# Phenomenological models and applications to the SARS-CoV-2 epidemic

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Bordeaux IMB Infectious Disease Outbreaks

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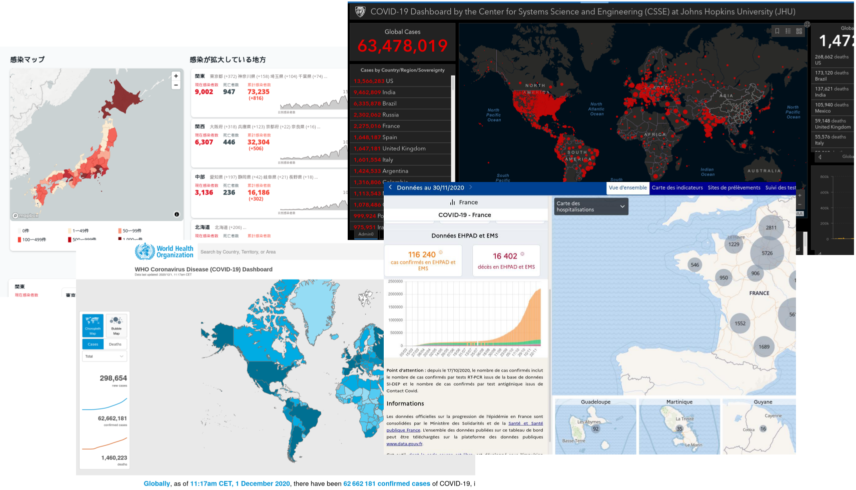
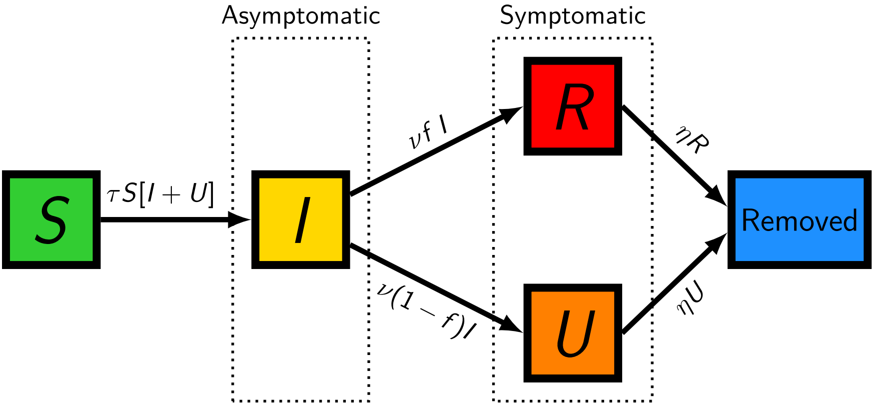
# Coronavirus outbreak: an explosion of data




...How to exploit these data ?

# PART I:
# Early results on the SIUR model

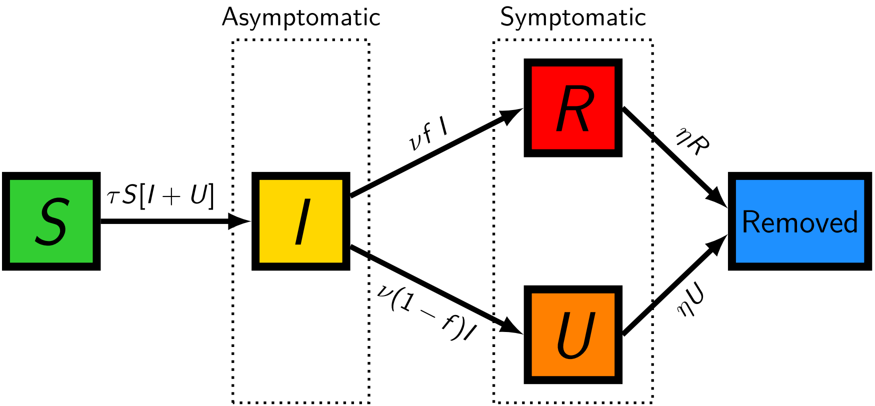
# A model for the COVID-19: the SIUR model




[1] Z Liu et al. "Understanding unreported cases in the COVID-19 epidemic outbreak in Wuhan, China, and the importance of major public health interventions". *Biology* 9.3 (2020), p. 50. DOI: 10.3390/biology9030050.

[2] J Qiu. "Covert coronavirus infections could be seeding new outbreaks.". *Nature (Lond.)* (2020). DOI: 10.1038/d41586-020-00822-x.

# A model for the COVID-19: the SIUR model




**R = Reported**

**U = Unreported**

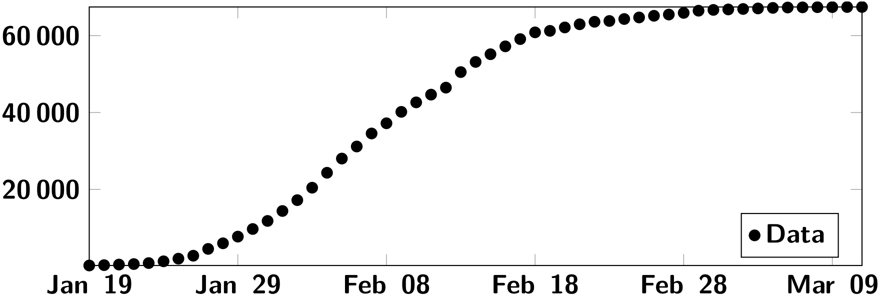
$f$ = fraction of reported cases

# Connection with the data

Reported cases are what goes inside the $R$ compartment,

$$\mathrm{CR}'(t) = \nu\, f\, I(t).$$

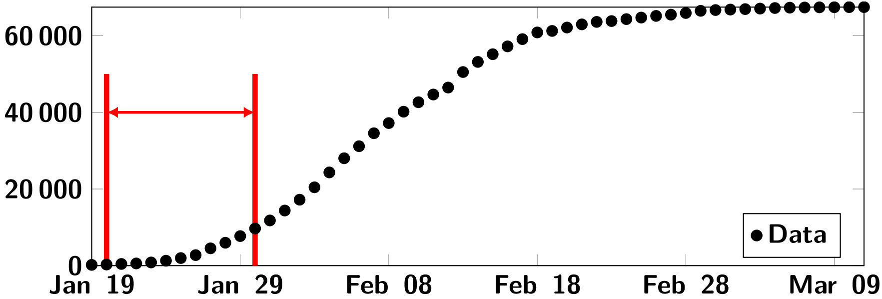
Here we plot the data of the first wave in Mainland China.



# A first phenomenological model

**Phenomenological model: the exponential function**

We first focus on a period with exponential growth: Jan 20 – Jan 30



# A first phenomenological model

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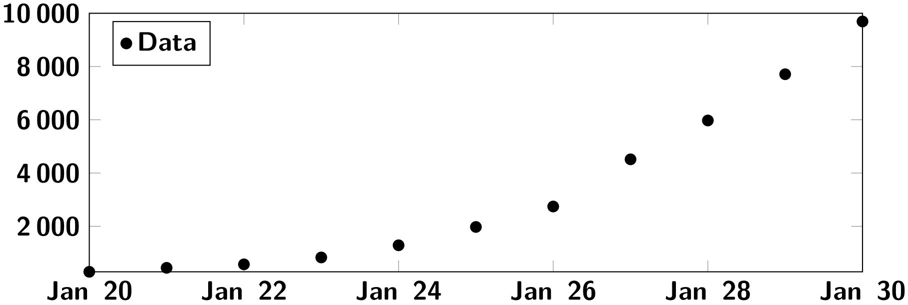
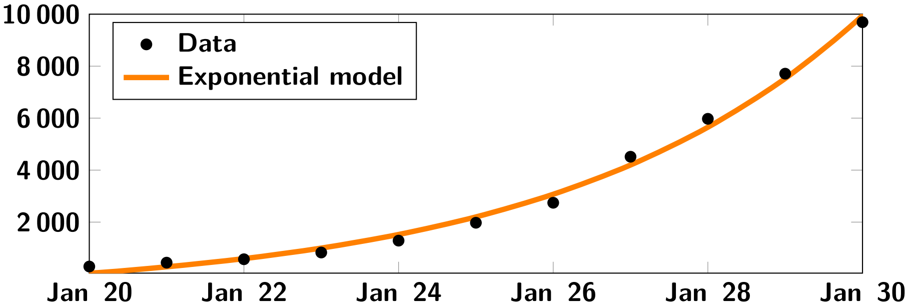


**Phenomenological model: the exponential function**

$I$ should be growing exponentially, so $\mathrm{CR}(t) = \chi_1 e^{\chi_2(t-t_0)} - \chi_3$.



# Identifying the parameters

We start from our phenomenological model

$$\mathrm{CR}(t) = \chi_1 e^{\chi_2(t-t_0)} - \chi_3.$$

Therefore $\mathrm{CR}'(t) = \chi_1\chi_2 e^{\chi_2(t-t_0)} = \nu f\, I(t)$, and we recover $I(t) = I_0 e^{\chi_2(t-t_0)}$:

$$I_0 = \frac{\chi_1\chi_2}{\nu f}$$

By using $U'(t) = \chi_2 U_0 e^{\chi_2(t-t_0)} = \nu(1-f)I(t) - \eta U(t)$, we identify $U_0$ and then $R_0$

$$U_0 = \frac{\nu(1-f)I_0}{\chi_2+\eta},$$
$$R_0 = \frac{\nu f\, I_0}{\chi_2+\eta},$$

and finally by $I'(t) = \tau S(t)\big(I(t)+U(t)\big) - \nu I(t)$:

$$\tau = \frac{(\chi_2+\nu)I_0}{S_0(I_0+U_0)}.$$

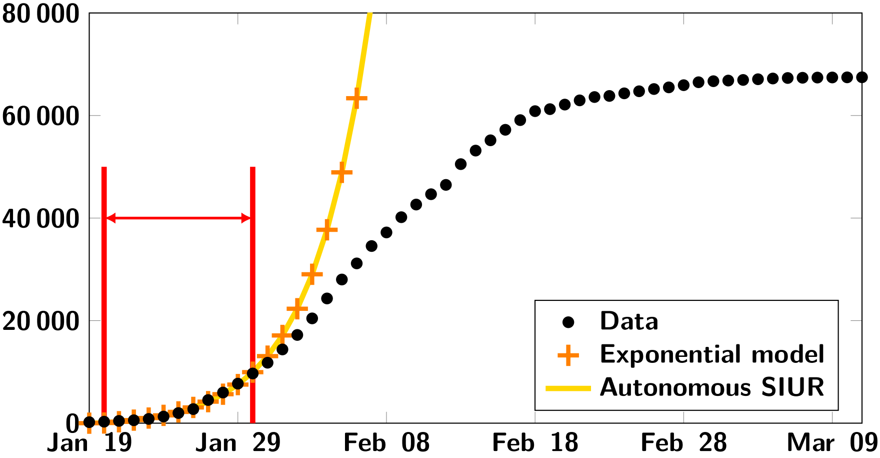
# Identification problem

$$I_0 = \frac{\chi_1\chi_2}{\nu f}, \qquad U_0 = \frac{(1-f)\chi_1\chi_2}{f(\chi_2+\eta)}, \qquad R_0 = \frac{\chi_1\chi_2}{\chi_2+\eta},$$

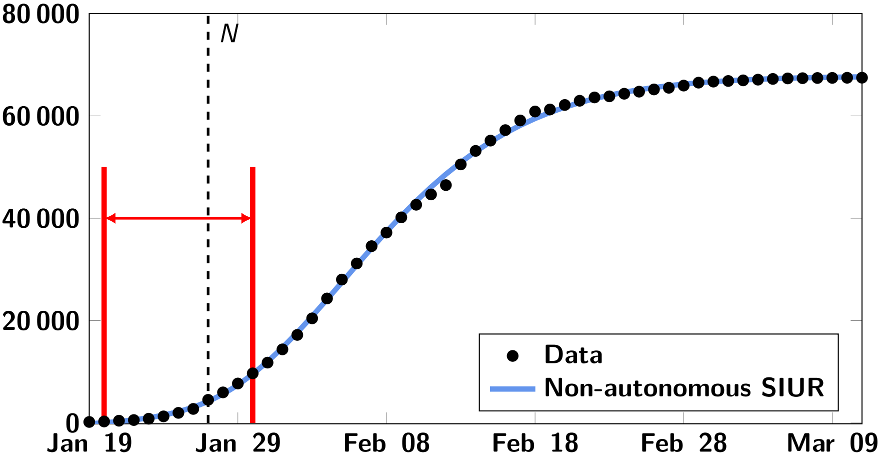
$$\tau = \frac{(\chi_2+\nu)(\chi_2+\eta)}{S_0((\chi_2+\eta)f + \nu(1-f))}.$$

**In particular, the parameters $\nu$, $f$, $\eta$ and $S_0$ cannot be identified from the data**

# The autonomous SIUR model does not match the data!



# Simulation with time-dependent $\tau(t)$




In blue we plot the best match for the full model with public intervention measures.

[1] Z Liu et al. "Predicting the cumulative number of cases for the COVID-19 epidemic in China from early data". *Math Biosci Eng* 17.4 (2020), pp. 3040–3051. DOI: 10.3934/mbe.2020172.

# PART II:
# Reconstruction of the transmission rate from the data.

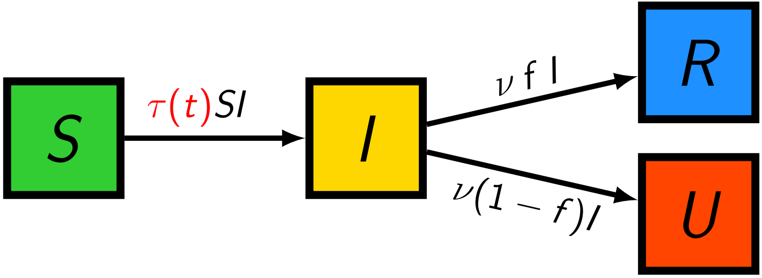
[1] J Demongeot, Q Griette, and P Magal. "SI epidemic model applied to COVID-19 data in mainland China". *Roy Soc Open Sci* 7.12 (2020), p. 201878. DOI: 10.1098/rsos.201878.

# Going further: identifying the transmission rate

**Jacques Demongeot**, Université Grenoble Alpes.

**Pierre Magal**, Université de Bordeaux.

# The SIR model with time-dependent transmission




**Given (non-identifiable) parameters:**

$$S_0, \nu, f.$$

**Goal: identifying $\tau(t)$ and $I_0$.**

# Identification of the transmission rate

**Theorem (Identification of the transmission rate)**

*Let $S_0 > 0, \nu > 0, f \in (0,1)$, and $t_0 < T$ be given. Assume that $N(t) \in C^2$ is a given positive function of time. There is at most one function $\tau(t) > 0$ such that*

$$\mathrm{CR}(t) = N(t) \text{ for all } t \in [t_0, T],$$

*where $\mathrm{CR}(t)$ is the cumulative number of reported cases given by the time-dependent SIR model. $\tau(t)$ exists and is given by the formula*

$$\tau(t) = \frac{\nu f \left(\frac{N''(t)}{N'(t)} + \nu\right)}{\nu f(I_0 + S_0) - N'(t) - \nu(N(t) - N(t_0))}$$

*whenever $N(t)$ is strictly increasing and the denominator of the right-hand side is positive for all $t \in [t_0, T]$. $I_0$ is given by*

$$I_0 = \frac{\mathrm{CR}'(t_0)}{\nu f} = \frac{N'(t_0)}{\nu f}.$$

# Phenomenological model

Among the many phenomenological models used to fit the COVID-19 data, we chose the solution to the **Bernoulli-Verhulst equation**

$$N'(t) = \chi N(t) \left(1 - \left(\frac{N(t)}{N_\infty}\right)^\theta\right),$$

which has an **explicit expression**

$$N(t) = \frac{N_0 e^{\chi(t-t_0)}}{\left(1 + \left(\frac{N_0}{N_\infty}\right)^\theta \left(e^{\chi\theta(t-t_0)} - 1\right)\right)^{\frac{1}{\theta}}}.$$

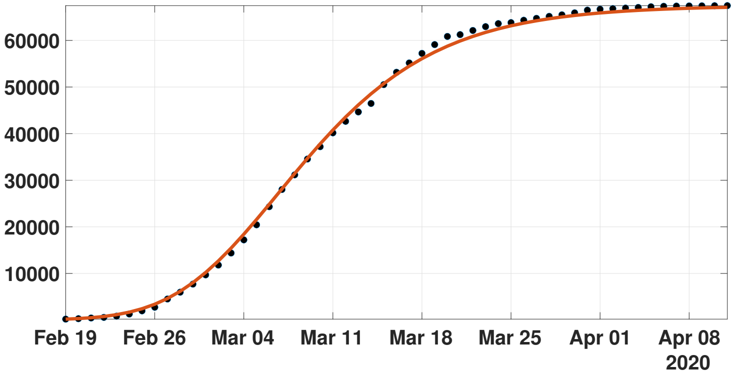



Figure: *In this figure, we plot the best fit of the Bernoulli-Verhulst model to the cumulative number of reported cases of COVID-19 in China. We obtain* $\chi_2 = 0.66$ *and* $\theta = 0.22$. *The black dots correspond to data for the cumulative number of reported cases and the blue curve corresponds to the model.*

## Estimated rate of transmission

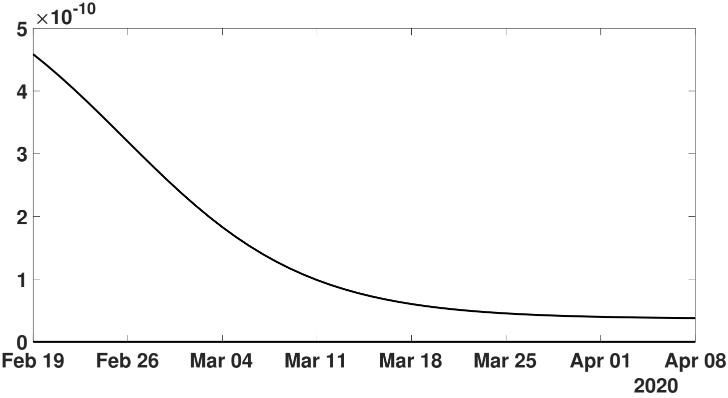
By using the Bernoulli-Verhulst equation we obtain

$$\tau(t) = \frac{f\left(\chi\left(1-(1+\theta)\left(\frac{N(t)}{N_\infty}\right)^\theta\right)+\nu\right)}{f\left(I_0+S_0\right)+\nu N_0 - N(t)\left(\chi\left(1-\left(\frac{N(t)}{N_\infty}\right)^\theta\right)+\nu\right)}. \quad (1)$$

This formula (1) combined with the explicit formula for $N(t)$ gives an explicit formula for the rate of transmission.

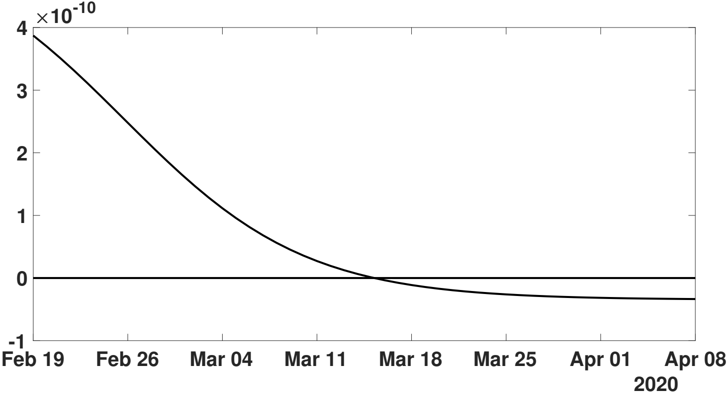
# Transmission rate

$\nu = 0.2 > 0.14 = \chi_2\,\theta$



# Transmission rate

$$\nu = 0.1 < 0.14 = \chi_2\,\theta$$




$\nu = 0.1$ **is not compatible with the data !**

## Compatibility of the model SI with the COVID-19 data for mainland China

The model SI is compatible with the data only when $\tau(t)$ stays positive for all $t \geq t_0$. From the formula we deduce that model is compatible with the data only when

$$1/\nu \leq 1/0.14 = 3.3 \text{ days}. \tag{2}$$

This means that the average duration of infectious period $1/\nu$ must be shorter than 3.3 days.

Similarly we get a condition on $f$:

$$f \geq \frac{N_\infty \chi + (N_\infty - N_0)\,\nu}{S_0 + I_0} \geq \frac{N_\infty \chi + (N_\infty - N_0)\,\chi\,\theta}{S_0 + I_0}$$

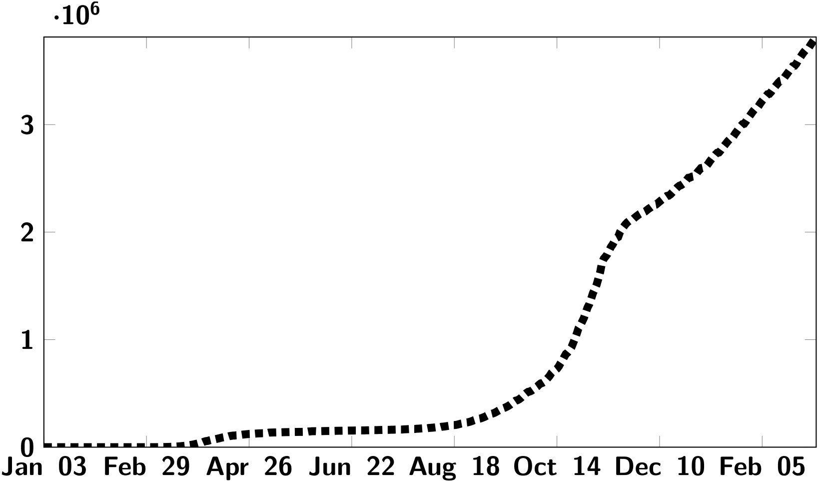
and since we have $CR_0 = 198$ and $N_\infty = 67102$, we obtain

$$f \geq \frac{67102 \times 0.66 + (67102 - 198) \times 0.14}{1.4 \times 10^9} \geq 3.83 \times 10^{-5}. \tag{3}$$

# PART III:
Connecting the waves.

[1] Q Griette, J Demongeot, and P Magal. "A robust phenomenological approach to investigate COVID-19 data for France". *medRxiv* (2021). DOI: 10.1101/2021.02.10.21251500.

# Successive waves: the case of France



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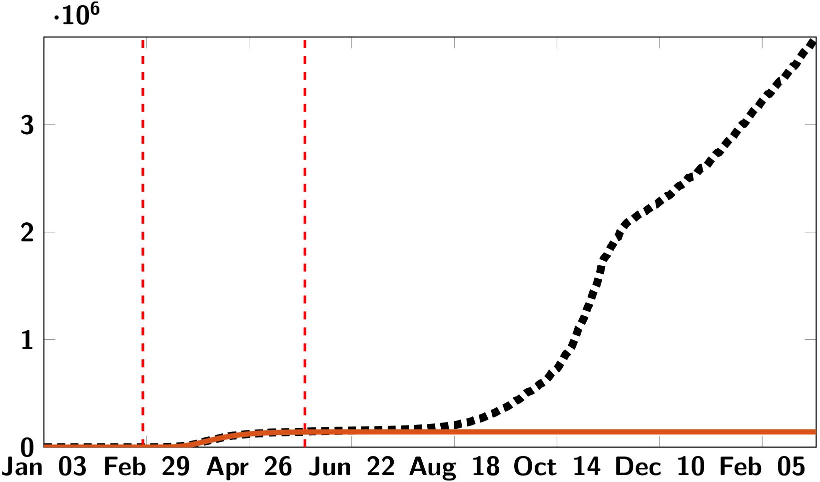
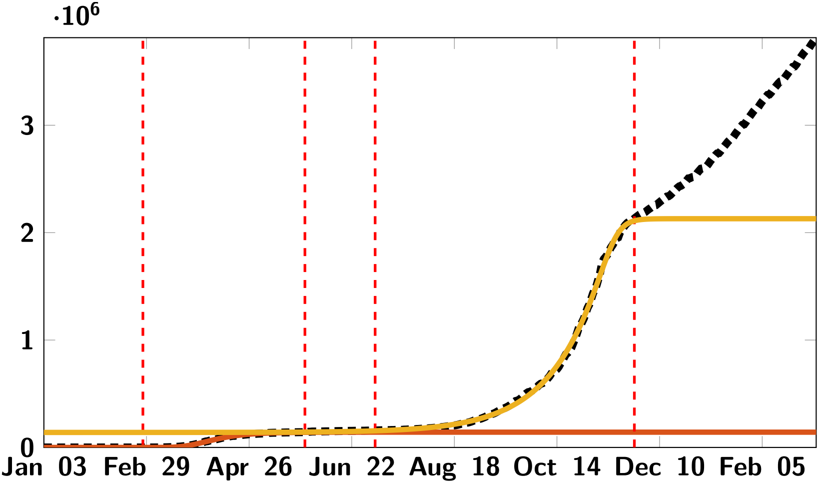


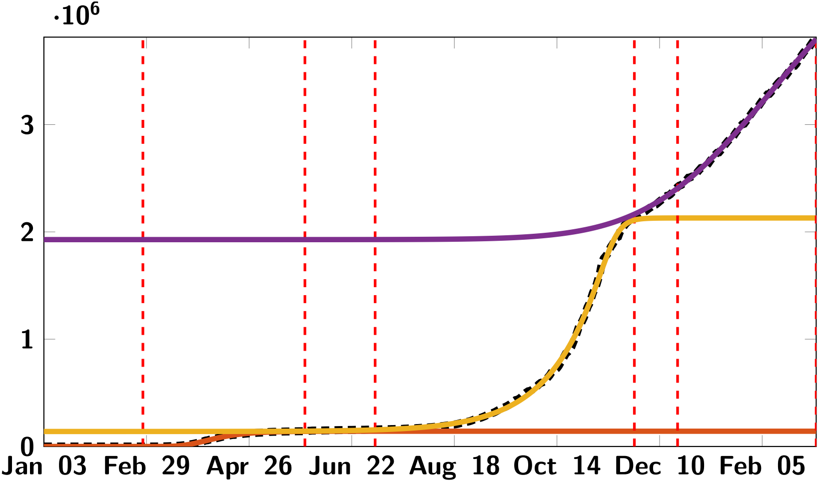

First wave: Feb 27, 2020 – May 27, 2020

# Successive waves: the case of France



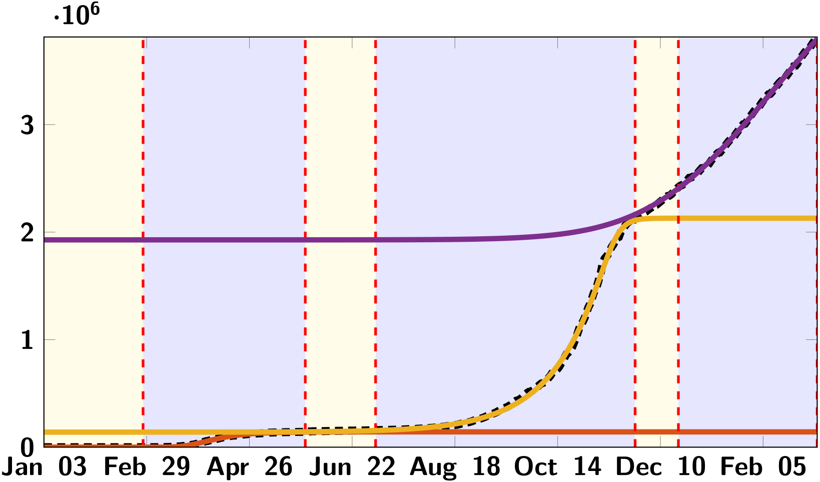

Second wave: Jul 05, 2020 – Nov 26, 2020

# Successive waves: the case of France




Third wave: Dec 20, 2020 – Mar 03, 2021

# Epidemic & endemic phases




Blue = epidemic phase, yellow = endemic phase

# Epidemic phase

Phenomenological model: $\mathrm{CR}(t) = N_{base} + N(t)$, where

$$N'(t) = \chi N(t)\left(1 - \left(\frac{N(t)}{N_\infty}\right)^\theta\right)$$

We can compute:

- the **transmission rate**

$$\tau(t) = \frac{\nu f\left(\chi\left[1-(1+\theta)\left(\frac{N(t)}{N_\infty}\right)^\theta\right]+\nu\right)}{\nu f\,(I_0+S_0) - \chi\,N(t)\left[1-\left(\frac{N(t)}{N_\infty}\right)^\theta\right] - \nu\,(N(t)-N_0)}$$

- the **(effective) basic reproduction number**

$$\mathcal{R}_0(t) = \frac{S(t)\tau(t)}{\nu}.$$

# Endemic phase

Phenomenological model:

$$\mathrm{CR}(t) = N(t) = N_0 + a \times (t - t_0).$$

We can compute:

- the **transmission rate**

$$\tau(t) = \frac{\nu^2 f}{\nu f\,(I_0 + S_0) - a - \nu(t - t_0) \times a}$$

- the **(effective) basic reproduction number**

$$\mathcal{R}_0(t) = \frac{S(t)\tau(t)}{\nu}.$$

# A global model

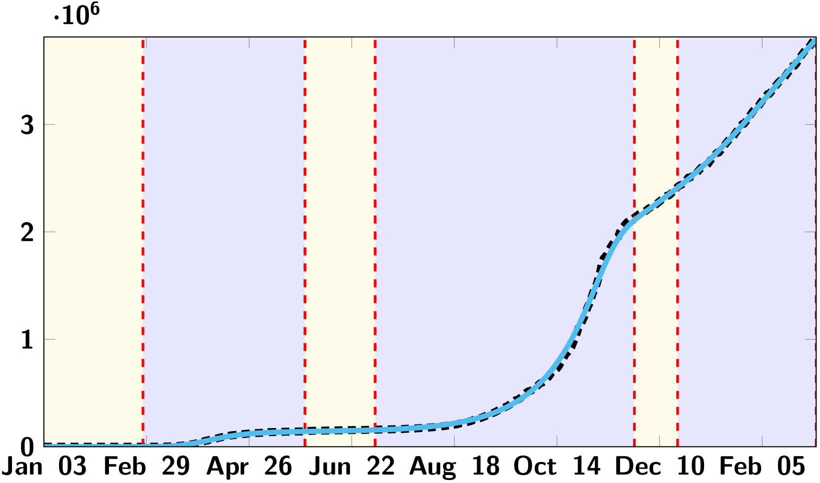
We want to **connect the phases** while keeping the information on the **transmission rate** and **basic reproductive number**.

**Theoretical formula for the transmission rate:**

$$\tau(t) = \frac{\nu f\left(\frac{\mathrm{CR}''(t)}{\mathrm{CR}'(t)} + \nu\right)}{\nu f\left(I_0 + S_0\right) - \mathrm{CR}'(t) - \nu\left(\mathrm{CR}(t) - \mathrm{CR}_0\right)}.$$

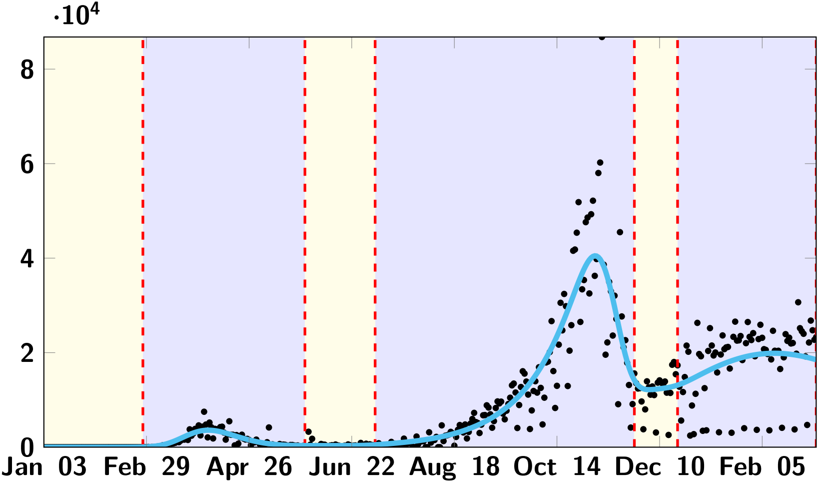
$\rightsquigarrow$ we need a **smooth interpolation** of the phases.

# The global model: cumulative cases



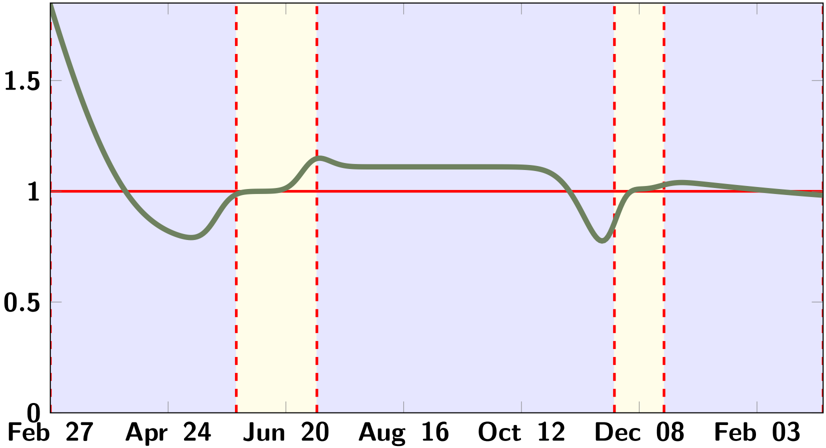

Blue = epidemic phase, yellow = endemic phase

# The global model: daily cases



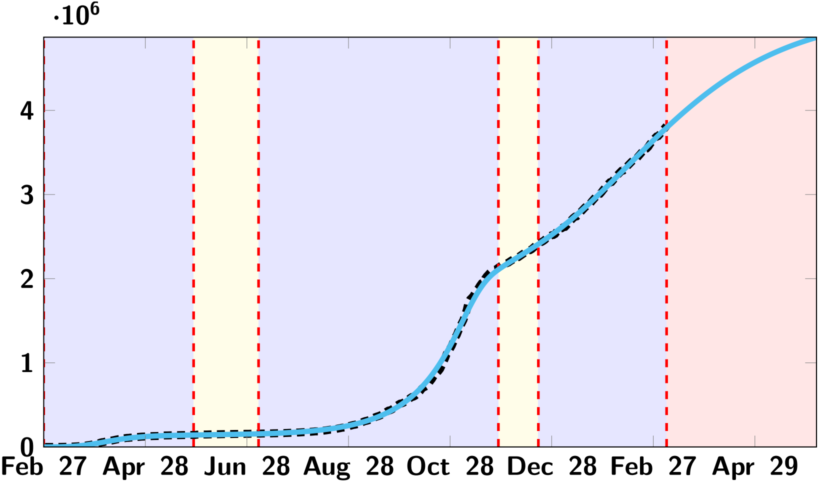

Blue = epidemic phase, yellow = endemic phase

# The global model: $\mathcal{R}_0(t)$



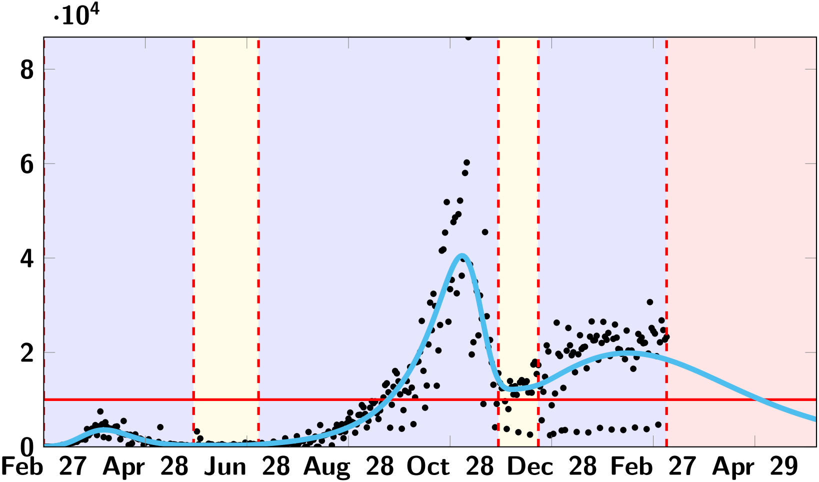

Blue = epidemic phase, yellow = endemic phase

# Projections: cumulative cases



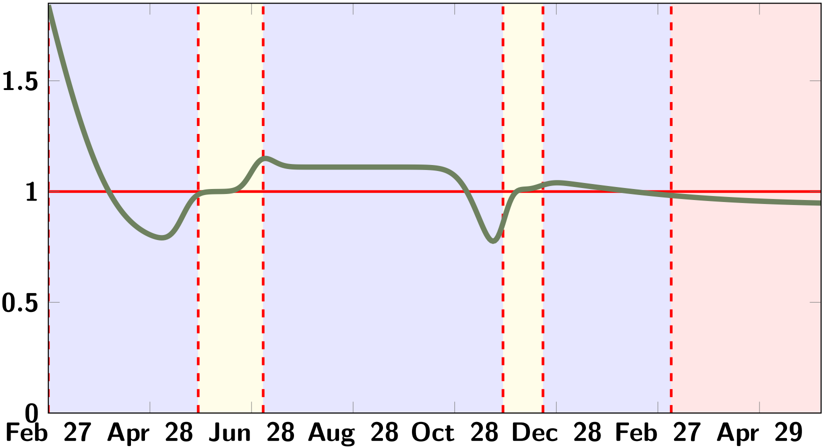

Blue = epidemic phase, yellow = endemic phase, red = projection
Last day: June 5, 2021.

# Projections: daily cases




Blue = epidemic phase, yellow = endemic phase, red = projection
Last day: June 5, 2021. Red line: 10 000 cases/day.

# The global model: $\mathcal{R}_0(t)$




Blue = epidemic phase, yellow = endemic phase, red = projection
Last day: June 5, 2021.

Thank you !