





Image: A math a math



# Estimations of mechanistics models by sequential and variational approach. Application to SARS-CoV-2.

#### Florian Robert

Master 2 Probability and random models Sorbonne University

13 september 2022

Under the supervision of Mélanie Prague

#### Equipe SISTM Bordeaux Population Health

Florian Robert

Estimations of mechanistics models.

13 september 2022 1 / 29

Objectives of this internship :

- Comparing sequential and variational approach
- Apply variational approach to a modelling problem for SARS-Cov-2

Image: A matched and A matc

# Table of contents

#### Thematic of study

- About data
- A mechanistic model

#### 2 Sequential approach

- A simplified model
- Comparison of time-schemes

#### 3 Variational approach

- Simulation scheme
- Application of simulation scheme

#### 4 Modelization

- Basic reproduction number
- Mathematical models
- Results

Image: A math a math

# Thematic of study

メロト メロト メヨト メ

### Case study



(a) Study design



(b) Prelevement design





Estimations of mechanistics models

# A mechanistic model



For  $X \in \{N = Nasopharynx ; T = Trachea\}$ , we define mathematical model <sup>1</sup> by :

$$\begin{aligned} \dot{T}^{X} &= -\beta T^{X} V_{i}^{X} - \mu \beta T^{X} V_{S}^{X} \\ \dot{I}_{1}^{X} &= \beta T^{X} V_{i}^{X} + \mu \beta T^{X} V_{S}^{X} - k I_{1}^{X} \\ \dot{I}_{2}^{X} &= k I_{1}^{X} - \delta I_{2}^{X} \\ \dot{V}_{i}^{X} &= \mu P^{X} I_{2}^{X} - c V_{i}^{X} - \beta T^{X} V_{i}^{X} \\ \dot{V}_{ni}^{X} &= (1 - \mu) P^{X} I_{2}^{X} - c V_{ni}^{X} \\ \dot{V}_{S}^{X} &= -\mu \beta T^{X} V_{S}^{X} - c_{I} V_{S}^{X} \end{aligned}$$

<sup>1</sup>Marie Alexandre et al. (2022). "Modelling the response to vaccine in non-human primates to define SARS-CoV-2 mechanistic correlates of protection". In: *eLife*  $\bigcirc$  +  $\bigcirc$  + 0

# A mechanistic model



The statistical model is defined by :

$$\begin{cases} \log_{10}(\beta_i) = \log_{10}(\beta_{pop}) + u_i^{\beta} \\ \log(\delta_i) = \log(\delta_{pop}) + u_i^{\delta} \end{cases}$$

where 
$$u_i^eta \sim \mathcal{N}(0,\omega_eta^2)$$
 and  $u_i^\delta \sim \mathcal{N}(0,\omega_\delta^2).$ 

And, the observation model is defined by :  $\begin{cases}
gRNA_{ij}^{X} = \log_{10}(V_{i}^{X} + V_{ni}^{X} + V_{S}^{X})(t_{ij}, \psi_{i}^{X}) + \epsilon_{ij,g}^{X} \\
sgRNA_{ij}^{X} = \alpha_{sgRNA} \log_{10}(l_{1}^{X} + l_{2}^{X})(t_{ij}, \psi_{i}^{X}) + \epsilon_{ij,sg}^{X} \\
where \epsilon_{ij,g}^{X} \sim \mathcal{N}(0, \sigma_{g,X}^{2}), \ \epsilon_{ij,sg}^{X} \sim \mathcal{N}(0, \sigma_{sg,X}^{2}).
\end{cases}$ 

イロト イヨト イヨト

 $\implies$  These 3 models define our **non linear mixed effects model**.

# Two approaches to estimating parameters



Image: A math a math

# Sequential approach

イロト イロト イヨト イヨ

# Simplified model

We only focus on nasopharynx compartment with the mathematical model :

$$\dot{T} = -\beta T V_i - \mu \beta T V_S$$

$$\dot{I}_1 = \beta T V_i + \mu \beta T V_S - k I_1$$

$$\dot{I}_2 = k I_1 - \delta I_2$$

$$\dot{V}_i = \mu P I_2 - c V_i - \beta T V_i$$

$$\dot{V}_{ni} = (1 - \mu) P I_2 - c V_{ni}$$

$$\dot{V}_S = -\mu \beta T V_S - c_I V_S$$
(1)

and the observation model :

$$gRNA_{ij} = log_{10}(V_i + V_{ni} + V_S)(t_{ij}, \psi_i) + \epsilon_{ij}$$
(2)

Image: A math a math

where  $\epsilon_{ij} \sim \mathcal{N}(0, \sigma^2)$ .

Florian Robert

# Stiffs equations

Figure: Simulation of the dynamics of the compartments of the previous model for different values of  $\beta$  and  $\delta = 0.85$ . dashed line :  $\beta = 10^{-5.5}$ , continuous line :  $\beta = 10^{-5}$ .



### Comparison of explicit and implicit time-schemes



# Working prospects

For the two next weeks, we have to :

- Solve issue about the numerical resolution method.
- Finish implementation of Kalman filter algorithm.
- Compare sequential approach with the variational approach.

Image: A matched a matc

# Variational approach

メロト メロト メヨトメ

# Simulation scheme

$$\begin{cases} \dot{T} = -\beta TV_i - \mu\beta TV_S \\ \dot{I}_1 = \beta TV_i + \mu\beta TV_S - kI_1 \\ \dot{I}_2 = kI_1 - \delta I_2 \\ \dot{V}_i = \mu PI_2 - cV_i - \beta TV_i \\ \dot{V}_{ni} = (1 - \mu)PI_2 - cV_{ni} \\ \dot{V}_S = -\mu\beta TV_S - c_I V_S \\ he observation model : \end{cases}$$

Т

 $gRNA_{ij} = log_{10}(V_i + V_{ni} + V_S)(t_{ij}, \psi_i) + \epsilon_{ij}$ where  $\epsilon_{ij} \sim \mathcal{N}(0, \sigma^2)$ .

- Variability on  $\beta$  and  $\delta$  + others parameters are fixed
- Simulation of 100 groups of 10 fictive monkeys on days 0, 1, 2, 3, 4, 6, 9, 14 and 20.
- Estimation of parameters with simulated data with MONOLIX software
- Comparison between estimated and real parameters

• • • • • • • • • • •

## Application of simulation scheme



イロト イヨト イヨト イヨ

# Application of simulation scheme

Approach	Parameters	Population		Individual		
		Relative bias	Coverage rate	Individual bias	Coverage rate	
Variational	β	$0.01\pm0.056$	0.95	$-0.016 \pm 0.475$	0.92	
	$\omega_{\beta}$	$\textbf{0.134} \pm \textbf{0.44}$	0.85	Undefined		
	δ	$-0.09\pm0.559$	0.90	$-0.009 \pm 0.155$	0.88	
	$\omega_{\delta}$	$-0.122\pm0.364$	0.92	Undefin	efined	
	σ	$0.005\pm0.089$	0.94	Undefined		
Sequential						

メロト メタト メヨト メヨト

# Modelization

Florian Robert

イロト イヨト イヨト イヨト

## A new model



イロト イヨト イヨト イヨト

# Basic reproduction number

By taking the spectral radius of  $FV^{-1}$ , we get the basic reproduction number in  $X \in \{N; T\}^2$ :

$$R_0^X = \frac{\beta T^X(0)\mu P^X}{\delta(c+\beta T^X(0))} \tag{3}$$

<sup>2</sup>Odo Diekmann, J.A.P. Heesterbeek, and Johan Metz (1990). "On the Definition and the Computation of the Basic Reproduction Ratio R0 in Models For Infectious-Diseases in Heterogeneous Populations". In: *Journal of mathematical biology*; Odo Diekmann, J.A.P. Heesterbeek, and M.G. Roberts (2009). "The construction of next-generation matrices for compartmental epidemic models". In: *Journal of the Royal Society, Interface / the Royal Society*; Jane Heffernan, R.J. Smith, and L.M. Wahl (2005). "Perspectives on the Basic Reproductive Ratio". In: *Journal of the Royal Society, Interface / the Royal Society*.

Florian Robert

# Distribution of R<sub>0</sub> by group

$$R_0^X = \frac{\beta T^X(0)\mu P^X}{\delta(c+\beta T^X(0))} \tag{4}$$

・ロト ・日下 ・日

Figure: Distribution of basic reproduction number  $R_0$  in nasopharynx by group



# The starting mathematical model



For  $X \in \{N = Nasopharynx ; T = Trachea\}$ , we define mathematical model by :

$$\begin{aligned} \dot{T}^{X} &= -(1 - \varepsilon_{Ab})\beta V_{i}^{X}T^{X} - \mu(1 - \varepsilon_{Ab})\beta V_{S}^{X}T^{X} \\ \dot{I}_{1}^{X} &= (1 - \varepsilon_{Ab})\beta V_{i}^{X}T^{X} + \mu(1 - \varepsilon_{Ab})\beta V_{S}^{X}T^{X} - kI_{1}^{X} \\ \dot{I}_{2}^{X} &= kI_{1}^{X} - \delta I_{2}^{X} - \xi Ab_{2}I_{2}^{X} \\ \dot{V}_{i}^{X} &= P^{X}\mu I_{2}^{X} - cV_{i}^{X} - (1 - \varepsilon_{Ab})\beta V_{i}^{X}T^{X} \\ \dot{V}_{ni}^{X} &= P^{X}(1 - \mu)I_{2}^{X} - cV_{ni}^{X} \\ \dot{V}_{s}^{X} &= -c_{I}V_{S}^{X} - \mu(1 - \varepsilon_{Ab})\beta V_{S}^{X}T^{X} \\ \dot{Ab}_{1} &= \gamma V + r_{A}\left(1 - \frac{Ab_{1}}{Ab_{max}}\right)Ab_{1} - k_{Ab}Ab_{1} \\ \dot{Ab}_{2} &= k_{Ab}Ab_{1} - \xi Ab_{2}I_{2} - \delta_{Ab}Ab_{2} \end{aligned}$$

< □ > < □ > < □ > < □ > < □ >

# Review of scientific literature

Figure: Models incorporating a refractory cell compartment.



(a) Voir Kasia A. PAWELEK and al. <sup>3</sup>

(b) See Pranesh PADMANABHAN and al. 4

 <sup>3</sup>Kasia A. Pawelek et al. (2012). "Modeling Within-Host Dynamics of Influenza Virus Infection Including Immune Responses". In: *PLOS Computational Biology* <sup>4</sup>Pranesh Padmanabhan, Rajat Desikan, and Narendra Dixit (2022). "Modeling how antibody responses may determine the efficacy of COVID-19 vaccines". In: *Nature Computational Science*

Florian Robert

# A new model



For  $X \in \{N = Nasopharynx ; T = Trachea\}$ , we define mathematical model <sup>5</sup> by :

$$\begin{split} \dot{T}^{X} &= -(1-\varepsilon_{Ab})\beta V_{i}^{X}T^{X} - \mu(1-\varepsilon_{Ab})\beta V_{S}^{X}T^{X} \\ \dot{I}_{1}^{X} &= (1-\varepsilon_{Ab})\beta V_{i}^{X}T^{X} + \mu(1-\varepsilon_{Ab})\beta V_{S}^{X}T^{X} - kI_{1}^{X} \\ \dot{I}_{2}^{X} &= kI_{1}^{X} - \delta(I_{2}^{X})^{H}I_{2}^{X} \\ \dot{V}_{i}^{X} &= P^{X}\mu I_{2}^{X} - cV_{i}^{X} - (1-\varepsilon_{Ab})\beta V_{i}^{X}T^{X} \\ \dot{V}_{ni}^{X} &= P^{X}(1-\mu)I_{2}^{X} - cV_{ni}^{X} \\ \dot{V}_{s}^{X} &= -c_{i}V_{S}^{X} - \mu(1-\varepsilon_{Ab})\beta V_{S}^{X}T^{X} \\ \dot{M}_{1} &= \gamma I_{2} + r_{A}\left(1 - \frac{M_{1}}{Ab_{max}}\right)M_{1} - k_{Ab}M_{1} \\ \dot{M}_{2} &= k_{Ab}M_{1} - k_{Ab}M_{2} \\ \dot{Ab} &= k_{Ab}M_{2} - \delta_{Ab}Ab \end{split}$$

<sup>5</sup>Ashish Goyal, E. Fabian Cardozo-Ojeda, and Joshua T. Schiffer (2020). "Potency and timing of antiviral therapy as determinants of duration of SARS-CoV-2 shedding and intensity of inflammatory response". In: *Science Advances* 

Florian Robert

# Results Individual plots

#### Figure: Individual plots for the starting and the previous model.



13 september 2022

CU494

CGB103

CGC005

DB331

CGC011

060021

25 / 29

he starting model :  

$$\begin{split} \vec{T}^{X} &= -(1 - \varepsilon_{Ab})\beta V_{i}^{X}T^{X} - \mu(1 - \varepsilon_{Ab})\beta V_{S}^{X}T^{X} \\ \vec{I}_{1}^{X} &= (1 - \varepsilon_{Ab})\beta V_{i}^{X}T^{X} + \mu(1 - \varepsilon_{Ab})\beta V_{S}^{X}T^{X} - kI_{1}^{X} \\ \vec{I}_{2}^{X} &= kI_{1}^{X} - \overline{\delta I_{2}^{X} - \xi Ab_{2}I_{2}^{X}} \\ \vec{V}_{i}^{X} &= P^{X}\mu I_{2}^{X} - cV_{i}^{X} - (1 - \varepsilon_{Ab})\beta V_{i}^{X}T^{X} \\ \vec{V}_{ni}^{X} &= P^{X}(1 - \mu)I_{2}^{X} - cV_{ni}^{X} \\ \vec{V}_{S}^{X} &= -c_{I}V_{S}^{X} - \mu(1 - \varepsilon_{Ab})\beta V_{S}^{X}T^{X} \\ \vec{Ab}_{1} &= \gamma V + r_{A}\left(1 - \frac{Ab_{1}}{Ab_{max}}\right)Ab_{1} - k_{Ab}Ab_{1} \\ \vec{Ab}_{2} &= k_{Ab}Ab_{1} - \xi Ab_{2}I_{2} - \delta_{Ab}Ab_{2} \end{split}$$

 $I_{1}^{X} = new model :$   $\begin{cases}
\dot{T}^{X} = -(1 - \varepsilon_{Ab})\beta V_{i}^{X}T^{X} - \mu(1 - \varepsilon_{Ab})\beta V_{S}^{X}T^{X} \\
\dot{I}_{1}^{X} = (1 - \varepsilon_{Ab})\beta V_{i}^{X}T^{X} + \mu(1 - \varepsilon_{Ab})\beta V_{S}^{X}T^{X} - kI_{1}^{X} \\
\dot{I}_{2}^{X} = kI_{1}^{X} - \delta I_{2}^{X} I_{2}^{H} I_{2}^{X} \\
\dot{V}_{i}^{X} = P^{X}\mu I_{2}^{X} - cV_{i}^{X} - (1 - \varepsilon_{Ab})\beta V_{i}^{X}T^{X} \\
\dot{V}_{ni}^{X} = P^{X}(1 - \mu)I_{2}^{X} - cV_{ni}^{X} \\
\dot{V}_{S}^{X} = -c_{I}V_{S}^{X} - \mu(1 - \varepsilon_{Ab})\beta V_{S}^{X}T^{X} \\
\dot{M}_{1} = \gamma I_{2}^{L} + r_{A} \left(1 - \frac{M_{1}}{Ab_{max}}\right)M_{1} - k_{Ab}M_{1} \\
\dot{M}_{2} = k_{Ab}M_{1} - k_{Ab}M_{2} \\
\dot{Ab} = k_{Ab}M_{2} - \delta_{Ab}Ab
\end{cases}$ 

#### $BICc = -2\mathcal{LL}_{y}(\theta) + \dim(\theta_{R})\log(N) + \dim(\theta_{F})\log(n_{tot})$

Basic model	Modification	BICc
The starting model	None	
	$\dot{Ab_1} = \gamma l_2 + r_A \left(1 - \frac{Ab_1}{Ab_{max}}\right) Ab_1 - k_{Ab}Ab_1$	800
	$\dot{l_2}^X = k l_1^X - \delta(l_2^X)^H l_2^X$	$\geq$ 1000
The new model	None	
	$\dot{M}_1 = \gamma V + r_A \left( 1 - \frac{M_1}{Ab_{max}} \right) M_1 - k_{Ab} M_1$	789
	$\dot{l_2}^{X} = k l_1^X - \delta l_2^X$	964

メロト メタト メヨト メヨト

## Conclusion

- After a review of the literature, the starting model is the best one among those that we have estimated.
- Finalize the implementation of sequential approach, apply simulation scheme and compare results with those of the variational approach.

・ロト ・日下・ ・ ヨト・

Thanks for listening !

Any questions ?

メロト メロト メヨト メヨト