

Viral dynamics of SARS-CoV2 and role of antiviral treatments

Jérémie Guedj

INSERM UMR 1137, Paris, France

jeremie.guedj@inserm.fr

www.viral-dynamics.com



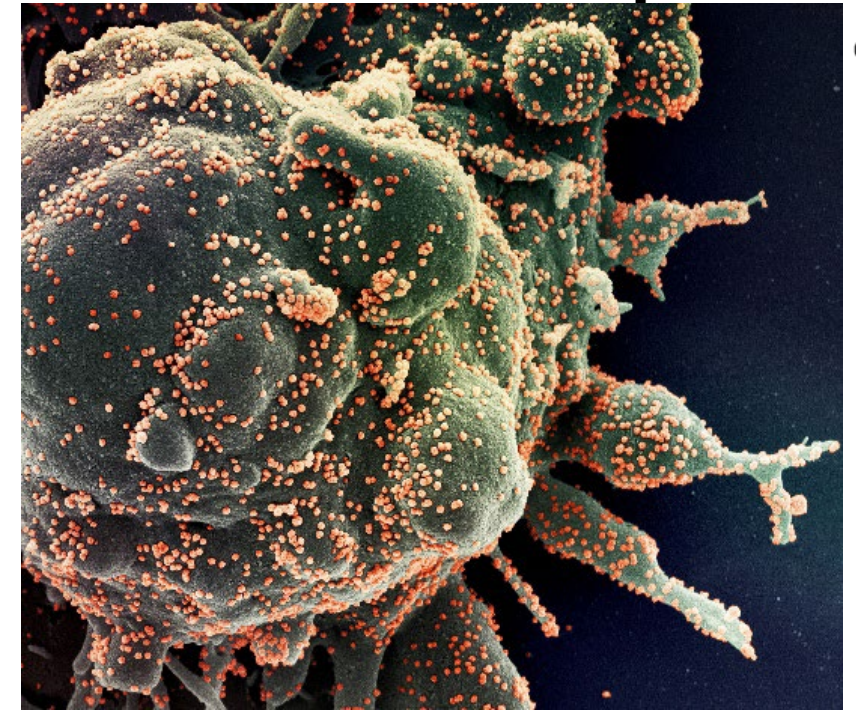
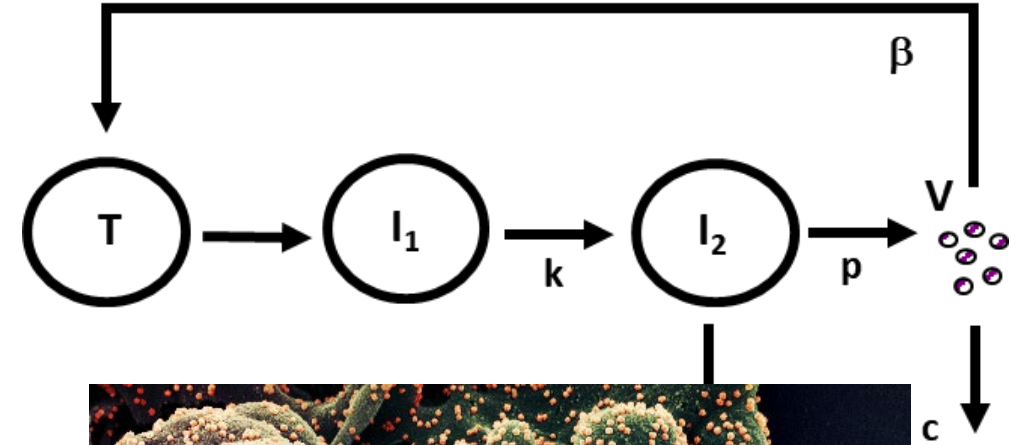
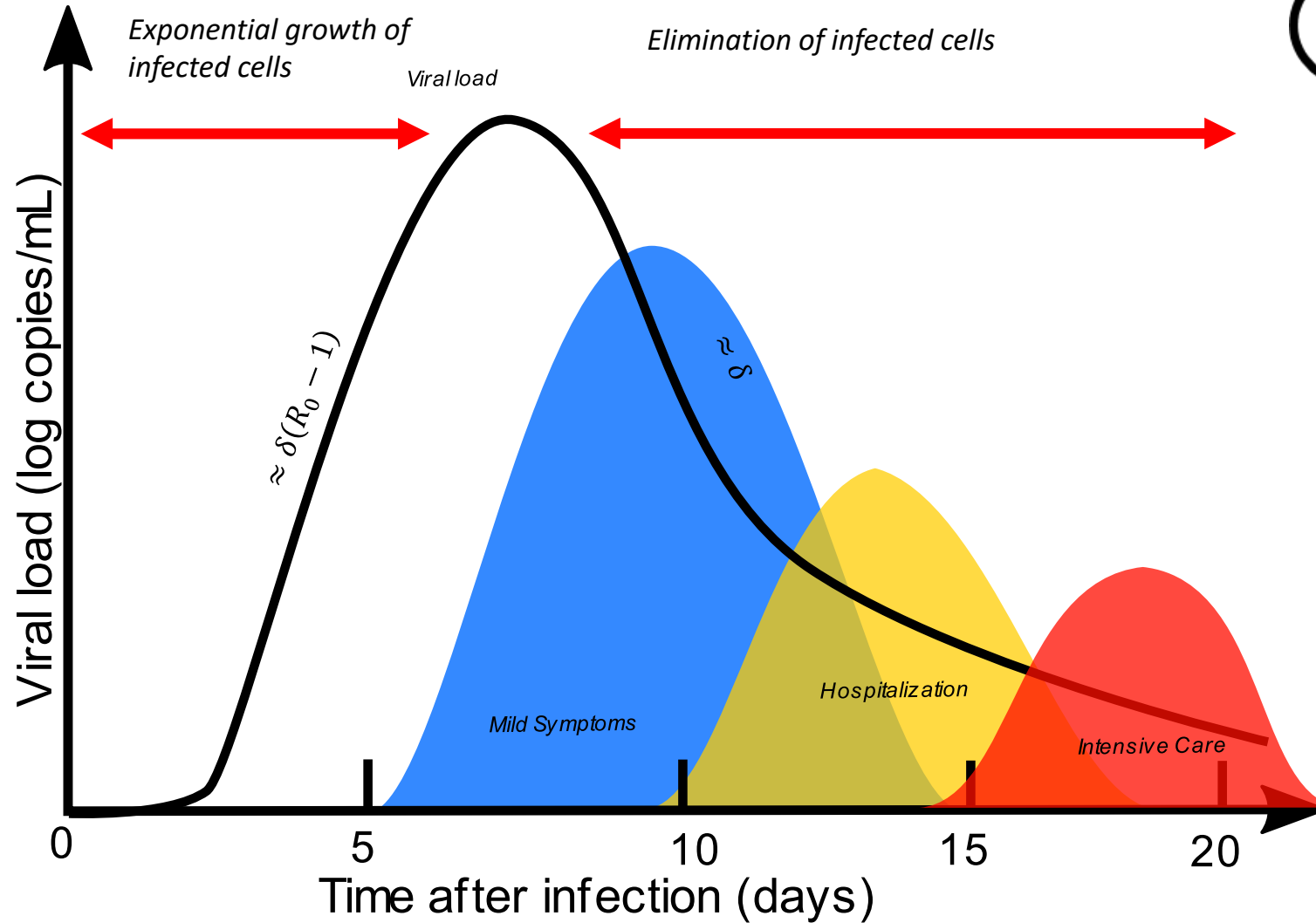
La science pour la santé
From science to health



BILL & MELINDA
GATES *foundation*

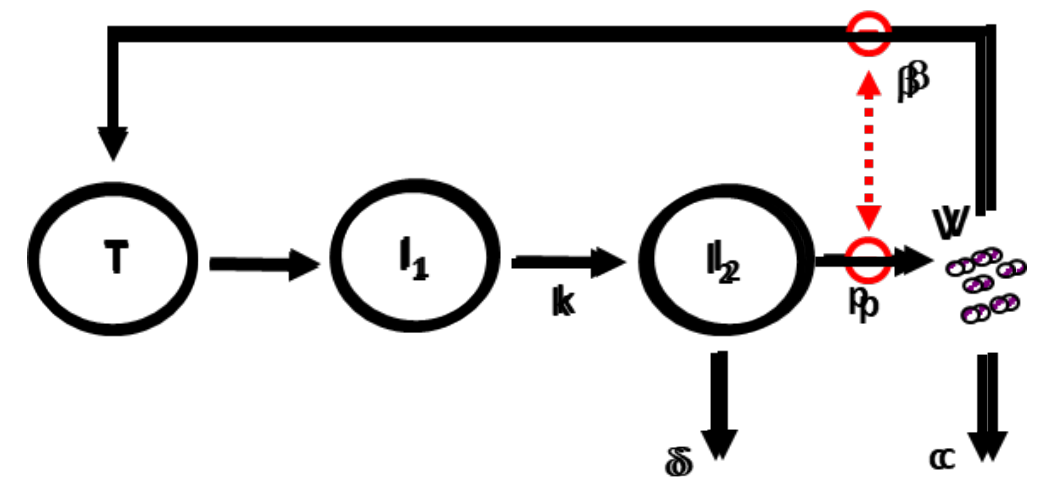
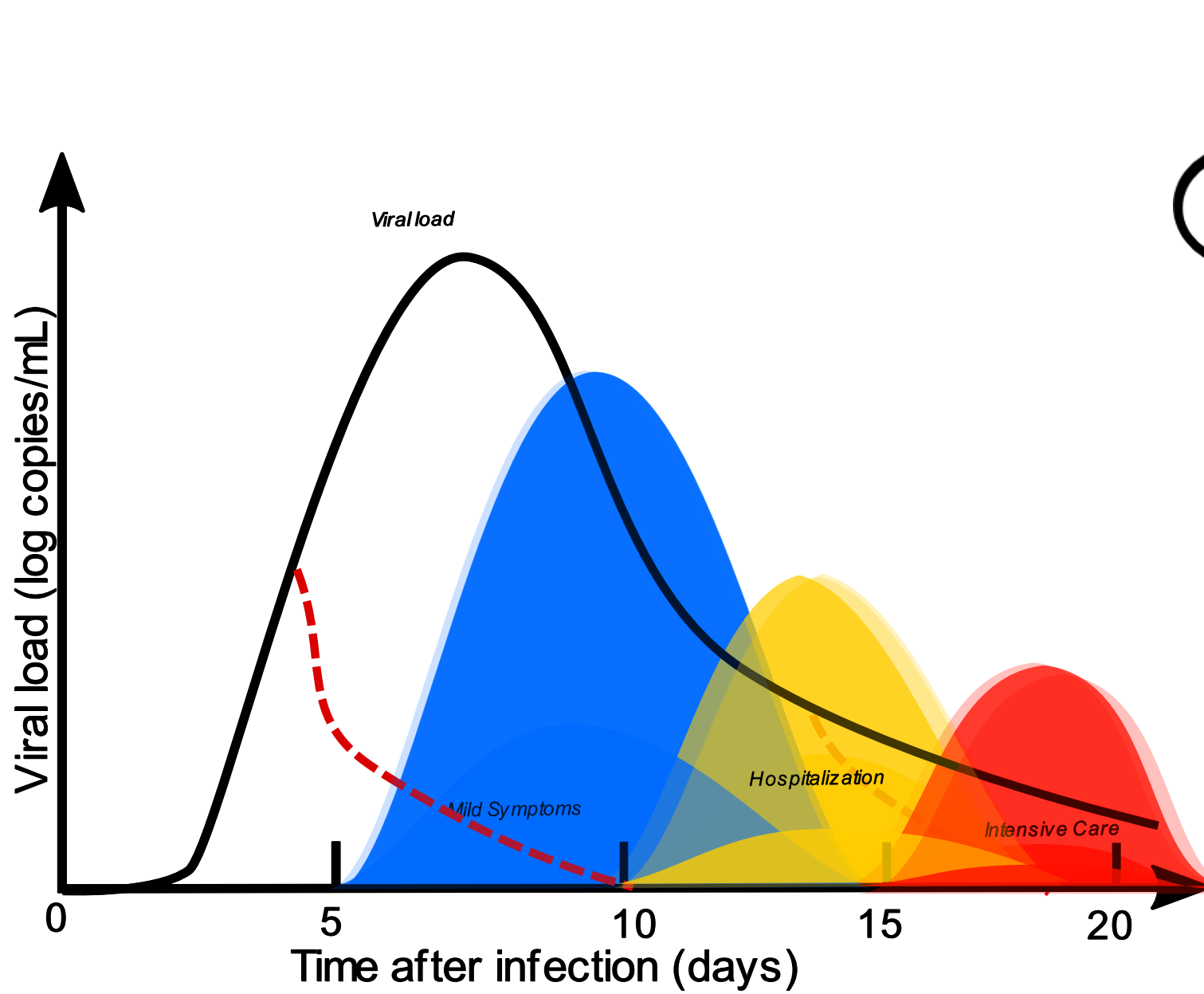
Viral dynamics during acute infection

Peak viral load \approx Target cell exhaustion

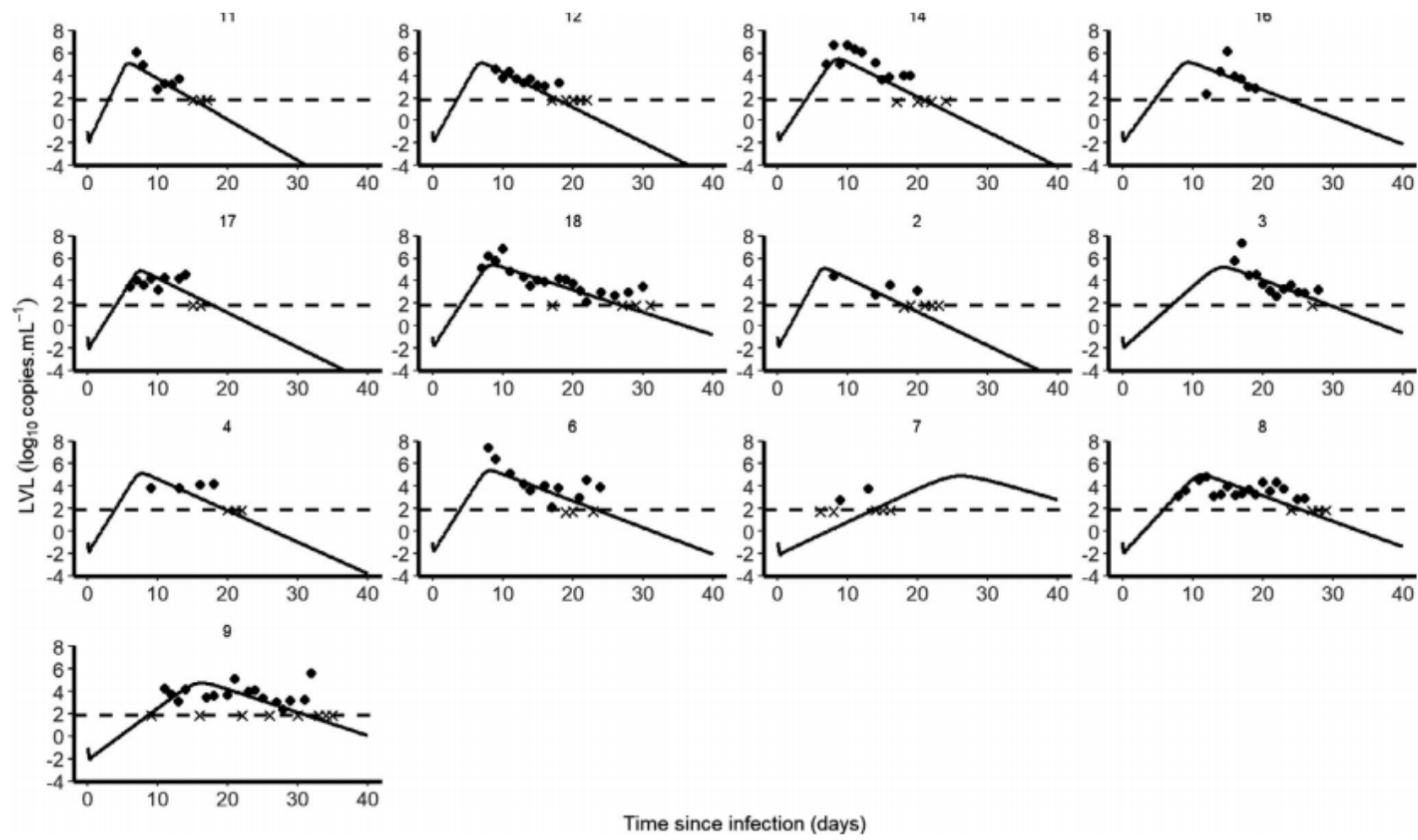


Credit: NIAID Bonhoeffer et al, PNAS (1996)

Timing of antiviral treatment is key to avoid disease progression

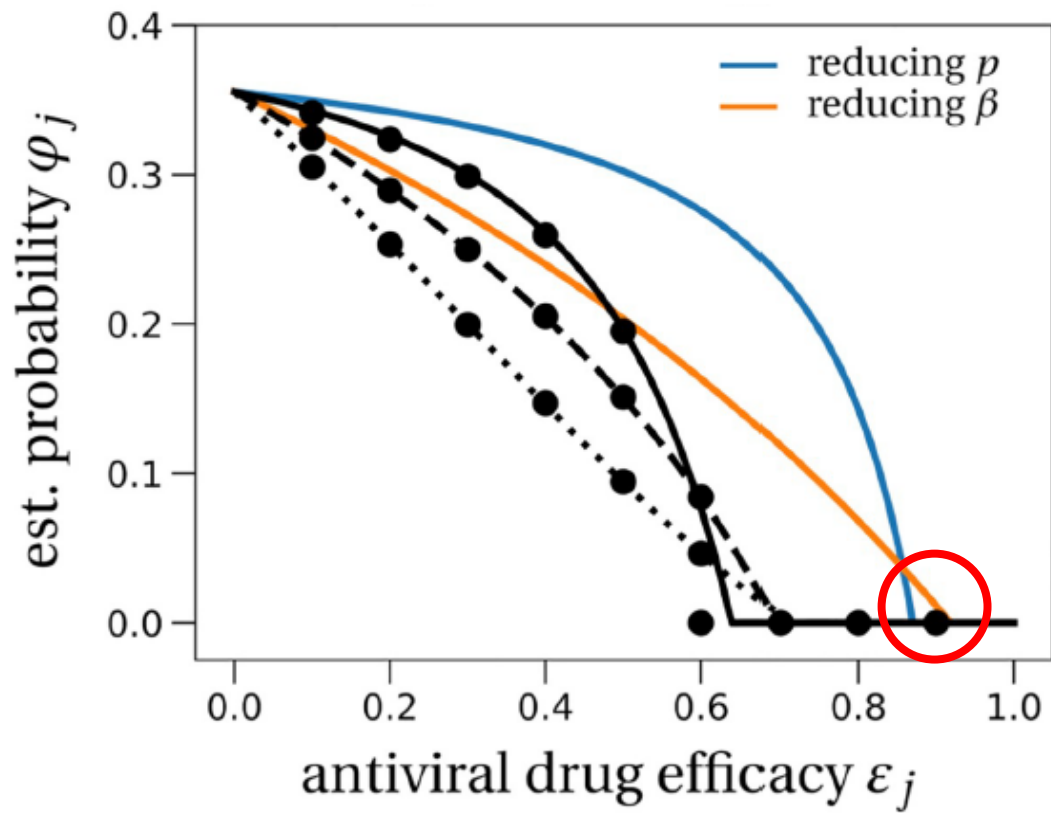
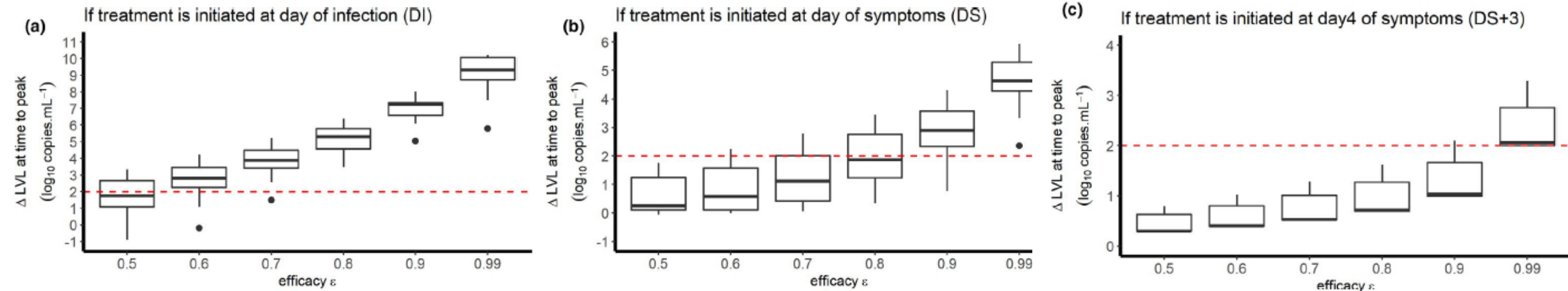


SARS-CoV-2 viral dynamics in mild patients



$R_0 \sim 10$ in mild infections

Timing is (almost) everything

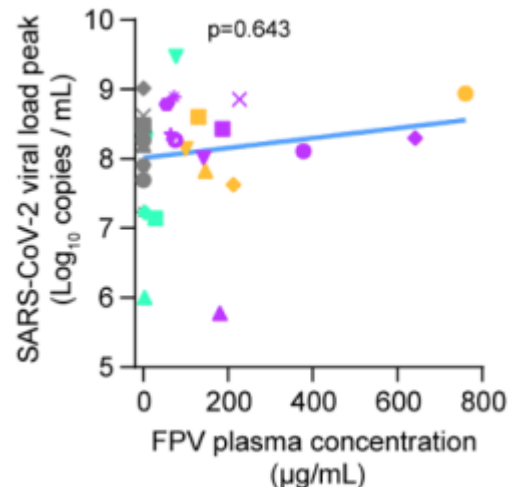
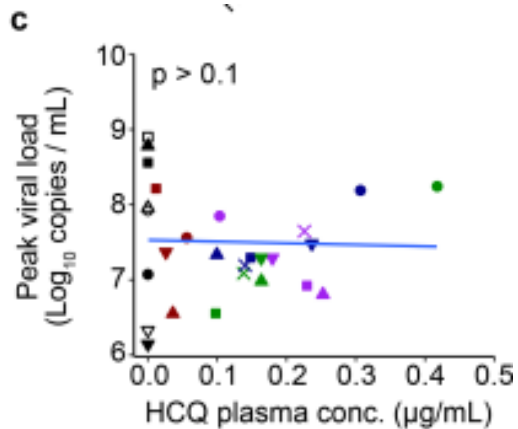


$$\varepsilon_c = 1 - \frac{1}{R_0} = 90\%$$

Effects of repurposed drugs in experimental infection models

Drug	PK parameter	EC ₅₀	Dosing regimen D0–D7	$\bar{\epsilon} = \frac{1}{N} \times \frac{1}{7} \times \int_0^7 \frac{C(u)}{C(u)+EC_{50}} du$
Lopinavir/ritonavir	Wang <i>et al.</i> ¹³	5.2 μM (unpublished)	400/100 b.i.d.	66%
Hydroxychloroquine	Morita <i>et al.</i> ¹⁴	4.2 μM ²⁷	400 mg b.i.d. at D0, followed by 400 mg q.d.	6%
IFN-β-1a	Hu <i>et al.</i> ¹⁵	175 IU/mL ²⁹	12 MIU at D0, D2, D5	18%
Remdesivir	EMA guidelines ¹⁶	1 μM ¹⁷	200 mg q.d. at D0, followed by 100 mg q.d.	87%

- None is likely to have major effect if given after peak viral load
- Even worse in Non-Human Primate model of experimental infection !



Article

Hydroxychloroquine use against SARS-CoV-2 infection in non-human primates

Article

Antiviral efficacy of favipiravir against Zika and SARS-CoV-2 viruses in non-human primates

<https://doi.org/10.1038/s41467-022-32565-w>

More details on preclinical models : Maisonnasse *et al*, *Nature* (2020) ; Eloy *et al*, *CPT* (2020) ; Driouich *et al*, *Nature Comm* (2021); Marlin *et al*, *Nature Communications* (2022)

Can we use viral dynamics to optimize the use of antiviral drugs ?

- **Viral kinetics in hospitalized non-treated patients**
- **Antiviral efficacy of remdesivir in hospitalized patients**
- **What can we expect from monoclonal antibodies ?**

Data used in this presentation (<2021)

Study	Patients	Intervention & Design	Objectives
French Covid cohort	665 untreated patients hospitalized between February and April 2020	No antiviral	Build a model of viral dynamics in hospitalized patients and explore the link with mortality
Discovery clinical trial	655 hospitalized patients between February 2020 and January 2021	Randomized to remdesivir or placebo	Estimate remdesivir antiviral efficacy
Regeneron phase 2/3 clinical trials	4,500 outpatients between September 2020 and January 2021	Randomized to REGN-CoV-2 or placebo	Estimate REGN-CoV-2 antiviral efficacy and association with risk of hospitalization

Can we use viral dynamics to better understand the role of treatment

- **Viral kinetics in hospitalized non-treated patients**
- Antiviral efficacy of remdesivir in hospitalized patients
- Antiviral efficacy of monoclonal antibodies in outpatients

French Covid Cohort

National prospective cohort (NCT04262921, PI: Jade Ghosn)

2020

26th January

5th february

Today

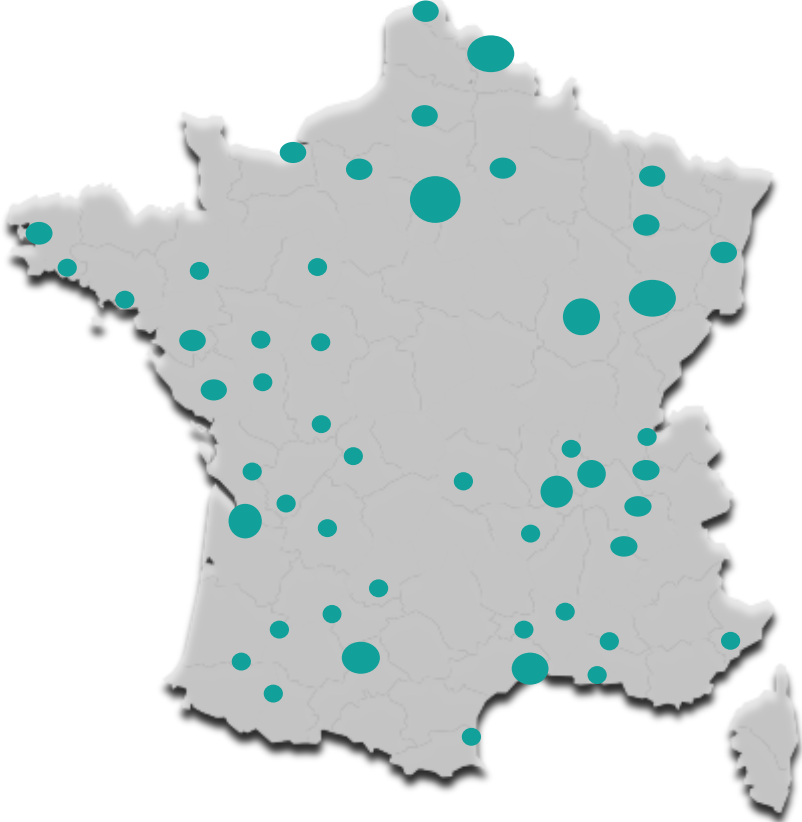
First patients in a French hospital (Bichat, Paris)

Cohort launch

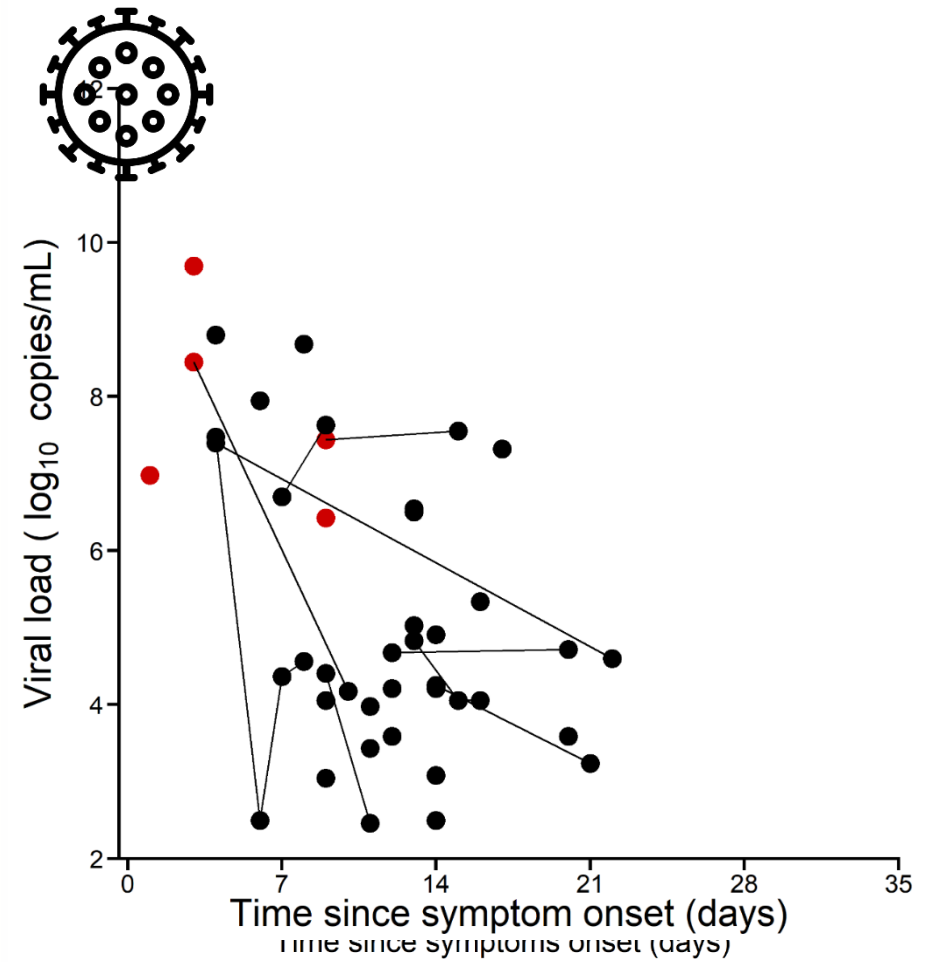
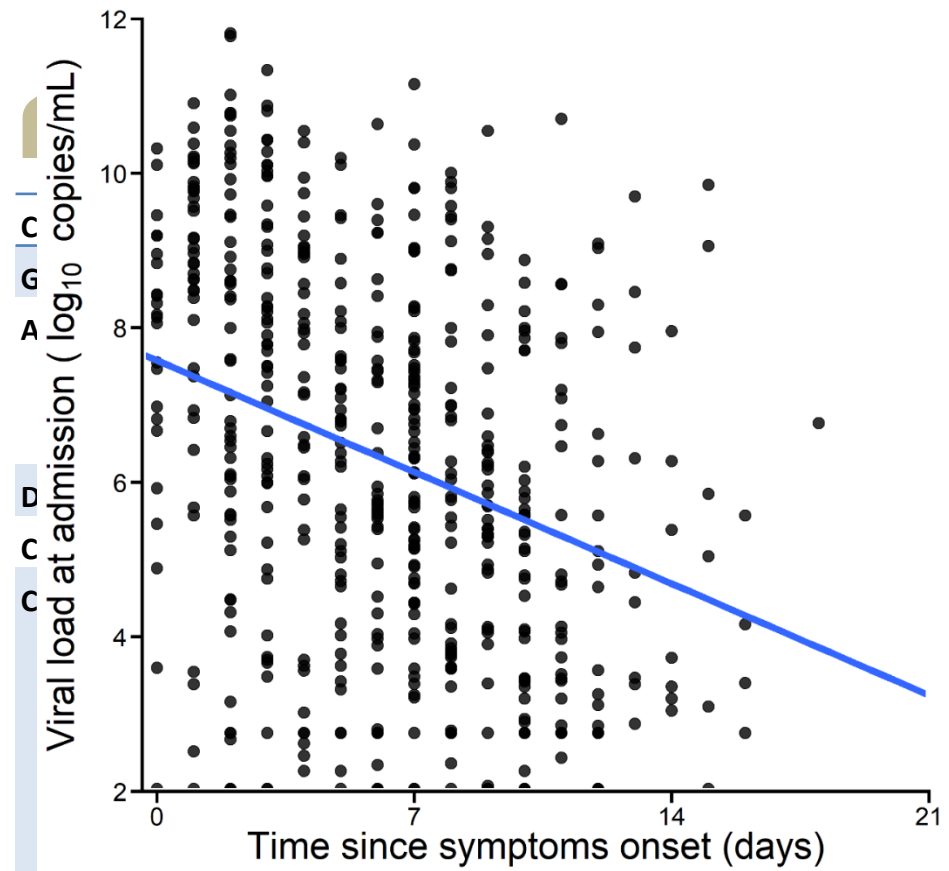
4000+ patients
150+ centers

Data collected during hospitalization, up until 18 months after hospital discharge

FRENCH COVID

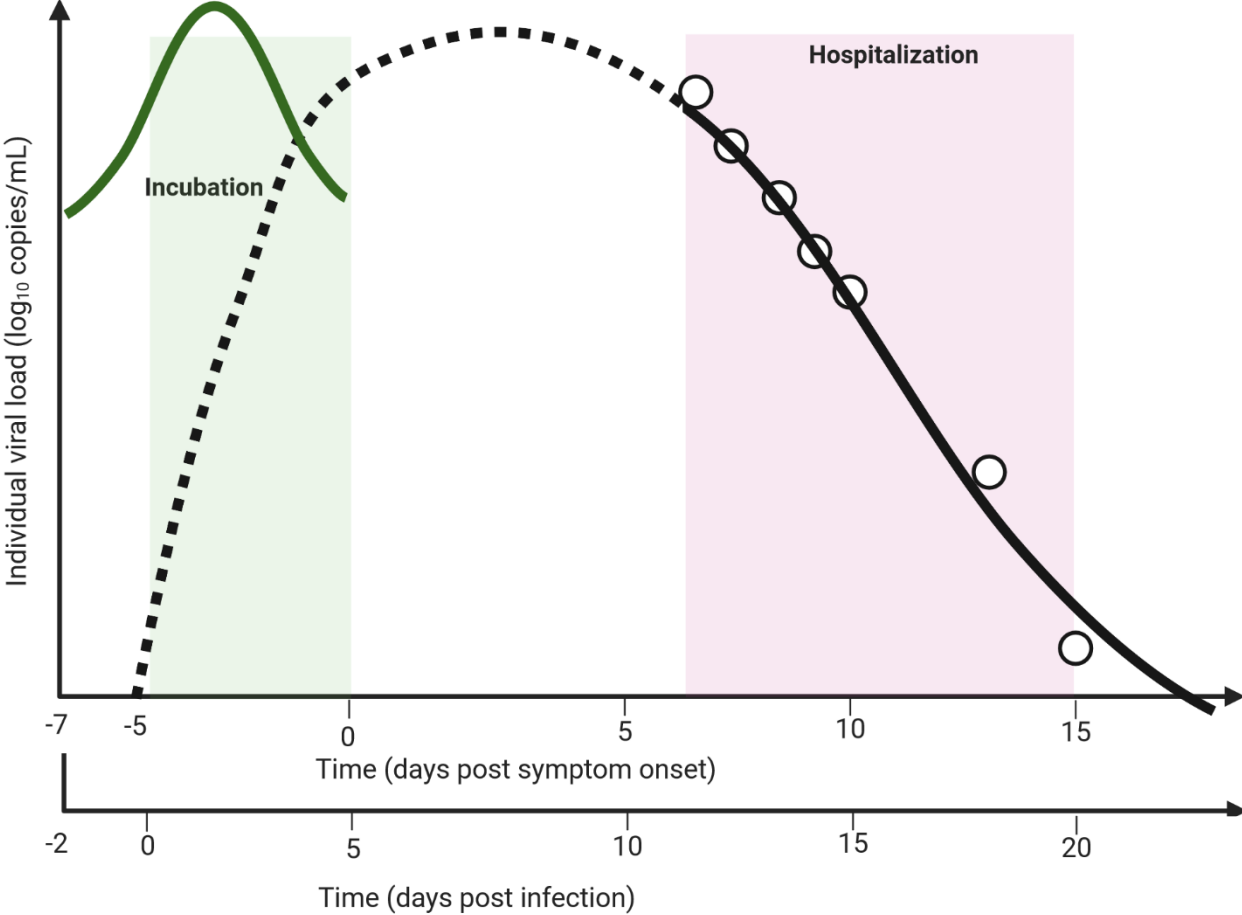


Data

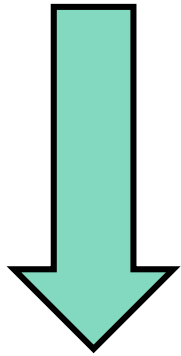


VIRAL DYNAMIC MODEL

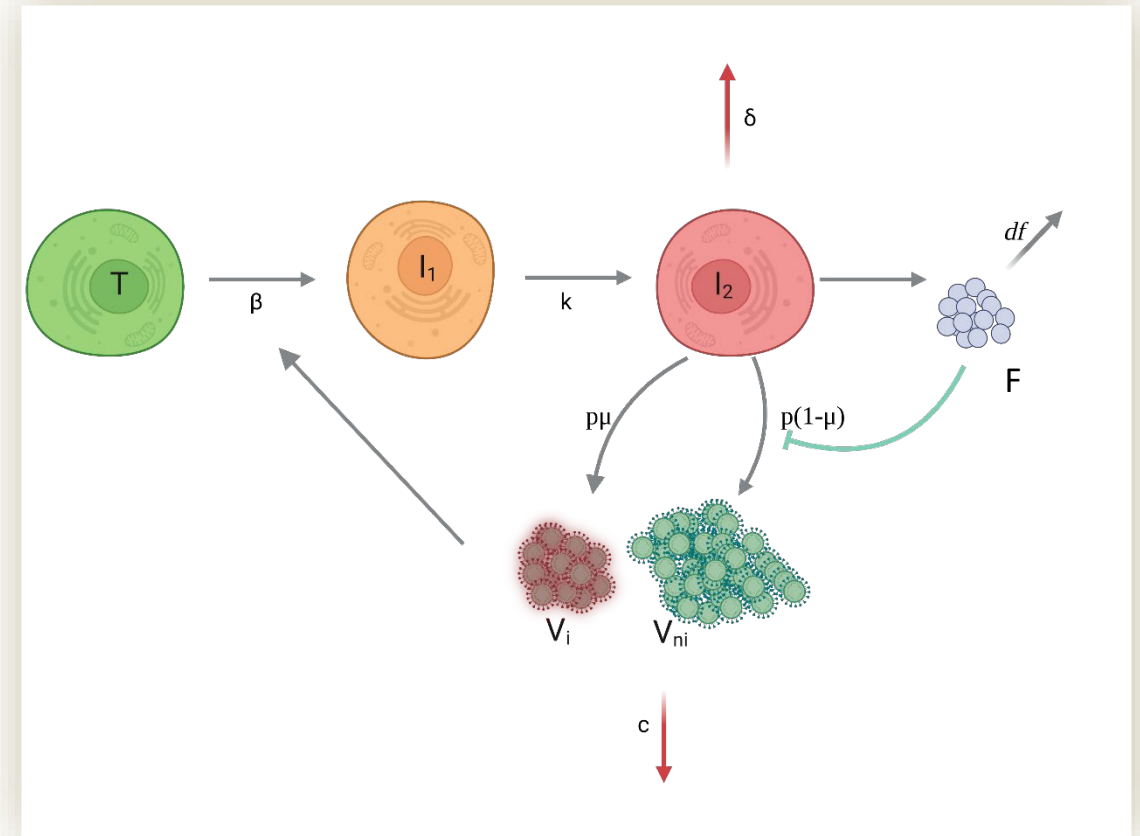
Reconstituting the time of infection based on the viral load data and the time of symptom onset



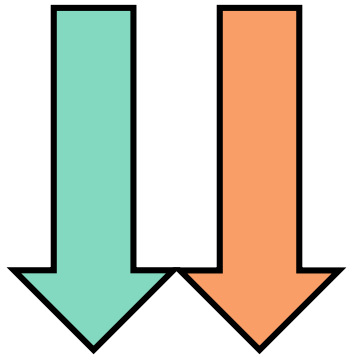
Modeling the immune response



$$\frac{V_i}{dt} = p\mu \left(1 - \frac{\phi F}{F + \theta}\right) I_2 - cV_i$$
$$\frac{dV_{ni}}{dt} = p(1 - \mu) \left(1 - \frac{\phi F}{F + \theta}\right) I_2 - cV_{ni}$$

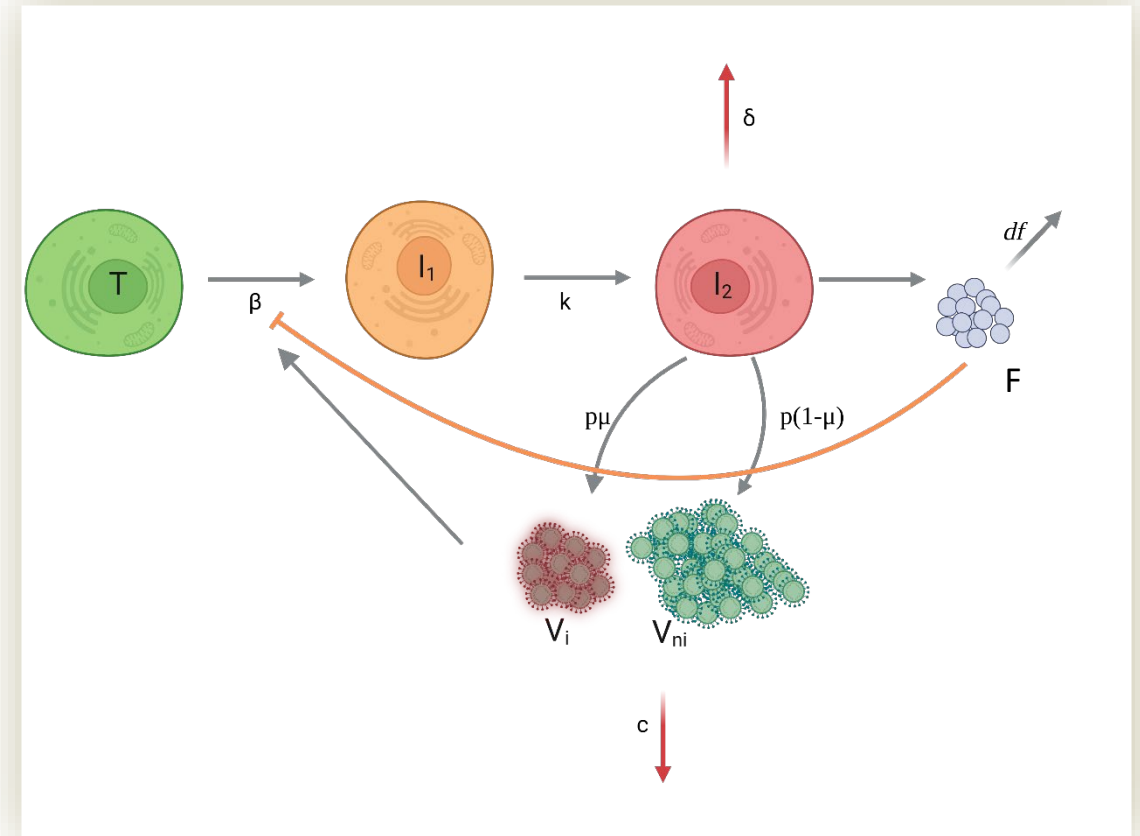


Modeling the immune response

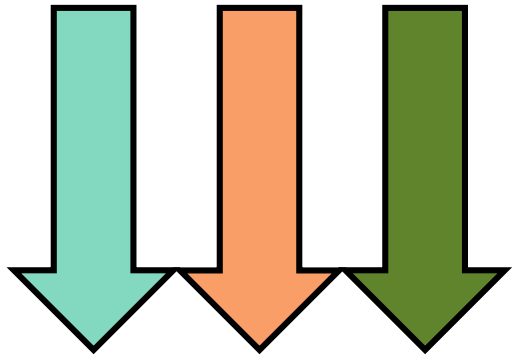


$$\frac{dT}{dt} = -\beta \left(1 - \frac{\phi F}{F + \theta}\right) V_I T$$

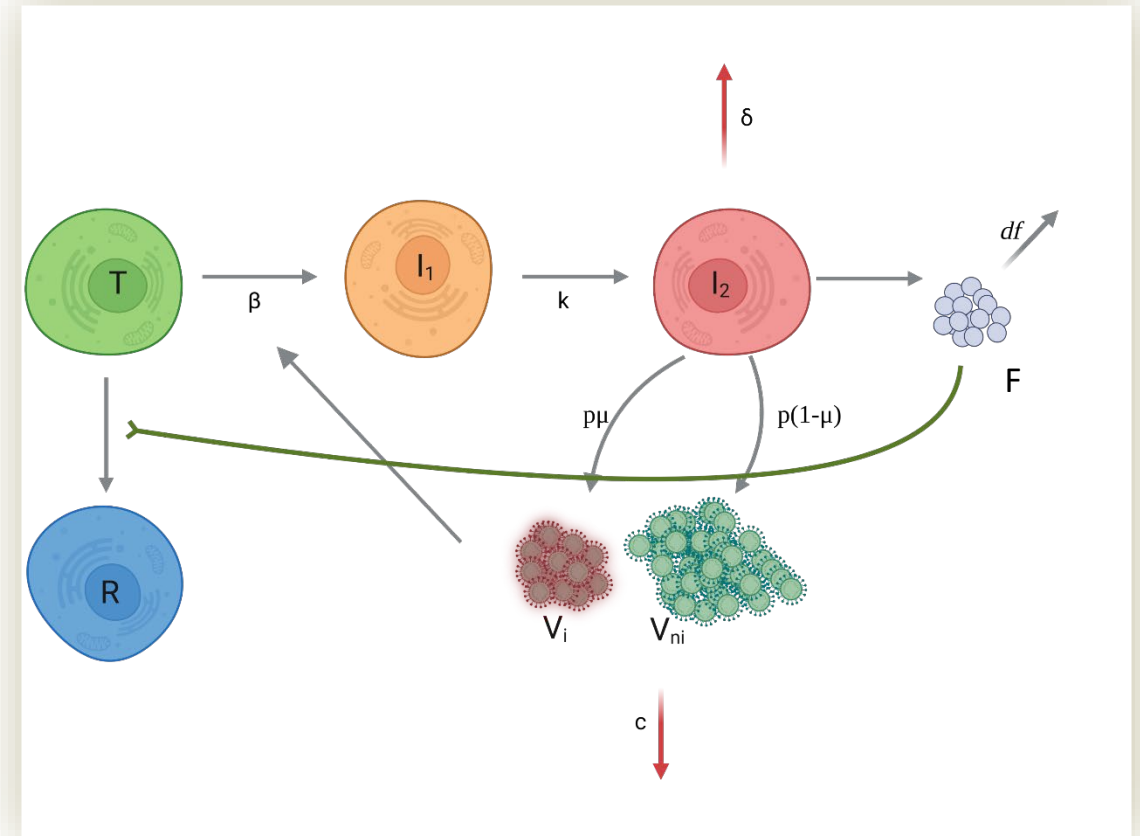
$$\frac{dI_1}{dt} = \beta \left(1 - \frac{\phi F}{F + \theta}\right) V_I T - k I_1$$



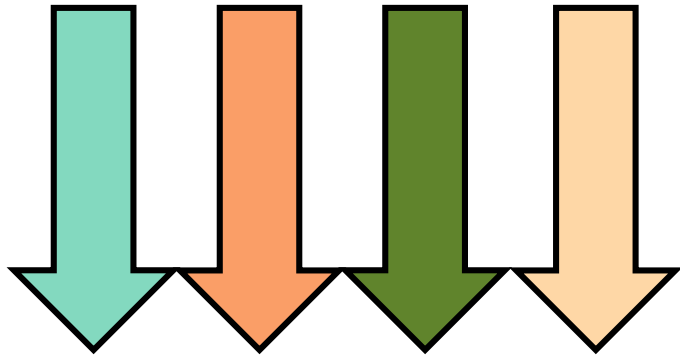
Modeling the immune response



$$\frac{dT}{dt} = -\beta V_I T - \frac{\phi F}{F + \theta} T$$
$$\frac{dR}{dt} = \frac{\phi F}{F + \theta} T$$

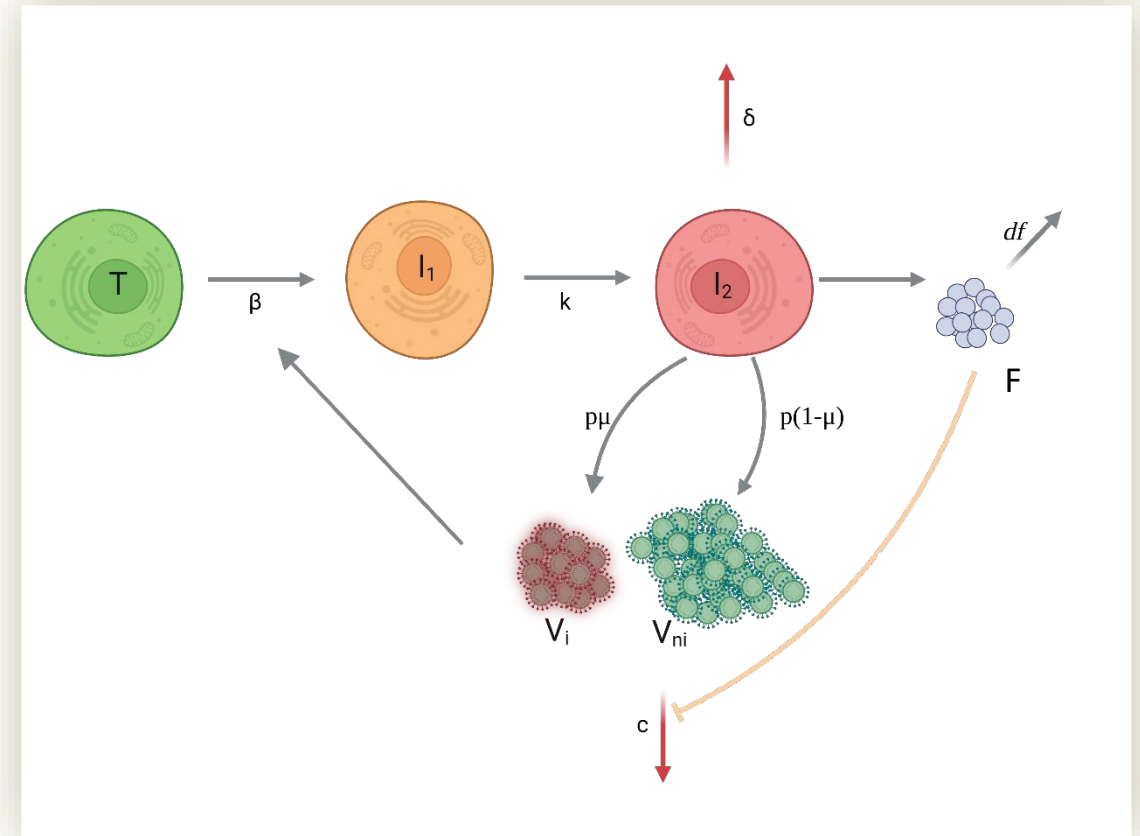


Modeling the immune response

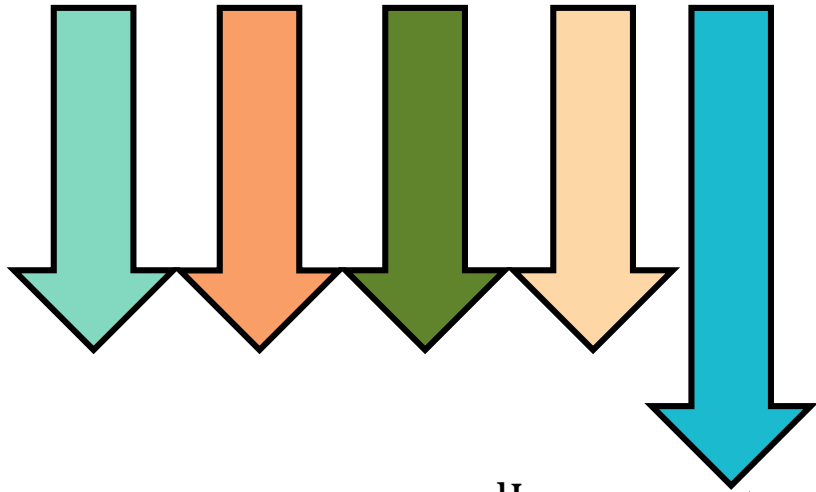


$$\frac{dV_i}{dt} = p\mu I_2 - \left(c + \phi \frac{F}{F + \theta}\right) V_i$$

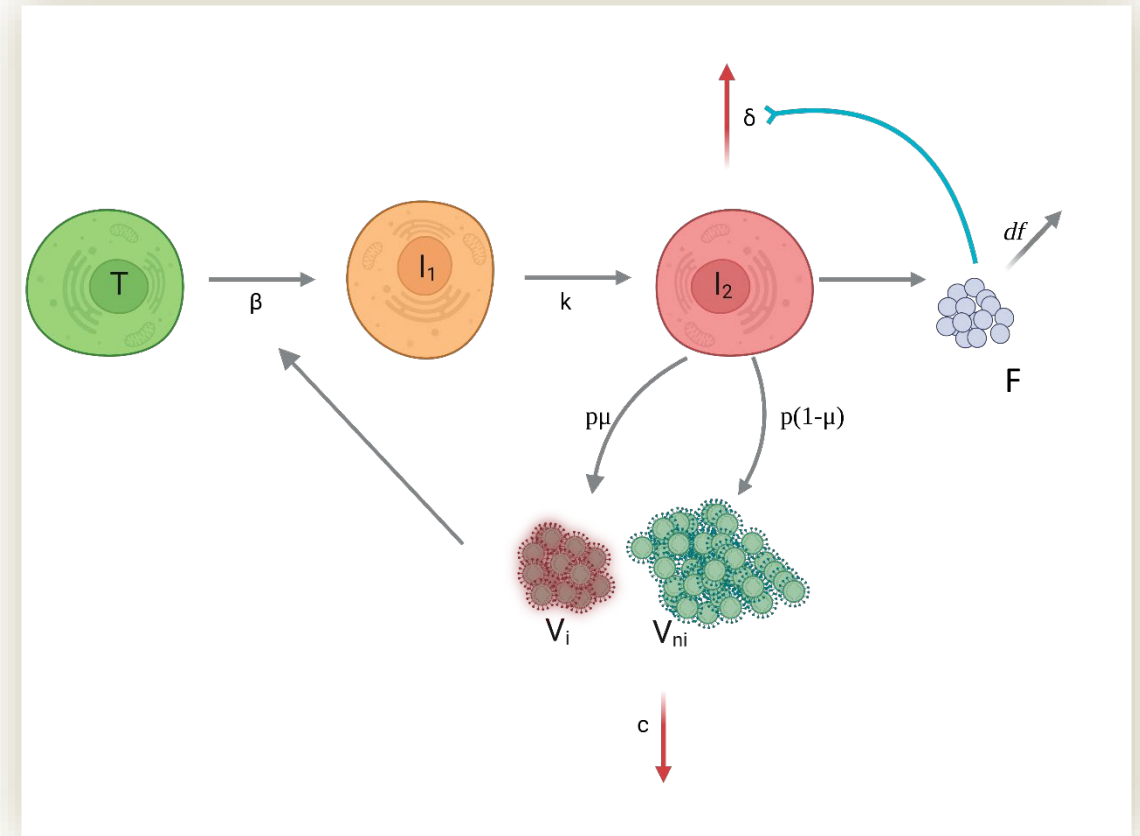
$$\frac{dV_{ni}}{dt} = p(1 - \mu)I_2 - \left(c + \phi \frac{F}{F + \theta}\right) V_{ni}$$



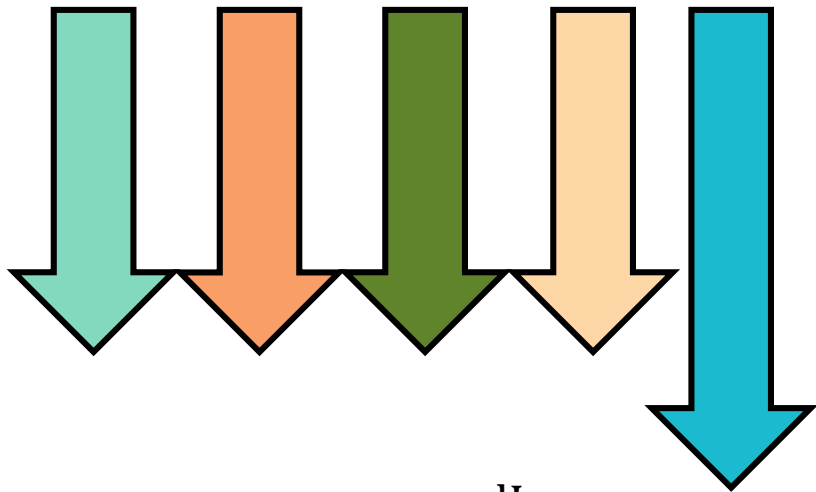
Modeling the immune response



$$\frac{dI_2}{dt} = kI_1 - \left(\delta + \phi \frac{F}{F + \theta} \right) I_2$$



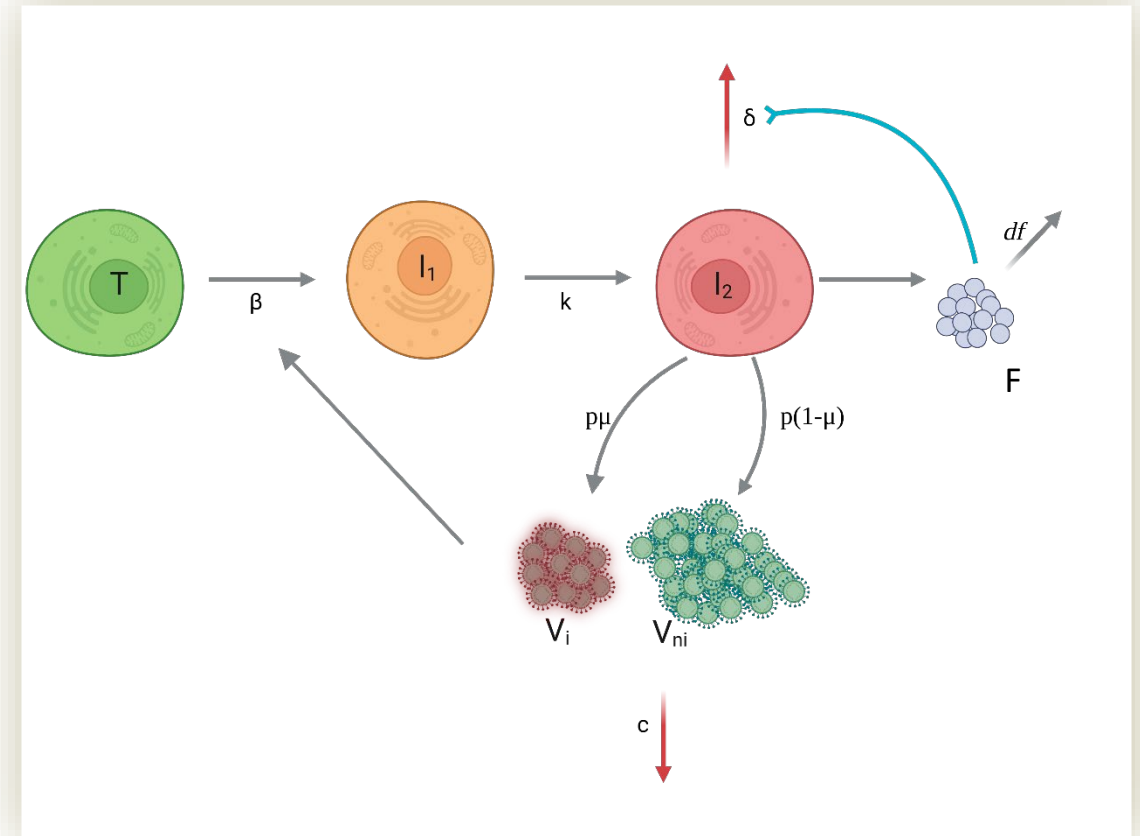
Modeling the immune response



$$\frac{dI_2}{dt} = kI_1 - \left(\delta + \phi \frac{F}{F + \theta} \right) I_2$$

Covariate screening

	β	p	ϕ	δ
Age				
Sexe				
MCC				
MPC				
HTA				
Obésité				
Diabète				



MORTALITY AND RISK FACTORS

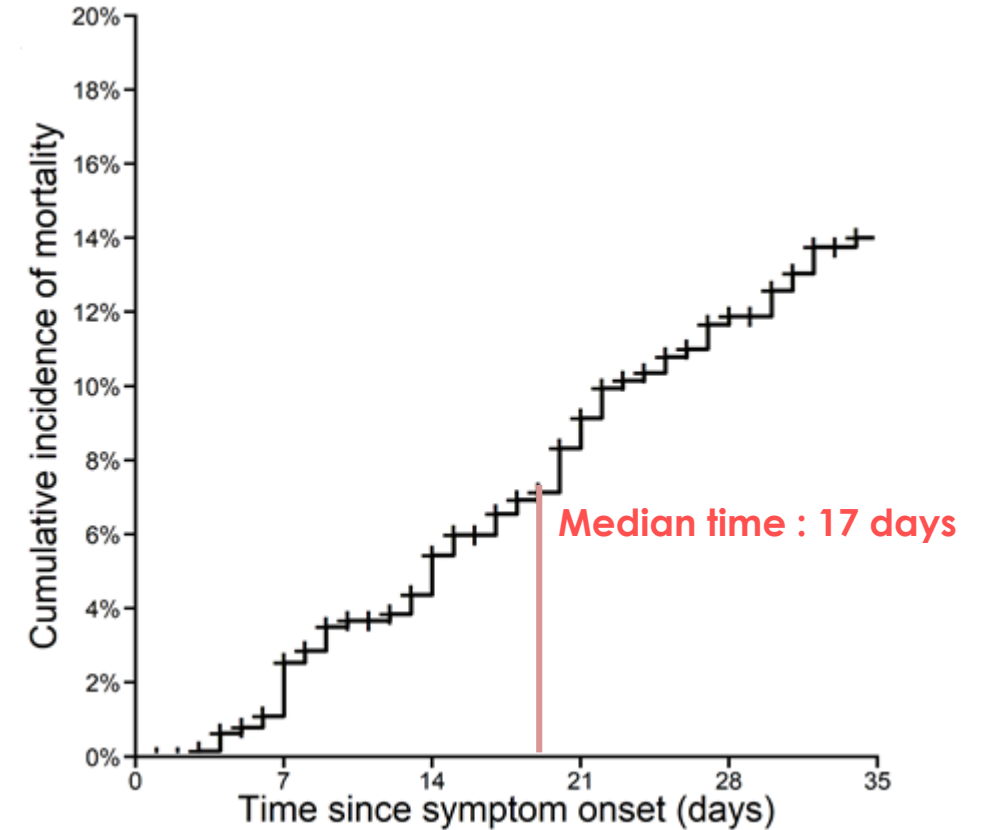
12 % patients died, 231 lost to follow up at D35

MULTIVARIATE SURVIVAL ANALYSIS

Male gender : HR = 2.63 p -value < 10^{-4}

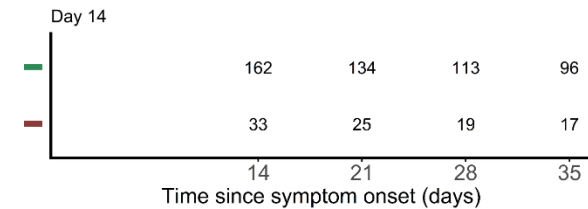
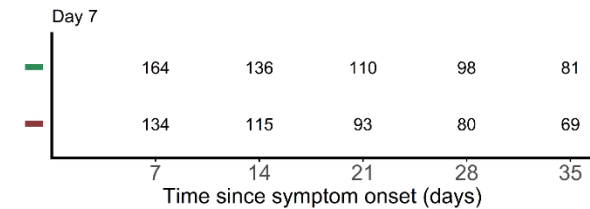
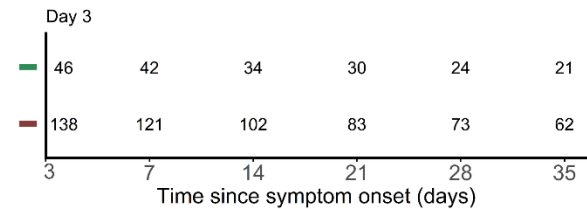
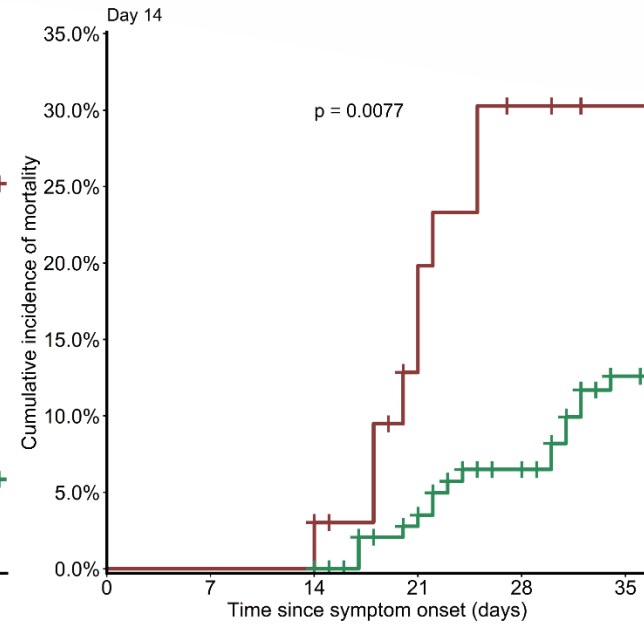
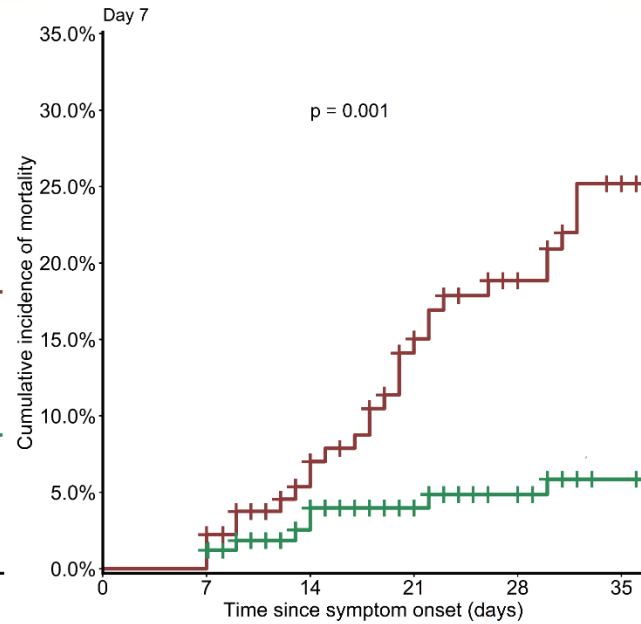
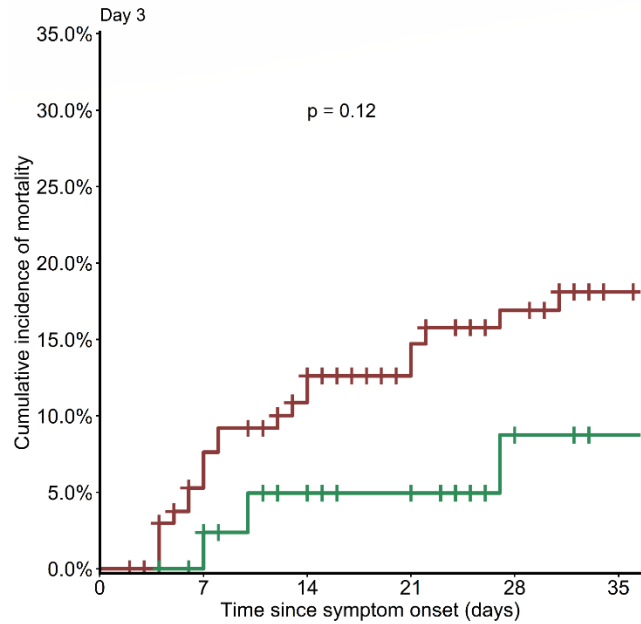
≥ 65 years old : HR = 3.02 p -value < 10^{-4}

Chronic pulmonary disease : HR = 2.47 p -value < 10^{-4}



MORTALITY AND VIRAL LOAD

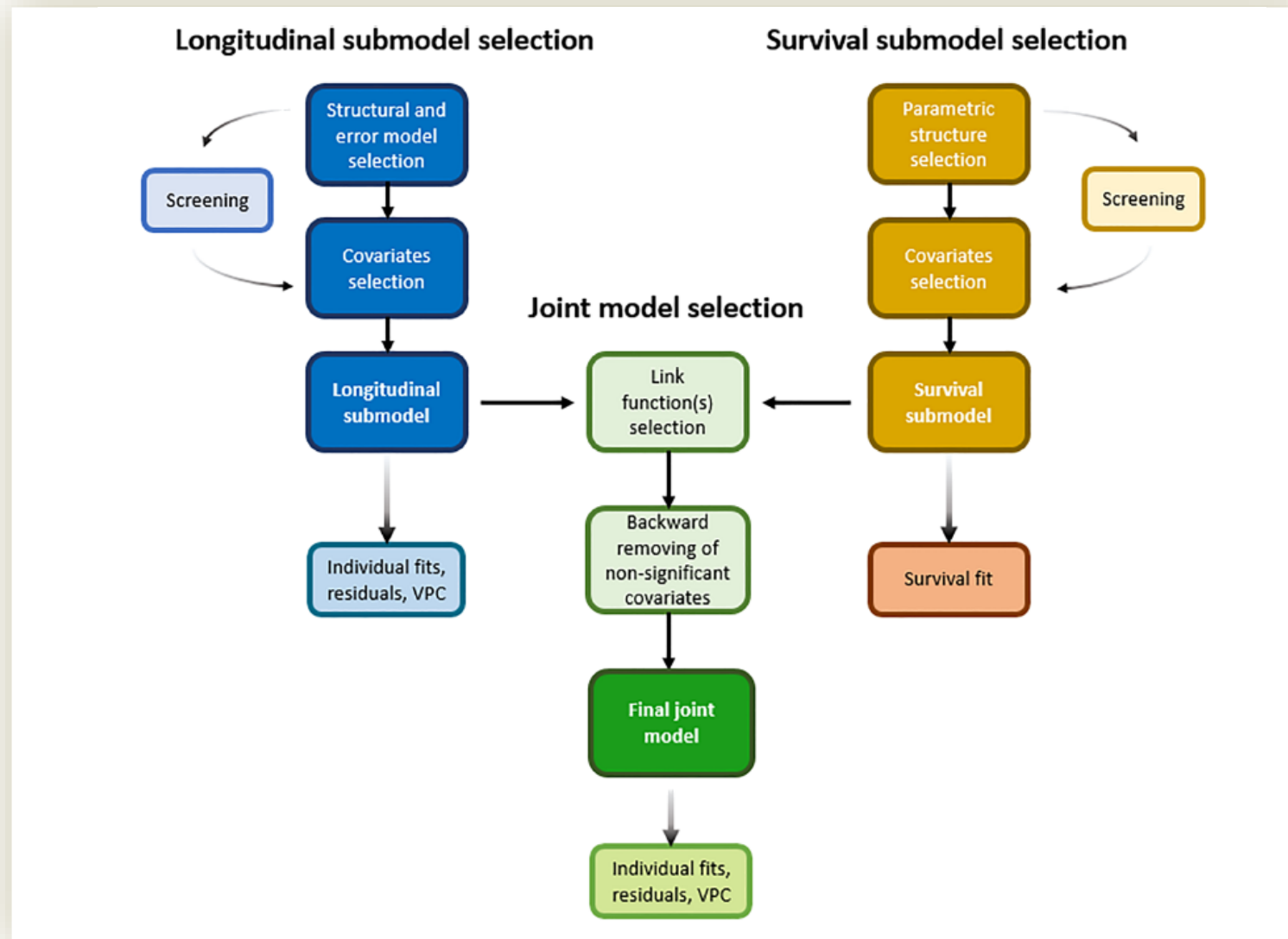
Mortality according to viral load at different landmark times since symptom onset



— $< 6 \log_{10}$ copies/mL

— $\geq 6 \log_{10}$ copies/mL

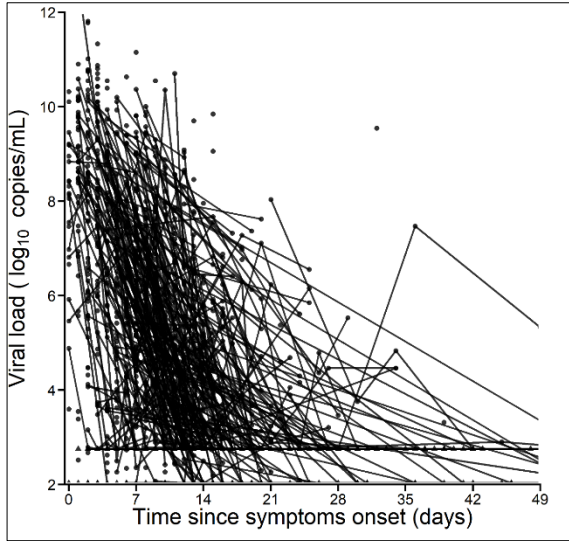
Joint modeling



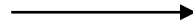
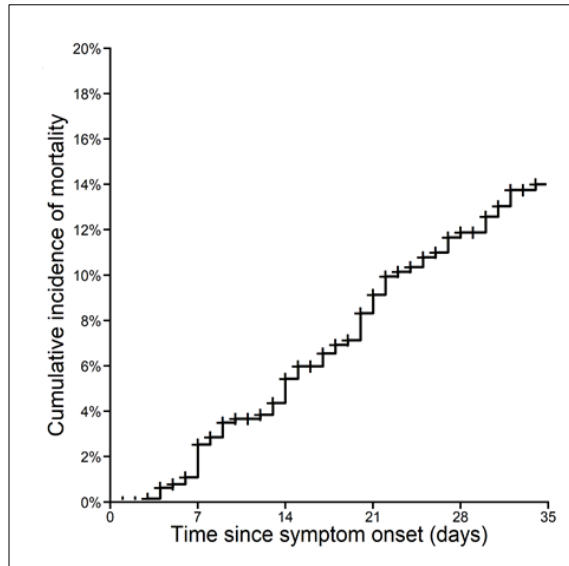
Kerioui et al . *Br J Clin Pharmacol*. 2022

JOINT MODELLING

Virological data



Survival data



$$\frac{dT}{dt} = -\beta V_I T$$

$$\frac{dI_1}{dt} = \beta V_I T - k I_1$$

$$\frac{dI_2}{dt} = k I_1 - \delta I_2 - \phi \frac{I_2 F}{F + \theta}$$

$$\frac{dV_I}{dt} = p \mu I_2 - c V_I$$

$$\frac{dV_{NI}}{dt} = p(1 - \mu) I_2 - c V_{NI}$$

$$\frac{dF}{dt} = q I_2 - d_f F$$

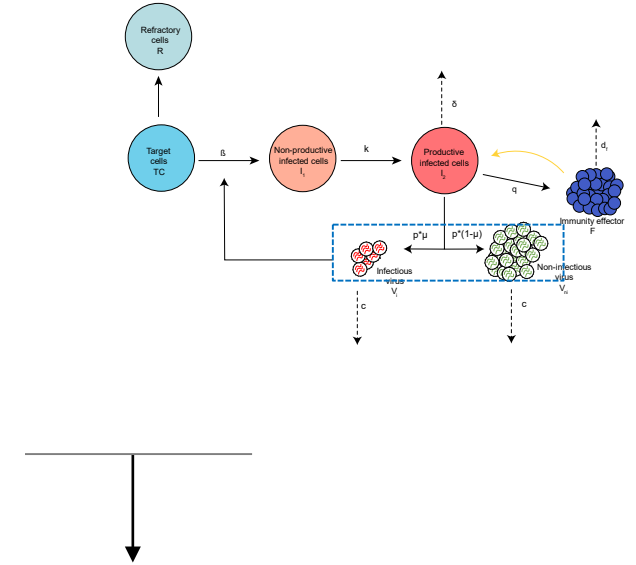
The survival function of patient i

$$S_i(t) = P(T_i \geq t) = \exp \left[- \int_0^t h_i(u) du \right]$$

depends on its instantaneous hazard function

$$h_i(t) = 0 \text{ if } t \leq 0 \text{ ie until admission}$$

$$h_i(t) = h_0 \times \exp(\gamma_{RF} \times z_{RF} + \nu \times \log_{10}(V_I + V_{NI})(t)) \text{ if } t > 0$$



With

T_i : Last time of observation

h_0 : Baseline hazard function

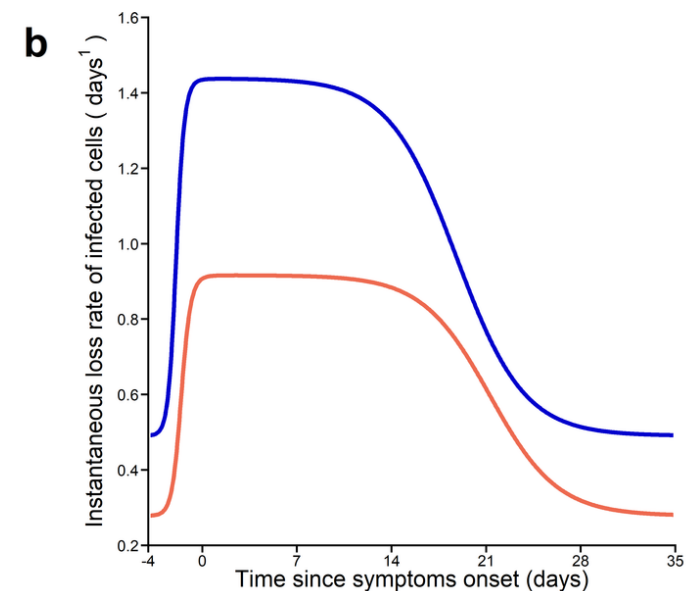
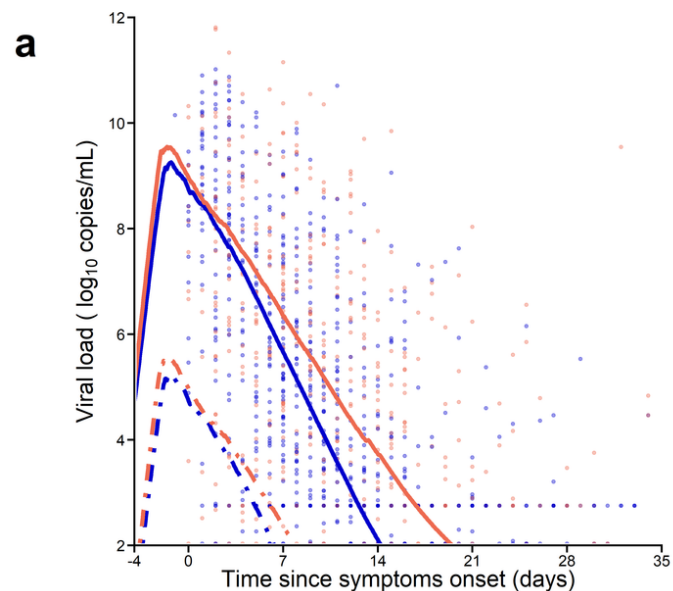
z_{RF} : Presence of risk factors

γ_{RF} : log(HR) associated with the risk factors

ν : log(HR) associated with \log_{10} viral load

Viral dynamic submodel

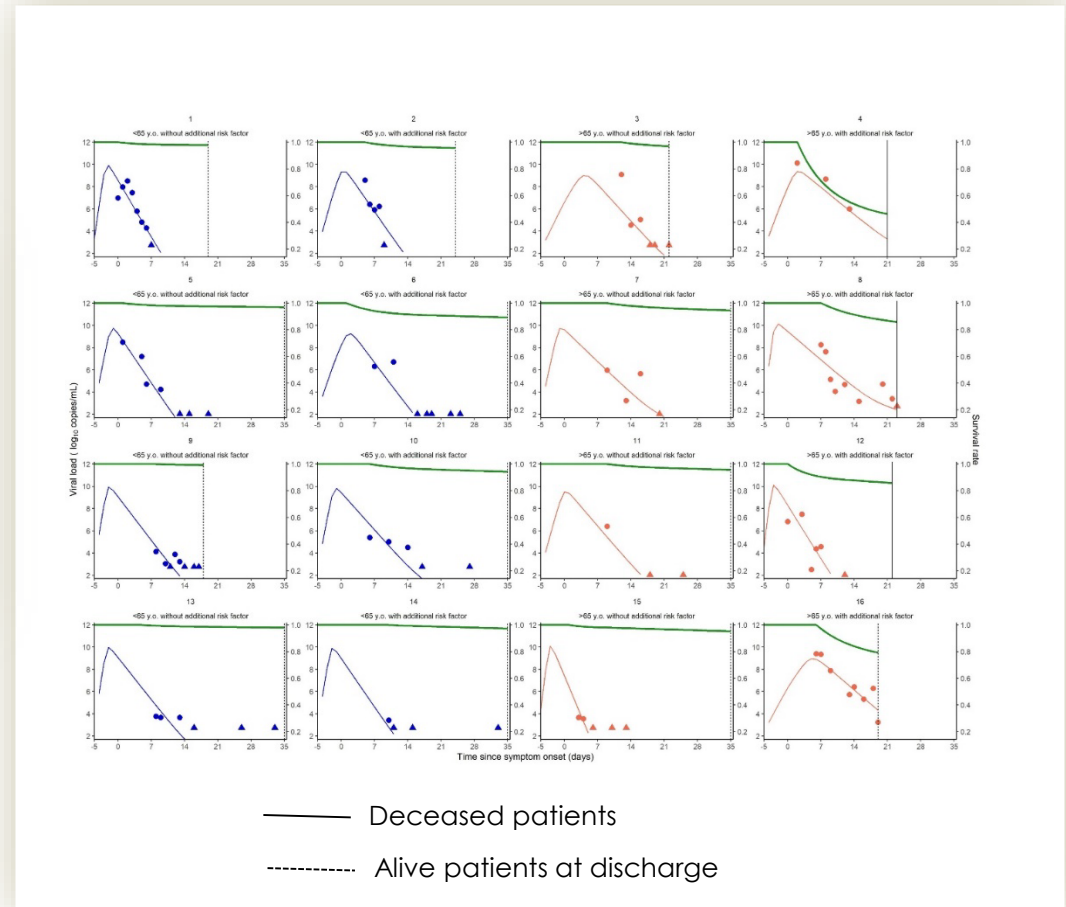
Parameter	Estimation (RSE. %)
Incubation period (d)	4.8 (3.24)
β (mL.j ⁻¹)	1.46×10^{-5} (23.4)
pT_0 (virus.mL ⁻¹ .j ⁻¹)	1.48×10^{11} (26.8)
$\delta + \phi_{age}(< 65)$ (j ⁻¹)	1.25 (8.66)
$\delta + \phi_{age}(\geq 65)$ (j ⁻¹)	0.98 (23.3)
θ (F.mL ⁻¹)	70 (80.8)



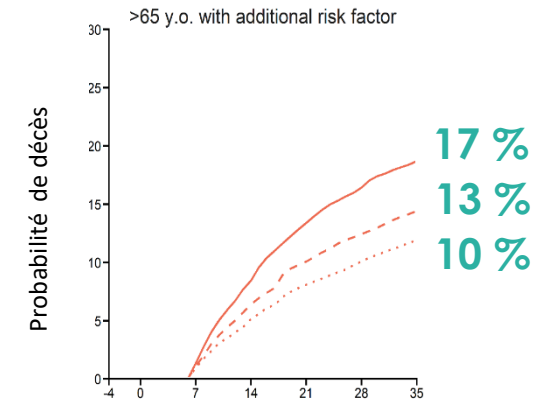
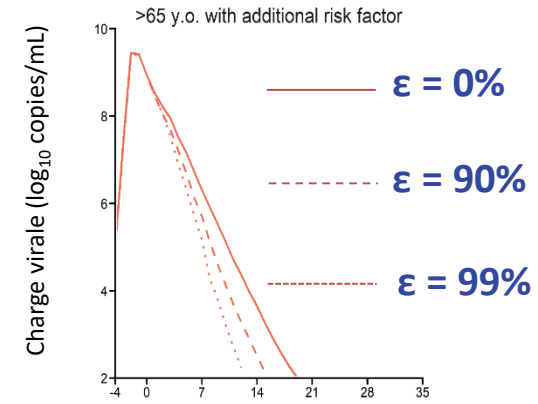
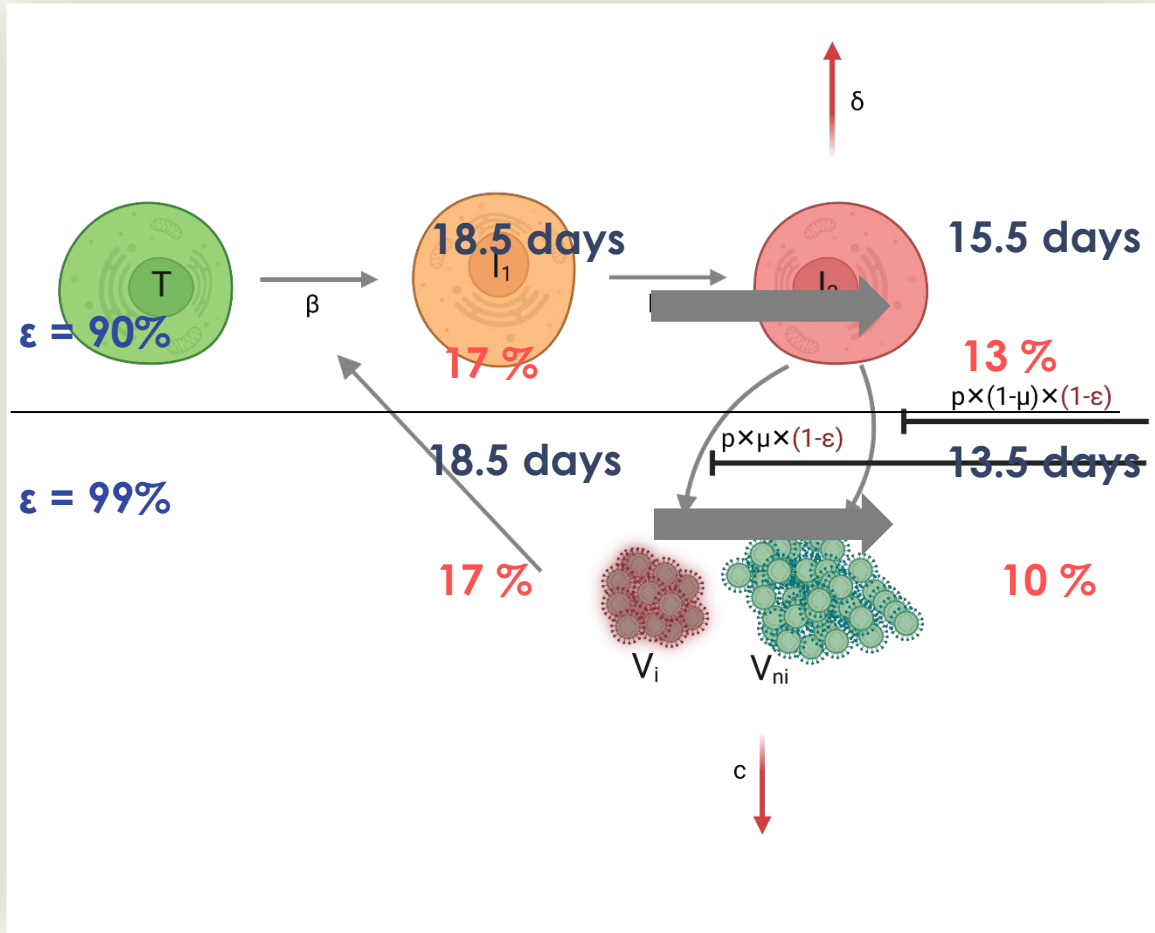
— Age < 65 y
— Age ≥ 65 y 23

Survival submodel

Parameter	Hazard Ratio (RSE%)
Male gender	2.55 (25.2)
Age ≥ 65	2.58 (37.9)
Chronic pulmonary disease	2.31 (36.8)
Current viral load (log₁₀ copies/mL)	1.31 (17)



Prédictions

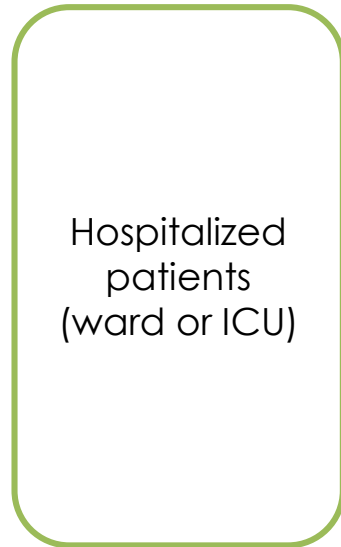
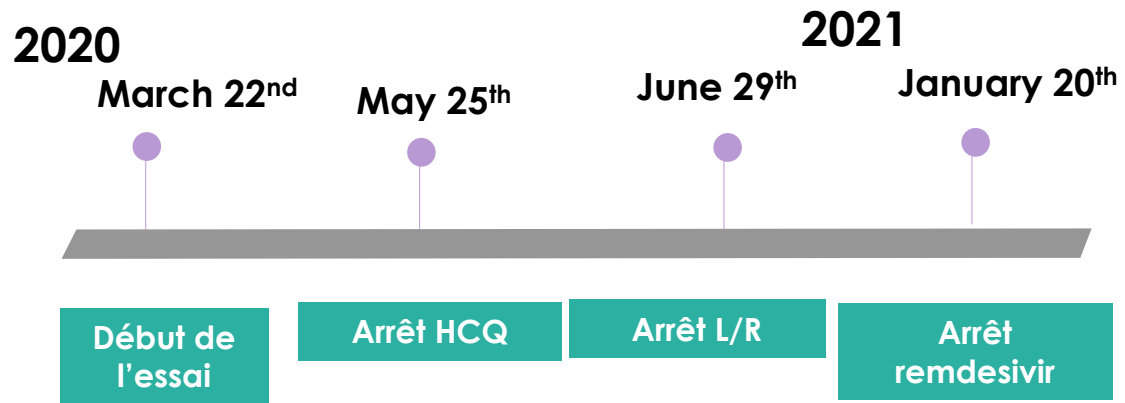


Can we use viral dynamics to better understand the role of treatment

- Viral kinetics in hospitalized non-treated patients
- **Antiviral efficacy of remdesivir in hospitalized patients**
- Antiviral efficacy of monoclonal antibodies in outpatients

DisCoVeRy trial

European randomized clinical trial
(NCT04315948, PI: Florence Ader,
Méthodology: France Mentré)



DISCOVeRY

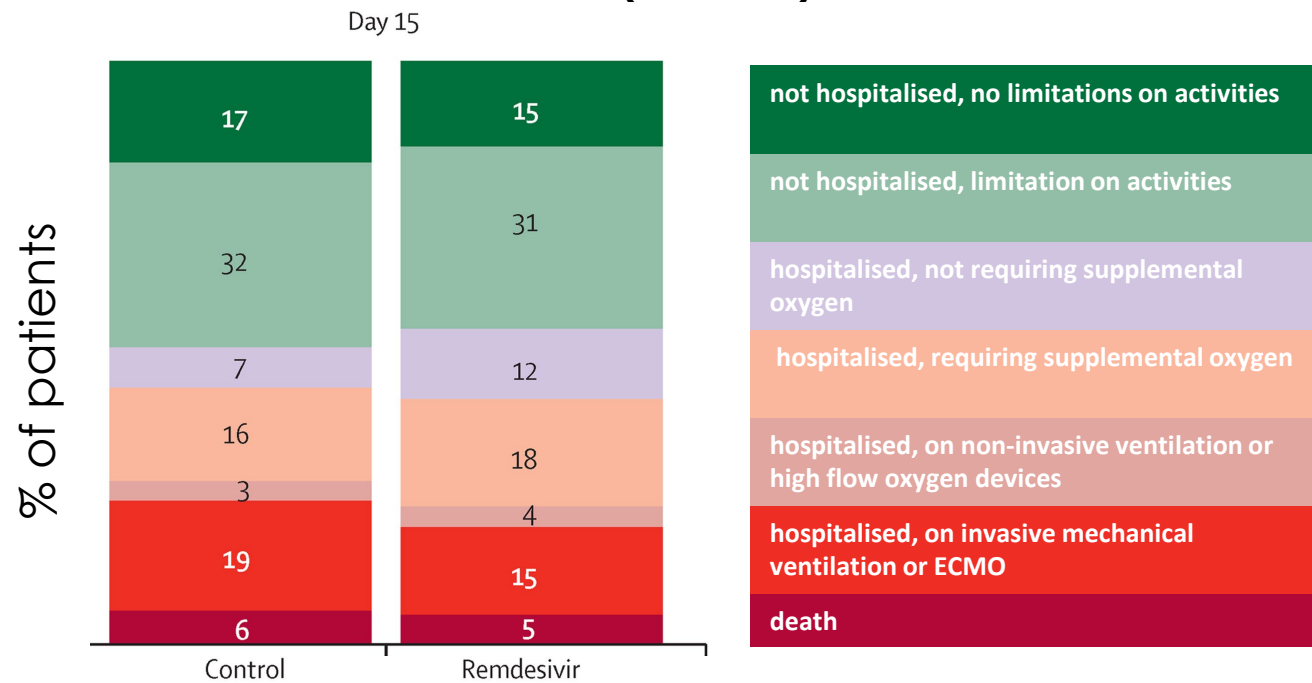
Control, standard of Care (SoC)

REMDESIVIR + SoC
IV 200 mg/j puis 100 mg pendant 9
days

Primary outcome measure: clinical status at day 15

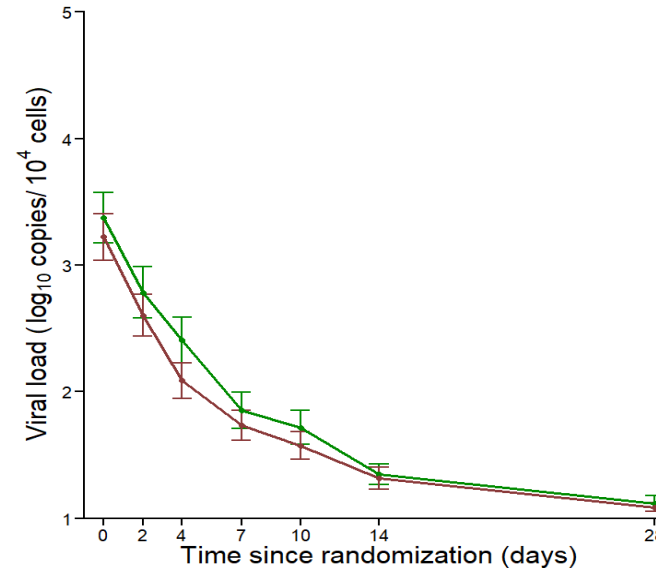
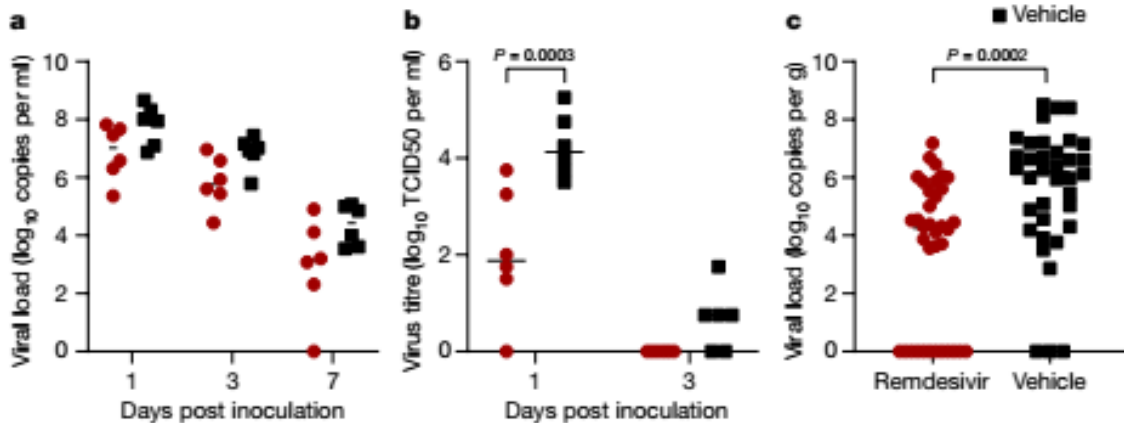
N=832 patients

OR = 0.98 (0.77-1.25), P=0.85

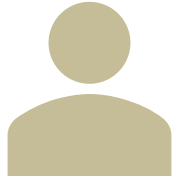


No clinical efficacy in hospitalized patients, but is there any virological signal ?

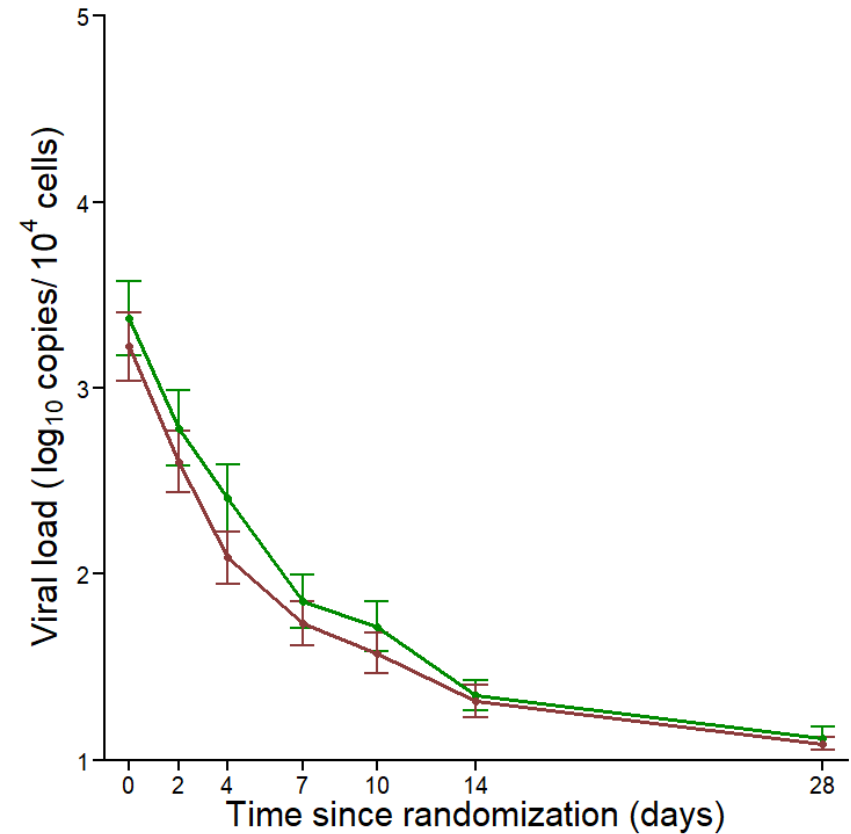
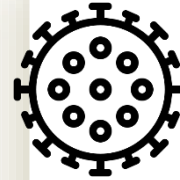
- The preclinical efficacy of remdesivir is well documented
- But contradictory findings on clinical and antiviral efficacy but large between and within-study heterogeneity
- Discovery trial had frequent and normalized viral load data in a large cohort of patients



Patients and data

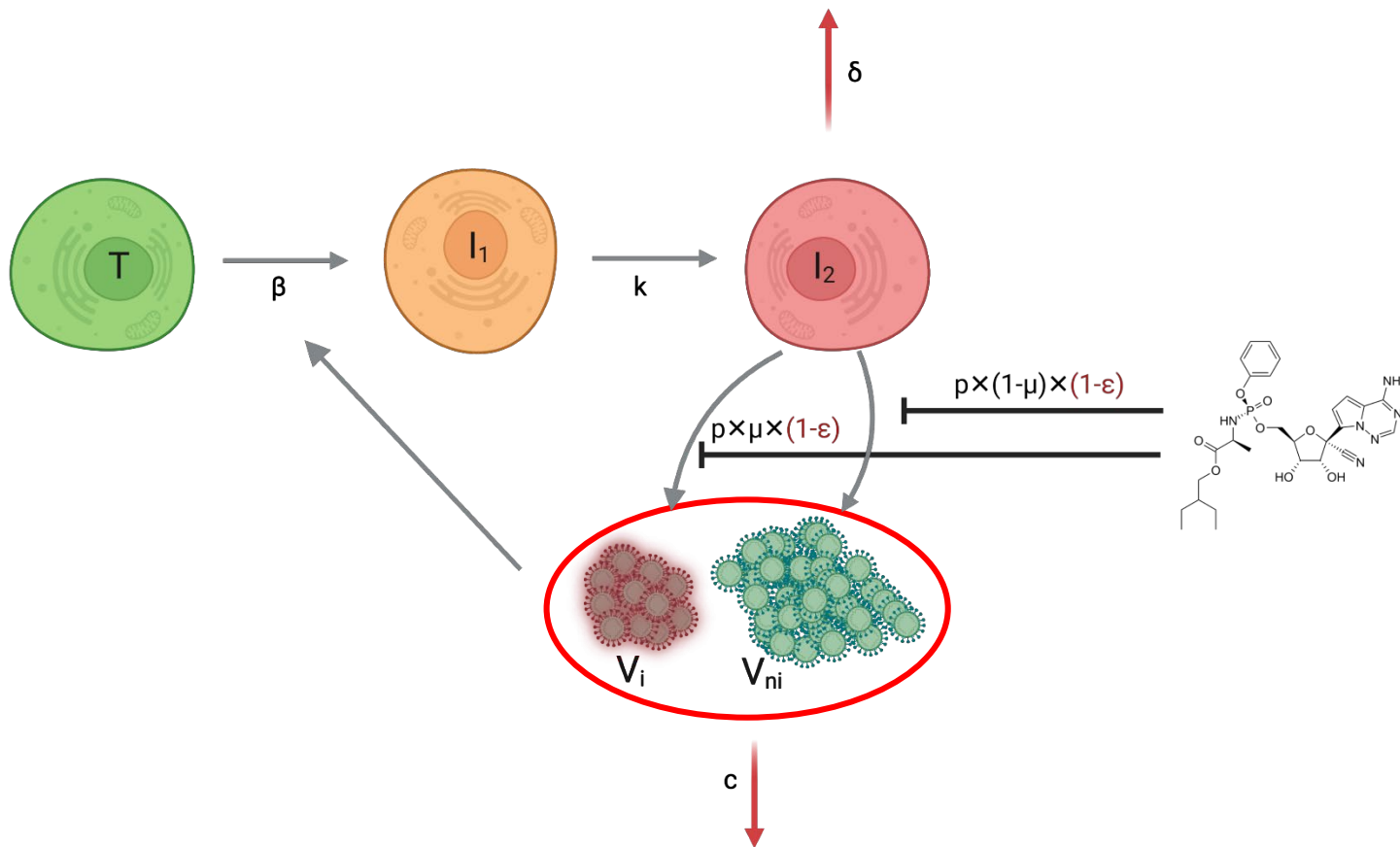


Characteristics	Standard of care	Standard of care + Remdesivir
	(N=329)	(N=336)
	Médiane (IQR) or n (%)	Médiane (IQR) or n (%)
Male gender	222 (67.5%)	235 (69.9%)
Age	64 (53-72)	63 (55-73)
<65	169 (51.4%)	180 (53.6%)
≥65	160 (48.6%)	156 (46.4%)
Delay between symptom onset and randomization (d)	9 (7-11)	9 (7-11)
Viral load at randomization (log ₁₀ copies/10 ⁴ cells)	3.2 (1.9-4.5)	3.2 (1.8-4.5)



Viral dynamic model

Target cell limited model with eclipse phase



$$\frac{dT}{dt} = -\beta \times V_i T$$

$$\frac{dI_1}{dt} = \beta \times V_i T - k I_1$$

$$\frac{dI_2}{dt} = k I_1 - \delta I_2$$

$$\frac{dV_i}{dt} = p(\mu_2 - \epsilon) I_2 - c V_i$$

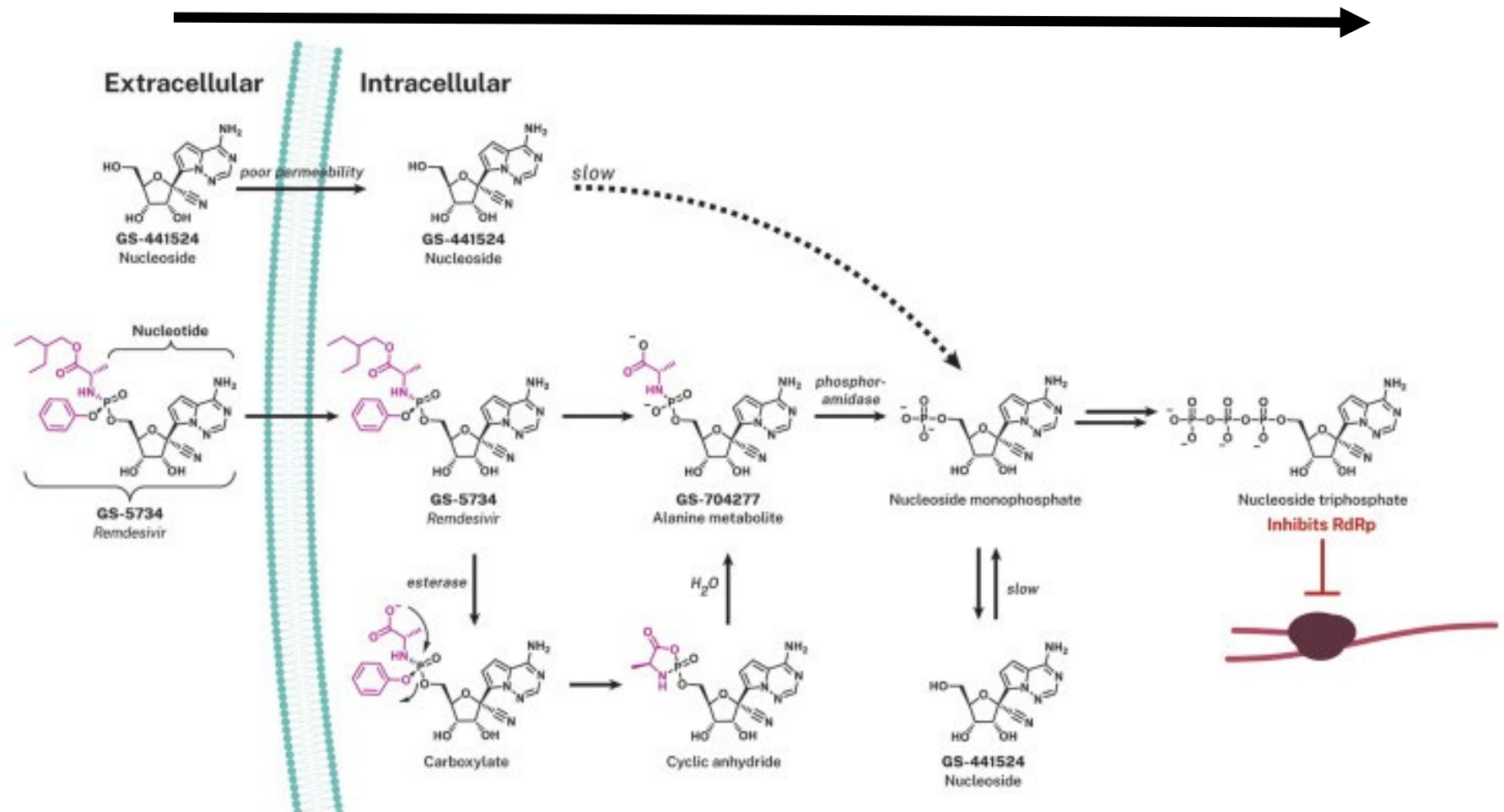
$$\frac{dV_{NI}}{dt} = p(1 - \epsilon) I_2 - \mu V_{NI} - c V_{NI}$$

Pharmacological delay of treatment



$\tau = 0-5$ days

- Model averaging [1] to take into account the uncertainty on delay τ



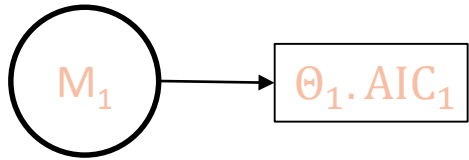
[1] Gonçalves et al. AAPS (2020)

Eastman et al. ACS Cent. Sci. (2020)

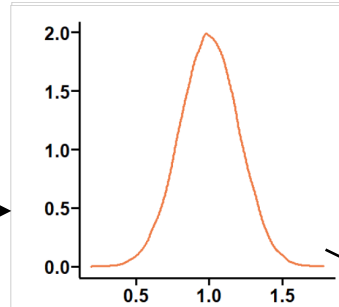
Model averaging



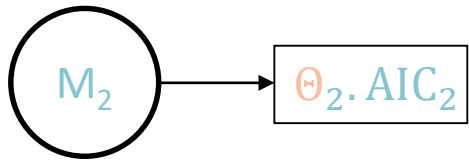
$$\Delta AIC_m = AIC_m - AIC_{\min}$$



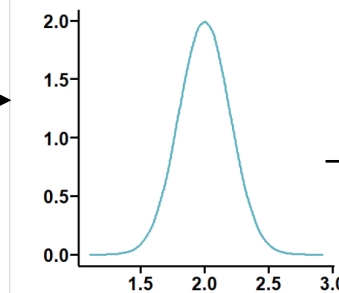
$$w_1 = \frac{e^{-\frac{\Delta AIC_1}{2}}}{\sum_{m=1}^M e^{-\frac{\Delta AIC_m}{2}}}$$



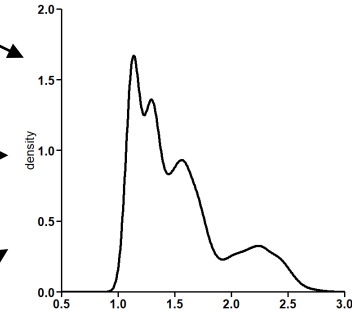
$N \times w_1$



$$w_2 = \frac{e^{-\frac{\Delta AIC_2}{2}}}{\sum_{m=1}^M e^{-\frac{\Delta AIC_m}{2}}}$$



$N \times w_2$

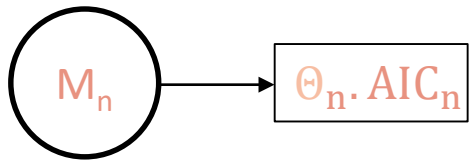


$N \times w_n$

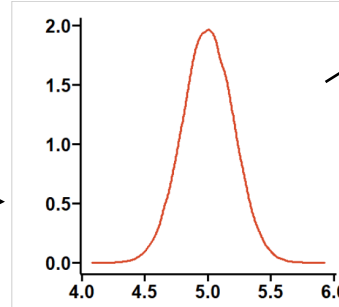
Estimation

Calculation of the weight of each model

Sampling of N individual parameters

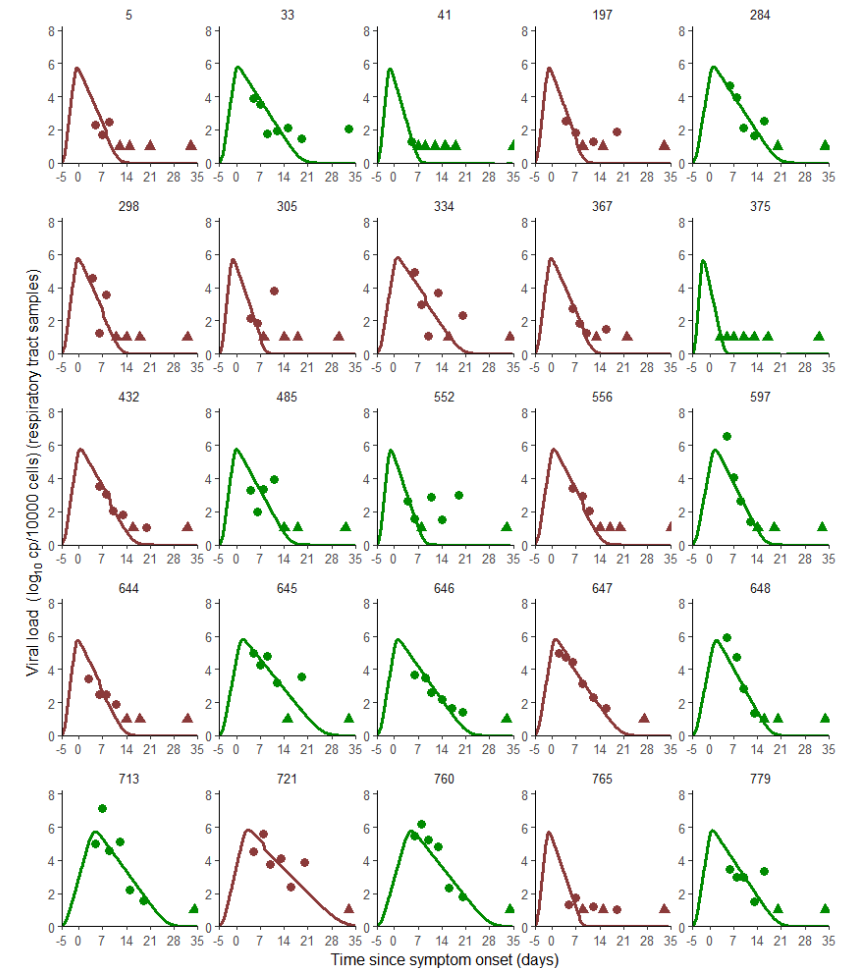


$$w_n = \frac{e^{-\frac{\Delta AIC_n}{2}}}{\sum_{m=1}^M e^{-\frac{\Delta AIC_m}{2}}}$$



Treatment efficacy

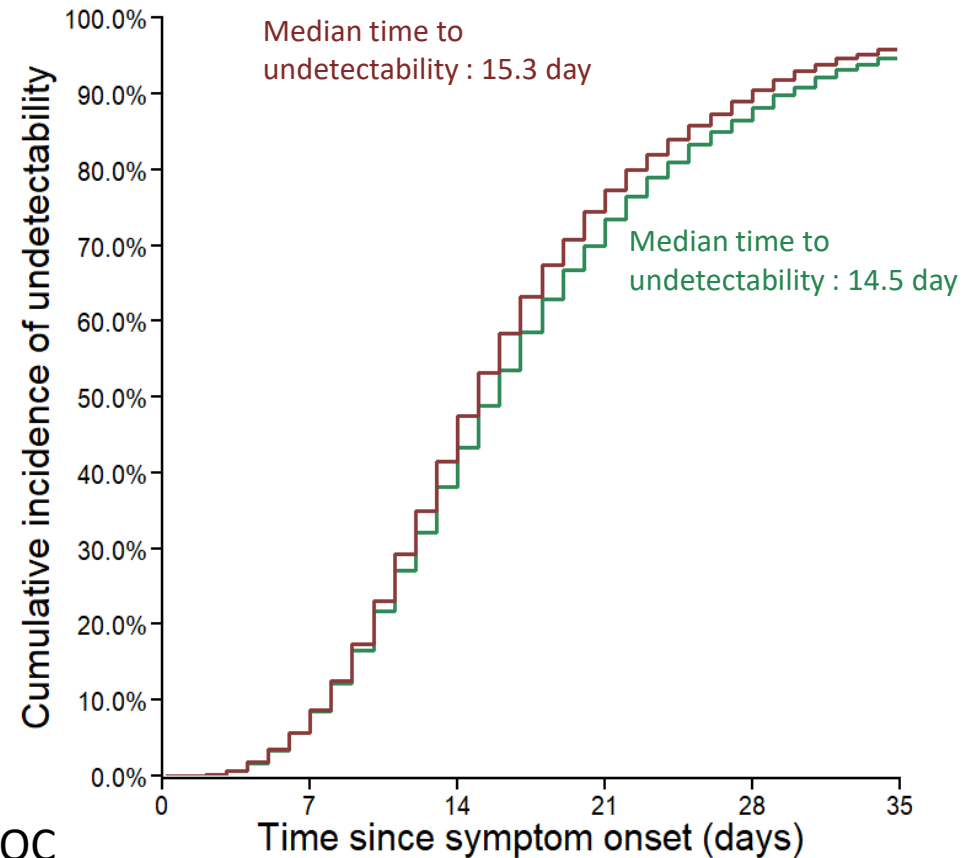
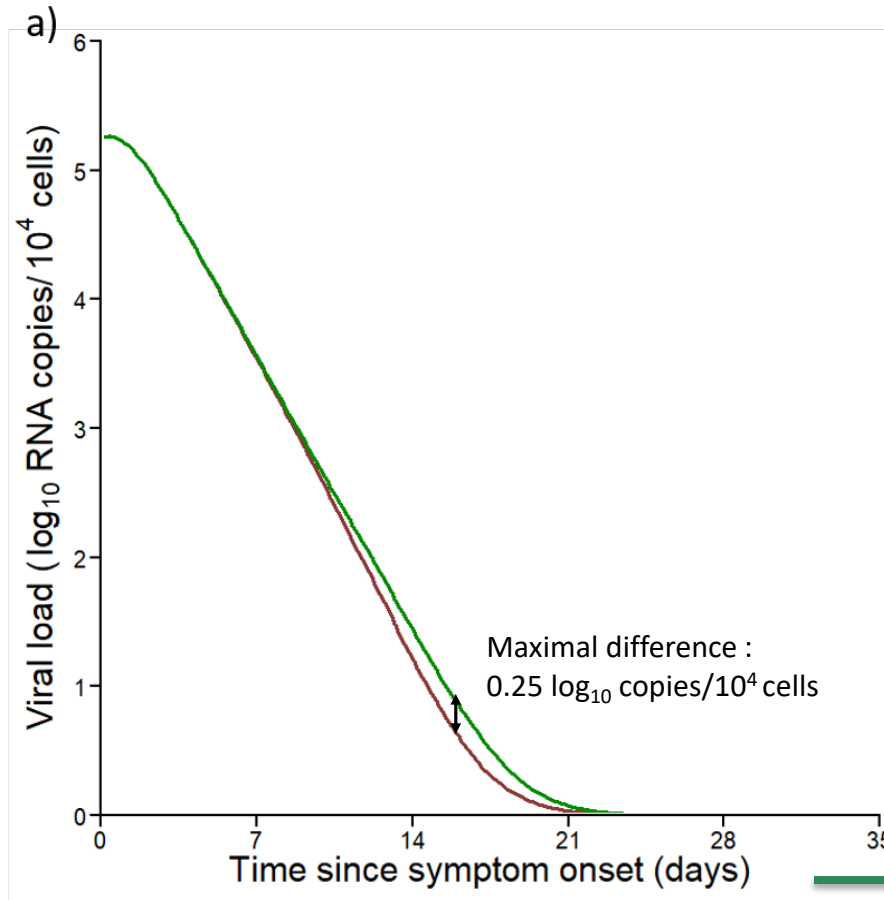
Parameter estimates		
Parameter	Fixed effects (Median, 95% CI)	SD of the random effect (Median, 95% CI)
R_0	10.60 (8.53-12.68)	0.50
$\delta_{<65}$ (d ⁻¹)	0.88 (0.80-0.96)	0.46 (0.41-0.51)
$\delta_{\geq 65}$ (d ⁻¹)	0.76 (0.67-0.84)	
p (10 ⁶ virus.cell ⁻¹ .d ⁻¹)*	1.20 (0.66-1.72)	0.38 (0.14-0.63)
ϵ (%)	52 (35-69)	0.77 (0.18-1.37)
σ (log ₁₀ RNA copies/10 ⁴ cells)	1.14 (1.09-1.19)	-



Analysis in all patients



Remdesivir reduces viral production by 52% (95%CI: 35-69%, p=0.0031)

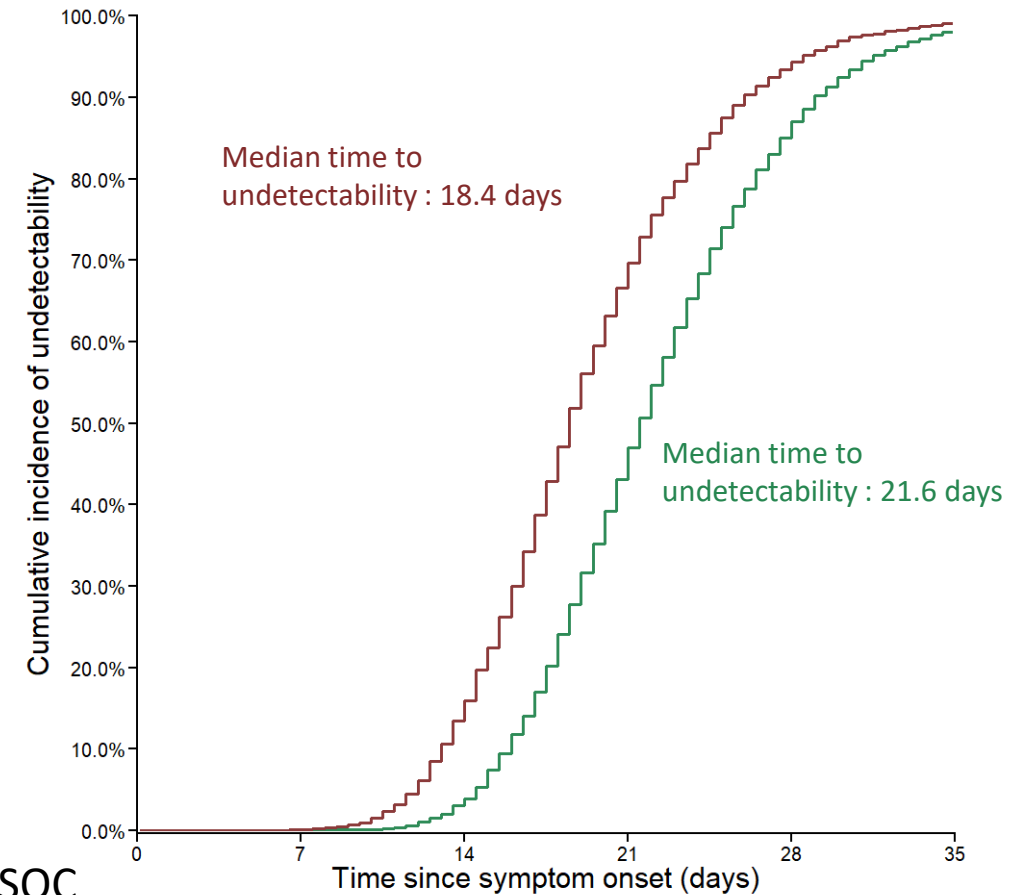
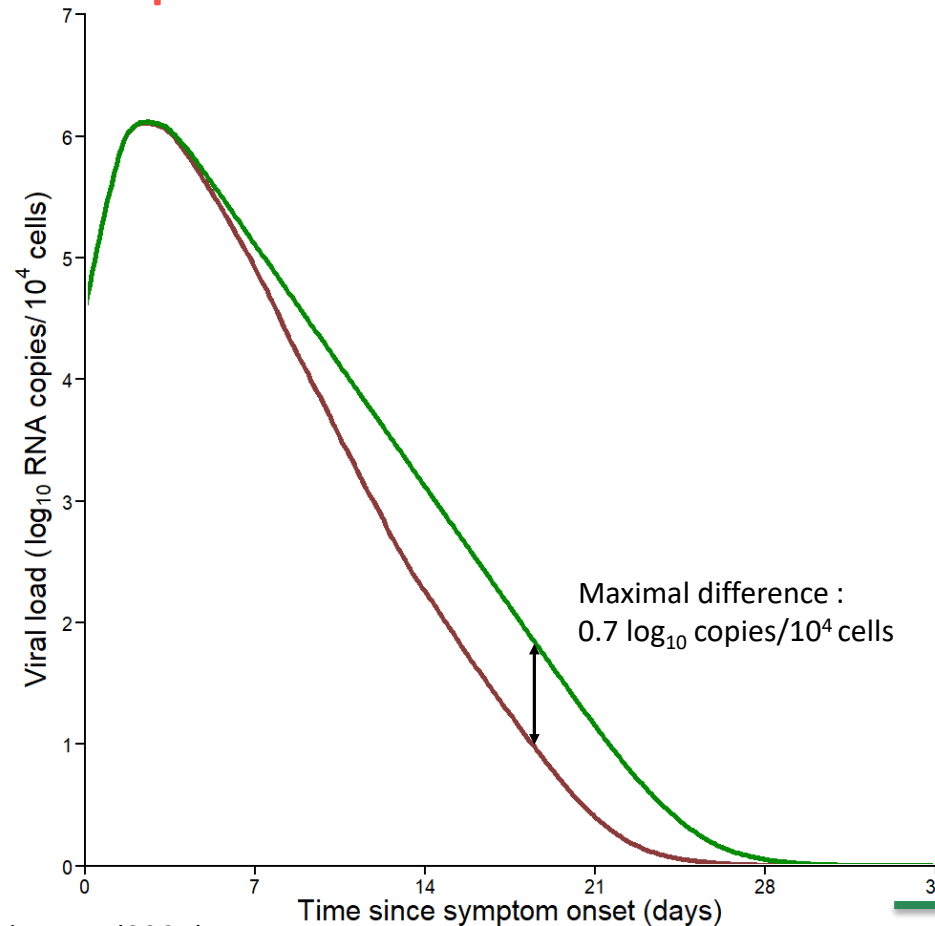


— SOC
— SOC+ remdesivir

Exploratory results in patients with high viral load at admission



Remdesivir reduces viral production by 80% (95%CI: 64-96%, $p < 10^{-5}$)
in patients with viral load at admission $\geq 3.5 \log_{10}$ copies/ 10^4 cells (Infectiosity threshold [1])



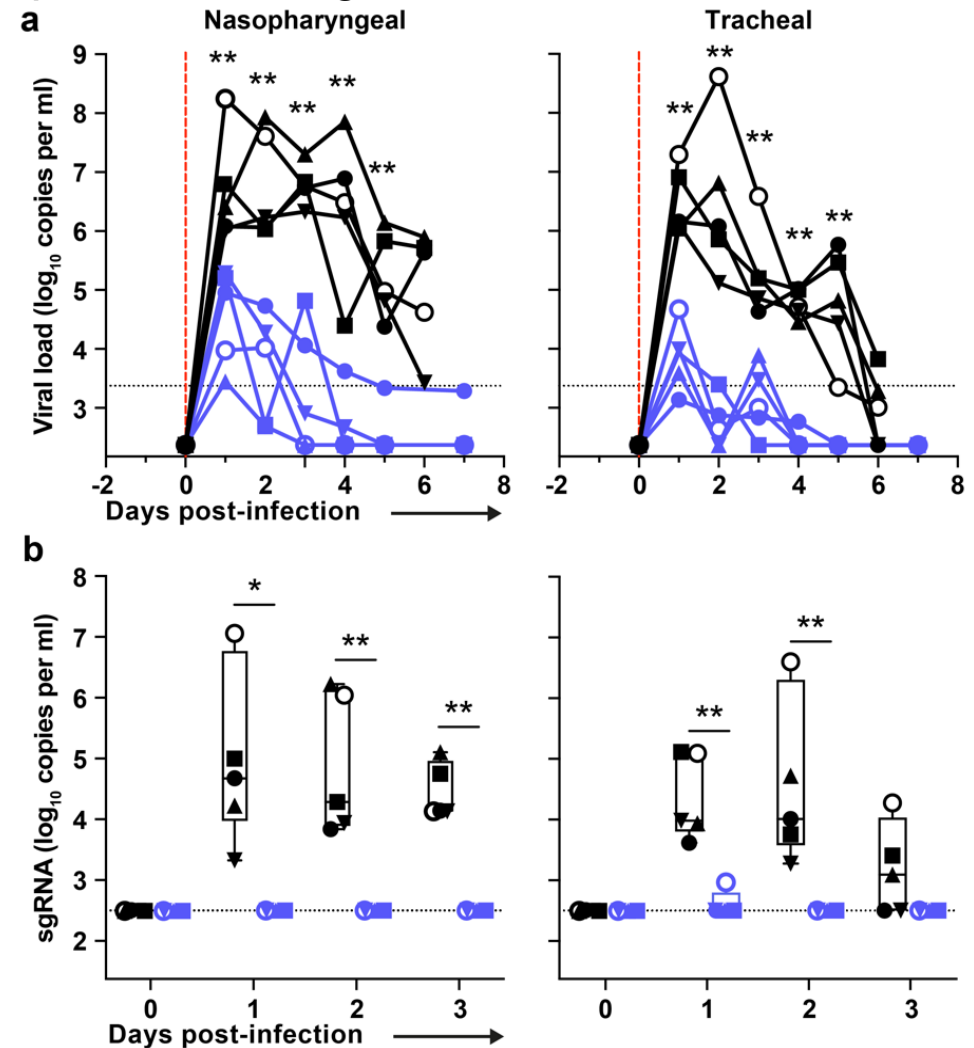
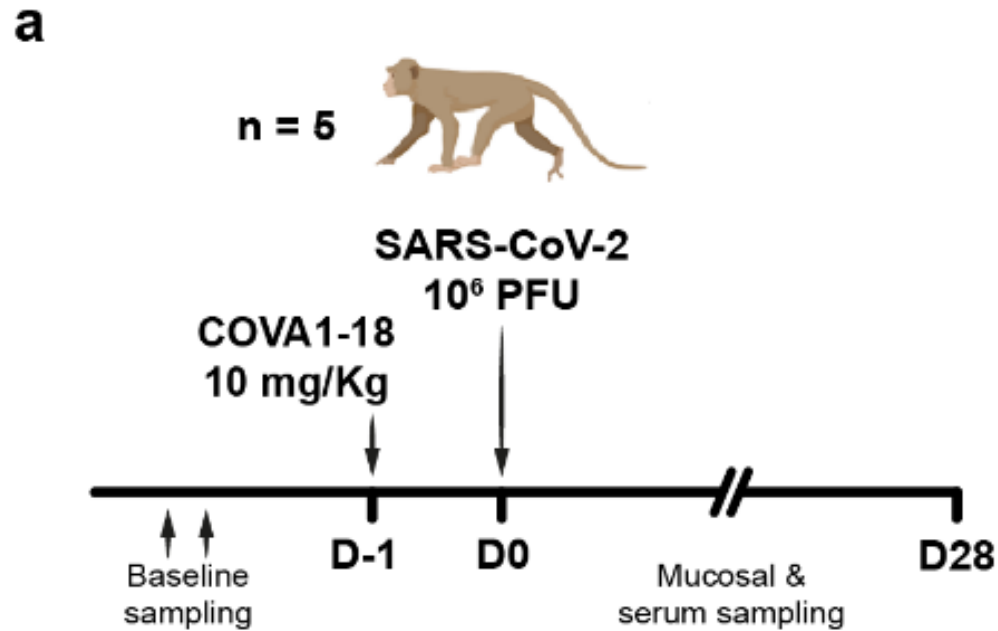
[1] Bal et al. *Sci. Rep.* (2021)

Can we use viral dynamics to better understand the role of treatment

- Viral kinetics in hospitalized non-treated patients
- Antiviral efficacy of remdesivir in hospitalized patients
- **Antiviral efficacy of monoclonal antibodies in outpatients**

Using modeling and animal data to quantify the effect of mAbs

- Most mAbs target the RBD domain of SARS-CoV-2 to prevent virus-cell interaction
- Cova1-18 is a highly efficacious mAb with efficacy in the picomolar range
- Treatment initiated prophylactically



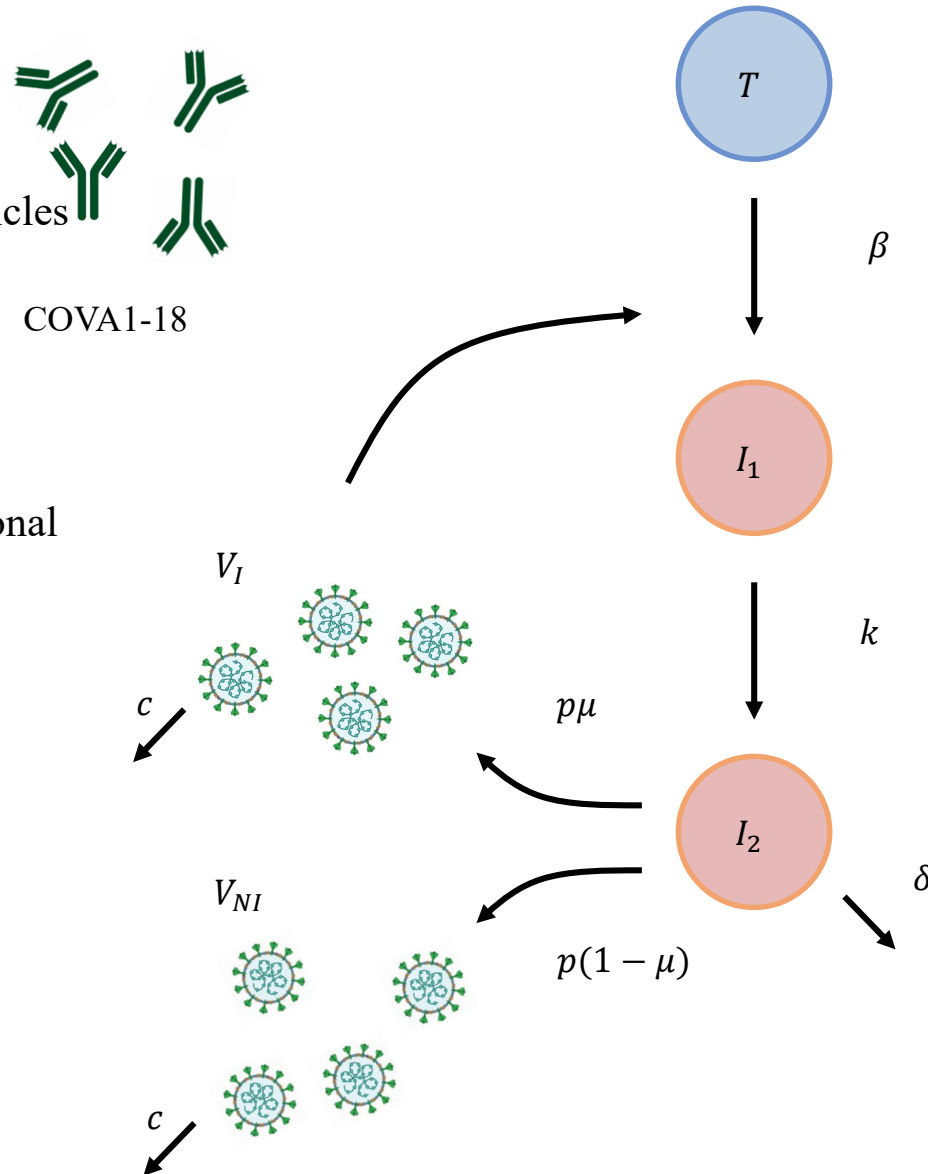
Viral dynamics during treatment with monoclonal antibodies

- Genomic RNA is a reflect of Infectious viral particles (V_I) and Non-infectious viral particles (V_{NI}).

$$V_g = V_I + V_{NI}$$

- Subgenomic RNA (V_{sg}) as a reflect of transcriptional activity:

$$V_{sg} \propto (I_1 + I_2)$$



ODE system :

$$\frac{dT}{dt} = -\beta VT$$

$$\frac{dI_1}{dt} = \beta VT - kI_1$$

$$\frac{dI_2}{dt} = kI_1 - \delta I_2$$

$$\frac{dV_I}{dt} = p\mu I_2 - cV_I$$

$$\frac{dV_{NI}}{dt} = p(1-\mu)I_2 - cV_{NI}$$

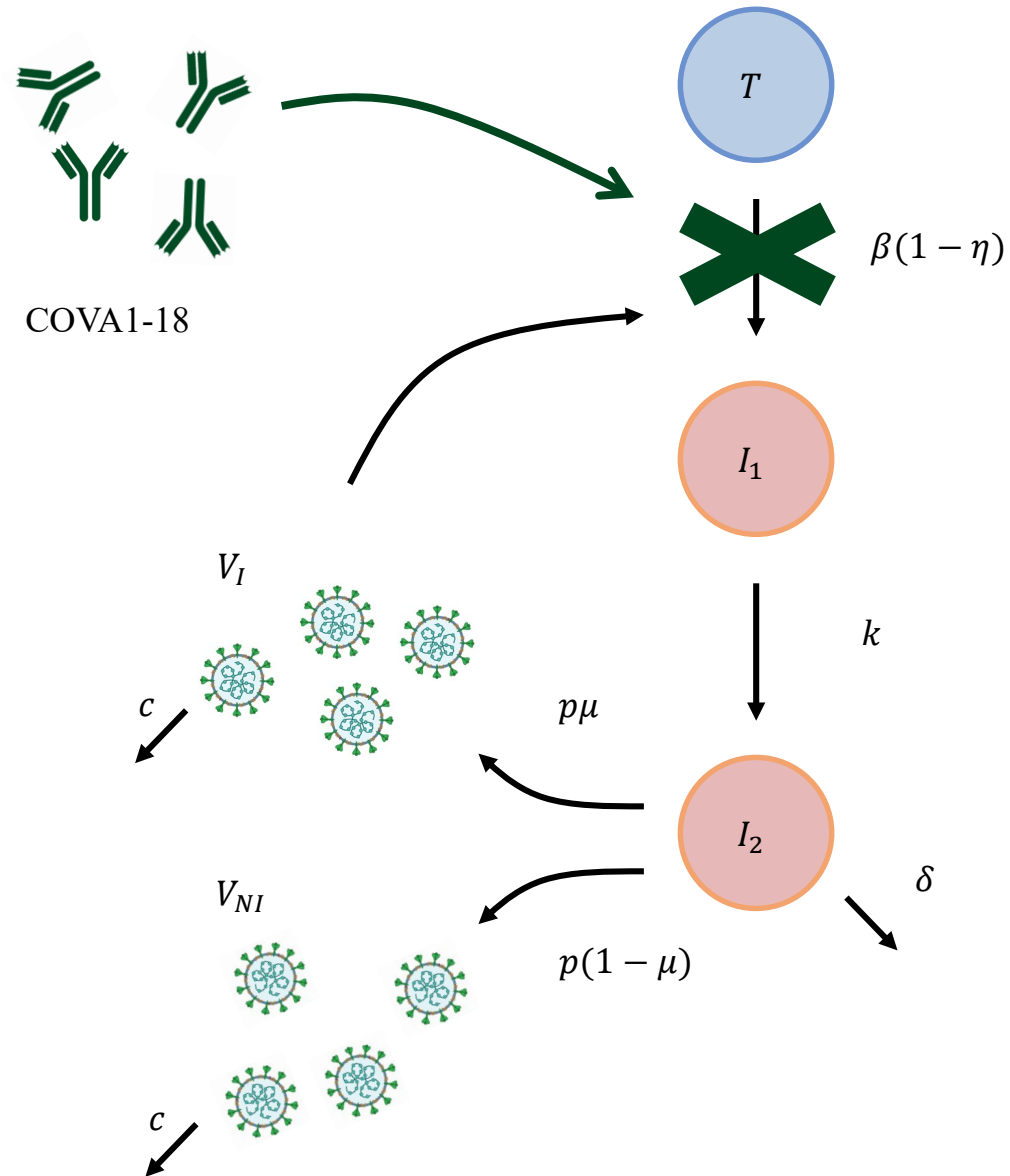
Viral dynamics during treatment with monoclonal antibodies

COVA1-18 blocks the virus/cell attachment

$$\eta(t) = \frac{C(t)}{C(t) + EC_{50}}$$

With :

- $C(t)$: COVA1-18 **plasma** concentration used as a driver of the efficacy
- EC_{50} : Concentration required to obtain 50% efficacy.



ODE system :

$$\frac{dT}{dt} = -\beta(1 - \eta)VT$$

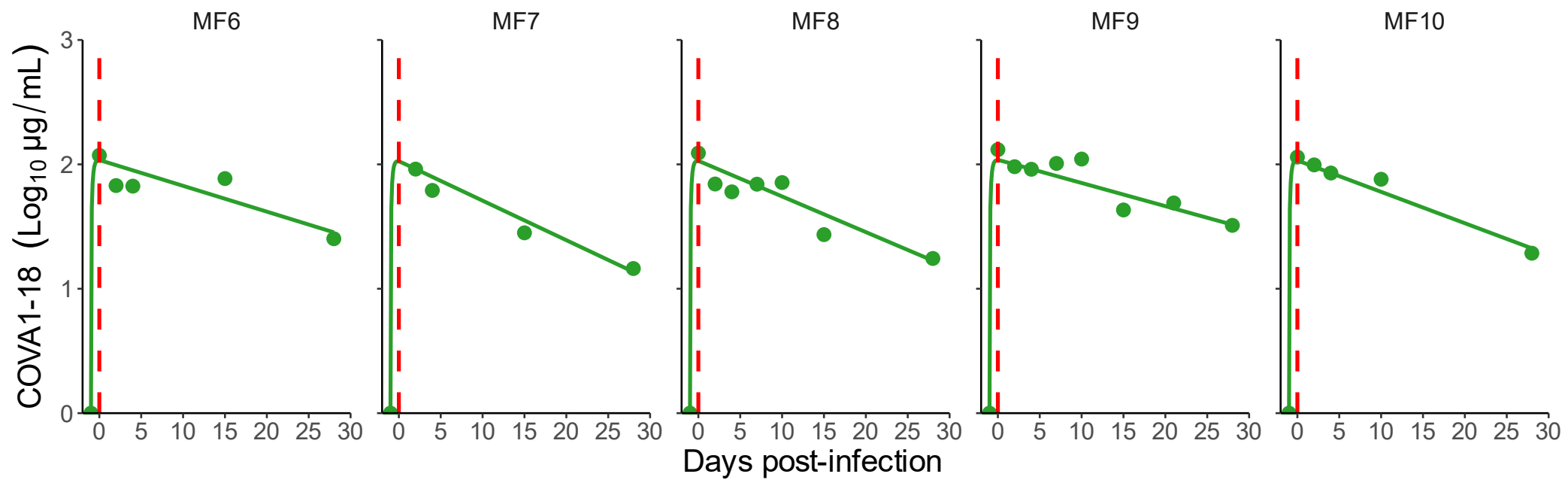
$$\frac{dI_1}{dt} = \beta(1 - \eta)VT - kI_1$$

$$\frac{dI_2}{dt} = kI_1 - \delta I_2$$

$$\frac{dV_I}{dt} = p\mu I_2 - cV_I$$

$$\frac{dV_{NI}}{dt} = p(1 - \mu)I_2 - cV_{NI}$$

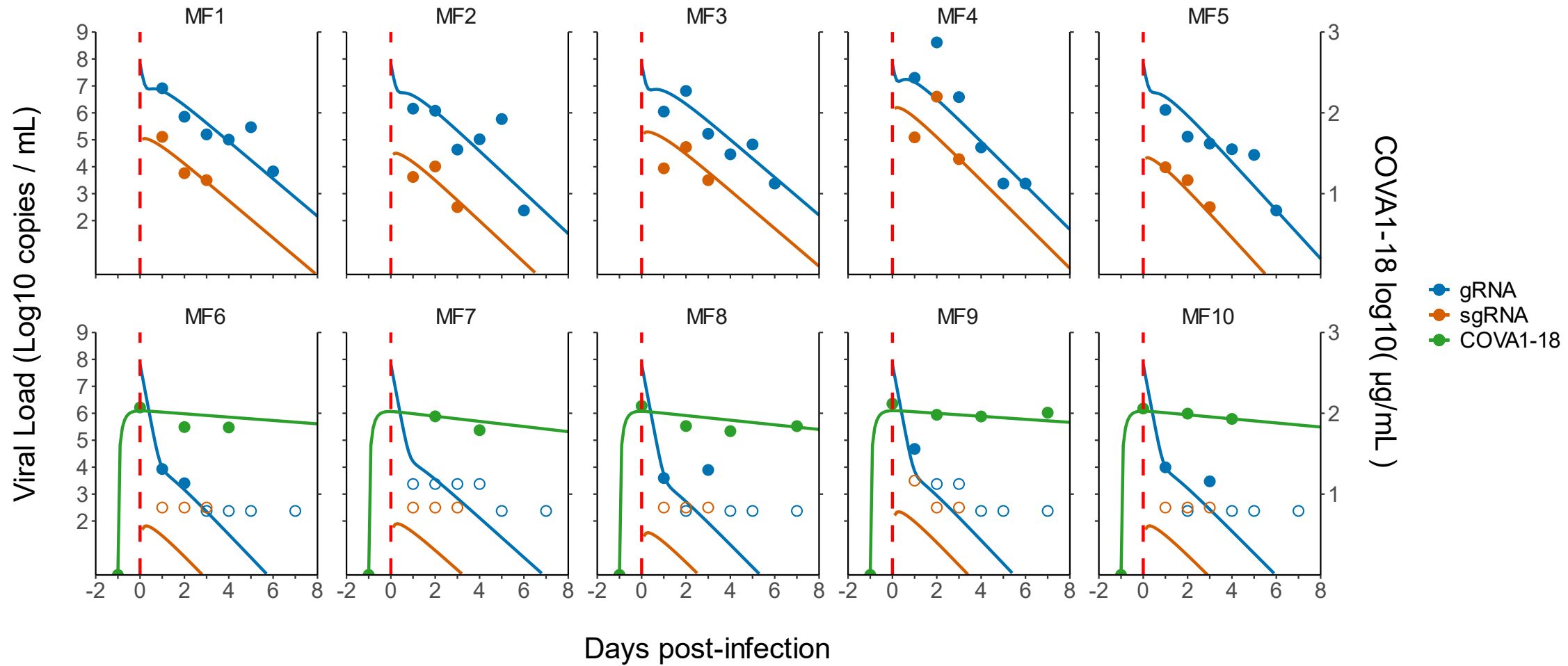
Plasma PK of COVA1-18



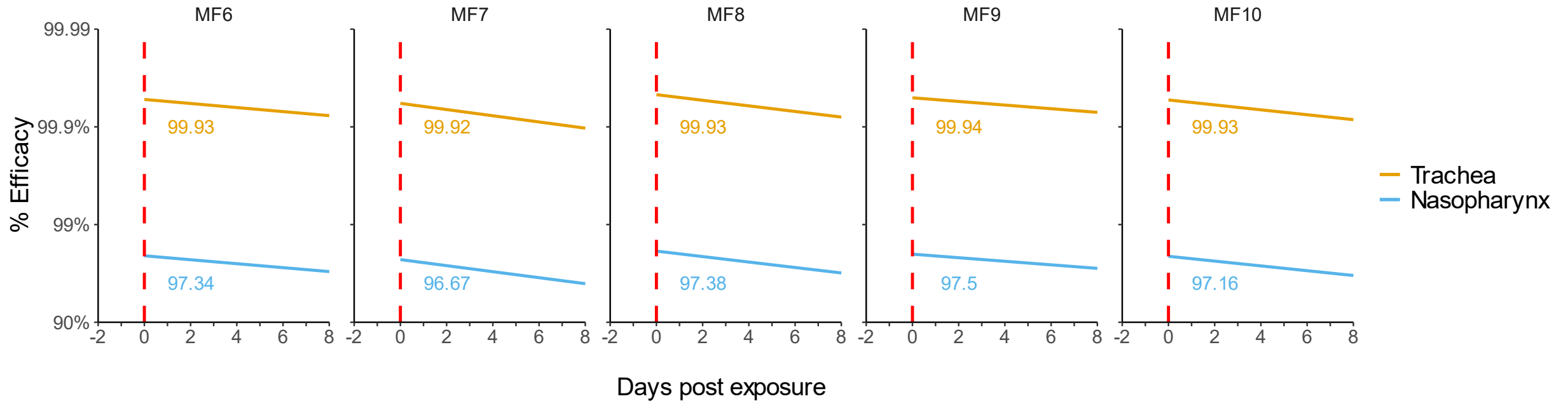
 **Antibody Half-life of 12.7 days**

4 Individual fits

Trachea



Drug efficacy in blocking viral infection is >95%



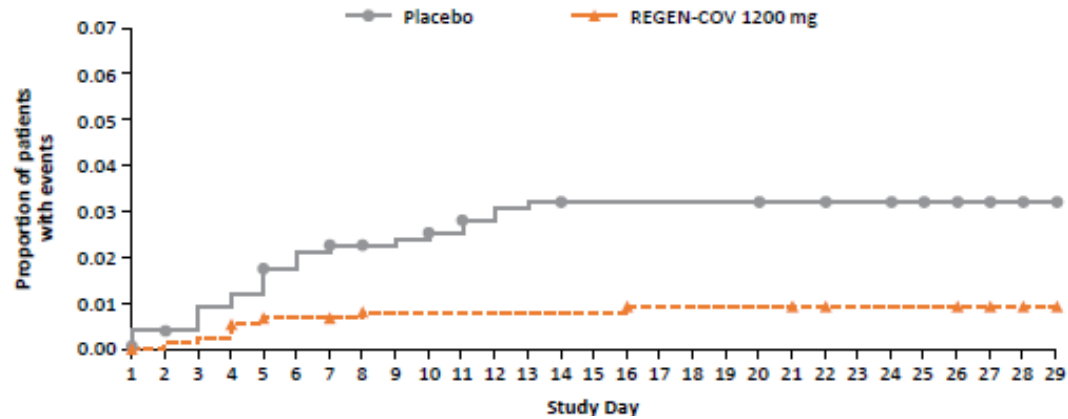
Efficacy is consistent over all animals :

- $\bar{\eta}_{trachea} > 99.9 \%$
- $\bar{\eta}_{nose} > 96 \%$

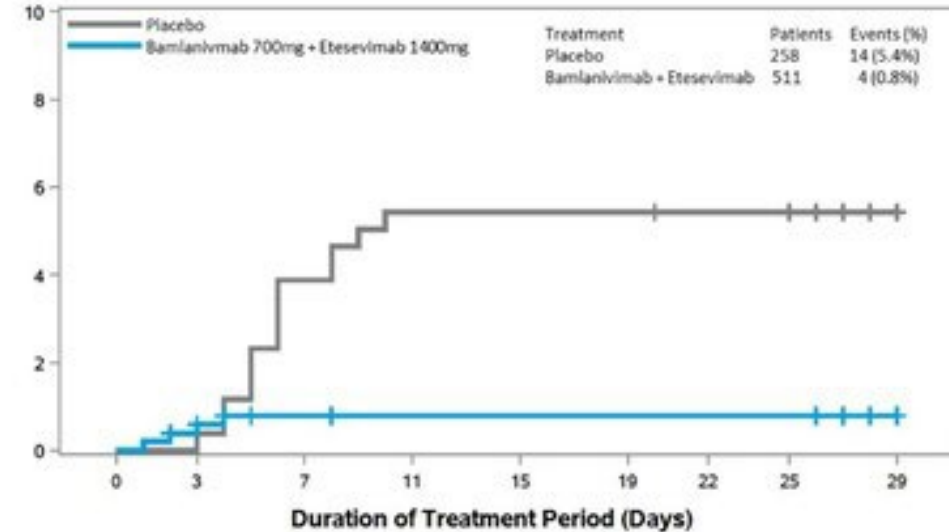
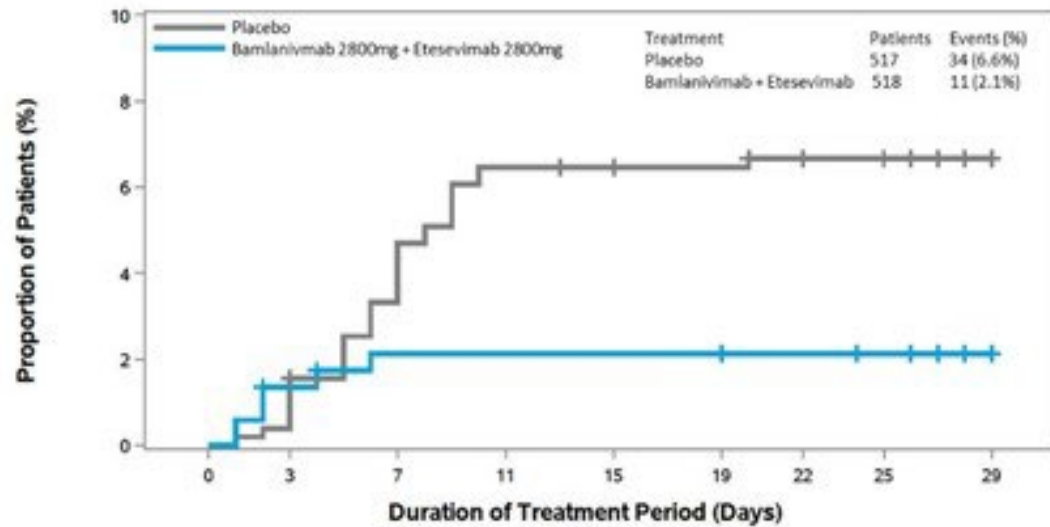
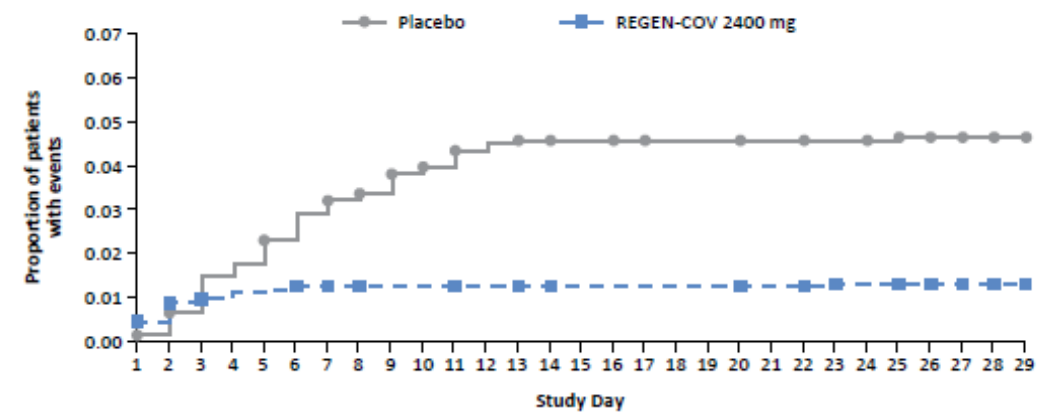
Could be relevant as a PreP in human infections with a lower viral inoculum

Monoclonal antibodies reduce the risk of disease progression by ~70% if given <7 days from symptom onset

A. Covid-19-related Hospitalization or All-Cause Death* – REGEN-COV 1200 mg IV Single Dose



B. Covid-19-related Hospitalization or All-Cause Death* – REGEN-COV 2400 mg IV Single Dose



Modeling and the role of antiviral treatment

- Modeling identifies some important features of viral dynamics
 - Incubation period is ~5 days (prior to Omicron) and the peak of viral load is close to symptom onset
 - Age is associated with prolonged viral shedding
 - Viral dynamics is an independent predictor of disease progression in both outpatients and hospitalized patients
- Timing of antiviral treatment is key to reduce the risk of disease progression
 - **Blocking viral production or infection >90% is needed to prevent progression**
 - Even if administered late, antiviral treatment can reduce the mortality in patients that have high viral load (eg, positive antigen test)
 - Monoclonal antibodies have a high efficacy and reduce the number of at risk patients with extended shedding
 - Efficacy jeopardized by Voc and need now to account for resistance and relapse
 - Small molecules can be alternatives to monoclonal antibodies if they pass the pharmacological threshold

Implications



2021

April 12th

First inclusion in France

Patients hospitalisés avec le COVID-19 sous assistance respiratoire (service de salle)

Placebo + standard of Care (SoC)

AZD7442 + SoC
IV 600 mg day 1

Primary end-point : WHO 7-point ordinal scale at day 15 (antigene positive patients)

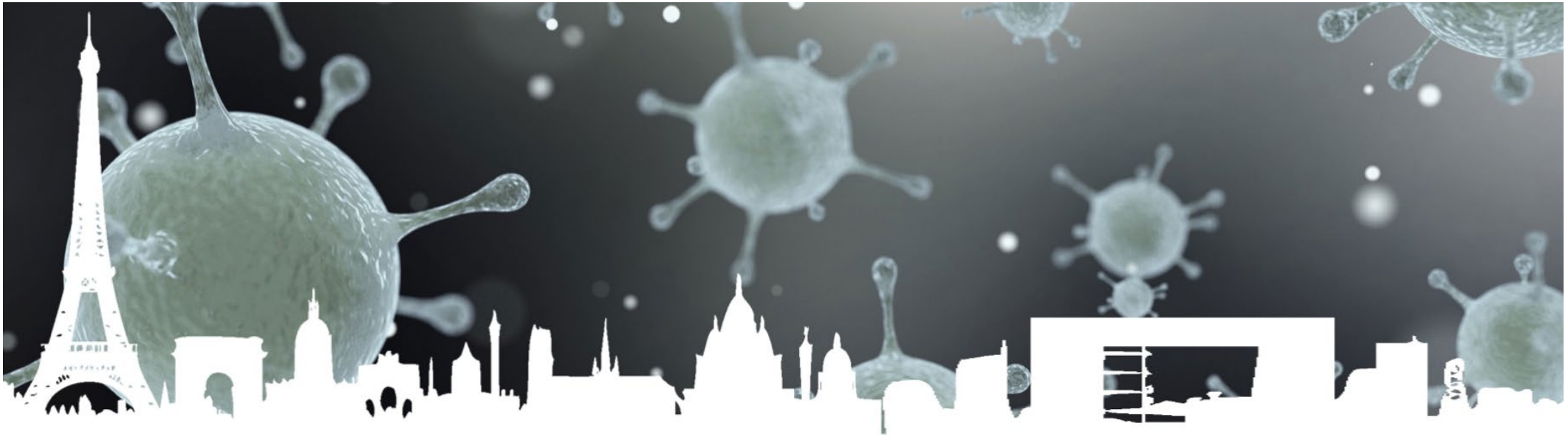
Key secondary end point: Time from randomization to sustained recovery

(being alive and at home for 14 consecutive days prior to Day 90)

AZD7442 [1] : cocktail de deux mAb synthétisés avec une technologie d'extension de la demi vie

[1] Dong et al. *Nat Microbiol.* (2021)

Join our group for a Postdoc in Paris !



Post doctoral position in mathematical modelling (COVID19) in Paris

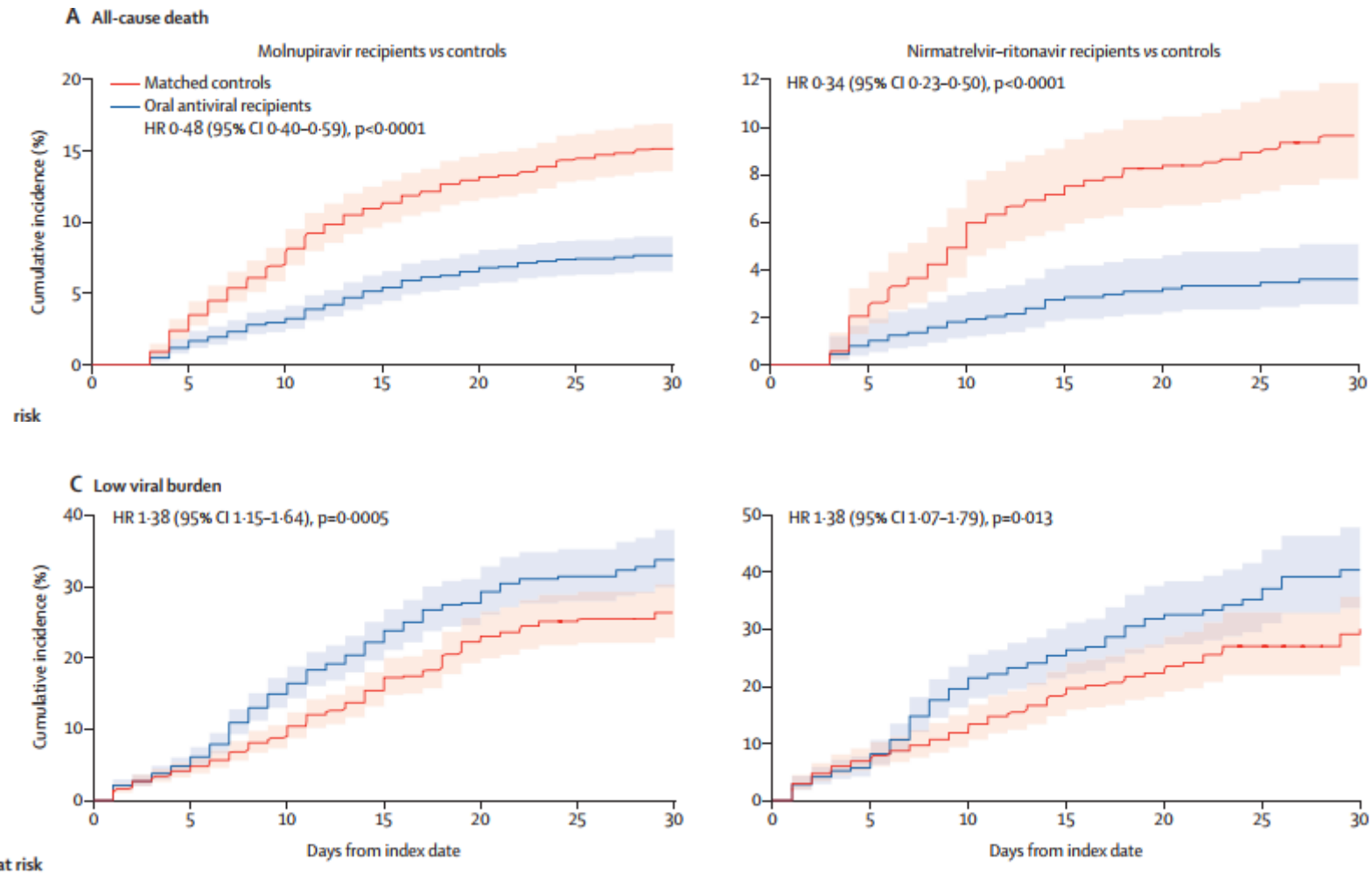
Two post-doctoral positions in mathematical modelling of infectious diseases of 24 months each are available to work in Paris between Institut Pasteur and Inserm (UMR 1137) within the European project ORCHESTRA.

PostDoc position (2y) in Paris for studying viral and immune dynamics of SARS-CoV-2 infection



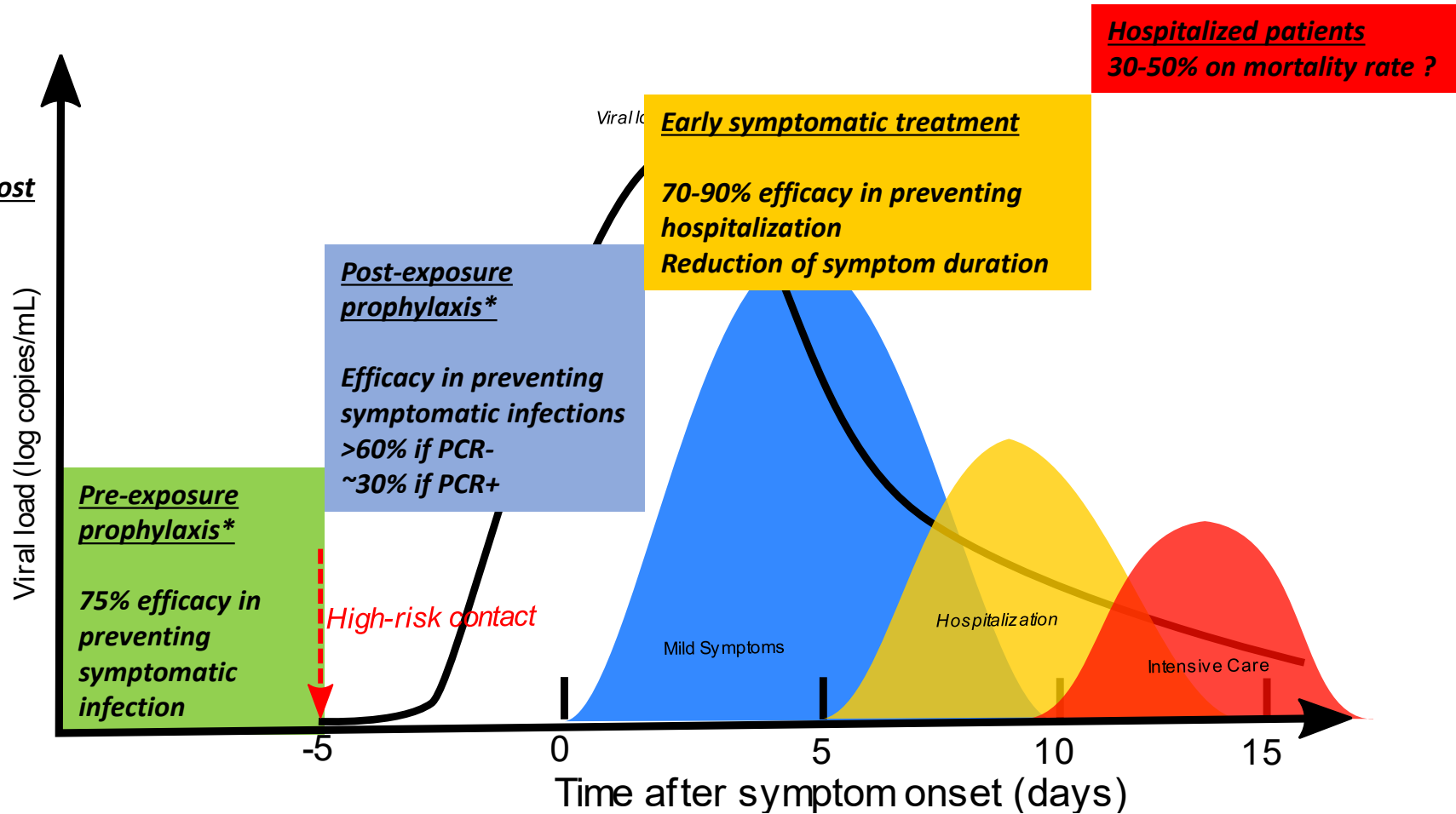
For more information: jeremie.guedj@inserm.fr

Effectiveness of early oral antivirals in hospitalized patients



Antiviral treatments and treatment efficacy : where are we ?

** Results obtained in 2020-2021 with mAbs that have lost most or all activity against omicron variants*



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DISCOVERY

FRENCH COVID

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