

# COVID 19 — From modeling to estimation using Kalman based estimators

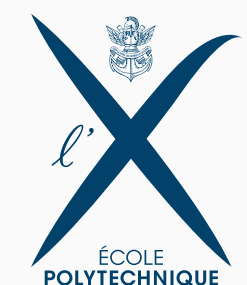
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Part of joint work with

Linda Wittkop<sup>1,2,3,5</sup>, Dan Dutartre<sup>1</sup>, Quentin Clairon<sup>2,3,4</sup>, Rodolphe Thiébaut<sup>1,2,3,4,5</sup>, Boris P. Hejblum<sup>1,2,3,4</sup>

*1: Inria, 2: Université de Bordeaux - CNRS, 3: Inserm, 4: Vaccine Research Institute, 5: CHU Bordeaux, 6: Ecole Polytechnique - CNRS*



# History and disclaimer

- Since 2015
  - A longstanding collaboration between A. Collin, P. Moireau (Analysis, Num Anal, Scientific Comp) about Kalman based estimators for “large dimensional” (classically distributed in our case) systems.
- Since 2018
  - A joint work with M. Prague (Biostatistics) on alternative to non-linear mixed effect model approaches (NLME) for estimating mechanistic models in pharmacokinetics, epidemiology



*A. Collin, M. Prague, P. Moireau – Estimation for dynamical systems using a population-based Kalman filter – Applications to pharmacokinetics models hal-02869347 – Submitted.*

- End of march 2020
  - A. Collin, P. Moireau test kalman estimation for COVID models
  - While M. Prague is using SAEM methods for COVID predictions with B. P. Hejblum, L. Wittkop, R. Thiébaud, D. Dutartre, Q. Clairon.
- Early June 2020
  - Can we give some **supplementary** grounds with our Kalman-based approach about some of the modeling choices and estimation assumptions used the NLME approach?
- Early July 2020
  - Submission of a paper with supplementary materials

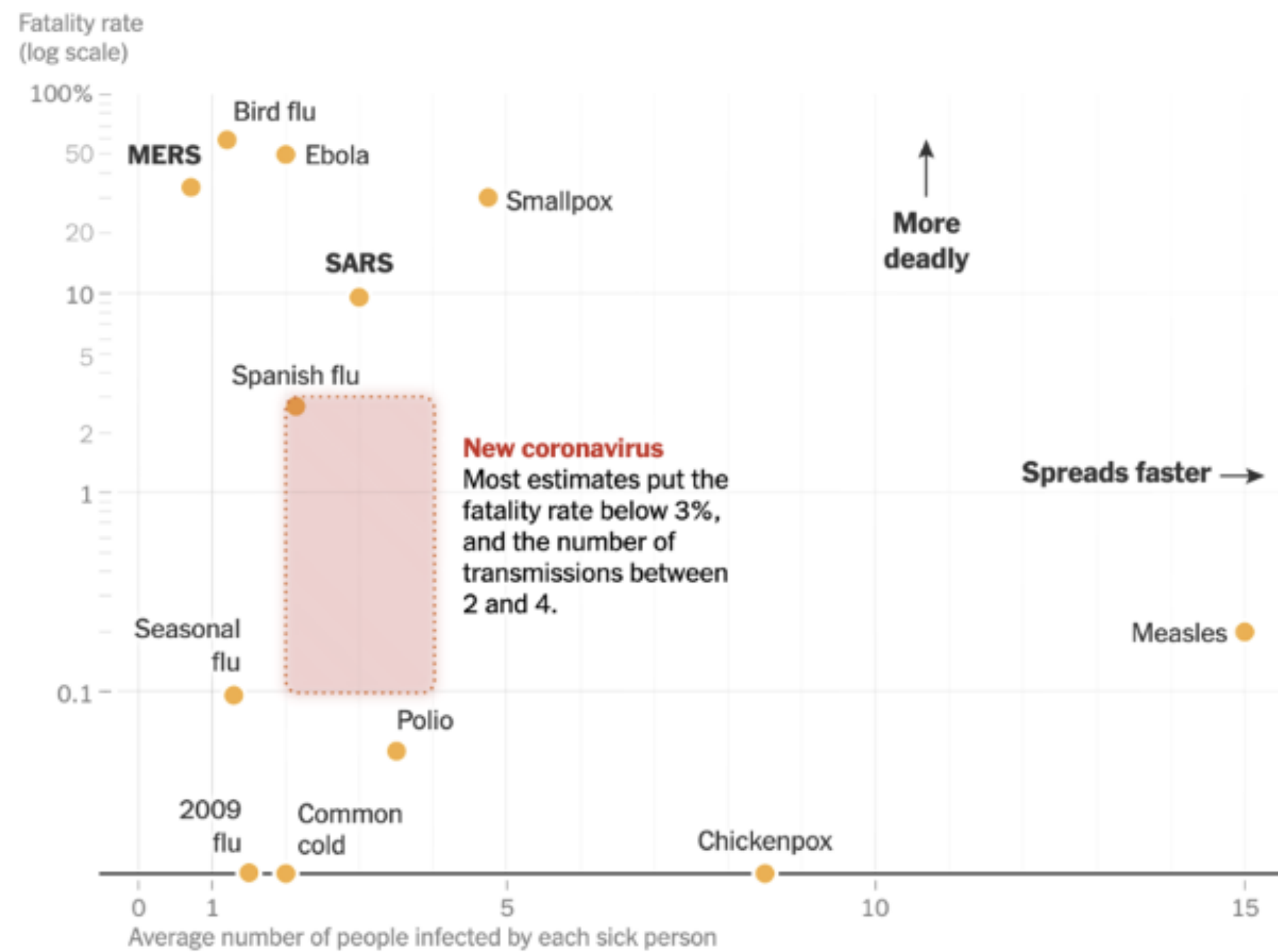


*M. Prague, L. Wittkop, A. Collin, Dan Dutartre, Q. Clairon, P. Moireau, R. Thiébaud, B. P. Hejblum – Multi-level modeling of early COVID-19 epidemic dynamics in French regions and estimation of the lockdown impact on infection rate – Submitted.*

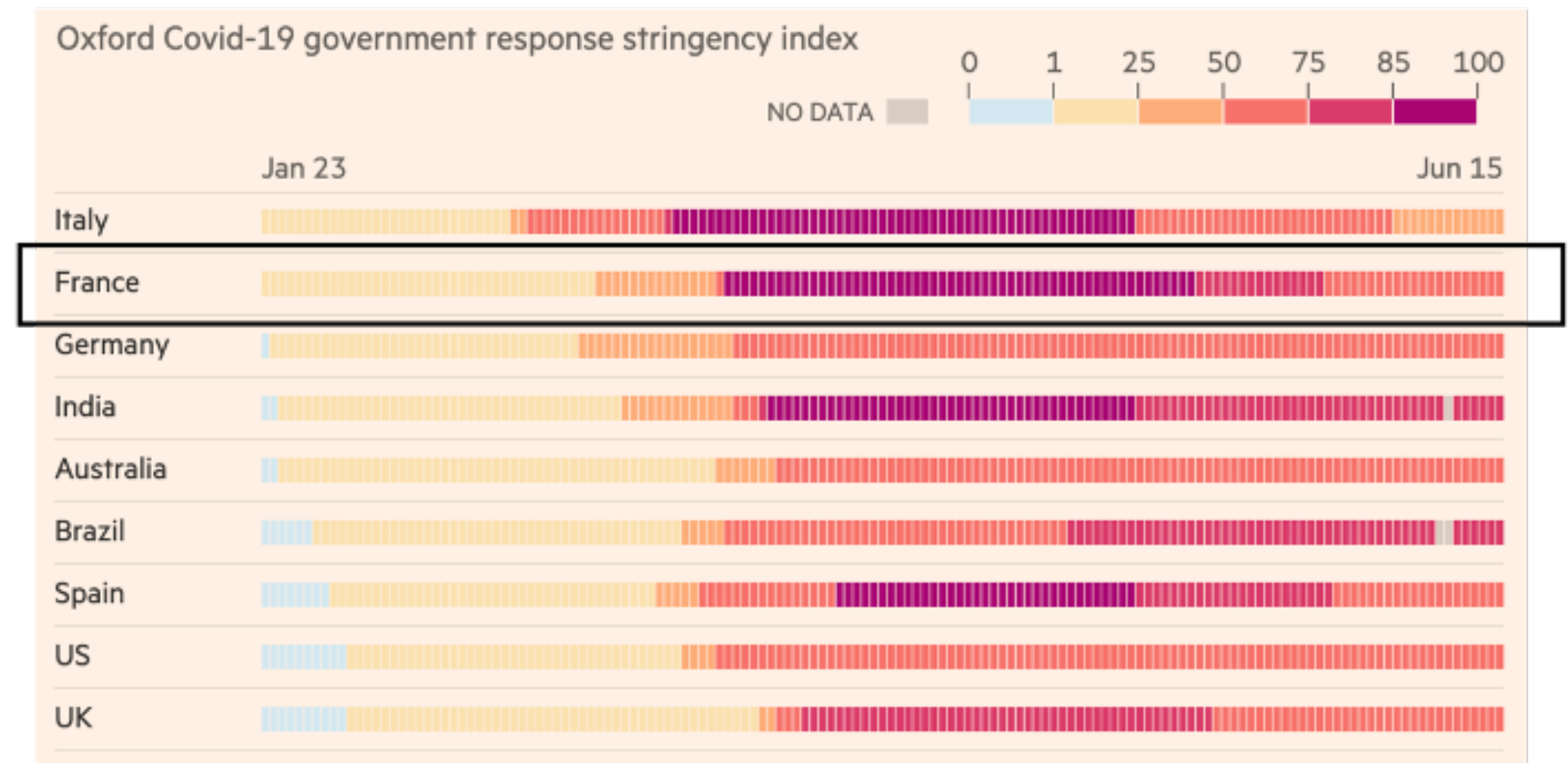
# A little bit of context

**SARS-Cov-2** appeared in Wuhan (China) in December 2019  
**No Vaccine** until December 11th 2020

Worldwide implementation of **Non-pharmaceutical Intervention**  
 from less stringent (masks, hand washing...) to most stringent complete lock-down.

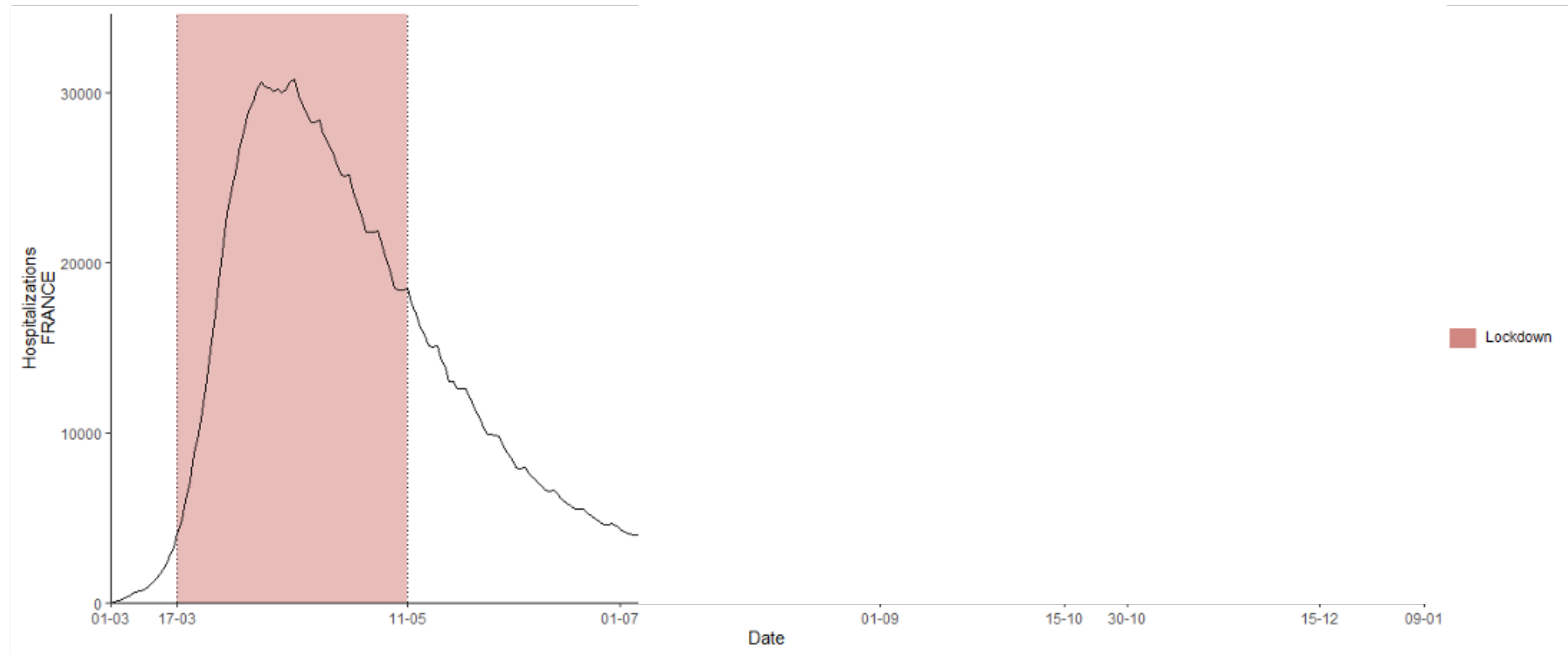


Note: Average case-fatality rates and transmission numbers are shown. Estimates of case-fatality rates can vary, and numbers for the new coronavirus are preliminary estimates.



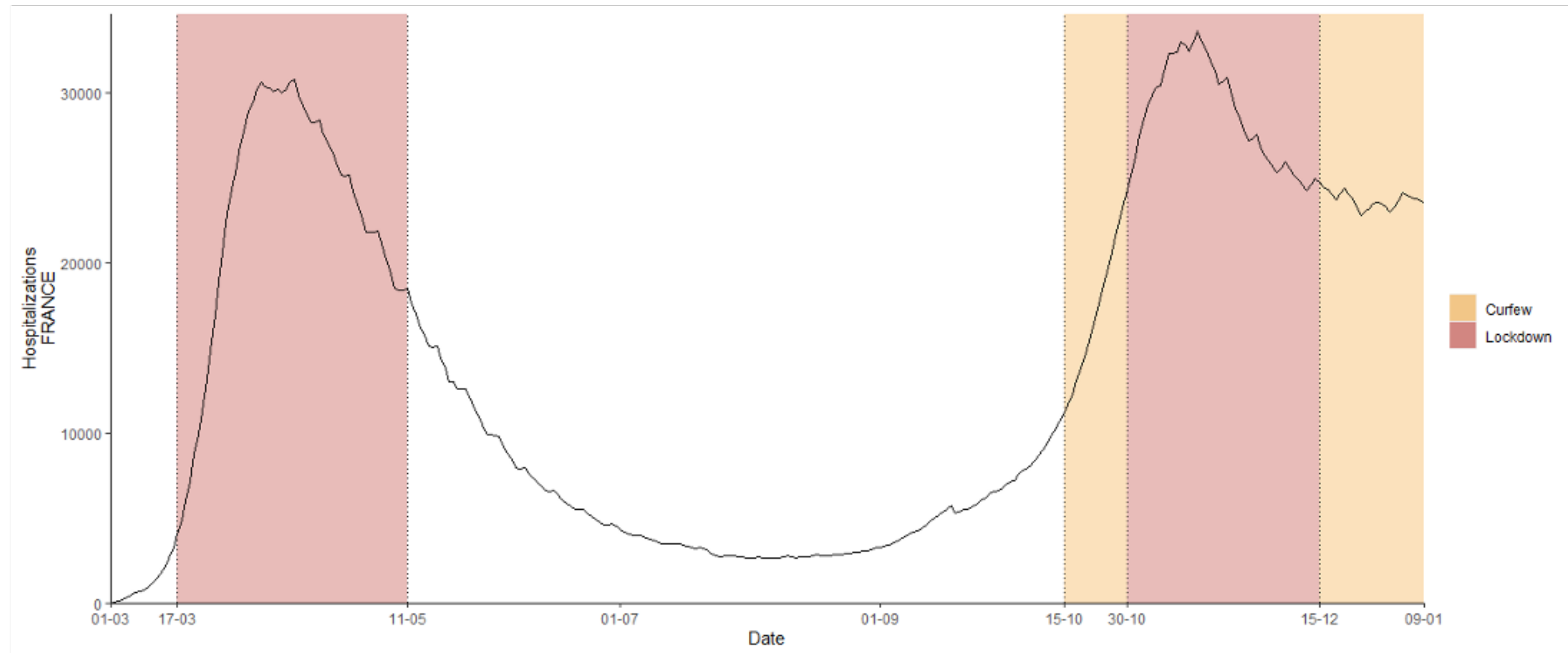
# Main goals

How to **estimate the effect** of lock-down on first wave?



# Main goals

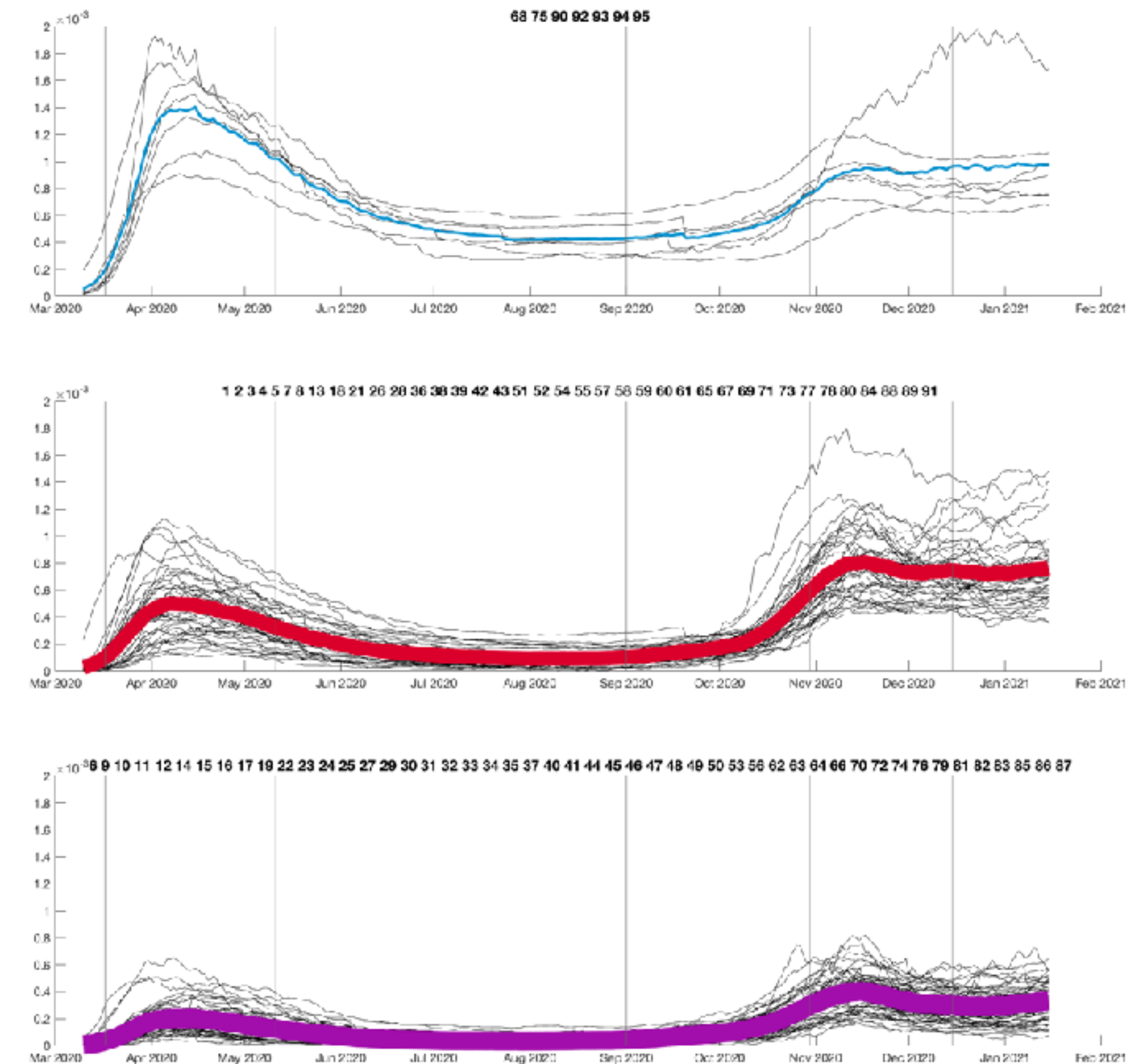
Can it **inform and predict** the second, third ... and so on ... waves ?



# Available data

- **Statistical analysis** only so good as the **data** :  
« Garbage in, garbage out »
- **Data is crucial**, but hardly a hospital priority when there are not enough respirators...
- **Public / Semi-Public data on Covid-19:**
  - Multiple sources
  - Multiple formats
  - Multiple geographical resolutions
  - Multiple interpretation (phase 2 vs phase 3, cf # of tests...)
  - Background noise

Percent of hospitalization data by departments  
Means clustering with 3 clusters



# Available data

- **Infection Data (# positive tests)**

- Sante Publique France: March 1st -> March 25th
- SI-dep: May 15th -> now

Partial data collection with change of sources & change of collection mode

- **Infection Data (Sentinelle)**

- Number of individual seen by GP with COVID-19 related symptoms

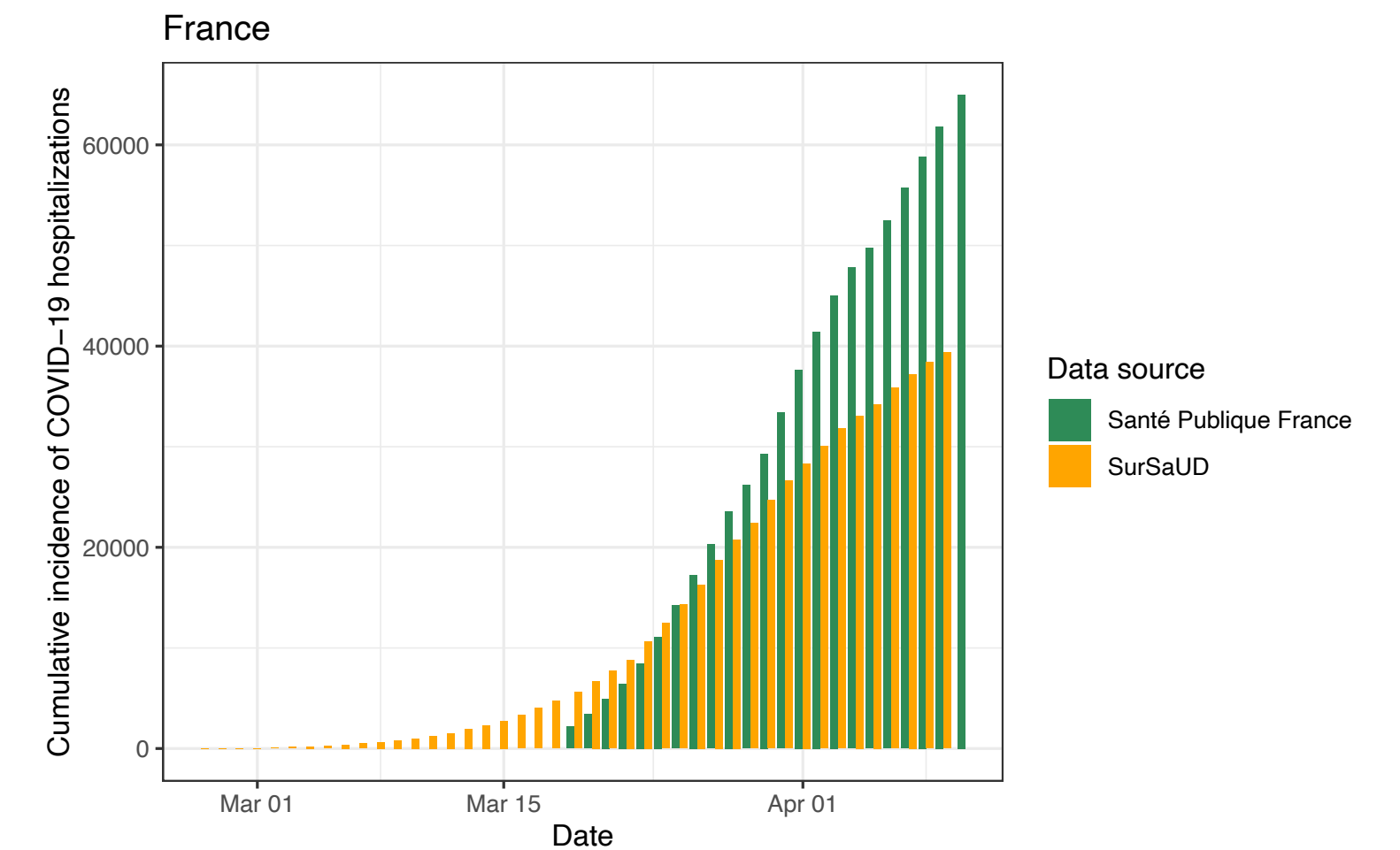
- **Hospital Data (SurSaUD)**

- Admission through urgent care

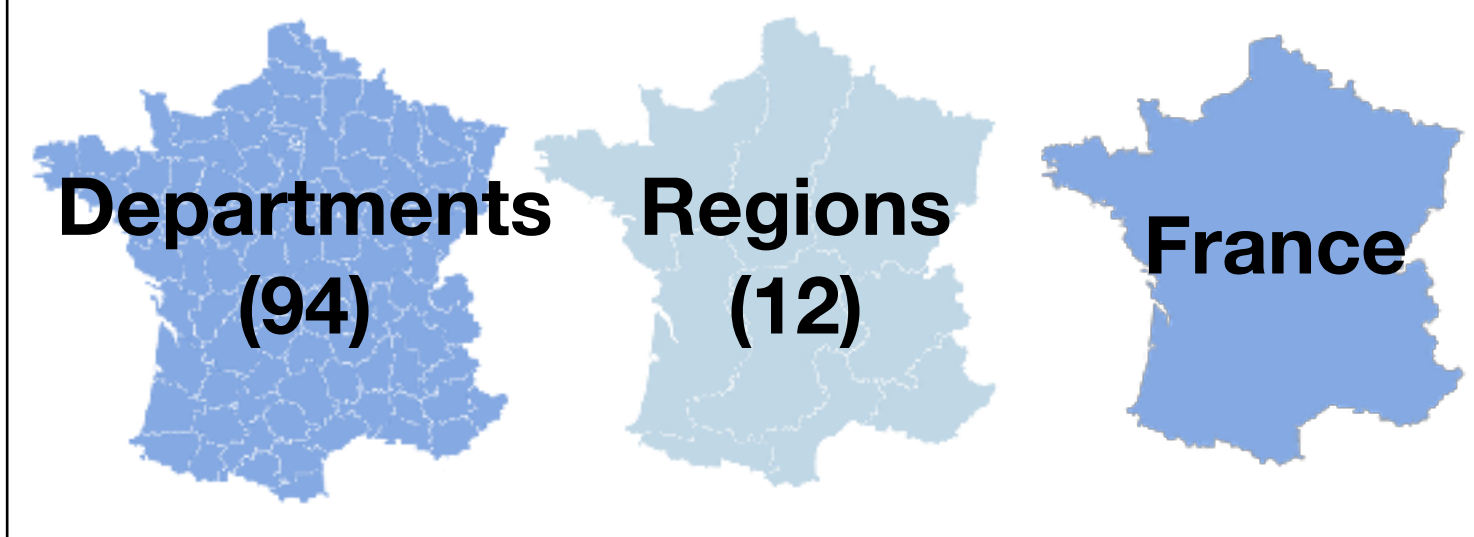
Multiple sources & format With inconsistencies

- **Hospital Data (SI-VIC available June 1st)**

- Hospitalisation Admission
- ICU
- Death



## Multiple geographic levels



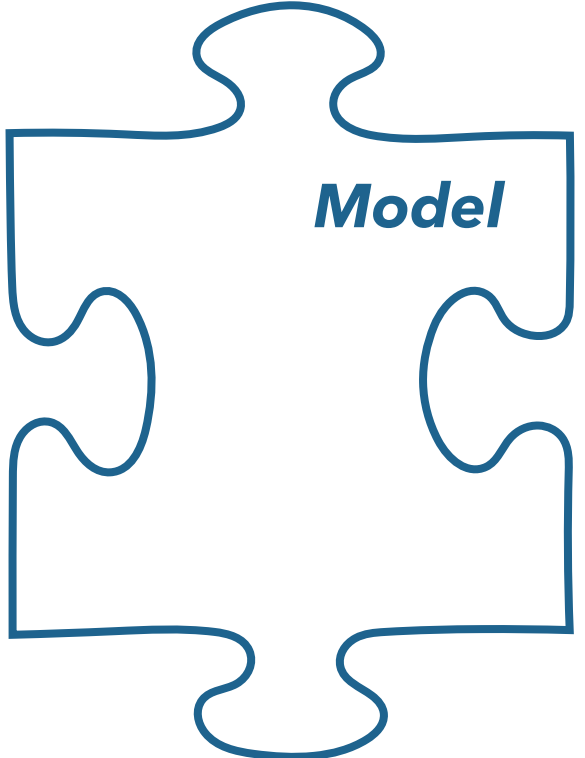
# Estimation paradigms

**State**  
 Exposed (E)  
 Infectious (I, A)  
 Removed (R)  
 Hospitalized (H)  
 -> **ODE system**

**State:**  $x = \begin{pmatrix} E \\ I \\ \vdots \\ H \end{pmatrix}$

**Augmented state:**

$z = \begin{pmatrix} x \\ \theta \end{pmatrix}$

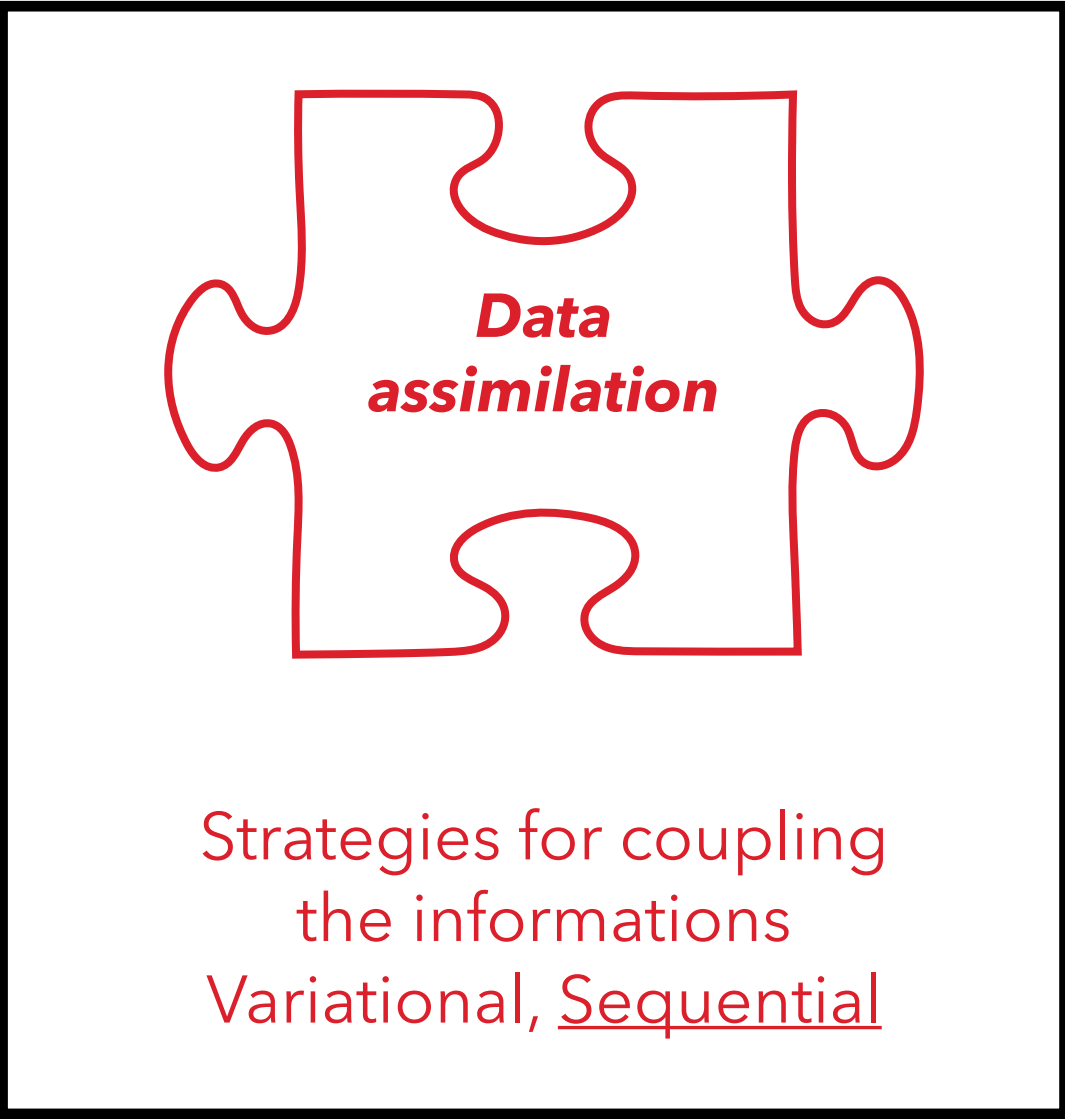


Uncertainties on parameters  $\theta$  and initial conditions ...

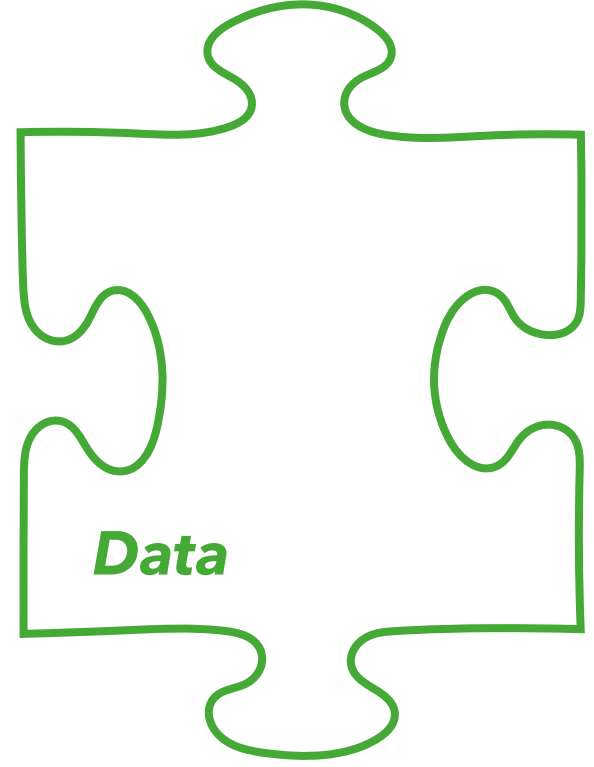
$$\dot{x} = f(x, \theta, t) + B_x v$$

$$\begin{aligned} \dot{\theta} &= 0 \\ x(0) &= x_0 + \xi_x \\ \theta(0) &= \theta_0 + \xi_\theta \end{aligned}$$

$$\begin{aligned} \dot{z} &= F(z, t) + Bv \\ z(0) &= z_0 + \xi \end{aligned}$$



**Goal: minimize a discrepancy comparing  $z$  and  $y$**



Observations  $y$

Observation operator  $h$

$$y = h(z, t) + \chi$$



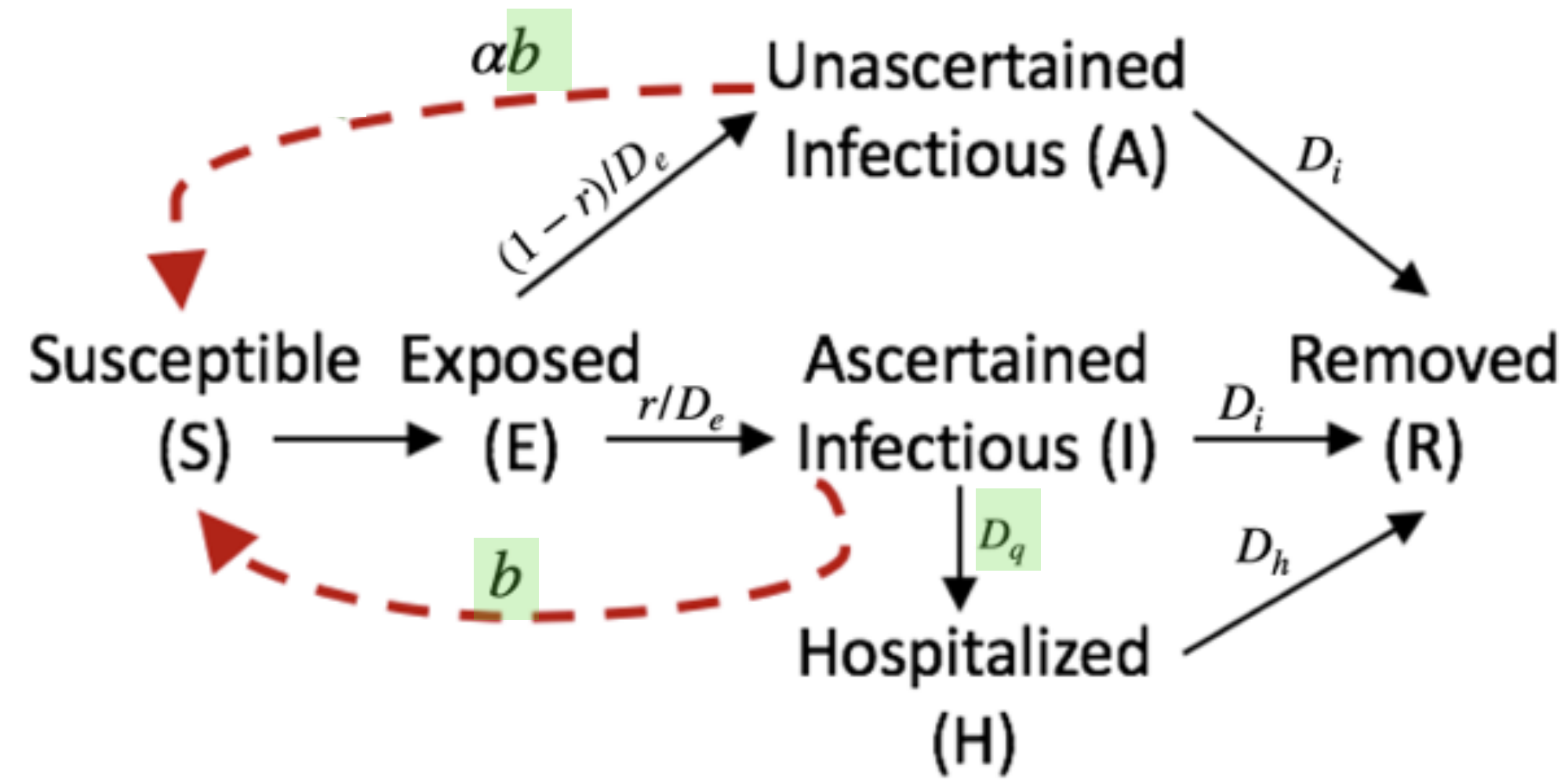
# Mixed effect dynamical model

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# The mathematical model

- The SEIRAH model : An extended Susceptible-Exposed-Infectious-Recovered (SEIR) model

$$\begin{cases} \dot{S} = \frac{b(t)S(I + aA)}{N} \\ \dot{E} = \frac{b(t)S(I + aA)}{N} - \frac{E}{D_e} \\ \dot{I} = \frac{rE}{D_e} - \frac{I}{D_q} - \frac{I}{D_i}, \\ \dot{R} = \frac{I + A}{D_i} + \frac{H}{D_h} \\ \dot{A} = \frac{(1-r)E}{D_e} - \frac{A}{D_i} \\ \dot{H} = \frac{I}{D_q} - \frac{H}{D_h}. \end{cases}$$



[1] Li, R., Pei, S., Chen, B., Song, Y., Zhang, T., Yang, W. et al. (2020), Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV2). *Science* 368 (6490), 489-493.

[2] Lauer, S.A., Grantz, K.H., Bi, Q., Jones, F.K., Zheng, Q., Meredith, H.R. et al. (2020), The incubation period of coronavirus disease 2019 (COVID-19) from publicly reported confirmed cases: Estimation and application. *Annals of Internal Medicine* 172 (9), 577-582.

[3] Wang, C., Liu, L., Hao, X., Guo, H., Wang, Q., Huang, J. et al. (2020). Evolving epidemiology and impact of non-pharmaceutical interventions on the outbreak of coronavirus disease 2019 in Wuhan, China. *medRxiv* 2020.03.03.20030593. doi: 10.1101/2020.03.03.20030593.

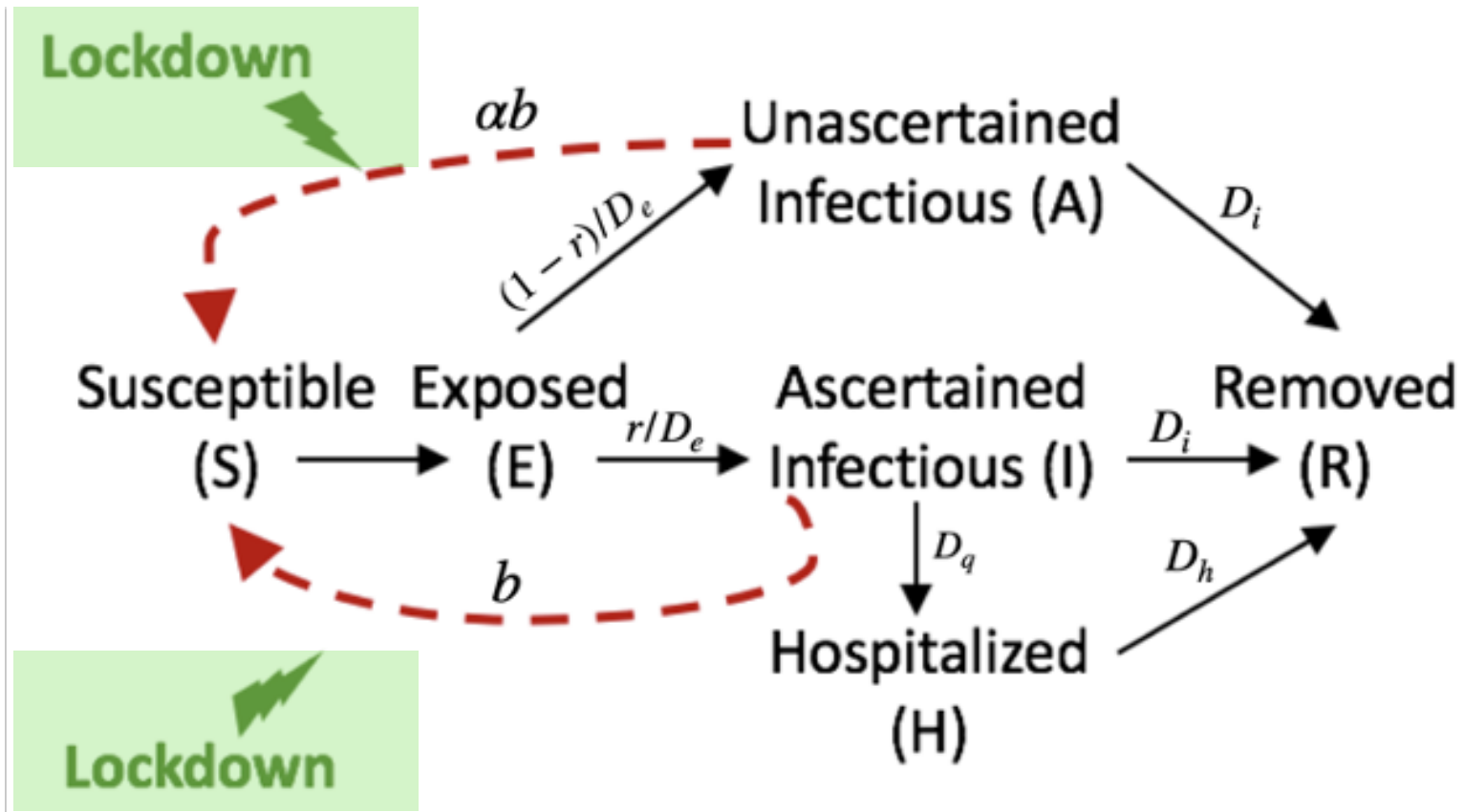
[4] INED (2020). Insee: Recensements de population, Estimations de population. [https://www.ined.fr/fichier/s\\_rubrique/159/estim.pop.nreg.sexe.gca.1975.2020.fr.xls](https://www.ined.fr/fichier/s_rubrique/159/estim.pop.nreg.sexe.gca.1975.2020.fr.xls). Accessed: 2020-03-25.

Parameter	Interpretation	Value	References
$b$	Transmission rate of ascertained cases	Region Specific	<b>Estimated</b>
$r$	Ascertainment rate	Region Specific	<i>Réseau Sentinelle</i>
$a$	Ratio of transmission between A and I	1.5	[1]
$D_e$	Latent (incubation) period (days)	5.2	[2]
$D_i$	Infectious period (days)	2.3	[1,3]
$D_q$	Duration from I onset to H (days)	Region Specific	<b>Estimated</b>
$D_h$	Hospitalization period (days)	30	[1,3]
$N$	Population size	Region Specific	[4]

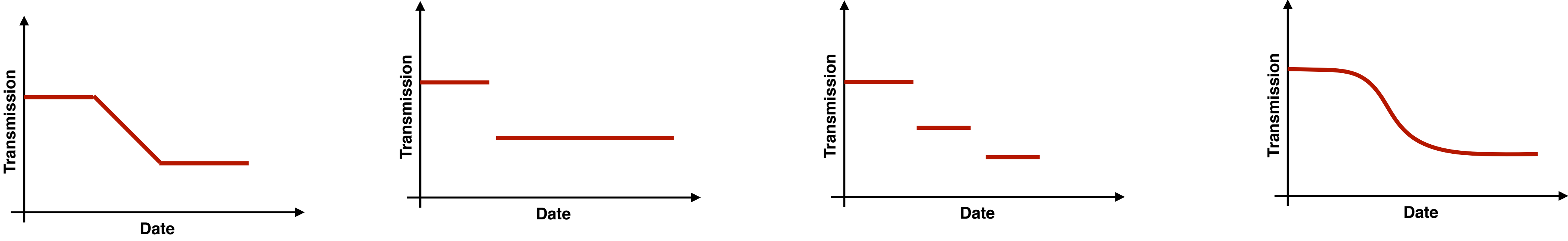
# Definition of the transmission change over time

- We assume that non-pharmaceutical intervention (NPI) reduces the transmission  $b$ .

$$\begin{cases} \dot{S} = -\frac{b(t)S(I+aA)}{N} \\ \dot{E} = \frac{b(t)S(I+aA)}{N} - \frac{E}{D_e} \\ \dot{i} = \frac{rE}{D_e} - \frac{I}{D_q} - \frac{I}{D_i} \\ \dot{R} = \frac{I+A}{D_i} + \frac{H}{D_h} \\ \dot{A} = \frac{(1-r)E}{D_e} - \frac{A}{D_i} \\ \dot{H} = \frac{I}{D_q} - \frac{H}{D_h} \end{cases}$$



- Major contribution of this work consist in using sequential methods to inform the parametric shape of the effect of NPI

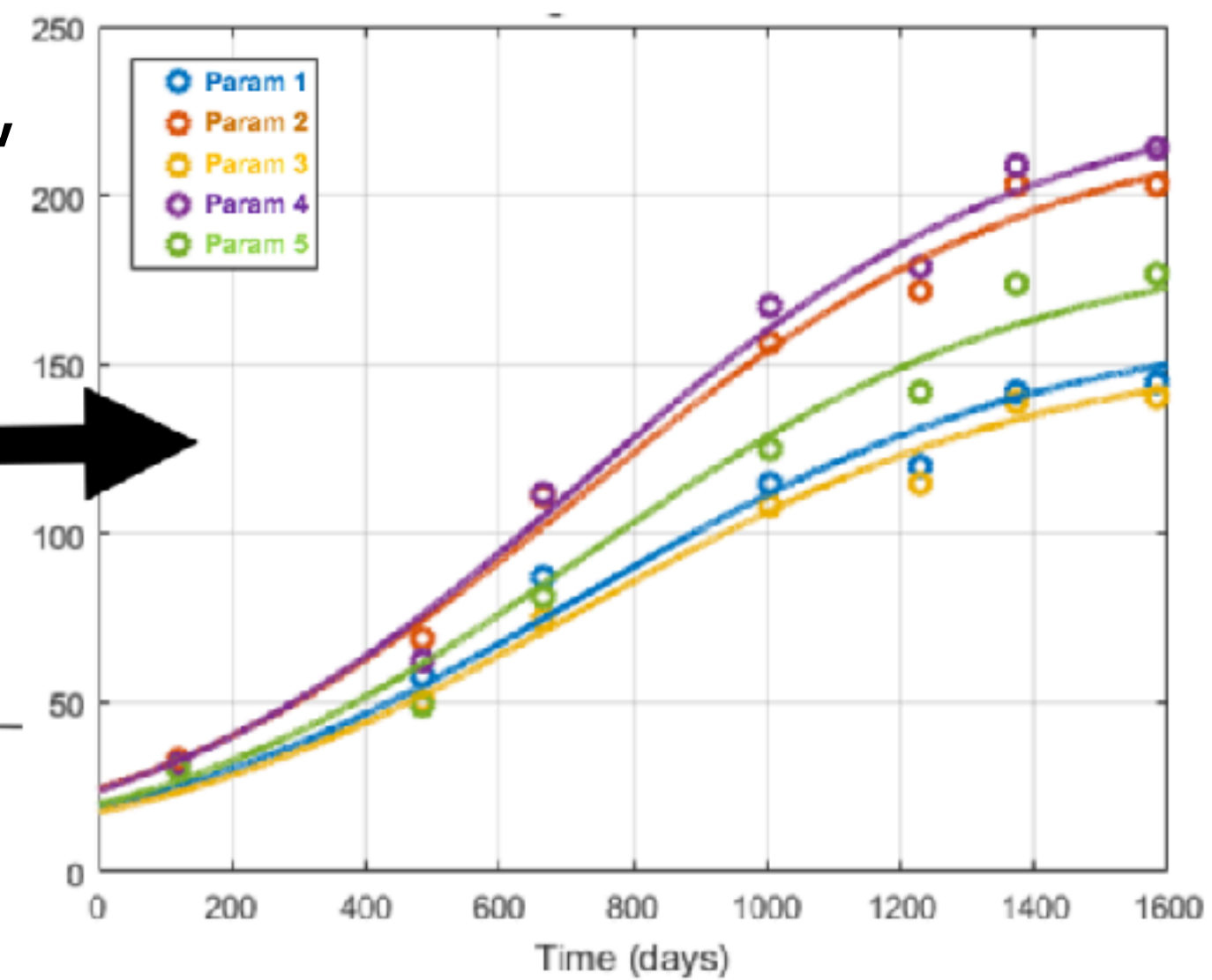
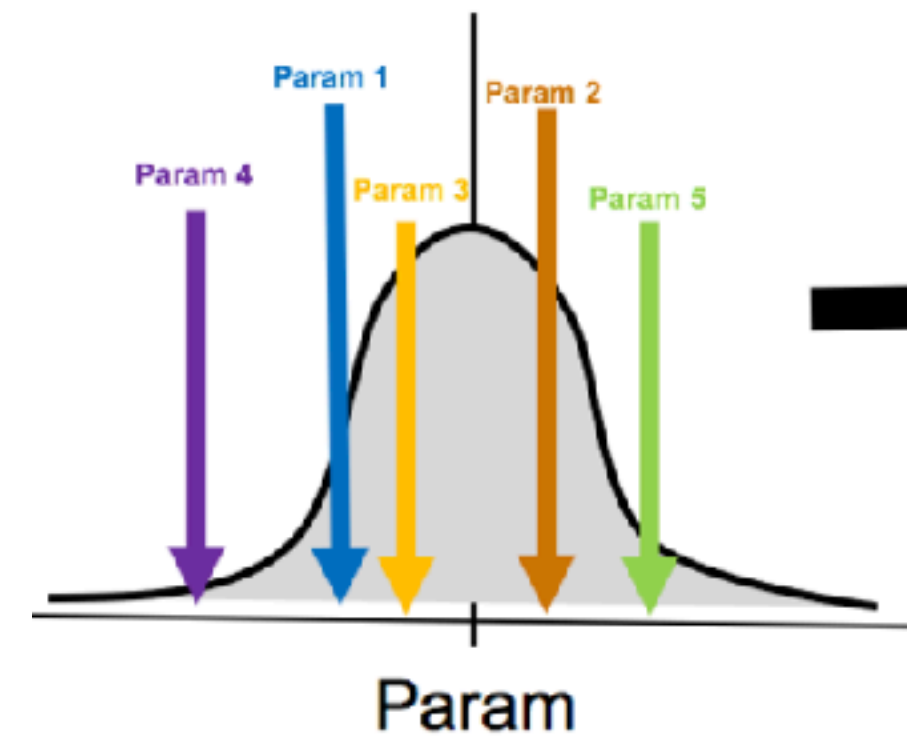


# The statistical model

- We use a mixed effect model on parameters to account for **inter-department / inter-region variability (denoted i)**.

$$\begin{aligned}\log(b_i(t)) &= g(t) + u_i^b, & \text{with } u_i^b &\simeq \mathcal{N}(0, \sigma_b^2) \\ \log(D_{qi}) &= D_{q_0} + u_i^{D_q}, & \text{with } u_i^{D_q} &\simeq \mathcal{N}(0, \sigma_{D_q}^2) \\ \log(E_i(0)) &= E(0) + u_i^{E_0}, & \text{with } u_i^{E_0} &\simeq \mathcal{N}(0, \sigma_{E_0}^2) \\ \log(I_i(0)) &= I(0) + u_i^{I_0}, & \text{with } u_i^{I_0} &\simeq \mathcal{N}(0, \sigma_{I_0}^2) \\ \log(H_i(0)) &= H(0) + u_i^{H_0}, & \text{with } u_i^{H_0} &\simeq \mathcal{N}(0, \sigma_{H_0}^2)\end{aligned}$$

Each geographical unit has a different parameter value with variability constrained by a normal law



# The observation model

We observe five variables :

$Y_1$ : Incident number of cases tested positive

$$Y_1(t) = \frac{rE}{D_e}$$

$Y_2$ : Incident number of hospitalized

$$Y_2(t) = \frac{I}{D_q}$$

$Y_3$ : Prevalent number of hospitalized

$$Y_3(t) = H$$

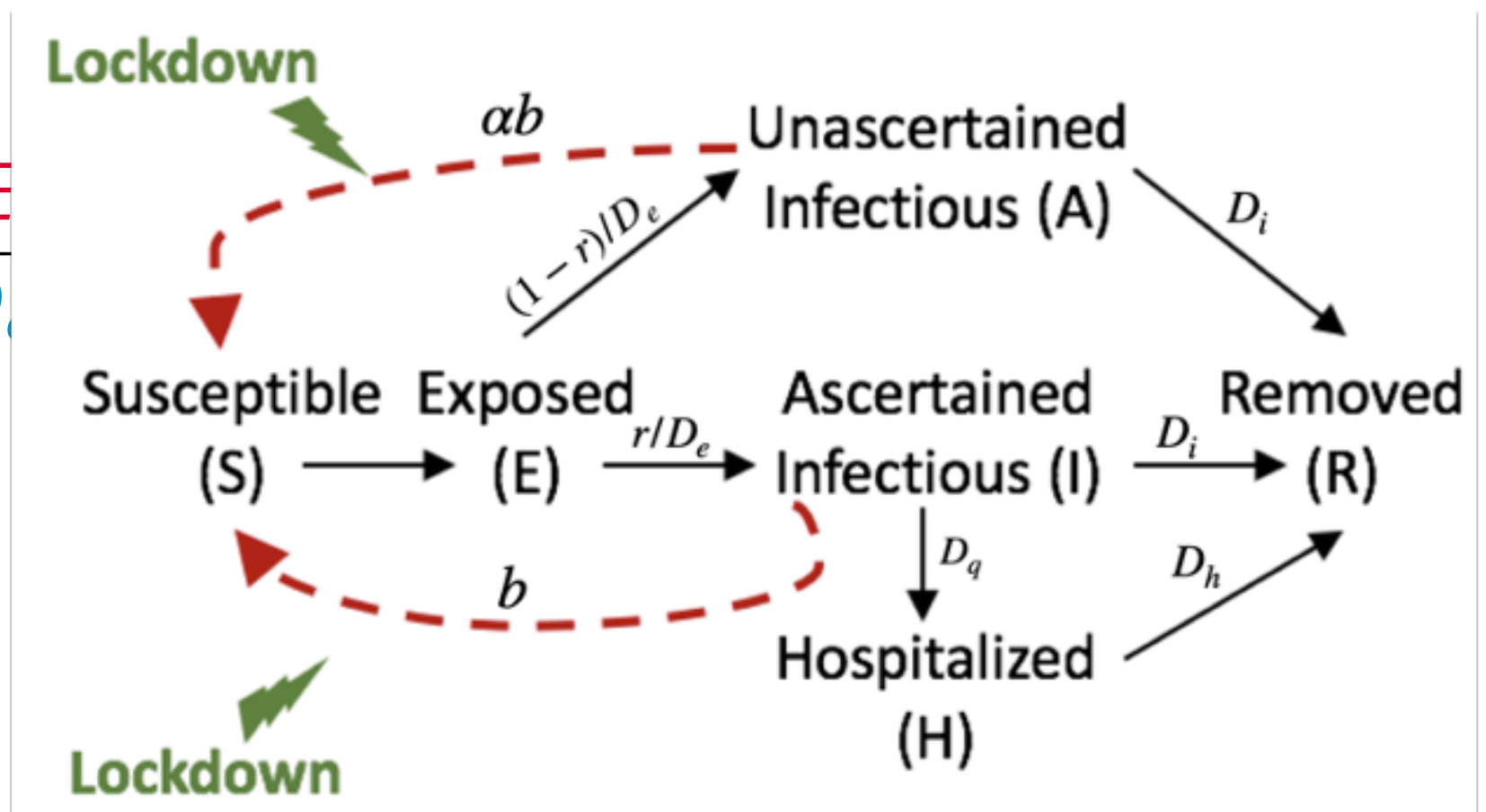
$Y_4$ : Prevalent number of cases in ICU

$$Y_4(t) = 0.25 \times H$$

$Y_5$ : Number of deaths

$$Y_5(t) = 0.005 \times R$$

$$\begin{cases} \dot{S} = -\frac{b(t)S(I + aA)}{N} \\ \dot{E} = \frac{b(t)S(I + aA)}{N} - \frac{E}{D_e} \\ \dot{I} = \frac{rE}{D_e} - \frac{I}{D_q} - \frac{I}{D_i}, \\ \dot{R} = \frac{I + A}{D_i} + \frac{H}{D_h} \\ \dot{A} = \frac{(1-r)E}{D_e} - \frac{A}{D_i} \\ \dot{H} = \frac{I}{D_q} - \frac{H}{D_h}. \end{cases}$$



# Reduced-order population Unscented Kalman filter

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# Maximum likelihood estimation (variational approach)

- Minimize the criterion with respect to the uncertainties under the constraint of the model dynamics

$$(\hat{\xi}, \hat{v}) = \operatorname{argmax}(\log \mathcal{L}_T((\zeta, v); y(t_1), \dots, y(t_{N_T})))$$

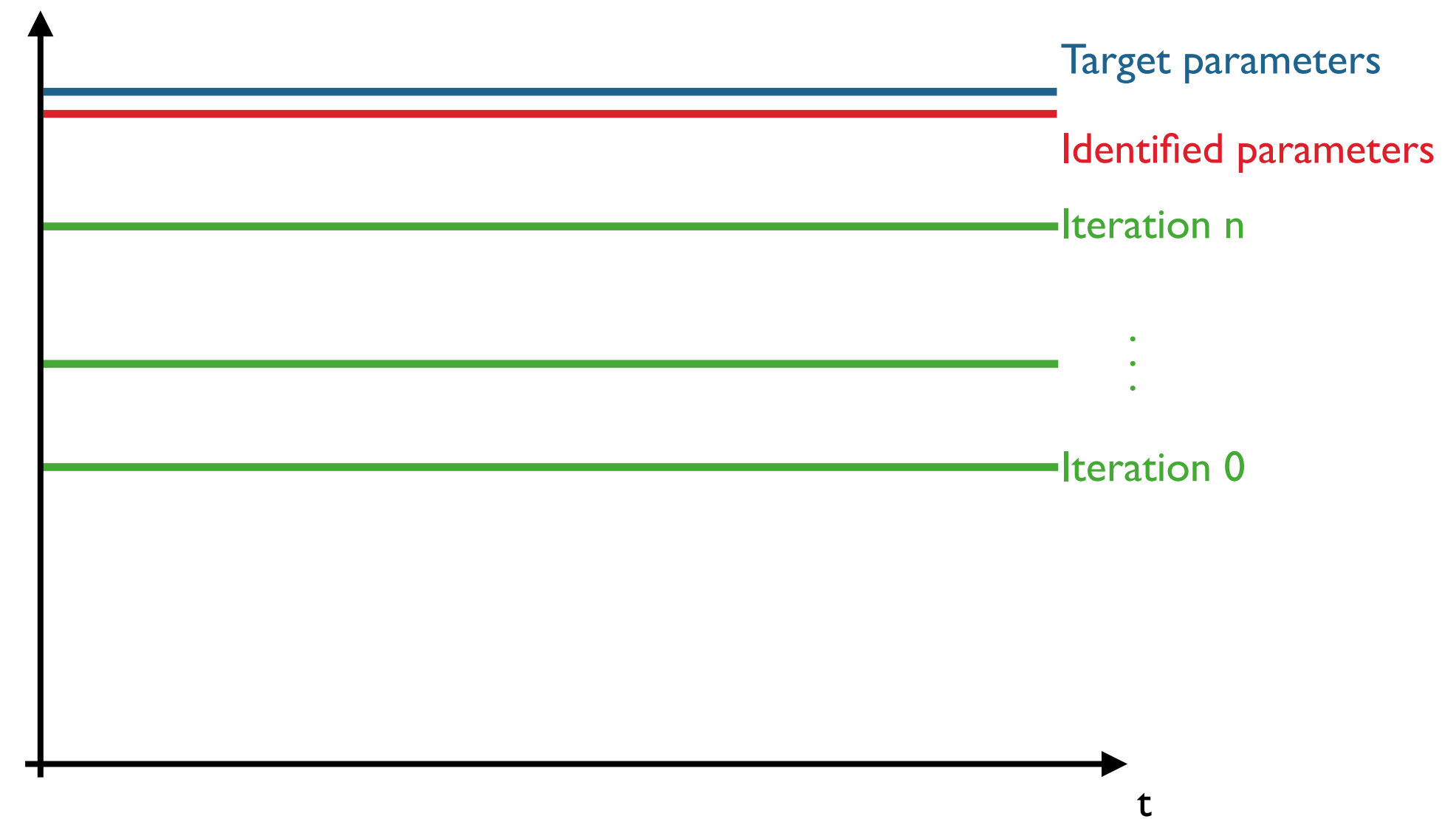
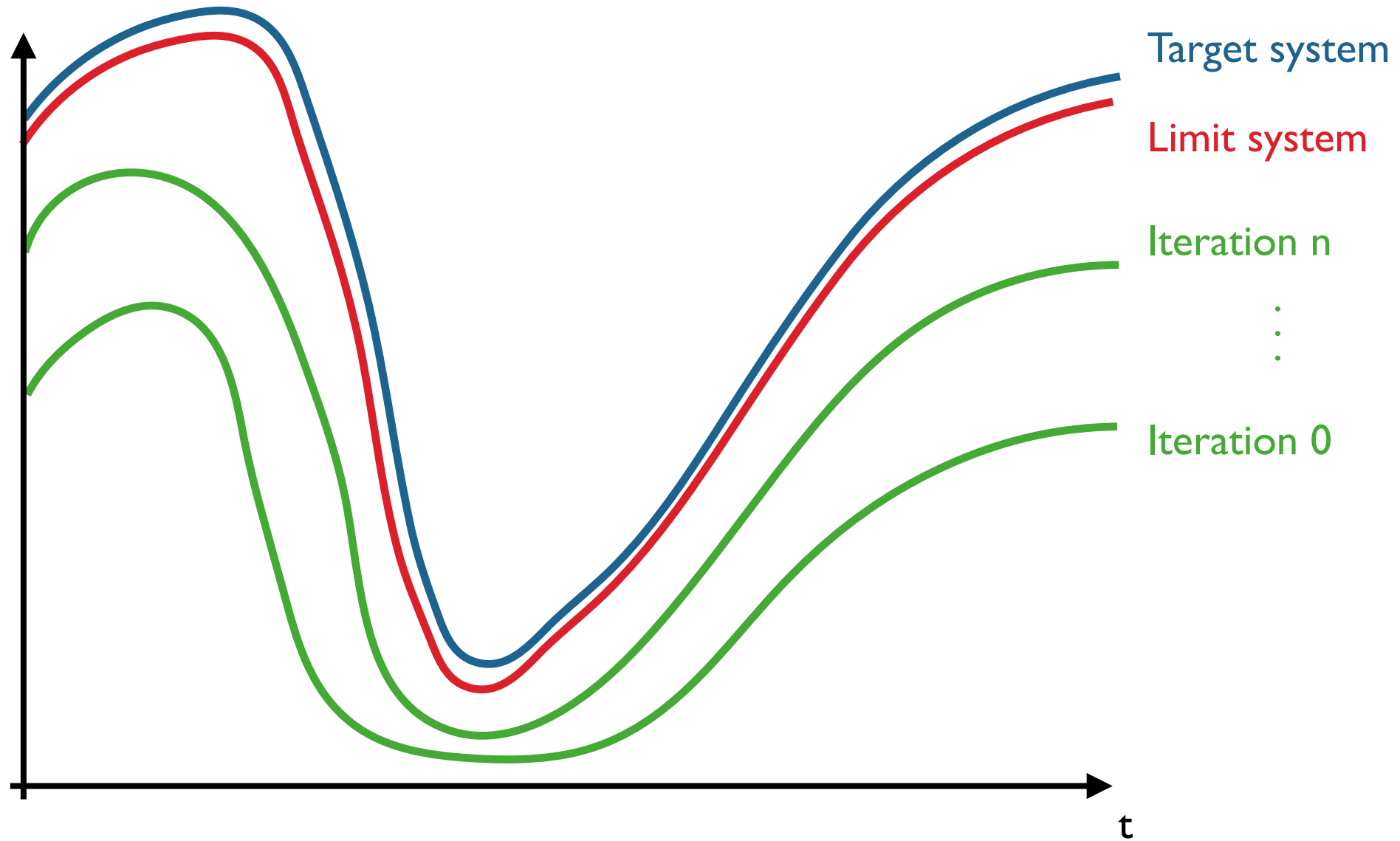
$\zeta$  Uncertainties (parameters / initial conditions)  
 $v$  Model error  
 $y$  Observations

- Corresponds to least-square minimisation when Gaussian laws are considered

$$\min_{\xi, v} \left\{ \mathcal{J}_T(\xi, v) = \underbrace{\frac{1}{2} \langle \xi, P_{\diamond}^{-1} \xi \rangle}_{\text{uncertainties priors}} + \underbrace{\frac{1}{2} \int_0^T \langle v(t), Q(t)^{-1} v(t) \rangle dt}_{\text{model error}} + \underbrace{\frac{1}{2} \sum_{k=0}^{N_{T, \text{obs}}} \langle y_k - h(z(t_k)), (W_k)^{-1} (y_k - h(z(t_k))) \rangle}_{\text{comparison between } y \text{ and } z} \right\}$$

Rk: It is possible to rewrite this functional in order to take into account mixed-effects model (SAEM algorithm)

with  $\dot{z} = F(z, t) + Bv$   
 $z(0) = z_0 + \xi$



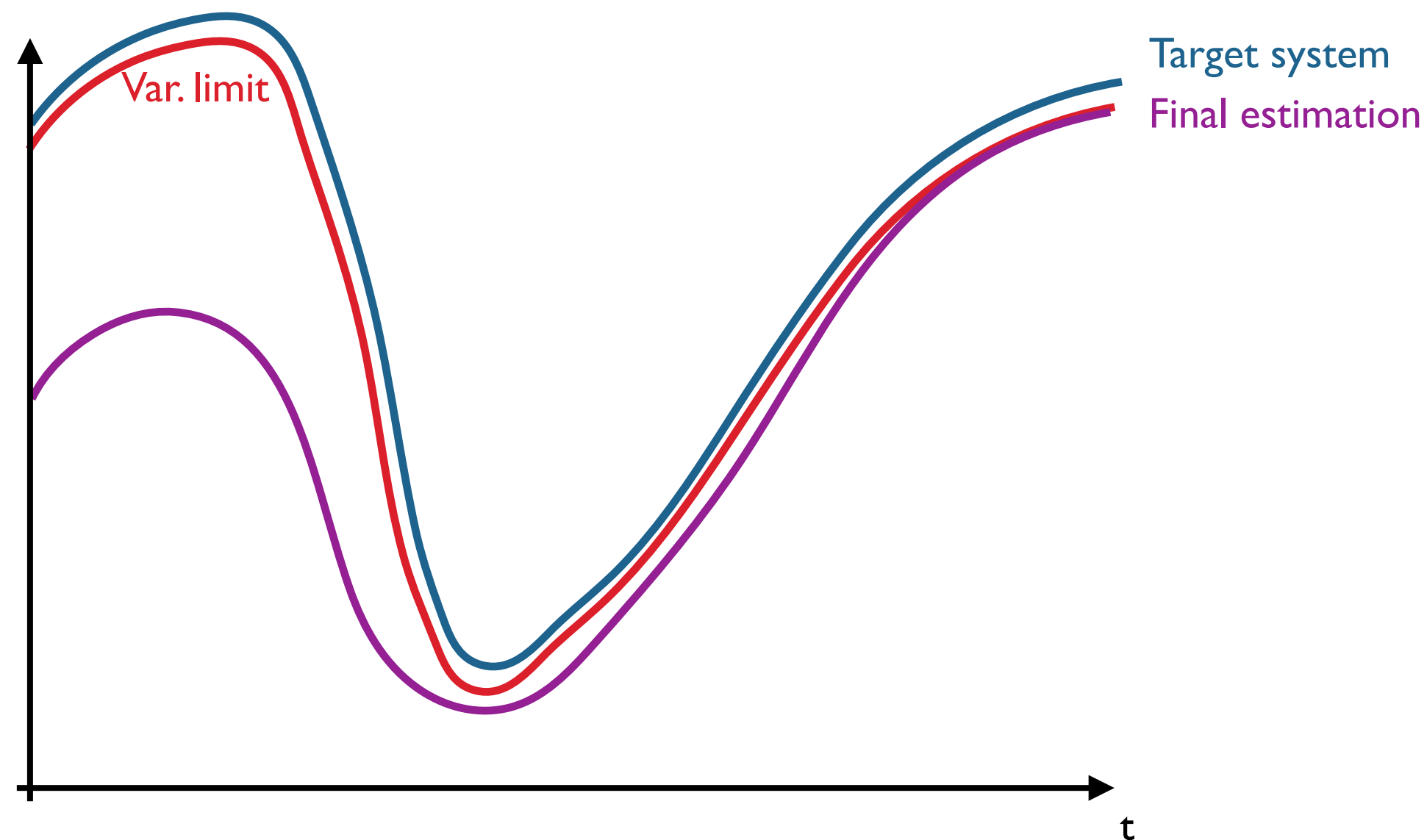
# Sequential Approach

- Correct the dynamics by a feedback based on the discrepancy combining the data and the model state

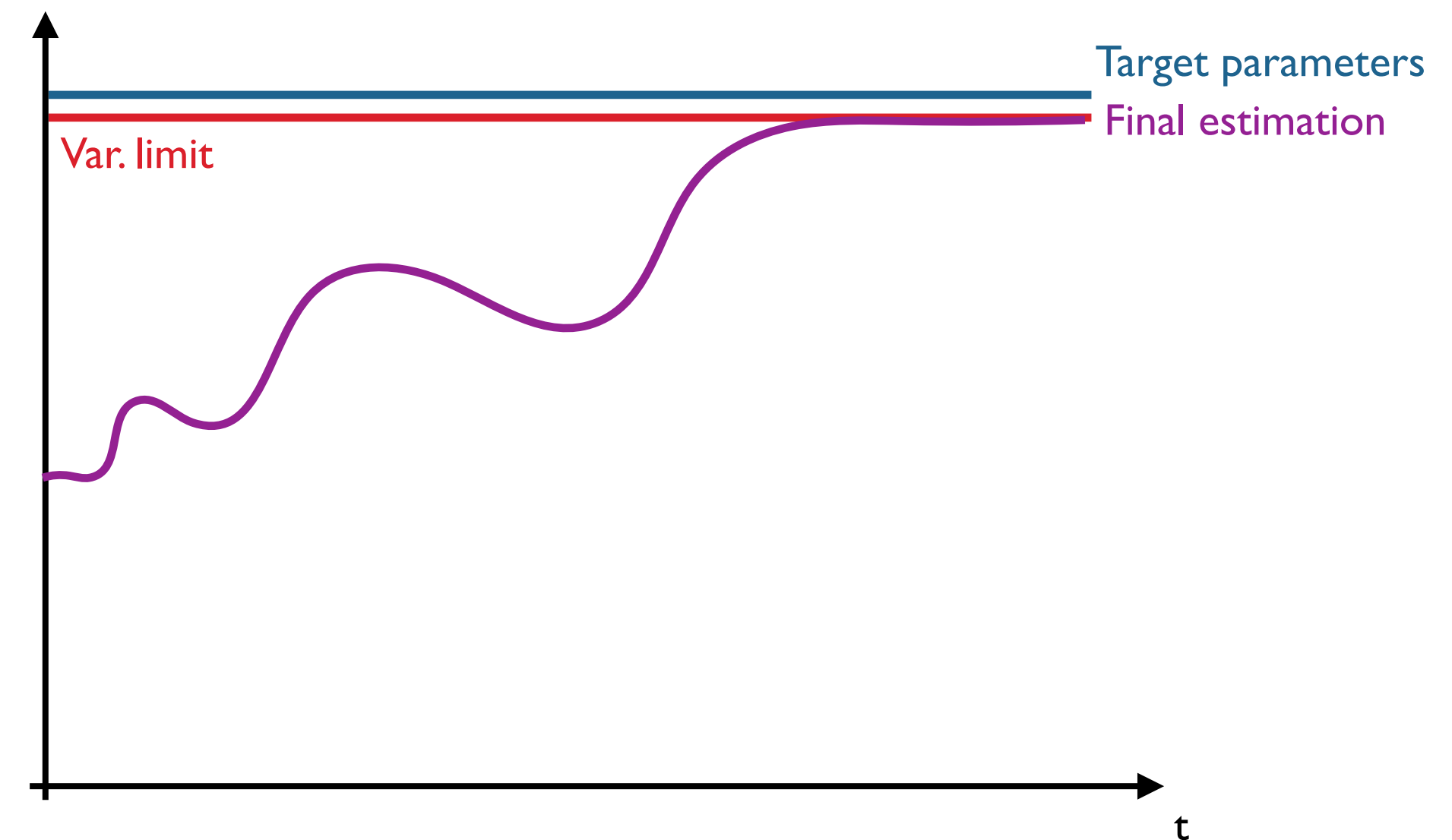
$$\dot{z} = f(z, t) + Bv + k(y, x)$$
$$z(0) = z_0 + \xi$$

with  $z = \begin{pmatrix} x \\ \theta \end{pmatrix}$  state  
parameters

- Rk: Allow also to estimate initial conditions and model error.



The parameters have a dynamics too !



- More precisely we consider a **reduced-order** version of a **population Unscented Kalman** filter:
  - i) Define a **population** criterion: we need a least square criterion
  - ii) Introduction to **Kalman** filter in a linear context
  - iii) Presentation of the **Unscented** Kalman filter (UKF)
  - iv) Presentation of the **reduced-order** version



# i) A population criterion

- Population approach: compensate the lack of data by an available population
- A population made of groups indexed by  $i$

$$\xi^i(t) = \xi_{\diamond}^0 + \tilde{\xi}^i, \quad \xi = \begin{pmatrix} \xi^1 \\ \vdots \\ \xi^{N_P} \end{pmatrix} \in (\mathcal{Z})^{N_P} \simeq \mathbb{R}^{N_z},$$

Mixed-effect approach: pooling all the patients together and estimating a global distribution of the model parameters in the population.

- Criterion:

$$\min_{\xi, v} \left\{ \mathcal{J}_T(\xi, v) = \frac{1}{2} \langle \xi_{\diamond}^0, (P_{\diamond}^0)^{-1} \xi_{\diamond}^0 \rangle + \sum_{i=1}^{N_P} \left[ \frac{1}{2} \langle (\xi^i - \xi_{\diamond}^0), (\tilde{P}_{\diamond}^i)^{-1} (\xi^i - \xi_{\diamond}^0) \rangle + \frac{1}{2} \int_0^T \langle v^i(t), Q^i(t)^{-1} v^i(t) \rangle dt + \frac{1}{2} \sum_{k=0}^{N_{T, \text{obs}}} \langle y_k^i - C(z^i(t_k)), (W_k^i)^{-1} (y_k^i - C(z^i(t_k))) \rangle \right] \right\}$$

- Assuming that the population share the same weighted mean value:  $\xi_{\diamond}^0 = \mathbb{E}_{\alpha, N_P}(\xi) \stackrel{\text{def}}{=} \sum_{i=1}^{N_P} \alpha^i \xi^i$  with  $\sum_{i=1}^{N_P} \alpha^i = 1$ ,

$$\min_{\xi, v} \left\{ \mathcal{J}_T(\xi, v) = \frac{1}{2} \langle \mathbb{E}_{\alpha, N_P}(\xi), (P_{\diamond}^0)^{-1} \mathbb{E}_{\alpha, N_P}(\xi) \rangle + \sum_{i=1}^{N_P} \left[ \frac{1}{2} \langle (\xi^i - \mathbb{E}_{\alpha, N_P}(\xi)), (\tilde{P}_{\diamond}^i)^{-1} (\xi^i - \mathbb{E}_{\alpha, N_P}(\xi)) \rangle + \frac{1}{2} \int_0^T \langle v^i(t), Q^i(t)^{-1} v^i(t) \rangle dt + \frac{1}{2} \sum_{k=0}^{N_{T, \text{obs}}} \langle y_k^i - C(z^i(t_k)), (W_k^i)^{-1} (y_k^i - C(z^i(t_k))) \rangle \right] \right\}$$

- Rewriting

$$\langle \mathbb{E}_{\alpha, N_P}(\xi), (P_{\diamond}^0)^{-1} \mathbb{E}_{\alpha, N_P}(\xi) \rangle + \sum_{i=1}^{N_P} \langle (\xi^i - \mathbb{E}_{\alpha, N_P}(\xi)), (\tilde{P}_{\diamond}^i)^{-1} (\xi^i - \mathbb{E}_{\alpha, N_P}(\xi)) \rangle = \sum_{i,j=1}^{N_P} \langle \xi^i, \left[ \alpha^i \alpha^j (P_{\diamond}^0)^{-1} + \delta_{ij} (\tilde{P}_{\diamond}^i)^{-1} - (\alpha^i (\tilde{P}_{\diamond}^j)^{-1} + \alpha^j (\tilde{P}_{\diamond}^i)^{-1}) + \alpha^i \alpha^j \sum_{\ell=1}^{N_P} (\tilde{P}_{\diamond}^{\ell})^{-1} \right] \xi^j \rangle.$$

$$= (\mathbf{P}_0^{-1})_{i,j}$$

# i) A population criterion

- We obtain a classical estimation framework: Minimize

$$\min_{\xi, v} \left\{ \mathcal{J}_T(\xi, v) = \sum_{i=1}^{N_P} \left[ \frac{1}{2} \langle \xi^i, \mathbf{P}_0^{-1} \xi^i \rangle + \frac{1}{2} \int_0^T \langle v^i(t), Q^i(t)^{-1} v^i(t) \rangle dt + \frac{1}{2} \sum_{k=0}^{N_{T, \text{obs}}} \langle y_k^i - C(z^i(t_k)), (W_k^i)^{-1} (y_k^i - C(z^i(t_k))) \rangle \right] \right\}.$$

with

$$\begin{cases} \dot{z}(t) = F(z(t), t) + B(t)v(t), & \forall t \in [0, T] \\ z(0) = z_0, \end{cases} \quad z = (z^1 \dots z^{N_P})^\top \in (\mathcal{Z})^{N_P}$$

$$y_k = H_k(z(t_k)) + \chi_k, \quad 1 \leq k \leq N_{T, \text{obs}},$$

with

$$\begin{cases} F(z(t), t) = \begin{pmatrix} F(z^1(t), t) \\ \vdots \\ F(z^{N_P}(t), t) \end{pmatrix} \text{ and } z_0 = z_\diamond \times \begin{pmatrix} 1 \\ \vdots \\ 1 \end{pmatrix} + \xi, \\ H_k(z(t_k)) = \begin{pmatrix} h_k(z^1) \\ \vdots \\ h_k(z^{N_P}) \end{pmatrix} \end{cases}$$

- The key of our **uncertainty modeling** is that  $\mathbf{P}_0$  couples the population members since indeed

$$\mathbf{P}_0 \neq \begin{pmatrix} P_0 & & 0 \\ & \ddots & \\ 0 & & P_0 \end{pmatrix}$$

## ii) The Kalman and Bucy filter (linear context)

- Kalman and Bucy in 1961 have shown that the minimizer of the following least-square minimisation

$$\min_{\xi, v} \left\{ \mathcal{J}_T(\xi, v) = \frac{1}{2} \langle \xi, P_{\diamond}^{-1} \xi \rangle + \frac{1}{2} \int_0^T \langle v(t), Q(t)^{-1} v(t) \rangle dt + \frac{1}{2} \sum_{k=0}^{N_{T, \text{obs}}} \langle y_k - h(z(t_k)), (W_k)^{-1} (y_k - h(z(t_k))) \rangle \right\}$$

(population or not criterion)

with  $\dot{z} = F(z, t) + Bv$   
 $z(0) = z_0 + \xi$

when the model and the observer operator are **linear** corresponds to the solution of (time discrete version!)

Model

$$\left( \begin{array}{l} z_{k+1} = F_{k+1|k} z_k \\ \text{discrete transition operator} \end{array} \right)$$

**Observer model**

$$\left\{ \begin{array}{l} \hat{z}_{k+1} = F_{k+1|k} \hat{z}_k + K_k (y_k - H_k \hat{z}_k) \\ \boxed{P_{k+1}} = F_{k+1|k} P_k F_{k+1|k}^T - K_k H_k P_k, \end{array} \right.$$

Covariance matrix  
(full matrix of size  $N_z \times N_z$ )

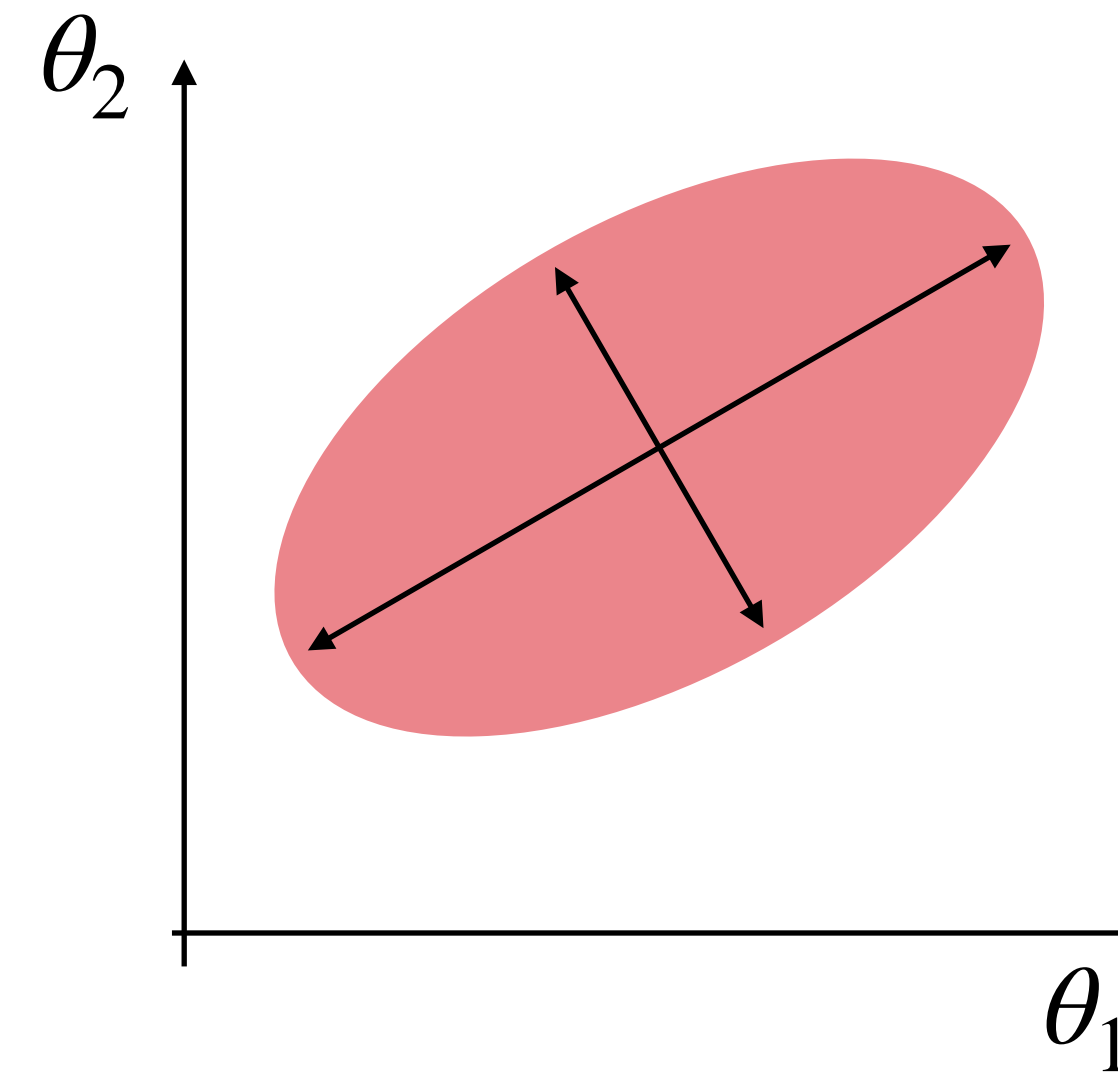
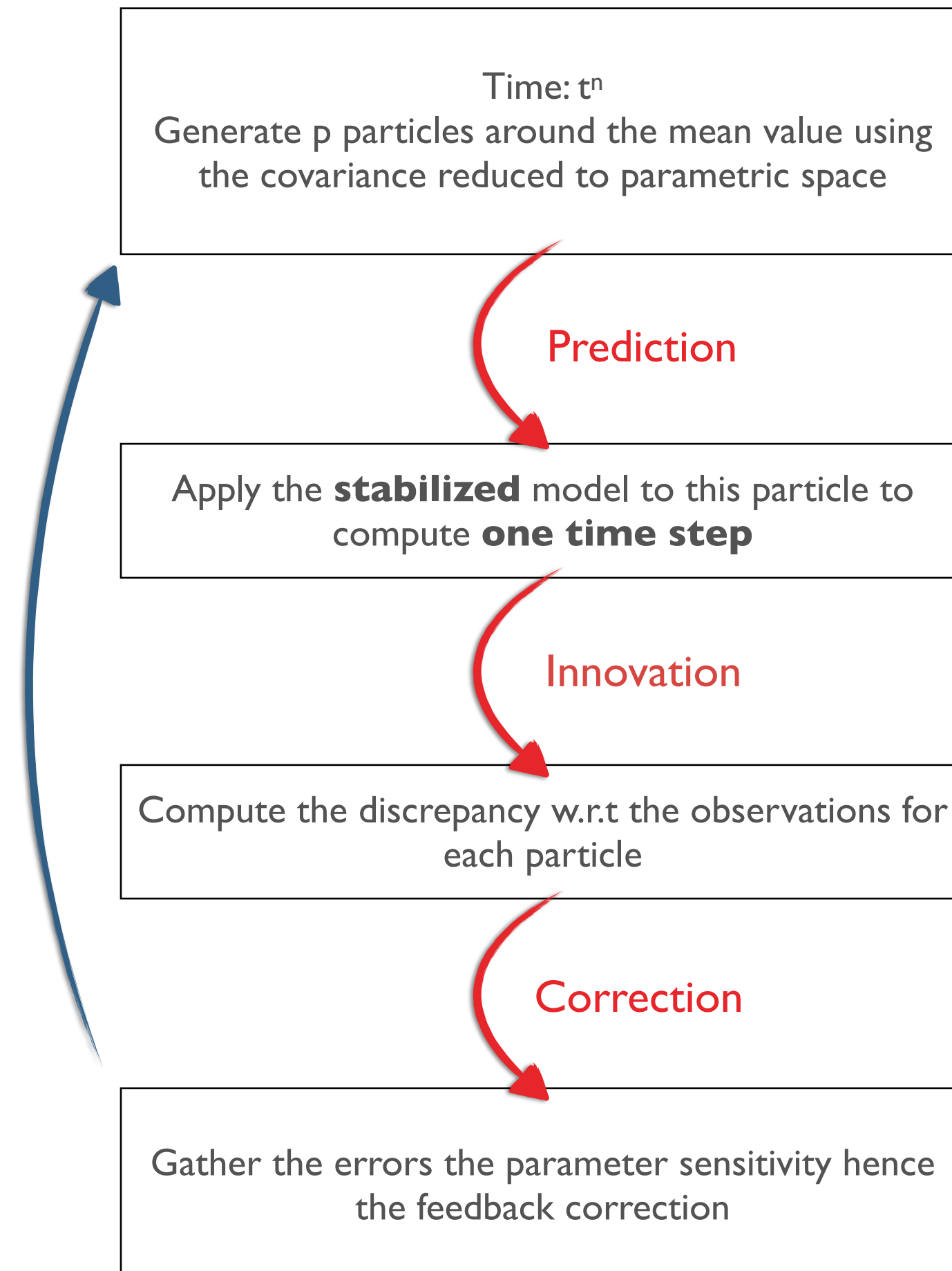
with  $K_k = P_k H_k^T (H_k P_k H_k^T + W)^{-1}$

$z$  state and parameters  
 $H$  observation operator  
 $y$  observations  
 $W$  covariance matrix of the observation error  
 $P$  covariance matrix of the estimation error

- And if it is not linear?** It is classical to rely on approximate optimal sequential estimator based on the generalization of the Kalman filter to non-linear operators.

# iii) The Unscented Kalman Filter

- Here we consider an *Unscented Kalman Filter*.
- The non linear operators are replaced by finite difference approximations based on sampling points.
- Sampling points can be seen as well-chosen “interpolation points” which propagate the mean and covariance of a random variable



S. Julier, J. Uhlmann and H. Durrant-Whyte, A new approach for filtering nonlinear systems, in American Control Conference (1995).

# iv) A reduced order version

- The main idea behind the reduced order strategy is to consider a SVD decomposition of the covariance matrix  $P$  of the form

$$P = LU^{-1}L^T$$

with  $U$  an invertible matrix of small size and  $L$  an extension operator.

- For linear operators, this decomposition is stable over time and the equation on  $P$  leads to the two following systems with admissible computational times:

$$\dot{L} = AL \text{ and } \dot{U} = L^T C^T W^{-1} C L$$

- In non-linear cases, extensions of these two systems have been developed.



P. Moireau, D. Chapelle, Reduced-Order Unscented Kalman Filtering with Application to Parameter Identification in Large-Dimensional Systems — COCV 2011.

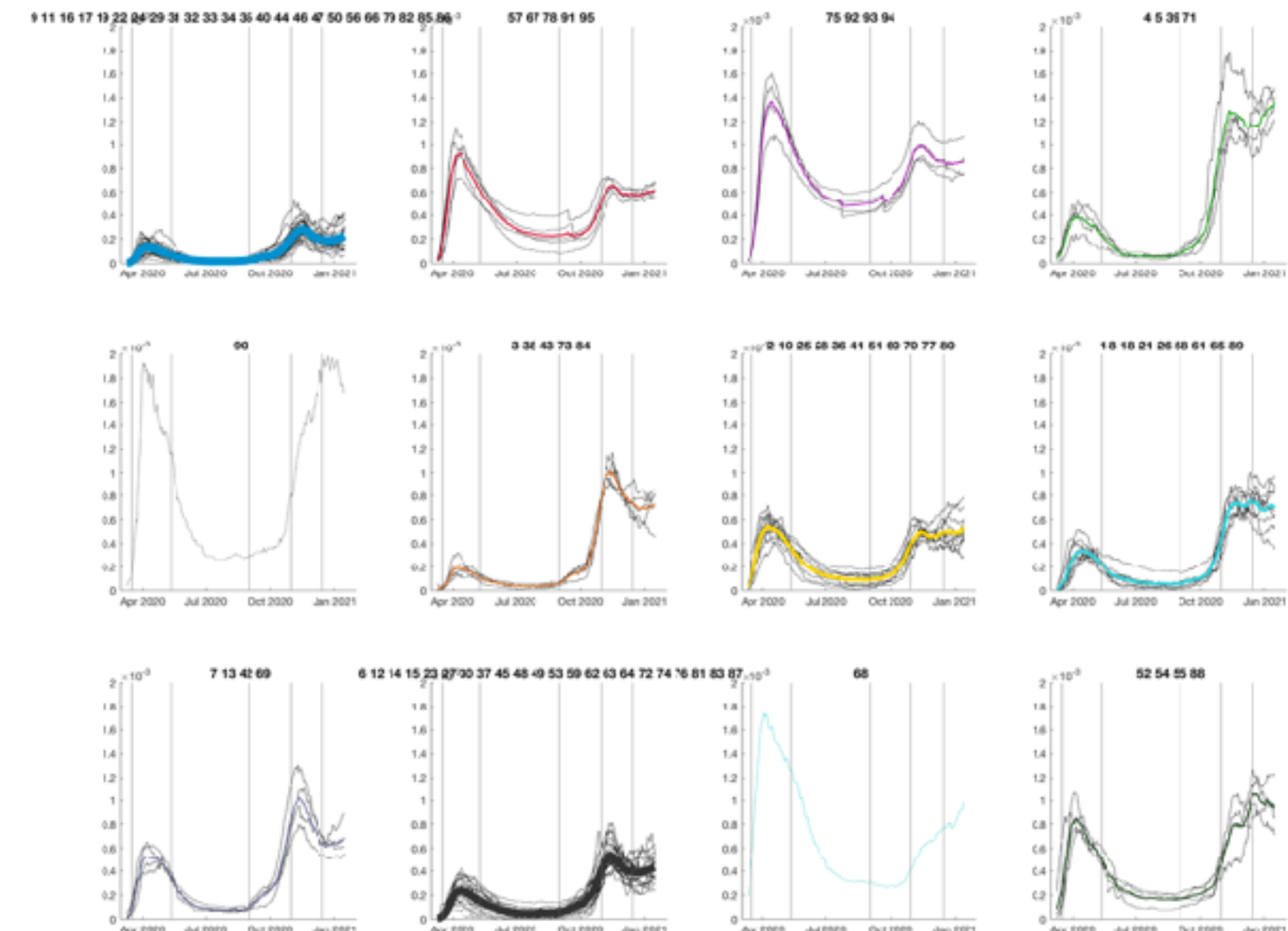
- Missing step: define the initial reduced covariance matrix  $U_0^{-1}$  and the initial extension matrix  $L_0$  from the initial covariance matrix  $P_0$ . Our strategy is based on a clustering approach applied to the observations sequence using the **k-means algorithm**.

$$(U_0^{-1})_{r,s} = \frac{1}{n_{c_r} n_{c_s}} \sum_{i \in c_r} \sum_{j \in c_s} (P_0)_{i,j}$$

$$(L_0)_{i,r} = \beta_{i,r} \mathbb{1}_{N_z, N_z}$$

how much each region/  
department  $i$  belongs to  
cluster  $c_r$

Means clustering with 12 clusters on H/Npop for 94 departments



# Application to the COVID crisis

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# Details about the estimation

- "State" variable for the dynamics with a Backward-Euler time scheme by regions without the S variables

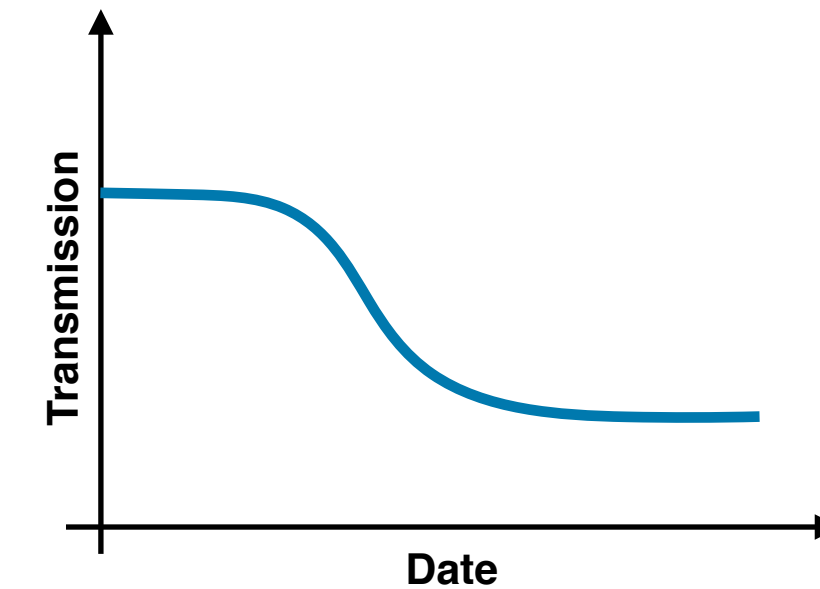
$$\begin{pmatrix} x_{n+1}^i \\ \log b_{n+1}^i \\ \theta_{n+1}^i \end{pmatrix} = \begin{pmatrix} x_n^i + \tau f(x_n^i, b_n^i, \theta_n^i) \\ \log b_n^i + \tau g^i(t_n, \theta_n^i) \\ \theta_n^i \end{pmatrix} + \begin{pmatrix} 0_5 \\ 1 \\ 0_{N_p} \end{pmatrix} v_n \quad x = (E, I/D_q, R, A, H)^T \in \mathbb{R}^5$$

as the shape of  $b$  is undetermined

- $b(t)$  modeled by a logistic function during the first lockdown

$$b(t) = G(t) \stackrel{\text{def}}{=} b_M - \frac{(b_M - b_m)}{1 + e^{-\frac{(t-t_\ell)}{\tau}}} \quad \xrightarrow{\text{dynamics}} \quad d(\log b) = g(t)dt + dv(t)$$

Wiener process



- State transformation ("Twisted" UKF)

$$\psi(x) = \text{logit}\left(\frac{E(0)}{N}\right), \text{logit}\left(\frac{I(0)}{D_q N}\right), \text{logit}\left(\frac{R(0)}{N}\right), \text{logit}\left(\frac{A(0)}{N}\right), \text{logit}\left(\frac{H(0)}{N}\right).$$

- Parameters

$$\theta = (\log(D_q^i), \log(b_M), \log(b_m), \log(\tau), \log(t_\ell), \text{logit}(E(0)), \text{logit}(I(0)), \text{logit}(H(0)))^T$$

- Observations: Incident number of cases tested positive  $rE/D_E$  and Incident number of hospitalized  $I/D_q$  for each region

For estimation of initial conditions

$$P_0^i = \begin{pmatrix} \sigma_{E_0}^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma_{E_0}^2 & 0 & 0 \\ 0 & \sigma_{I_0}^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma_{I_0}^2 & 0 \\ 0 & 0 & \sigma_{R_0}^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \sigma_{A_0}^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \sigma_{H_0}^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma_{H_0}^2 \\ 0 & 0 & 0 & 0 & 0 & \sigma_{b_M}^2 & 0 & \sigma_{b_M}^2 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \sigma_{D_q}^2 & \sigma_{b_M}^2 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma_{b_M}^2 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma_{b_m}^2 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma_\tau^2 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma_{t_\ell}^2 & 0 & 0 & 0 \\ \sigma_{E_0}^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma_{E_0}^2 & 0 & 0 \\ 0 & \sigma_{I_0}^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma_{I_0}^2 & 0 \\ 0 & 0 & 0 & 0 & \sigma_{H_0}^2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & \sigma_{H_0}^2 \end{pmatrix}$$

Covariance per department / region

# Estimation using our Kalman filter in 3 steps (first lockdown + regions)

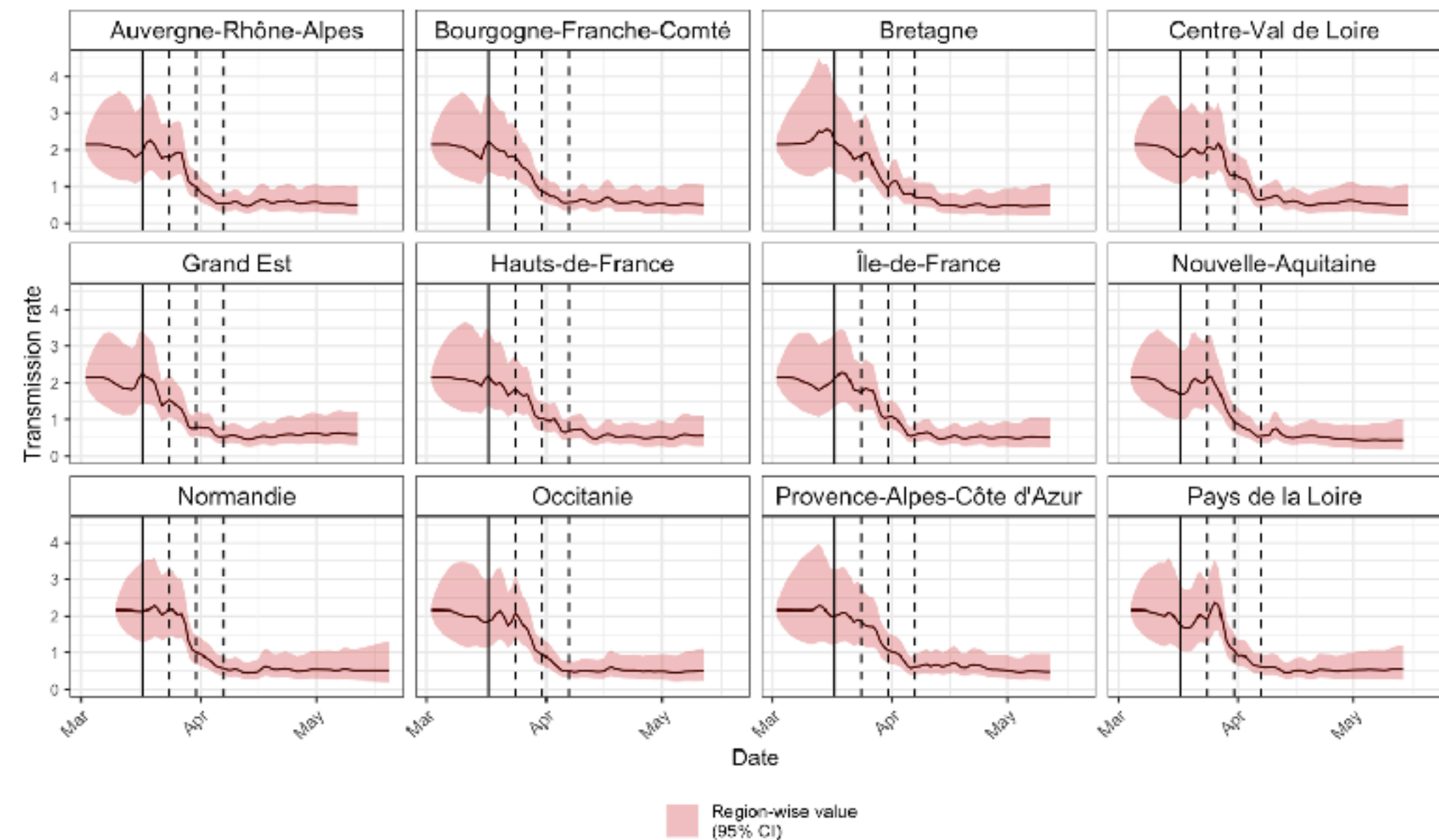
## 1. Estimation of region-wise model parameters and national weighted averages using logistic function $b$

$$d(\log b) = g(t)dt$$

Region	$b_M$	$b_m$	$\tau$	$t_\ell$	$D_q$	$I_0$	$H_0$	$E_0$
Auvergne-Rhône-Alpes	-	0.54 [0.50;0.58]	2.49 [1.51;3.47]	22.22 [20.91;23.53]	-	4 [1;14] (vs 9)	9 [2;34] (vs 9)	2157 [1667; 2790]
Bourgogne-Franche-Comté	-	0.56 [0.52;0.60]	2.56 [1.58;3.53]	21.15 [19.81;22.49]	-	4 [1;12] (vs 8)	2 [0; 8] (vs 2)	1292 [ 944; 1767]
Bretagne	-	0.53 [0.48;0.58]	3.82 [2.81;4.82]	20.30 [18.67;21.94]	-	5 [2;12] (vs 13)	5 [1;19] (vs 5)	45 [ 16; 128]
Centre-Val de Loire	-	0.55 [0.50;0.60]	2.80 [1.82;3.77]	21.91 [20.61;23.20]	-	1 [0; 3] (vs 2)	4 [1;15] (vs 4)	790 [ 611; 1021]
Grand Est	-	0.55 [0.50;0.59]	2.68 [1.76;3.60]	20.03 [18.70;21.36]	-	6 [2;18] (vs 12)	24 [6;95] (vs 25)	6752 [5733; 7951]
Hauts-de-France	-	0.56 [0.52;0.60]	3.31 [2.34;4.27]	21.91 [20.51;23.30]	-	4 [1;14] (vs 9)	4 [1;15] (vs 4)	1794 [1315; 2448]
Île-de-France	-	0.52 [0.48;0.56]	3.10 [2.19;4.00]	22.61 [21.47;23.73]	-	16 [5;49] (vs 34)	4 [1;15] (vs 4)	8506 [6669;10849]
Normandie	-	0.49 [0.44;0.55]	2.18 [1.23;3.14]	16.33 [14.77;17.88]	-	4 [1;11] (vs 9)	8 [2;34] (vs 9)	1335 [1105; 1611]
Nouvelle-Aquitaine	-	0.52 [0.46;0.56]	2.34 [1.33;3.33]	21.11 [19.77;22.45]	-	2 [1; 7] (vs 5)	1 [0; 4] (vs 1)	789 [ 546; 1141]
Occitanie	-	0.49 [0.44;0.54]	2.42 [1.44;3.40]	22.10 [20.81;23.37]	-	3 [1; 9] (vs 6)	3 [1;11] (vs 3)	906 [ 594; 1382]
Pays de la Loire	-	0.51 [0.46;0.56]	2.30 [1.37;3.23]	22.21 [21.10;23.31]	-	3 [1;10] (vs 7)	2 [0; 8] (vs 2)	575 [ 256; 1290]
Provence-Alpes-Côte d'Azur	-	0.59 [0.55;0.63]	3.02 [2.05;4.00]	22.05 [20.63;23.47]	-	4 [1;13] (vs 9)	2 [0; 8] (vs 2)	1124 [ 753; 1677]
France	2.16 [2.02;2.31]	0.53 [0.51;0.56]	2.78 [2.29;3.27]	21.49 [20.82;22.16]	0.26 [0.20;0.34]			

## 2. Estimation of $b$ without the logistic function *a priori*

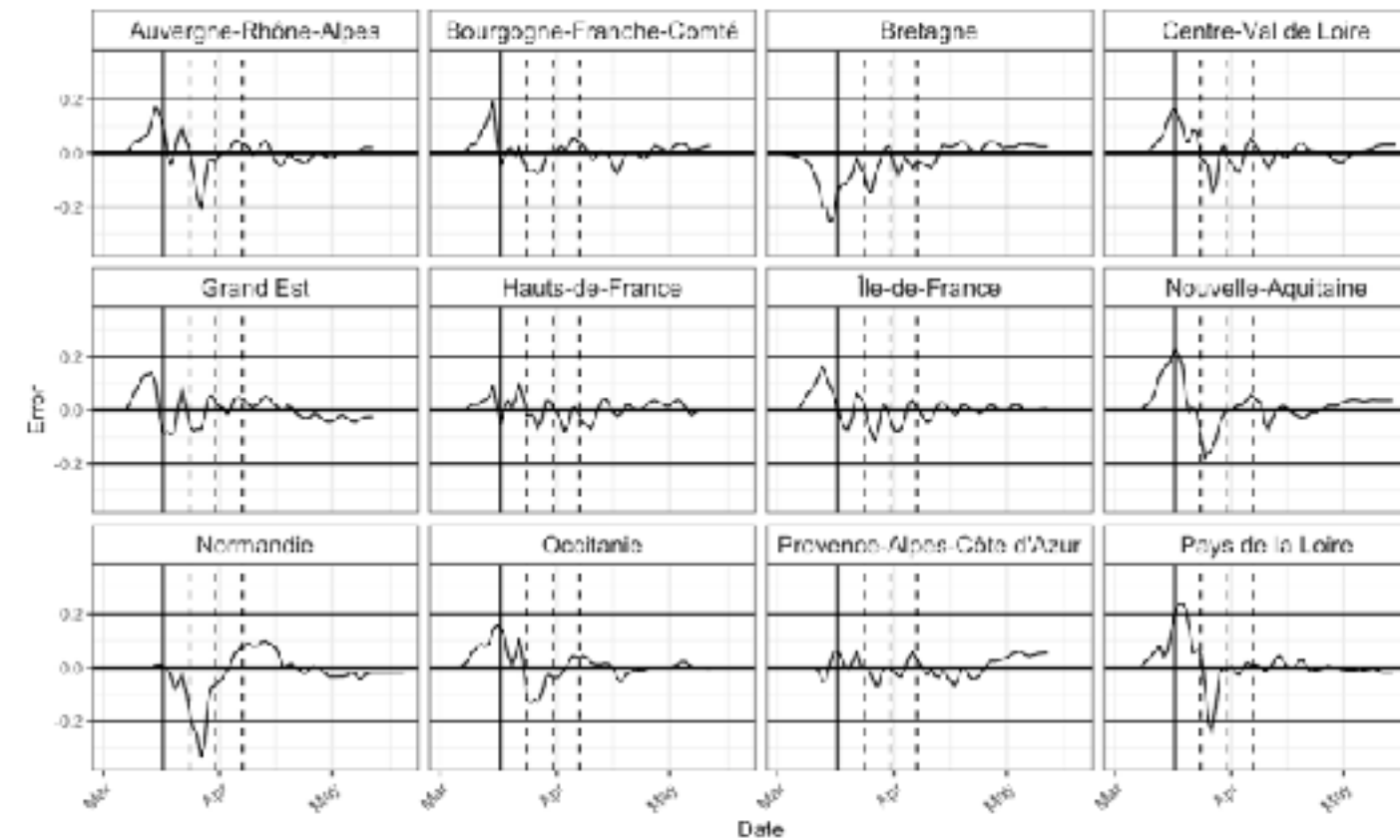
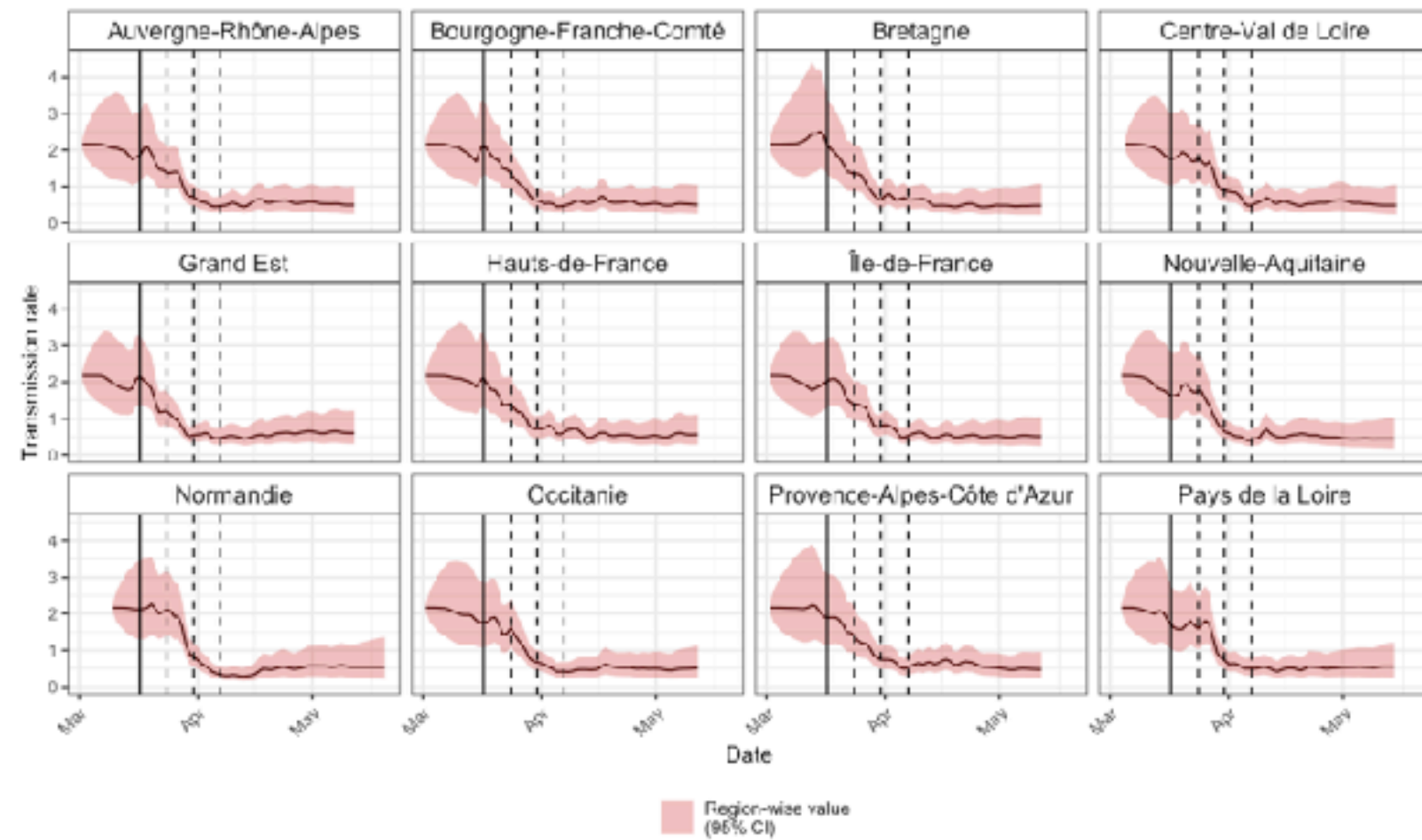
$$d(\log b) = dv(t)$$





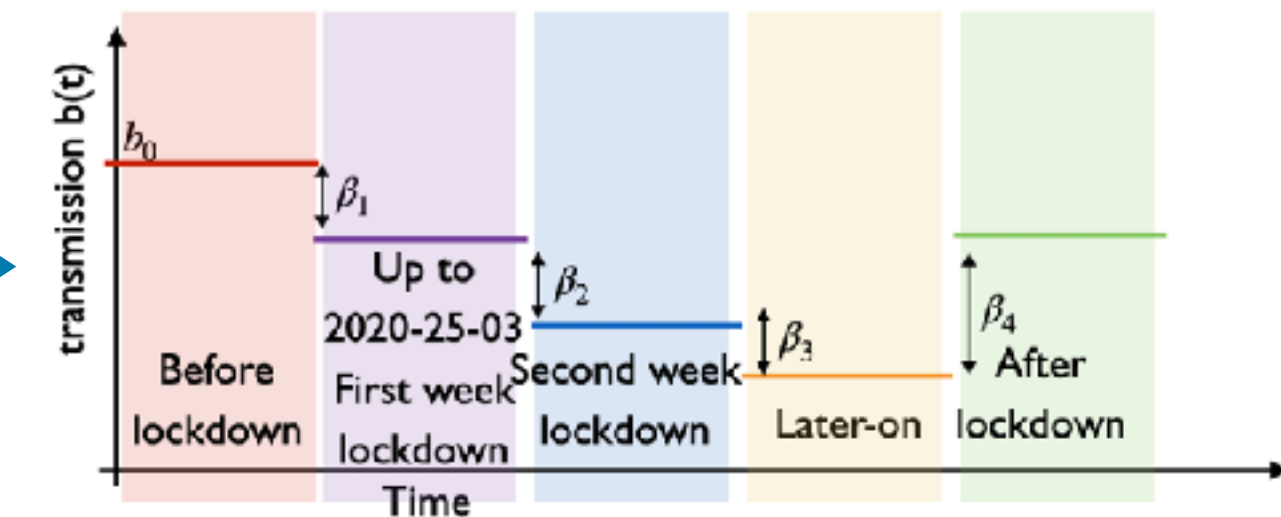
# Estimation using our Kalman filter in 3 steps (first lockdown + regions)

## 3. Estimation of region-wise model parameters and national weighted averages using logistic function $b$



$$d(\log b) = g(t)dt + dv(t)$$

Choice of a step function



→ Final prediction of effective reproductive number

$$R_e(t, \xi_i) = \frac{D_I b_i}{A(t, \xi_i) + I(t, \xi_i)} \left( aA(t, \xi_i) + \frac{D_{q_i} I(t, \xi_i)}{D_I + D_{q_i}} \right)$$

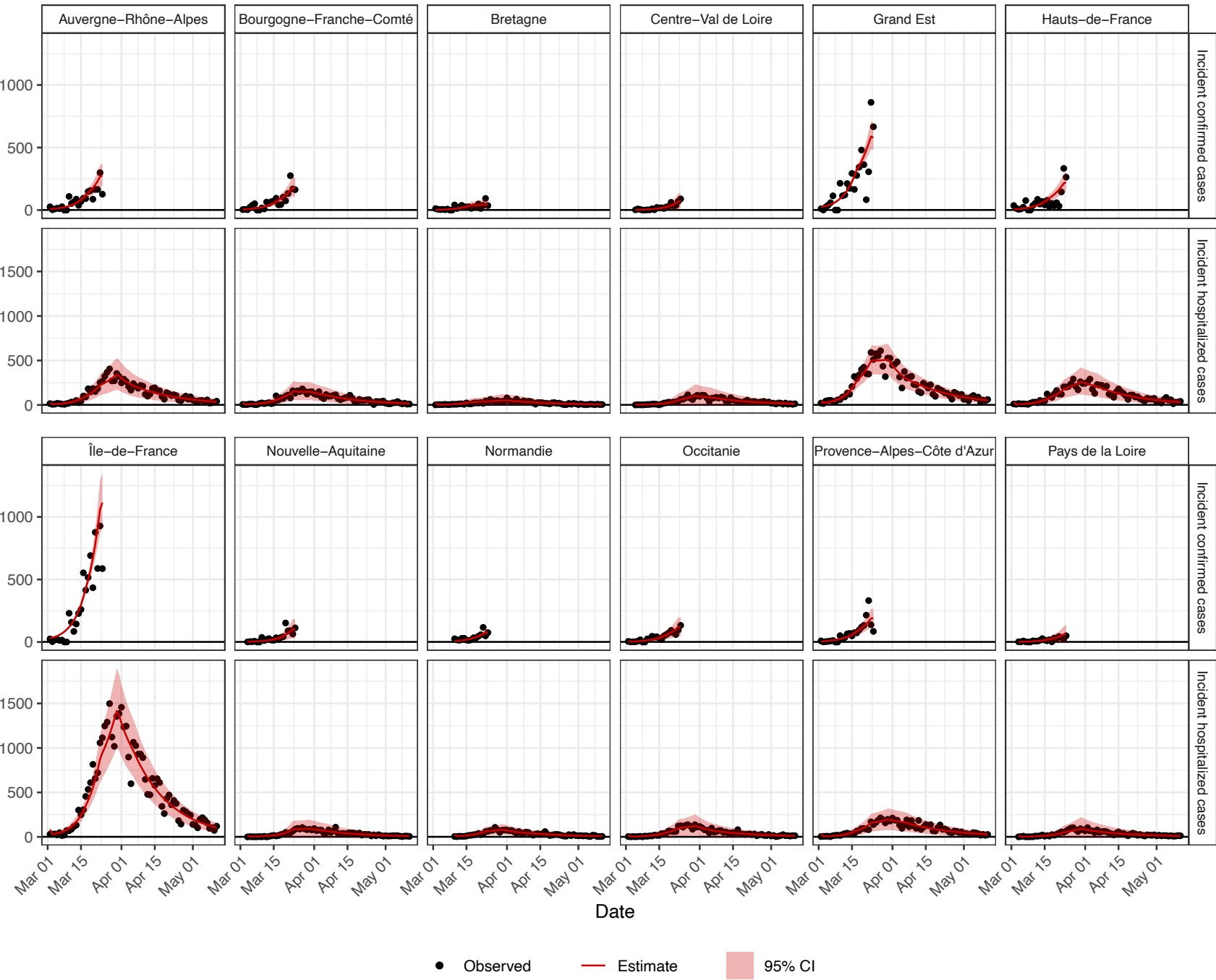
and attack rates = people at risk / population

Our results are comparable to the results obtained by Salje et al. (Pasteur institute); Crepey et al. (EHESP); Alizon et al. (ETE CNRS)

Region	$R_e$ (before lockdown) on 2020-03-15	$R_e$ (during lockdown) on 2020-03-29	$R_e$ (end lockdown) on 2020-05-11	Attack rates: Infected proportion of the population in % computed as (E+I+A+H+R)/N	
Geographical region				2020-03-17	2020-05-11
Auvergne-Rhône-Alpes	2.20 [1.68;2.87]	1.01 [0.83;1.23]	0.62 [0.44;0.90]	0.28 [0.21;0.36]	3.85 [3.71;3.99]
Bourgogne-Franche-Comté	2.12 [1.63;2.77]	0.93 [0.76;1.15]	0.63 [0.43;0.92]	0.47 [0.37;0.60]	5.52 [5.32;5.75]
Bretagne	3.15 [2.40;4.11]	0.99 [0.79;1.24]	0.61 [0.40;0.91]	0.17 [0.12;0.23]	1.52 [1.45;1.60]
Centre-Val de Loire	2.38 [1.8;3.14]	1.33 [1.08;1.64]	0.62 [0.43;0.88]	0.20 [0.15;0.26]	3.74 [3.59;3.89]
Grand Est	2.30 [1.81;2.93]	0.71 [0.58;0.87]	0.76 [0.53;1.08]	1.19 [0.99;1.44]	9.47 [9.15;9.83]
Hauts-de-France	2.35 [1.81;3.04]	0.97 [0.79;1.19]	0.71 [0.50;1.00]	0.35 [0.27;0.45]	4.39 [4.23;4.56]
Île-de-France	2.38 [1.85;3.06]	1.02 [0.84;1.23]	0.65 [0.49;0.93]	0.74 [0.60;0.93]	9.94 [9.65;10.3]
Normandie	2.68 [2.14;3.35]	1.45 [1.19;1.75]	0.68 [0.46;0.99]	0.12 [0.11;0.14]	2.11 [2.02;2.21]
Nouvelle-Aquitaine	2.23 [1.67;2.97]	1.11 [0.91;1.36]	0.55 [0.37;0.83]	0.10 [0.08;0.14]	1.43 [1.37;1.49]
Occitanie	2.29 [1.77;2.96]	0.96 [0.79;1.18]	0.64 [0.43;0.95]	0.17 [0.14;0.22]	1.83 [1.76;1.91]
Pays de la Loire	2.55 [1.95;3.31]	1.18 [0.97;1.44]	0.70 [0.48;1.01]	0.16 [0.13;0.21]	2.10 [2.01;2.19]
Provence-Alpes-Côte d'Azur	2.59 [1.99;3.36]	1.11 [0.90;1.37]	0.60 [0.42;0.85]	0.33 [0.25;0.44]	4.10 [3.95;4.26]
France	2.40 [1.85;3.10]	1.04 [0.85;1.27]	0.65 [0.45;0.94]	0.41 [0.33;0.52]	4.90 [4.74;5.08]

# Estimation using SAEM approach (first lockdown + regions)

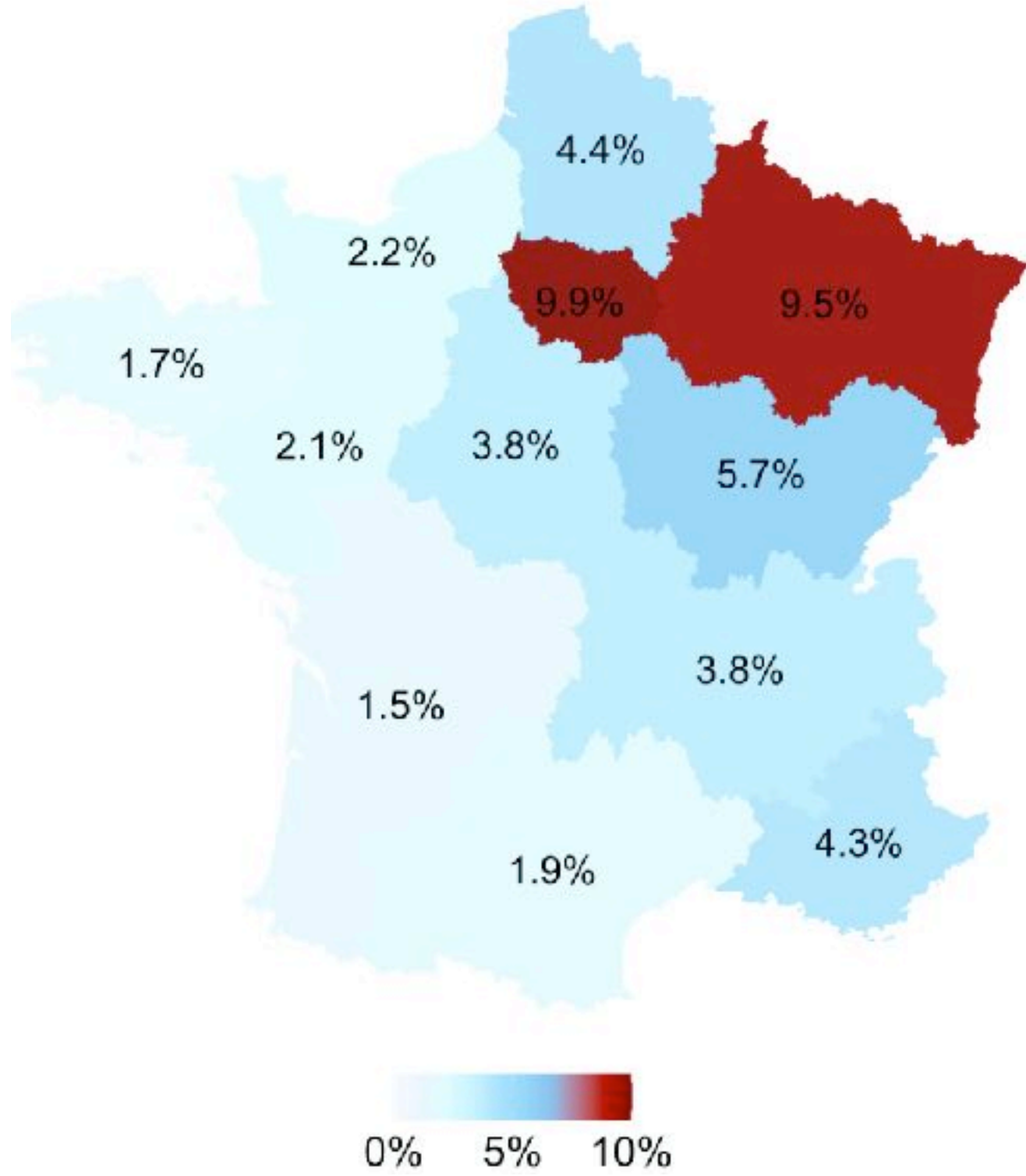
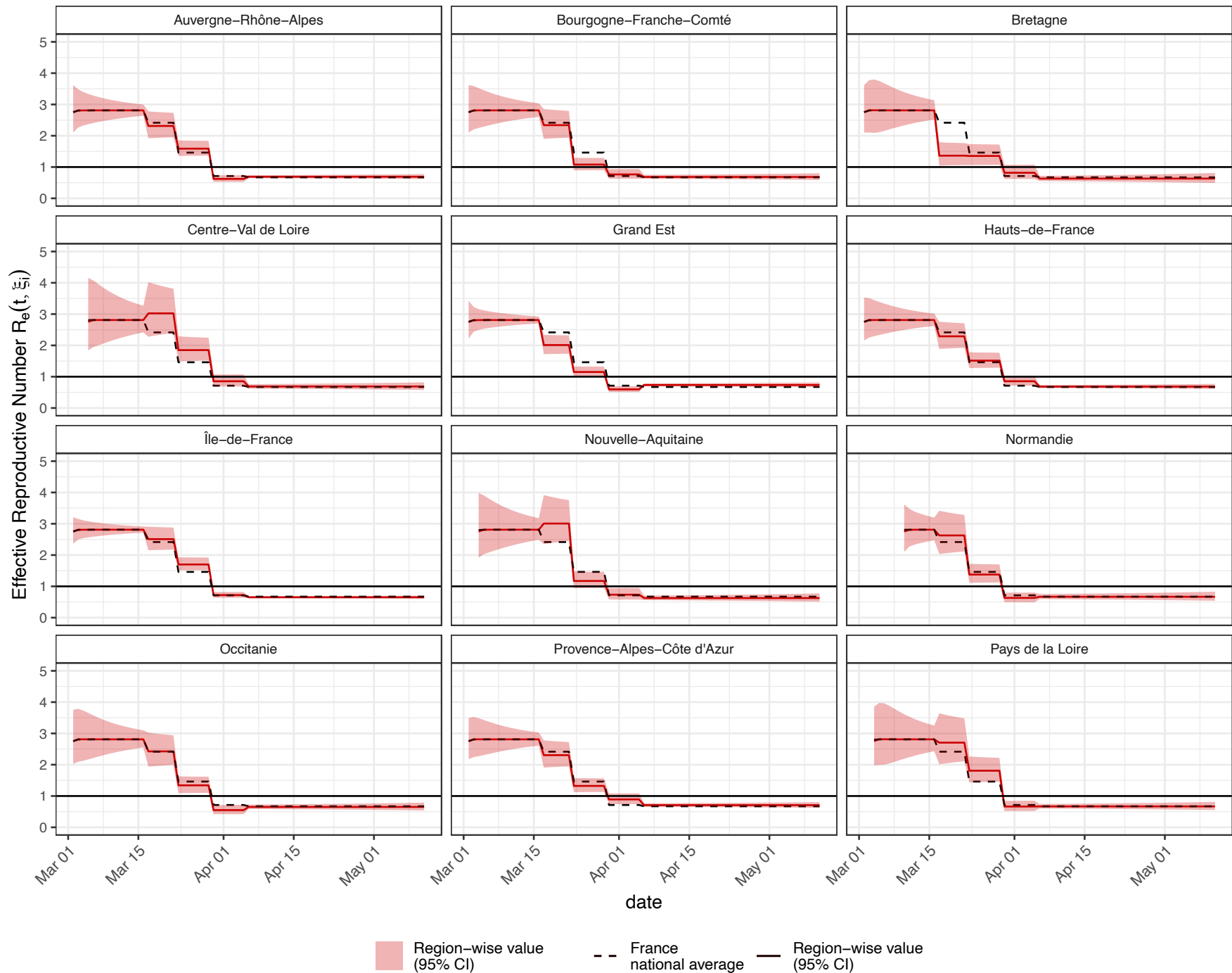
- In order to validate our Kalman estimation approach, an estimation using SAEM approach with a step function for  $b$  has been done.



Fitting curves of incident number of cases tested positive ( $rE/D_E$ ) and Incident number of hospitalized ( $I/D_q$ ) for each region with the SEIRAH model

Our results are comparable to the results obtained by Salje et al. (Pasteur institute); Crepey et al. (EHESP); Alizon et al. (ETE CNRS)

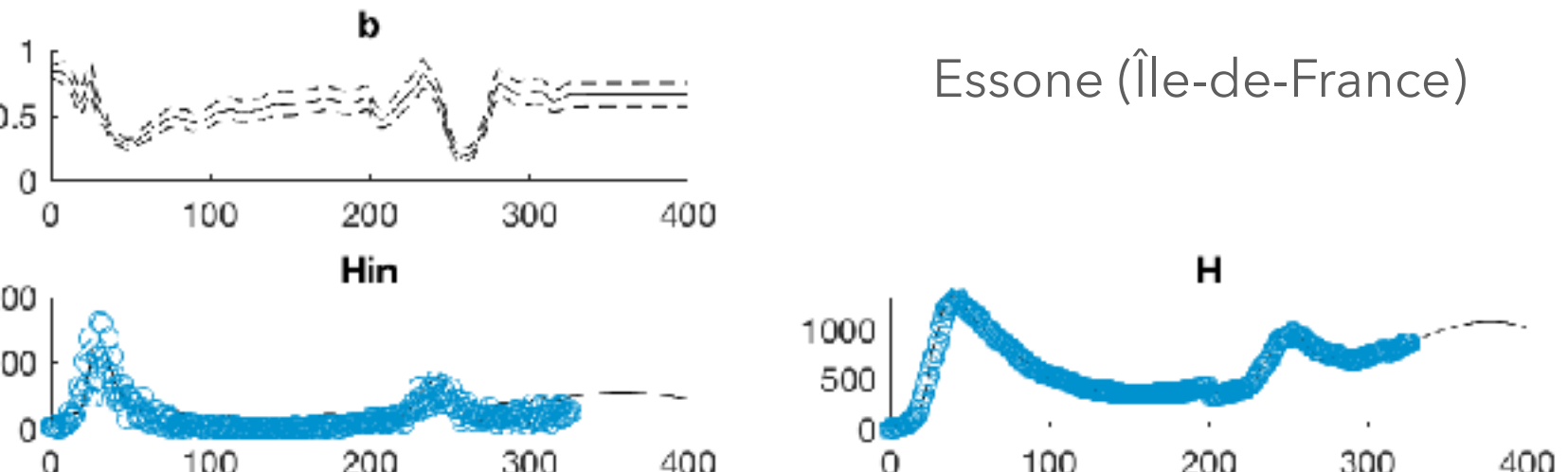
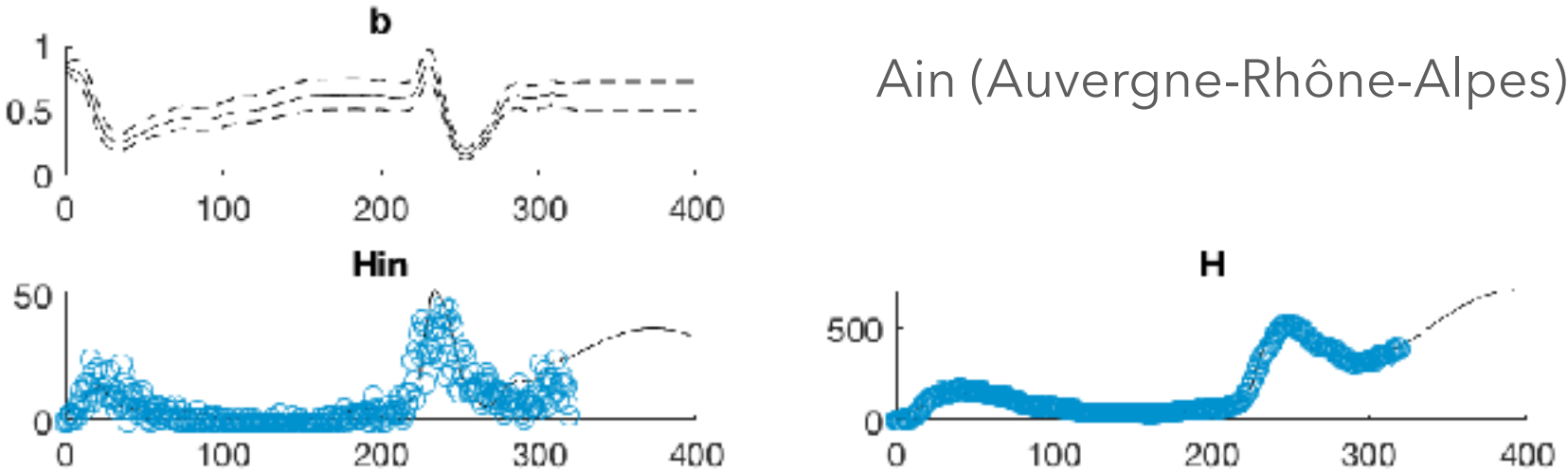
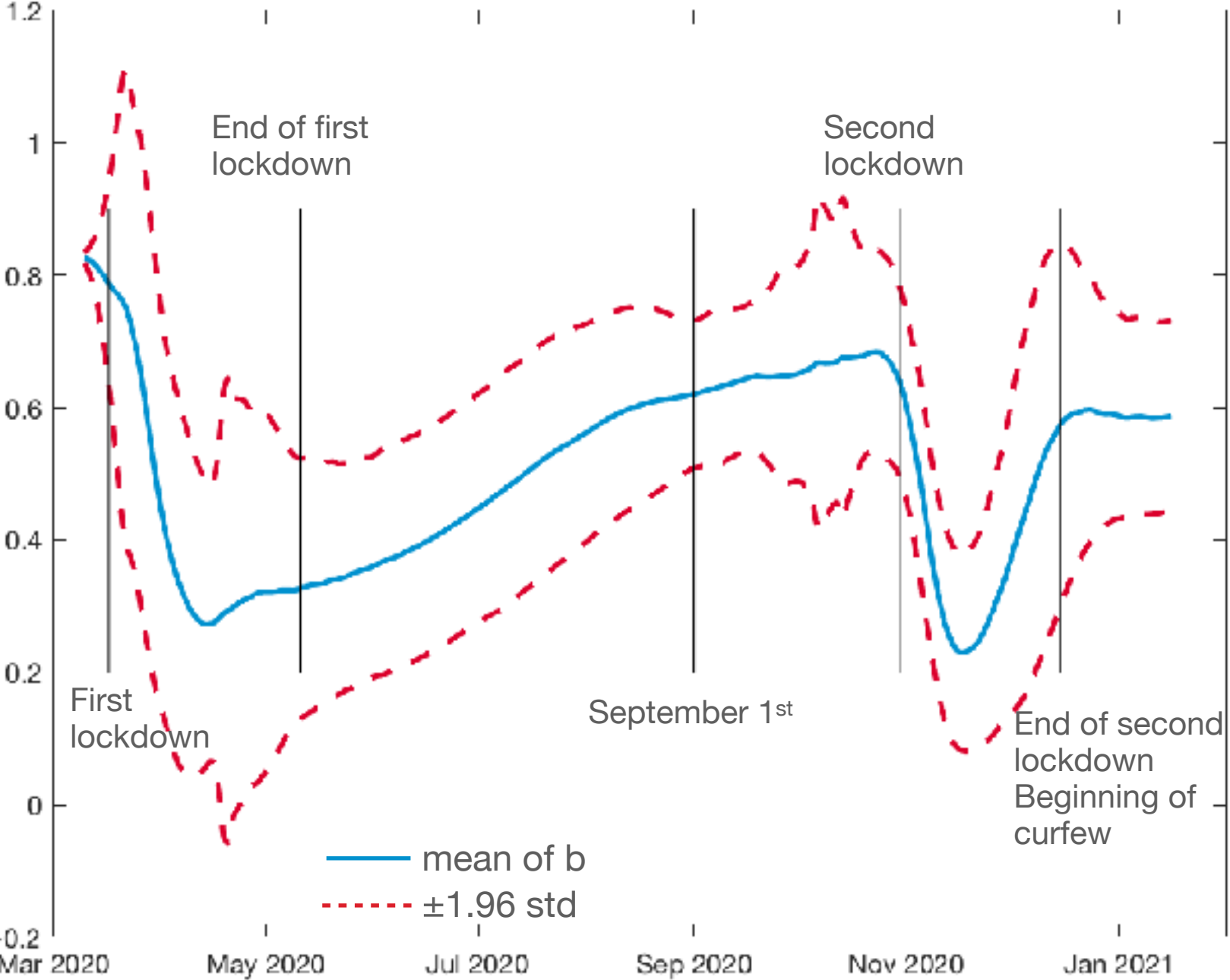
Region specific  $R_e$  compared to the national average. Lockdown started on March 17.



Model estimation for the proportion of Immunized individual in the population (deaths not taken into account), also referred as attack rate, on May 11th, 2020 (end of the first lockdown)

# Departments results until today

- Since the first lockdown, new data are available (Hospitalizations H and Incident number of hospitalized  $H_{in}$ )
- Refined level (94 departments instead of 12 regions)
- Reduced-order version of our population Unscented Kalman filter (on 12 clusters)
- Prediction assuming  $b$  stays constant (different values for each department) ...



	January 25th -> February 1st	January 25th -> February 8th
Number of hospitalisations	+ 2378	+ 4987

# Conclusions and Perspectives

- Conclusions
  - Validation of our reduced-order population-based Kalman filter
    - Able to deal with mixed effects
    - Able to deal with error model
    - Very efficient in terms of computational times
  - Very interesting results obtained on the first lockdown in terms of immunity and effective reproducer number
  - Main limitation: do not take into account travels between regions / departments
- Perspectives for the application
  - Evaluate the acceptability of lockdown strategy
  - Evaluate the predicting of second- and third- waves of COVID-19 using only the information of first wave
  - Account for vaccination and waning immunity
- Perspective for methodological developments
  - Deal with large systems (ODE or even PDE systems)