Modeling the evolution of COVID-19 in France

Gary Mamon
Modeling the evolution of COVID-19 in France

... by an Astrophysicist!

Gary Mamon
The current situation
The current situation
Charts from GM's web site
Did France confine too late?
Did France confine too late?

Doubling time rises:
- exponentially
- or double-exp’ly

Daddi & Giavalisco 20
Deaths

weekly periodicity?
lower values on Mondays!
A. Moneti

Deaths

weekly periodicity?
lower values on Mondays!
A. Moneti

France = #1 in fatality rate!
• worse hospital care?
• nursing homes now counted
• France is last in testing
By *département*, daily for COVID-19 patients
- hospital arrivals
- critical care arrivals
- releases
- deaths

17000+ points of data
By *département*, daily for COVID-19 patients
- hospital arrivals
- critical care arrivals
- releases
- deaths

**17000+ points of data**

### Data Table

<table>
<thead>
<tr>
<th>dep</th>
<th>jour</th>
<th>incid_hosp</th>
<th>incid_rea</th>
<th>incid_dc</th>
<th>incid_rad</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>2020-03-19</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>2020-03-20</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>2020-03-21</td>
<td>4</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>3</td>
<td>2020-03-22</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>4</td>
<td>2020-03-23</td>
<td>14</td>
<td>1</td>
<td>0</td>
<td>5</td>
</tr>
<tr>
<td></td>
<td>2020-04-29</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>4641</td>
<td>2020-04-30</td>
<td>7</td>
<td>0</td>
<td>0</td>
<td>9</td>
</tr>
<tr>
<td>4642</td>
<td>2020-05-01</td>
<td>6</td>
<td>2</td>
<td>2</td>
<td>8</td>
</tr>
<tr>
<td>4643</td>
<td>2020-05-02</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>4644</td>
<td>2020-05-03</td>
<td>8</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
</tbody>
</table>
Epidemic modeling data

By département, daily for COVID-19 patients
- hospital arrivals
- critical care arrivals
- releases
- deaths

17000+ points of data

This data neglects deaths outside hospitals
- nursing homes
- private homes
- homeless
≈ half of all??
Epidemic modeling data

By département, daily for COVID-19 patients
- hospital arrivals
- critical care arrivals
- releases
- deaths

17000+ points of data

This data neglects deaths outside hospitals
- nursing homes
- private homes
- homeless
≈ half of all??

I stopped at 95 for more genetically homogenous départements

**SIR model**

Kermack & McKendrick 27

thanks to Avishai Dekel for introducing me to SIR!

Susceptible $\rightarrow$ Infectious $\rightarrow$ Removed (Recovered & Dead)

\[
\frac{dS}{dt} = -\beta SI
\]

\[
\frac{dI}{dt} = \beta SI - \gamma I
\]

\[
\frac{dR}{dt} = -\gamma I
\]
The SIR model, developed by Kermack & McKendrick in 1927, is used to model the evolution of COVID-19 in France. It categorizes the population into three groups: Susceptible, Infectious, and Removed (Recovered & Dead).

The model equations are:

\[
\begin{align*}
\frac{dS}{dt} &= - \beta SI \\
\frac{dI}{dt} &= \beta SI - \gamma I \\
\frac{dR}{dt} &= - \gamma I
\end{align*}
\]

The reproductive factor, \( R_0 \), is given by:

\[ R_0 = \frac{\beta}{\gamma} = \text{number of S contaminated by I} \]

Thanks to Avishai Dekel for introducing me to SIR!
**SIR model**  Kermack & McKendrick 27

**Susceptible** → **Infectious** → **Removed**  
(Recovered & Dead)

\[
\begin{align*}
\frac{dS}{dt} &= -\beta SI \\
\frac{dI}{dt} &= \beta SI - \gamma I \\
\frac{dR}{dt} &= -\gamma I
\end{align*}
\]

\[
\begin{aligned}
\dot{S} &= -R_0 S \frac{I}{T_{I\to R}} \\
\dot{I} &= (R_0 S - 1) \frac{I}{T_{I\to R}} \\
\dot{R} &= \frac{I}{T_{I\to R}}
\end{aligned}
\]

**Reproductive factor**: \( R_0 = \frac{\beta}{\gamma} = \) number of S contaminated by I

\( S \sim 1 \): Exponential increase of Infectious if \( R_0 > 1 \)

thanks to Avishai Dekel for introducing me to SIR!
**SIR model**

Kermack & McKendrick 27

**Reproductive factor**: \( R_0 = \frac{\beta}{\gamma} = \text{number of } S \text{ contaminated by } I \)

\[
\begin{align*}
\frac{dS}{dt} &= -\beta SI \\
\frac{dI}{dt} &= \beta SI - \gamma I \\
\frac{dR}{dt} &= -\gamma I
\end{align*}
\]

\[
\begin{align*}
\dot{S} &= -R_0 S \frac{I}{T_{I\rightarrow R}}, \\
\dot{I} &= (R_0 S - 1) \frac{I}{T_{I\rightarrow R}}, \\
\dot{R} &= \frac{I}{T_{I\rightarrow R}}.
\end{align*}
\]

**S ~ 1**: Exponential increase of Infectious if \( R_0 > 1 \)

observed doubling time \( T_2 = \frac{\ln 2}{R_0 - 1} T_{I\rightarrow R} \Rightarrow \text{need to know } R_0 \text{ or } T_{I\rightarrow R} \)

**SIR evolution before lockdown:**

\[ R_0 = \text{cst} \]

*Figure 7: Evolution of fraction of infectious people for different values of \( R_0 \), for fixed infectious duration \( T_I = 7 \) days. The doubling times are 9.7, 2.4, and 1.2 days for \( R_0 = 1.5 \), 3, and 5.*

*Figure 8 shows the evolution of such a 3-zone clustered country. The infection spreads rapidly to other villages, then almost immediately to cities, whose greater promiscuity, hence larger \( R_0 \) factor, leads to a faster relative rise in number of infectious. The number of infectious in the country has two peaks: in cities after 45 days, and in villages after 270 days. Moreover, while up to 10% of the inhabitants of the origin and of villages are infectious at the peak of their respective epidemics, the peak fraction of infectious is as high as 50% in the cities.*

*Containment*

The top panel of Figure 9 displays the effects of a 90-day period of containment that reduces \( R_0 \) from 3 to 0.5. The figure indicates that containment represents a delay in the contamination, but the final cumulative fraction of contaminated people remains the same. Indeed, while containment does reduce drastically the number of infectious (decreasing portion of red line), the infectious rises exponentially (seen linearly in logarithmic y axis) as soon as containment is ended. The post-containment period matches the evolution of the no-containment case (dashed lines), but with the delay of the containment period. The delayed effects of lower \( R_0 \)
Evolution with lockdown

Figure 9: Effect of Containment (during times shown as gray shaded region) on fractions of cumulative cases and of Infectious. The Infectious duration is assumed to be 7 days. The basic reproduction number is $R_0=3$ before and after Containment, and $R_0=0.5$ (top) or 0 (bottom) during Containment. The dashed and solid curves show the cases without and with Containment. The lower panel is a case of possibly successful Containment, since the fraction of Infectious is reduced to less than one person in a medium-size country (in which case the second peak will not occur).

$R_0=3$, then 0, Final total infected fraction= 0.94

Exponential decreases $\geq 2 \times$ slower than increase
Evolution with lockdown

Figure 9: Effect of Containment (during times shown as gray shaded region) on fractions of cumulative cases and of Infectious. The Infectious duration is assumed to be 7 days. The basic reproduction number is $R_0=3$ before and after Containment, and $R_0=0.5$ (top) or 0 (bottom) during Containment. The dashed and solid curves show the cases without and with Containment. The lower panel is a case of possibly successful Containment, since the fraction of Infectious is reduced to less than one person in a medium-size country (in which case the second peak will not occur).

How long a lockdown to eradicate the virus? 75 days (SIR model)? OR 15 days (quarantine)
**Distribution of phase durations**

SIR model assumes exponential distribution of duration of Infectious phase

\[ \frac{dI}{dt} = \beta SI - \gamma I \]
**Distribution of phase durations**

SIR model assumes exponential distribution of duration of Infectious phase

\[
\frac{dI}{dt} = \beta SI - \gamma I
\]

More complex models (SEIR etc.) effectively split single exponential into many

\[\Rightarrow E+I \equiv \text{convolution of exponentials (Gamma or Erlang)}\]

e.g. Vergu+10

---

**Figure 13:** Different models for the distribution of the durations of the Infectious phase. The SIR model uses the exponential model.

**Figure 14:** Illustration of the underestimation of the fatality rate when the doubling time increases. The figure assumes that the fatality rate and time in hospital are both constant in time, and yet the measured fatality rate, obtained by dividing the number of total deaths by the number of total cases (green) underestimates the true fatality rate (black vertical arrow).

---

More complex models (SEIR etc.) effectively split single exponential into many

\[\Rightarrow E+I \equiv \text{convolution of exponentials (Gamma or Erlang)}\]

e.g. Vergu+10

---

**Figure:**

- Red: exponential
- Green: gamma distribution \(\Gamma(3,3/T_I)\)
- Blue: constant duration \(T_I\)
The trouble with SIR

SIR: sharp transition

data: very slow transition
simplest model to fit hospital data: SIHCDRO

Susceptible → Infectious → Hospitalized → Critical → Dead

Other-recovered → Released

Immunized

Hospital data
simplest model to fit hospital data: \textit{SIHCDRO}

\begin{align*}
\dot{S} &= -R_0 S \frac{I}{T_{1\to}} = -R_0 S \left[ \frac{f_{I\to H}}{T_{1\to H}} + \frac{(1 - f_{I\to H})}{T_{1\to O}} \right] I, \\
\dot{I} &= (R_0 S - 1) \frac{I}{T_{1\to}} = (R_0 S - 1) \left[ \frac{f_{I\to H}}{T_{1\to H}} + \frac{(1 - f_{I\to H})}{T_{1\to O}} \right] I, \\
\dot{H} &= f_{I\to H} \frac{I}{T_{1\to H}} - f_{H\to C} \frac{H}{T_{H\to C}} - (1 - f_{H\to C}) \frac{H}{T_{H\to R}}, \\
\dot{C} &= f_{H\to C} \frac{H}{T_{H\to C}} - f_{C\to D} \frac{C}{T_{C\to D}} - (1 - f_{C\to D}) \frac{C}{T_{C\to R}}, \\
\dot{D} &= f_{C\to D} \frac{C}{T_{C\to D}}, \\
\dot{R} &= (1 - f_{H\to C}) \frac{H}{T_{H\to R}} + (1 - f_{C\to D}) \frac{C}{T_{C\to R}}, \\
\dot{O} &= (1 - f_{I\to H}) \frac{I}{T_{I\to O}}.
\end{align*}
It is advisable to incorporate an additional, non-contagious, incubation phase. We introduce the 2.3 SEIHCDRO model where

\[
\begin{align*}
\dot{S} &= -R_0 S \frac{I}{T_{I\rightarrow}} = -R_0 S \left[ \frac{f_{I\rightarrow H}}{T_{I\rightarrow H}} + \frac{(1 - f_{I\rightarrow H})}{T_{I\rightarrow O}} \right] I, \\
\dot{I} &= (R_0 S - 1) \frac{I}{T_{I\rightarrow}} = (R_0 S - 1) \left[ \frac{f_{I\rightarrow H}}{T_{I\rightarrow H}} + \frac{(1 - f_{I\rightarrow H})}{T_{I\rightarrow O}} \right] I, \\
\dot{H} &= f_{I\rightarrow H} \frac{I}{T_{I\rightarrow H}} - f_{H\rightarrow C} \frac{H}{T_{H\rightarrow C}} - (1 - f_{H\rightarrow C}) \frac{H}{T_{H\rightarrow R}}, \\
\dot{C} &= f_{H\rightarrow C} \frac{H}{T_{H\rightarrow C}} - f_{C\rightarrow D} \frac{C}{T_{C\rightarrow D}} - (1 - f_{C\rightarrow D}) \frac{C}{T_{C\rightarrow R}}, \\
\dot{D} &= f_{C\rightarrow D} \frac{C}{T_{C\rightarrow D}}, \\
\dot{R} &= (1 - f_{H\rightarrow C}) \frac{H}{T_{H\rightarrow R}} + (1 - f_{C\rightarrow D}) \frac{C}{T_{C\rightarrow R}}, \\
\dot{O} &= (1 - f_{I\rightarrow H}) \frac{I}{T_{I\rightarrow O}}.
\end{align*}
\]

Free parameters:
6 timescales over fractions
\( R_0 \) before confinement
\( R_0 \) during confinement
normalization of Infectious
\( \rightarrow 6 + 3 N \) (zones)

timescales & branching fractions
It is advisable to incorporate an additional, non-contagious, incubation phase. We introduce the 2.3 SEIHCDRO model where

\[ \text{The SIHCDRO model equations can be written} \]

\[
\begin{align*}
\dot{S} &= -R_0 S \frac{I}{T_{1\rightarrow}} = -R_0 S \left[ \frac{f_{1\rightarrow H}}{T_{1\rightarrow H}} + \frac{(1 - f_{1\rightarrow H})}{T_{1\rightarrow O}} \right] I, \\
\dot{I} &= (R_0 S - 1) \frac{I}{T_{1\rightarrow}} = (R_0 S - 1) \left[ \frac{f_{1\rightarrow H}}{T_{1\rightarrow H}} + \frac{(1 - f_{1\rightarrow H})}{T_{1\rightarrow O}} \right] I, \\
\dot{H} &= f_{1\rightarrow H} \frac{I}{T_{1\rightarrow H}} - f_{H\rightarrow C} \frac{H}{T_{H\rightarrow C}} - (1 - f_{H\rightarrow C}) \frac{H}{T_{H\rightarrow R}}, \\
\dot{C} &= f_{H\rightarrow C} \frac{H}{T_{H\rightarrow C}} - f_{C\rightarrow D} \frac{C}{T_{C\rightarrow D}} - (1 - f_{C\rightarrow D}) \frac{C}{T_{C\rightarrow R}}, \\
\dot{D} &= f_{C\rightarrow D} \frac{C}{T_{C\rightarrow D}}, \\
\dot{R} &= (1 - f_{H\rightarrow C}) \frac{H}{T_{H\rightarrow R}} + (1 - f_{C\rightarrow D}) \frac{C}{T_{C\rightarrow R}}, \\
\dot{O} &= (1 - f_{1\rightarrow H}) \frac{I}{T_{1\rightarrow O}}.
\end{align*}
\]

\[ \text{Hospital data points in red} \]

**Zones:**
- single department
- France as single zone
- 4-departments
- 8-departments
- 15 regions

**Free parameters:**
6 timescales over fractions
\( R_0 \) before confinement
\( R_0 \) during confinement normalization of Infectious
\( \rightarrow \) 6 + 3 \( N \) (zones)
Exposed (E)

SEIHCDRO model that incorporates the Exposed phase:

It is advisable to incorporate an additional, non-contagious, incubation phase. We introduce the

2.3 SEIHCDRO model

In equations (4b) to (4g), the terms

\[
\dot{S} = -R_0 S \frac{I}{T_{1-H}} = -R_0 S \left[ \frac{f_{I-H}}{T_{1-H}} + \frac{(1 - f_{I-H})}{T_{1-O}} \right] I ,
\]

\[
\dot{I} = (R_0 S - 1) \frac{I}{T_{1-H}} = (R_0 S - 1) \left[ \frac{f_{I-H}}{T_{1-H}} + \frac{(1 - f_{I-H})}{T_{1-O}} \right] I ,
\]

\[
\dot{H} = f_{I-H} \frac{I}{T_{1-H}} - f_{H-C} \frac{H}{T_{H-C}} - (1 - f_{H-C}) \frac{H}{T_{H-R}} ,
\]

\[
\dot{C} = f_{H-C} \frac{H}{T_{H-C}} - f_{C-D} \frac{C}{T_{C-D}} - (1 - f_{C-D}) \frac{C}{T_{C-R}} ,
\]

\[
\dot{D} = f_{C-D} \frac{C}{T_{C-D}} ,
\]

\[
\dot{R} = (1 - f_{H-C}) \frac{H}{T_{H-R}} + (1 - f_{C-D}) \frac{C}{T_{C-R}} ,
\]

\[
\dot{O} = (1 - f_{I-H}) \frac{I}{T_{1-O}} .
\]

Likelihood:

\[-\ln \mathcal{L} = - \sum_{\text{zones}} \sum_{\text{times}} \sum_{\mathcal{X}_i} \ln \text{Poisson} \left( \mathcal{X}_i \mid \text{Population}_{\text{zone} f \mathcal{X}_i} \right)\]

Zones:

- single department
- France as single zone
- 4-departments
- 8-departments
- 15 regions

Free parameters:

6 timescales over fractions

$R_0$ before confinement

$R_0$ during confinement

normalization of Infectious

$\rightarrow 6 + 3 N$ (zones)
Exposed (E)

It is advisable to incorporate an additional, non-contagious, incubation phase. We introduce the

\[ T \]

Replacing the rates by timescales, the equations of the SIHCDRO model become

\[ \text{The SIHCDRO model equations can be written} \]

**Analysis method**

**Likelihood:**
\[
-\ln \mathcal{L} = - \sum_{\text{zones}} \sum_{\text{times}} \sum_{\mathcal{X}_i} \ln \text{Poisson} \left( \mathcal{X}_i \mid \text{Population}_{\text{zone}} f(\mathcal{X}_i) \right)
\]

MCMC analysis: Python / **emcee**
flat log priors on (timescale-over-fraction)s
flat linear priors on \( R_0 \)
with \( R_0^\text{Confinement} < R_0^\text{Ini} \)
64+ walkers with 50 000+ steps (analysis on last 20%)
random uniform initial positions

**Zones:**
- single department
- France as single zone
- 4-departments
- 8-departments
- 15 regions

**Free parameters:**
- 6 timescales over fractions
- \( R_0 \) before confinement
- \( R_0 \) during confinement
normalization of Infectious
\[
\rightarrow 6 + 3 N \text{ (zones)}
\]

**Hospital data points in red**
Goodness-of-fit of model 1: SIHCDRO

France: $R_0^{init} = 1.40, R_0^{conf} = 1.06, I_{initial} = 5.6 \times 10^{-7}$

OK fit except for Critical-care arrivals
Goodness-of-fit of model 1: SIHCDRO

France

France: $R_0^{\text{initial}} = 1.40, R_0^{\text{confine}} = 1.06, I_{\text{initial}} = 5.6 \times 10^{-7}$

OK fit except for Critical-care arrivals

lockdown:
mean $R_0 = 1.95$
MLE $R_0 = 1.06$

pre-lockdown:
mean $R_0 = 4.36$

Do we need a better model?
model 2: SEIHCRO

model 1: SIHCDRO

Susceptible → Exposed → Infectious → Hospitalized

Other-recovered → Immunized → Released

Infectious

Hospitalized

Critical

Dead
model 2: SEIHCDRO

\[
\begin{align*}
\dot{S} &= -R_0 S \frac{I}{T_{I\rightarrow}} = -R_0 S \left[ \frac{f_{I\rightarrow H}}{T_{I\rightarrow H}} + \frac{(1 - f_{I\rightarrow H})}{T_{I\rightarrow O}} \right] I, \\
\dot{E} &= R_0 S \frac{I}{T_{I\rightarrow}} - f_{E\rightarrow I} \frac{E}{T_{E\rightarrow I}} = R_0 S \left[ \frac{f_{I\rightarrow H}}{T_{I\rightarrow H}} + \frac{(1 - f_{I\rightarrow H})}{T_{I\rightarrow O}} \right] I - f_{E\rightarrow I} \frac{E}{T_{E\rightarrow I}}, \\
\dot{I} &= f_{E\rightarrow I} \frac{E}{T_{E\rightarrow I}} - \frac{I}{T_{I\rightarrow}} = f_{E\rightarrow I} \frac{E}{T_{E\rightarrow I}} - \left[ \frac{f_{I\rightarrow H}}{T_{I\rightarrow H}} + \frac{(1 - f_{I\rightarrow H})}{T_{I\rightarrow O}} \right] I, \\
\dot{H} &= f_{I\rightarrow H} \frac{I}{T_{I\rightarrow H}} - f_{H\rightarrow C} \frac{H}{T_{H\rightarrow C}} - (1 - f_{H\rightarrow C}) \frac{H}{T_{H\rightarrow R}}, \\
\dot{C} &= f_{H\rightarrow C} \frac{H}{T_{H\rightarrow C}} - f_{C\rightarrow D} \frac{C}{T_{C\rightarrow D}} - (1 - f_{C\rightarrow D}) \frac{C}{T_{C\rightarrow R}}, \\
\dot{D} &= f_{C\rightarrow D} \frac{C}{T_{C\rightarrow D}}, \\
\dot{R} &= (1 - f_{H\rightarrow C}) \frac{H}{T_{H\rightarrow R}} + (1 - f_{C\rightarrow D}) \frac{C}{T_{C\rightarrow R}}, \\
\dot{O} &= (1 - f_{I\rightarrow H}) \frac{I}{T_{I\rightarrow O}}.
\end{align*}
\]

\(2.4 \text{ The SEAFHCDRO model}

We generalize the SEIFHCDRO model by splitting the Infectious stage into Asymptomatic and Feverish phases, where the Feverish people do not contaminate the Susceptibles, because they don't leave their dwelling.

Susceptibles (S)
People who may catch the virus infection, without being immune to it.

Exposed (E)
People who have been exposed to the virus without having become infectious.

Asymptomatic (A)
People who are in an infectious stage, but with no symptoms.

Feverish (F)
People who show COVID-19 symptoms, but have not been hospitalized.

Hospitalized (H)
People who are treated for COVID-19 in hospitals, but are not in the critical care.

Critical (C)
People who are in a critical care at a hospital.

Dead (D)
People who died of COVID-19 at a hospital.

Released (R)
People who have been released from a hospital for COVID-19 treatment.

Others (O)
People who have recovered from the virus, without having passed through a hospital.

\[8a\] \[8b\] \[8c\] \[8d\] \[8e\] \[8f\] \[8g\] \[8h\] no more \(R_0 S - 1\) term!
model 2: SEIHCDRO

\[ \begin{align*}
\dot{S} &= -R_0 S \frac{I}{T_{1\to}} = -R_0 S \left[ \frac{f_{I\to H}}{T_{I\to H}} + \frac{(1 - f_{I\to H})}{T_{I\to O}} \right] I, \\
\dot{E} &= R_0 S \frac{I}{T_{1\to}} - f_{E\to I} E \frac{E}{T_{E\to I}} = R_0 S \left[ \frac{f_{I\to H}}{T_{I\to H}} + \frac{(1 - f_{I\to H})}{T_{I\to O}} \right] I - f_{E\to I} \frac{E}{T_{E\to I}}, \\
\dot{I} &= f_{E\to I} E \frac{E}{T_{E\to I}} - \frac{I}{T_{1\to}} = f_{E\to I} E \frac{E}{T_{E\to I}} - \left[ \frac{f_{I\to H}}{T_{I\to H}} + \frac{(1 - f_{I\to H})}{T_{I\to O}} \right] I, \\
\dot{H} &= f_{I\to H} \frac{I}{T_{I\to H}} - f_{H\to C} \frac{H}{T_{H\to C}} - (1 - f_{H\to C}) \frac{H}{T_{H\to R}}, \\
\dot{C} &= f_{H\to C} \frac{H}{T_{H\to C}} - f_{C\to D} \frac{C}{T_{C\to D}} - (1 - f_{C\to D}) \frac{C}{T_{C\to R}}, \\
\dot{D} &= f_{C\to D} \frac{C}{T_{C\to D}}, \\
\dot{R} &= (1 - f_{H\to C}) \frac{H}{T_{H\to R}} + (1 - f_{C\to D}) \frac{C}{T_{C\to R}}, \\
\dot{O} &= (1 - f_{I\to H}) \frac{I}{T_{I\to O}}.
\end{align*} \]

Free parameters:
7 timescales over fractions
\( R_0 \) before confinement
\( R_0 \) during confinement
normalization of Infectious
\( \rightarrow 7 + 3 N \text{ (zones)} \)

Susceptible → Exposed → Infectious → Hospitalized
Other-recovered → Immunized → Released

Infectious
Critical → Dead

Susceptible
People who may catch the virus infection, without being immune to it.
Exposed
People who have been exposed to the virus without having become infectious.
Asymptomatic
People who are in an infectious stage, but with no symptoms.
Feverish
People who show COVID-19 symptoms, but have not been hospitalized.
Hospitalized
People who are treated for COVID-19 in hospitals, but are not in the critical care.
Critical
People who are in a critical care at a hospital.
Dead
People who died of COVID-19 at a hospital.
Released
People who have been released from a hospital for COVID-19 treatment.
Others
People who have recovered from the virus, without having passed through a hospital.
SEIHCDRO model (2) ctd.

single-France fits worse, but 8-department model fits (significantly) better
Problem with model or with data?
Problem with model or with data?

Cannot fit Critical-arrivals: lack of critical-care beds in Haut-Rhin?

Gary Mamon, Modeling the evolution of COVID-19 in France, 5 May 2020, IAP - Journal Club équipe Univers
### Model 2: lockdown is working!

**Before lockdown:**

- Mean: 6.00
- Allowed max: 6

**During lockdown:**

- Mean: 0.2

### Graphs

- **$R_0^{\text{ini}}$ (France):**
  - Mean = allowed max = 6

- **$R_0^{\text{confine}}$ (France):**
  - Mean = 0.2

### Tables

<table>
<thead>
<tr>
<th>$R_0^{\text{ini}}$ (France)</th>
<th>Mean</th>
<th>Allowed Max</th>
</tr>
</thead>
<tbody>
<tr>
<td>75</td>
<td>5.7</td>
<td></td>
</tr>
<tr>
<td>68</td>
<td>4.8</td>
<td></td>
</tr>
<tr>
<td>13</td>
<td>5.4</td>
<td></td>
</tr>
<tr>
<td>23</td>
<td>3.5</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>$R_0^{\text{confine}}$ (France)</th>
<th>Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>75</td>
<td>0.4</td>
</tr>
<tr>
<td>68</td>
<td>0.2</td>
</tr>
<tr>
<td>13</td>
<td>0.7</td>
</tr>
<tr>
<td>23</td>
<td>1.0</td>
</tr>
</tbody>
</table>

---

Model 2: *lockdown is working!*

**before lockdown**

- $R_0^{\text{Ini}}$ (France)
  - Mean: 6.00
  - Allowed max: 6

**during lockdown**

- $R_0^{\text{Confine}}$ (France)
  - Mean: 0.2

**except in rural areas!**

- $R_0^{\text{Confine}}$ (France)
  - Mean: 0.42
  - Allowed max: 6
The SEAFHCDRO model involves a single exponential pdf for the duration of the Infectious phase, in more complex models, transition functions (pdfs) for the durations of the phases (besides S, E, and I). But while the SIR model as those in the Released and Other phases that are not Infectious.

The Immunized group of people as those that are either in the Exposed or Neutralized phases, as well as those in the Released and Other phases, and some branching fractions finish with letter I for Infectious. Moreover, I define chemical branching ratios. For example, a Feverish person can either end up Hospitalized, or may return to the Asymptomatic phase, or may be released. People in the Exposed phase can either move to the Asymptomatic or the Feverish phase, or may die. The critical care has two possible evolutionary paths, shown by arrows in Fig. 1. These are the analogs to critical care and Other categories.

\[ \dot{S} = -R_0 S \frac{A}{T_A} = -R_0 S \left[ \frac{f_{A \to F}}{T_{A \to F}} + \frac{(1 - f_{A \to F})}{T_{A \to O}} \right] A, \]
\[ \dot{E} = R_0 S \frac{A}{T_A} - f_{E \to A} \frac{E}{T_{E \to A}} = R_0 S \left[ \frac{f_{A \to F}}{T_{A \to F}} + \frac{(1 - f_{A \to F})}{T_{A \to O}} \right] A - f_{E \to A} \frac{E}{T_{E \to A}}, \]
\[ \dot{A} = f_{E \to A} \frac{E}{T_{E \to A}} - \frac{A}{T_A} = f_{E \to A} \frac{E}{T_{E \to A}} - \left[ \frac{f_{A \to F}}{T_{A \to F}} + \frac{(1 - f_{A \to F})}{T_{A \to O}} \right] A, \]
\[ \dot{F} = f_{A \to F} \frac{A}{T_{A \to F}} - f_{F \to H} \frac{F}{T_{F \to H}} - (1 - f_{F \to H}) \frac{F}{T_{F \to O}}, \]
\[ \dot{H} = f_{F \to H} \frac{F}{T_{F \to H}} - f_{H \to C} \frac{H}{T_{H \to C}} - (1 - f_{H \to C}) \frac{H}{T_{H \to R}}, \]
\[ \dot{C} = f_{H \to C} \frac{H}{T_{H \to C}} - f_{C \to D} \frac{C}{T_{C \to D}} - (1 - f_{C \to D}) \frac{C}{T_{C \to R}}, \]
\[ \dot{D} = f_{C \to D} \frac{C}{T_{C \to D}}, \]
\[ \dot{R} = (1 - f_{H \to C}) \frac{H}{T_{H \to R}} + (1 - f_{C \to D}) \frac{C}{T_{C \to R}}, \]
\[ \dot{O} = (1 - f_{A \to F}) \frac{I}{T_{A \to O}} + (1 - f_{F \to H}) \frac{F}{T_{F \to O}}. \]

Free parameters: 8 timescales over fractions
\( R_0 \) before confinement
\( R_0 \) during confinement
normalization of Infectious phases
\[ \rightarrow 8 + 3 N \text{ (zones)} \]
9-phase evolution

Gary Mamon, Modeling the evolution of COVID-19 in France, 5 May 2020, IAP - Journal Club équipe Univers
Model 3: goodness of fits

France: \( R_{\text{initial}} = 4.25, R_0^{\text{confine}} = 0.00, A_{\text{initial}} = 0.00013 \)

Paris: \( R_{\text{initial}} = 4.50, R_0^{\text{confine}} = 0.52, A_{\text{initial}} = 2.8 \times 10^{-5} \)

model 3 also fails to fit Critical-care arrivals in 8-zone model
Model 3: goodness of fits

model 3 also fails to fit Critical-care arrivals

“we learned alot and now send fewer hospitalized to critical care”
Model 3 fits data better than other 2

<table>
<thead>
<tr>
<th>BIC evidence (lower = better)</th>
<th>Model 1: SIHCDRO</th>
<th>Model 2: SEIHCDRO</th>
<th>Model 3: SEAFHCDRO</th>
</tr>
</thead>
<tbody>
<tr>
<td>France</td>
<td>20976</td>
<td>22905</td>
<td>20074</td>
</tr>
<tr>
<td>4-zone</td>
<td>9102</td>
<td>8403</td>
<td>8134</td>
</tr>
<tr>
<td>8-zone</td>
<td>13849</td>
<td>13211</td>
<td>12627</td>
</tr>
</tbody>
</table>
~ same $R_0$ factors with model 3

<table>
<thead>
<tr>
<th>Region</th>
<th>ini (±0.6)</th>
<th>conf (±0.06)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Paris</td>
<td>4.1</td>
<td>0.65</td>
</tr>
<tr>
<td>Paris-Petite-Ceinture</td>
<td>3.3</td>
<td>0.70</td>
</tr>
<tr>
<td>Paris-Grande-Ceinture</td>
<td>2.1</td>
<td>0.75</td>
</tr>
<tr>
<td>Auvergne-Rhône-Alpes</td>
<td>3.0</td>
<td>0.65</td>
</tr>
<tr>
<td>Bourgogne-Franche-Comté</td>
<td>1.9</td>
<td>0.75</td>
</tr>
<tr>
<td>Bretagne</td>
<td>3.6</td>
<td>0.65</td>
</tr>
<tr>
<td>Centre-Val de Loire</td>
<td>5.6</td>
<td>0.80</td>
</tr>
<tr>
<td>Corse</td>
<td>5.0</td>
<td>0.10</td>
</tr>
<tr>
<td>Grand Est</td>
<td>2.9</td>
<td>0.60</td>
</tr>
<tr>
<td>Hauts-de-France</td>
<td>4.9</td>
<td>0.70</td>
</tr>
<tr>
<td>Normandie</td>
<td>2.0</td>
<td>0.55</td>
</tr>
<tr>
<td>Nouvelle-Aquitaine</td>
<td>3.1</td>
<td>0.60</td>
</tr>
<tr>
<td>Occitanie</td>
<td>3.4</td>
<td>0.60</td>
</tr>
<tr>
<td>Pays de la Loire</td>
<td>3.9</td>
<td>0.55</td>
</tr>
<tr>
<td>Provence-Alpes-Côte d’Azur</td>
<td>2.8</td>
<td>0.80</td>
</tr>
<tr>
<td><strong>Average France</strong></td>
<td><strong>3.3</strong></td>
<td><strong>0.65</strong></td>
</tr>
</tbody>
</table>
Marginal distributions of timescales-over-fractions

**single-zone France**

- $T_{E,A}/f_{OSA}$ [d] with mean = 6.4d
- $T_{A,R}/f_{AR}$ [d] with mean = 10.0d
- $T_{F,H}/f_{FH}$ [d] with mean = 35.9d
- $T_{H,C}/f_{HOC}$ [d] with mean = 28.9d
- $T_{C,D}/f_{COD}$ [d] with mean = 1.0d
- $T_{R,A}/(1 - f_{RAD})$ [d] with mean = 8.7d
- $T_{C,H}/f_{COD}$ [d] with mean = 78.6d
- $T_{C,R}/(1 - f_{COD})$ [d] with mean = 23.4d
- $T_{F,A}/(1 - f_{FAO})$ [d] with mean = 31.5d
- $T_{F,R}/(1 - f_{FRO})$ [d] with mean = 7.6d

**8 departments**

- $T_{E,A}/f_{OSA}$ [d] with mean = 4.8d
- $T_{A,R}/f_{AR}$ [d] with mean = 4.4d
- $T_{F,H}/f_{FH}$ [d] with mean = 9.4d
- $T_{H,C}/f_{HOC}$ [d] with mean = 29.1d
- $T_{C,D}/f_{COD}$ [d] with mean = 1.3d
- $T_{R,A}/(1 - f_{RAD})$ [d] with mean = 9.3d
- $T_{C,H}/f_{COD}$ [d] with mean = 50.0d
- $T_{C,R}/(1 - f_{COD})$ [d] with mean = 7.6d
- $T_{F,A}/(1 - f_{FAO})$ [d] with mean = 50.0d
- $T_{F,R}/(1 - f_{FRO})$ [d] with mean = 23.3d

**15 regions**

- $T_{E,A}/f_{OSA}$ [d] with mean = 5.0d
- $T_{A,R}/f_{AR}$ [d] with mean = 5.0d
- $T_{F,H}/f_{FH}$ [d] with mean = 12.6d
- $T_{H,C}/f_{HOC}$ [d] with mean = 23.7d
- $T_{C,D}/f_{COD}$ [d] with mean = 1.7d
- $T_{R,A}/(1 - f_{RAD})$ [d] with mean = 7.9d
- $T_{C,H}/f_{COD}$ [d] with mean = 10.5d
- $T_{C,R}/(1 - f_{COD})$ [d] with mean = 1.0d
- $T_{F,A}/(1 - f_{FAO})$ [d] with mean = 7.9d
- $T_{F,R}/(1 - f_{FRO})$ [d] with mean = 65.6d
Marginal distributions of timescales-over-fractions

single-zone France

8 departments

15 regions

incubation time < 5-6 days
Predictions

Use marginal distributions & re-solve differential equations
How many would have \textit{died} without the lockdown?

- **single-zone France**
- **Paris in 8-zone model**

17 March lockdown
How many would have died without the lockdown?

**single-zone France**

$R_0 = 4.3 \pm 0.1$

6±3% $\Rightarrow$ 3±1.5 million over France!

**Paris in 8-zone model**

$R_0 = 4.7 \pm 0.4$

Effects of lockdown on deaths: ~12 days later
Fraction of immunized people on May 11

single-zone France

Paris in 8-zone model

< 2% (95% c.l.)

< 4% (95% c.l.)

2nd wave is very possible!

Post May-11 evolution

For single-zone France:

- $R_0 = 0.5$
- $R_0 = 1$
- $R_0 = 2$

For Paris in 8 departments:

- $R_0 = 0.5$
- $R_0 = 1$
- $R_0 = 2$

**must re-lockdown in mid-June!**
Better model?
Better model?

Branching fraction $f_{H \rightarrow C}$ decreases with time
Better model?

Branching fraction $f_{H \to C}$ decreases with time

Better model?

Branching fraction $f_{H\rightarrow C}$ decreases with time

**SEAFHCDRON**

Better data!

- Random testing of 1000 people every week
  $\rightarrow$ S, E-O(N), A, F, vs time
- Data on anonymous hospitalized people with durations
  both: saved to data.gouv.fr

Conclusions

Modeling

SIR etc. models can be extended to account for hospital arrivals & departures
Extended SIR models are too simple
Extended SEIR models are somewhat better
SEAFDRO model has highest Bayesian evidence
Multi-zone preferable to single-zone

Results

The national lockdown is working!
$R_0$ has diminished from $\approx 3.5$ before lockdown to 0 (single-region-France) or 0.6 (15-regions)
Without the lockdown, France would have suffered 2+ million deaths
(less with improvised social-distancing)
< 2% of the French will be immunized on May 11
⇒ A 2nd wave is possible if $R_0 > 1$
In pessimistic scenario ($R_0=2$), we need to re-lockdown before mid June

Strategy

Random testing of 1000 people every week or less $\rightarrow$ data.gouv.fr
Data on anonymous individuals in hospitals $\rightarrow$ data.gouv.fr