

- Simulation et Monte Carlo, ENSAE 2019-2020

Dynamics of transmission of COVID-19

GHERMI Ridouane

SAMSON Marc-Antoine

SEKKAT Chloé



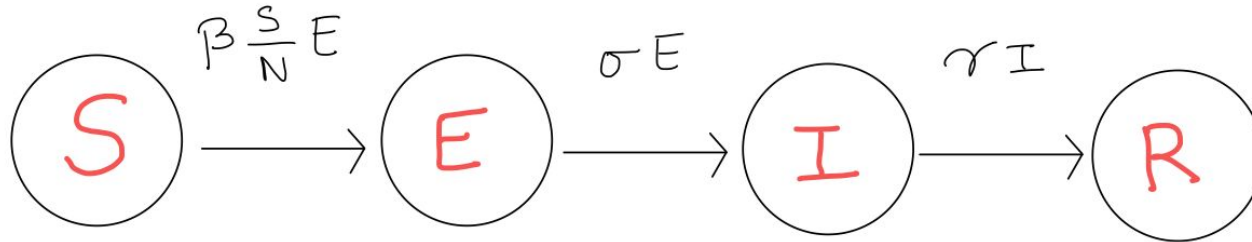
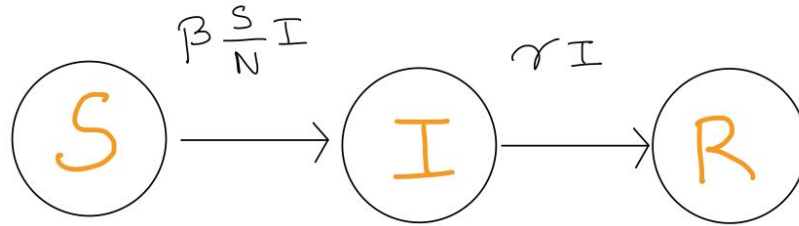
Quick introduction to compartmental models in epidemiology

Closed population:

$$N = S + I + R$$

or

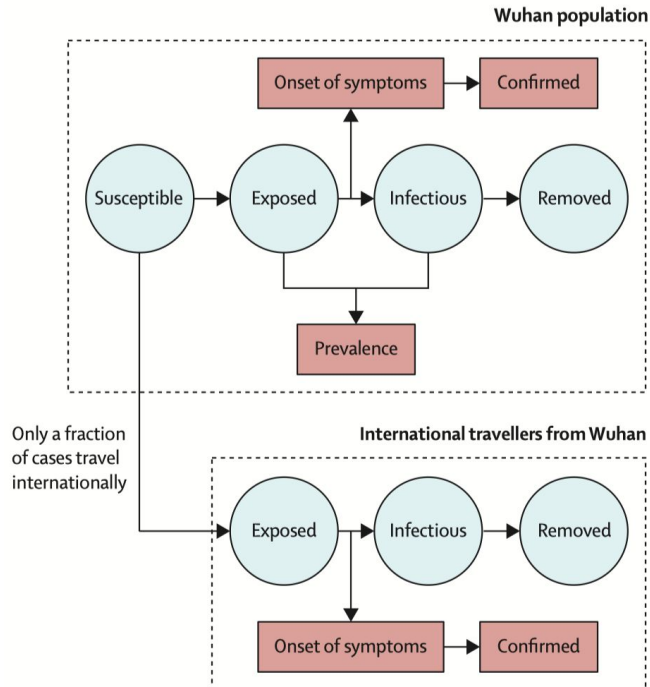
$$N = S + E + I + R$$





A mathematical modelling study in epidemiology

- An extended version of a SEIR model on Wuhan's population



$$S(t+1) = S(t) - \beta(t)S(t)[I_{1w}(t) + I_{2w}(t)] / N$$

$$E_{1w}(t+1) = E_{1w}(t) + (1-f)\beta(t)S(t)[I_{1w}(t) + I_{2w}(t)] / N - 2\sigma E_{1w}(t)$$

$$E_{2w}(t+1) = E_{2w}(t) + 2\sigma E_{1w}(t) - 2\sigma E_{2w}(t)$$

$$I_{1w}(t+1) = I_{1w}(t) + 2\sigma E_{2w}(t) - 2\gamma I_{1w}(t)$$

$$I_{2w}(t+1) = I_{2w}(t) + 2\gamma I_{1w}(t) - 2\gamma I_{2w}(t)$$

$$Q_w(t+1) = Q_w(t) + 2\sigma E_{2w}(t)e^{-\gamma\kappa} - \kappa Q_w(t)$$

$$D_w(t+1) = D_w(t) + 2\sigma E_{2w}(t)e^{-\gamma\kappa}$$

$$C_w(t+1) = C_w(t) + \kappa Q_w(t)$$

$$R_w(t+1) = R_w(t) + \gamma(I_{1w} + I_{2w})$$



Implementation of a deterministic model

Simulation up to 90 days (~3 months) with the following parameters (close to the paper ones):

$N = 11\,000\,000$

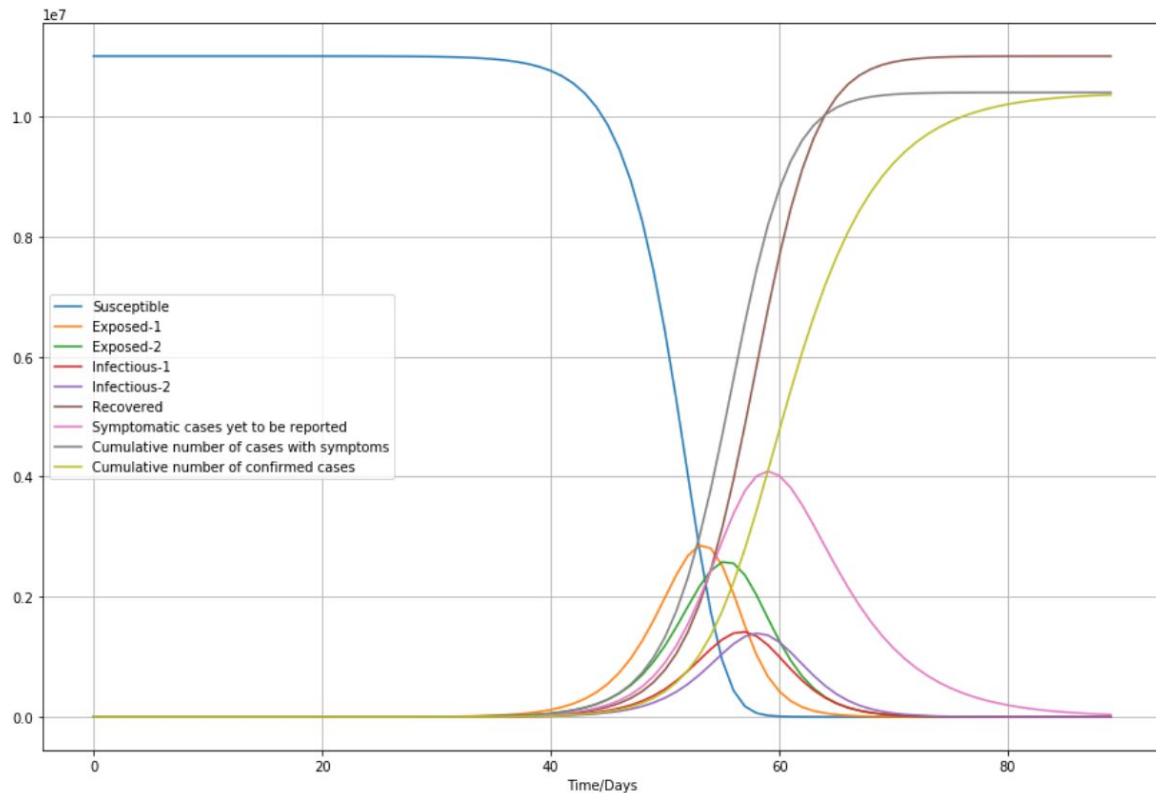
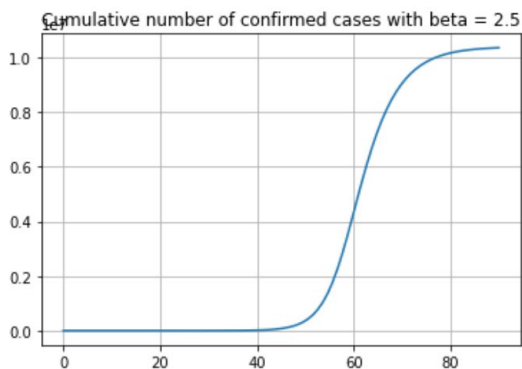
$\text{init_vals} = [N-1, 1, 0, 0, 0, 0, 0, 0, 0]$

$\beta = 2.5$

$\sigma = 1/5.2$

$\gamma = 1/2.9$

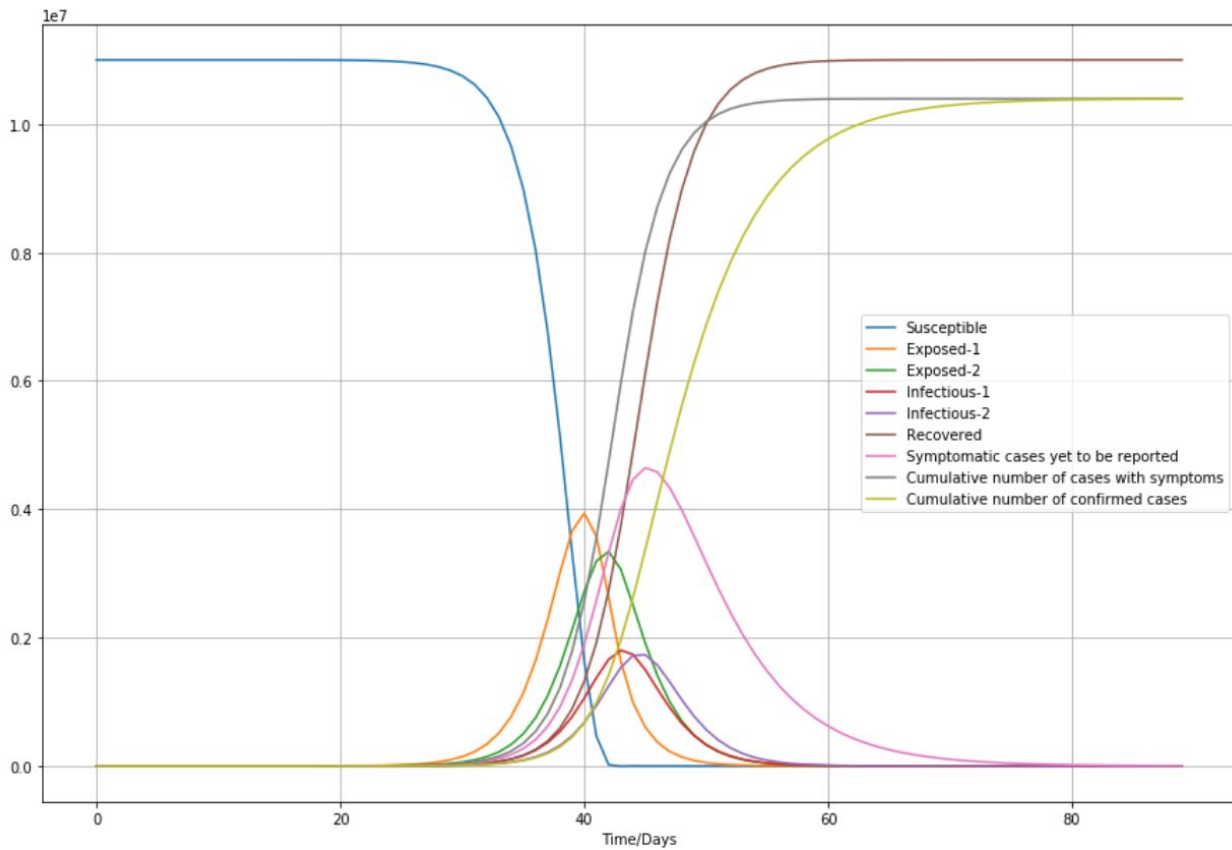
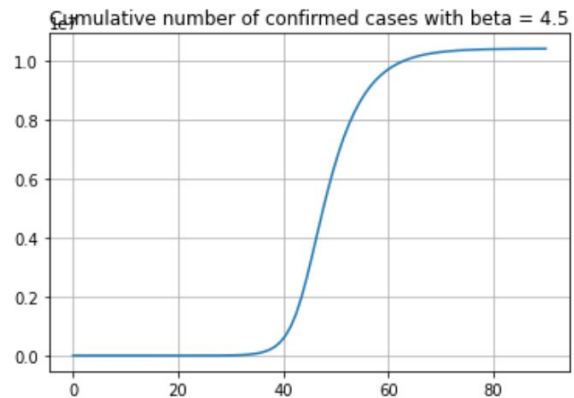
$\kappa = 1/6.1$





Implementation of a deterministic model

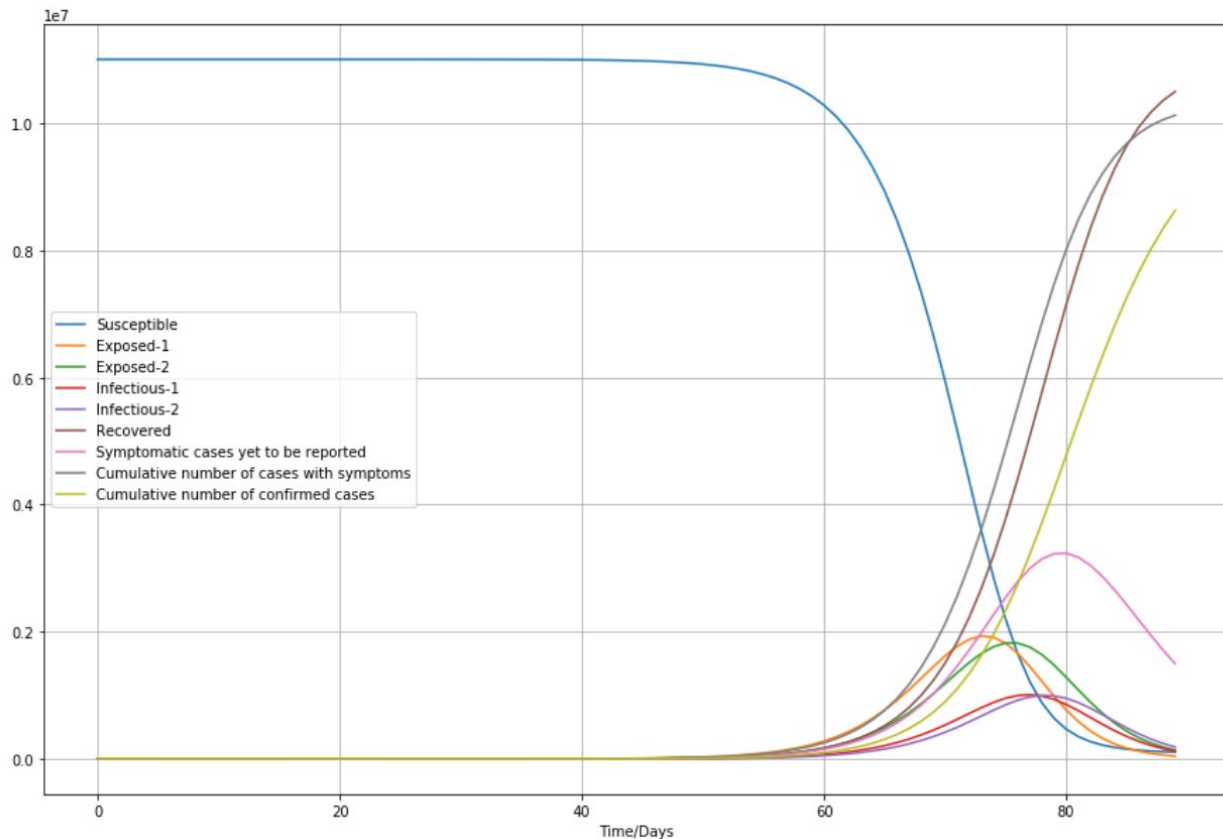
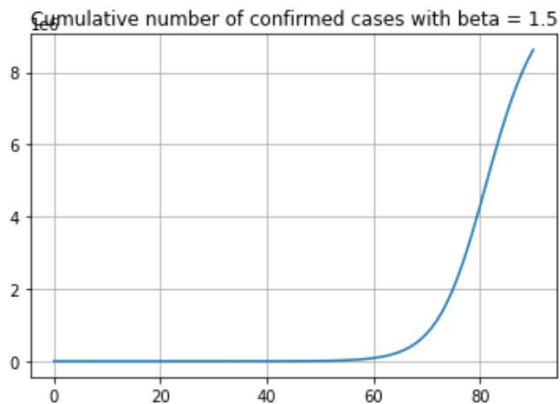
If we change beta to 4.5





Implementation of a deterministic model

If we change beta to 1.5

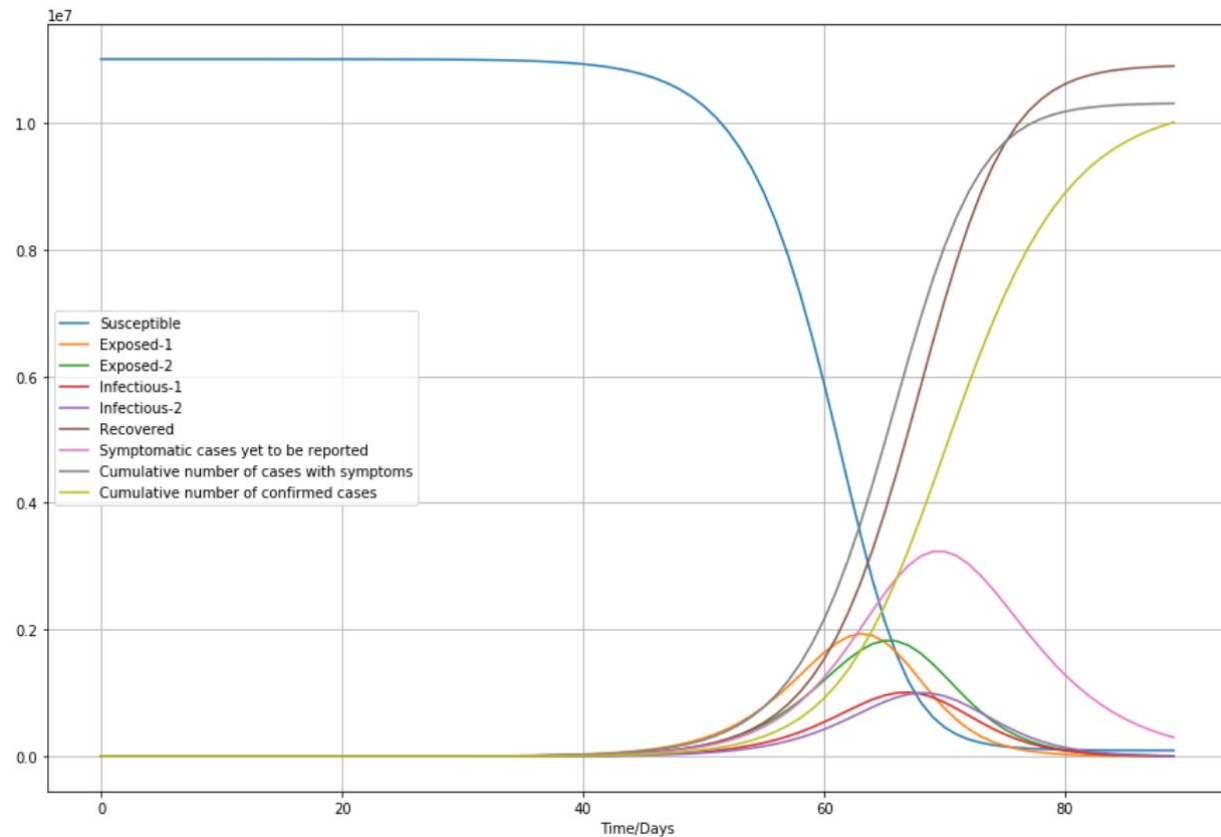
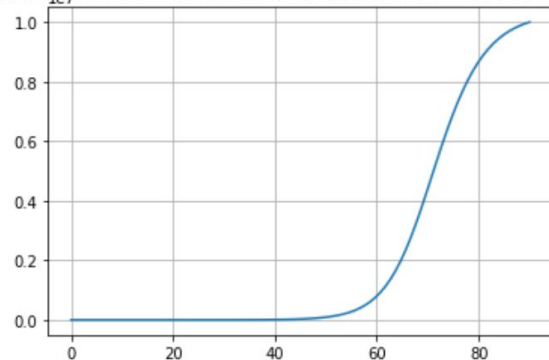




Implementation of a deterministic model

Back to $\beta = 2.5$ but the number of initial cases is now 10

Cumulative number of confirmed cases with $\beta = 2.5$ and $E_0 = 10$

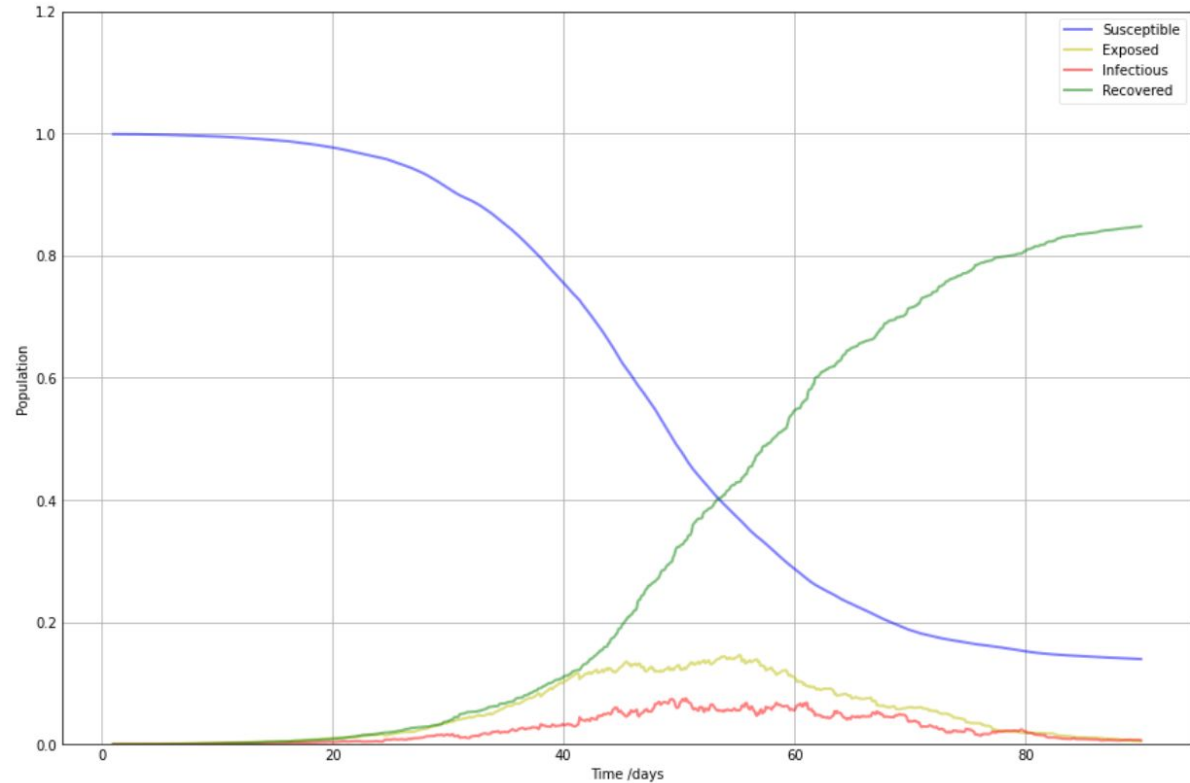


Stochastic implementation using Monte Carlo's methods



Stochastic modelling on SEIR

Here both sigma and gamma have exponential distribution





Stochastic modelling: transmission rate a Geometric Brownian Motion

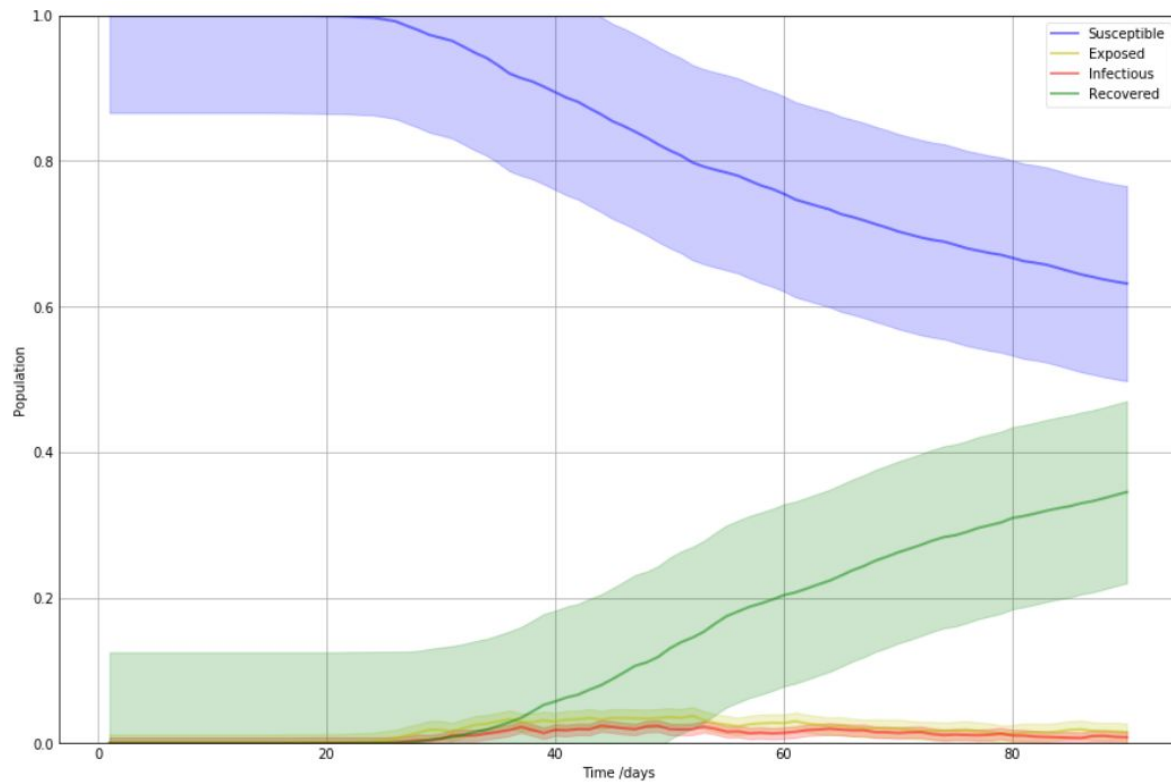
$$d \log(\beta(t)) = a dB_t$$

where a is the volatility of transmission over time and B_t is Brownian motion.

In the paper, they estimate $a = 0.395$

$$\beta(t+1) = \beta(t)e^X$$

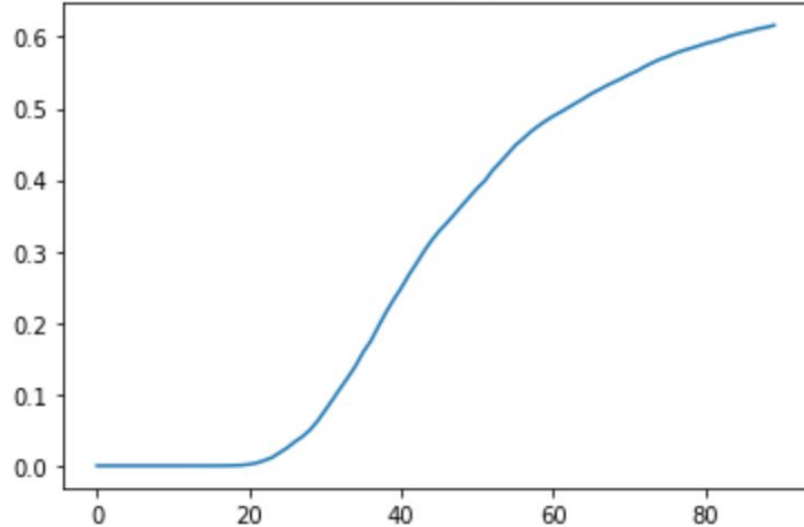
where $X \rightarrow N(0, a)$



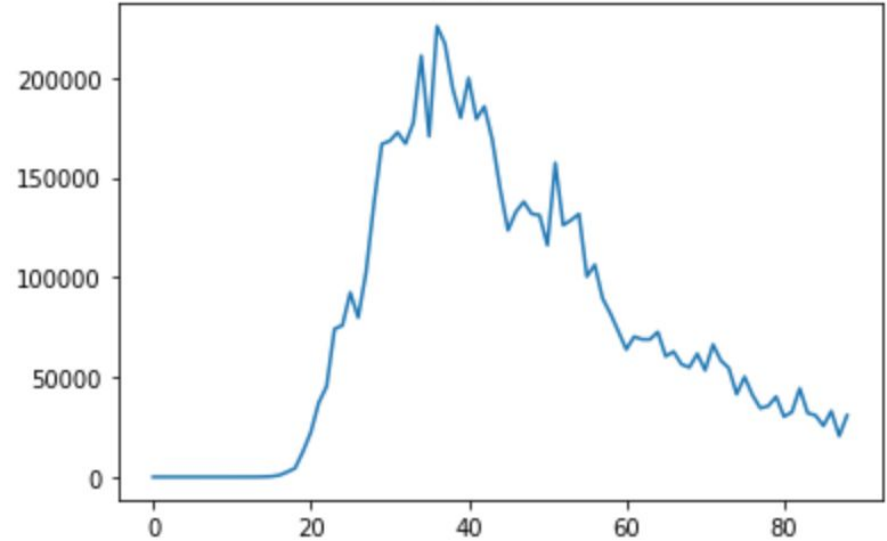


Stochastic modelling: simulation in order to estimate

Prevalence: Total number of symptomatic cases each day



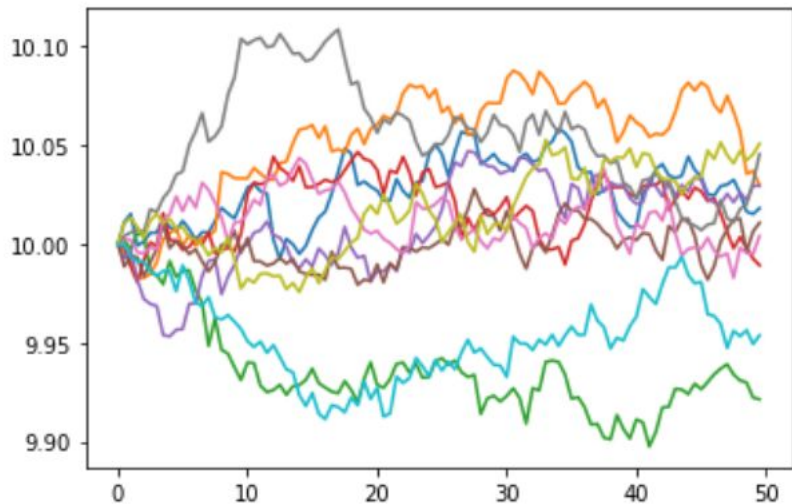
Incidence: Number of symptomatic new cases each day



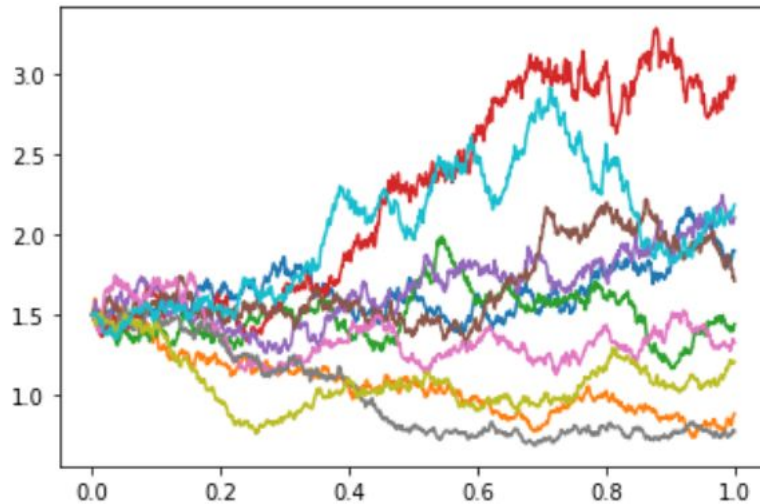


Stochastic modelling: Geometric Brownian Motion

First technique: using a random walk

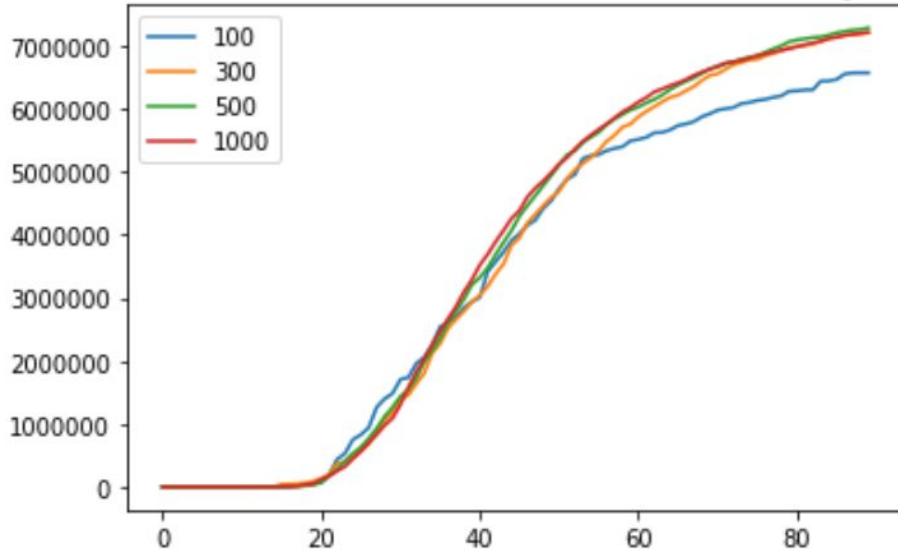


Second technique: RQMC with Sobol sequence

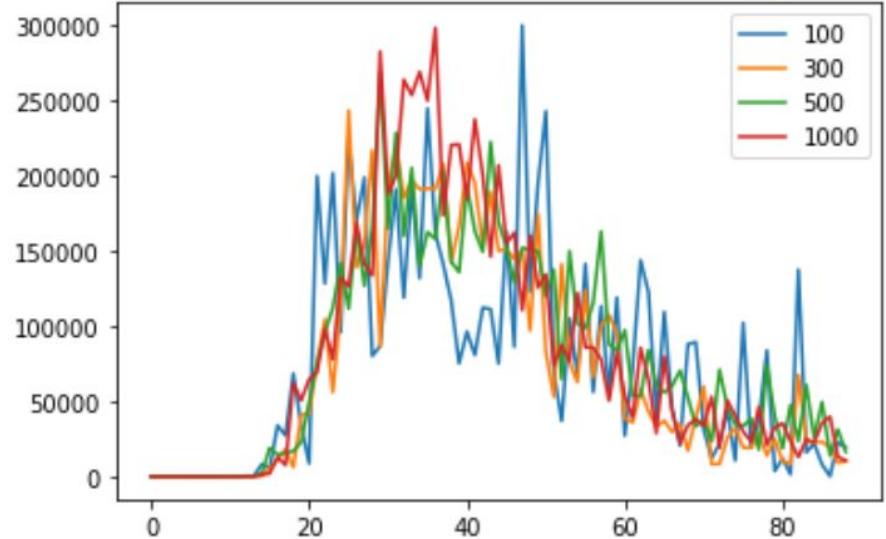


Stochastic modelling: RQMC has better convergence rate and smaller approximation error than MC

Cumulative number of confirmed cases each day



Number of new confirmed cases each day

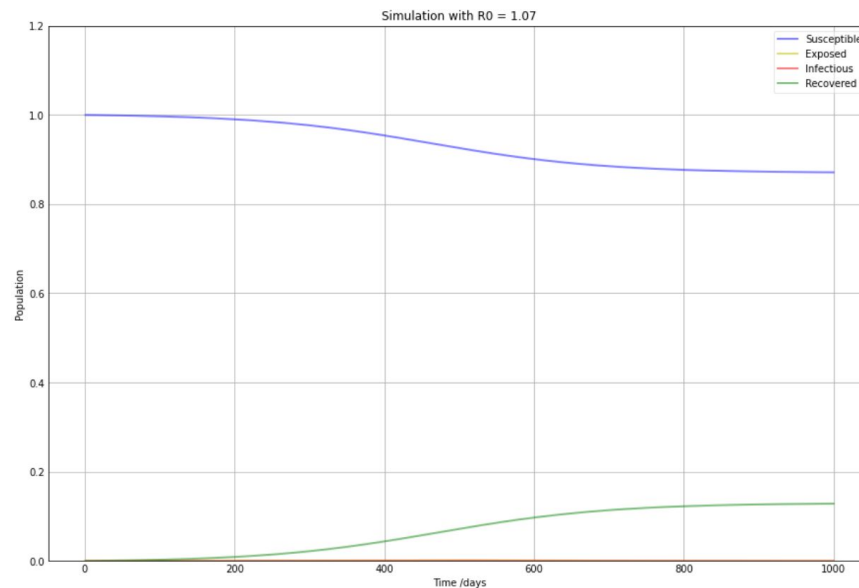
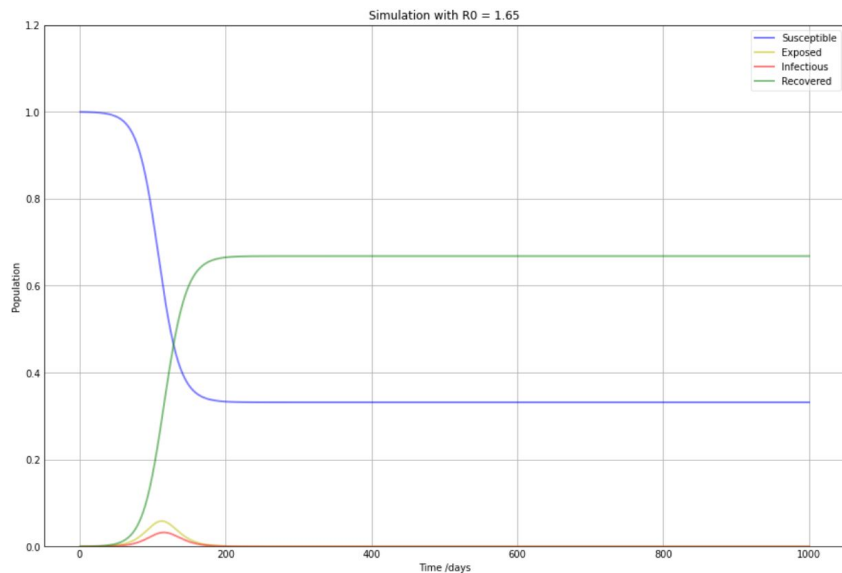




Application of the model on France: estimation of R_0

Linear estimation of R_0 between 25/03/2020 and 26/02/2020: 1.65

Linear estimation of R_0 after 18/03/2020 (after containment measures): 1.07



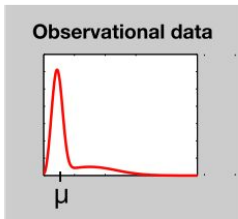
Estimate the posterior distribution
without the likelihood function



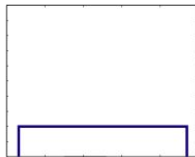
Approximate Bayesian Computation (ABC)

ABC rejection algorithm :

- sample many particles from a prior distribution (e.g. uniform)
- generate synthetic datasets from these particles and compare them to observed data
- accept particles with a given tolerance rate
- when N particles are accepted, estimate the posterior from the accepted particles (histogram)

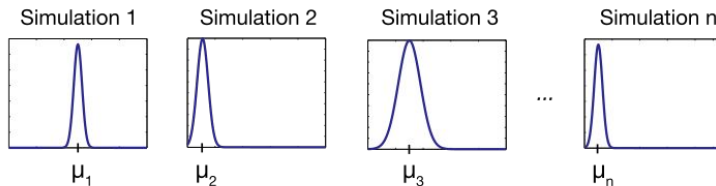
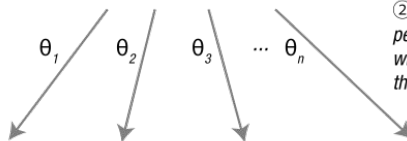


Prior distribution of model parameter θ



① Compute summary statistic μ from observational data

② Given a certain model, perform n simulations, each with a parameter drawn from the prior distribution



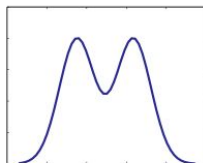
③ Compute summary statistic μ_i for each simulation

$$\rho(\mu_i, \mu) \stackrel{?}{\leq} \varepsilon$$



④ Based on a distance $\rho(\cdot, \cdot)$ and a tolerance ε , decide for each simulation whether its summary statistic is sufficiently close to that of the observed data.

Posterior distribution of model parameter θ

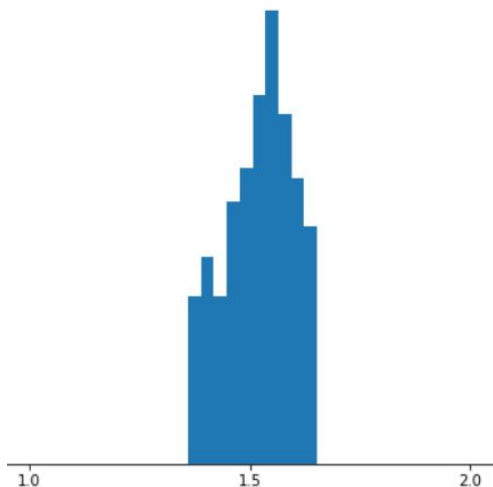


⑤ Approximate the posterior distribution of θ from the distribution of parameter values θ_i associated with accepted simulations.

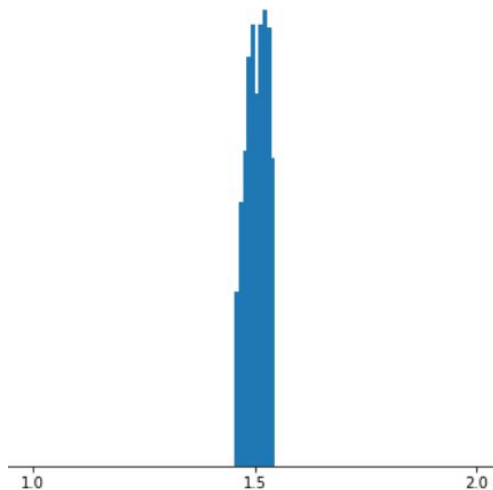


Approximate Bayesian Computation (ABC)

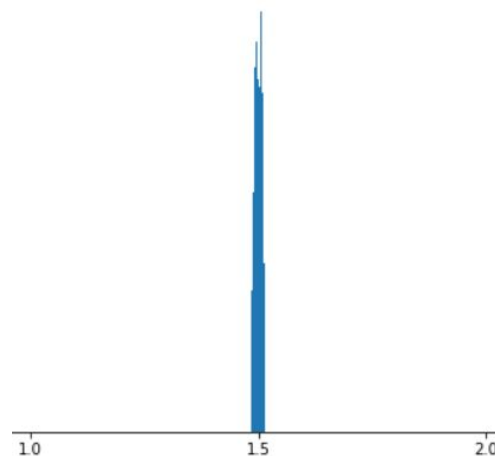
Accepted values of beta for threshold = 10



Accepted values of beta for threshold = 1



Accepted values of beta for threshold = 0.1



trade-off between the precision of the estimated posterior and the computation time



ABC-SMC (Sequential Monte Carlo)

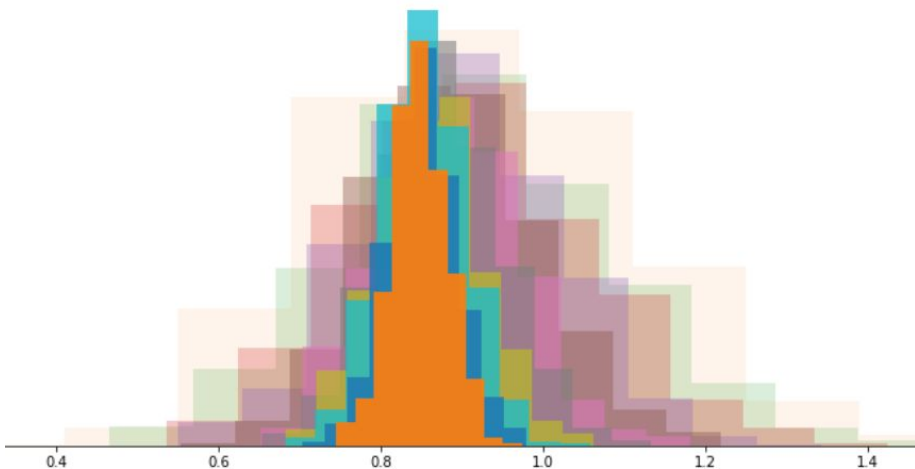
ABC-SMC rejection algorithm :

- define a list of tolerance rates : $\text{eps}_1 > \text{eps}_2 > \dots > \text{eps}_T$
- at first, run ABC algorithm with tolerance eps_1 and particles from prior distribution
- estimate the posterior
- then, run ABC with successive tolerance rates
- sample particles from intermediate posterior distribution
- refine the estimated posterior distribution
- repeat

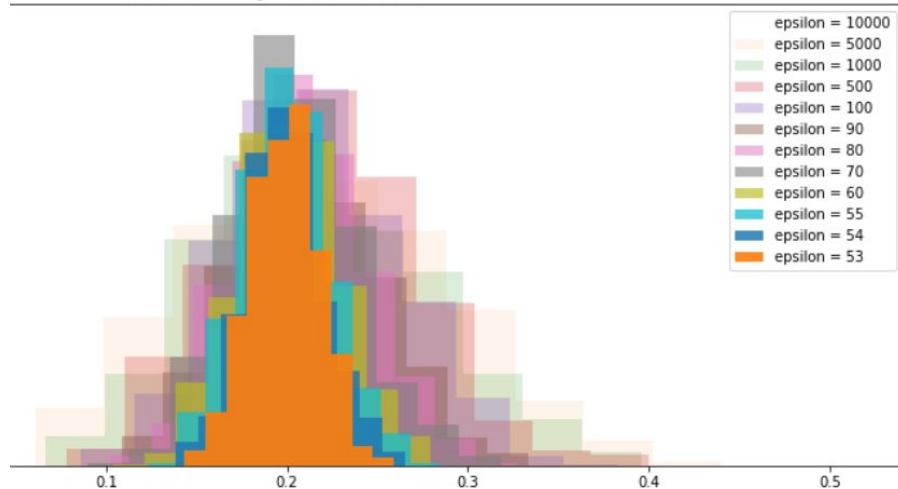


ABC-SMC (Sequential Monte Carlo)

Estimation of beta with SMC-ABC



Estimation of sigma with SMC-ABC



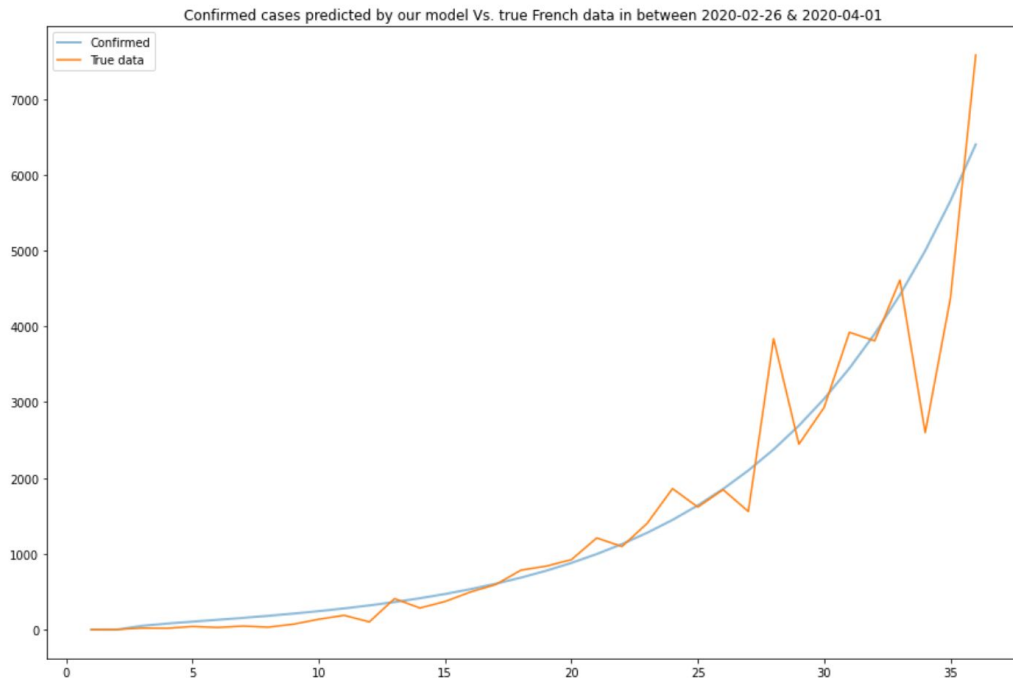
much faster and more precise, a lot of possible improvements (how to sample from intermediate posterior? how to choose tolerance rate? how to decide whether to accept a particle?)



Application on French covid-19 data

Setting:

- SEIR model with delay between symptomatic and confirmed cases
- from 26/02 to 31/03, before lockdown impact
- parameters to estimate: infection rate, incubation period, report delay, initial number of exposed/infected
- observed data: nb of new confirmed cases each day





Conclusion / Limitations

- SIR model : basic model of epidemics, good at predicting trends (not precise numbers), can be complexified
- Infection rate much more deterministic than expected
- ABC algorithm is very powerful for complex model with no obvious likelihood and latent variable model with partially observed data