Comment rendre prédictifs des modèles phénoménologiques ?

Yvon Maday,

Laboratoire Jacques-Louis Lions
Sorbonne Université, Paris, Roscoff, France,
Institut Universitaire de France

Paris — November 9 2021

Année de la mécanique
La mécanique à l'interface des autres disciplines
Paris

…….. à l’interface des autres disciplines

…….. à l’interface des autres disciplines

….. où l’on peut rencontrer pas mal de modèles mathématiques sur lesquels des incertitudes existent

…….. à l'interface des autres disciplines

….. où l'on peut rencontrer pas mal de modèles mathématiques sur lesquels des incertitudes existent

soit sur les mécanismes de réaction

……. à l’interface des autres disciplines

….. où l’on peut rencontrer pas mal de modèles mathématiques sur lesquels des incertitudes existent

soit sur les mécanismes de réaction

soit sur les valeurs de constantes

…….. à l’interface des autres disciplines

….. où l’on peut rencontrer pas mal de modèles mathématiques sur lesquels des incertitudes existent

soit sur les mécanismes de réaction

soit sur les valeurs de constantes

qui d’ailleurs peuvent ne pas être aussi constantes que celà

Dynamique de population

modèle de Verhulst:

$$\frac{\mathrm{d}N(t)}{\mathrm{d}t} = rN(t)\left(1 - \frac{N(t)}{K}\right)$$

et son équivalent discret en temps

$$N_{t+\Delta t} = rN_t\left(1 - \frac{N_t}{K}\right)$$

…. mais il y a aussi le modèle de Ricker $$N_{t+1} = N_t \exp\left(r(1 - \frac{N_t}{K})\right)$$

Dynamique de population

modèle de Verhulst:

$$\frac{\mathrm{d}N(t)}{\mathrm{d}t} = rN(t)\left(1 - \frac{N(t)}{K}\right)$$

et son équivalent discret en temps

$$N_{t+\Delta t} = rN_t\left(1 - \frac{N_t}{K}\right)$$

…. mais il y a aussi le modèle de Ricker $N_{t+1} = N_t \exp\left(r(1 - \frac{N_t}{K})\right)$

sans parler des interactions entre espèces

$$\begin{cases} \frac{\mathrm{d}N_1}{\mathrm{d}t} = r_1 N_1\left(1 - \left(\frac{N_1 + \alpha_{12} N_2}{K_1}\right)\right) \\ \frac{\mathrm{d}N_2}{\mathrm{d}t} = r_2 N_2\left(1 - \left(\frac{N_2 + \alpha_{21} N_1}{K_2}\right)\right) \end{cases}$$

On a aussi des systèmes spatio-temporels comme….

CHEMOTAXIS : mathematical models

The mathematical modelling of cell movement goes back to Patlak (1953), E. Keller and L. Segel (70's)

$$n(t,x) = \text{density of cells at time t and position } x,$$
$$c(t,x) = \text{concentration of chemoattractant},$$

In a collective motion, the chemoattractant is emited by the cells that react according to biased random walk.

$$\begin{cases} \frac{\partial}{\partial t} n(t,x) - \Delta n(t,x) + \mathrm{div}(n\chi\nabla c) = 0, \quad x \in R^d, \\ -\Delta c(t,x) = n(t,x), \end{cases}$$

The parameter χ is the sensitivity of cells to the chemoattractant.

emprunté dans un exposé de B. Perthame

ce sont des modèles phénoménologiques .. qualitatifs

peut on les transformer en modèles quantitatifs ?

(avec Edmond CHEN Gong)

Lets us assume that we have two population of bacterias

that interact in a mutualistic way as follows

$$\begin{cases} \dfrac{dn}{dt} &= \dfrac{n(1-n)+n\sqrt{m}}{4} \\ \dfrac{dm}{dt} &= \dfrac{m(1-m)+m\sqrt{n}}{4} \end{cases}$$

Lets us assume that we have two population of bacterias

that interact in a mutualistic way as follows

$$\begin{cases} \dfrac{dn}{dt} & = & \dfrac{n(1-n)+n\sqrt{m}}{4} \\ \dfrac{dm}{dt} & = & \dfrac{m(1-m)+m\sqrt{n}}{4} \end{cases}$$

actually we do not know that law

the only thing that we know is that *n* alone behaves like

$$\frac{dn}{dt} = \frac{n(n-1)}{4}$$

Lets us assume that we have two population of bacterias

that interact in a mutualistic way as follows

$$\begin{cases} \dfrac{dn}{dt} = \dfrac{n(1-n)+n\sqrt{m}}{4} \\ \dfrac{dm}{dt} = \dfrac{m(1-m)+m\sqrt{n}}{4} \end{cases}$$

actually we do not know that law

the only thing that we know is that n alone behaves like

$$\frac{dn}{dt} = \frac{n(n-1)}{4}$$

and that, in a natural environment, n behaves better so we propose a model for this interaction

$$\begin{cases} \dfrac{dn}{dt} = \dfrac{n(1-n) + Cmn}{4} \\ \dfrac{dm}{dt} = \dfrac{m(1-m) + Kmn}{4} \end{cases}$$

and we propose to fit C and K so that it matches with the data on n

the only thing that we know is that n alone behaves like

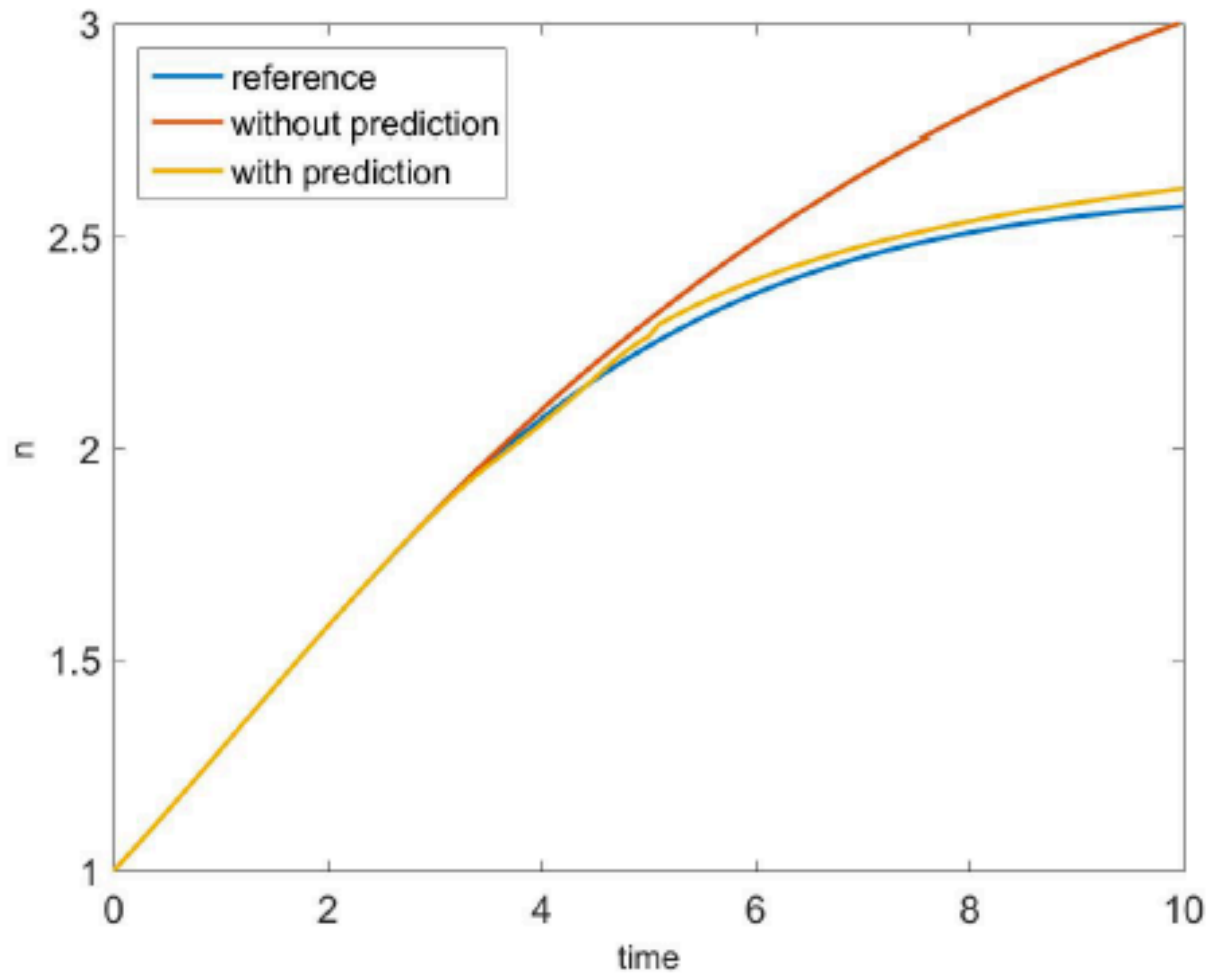
$$\frac{dn}{dt} = \frac{n(n-1)}{4}$$

and that, in a natural environment, n behaves better

actually we do not know m we only guess that there is a m

so we also fit m on known values of n

and we use this to extrapolate n



An example of results : extrapolation from [0, 2] —> [2, 10]

With prediction : extrapolation from [0, 2] —> [2, 3] —> [3, 10]

Different models

propagation of epidemics

Compartmental models of epidemics

When exposed to an infectious agent, the population is differentiated into several subsets (or compartments), all of which are exclusive to each other:

For example, the entire population can be broken down as follows

- Uninfected people, called susceptible (S),
- Infected and contagious people (I), with more or less marked symptoms,
- And people removed (R) from the infectious process, either because they are cured or unfortunately died after being infected.

The resulting three-compartment "SIR" model is the simplest of the models described, but it can be detailed by imagining several dozen compartments taking into account, for example, age, sex, professional activity, or even other characteristics of the disease such as

- Non-contagious infected persons without symptoms (E1),
- Infected and contagious persons who do not show symptoms (E2),
- Infected and contagious but asymptomatic persons (A)

…

Compartmental models of epidemics

During a given period of time (day, week, month), these compartmental models simulate, using differential equations, the average number of people moving from one compartment to another.

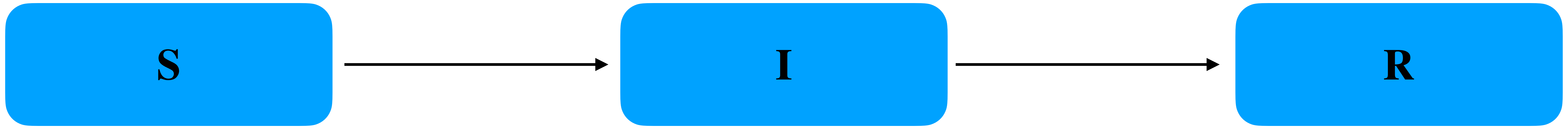
For example for the SIR model: S —> I and I —> R.

At the end of each period, the number of individual in each compartment at the beginning of the period is increased by the number of individual entering and decreased by the number of individual leaving.

It is possible to create a local compartmental model at the scale of a city, a region, a country, and to make these models interact through connections possible to account for exchanges between different areas.

Compartmental models of epidemics

Example of the SIR model: This is the model proposed by Kermack and McKendrick in 1927.



How does a healthy individual contract the disease?

by being in contact with a contagious infected people

this contact is proportional to the number of healthy individuals and the number of contagious individuals

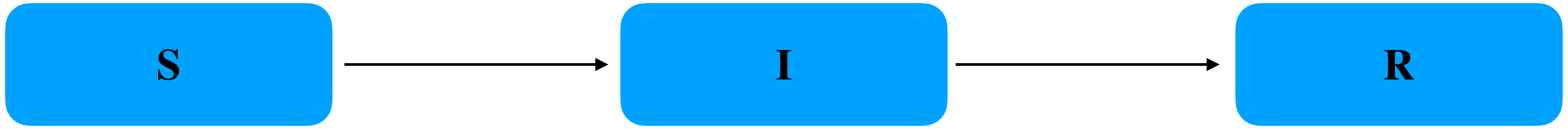
$$\frac{dS}{dt} = -\frac{\beta}{N} S I$$

where N represents the total number of individuals : $N= S+I+R$

and we neglect here the new born and « standard » death

Compartmental models of epidemics

Example of the SIR model: This is the model proposed by Kermack and McKendrick in 1927.



$$\frac{dS}{dt} = -\frac{\beta}{N}SI$$

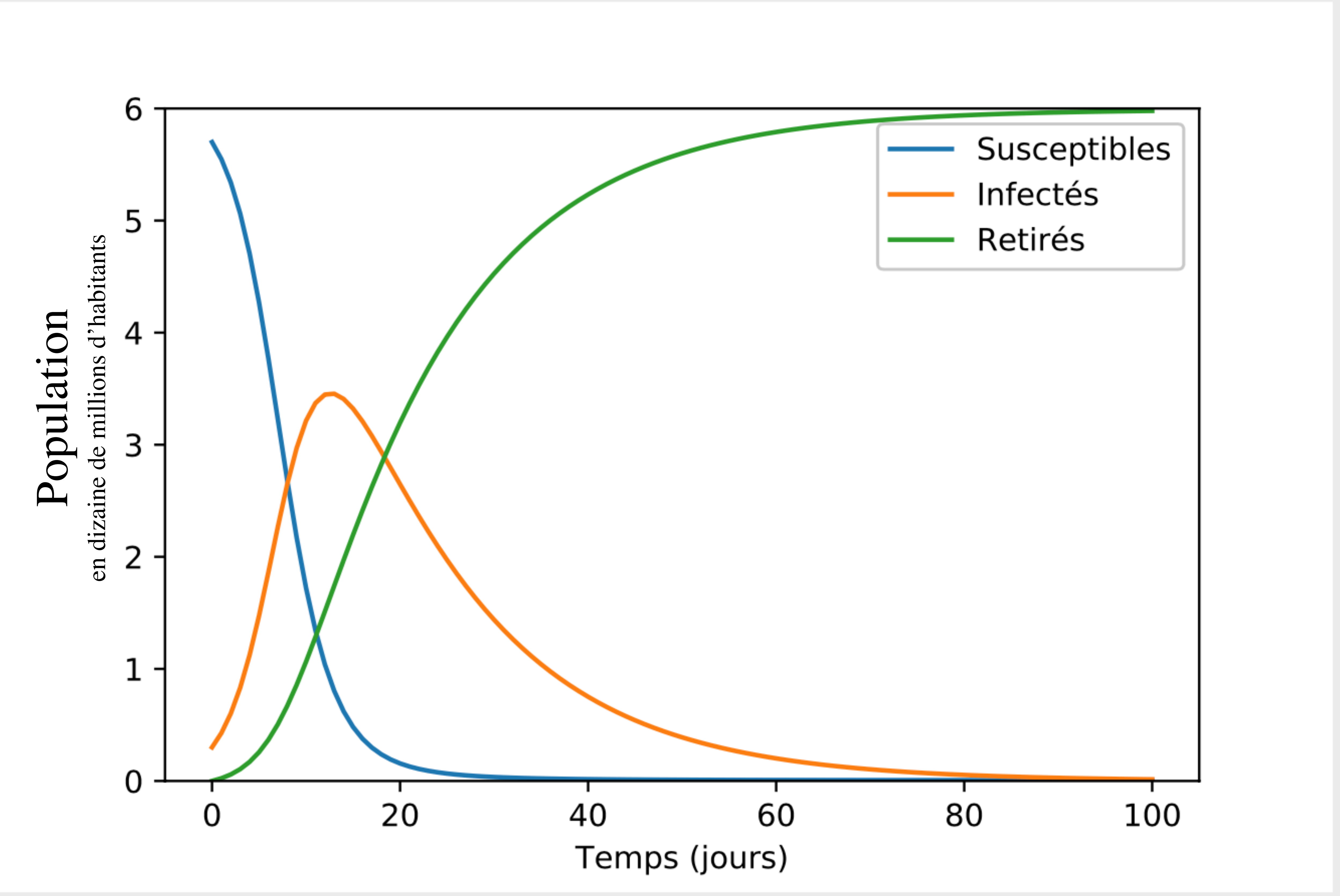
$$\frac{dI}{dt} = \frac{\beta}{N}SI - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

Compartmental models of epidemics

Example of the SIR model: This is the model proposed by Kermack and McKendrick in 1927.

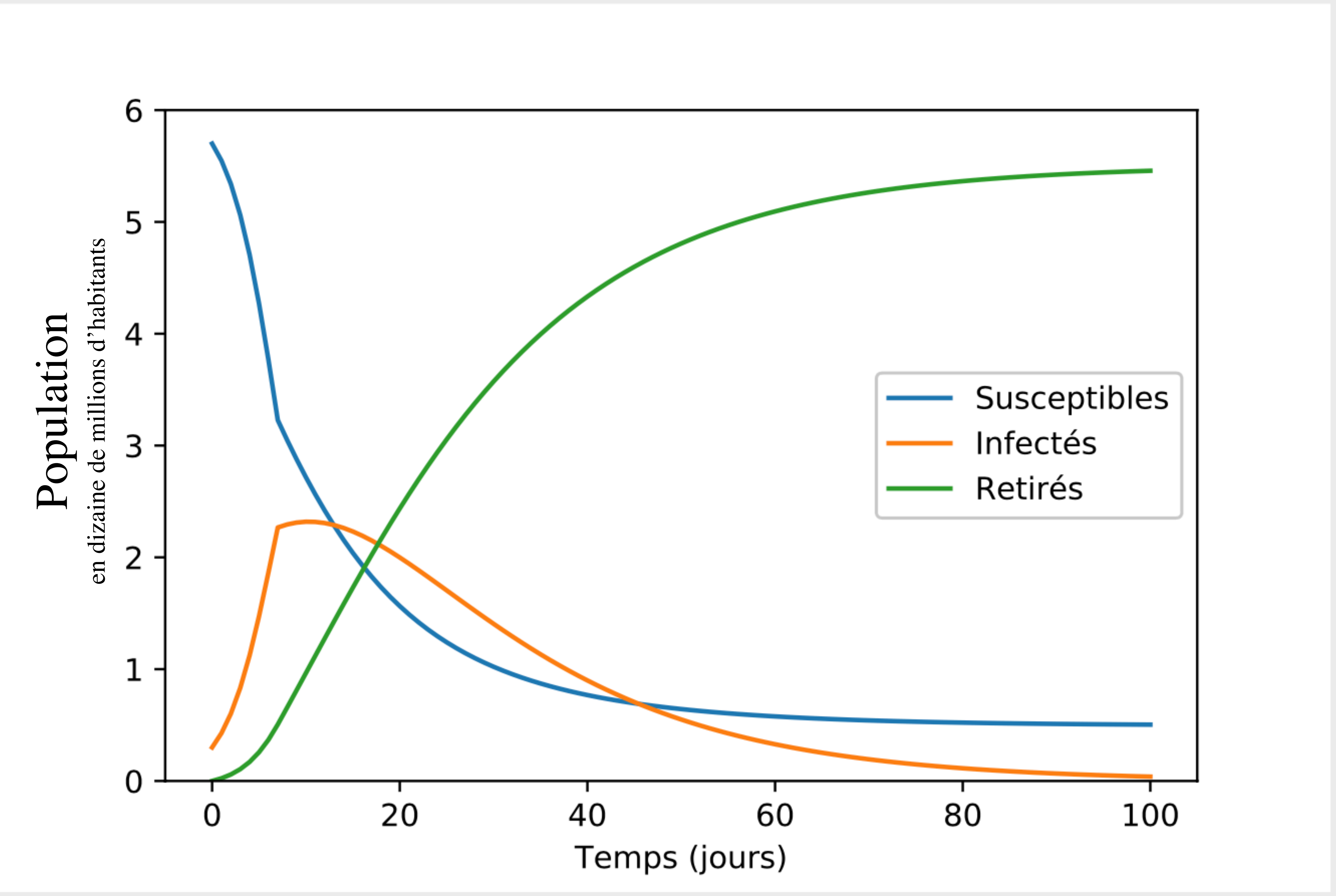
Here is what can be obtained, day after day, in France by the numerical resolution of such a model with a transmission rate $\beta = 0.45$ and a cure rate $\gamma = 1/15$:



Compartmental models of epidemics

Example of the SIR model: This is the model proposed by Kermack and McKendrick in 1927.

Such a model can also simulate the effect of a confinement by modifying (decreasing) the value of the transmission rate β, for example by increasing it from 0.45 to 0.15 after 7 days.



Compartmental models of epidemics

We can, as we said before, increase the number of compartments

an important effect that a SIR model does not see is the pre-infectious period, and the fact that many patients can go unnoticed (Asymptomatic and U
& Webb» model

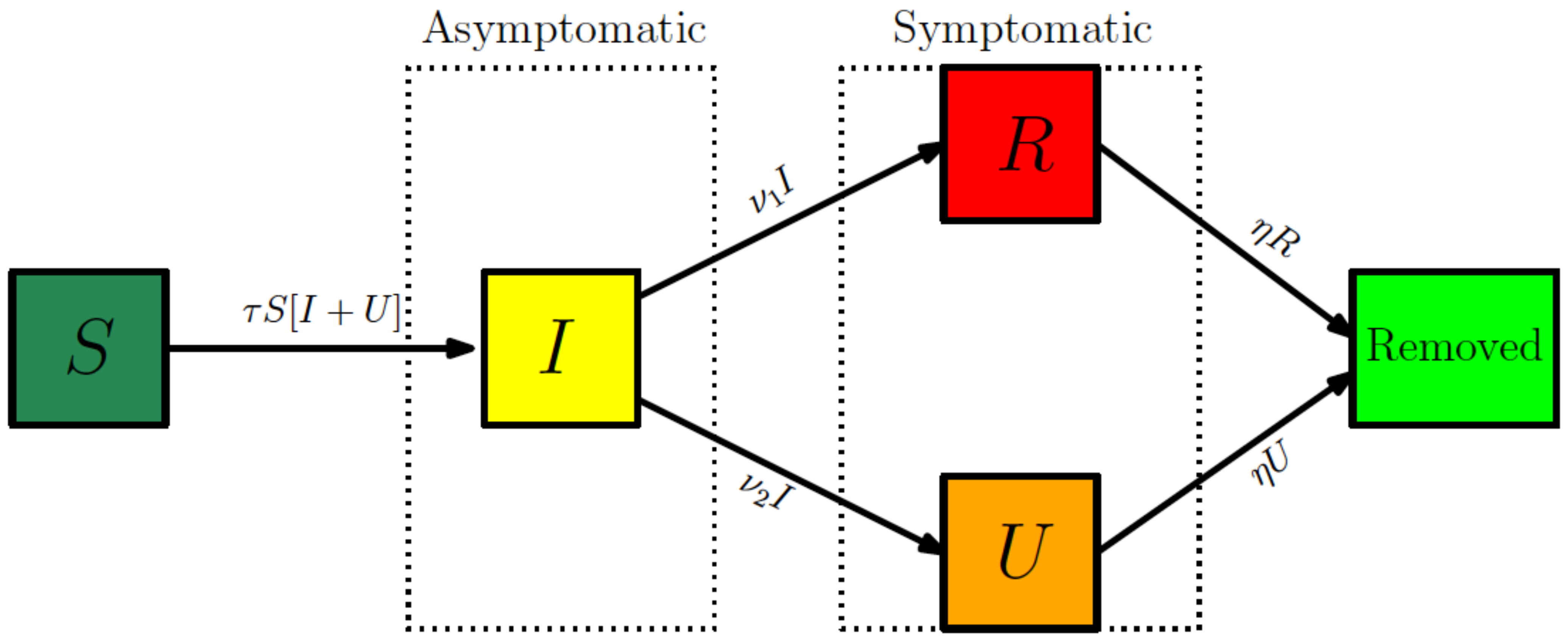


Figure: *Compartments and flow chart of the model.*

P. Magal and G. Webb, The parameter identification problem for SIR epidemic models: Identifying Unreported Cases, J. Math. Biol. (2018).
A. Ducrot, P. Magal, T. Nguyen, G. Webb, Identifying the Number of Unreported Cases in SIR Epidemic Models. Mathematical Medicine and Biology, (2019)

Compartmental models of epidemics

We can, as we said before, increase the number of compartments

an important effect that a SIR model does not see is the pre-infectious period, and the fact that many patients can go unnoticed (Asymptomatic and U
& Webb» model

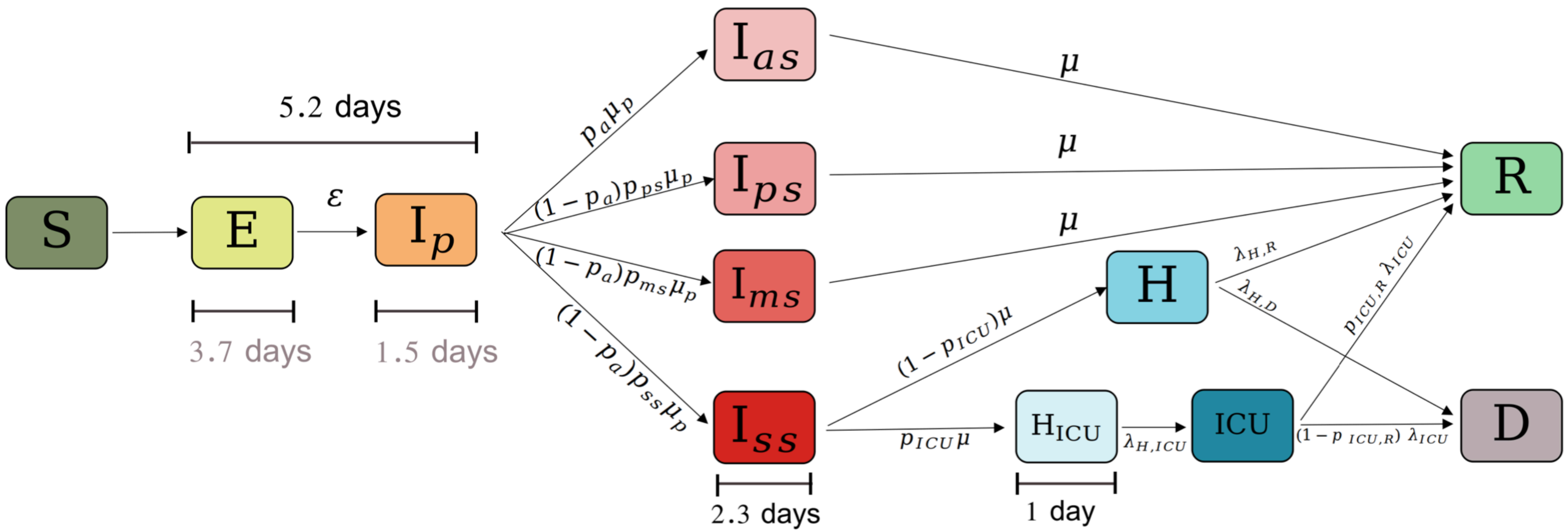
$$\begin{cases} S'(t) = -\tau S(t)[I(t) + U(t)], \\ I'(t) = \tau S(t)[I(t) + U(t)] - \nu I(t), \\ R'(t) = \nu_1 I(t) - \eta R(t), \\ U'(t) = \nu_2 I(t) - \eta U(t). \end{cases}$$

P. Magal and G. Webb, The parameter identification problem for SIR epidemic models: Identifying Unreported Cases, J. Math. Biol. (2018).
A. Ducrot, P. Magal, T. Nguyen, G. Webb, Identifying the Number of Unreported Cases in SIR Epidemic Models. Mathematical Medicine and Biology, (2019)

Compartmental models of epidemics

We can, as we said before, increase the number of compartments

But it is also possible to increase the number of compartments in a more substantial way : S=Susceptible, E=Exposed, I_p= Infectious in the prodromic phase (the length of time including E and I_p stages is the incubation period), I_a=Asymptomatic Infectious, I_{ps}=Paucysym I_{ms}=Symptomatic Infectious with mild symptoms, I_{ss}=Symptomatic Infectious with severe symptoms, H_{ICU}= severe case who will enter in ICU, ICU=se to ICU, H=severe case admitted to the hospital but not in intensive care, R=Recovered, D=Deceased



Expected impact of reopening schools after lockdown on COVID-19 epidemic in Île-de-France, Laura Di Domenico , Giulia Pullano , Chiara E. Sabbatini , Pierre-Yves Boëlle , Vittoria C

Compartmental models of epidemics

We can, as we said before, increase the number of compartments

But it is also possible to increase the number of compartments in a more substantial way : S=Susceptible, E=Exposed,
I_p= Infectious in the prodromic phase (the length of time including E and I_p stages is the incubation period), I_a=Asymptomatic Infectious, I_{ps}=Paucysym
I_{ms}=Symptomatic Infectious with mild symptoms, I_{ss}=Symptomatic Infectious with severe symptoms, H_{ICU}= severe case who will enter in ICU, ICU=se
to ICU, H=severe case admitted to the hospital but not in intensive care, R=Recovered, D=Deceased

It is easy to understand that the number of parameters to be set is very large here and this becomes a problem.

and this requires access to data

Expected impact of reopening schools after lockdown on COVID-19 epidemic in Île-de-France, Laura Di Domenico , Giulia Pullano , Chiara E. Sabbatini , Pierre-Yves Boëlle , Vittoria C

Compartmental models of epidemics

Let us come back to the Magal & Webb model

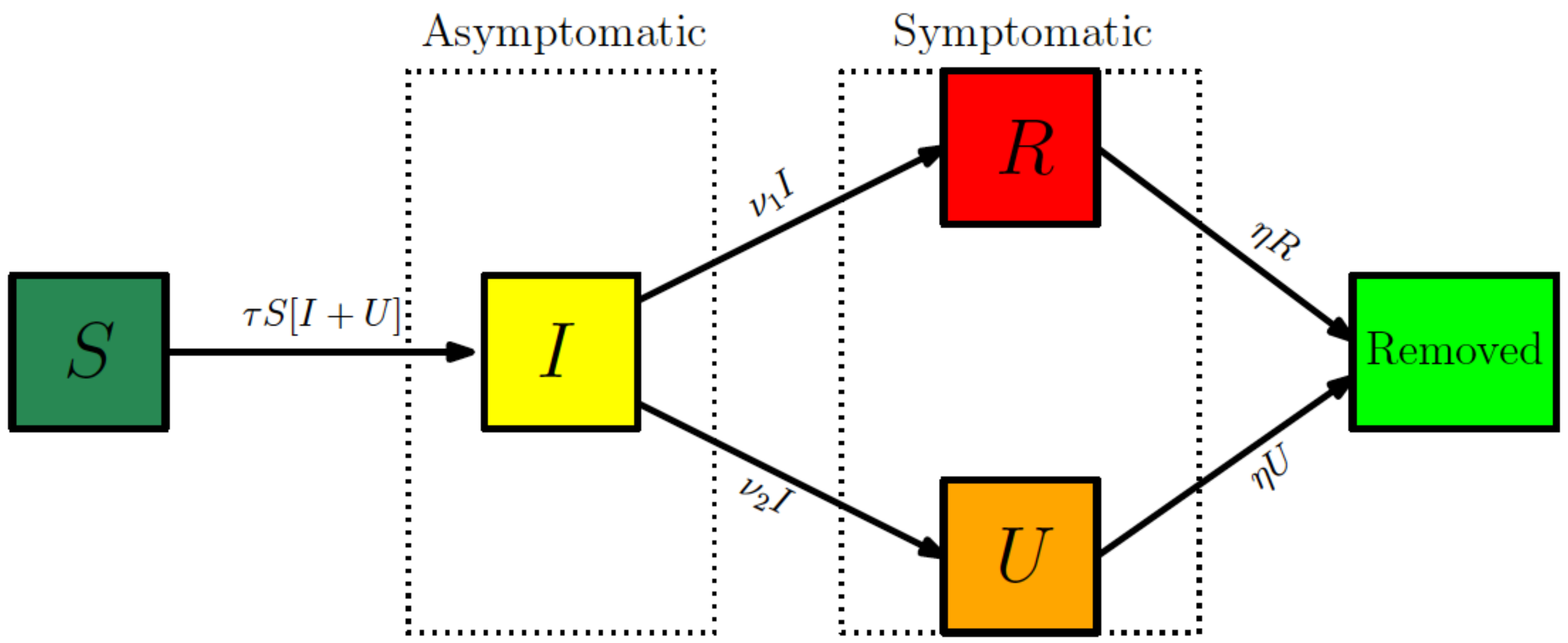


Figure: *Compartments and flow chart of the model.*

there is a bifurcation between « R » and « U »

another way of asking the question: what is the proportion of cases not carried over?

Compartmental models of epidemics

Alternative proposal that we started to study with Olga Mula, Thomas Boiveau, Athmane Bakhta

A SIR model with 2 coefficients $\beta(t)$ and $\gamma(t)$ that depend on time

$$\frac{dS}{dt}(t) = -\frac{\beta(t)I(t)S(t)}{N}$$

$$\frac{dI}{dt}(t) = \frac{\beta(t)I(t)S(t)}{N} - \gamma(t)I(t)$$

$$\frac{dR}{dt}(t) = \gamma(t)I(t)$$

We then have 2 coefficients to calibrate according to the data, by solving a minimization problem

$$\min_{\beta,\gamma}\{\|I_{data} - I_{\beta,\gamma}\| + \|R_{data} - R_{\beta,\gamma}\|\}$$

Bakhta, A., Boiveau, T., Maday, Y., & Mula, O. (2021).
Epidemiological Forecasting with Model Reduction of Compartmental Models. Application to the COVID-19 Pandemic. *Biology*, *10*(1), 22.

Compartmental models of epidemics

Alternative proposal that we started to study with Olga Mula, Thomas Boiveau, Athmane Bakhta

Proposition 4.1. *Let $N \in \mathbb{N}^*$ and $T > 0$. For any real-valued functions S_d, I_d, R_d defined on $[0, T]$ satisfying*

(i) $S_d(t) + I_d(t) + R_d(t) = N$ *for every* $t \in [0, T]$,

(ii) S_d *in nonincreasing on* $[0, T]$,

(iii) R_d *is nondeacreasing on* $[0, T]$,

there exists a unique minimizer (β^*, γ^*) *to problem 4.1.*

Bakhta, A., Boiveau, T., Maday, Y., & Mula, O. (2021).
Epidemiological Forecasting with Model Reduction of Compartmental Models. Application to the COVID-19 Pandemic. *Biology*, *10*(1), 22.

Compartmental models of epidemics

Alternative proposal that we started to study with Olga Mula, Thomas Boiveau, Athmane Bakhta

Proposition 4.1. *Let* $N \in \mathbb{N}^*$ *and* $T > 0$. *For any real-valued functions* S_d, I_d, R_d *defined on* $[0, T]$ *satisfying*

(i) $S_d(t) + I_d(t) + R_d(t) = N$ *for every* $t \in [0, T]$,

(ii) S_d *in nonincreasing on* $[0, T]$,

(iii) R_d *is nondeacreasing on* $[0, T]$,

there exists a unique minimizer (β^*, γ^*) *to problem 4.1.*

$$\beta(t) = -\frac{N}{I(t)S(t)}\frac{dS(t)}{dt}$$

$$\gamma(t) = \frac{1}{I(t)}\left[\frac{dI}{dt}(t) - \frac{\beta(t)I(t)S(t)}{N}\right]$$

Bakhta, A., Boiveau, T., Maday, Y., & Mula, O. (2021).
Epidemiological Forecasting with Model Reduction of Compartmental Models. Application to the COVID-19 Pandemic. *Biology*, *10*(1), 22.

And then!

Alternative proposal that we started to study with Olga Mula, Thomas Boiveau, Athmane Bakhta

$$\beta(t) = -\frac{N}{I(t)S(t)}\frac{dS(t)}{dt}$$

$$\gamma(t) = \frac{1}{I(t)}\left[\frac{dI}{dt}(t) - \frac{\beta(t)I(t)S(t)}{N}\right]$$

we can learn from different models (Magal, Colizza, … each one indexed by a generic μ) the behaviour of the coefficients

$$\mathcal{S} = \{\beta(t;\mu), \gamma(t;\mu)\}$$

Bakhta, A., Boiveau, T., Maday, Y., & Mula, O. (2021).
Epidemiological Forecasting with Model Reduction of Compartmental Models. Application to the COVID-19 Pandemic. *Biology*, *10*(1), 22.

And then!

Alternative proposal that we started to study with Olga Mula, Thomas Boiveau, Athmane Bakhta

$$\beta(t) = -\frac{N}{I(t)S(t)}\frac{dS(t)}{dt}$$
$$\gamma(t) = \frac{1}{I(t)}\left[\frac{dI}{dt}(t) - \frac{\beta(t)I(t)S(t)}{N}\right]$$

we can learn from different models (Magal, Colizza, … each one indexed by a generic μ) the behaviour of the coefficients

$$\mathcal{S} = \{\beta(t;\mu), \gamma(t;\mu)\}$$

$$\mathbf{S}_i^{\text{collapse}} = \mathbf{S}_i + \mathbf{E}_{1i}$$
$$\mathbf{I}_i^{\text{collapse}} = \mathbf{E}_{2i} + \mathbf{I}_i + \mathbf{U}_i$$
$$\mathbf{R}_i^{\text{collapse}} = \mathbf{R}_i$$

Bakhta, A., Boiveau, T., Maday, Y., & Mula, O. (2021).
Epidemiological Forecasting with Model Reduction of Compartmental Models. Application to the COVID-19 Pandemic. *Biology*, *10*(1), 22.

And then!

Alternative proposal that we started to study with Olga Mula, Thomas Boiveau, Athmane Bakhta

$$\beta(t) = -\frac{N}{I(t)S(t)}\frac{dS(t)}{dt}$$

$$\gamma(t) = \frac{1}{I(t)}\left[\frac{dI}{dt}(t) - \frac{\beta(t)I(t)S(t)}{N}\right]$$

we can learn from different models (Magal, Colizza, … each one indexed by a generic μ) the behaviour of the coefficients

$$\mathcal{S} = \{\beta(t;\mu), \gamma(t;\mu)\}$$

$$\mathbf{S}_i^{\text{collapse}} = \mathbf{S}_i + \mathbf{E}_{1i}$$
$$\mathbf{I}_i^{\text{collapse}} = \mathbf{E}_{2i} + \mathbf{I}_i + \mathbf{U}_i$$
$$\mathbf{R}_i^{\text{collapse}} = \mathbf{R}_i$$

$$\mathbf{S}_i^{\text{collapse}} = \mathbf{S}_i + \mathbf{E}_i$$
$$\mathbf{I}_i^{\text{collapse}} = \mathbf{I}_{p_i} + \mathbf{I}_{ai} + \mathbf{I}_{ps_i} + \mathbf{I}_{msi} + \mathbf{I}_{ssi} + \mathbf{C}_i + \mathbf{H}_i$$
$$\mathbf{R}_i^{\text{collapse}} = \mathbf{R}_i + \mathbf{D}_i$$

Bakhta, A., Boiveau, T., Maday, Y., & Mula, O. (2021).
Epidemiological Forecasting with Model Reduction of Compartmental Models. Application to the COVID-19 Pandemic. *Biology*, *10*(1), 22.

And then!

Alternative proposal that we started to study with Olga Mula, Thomas Boiveau, Athmane Bakhta

$$\beta(t) = -\frac{N}{I(t)S(t)}\frac{dS(t)}{dt}$$
$$\gamma(t) = \frac{1}{I(t)}\left[\frac{dI}{dt}(t) - \frac{\beta(t)I(t)S(t)}{N}\right]$$

we can learn from different models (Magal, Colizza, … each one indexed by a generic μ) the behaviour of the coefficients

$$\mathcal{S} = \{\beta(t;\mu), \gamma(t;\mu)\}$$

over a period of time beyond the current epidemic data window.

Bakhta, A., Boiveau, T., Maday, Y., & Mula, O. (2021).
Epidemiological Forecasting with Model Reduction of Compartmental Models. Application to the COVID-19 Pandemic. *Biology*, *10*(1), 22.

And then!

Model reduction approach

if $\mathcal{S}$ has a small Kolmogorov n-width

$$\mathcal{S} = \{\beta(t;\mu), \gamma(t;\mu)\} \simeq \text{Span}\{\beta_i, \gamma_i, i = 1, \ldots, N\}$$

And then!

Model reduction approach

if $\mathcal{S}$ has a small Kolmogorov n-width

$$\mathcal{S} = \{\beta(t;\mu), \gamma(t;\mu)\} \simeq \mathrm{Span}\{\beta_i, \gamma_i, i = 1, \ldots, N\}$$

meaning that, for a small value of N

$$\forall \mu, \quad \beta(.;\mu) \simeq \sum_{i=1}^{N} \alpha_i \beta_i(.)$$

And then!

Model reduction approach

if $\mathcal{S}$ has a small Kolmogorov n-width

$$\mathcal{S} = \{\beta(t;\mu), \gamma(t;\mu)\} \simeq \mathrm{Span}\{\beta_i, \gamma_i, i = 1, \ldots, N\}$$

how do we get the β_i and γ_i ?

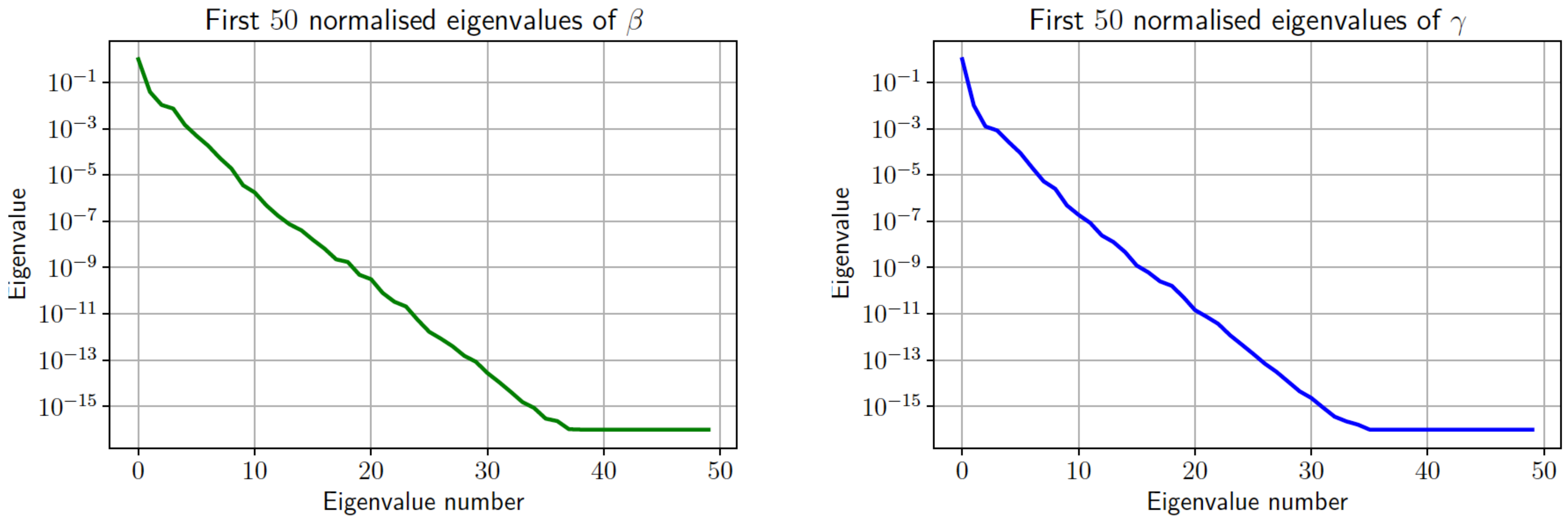
And then!

Model reduction approach

if $\mathcal{S}$ has a small Kolmogorov n-width

$$\mathcal{S} = \{\beta(t;\mu), \gamma(t;\mu)\} \simeq \text{Span}\{\beta_i, \gamma_i, i = 1, \ldots, N\}$$

how do we get the β_i and γ_i ? Through POD/SVD/KL



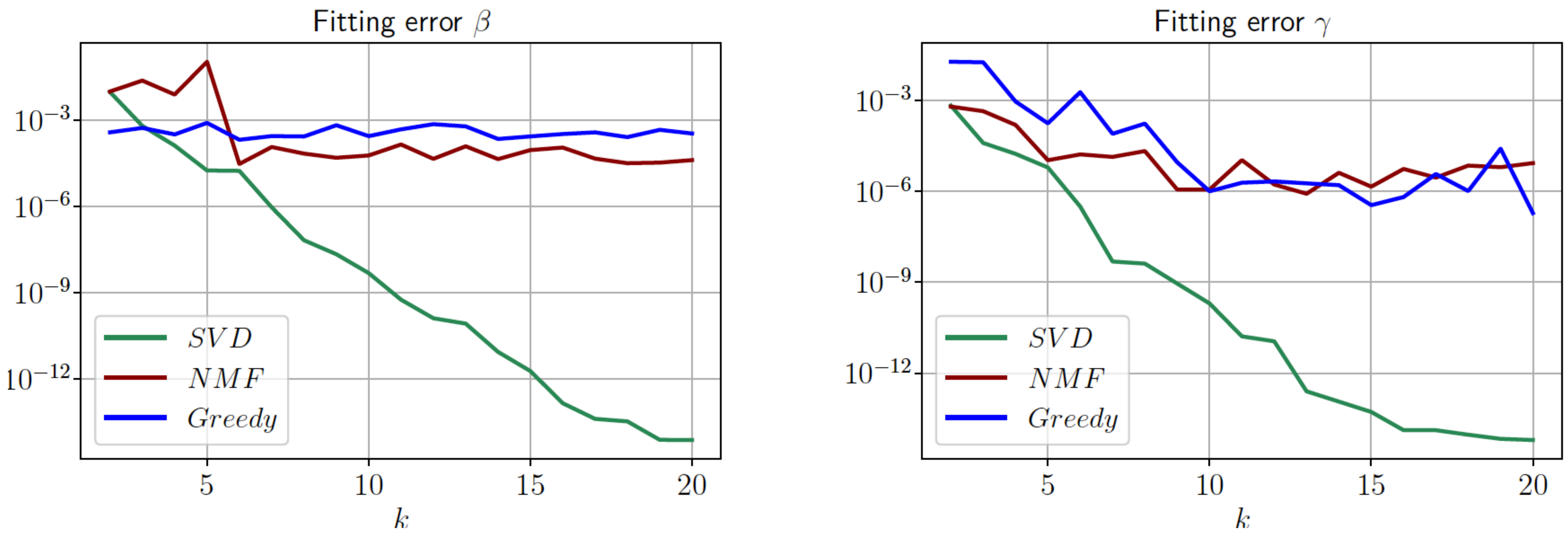
Eigenvalues decay

And then!

Model reduction approach

and provide a reduced basis for interpolation... and extrapolation...

$$\mathcal{S} = \{\beta(t;\mu), \gamma(t;\mu)\} \simeq \mathrm{Span}\{\beta_i, \gamma_i, i = 1, \ldots, N\}$$

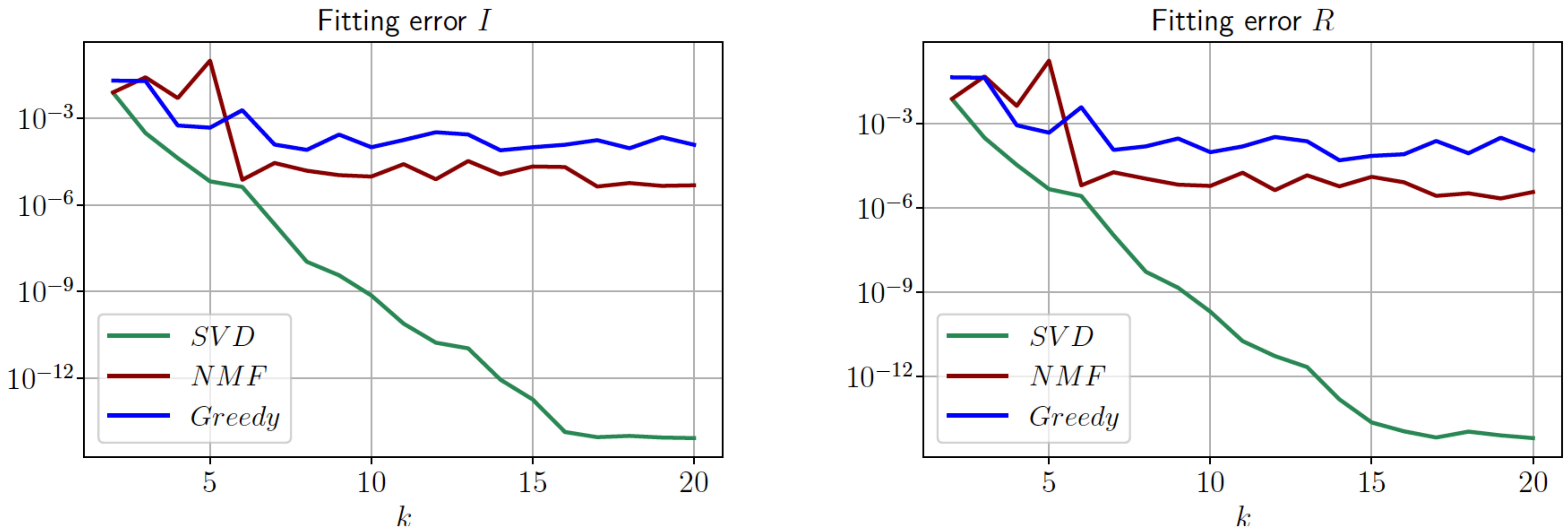


And then!

Model reduction approach

and provide a reduced basis for interpolation… and extrapolation…

$$\mathcal{S} = \{\beta(t;\mu), \gamma(t;\mu)\} \simeq \mathrm{Span}\{\beta_i, \gamma_i, i = 1, \ldots, N\}$$



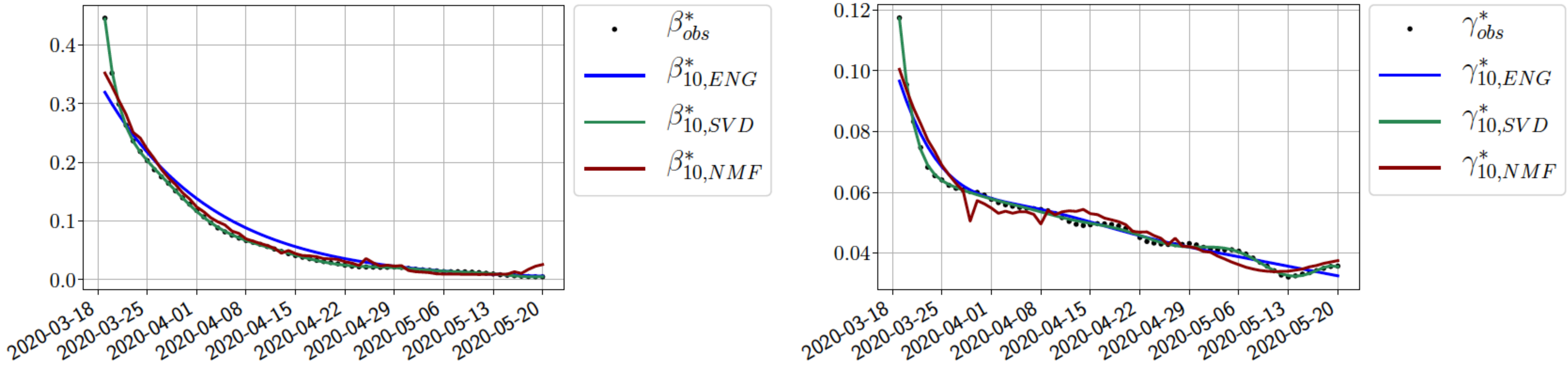
L^1 fitting error of I, L^∞ fitting error of R

And then!

Model reduction approach

and provide a reduced basis for interpolation... and extrapolation...

$$\mathcal{S} = \{\beta(t;\mu), \gamma(t;\mu)\} \simeq \text{Span}\{\beta_i, \gamma_i, i = 1, \dots, N\}$$

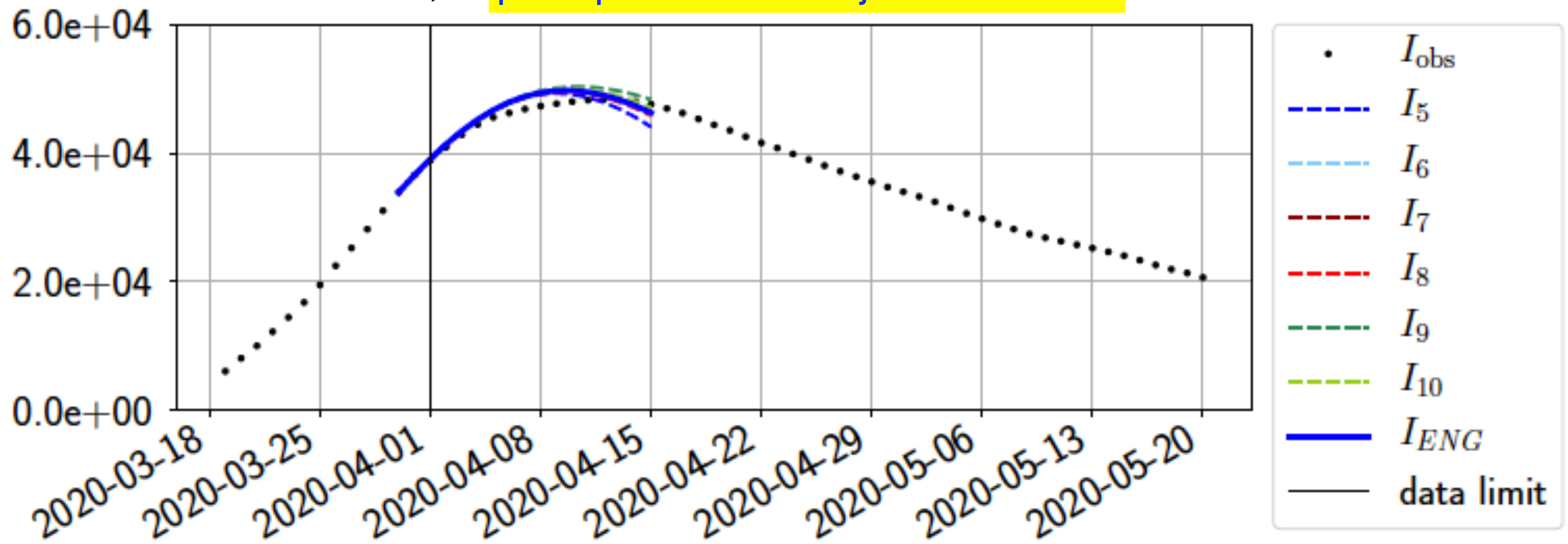


(a) β **(b)** γ

Figure 4. Fitting from $t_0 = 19/03/2020$ **to** $T = 20/05/2020$

on n’utilise que ces données

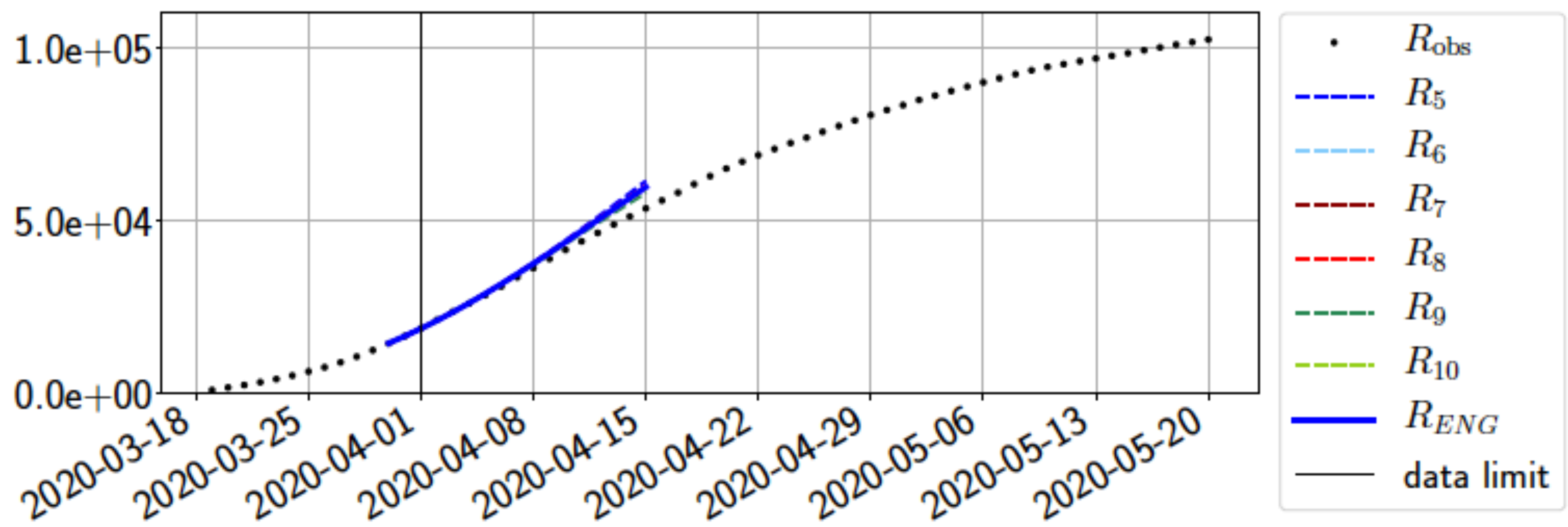
pour prédire les 14 jours suivants



(c) Infected

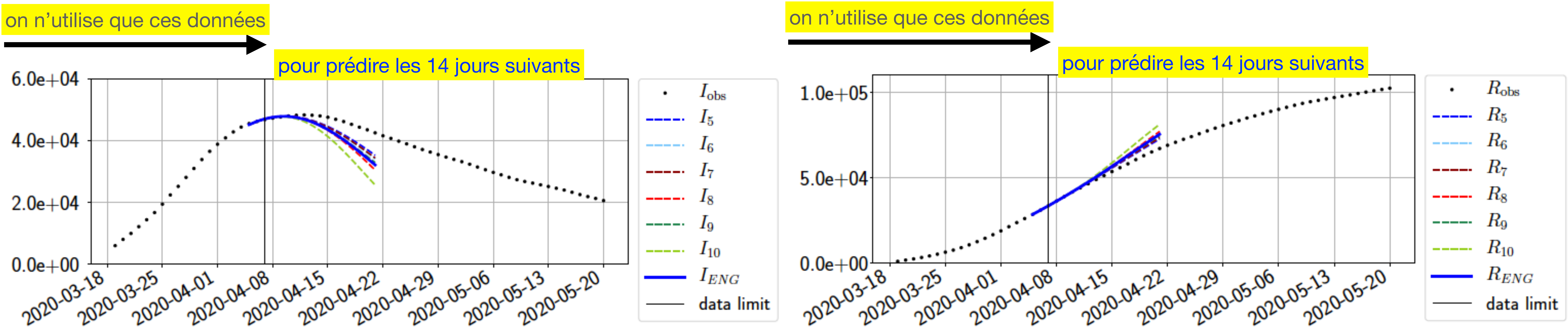
on n’utilise que ces données

pour prédire les 14 jours suivants



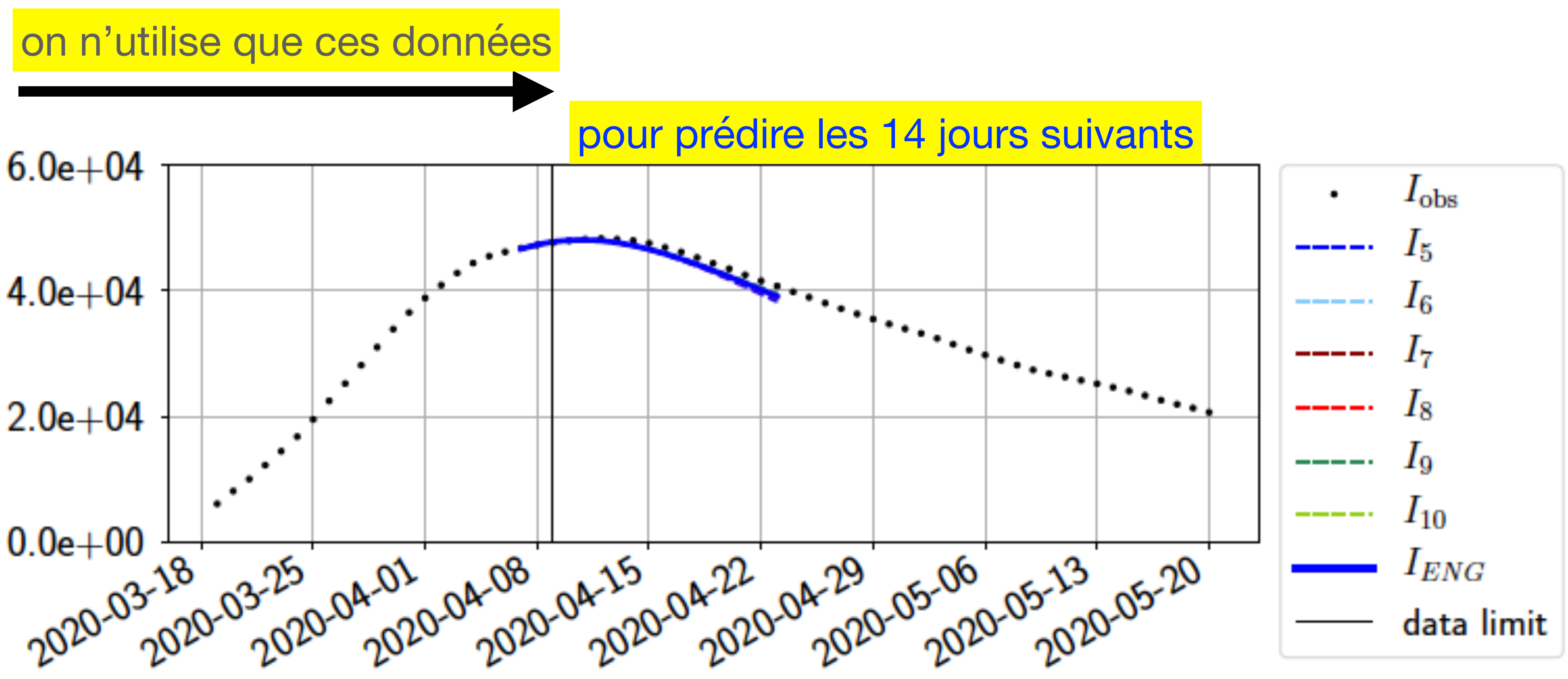
(d) Removed

Prévision au 1 Avril sur 14 jours/ comparaison avec les données Santé Publique France

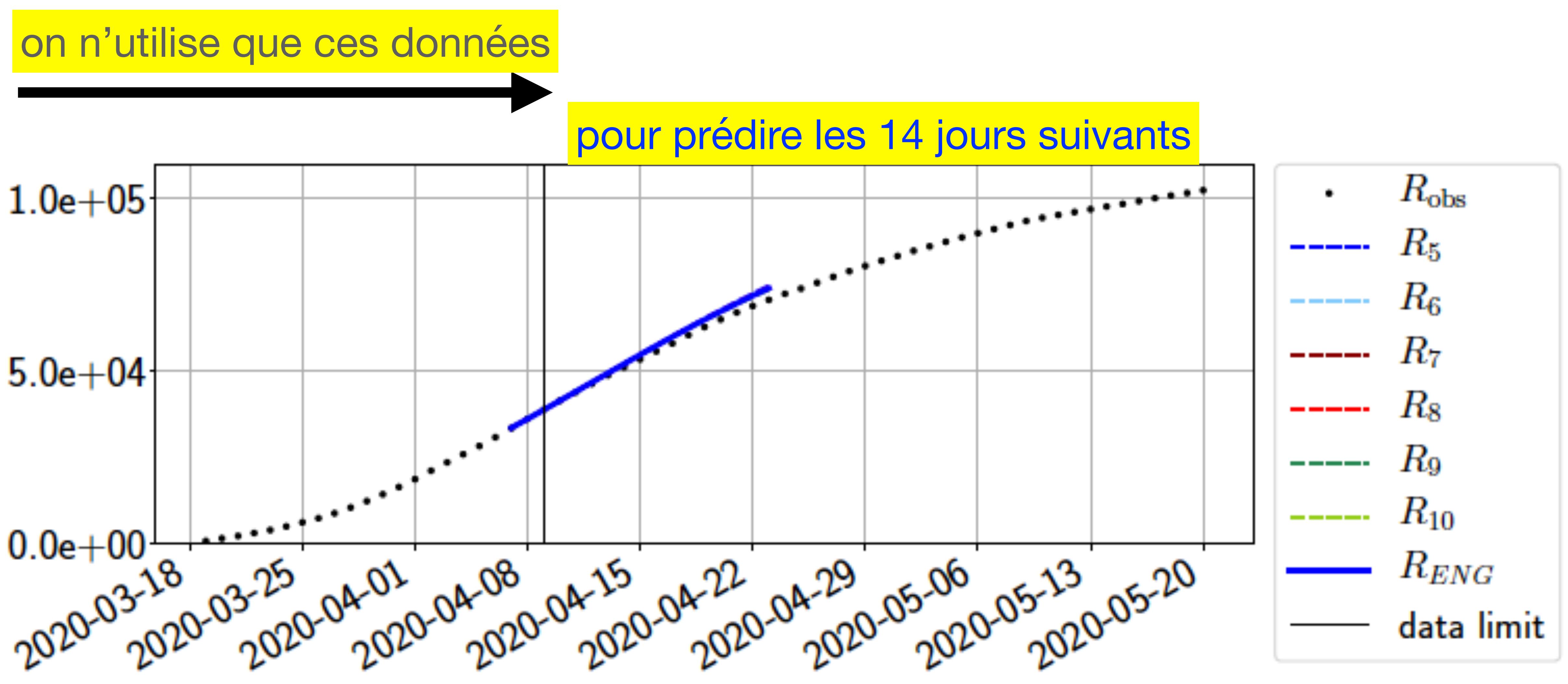


(c) Infected **(d)** Removed

Prévision au 7 avril sur 14 jours/ comparaison avec les données Santé Publique France

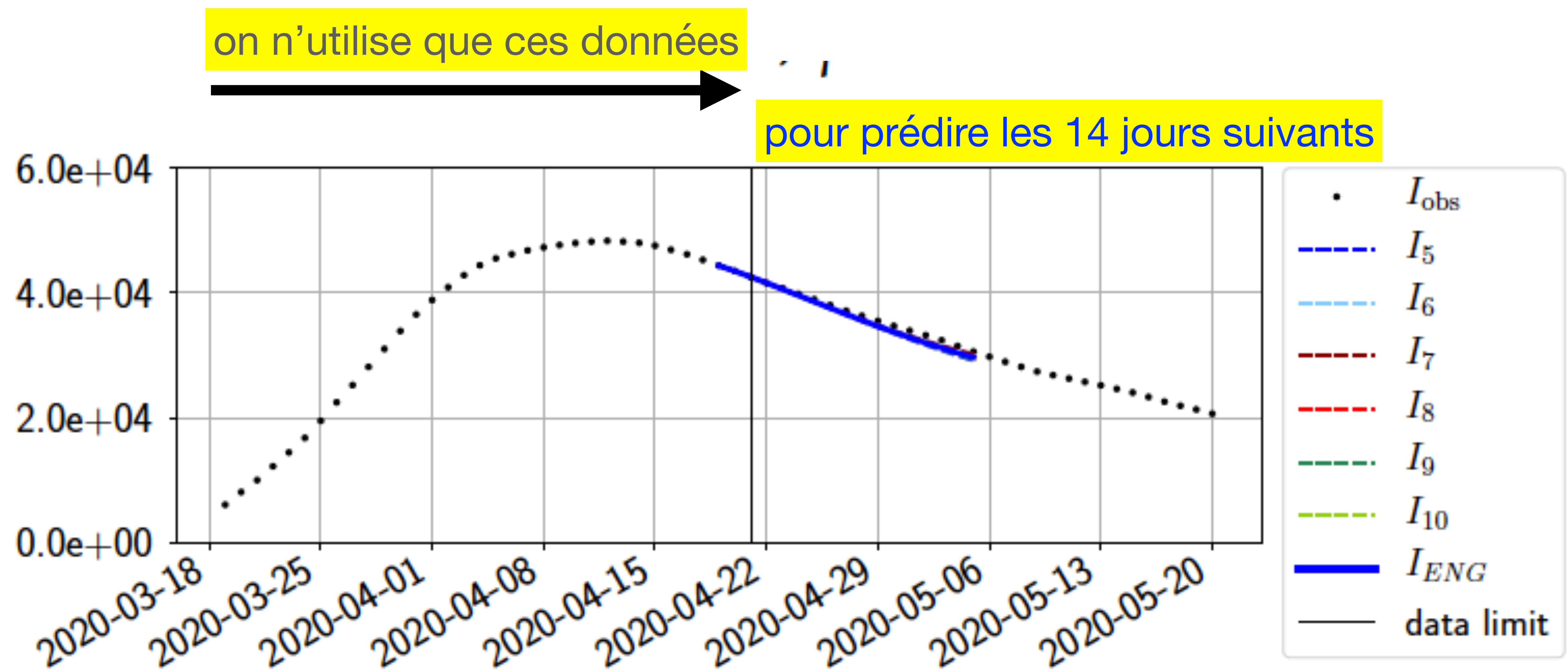


(c) Infected

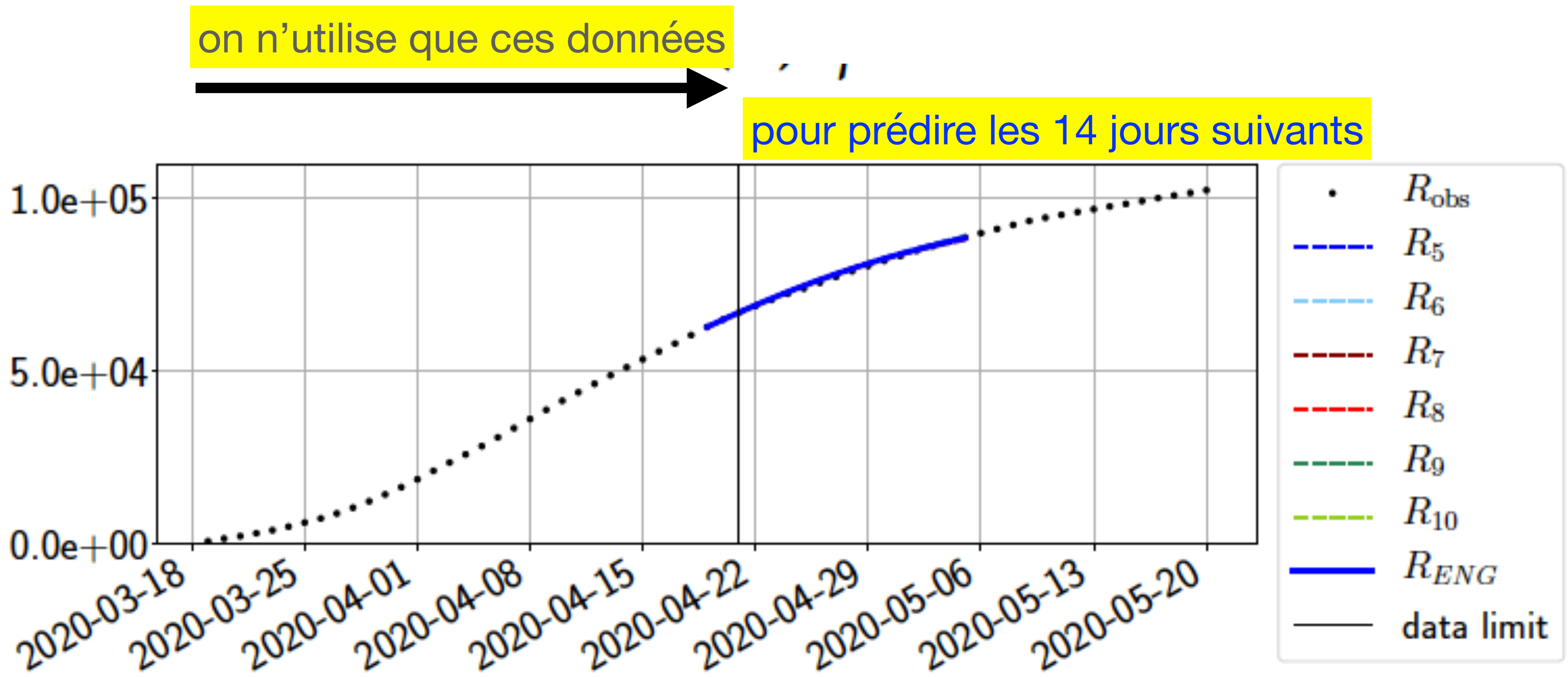


(d) Removed

Prévision au 9 avril sur 14 jours/ comparaison avec les données Santé Publique France



(c) Infected

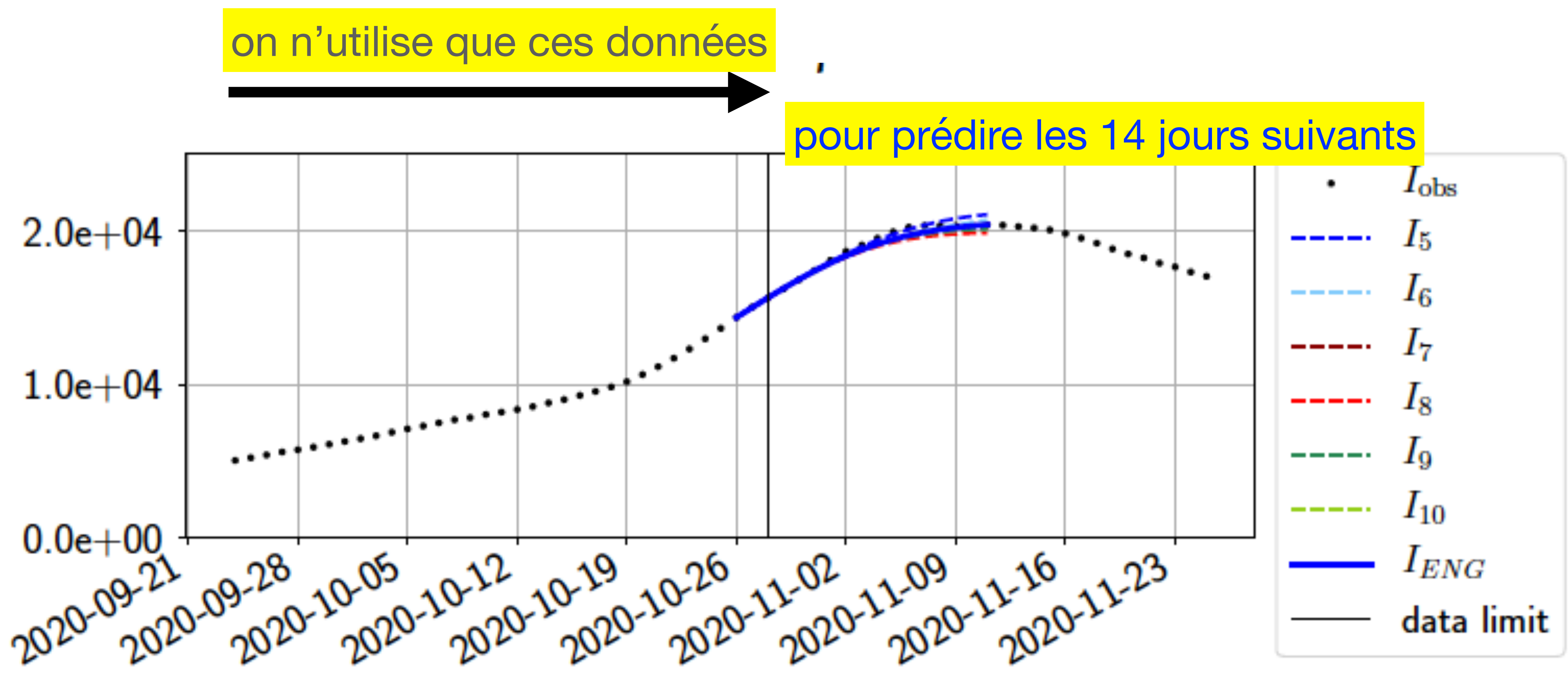


(d) Removed

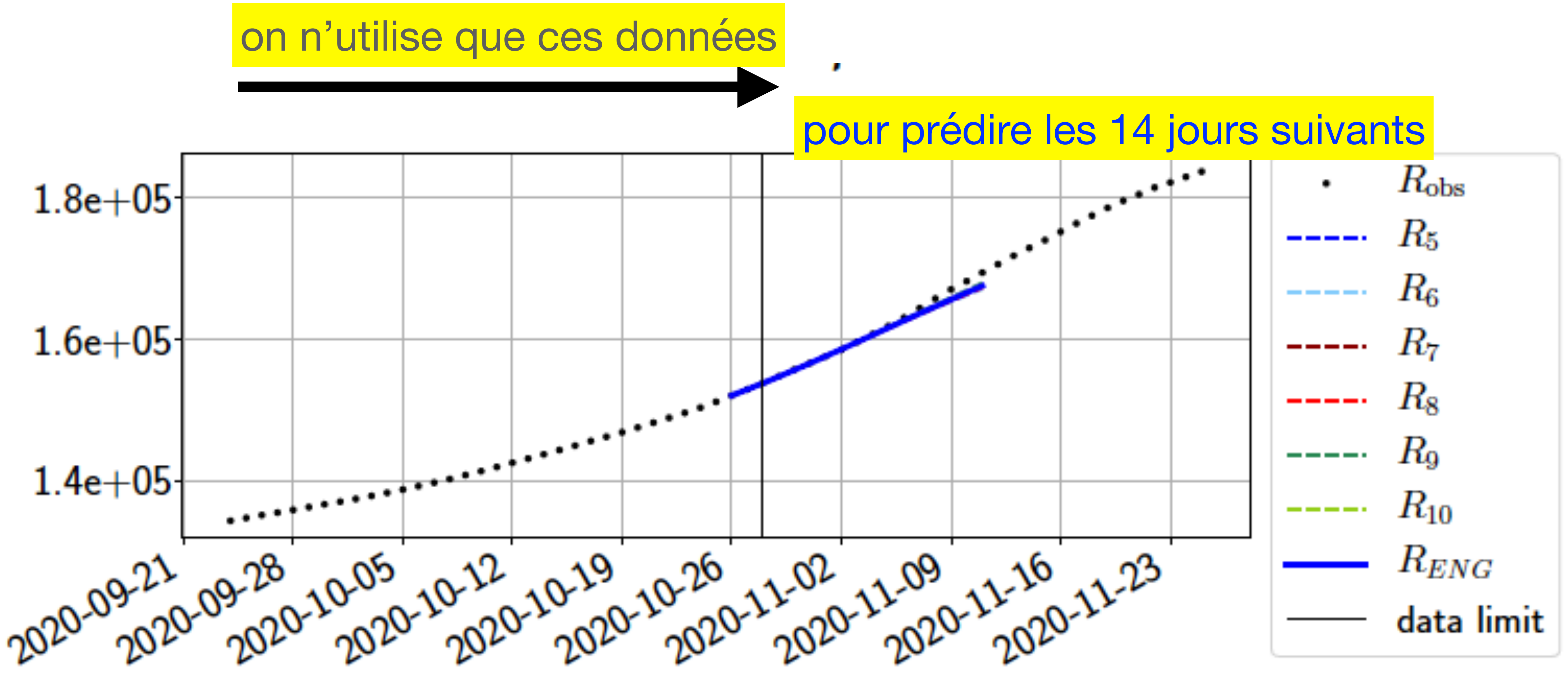
Prévision au 21 avril sur 14 jours/ comparaison avec les données Santé Publique France

Seconde vague

on connait la suite mais on ne l’utilise pas

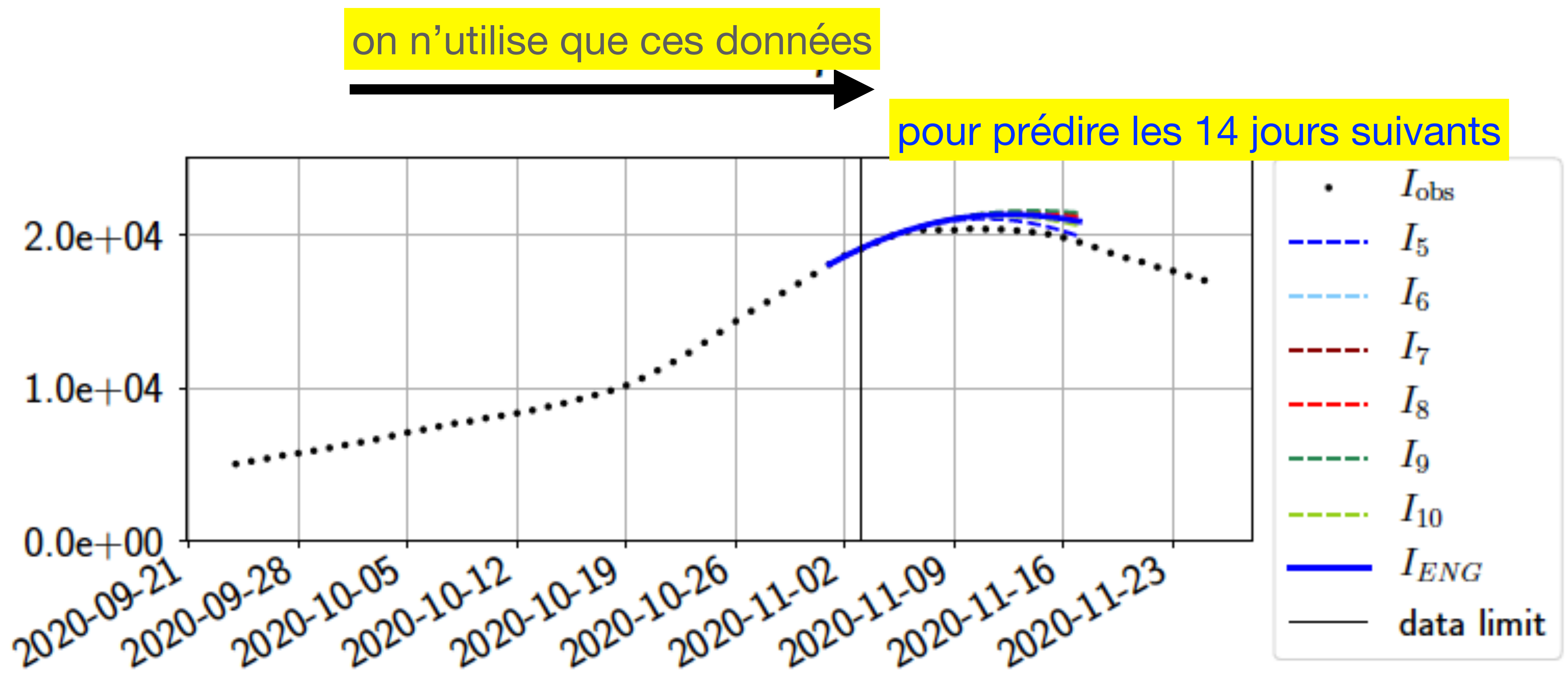


(c) Infected

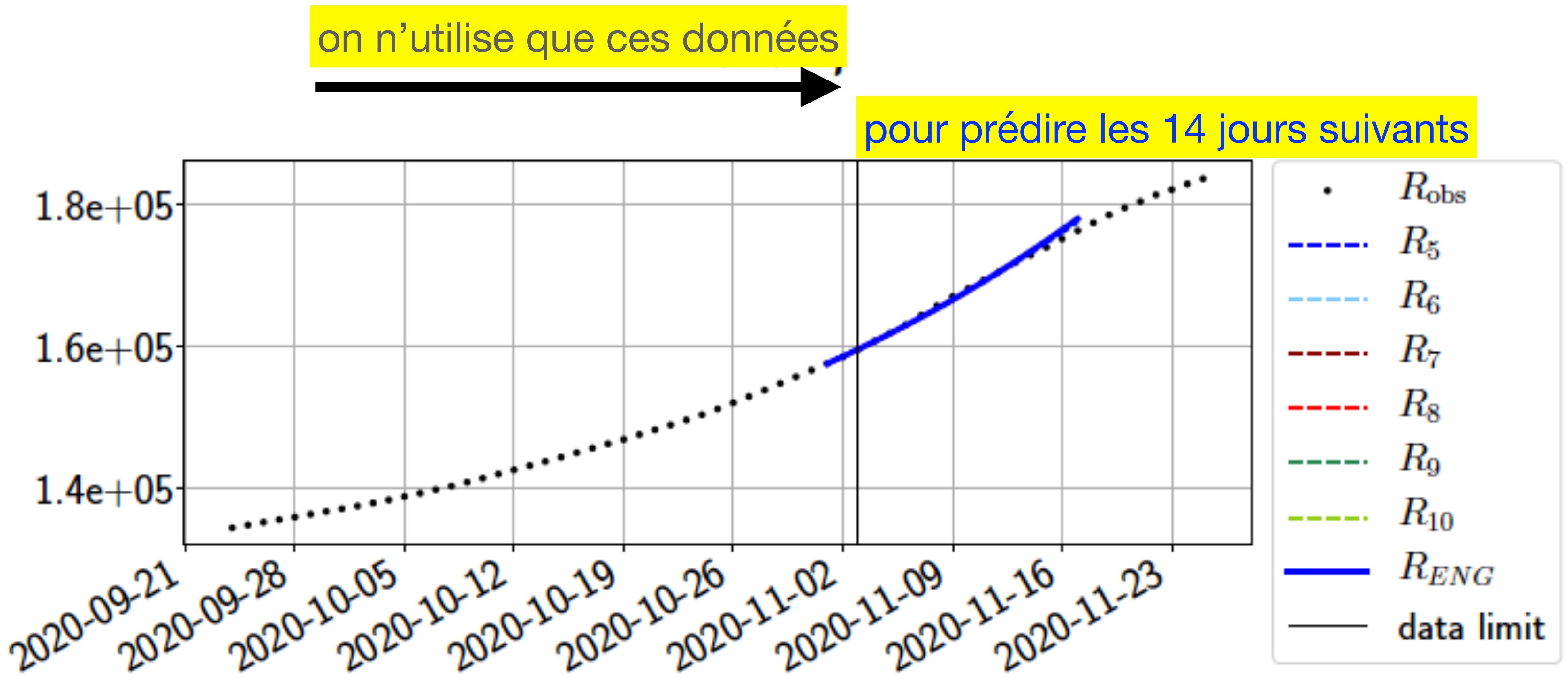


(d) Removed

Prévision au 28 Octobre sur 14 jours/ comparaison avec les données Santé Publique France



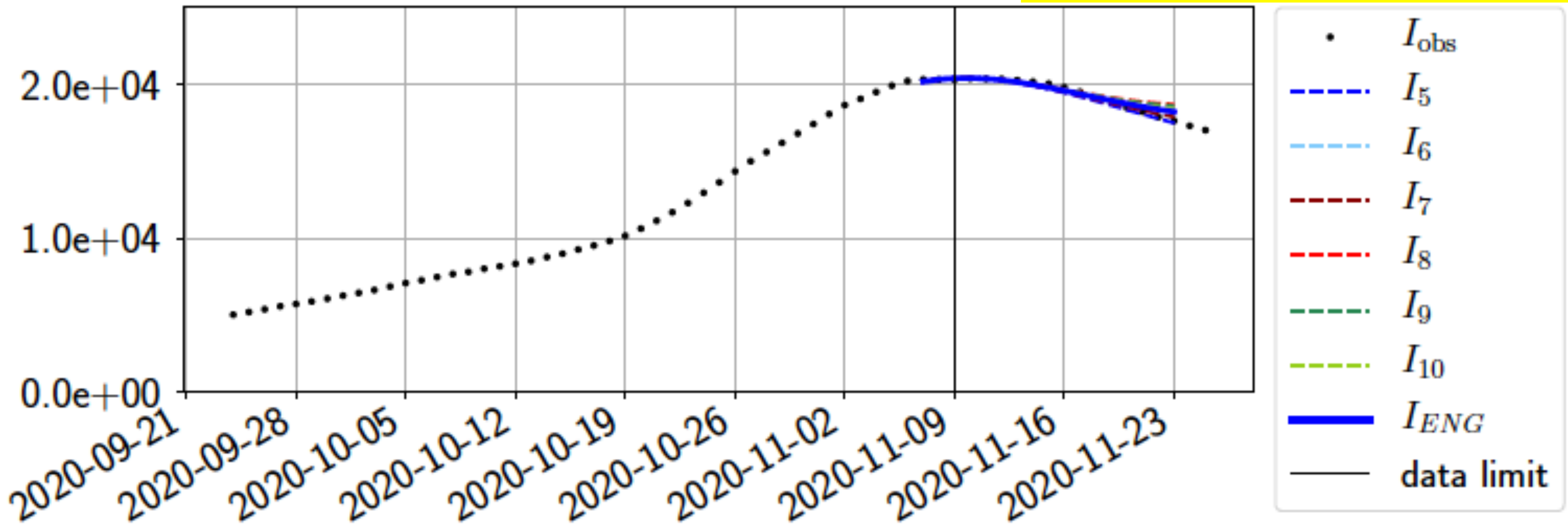
(c) Infected



(d) Removed

Prévision au 3 Novembre sur 14 jours/ comparaison avec les données Santé Publique France on n’utilise que ces données

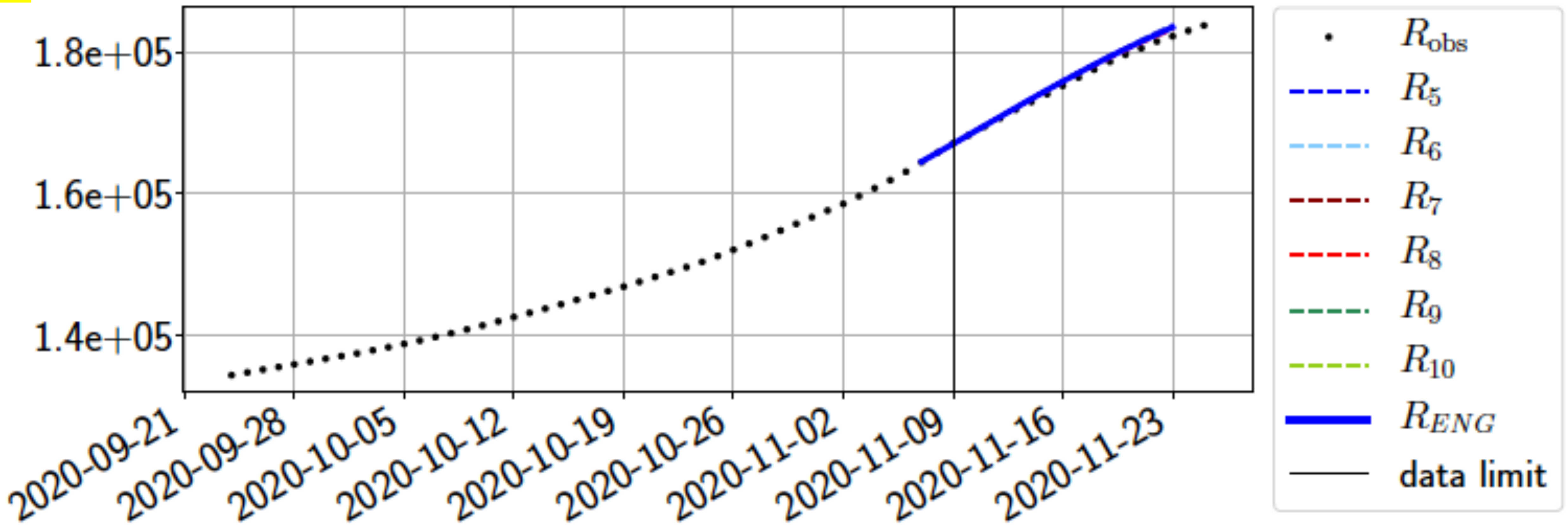
pour prédire les 14 jours suivants



(c) Infected

on n’utilise que ces données

pour prédire les 14 jours suivants



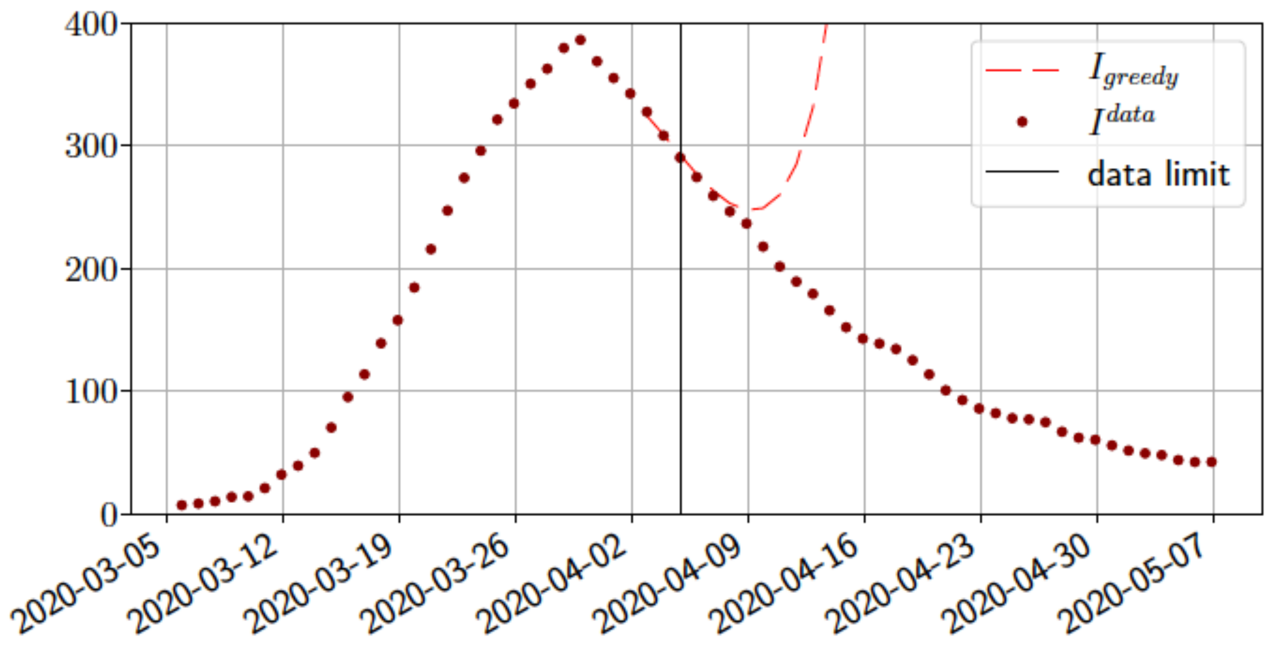
(d) Removed

Prévision au 9 Novembre sur 14 jours/ comparaison avec les données Santé Publique France

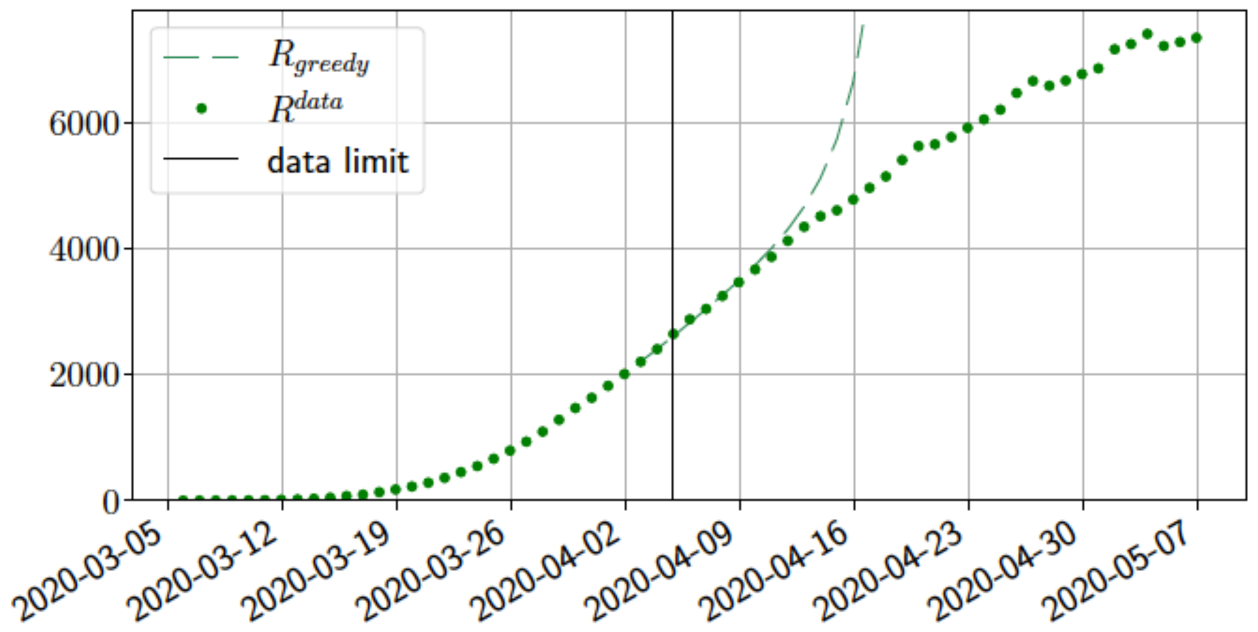
And then!

and provide a reduced basis for interpolation… and extrapolation…

actually it may not be so good !



(a) Infected, β, γ fit

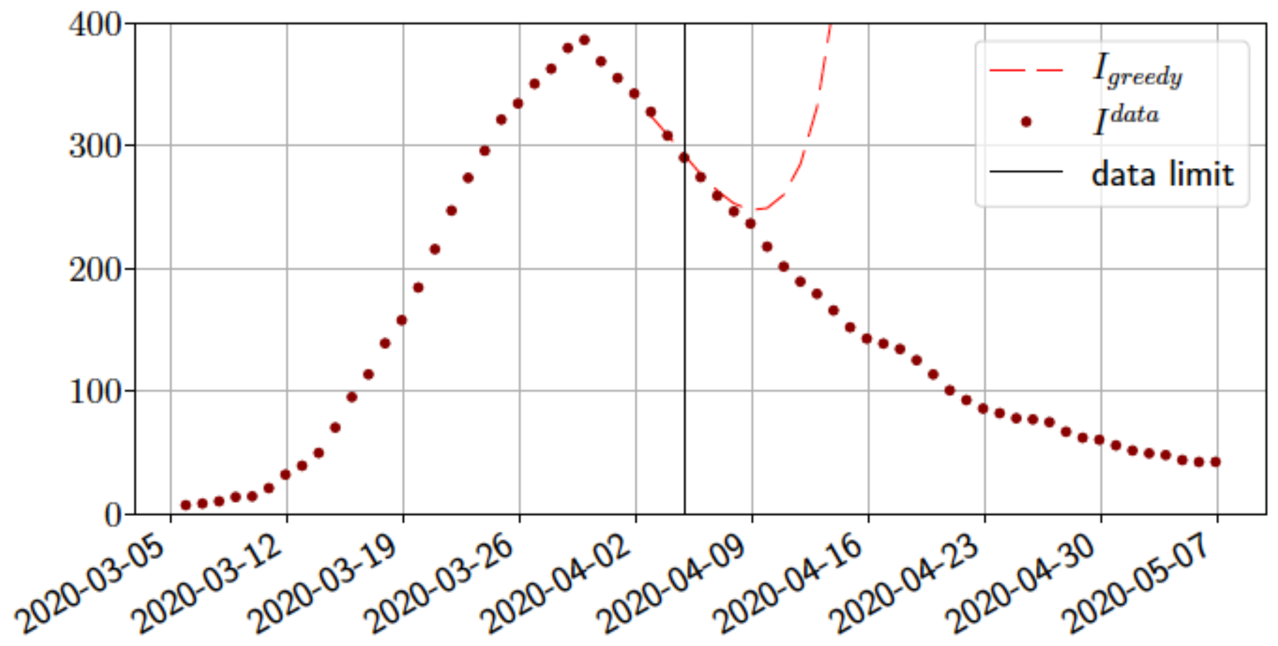


(c) Recovered, β, γ fit

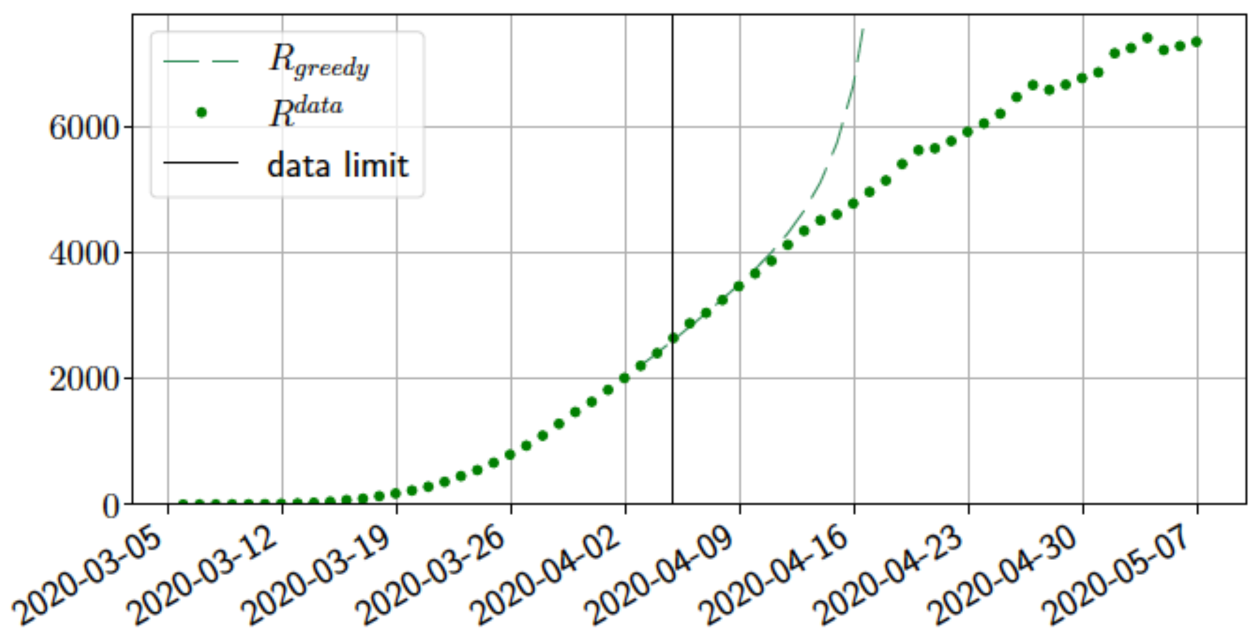
And then!

and provide a reduced basis for interpolation… and extrapolation…

actually it may not be so good !



(a) Infected, β, γ fit



(c) Recovered, β, γ fit

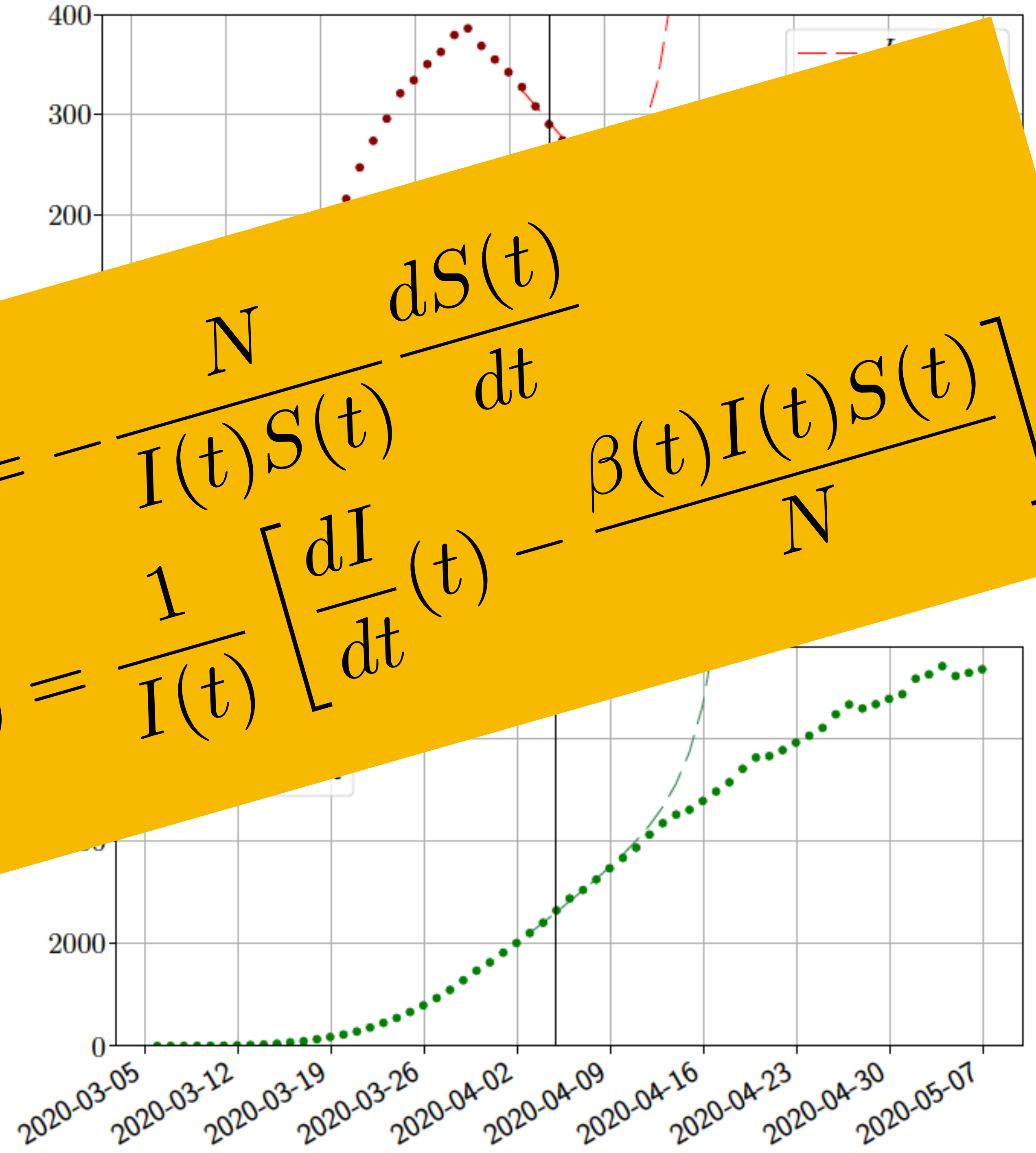
the reason is that β and γ should remain positive !

Bakhta, A., Boiveau, T., Maday, Y., & Mula, O. (2021).
Epidemiological Forecasting with Model Reduction of Compartmental Models. Application to the COVID-19 Pandemic. *Biology*, *10*(1), 22.

And then!

and provide a reduced basis for interpolation… and extrapolation…

actually it may not be so good !



$$\beta(t) = -\frac{N}{I(t)S(t)}\frac{dS(t)}{dt}$$

$$\gamma(t) = \frac{1}{I(t)}\left[\frac{dI}{dt}(t) - \frac{\beta(t)I(t)S(t)}{N}\right]$$

(c) Recovered, β, γ fit

the reason is that β and γ should remain positive !

And then!

and provide a reduced basis for interpolation… and extrapolation…

$$\forall \mu, \quad \beta(.;\mu) \simeq \sum_{i=1}^{N} \alpha_i \beta_i(.)$$

the precision is enough to assure the positivity for INTERPOLATION

but not for FORECASTING = EXTRAPOLATION

And then!

and provide a reduced basis for interpolation… and extrapolation…

$$\forall \mu, \quad \beta(.;\mu) \simeq \sum_{i=1}^{N} \alpha_i \beta_i(.)$$

the precision is enough to assure the positivity for INTERPOLATION

but not for FORECASTING = EXTRAPOLATION

CURE …..

Impose positive coefficients …

And then!

and provide a reduced basis for interpolation… and extrapolation…

$$\forall \mu, \quad \beta(.;\mu) \simeq \sum_{i=1}^{N} \alpha_i \beta_i(.)$$

the precision is enough to assure the positivity for INTERPOLATION

but not for FORECASTING = EXTRAPOLATION

CURE …..

Impose positive coefficients … not sufficient …

And then!

and provide a reduced basis for interpolation… and extrapolation…

$$\forall \mu, \quad \beta(.;\mu) \simeq \sum_{i=1}^{N} \alpha_i \beta_i(.)$$

CURE …..

Impose positive coefficients …

And then!

and provide a reduced basis for interpolation… and extrapolation…

$$\forall \mu, \quad \beta(.;\mu) \simeq \sum_{i=1}^{N} \alpha_i \beta_i(.)$$

enlarge the cone

CURE …..

Impose positive coefficients …

And then!

and provide a reduced basis for interpolation… and extrapolation…

enlarge the cone

Define a new basis set : $\tilde{\beta}_i$

$$\tilde{\beta}_i = \beta_i - \sum_{j \neq i} \lambda_j^i \beta_j$$

with positive coefficients λ_j^i

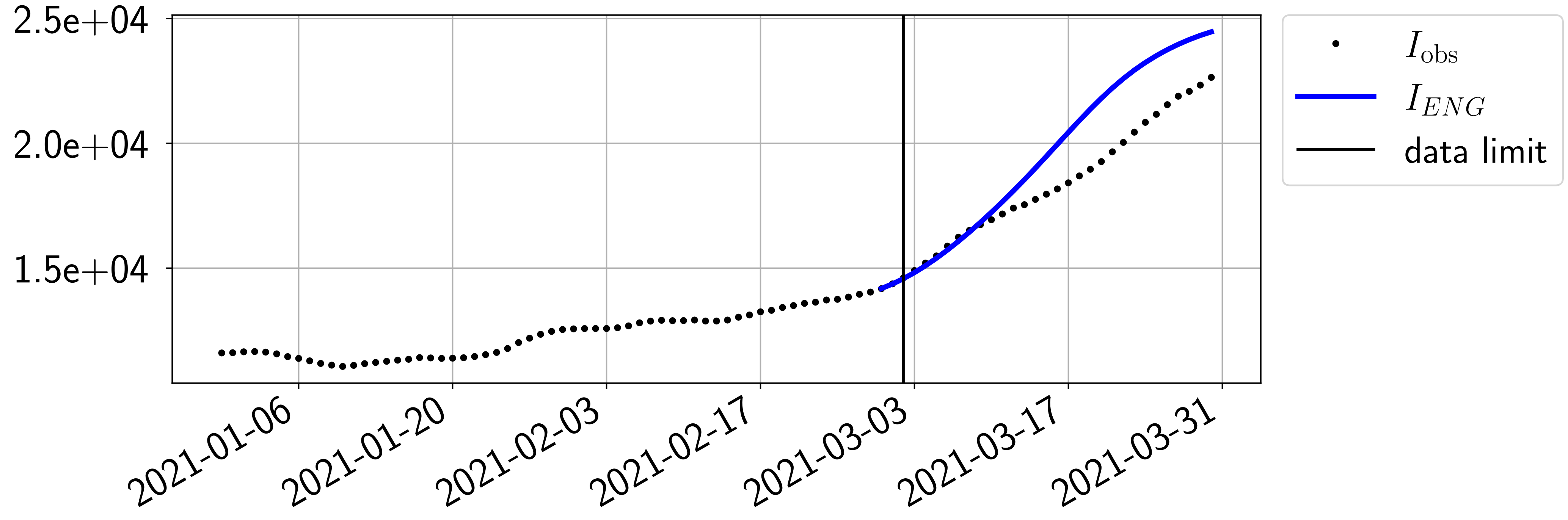
so as to maintain the positivity of $\tilde{\beta}_i$ but minimize its L^∞ norm

and then set

$$\forall \mu; \beta(.;\mu) \simeq \sum_{i=1}^{N} \alpha_i \tilde{\beta}_i(.)$$

on n'utilise que ces données

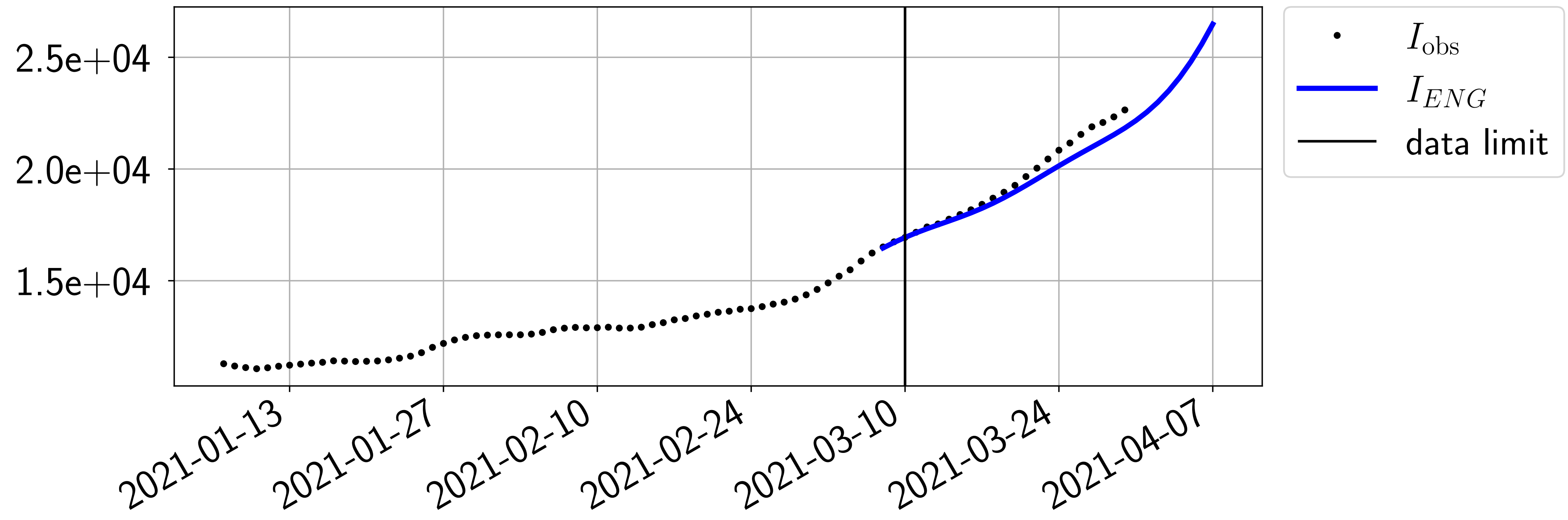
pour prédire les 14 jours suivants



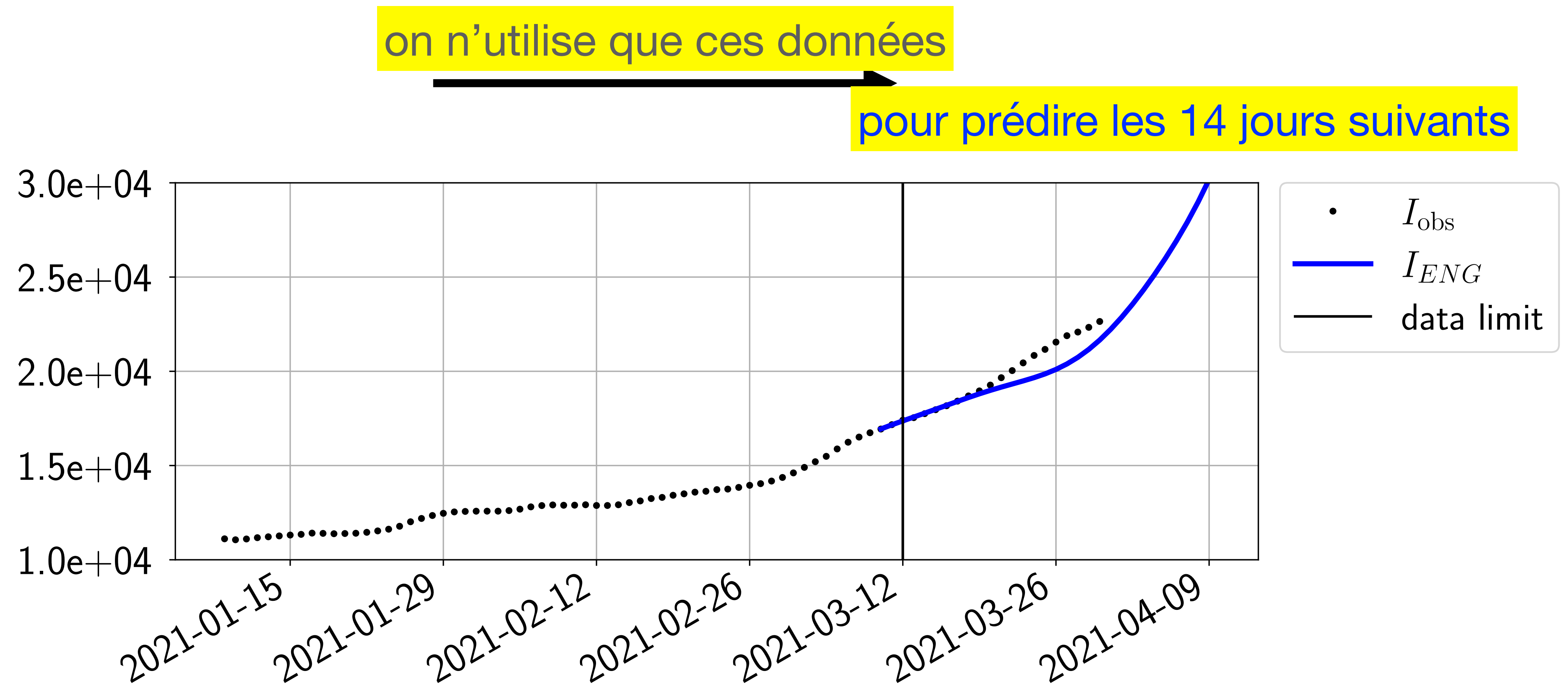
Prévision au 2 Mars sur 14 jours/ comparaison avec les données Santé Publique France

on n'utilise que ces données

pour prédire les 14 jours suivants



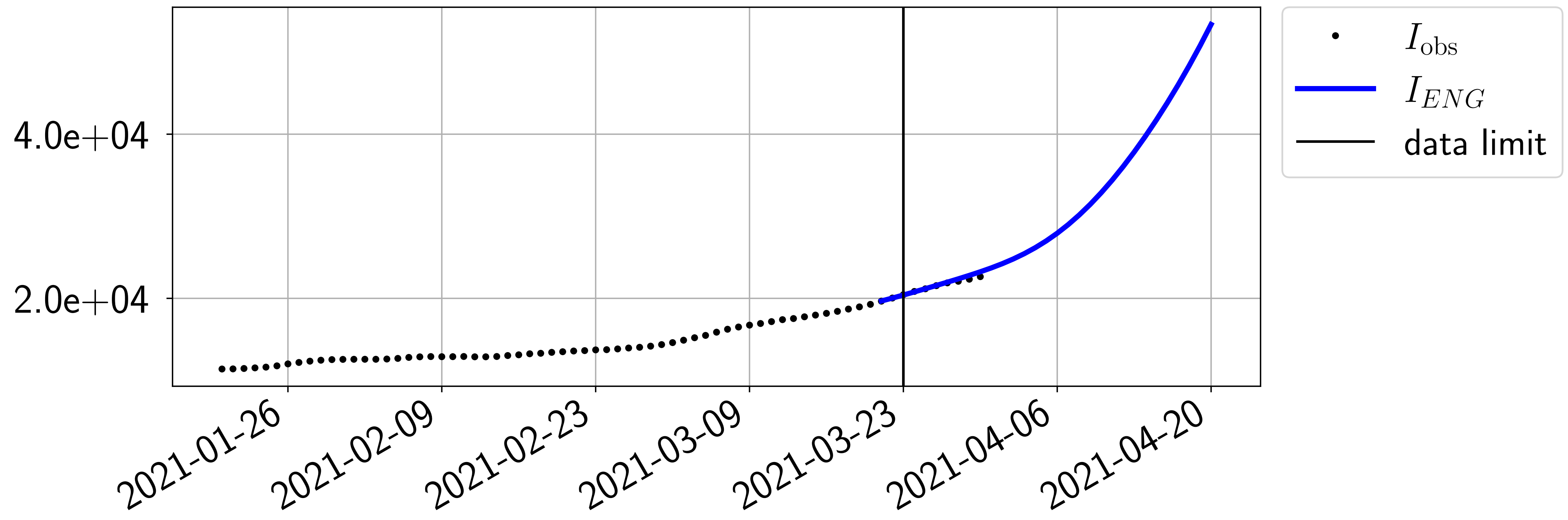
Prévision au 10 Mars sur 14 jours/ comparaison avec les données Santé Publique France



Prévision au 12 Mars sur 14 jours/ comparaison avec les données Santé Publique France

on n'utilise que ces données

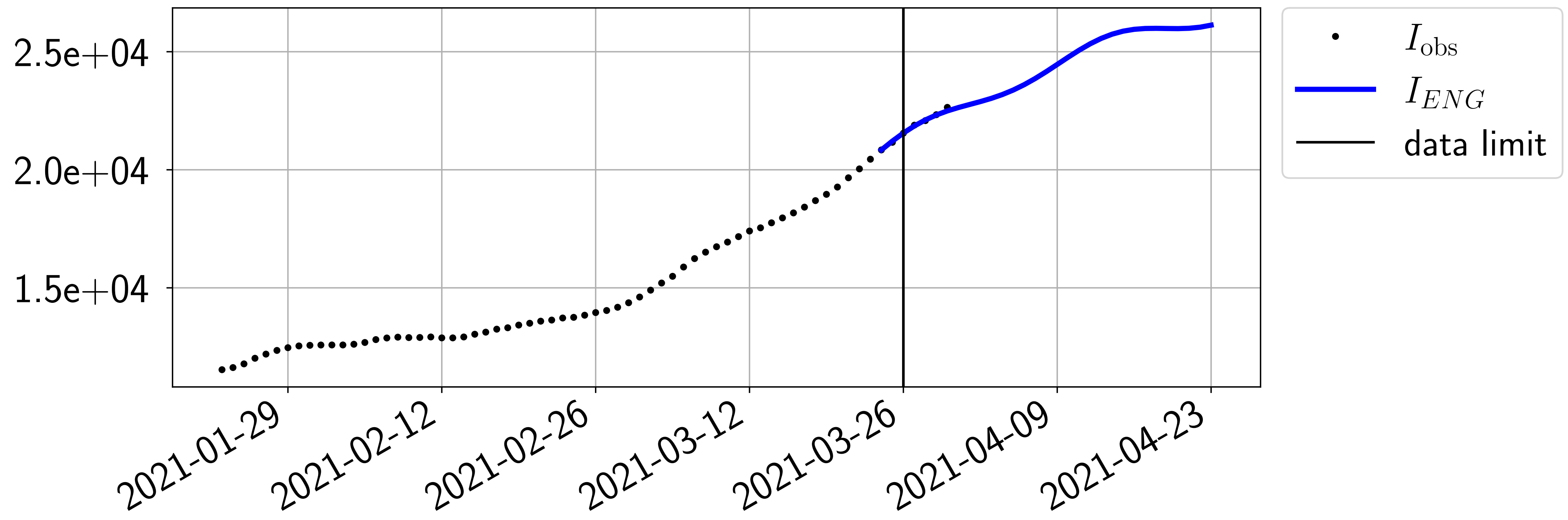
pour prédire les 14 jours suivants



Prévision au 23 Mars sur 14 jours/ comparaison avec les données Santé Publique France

on n'utilise que ces données

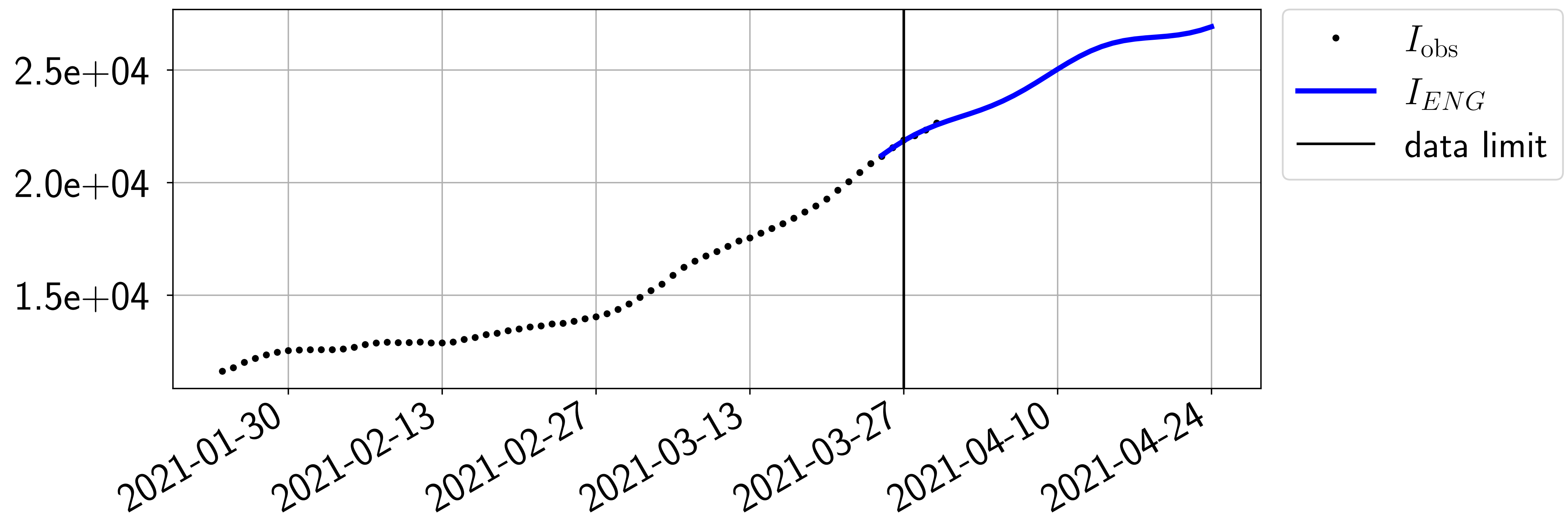
pour prédire les 14 jours suivants



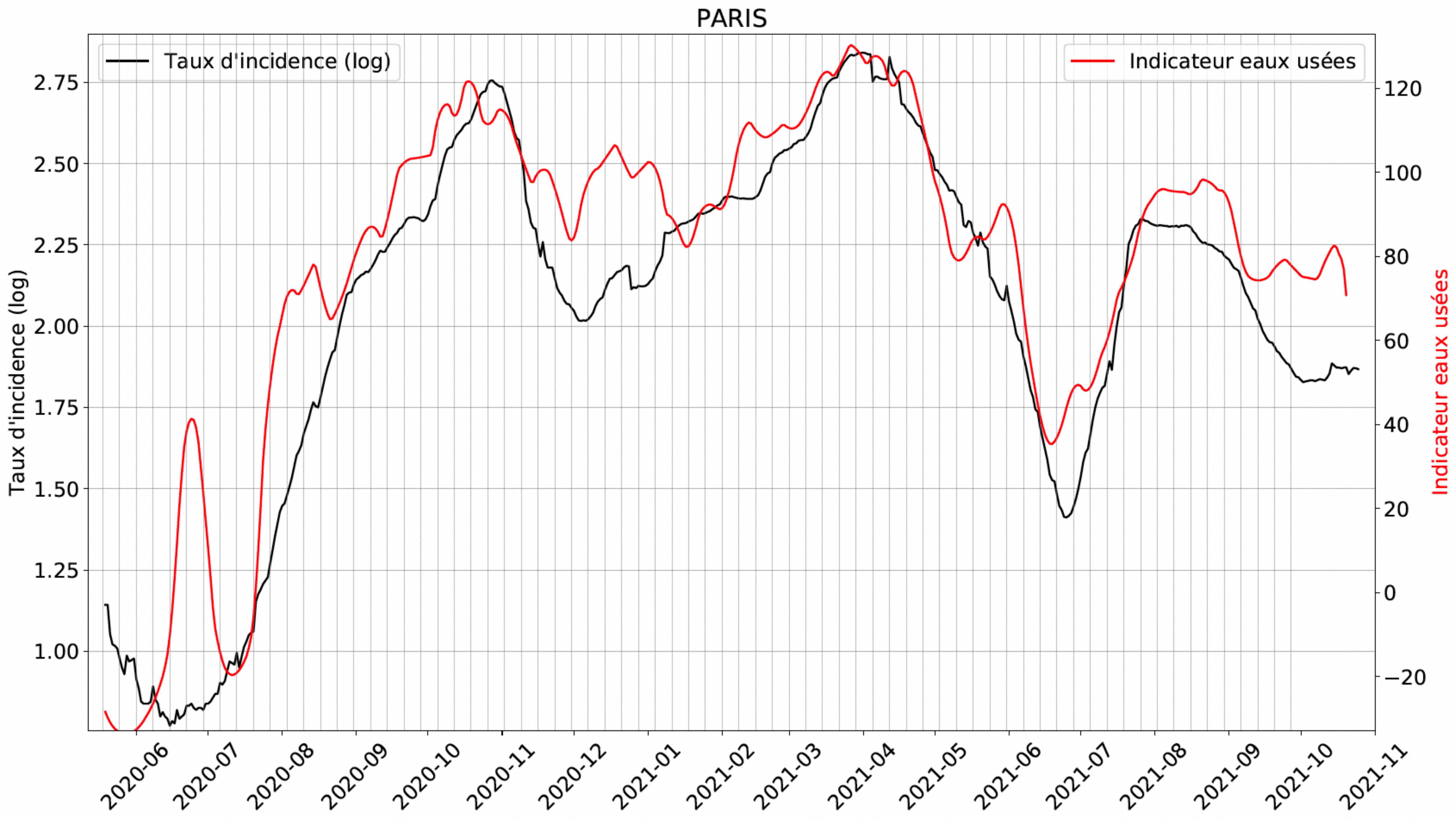
Prévision au 26 Mars sur 14 jours/ comparaison avec les données Santé Publique France

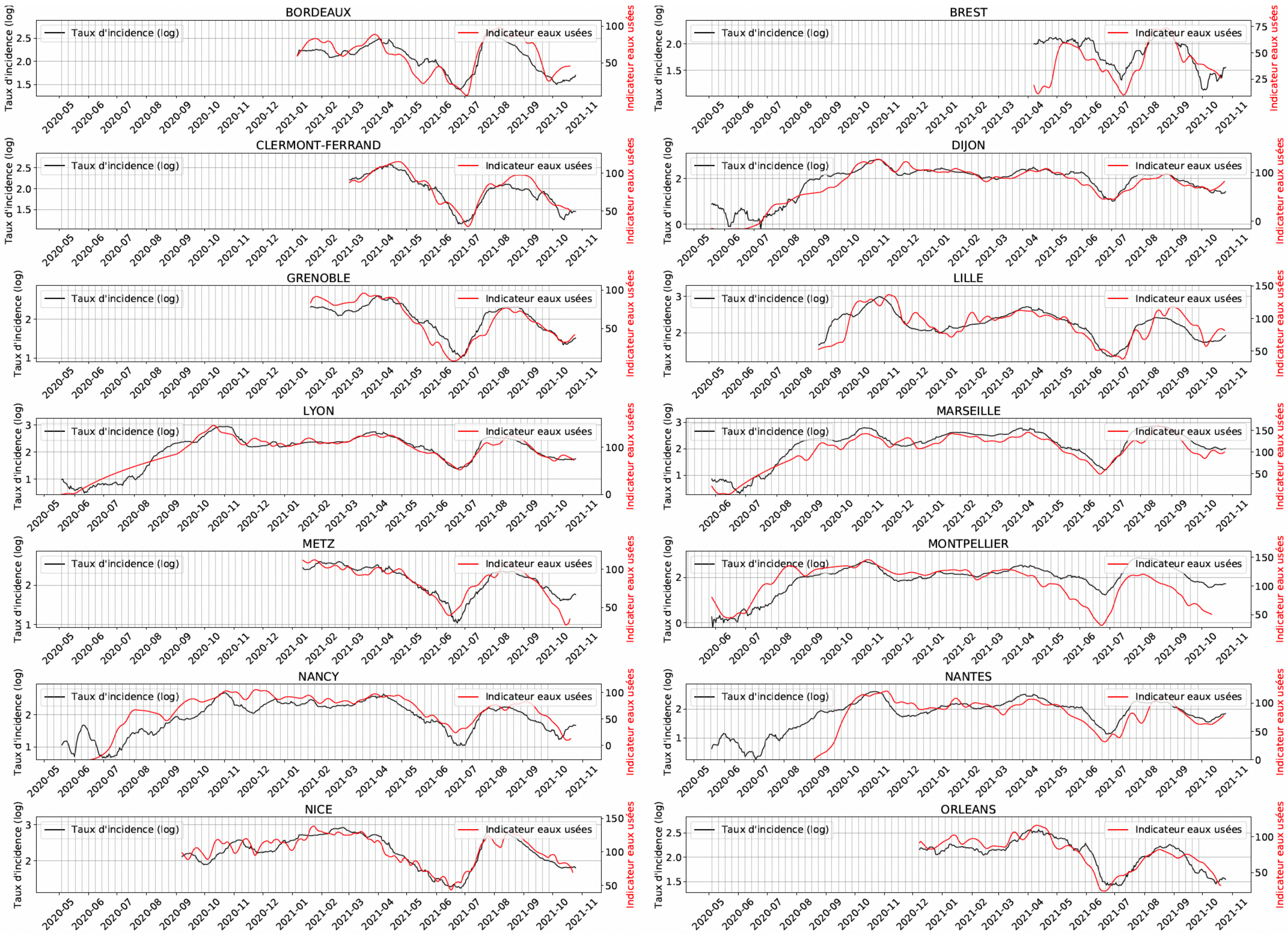
on n'utilise que ces données

pour prédire les 14 jours suivants



Prévision au 27 Mars sur 14 jours/ comparaison avec les données Santé Publique France


PARIS
Taux d'incidence (log)
Indicateur eaux usées
2.75
2.50
2.25
2.00
1.75
1.50
1.25
1.00
120
100
80
60
40
20
0
−20
2020-06
2020-07
2020-08
2020-09
2020-10
2020-11
2020-12
2021-01
2021-02
2021-03
2021-04
2021-05
2021-06
2021-07
2021-08
2021-09
2021-10
2021-11


BORDEAUX
BREST
CLERMONT-FERRAND
DIJON
GRENOBLE
LILLE
LYON
MARSEILLE
METZ
MONTPELLIER
NANCY
NANTES
NICE
ORLEANS
Taux d'incidence (log)
Indicateur eaux usées

La mécanique à l'interface des autres disciplines

en fait, en mécanique, il y a des modèles plus solides

avec des instruments pour mesurer les constantes

La mécanique à l’interface des autres disciplines

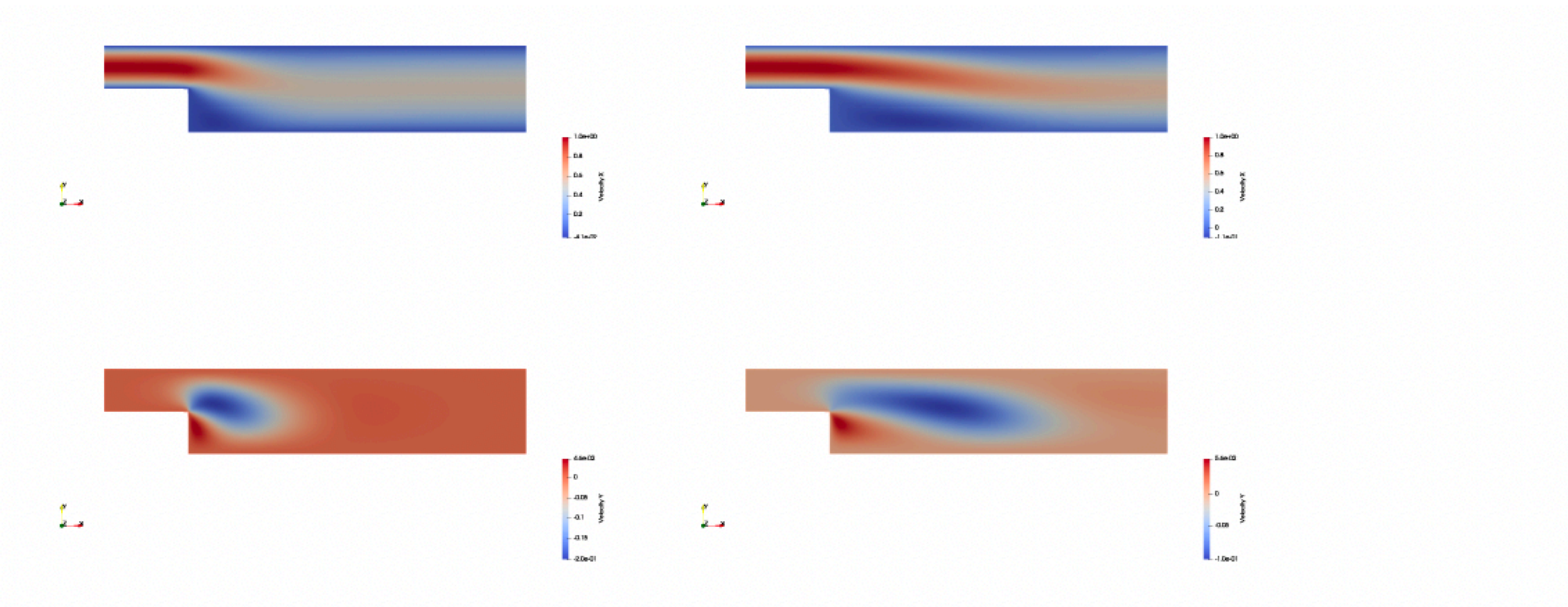
en fait, en mécanique, il y a des modèles plus solides

avec des instruments pour mesurer les constantes

mais il reste pas mal d’incertitudes

ou des approximations à réaliser

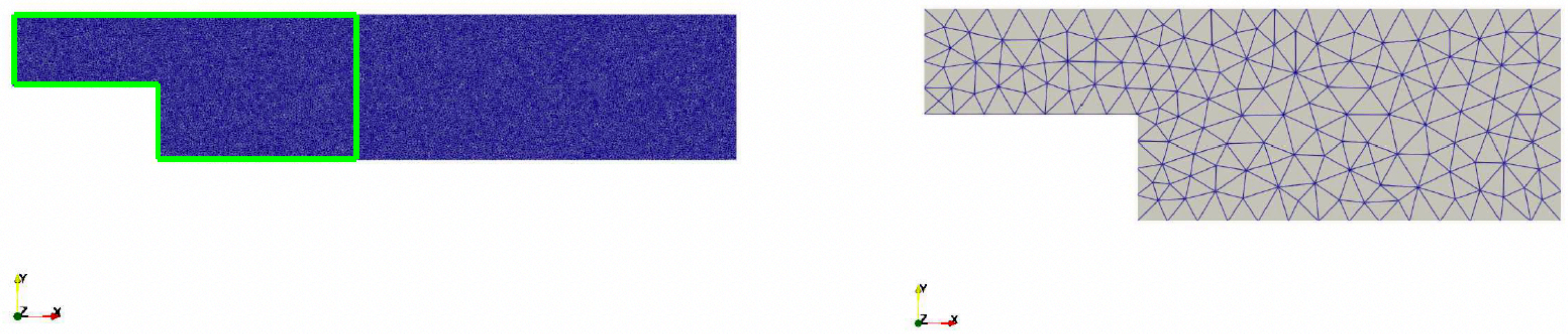
un exemple ou des approximations sont réaliseées



Velocities (u_1 and u_2) for Reynolds=52 (left) and Reynolds=233 (right)

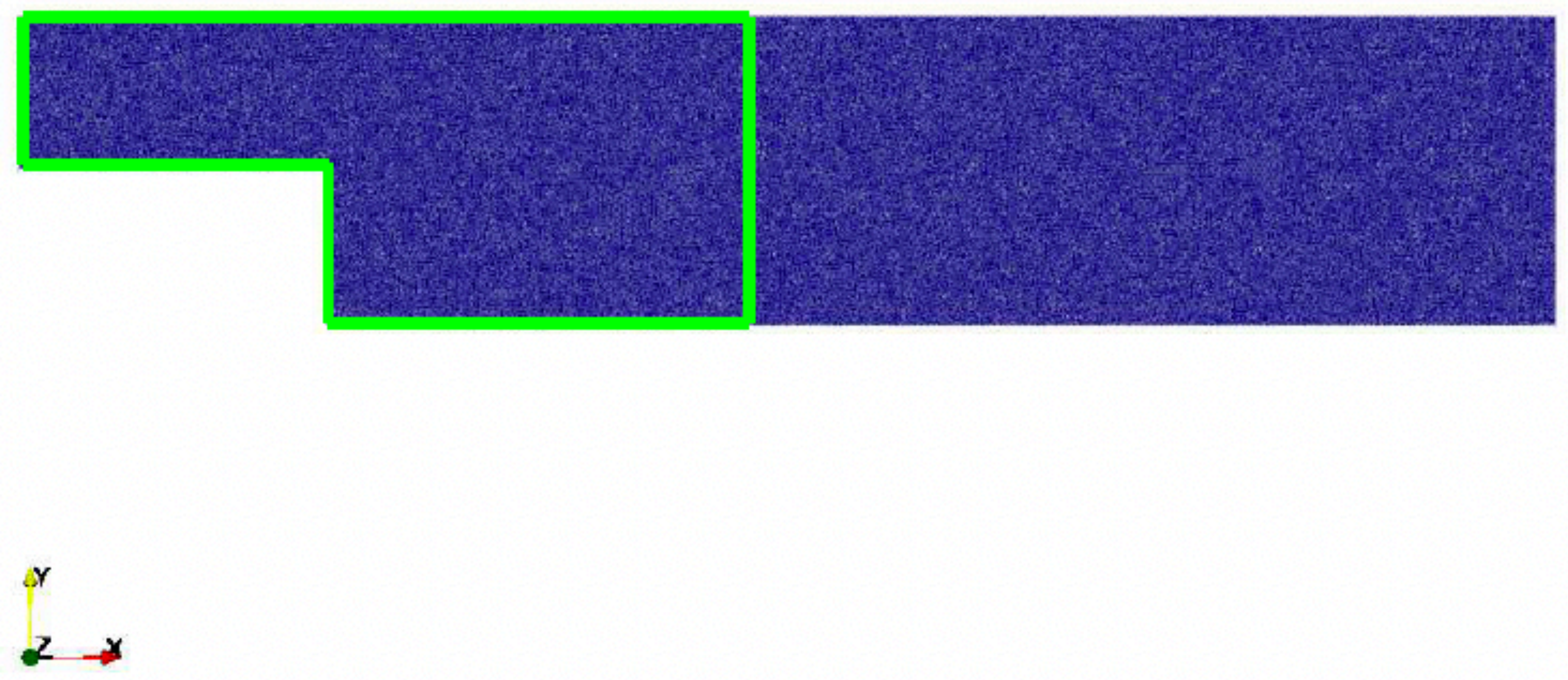
thèse de Elise Grosjean

un exemple ou des approximations sont réaliseées

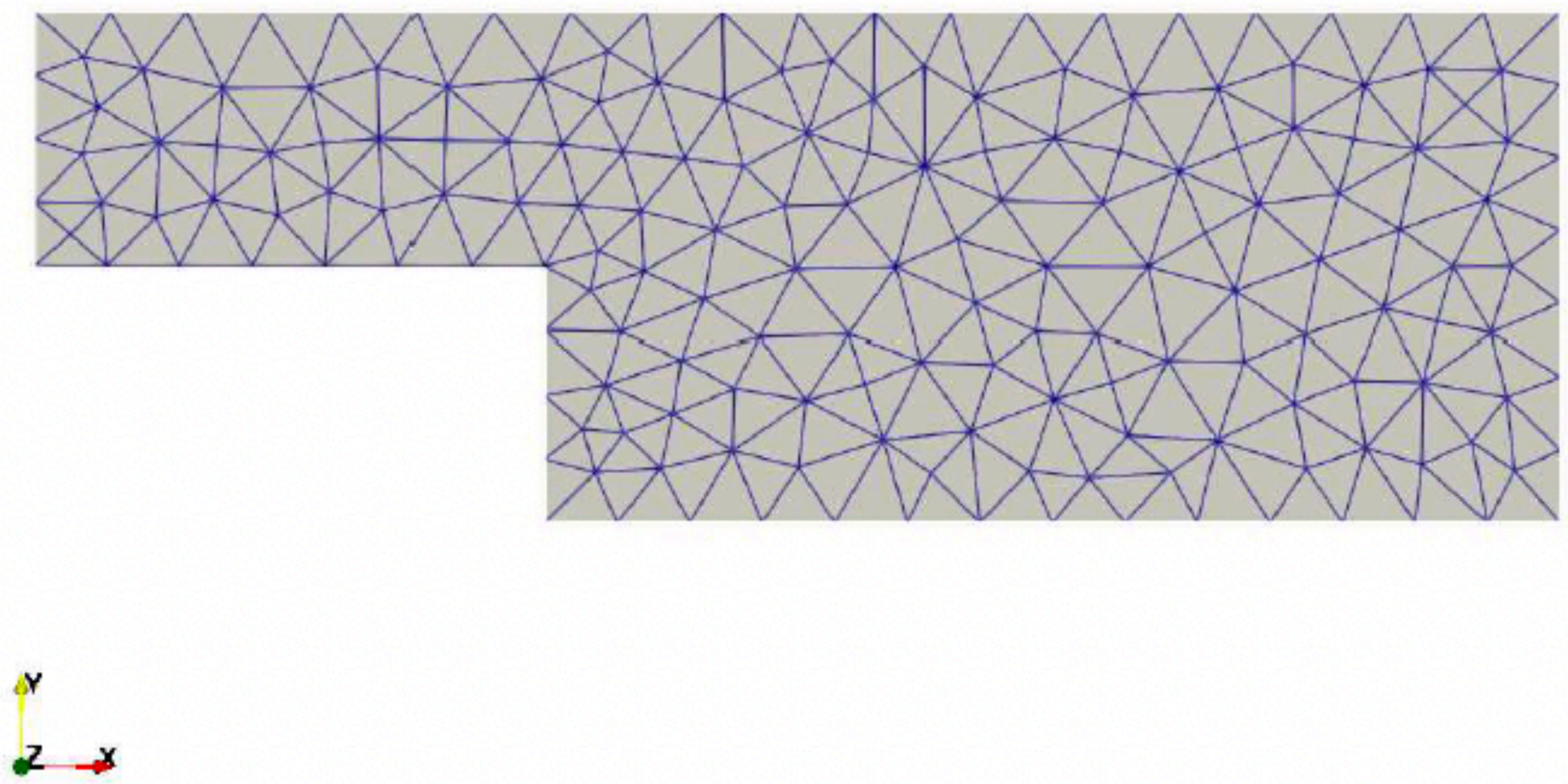


thèse de Elise Grosjean

un exemple ou des approximations sont réaliseées

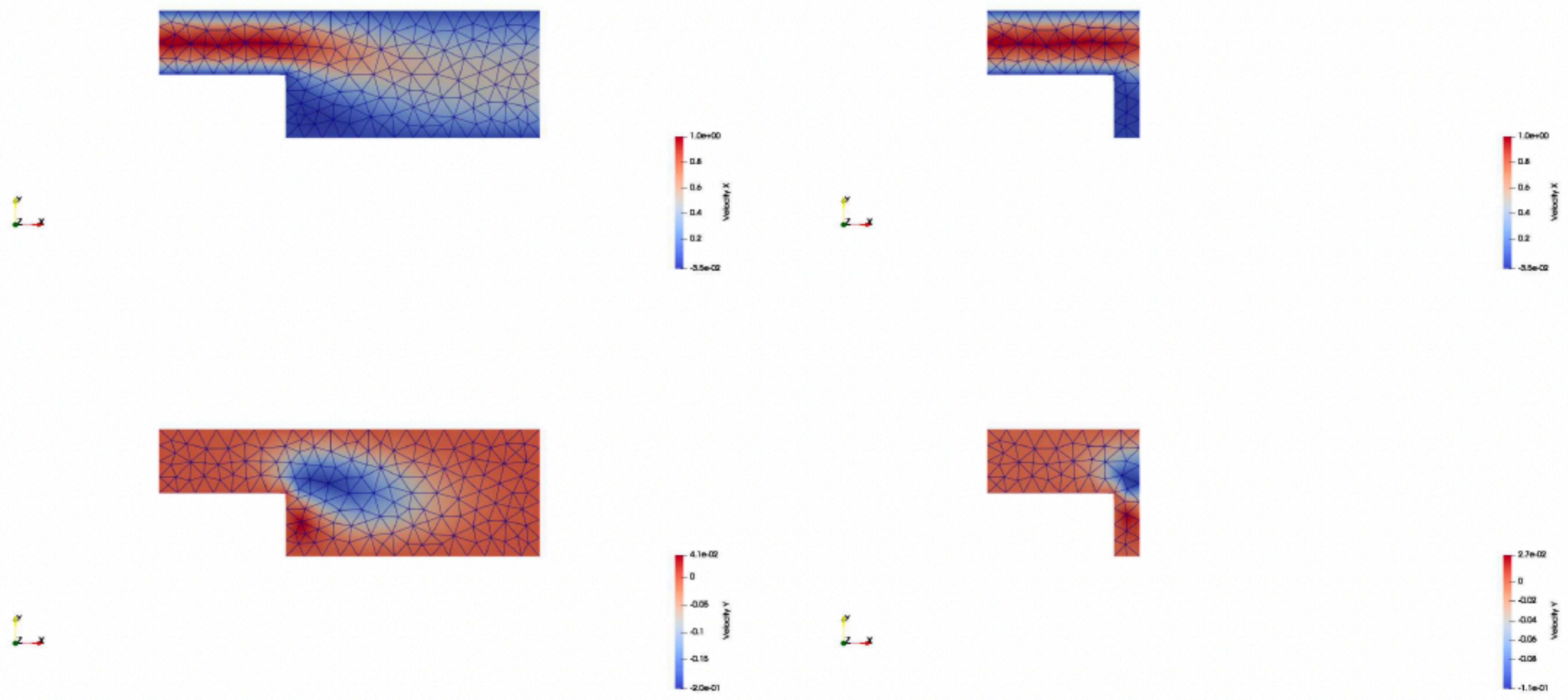


NIRB + réduction du domaine



thèse de Elise Grosjean

un exemple ou des approximations sont réaliseées

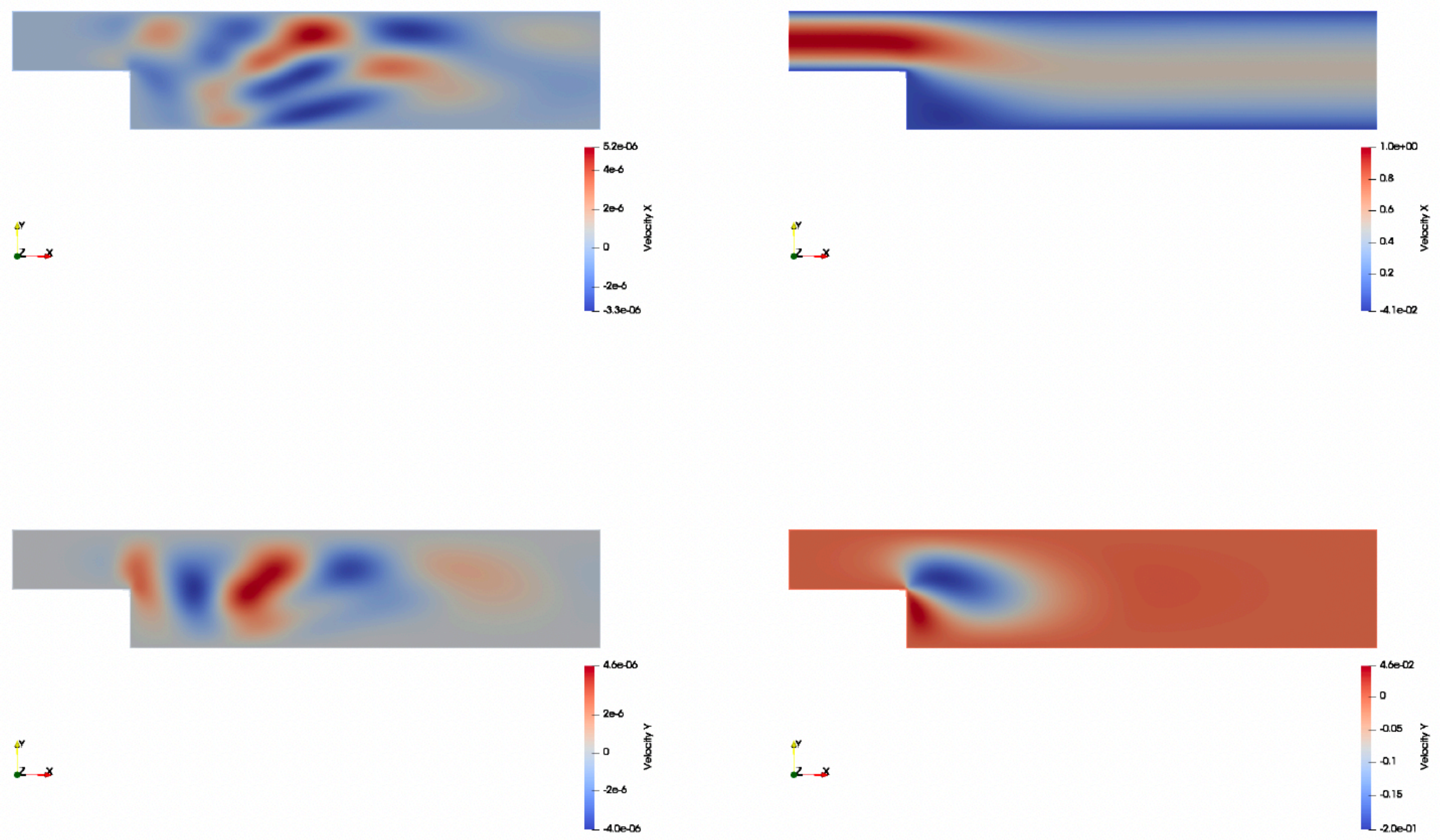


Coarse solution for Re=52 computed with the solver on the truncated domain with $L = 3$ (left), and with $L = 1.2$ (right)

NIRB + réduction du domaine

thèse de Elise Grosjean

un exemple ou des approximations sont réaliseées

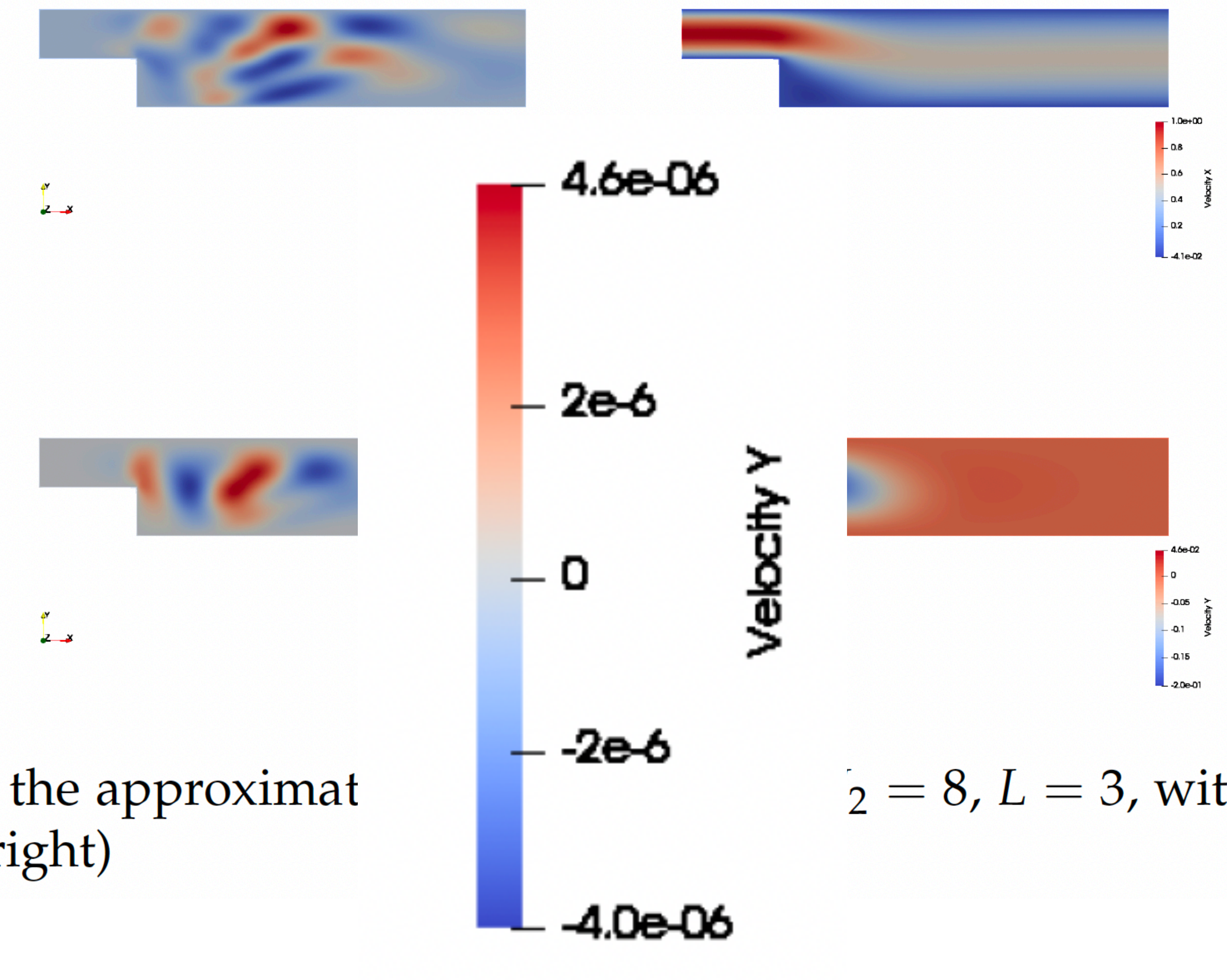


Error of the approximation for $N_1 = 7$ and $N_2 = 8$, $L = 3$, with $Re = 52$ (left) and the approximation (right)

NIRB + réduction du domaine

thèse de Elise Grosjean

un exemple ou des approximations sont réaliseées



Error of the approximat ... $_2 = 8$, $L = 3$, with $Re = 52$ (left) and the approximation (right)

NIRB + réduction du domaine

thèse de Elise Grosjean

un exemple ou des approximations sont réaliseées

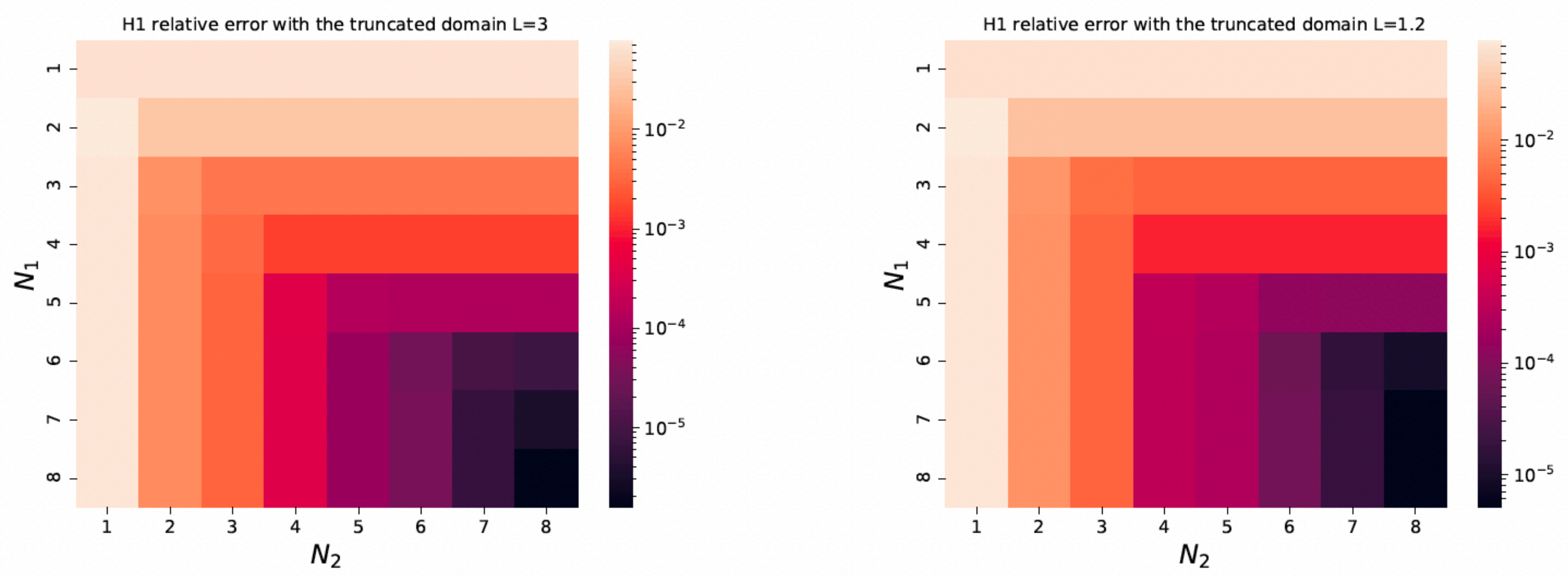
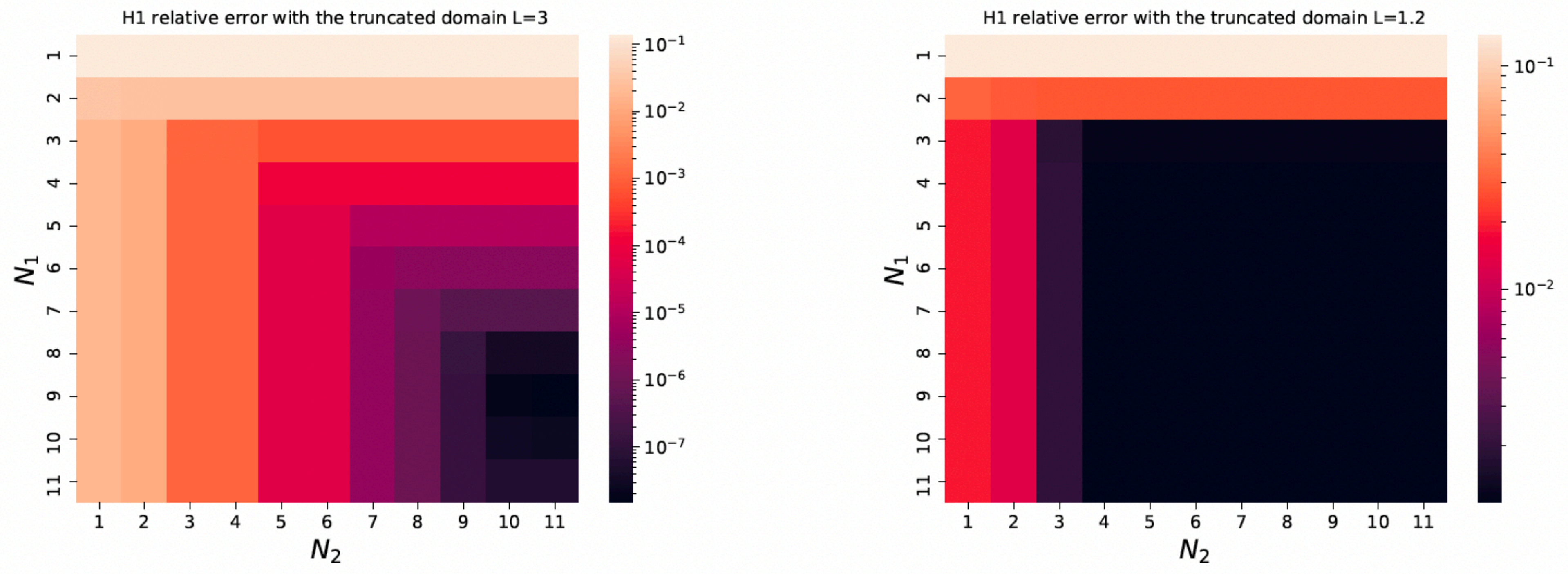


Figure 3.17: H_1 relative error for Re=52 with Greedy algorithm ($\lambda = 0$) on $\mathcal{G}_1$ with $L = 3$ (left), and with $L = 1.2$ ($\lambda = 0$) (right)



NIRB + réduction

Figure 3.18: H_1 relative error for Re=233 with Greedy algorithm ($\lambda = 0$) on $\mathcal{G}_2$ with $L = 3$ (left), and with $L = 1.2$ ($\lambda = 1e - 10$) (right)

these de Elise Grosjean

La mécanique à l’interface des autres disciplines

en fait, en mécanique, il y a des modèles plus solides

av… [illegible] pour mesurer les constantes

More to come ....

mais il reste pas mal d’incertitudes

ou des approximations à réaliser