# Estimation of the effective reproduction number in Madagascar

Our objective is to determine the spread of the coronavirus disease (Covid-19) from the number of daily infected cases. We use a model which considers the randomness of infections as a renewal process, in close connection to the Model 2 used in [2].

## 1/ The reproduction number

Let I(t-k) be the number of daily infected people at time t-k, (t-k < t, t: date, k: duration), then we can assume that a fraction of the same people at time t-k, of size I(t-k)f(t,k),  $(0 \le f(t,k) \le 1)$ , will transmit the virus to some individuals at time t. When we consider all cases before the time t (i.e. for all  $k \in [1,t-1]$ ,

then  $Iinf(t) = \sum_{k=1}^{t-1} I(t-k)f(t,k)$  will be the number of all people who contaminated those infected at time t.

For this setting, we can define the effective reproduction number Rt = R(t) at time t [2] by:

$$R(t) = \frac{I(t)}{I_{inf}(t)} \tag{1}$$

Therefore Rt is the average number of newly infected people at time t and contaminated by one person.

#### Remarks:

For R(t) > 1, the number of infection is fastly growing.

The coefficient f(t,k) is related to the infectiousness profile and is only estimated; in some models [2, 4, 5], this term depends only on the duration k and not explictly on the time t. It implies that the fraction of those who have transmitted the virus is completely determined when the duration k is known.

Because of the limitations to detect all chains of transmission among the infected population, the way of estimating f(t,k) is by means of data about the serial interval, i.e. the time between the symptom onsets for the infected and his or her transmitter. From such data, one can deduce the serial interval distribution w(k) of the duration k between symptom onsets. Then, one sets: f(t,k) = w(k).

## 2/ Our model

For models based on the renewal process [8, 7, 5, 4, 2], the purpose is not to compute Rt directly from the equality 1. Following the methods described further, we rather estimate:

- I(t): in our model, I(t) follows a Poisson distribution with mean equals to  $R(t)I_{inf}(t) = R(t)\sum_{k=1}^{t-1} I(t-k)w(k)$ . When R(t) and w(k) are known, then one can estimate I(t) using the Poisson distribution.
- Rt: We use Bayesian inference to estimate Rt which follows a Gamma distribution in the renewal process model. It is realistic to assume that Rt does not change considerably over a time period [t, t-k\*+1] for some k\* > 1. In this case, it is not difficult to show that the shape and the scale of the posterior Gamma distribution of Rt are respectively equal to  $(a + \sum_{k=1}^{t-1} I(t k))$  and  $(1/b + \sum_{s=t-k*+1}^{t-1} I_{inf}(s))$  where a and b are respectively the shape and the scale of the prior Gamma distribution of Rt. (See Methods).
- **w(k)**: In our model, the serial interval distribution w(k) is taken to follow a Gamma distribution with 6.48 days as mean and 3.83 days as standard deviation [2].
- 2/ Estimation of R(t= 6/06/20): See Figure 1. Each boxplot gives the minimum and maximum values, the 1st (25%), 2nd (median) and 3rd (75%) quartiles of the posterior Gamma distribution of Rt. For the numerical values, we give the mean, the 25% and 75% quartiles.

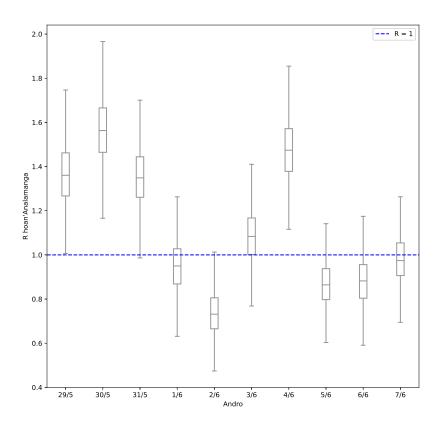
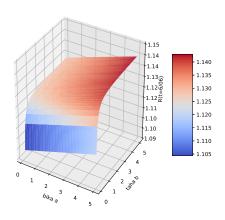


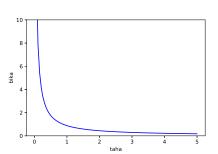
Figure 1: Data taken from 3/05/20 to 7/06/20. R(t=6/06)=0.88220 (75%-quartile: 0,95091; 25%-quartile: 0,80891) for a and b such that the prior and the posterior distribution of Rt are equal.

#### Discussions and limitations of the model:

1/ The estimation of Rt depends on the prior parameters a and b. For t = 6/06/20, this dependence is shown by the figure 2. The red region corresponds to values of Rt which does not change significantly with rapport to a and b. In the blue region, a and b are both usually less than 1, and Rt is lower than its values in the red region.

For example, R(t=6/06) = 0.78333 (75%-quartile: 0.84466; 25%-quartile: 0.71788) for a = b = 0.1. And R(t=6/06) = 0.94372 (75%-quartile: 1,01521; 25%-quartile: 0,86759) for a = b = 5.





rameters a and b.

Figure 2: Variation of R(t=6/06/20) according to pa- Figure 3: Curve of points (a,b) for which the prior and the posterior distributions of Rt are equal when t = 6/06/20.

- 2/ It is better to choose values for a and b such that the prior and the posterior distributions of Rt are equal. Indeed, both probabilities can be used to estimate Rt. In such cases, the values (a,b) which equalize the two distributions are situated on a particular curve in the space of possible parameter values.
- 3/ The time-windows [t,t-k\*-1] are chosen for a value of k\* such that 1) Rt is globally stable during the time period and 2) the posterior density probability Pr(daily infected = I(t),...,I(t-k\*-1)| Rt) given Rt is maximum so that the model fits closely to the data [4, 2].
- 5/ The estimation of Rt depends on the duration of the period associated to the collected data. This duration have to be taken into account when one computes the optimal duration k\*. In fact, it should be largely greater than k\*.
- 6/ The estimation of Rt depends on the the optimal value k\*. However, one can compare the estimated Rt with the one obtained directly from the equality 1.
- 7/ Because we have taken w(k) with mean equal to 6.5 days, i.e. because we admit that there are about 6.5 days between the symptom onsets for the infected and his or her transmitter, our model cannot give an estimation of Rt for the first 7 days of the outbreak.

## Weekly evaluation:

The numbers of daily infections, collected during a week W, can be analyzed so that one can estimate a global reproduction number associated to the week W. In our model, this weekly reproduction is chosen so that for each  $t \in W$ , the average value of I(t), given by the product  $R(t) \sum_{k=1}^{t-1} I(t-k)w(k)$ , is close to the obsered data.

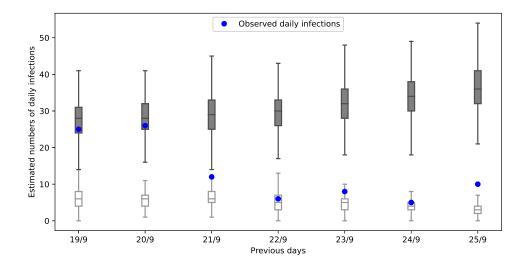


Figure 4: Week evaluation for the period of 19-25/09/20 in **Analamanga**. Transparent boxplots correspond to estimated average values of I(t) when the reproductive number is constantly equal to R(14/09) = 0.33014 (75%-kartily: 0.37450; 25%-kartily: 0.28034) during the period of 19-25/09/20.

Colored boxplots correspond to estimated average values of I(t) when the reproductive number is constantly equal to R(19/09) = 1,40746 (75%-kartily: 1,52539; 25%-kartily: 1,28102) during the period of 19-25/09/20.

#### 4/ Methods

A renewal process describes random events K1, K2,... which occur independently between different random time intervals, k1, k2, ... These events (eg. time intervals between consecutive infections) are independently and identically distributed probability distribution.

For a renewal process K1, K2,... following an exponential distribution with rate r, one can prove that:

- 1/ the random variable  $TK_i = \sum_{j=1}^{i} Kj$ , (i = 1,2,...), which gives the time of apparition of the event Ki (i
- = 1,2,...), follows a Gamma distribution with shape i and rate r;
- 2/ the random variable IK(k) which computes the number of all events K1, K2, ... happening before the time k, follows a Poisson distribution with mean rk.

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Pr.pdf(taha = r|antontan'isa = Ivao) = Gamma.pdf(r, a + I, 1/(1/b + w)).

Mahasedra, 27/09/2020.

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