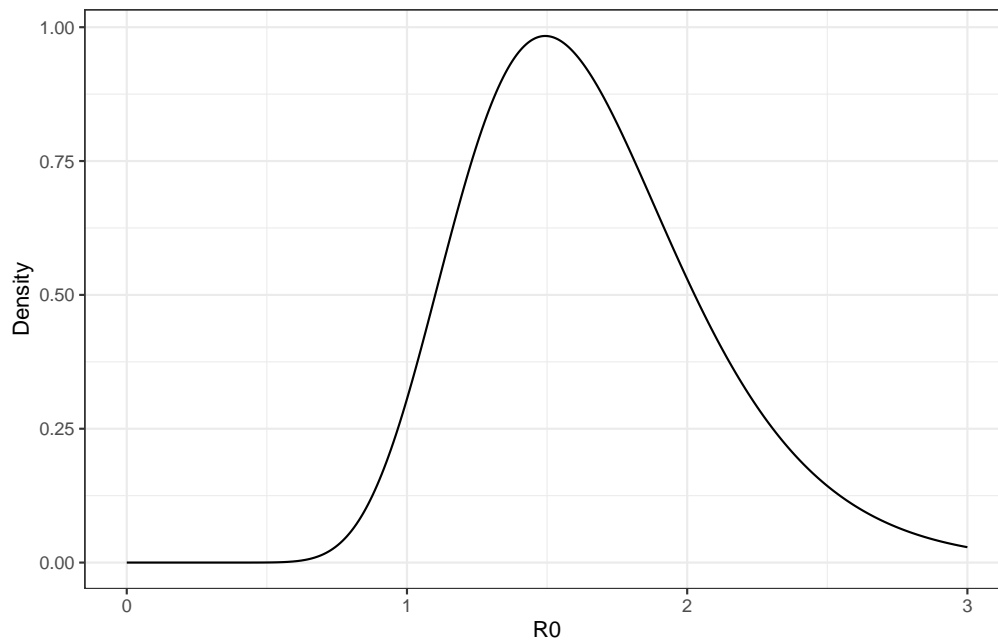


Figure 6: Prior for R0

Rates of zoonotic introductions are usually harder to estimate, so we use a flat, uninformative priors for λ_z , uniformly distributed from 0 to 10:

```
prior_zoo <- function(x, log = FALSE) dunif(x, 0, 10, log = log)

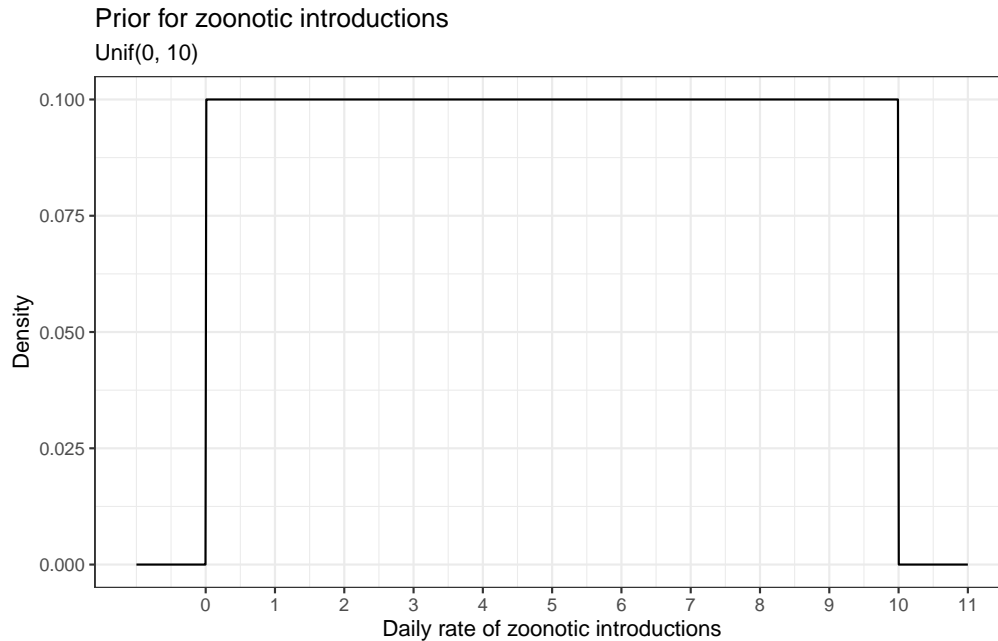
prior_zoo_dat <- tibble(
  x = seq(-1, 11, length.out = 1000),
  d = prior_zoo(seq(-1, 11, length.out = 1000))
)

ggplot(prior_zoo_dat, aes(x = x, y = d)) +
  geom_line() +
  theme_bw() +
  labs(
    x = "Daily rate of zoonotic introductions",
    y = "Density",
    title = "Prior for zoonotic introductions",
  )
)
```

```

  subtitle = "Unif(0, 10)"
) +
scale_x_continuous(breaks = 0:11)

```



5.4 Implementation

The following code implements the model. Since Corrégac and La Canourgue had vastly different populations (respectively 111 and 1370 inhabitants), we restrict the analysis of the early stage of the outbreak to Corrégac. Note that for such a small population, accounting for the depletion of susceptibles is a key feature of our model.

```

## Function to generate augmented data
## This will return a list with all the data needed for likelihood calculation.
## Note that dates of deaths are converted to integers, with 0 the earliest death.

```

```

make_aug_data <- function(date_death,
                           r_incub = incub$r,
                           r_infec = infec$r
                           ) {
  if (any(is.na(date_death))) {
    msg <- "Some dates of death are missing"
    stop(msg)
  }
  n <- length(date_death)
  date_death <- as.integer(date_death - min(date_death))
  date_onset <- date_death - r_infec(n)
  date_infection <- date_onset - r_incub(n)
  out <- data.frame(
    infection = date_infection,
    onset = date_onset,
    death = date_death
  )
}

```

```

## Use this to have 0 as the earliest date; otherwise we do get some negative
## dates:
## data.frame(lapply(a, function(x) x - min(a)))
out
}

## Function to move augmented data
## 'x' is a data.frame as output but make_aug_data()
## 'p' is the proportion of data to move
move_aug_data <- function(x, p = 0.1,
                          r_incub = incub$r,
                          r_infec = infec$r) {
  n <- nrow(x)
  to_move <- sample(c(TRUE, FALSE), n, prob = c(p, 1 - p), replace = TRUE)
  n_to_move <- sum(to_move)

  x[to_move, ]$onset <- x[to_move, ]$death - r_infec(n_to_move)
  x[to_move, ]$infection <- x[to_move, ]$onset - r_incub(n_to_move)
  x
}

## Function to calculate the log-likelihood
##
## @param data: a data.frame with 3 columns as returned by make_aug_data()
## @param params: a list with two items: zoo, and R, in this order
## @param d_incub: a PMF function for the incubation period
## @param d_infec: a PMF function for the infectious period
## @param d_gentime: a PMF function for the generation time

compute_loglike <- function(data,
                             params,
                             d_incub = incub$d,
                             d_infec = infec$d,
                             d_gentime = gentime$d,
                             pop_size = 111) {

  ### There are 3 components to the likelihood: ^
  ###
  ### 1. delay from onset to death (infectious period)
  ### 2. delay from infection to onset (incubation time)
  ### 3. incidence of infections from Hawkes process

  ### Component 1
  p_1 <- sum(d_infec(data$death - data$onset, log = TRUE))

  ### Component 2
  p_2 <- sum(d_incub(data$onset - data$infection, log = TRUE))

  ### Component 3

```

```

first_day <- min(data$infection)
last_day <- max(data$infection)

#### calculate incidence for the whole time period, do no miss the zeros
incid <- sapply(
  seq(first_day, last_day, by = 1),
  function(i) sum(data$infection == i)
)

#### calculate the corresponding number of susceptibles over time
total_inf <- cumsum(incid)
if (any(total_inf > pop_size)) stop("total infected > pop_size")
total_sus <- pop_size - total_inf
p_sus <- total_sus / pop_size

#### get relative FOIs - check that w indeed start at 1 in EpiEstim
lambdas_p2p <- EpiEstim::overall_infectivity(incid, d_gentime(0:100))
lambdas <- params$zoo + (lambdas_p2p * params$R * p_sus)

#### we omit the first entry as it is by definition NA
p_3 <- sum(na.omit(dpois(incid, lambdas, log = TRUE)))

p_1 + p_2 + p_3
}

## Function to calculate log-priors
compute_priors <- function(params,
  d_zoo = prior_zoo,
  d_R = prior_R) {
  d_zoo(params$zoo, log = TRUE) + d_R(params$R, log = TRUE)
}

## Compute log-posterior
compute_post <- function(data,
  params,
  d_incub = incub$d,
  d_infec = infec$d,
  d_gentime = gentime$d,
  d_zoo = prior_zoo,
  d_R = prior_R,
  pop_size = 111
) {
  compute_loglike(data, params, d_incub, d_infec, d_gentime, pop_size) +
  compute_priors(params, d_zoo, d_R)
}

## Function implementing the whole MCMC procedure

## @param n_iter the number of iterations of the MCMC; defaults to 1000
## @param sd_zoo the standard deviation of the normal proposal distribution for
##   the rate of zoonotic introductions
## @param sd_R the standard deviation of the normal proposal distribution for

```

```

## the effective reproduction number
## @param ini_zoo the initial value of the daily rate of zoonotic introduction
## @param ini_R the initial value of the effective reproduction number
## @param p_aug_data the proportion of augmented data moved at each step

estimate_params <- function(date_death,
                             n_iter = 1e3,
                             d_incub = incub$d,
                             d_infec = infec$d,
                             d_gentime = gentime$d,
                             d_zoo = prior_zoo,
                             d_R = prior_R,
                             r_incub = incub$r,
                             r_infec = infec$r,
                             sd_zoo = 0.1,
                             sd_R = 0.4,
                             p_aug_data = 0.1,
                             ini_zoo = runif(1, 0, 1),
                             ini_R = runif(1, 0, 3),
                             pop_size = 111) {

  ### Initialize MCMC
  params <- list(zoo = ini_zoo, R = ini_R)
  aug_data <- make_aug_data(date_death, r_incub, r_infec)
  ini_post <- compute_post(aug_data,
                           params,
                           d_incub,
                           d_infec,
                           d_gentime,
                           d_zoo,
                           d_R,
                           pop_size)

  new_params <- current_params <- params

  ### Build output structure
  mcmc <- list(
    step = seq_len(n_iter),
    post = double(n_iter),
    zoo = double(n_iter),
    R = double(n_iter)
  )
  accept_zoo <- 0
  accept_R <- 0
  accept_aug_data <- 0

  for (i in seq_len(n_iter)) {

    #### /// move augmented data
    #### calculate current log-post
    current_post <- compute_post(aug_data,
                                 current_params,
                                 d_incub,
                                 d_infec,

```

```

        d_gentime,
        d_zoo,
        d_R,
        pop_size)

#### propose new augmented data
new_aug_data <- move_aug_data(aug_data, p_aug_data)

new_post <- compute_post(new_aug_data,
                        current_params,
                        d_incub,
                        d_infec,
                        d_gentime,
                        d_zoo,
                        d_R,
                        pop_size)

#### accept/reject new augmented data
p_accept_aug_data <- exp(new_post - current_post)
if (runif(1) <= p_accept_aug_data) { # accept move
  aug_data <- new_aug_data
  current_post <- new_post
  accept_aug_data <- accept_aug_data + 1
}

#### // move daily rate of zoonotic introduction
#### propose new zoo
new_params$zoo <- current_params$zoo + rnorm(1, sd = sd_zoo)

#### accept/reject zoo
new_post <- compute_post(aug_data,
                        new_params,
                        d_incub,
                        d_infec,
                        d_gentime,
                        d_zoo,
                        d_R,
                        pop_size)
p_accept_zoo <- exp(new_post - current_post)
if (runif(1) <= p_accept_zoo) { # accept move
  current_params$zoo <- new_params$zoo
  current_post <- new_post
  accept_zoo <- accept_zoo + 1
} else { # reject move
  new_params$zoo <- current_params$zoo
}

#### // move R
#### propose new R
new_params$R <- current_params$R + rnorm(1, sd = sd_R)

#### accept/reject R

```



```

new_post <- compute_post(aug_data,
                        new_params,
                        d_incub,
                        d_infec,
                        d_gentime,
                        d_zoo,
                        d_R,
                        pop_size)
p_accept_R <- exp(new_post - current_post)
if (runif(1) <= p_accept_R) { # accept move
  current_params$R <- new_params$R
  current_post <- new_post
  accept_R <- accept_R + 1
} else { # reject move
  new_params$R <- current_params$R
}

### store info from this iteration
mcmc$post[i] <- current_post
mcmc$zoo[i] <- current_params$zoo
mcmc$R[i] <- current_params$R
}

list(
  mcmc = data.frame(mcmc),
  accept_zoo = accept_zoo / n_iter,
  accept_R = accept_R / n_iter,
  accept_aug_data = accept_aug_data / n_iter
)
}

```

We run the chains for a few iterations to check all runs smoothly:

```

system.time(res <- estimate_params(
  x_cor$date_of_death,
  pop_size = 111,
  n_iter = 30)
)

```

```

##      user  system elapsed
##    6.050    0.605    6.684

```

```
head(res)
```

```

## $mcmc
##   step      post      zoo      R
## 1     1 -437.4312 0.95761861 1.8981867
## 2     2 -433.6898 0.95761861 1.8981867
## 3     3 -402.6600 0.81251220 1.9054229
## 4     4 -402.6600 0.81251220 1.9054229
## 5     5 -401.3267 0.81251220 1.9054229
## 6     6 -396.4616 0.81251220 1.7387401
## 7     7 -380.8859 0.81251220 1.0591397

```

```
## 8      8 -360.3294 0.74502482 0.6118053
## 9      9 -351.5749 0.69850895 0.6118053
## 10     10 -345.4235 0.69850895 0.6117011
## 11     11 -314.7065 0.54353824 0.6117011
## 12     12 -314.7065 0.54353824 0.6117011
## 13     13 -300.5487 0.48791269 0.6117011
## 14     14 -300.3594 0.48791269 0.6117011
## 15     15 -300.3594 0.48791269 0.6117011
## 16     16 -300.3594 0.48791269 0.6117011
## 17     17 -300.3594 0.48791269 0.6117011
## 18     18 -272.7574 0.32358387 0.6117011
## 19     19 -272.7574 0.32358387 0.6117011
## 20     20 -259.4449 0.22742945 0.6228685
## 21     21 -254.2499 0.17980965 0.6228685
## 22     22 -254.4597 0.17882641 0.6228685
## 23     23 -254.4597 0.17882641 0.6228685
## 24     24 -250.8536 0.12999990 0.6228685
## 25     25 -248.5725 0.12999990 0.8067163
## 26     26 -246.9901 0.12999990 0.8350806
## 27     27 -245.1217 0.09728707 0.8350806
## 28     28 -245.5353 0.09728707 0.7445495
## 29     29 -245.5353 0.09728707 0.7445495
## 30     30 -245.0704 0.09728707 0.7445495
```

```
##
```

```
## $accept_zoo
```

```
## [1] 0.3666667
```

```
##
```

```
## $accept_R
```

```
## [1] 0.3
```

```
##
```

```
## $accept_aug_data
```

```
## [1] 0.4666667
```

```
tail(res)
```

```
## $mcmc
```

```
##      step      post      zoo      R
## 1      1 -437.4312 0.95761861 1.8981867
## 2      2 -433.6898 0.95761861 1.8981867
## 3      3 -402.6600 0.81251220 1.9054229
## 4      4 -402.6600 0.81251220 1.9054229
## 5      5 -401.3267 0.81251220 1.9054229
## 6      6 -396.4616 0.81251220 1.7387401
## 7      7 -380.8859 0.81251220 1.0591397
## 8      8 -360.3294 0.74502482 0.6118053
## 9      9 -351.5749 0.69850895 0.6118053
## 10     10 -345.4235 0.69850895 0.6117011
## 11     11 -314.7065 0.54353824 0.6117011
## 12     12 -314.7065 0.54353824 0.6117011
## 13     13 -300.5487 0.48791269 0.6117011
## 14     14 -300.3594 0.48791269 0.6117011
## 15     15 -300.3594 0.48791269 0.6117011
## 16     16 -300.3594 0.48791269 0.6117011
## 17     17 -300.3594 0.48791269 0.6117011
## 18     18 -272.7574 0.32358387 0.6117011
```

```
## 19 19 -272.7574 0.32358387 0.6117011
## 20 20 -259.4449 0.22742945 0.6228685
## 21 21 -254.2499 0.17980965 0.6228685
## 22 22 -254.4597 0.17882641 0.6228685
## 23 23 -254.4597 0.17882641 0.6228685
## 24 24 -250.8536 0.12999990 0.6228685
## 25 25 -248.5725 0.12999990 0.8067163
## 26 26 -246.9901 0.12999990 0.8350806
## 27 27 -245.1217 0.09728707 0.8350806
## 28 28 -245.5353 0.09728707 0.7445495
## 29 29 -245.5353 0.09728707 0.7445495
## 30 30 -245.0704 0.09728707 0.7445495
##
## $accept_zoo
## [1] 0.3666667
##
## $accept_R
## [1] 0.3
##
## $accept_aug_data
## [1] 0.4666667
```

5.5 Results for Corr  jac

Parameters are estimated for all cases from Corr  jac, using 12 separate chains run in parallel (works only on linux), with a burn-in of 100 iterations. For simplicity, chains have been saved in a separate RDS file.

```
# n_iter <- 2000

n_iter <- 1e4

library(parallel)
res <- mclapply(1:12, function(i)
  cbind.data.frame(
    estimate_params(
      x_cor$date_of_death,
      pop_size = 111,
      n_iter = n_iter),
    chain = i),
  mc.cores = 12
)
saveRDS(res, file = "res_1e4iter_12chains_correjac.rds")

res <- readRDS("res_1e4iter_12chains_correjac.rds")

## Some diagnostics
library(coda)
lapply(res, function(e) effectiveSize(mcmc(e))) %>%
  bind_rows()
```

```
## # A tibble: 12 x 8
##   mcmc.step mcmc.post mcmc.zoo mcmc.R accept_zoo accept_R accept_aug_data chain
##   <dbl>      <dbl>    <dbl> <dbl>    <dbl>    <dbl>        <dbl> <dbl>
## 1         0      111.    1266.  1867.         0         0           0     0
## 2         0      197.     486.  1429.         0         0           0     0
```

```
## 3      0      180.      395.  1820.      0      0      0      0
## 4      0      68.6     1379.  1587.      0      0      0      0
## 5      0      93.8     1265.  1925.      0      0      0      0
## 6      0      75.5     1336.  1709.      0      0      0      0
## 7      0     161.      1048.  1473.      0      0      0      0
## 8      0     151.      1334.  1820.      0      0      0      0
## 9      0     168.       479.  1770.      0      0      0      0
## 10     0     154.      1228.  1755.      0      0      0      0
## 11     0     281.       890.  1477.      0      0      0      0
## 12     0      78.4     1335.  1765.      0      0      0      0
```

```
## Putting chains together and thinning
## Given the reported ESS a thinning of 1/100 seems reasonable
to_keep <- seq(from = 1, to = n_iter, by = 100)
chains <- Reduce(rbind, lapply(1:length(res), function(i) res[[i]][to_keep, ]))
names(chains) <- gsub("mcmc.", "", names(chains))
chains$chain <- factor(chains$chain)
```

Figure of log-posterior traces:

```
## Plots
ggplot(chains) +
  geom_line(aes(x = step, y = post, color = chain), alpha = 0.5) +
  labs(x = "Iteration", y = "Log-posterior")
```

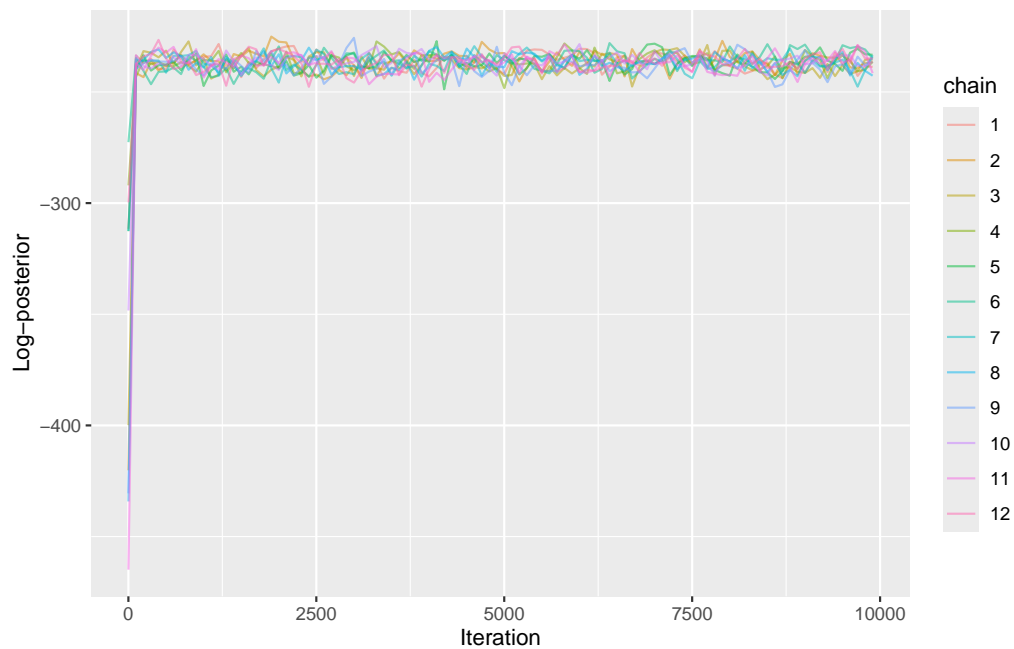
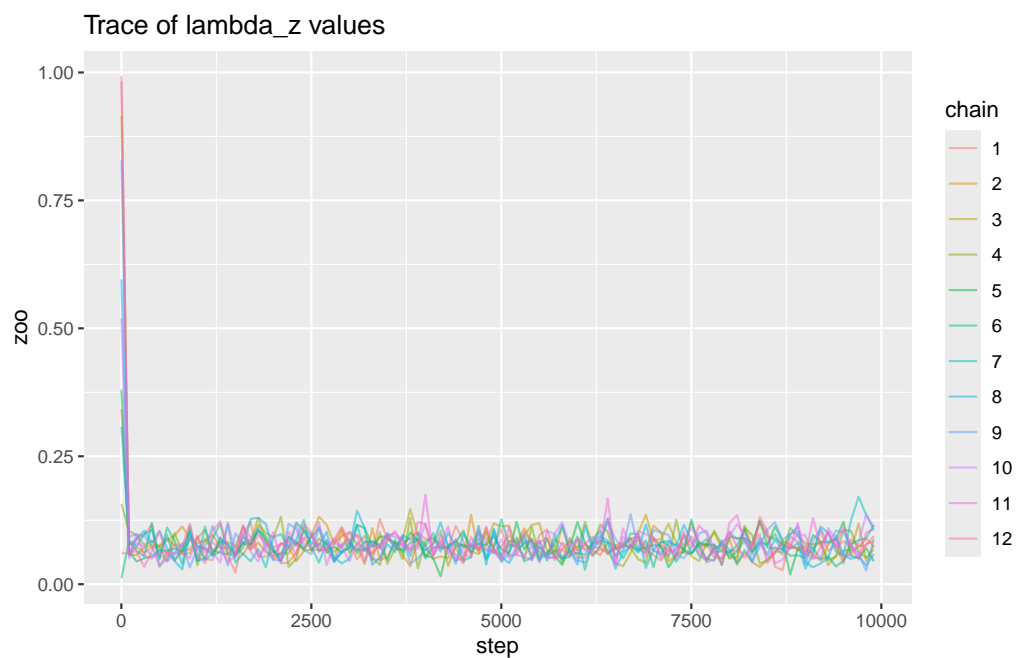


Figure 7: Log-posterior traces

```
## Plots
ggplot(chains) +
  geom_line(aes(x = step, y = R, color = chain), alpha = 0.5) +
  labs(title = "Trace of R values")
```



```
ggplot(chains) +
  geom_line(aes(x = step, y = zoo, color = chain), alpha = 0.5) +
  labs(title = "Trace of lambda_z values")
```

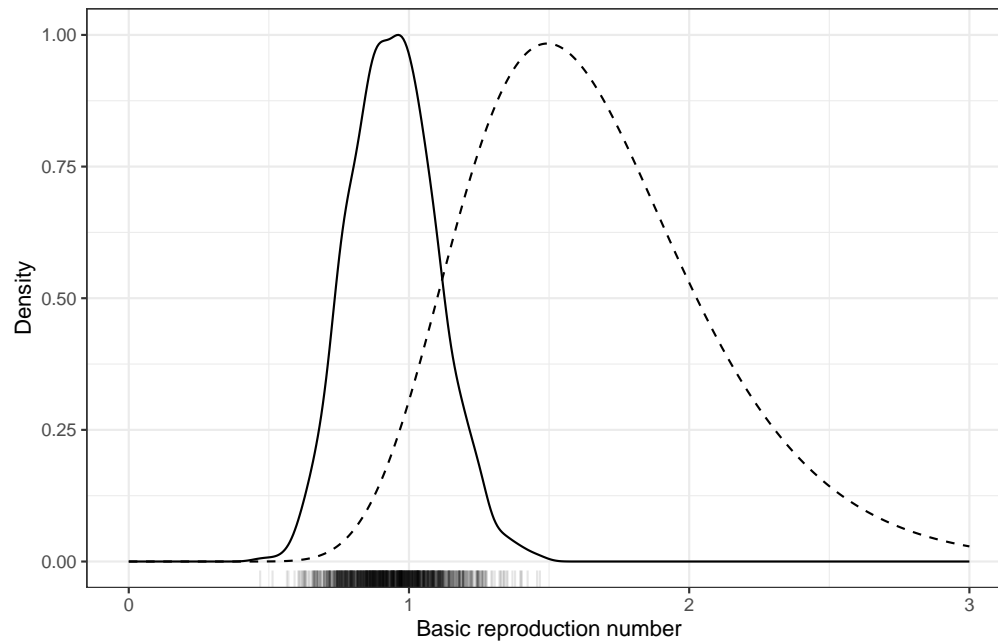


```
figure_4A <- chains %>%
  filter(step > 100) %>%
  ggplot(aes(x = R)) +
  stat_density(aes(y = after_stat(scaled)), geom = "line") +
  geom_rug(alpha = .1) +
  geom_line(data = prior_R_dat, aes(x = x, y = d), linetype = 2) +
  theme_bw() +
  labs(
```

```

  x = "Basic reproduction number",
  y = "Density"
)
figure_4A

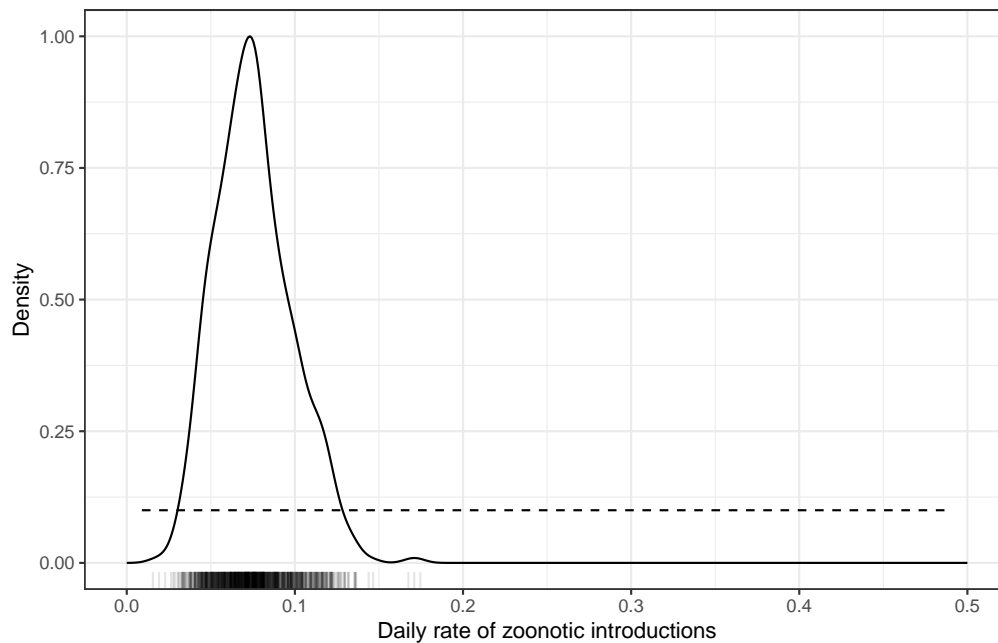
```



```

figure_4B <- chains %>%
  filter(step > 100) %>%
  ggplot(aes(x = zoo)) +
  stat_density(aes(y = after_stat(scaled)), geom = "line") +
  geom_rug(alpha = .1) +
  geom_line(data = prior_zoo_dat, aes(x = x, y = d), linetype = 2) +
  theme_bw() +
  labs(
    x = "Daily rate of zoonotic introductions",
    y = "Density"
  ) +
  xlim(0, 0.5)
figure_4B

```



We can report the mean, median and 95% CrI for each parameter:

```
chains_smry <- chains %>%
  filter(step > 100) %>%
  select(R, zoo) %>%
  lapply(function(x) data.frame(
    mean = mean(x),
    median = median(x),
    CrI_low = quantile(x, 0.025),
    CrI_up = quantile(x, 0.975)
  )) %>%
  bind_rows()

rownames(chains_smry) <- c("R", "Zoo")
chains_smry
```

```
##           mean    median   CrI_low  CrI_up
## R    0.94592595 0.9426328 0.66419015 1.259642
## Zoo 0.07569794 0.0738325 0.03734615 0.122518
```

We can also check acceptance rates:

```
chains %>%
  filter(step > 100) %>%
  select(accept_R, accept_zoo) %>%
  summarise_all(mean)
```

```
##   accept_R accept_zoo
## 1  0.40735  0.254025
```

We finally check the proportion of R_0 above 1:

```
p_R_above_1 <- chains %>%
  filter(step > 100) %>%
  summarise(mean(R > 1))
p_R_above_1
```

```
## mean(R > 1)
## 1 0.3577441
```

We calculate the respective overall daily force of infection from humans, and from zoonotic introductions:

```
n_cases <- nrow(x_cor)
n_days <- as.integer(diff(range(x_cor$date_of_death))) + gentime_mean
```

```
# average daily FOI from humans
foi_humans <- chains %>%
  filter(step > 100) %>%
  pull(R) * n_cases / n_days
```

```
summary(foi_humans)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.0788 0.1404 0.1584 0.1590 0.1763 0.2465
```

```
quantile(foi_humans, c(0.025, 0.975))
```

```
##      2.5%      97.5%
## 0.1116115 0.2116721
```

```
# average daily FOI from zoonotic infections
foi_zoo <- chains %>%
  filter(step > 100) %>%
  pull(zoo)
```

```
summary(foi_zoo)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.01553 0.05914 0.07383 0.07570 0.08963 0.17464
```

```
quantile(foi_zoo, c(0.025, 0.975))
```

```
##      2.5%      97.5%
## 0.03734615 0.12251802
```

```
# ratio
foi_total <- foi_humans + foi_zoo
prop_foi_humans <- foi_humans / foi_total
summary(prop_foi_humans)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.4172 0.6214 0.6834 0.6787 0.7394 0.9283
```

```
quantile(prop_foi_humans, c(0.025, 0.975))
```

```
##      2.5%      97.5%
## 0.5117801 0.8292291
```

```
source_colors <- c("Human to human" = "#548ecf",
  "Rodent to human" = "#aacf54")
```

```
figure_4C <- tibble(
  "Human to human" = foi_humans / foi_total,
  "Rodent to human" = foi_zoo / foi_total) %>%
  pivot_longer(1:2, values_to = "p", names_to = "source") %>%
  mutate("source" = factor(source, levels = c("Rodent to human", "Human to human"))) %>%
```



```

ggplot(aes(x = p, color = source)) +
  geom_density(aes(fill = source), alpha = 0.5) +
  geom_rug(alpha = .1) +
  theme_bw() +
  scale_fill_manual("", values = source_colors) +
  scale_color_manual("", values = source_colors) +
  labs(x = "Proportion of daily transmission",
       y = "Density") +
  scale_x_continuous(labels = scales::percent,
                     breaks = seq(0, 1, by = 0.1),
                     limits = c(0, 1.1)) +
  theme(legend.position = c(0.85, 0.75),
        legend.title = element_blank(),
        legend.background = element_rect(color = NA, fill = NA))

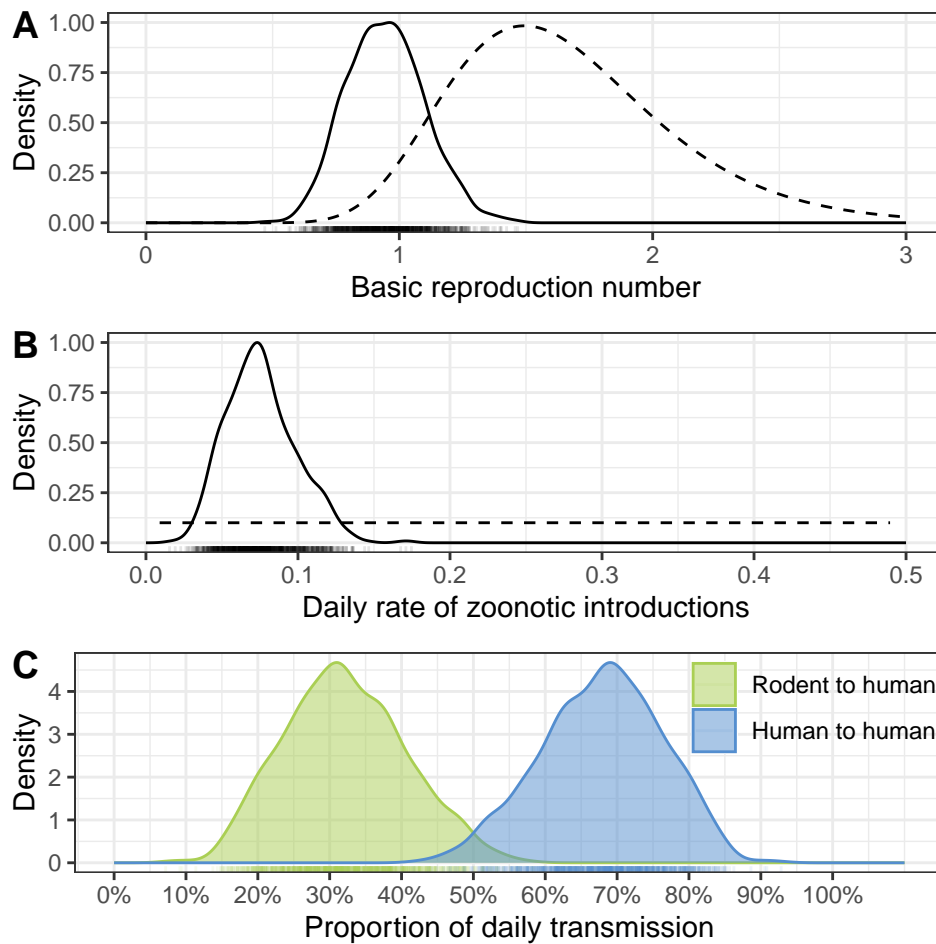
```

We make a joint figure for the paper:

```

library(cowplot)
plot_grid(figure_4A, figure_4B, figure_4C,
          nrow = 3, labels = c("A", "B", "C"))

```



Results suggest that:

- the data is informative on R_0 and λ_z , with posterior distributions well different from the priors

- the average value of estimated R_0 is 0.95 (95% CrI: 0.66 - 1.26), with only 0.36% of posterior values above 1, suggesting that person-to-person transmission only is unlikely to have sustained the epidemic
- the estimated rate of zoonotic introductions confirms that re-introduction played a substantial role in transmission, with a mean rate of introduction of 0.08 (95% CrI: 0.04 - 0.12), corresponding to an average of one introduction every 13.2 days
- overall, human-to-human transmission accounted for 68% of the total transmission (95% CrI: 51% - 83%)

5.6 Results on all data

As a sensitivity study, we re-run the same analyses but including all cases.

```
library(parallel)

res <- mclapply(1:12, function(i)
  cbind.data.frame(
    estimate_params(
      x$date_of_death,
      pop_size = 111,
      n_iter = n_iter),
    chain = i),
  mc.cores = 12
)
saveRDS(res, file = "res_1e4iter_12chains_all_cases.rds")

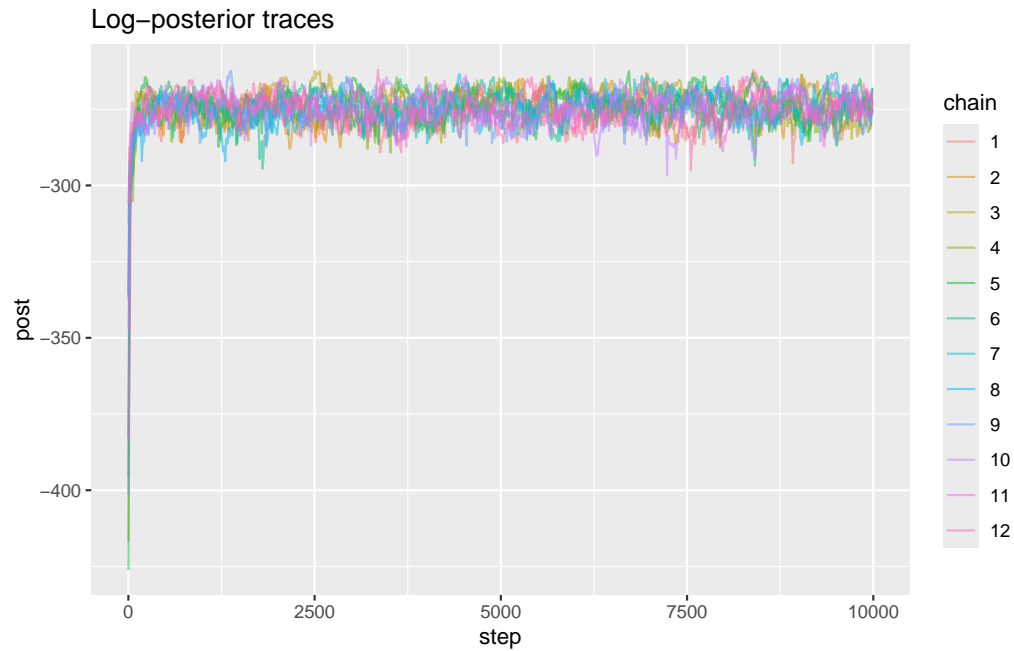
res <- readRDS("res_1e4iter_12chains_all_cases.rds")

## Some diagnostics
lapply(res, function(e) effectiveSize(mcmc(e))) %>%
  bind_rows()

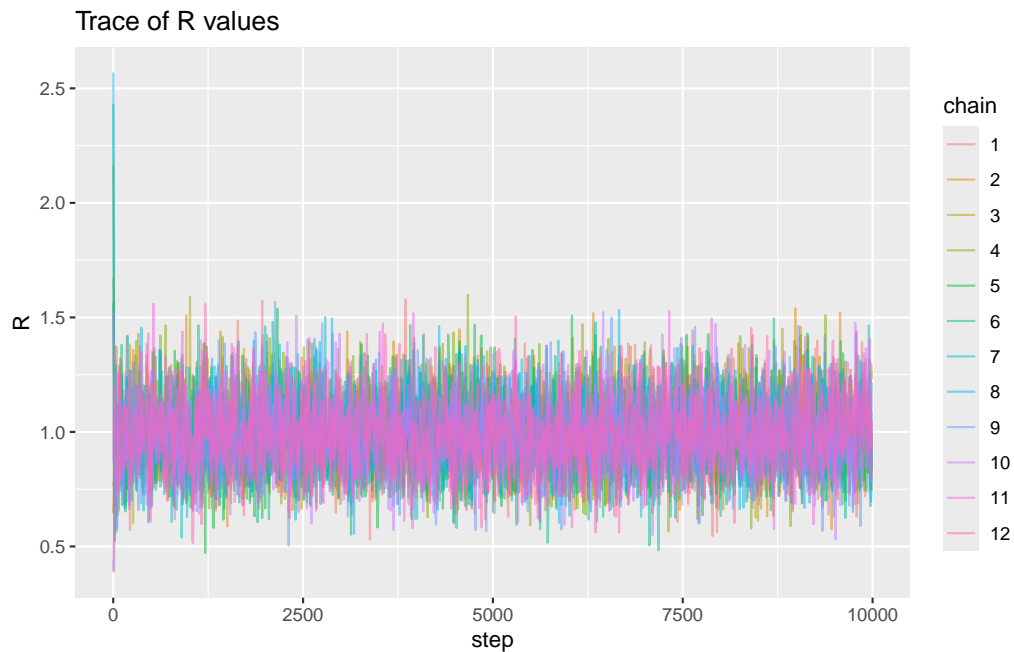
## # A tibble: 12 x 8
##   mcmc.step mcmc.post mcmc.zoo mcmc.R accept_zoo accept_R accept_aug_data chain
##   <dbl>      <dbl>    <dbl>  <dbl>    <dbl>    <dbl>        <dbl> <dbl>
## 1         0        68.3   1055.  1613.         0         0           0      0
## 2         0        94.5   1273.  1507.         0         0           0      0
## 3         0        71.1   1314.  1615.         0         0           0      0
## 4         0        91.3    960.  1307.         0         0           0      0
## 5         0       103.    757.  1515.         0         0           0      0
## 6         0        65.8  1284.  1627.         0         0           0      0
## 7         0       117.    890.  1493.         0         0           0      0
## 8         0        63.1   971.  1555.         0         0           0      0
## 9         0       112.    881.  1512.         0         0           0      0
## 10        0       73.7  1240.  1715.         0         0           0      0
## 11        0        68.7  1203.  1679.         0         0           0      0
## 12        0       115.   562.  1605.         0         0           0      0

## Putting chains together and thinning
## Given the reported ESS a thinning of 1/10 seems reasonable
to_keep <- seq(from = 1, to = n_iter, by = 10)
chains <- Reduce(rbind, lapply(1:length(res), function(i) res[[i]][to_keep, ]))
names(chains) <- gsub("mcmc.", "", names(chains))
chains$chain <- factor(chains$chain)
```

```
## Plots
ggplot(chains) +
  geom_line(aes(x = step, y = post, color = chain), alpha = 0.5) +
  labs(title = "Log-posterior traces")
```

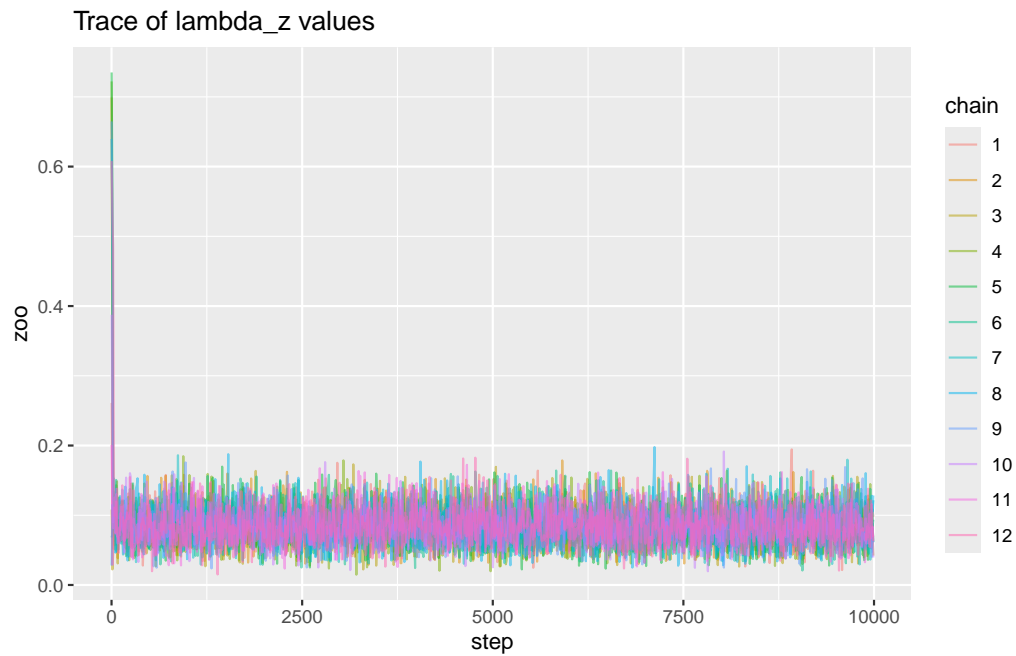


```
## Plots
ggplot(chains) +
  geom_line(aes(x = step, y = R, color = chain), alpha = 0.5) +
  labs(title = "Trace of R values")
```

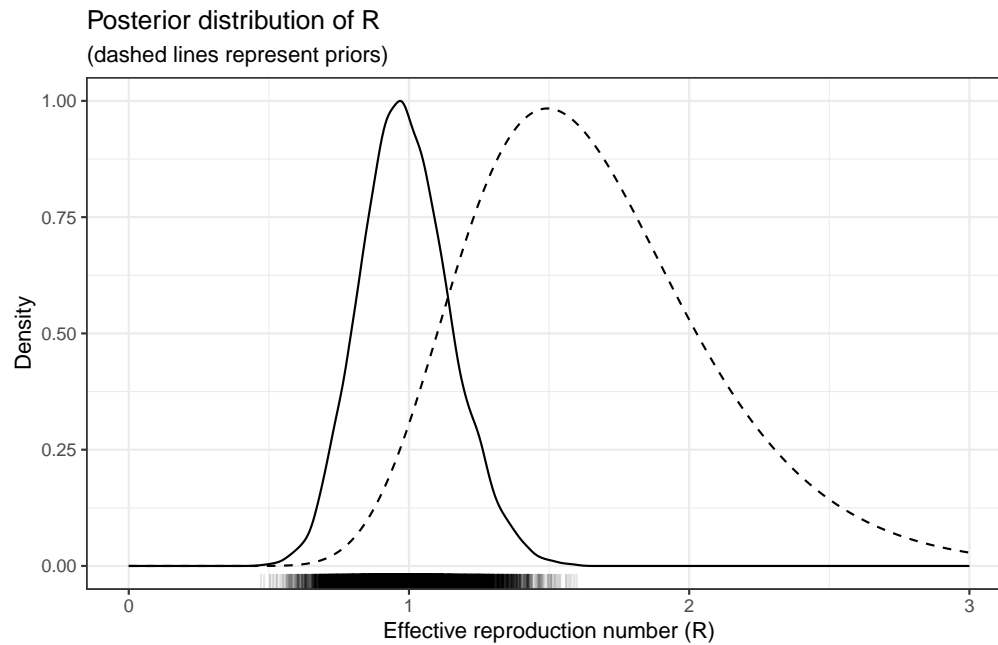


```
ggplot(chains) +
  geom_line(aes(x = step, y = zoo, color = chain), alpha = 0.5) +
```

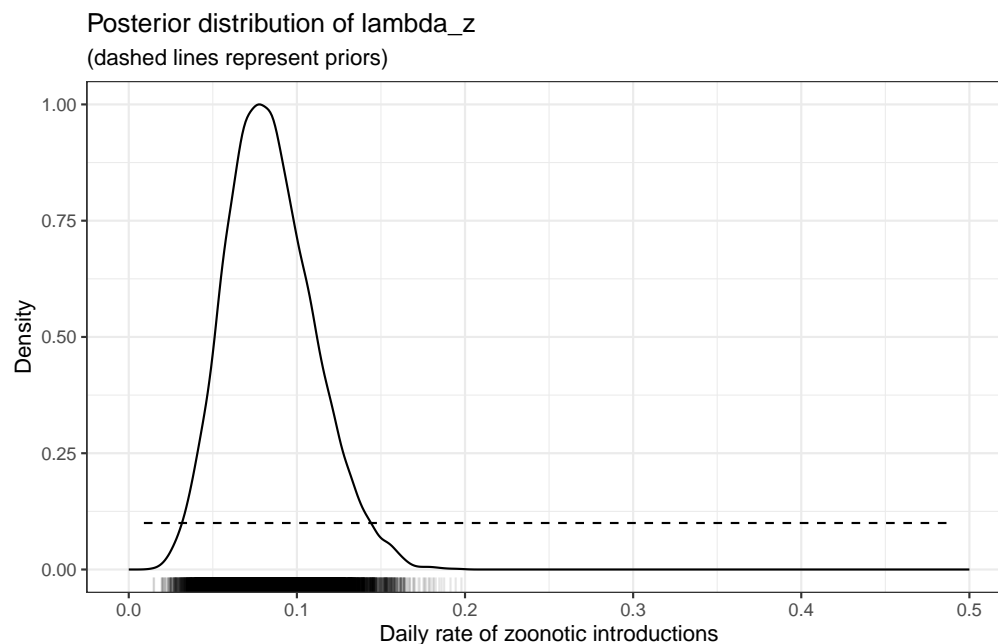
```
labs(title = "Trace of lambda_z values")
```



```
chains %>%
  filter(step > 100) %>%
  ggplot(aes(x = R)) +
  stat_density(aes(y = after_stat(scaled)), geom = "line") +
  geom_rug(alpha = .1) +
  geom_line(data = prior_R_dat, aes(x = x, y = d), linetype = 2) +
  theme_bw() +
  labs(
    x = "Effective reproduction number (R)",
    y = "Density",
    title = "Posterior distribution of R",
    subtitle = "(dashed lines represent priors)")
```



```
chains %>%
  filter(step > 100) %>%
  ggplot(aes(x = zoo)) +
  stat_density(aes(y = after_stat(scaled)), geom = "line") +
  geom_rug(alpha = .1) +
  geom_line(data = prior_zoo_dat, aes(x = x, y = d), linetype = 2) +
  theme_bw() +
  labs(
    x = "Daily rate of zoonotic introductions",
    y = "Density",
    title = "Posterior distribution of lambda_z",
    subtitle = "(dashed lines represent priors)" +
    xlim(0, 0.5)
```



We can report the mean, median and 95% CrI for each parameter:

```
chains_smry <- chains %>%
  filter(step > 100) %>%
  select(R, zoo) %>%
  lapply(function(x) data.frame(
    mean = mean(x),
    median = median(x),
    CrI_low = quantile(x, 0.025),
    CrI_up = quantile(x, 0.975))
  ) %>%
  bind_rows()

rownames(chains_smry) <- c("R", "Zoo")
chains_smry
```

```
##           mean      median   CrI_low   CrI_up
## R    0.989239 0.9811922 0.69661797 1.3265393
## Zoo 0.084418 0.08237575 0.03919699 0.1410418
```

We can also check acceptance rates:

```
chains %>%
  filter(step > 100) %>%
  select(accept_R, accept_zoo) %>%
  summarise_all(mean)
```

```
##      accept_R accept_zoo
## 1 0.4024417      0.2777
```

We finally check the proportion of R_0 above 1:

```
p_R_above_1 <- chains %>%
  filter(step > 100) %>%
  summarise(mean(R > 1))
p_R_above_1
```

```
##      mean(R > 1)
## 1      0.4531987
```

We calculate the respective overall daily force of infection from humans, and from zoonotic introductions:

```
n_cases <- nrow(x)
n_days <- as.integer(diff(range(x$date_of_death))) + gentime_mean

# average daily FOI from humans
foi_humans <- chains %>%
  filter(step > 100) %>%
  pull(R) * n_cases / n_days

summary(foi_humans)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.09589 0.17850 0.19938 0.20103 0.22213 0.32481
```

```
quantile(foi_humans, c(0.025, 0.975))
```

```
##           2.5%      97.5%
## 0.1415617 0.2695699
```

```

# average daily FOI from zoonotic infections
foi_zoo <- chains %>%
  filter(step > 100) %>%
  pull(zoo)

summary(foi_zoo)

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.01473 0.06586 0.08238 0.08442 0.10102 0.19787

quantile(foi_zoo, c(0.025, 0.975))

##      2.5%      97.5%
## 0.03919699 0.14104176

# ratio
foi_total <- foi_humans + foi_zoo
prop_foi_humans <- foi_humans / foi_total
summary(prop_foi_humans)

##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.3930 0.6500 0.7084 0.7046 0.7636 0.9356

quantile(prop_foi_humans, c(0.025, 0.975))

##      2.5%      97.5%
## 0.5339988 0.8565850

```

Results of the sensitivity analysis on all data:

- the average value of estimated R_0 using all cases is 0.99 (95% CrI: 0.7 - 1.33), with 0.45% of posterior values above 1
- the mean rate of zoonotic introductions estimated on all data was 0.08 (95% CrI: 0.04 - 0.14), corresponding to an average of one introduction every 11.8 days
- overall, human-to-human transmission accounted for 70% of the total transmission (95% CrI: 53% - 86%)

6 Conclusions

The statistical analysis of historical data suggests the established scenario of how the Plague epidemic in Gévaudan started may not be accurate. In short:

- It is rather unlikely that an individual would have travel with an infected wood bundle without getting infected the entire trip, to then infect a new person overnight.
- The delays between Jean Quintin's infection and his son's death are not compatible with direct transmission.
- Epidemic modelling suggests that person-to-person transmission was insufficient to sustain the epidemic, and that zoonotic transmission, while low, indeed played a role in the epidemic.

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