Comparing forecast performance on different synthetic pandemics

Sous-titre du Rapport

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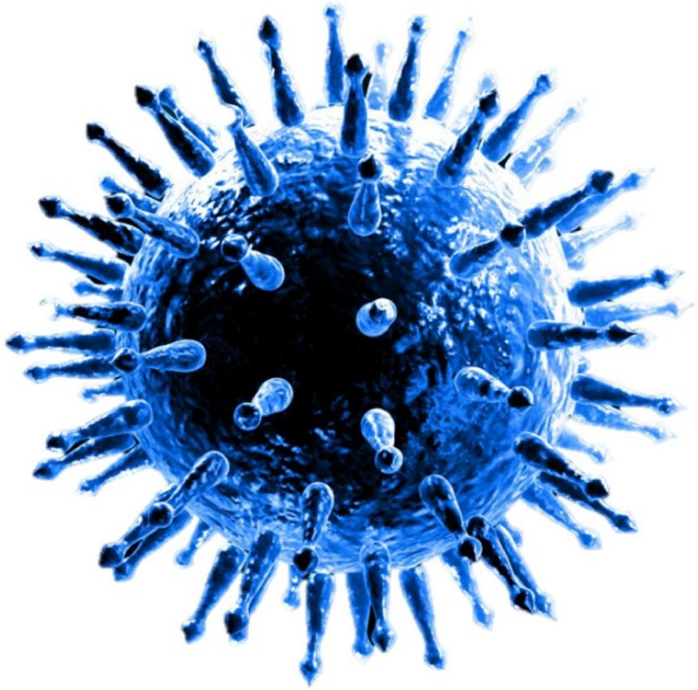
Internship at
Chalmers University



Under the supervision of
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Contents

1 Plagiarism integrity statement

By this statement, I declare that the content of this work is fully original and has not been copied. Some previous results have been used, and they are always explicitely cited. Moreover, the work presented in this report led to a publication. Some parts of this report are directly taken from this publication, as they referred to the exact same work and results. Those parts were fully written by me, and present results based only on my personal work.

2 Introduction

The recent outbreak of COVID-19 has enlighted the importance of accurate forecasting models, for policymakers and population alike. The number of hospitalized has shown to be a key indicator in the last pandemic, as maintaining the number of hospitalized individuals below the capacity of the healthcare system was a major concern. Predicting the trajectory of a pandemic is a complex task, considering the number of parameters that have an influence on the outbreak. I will relate in this report the work that was done during an research internship of 16 weeks in Chalmers, whose goal was to develop predictive models and assess their performance on a set of diverse pandemics. The elaboration of the set of pandemic was also an important part of the work.

I implemented 13 individual models and an ensemble model to forecast the number of hospitalizations 7 and 14 days ahead, given the data up to the current day. These models are divided into two categories: those trained only on hospitalization data and those incorporating additional time-series such as mobility data and the number of infected agents. The individual models are: variations of the SIRH (Susceptible, Infected, Recovered, Hospitalized) model, ARIMA, VAR, moving average, exponential regressions, bayesian and linear regressors.

A complex agent-based model was used to simulate pandemics of a wide diversity. By varying key parameters and using different mobility patterns, I created a diverse set of 324 synthetic pandemic scenarios (consisting into daily reports of key quantities). This diversity allows for a robust evaluation of the models across various conditions.

The models were trained and tested on many points of these pandemics, allowing for a consistent analysis of their performance. Additionally, I classified the points in the pandemic trajectories based on the reproductive number to understand model performance at different phases of the pandemic.

This paper aims to determine the most consistent and reliable models for forecasting hospitalizations during pandemics, at different phases of the outbreak. These prediction are not spatial or biological predictions, but forecasts of time series representing the evolution of key values in an area (number of hospitalized, of deaths...). By analyzing the performance of various models across a wide range of synthetic pandemic scenarios, the objective is to provide insights that can guide the selection and development of predictive models for real-world applications. The findings of this internship highlight the strengths and weaknesses of different modeling approaches and underscore the value of ensemble models in achieving robust and accurate predictions.

The simulations that are described in this report and lead to all the figures presented below are available on this GitHub Repository.

3 Literature review and objectives

3.1 Literature review

The literature of pandemic forecastings is well documented, as many studies have been conducted during the outbreak of Covid 19. The huge amount of article published makes it difficult to identify relevant articles with interesting results. The first part of the internship was dedicated

to the analysis of the literature, to find useful ideas for the project, such as models, methods or clever ways to present the results. I found that early predictions on the number of cases (such as [4]) almost overestimated the real spread of the virus, and aknowledge the difficulty to estimate the impacts of governments strategies to mitigate the outbreak.

Some model performances were pointed out. Indeed, the autoregressive models such as the Arima model seem to outperform the other model in short-terms predictions ([10] and [16]), whereas compartemental models such as the SIR model are more performant for long term predictions ([13]).

Many article about the ensemble models were found ([2], [14], [7]). The ensemble models aggregate the predictions of many models, and output a function of these predictions. It can be simple functions (such as median), our more complexe ones such as stacking (as it is done in [14]) or linear opinion pool (see [7]). These studies all enhance the following results : the ensemble models are rarely the best, but never the last. Indeed, when compared to individuals models, the ensemble models seems very consistent in their predictions, and their distribution of ranking among the other models is very little scattered.

Many papers on the variations of SIR model were found ([5], [8], [17]) If this simple model does not manage to catch the complexity of an outbreak, some variations can have very good results. For instance, in [5], the authors manage to find a strong correlation between the mobility data and the number of cases, with a three weeks lag.

Other interesting results were also pointed out. For instance, [8] pointed out the relevance of testing to estimate the proportions of infected. [17] focused on ICU occupancy for its predictive model, which is a key variable to monitor.

3.2 Objectives

After this review, a general direction was taken. It was decided to implement some simple models (Arima, SIR, exponential regression...) to compare their performances on a wide range of pandemics. Indeed, the models that were found in the literature were often tested on a single pandemic, which might lead to a bias in the results and could limit their generalization.

4 Generating diverse pandemics

To be able to compare the performances of the models, one need pandemic data to compare them. As the objective was to obtain the most consistent results, I decided not to train and compare the models on real data as this data is limited and biaised: the results would not have been relevant when facing a new pandemic. All the simulations in this paper are made on a fixed population of 10^6 agents.

4.1 Covasim

To generate the pandemics, Covasim [9], a python library that can simulate the evolution of a pandemic, was used. Covasim is an agent-based model that can simulate the spread of a pandemic in a population. This model takes as an input many parameters such as the population type, the population size, the age repartition... and outputs a complete description of the pandemic,

with real-time values of each relevant piece of information, such as the number of severe, of asymptomatic... but also physical values such as the value of the reproduction number. Covasim enables to generate a huge diversity of pandemics, thanks to the plurality of parameters that can be given as input to the model, but also with interventions that can be planned by the users. These interventions can help to assess the impact of a vaccination campaign, or lockdown scenarios. They represent relatives changes in the probabilities of transmission. Covasim was used by policymakers during the Covid 19 outbreak to adapt their strategies of mitigation, for instance in Australia,Vietnam, India and United States ([9]).

4.2 First pandemics

For the implementation and the first tests of the models, two pandemics were generated. The first one focusing on the new deaths count and the second one focusing on the number of hospitalized count. I quickly decided to move to the second pandemic, as the variable 'new deaths' is neither relevant nor continuous (which caused problems in the implementation of some models, namely SIRH models).

The different interventions were based on mobility reports from Västtrafik (see appendix 7), the public transport company of the city of Gothenburg. They were reported during the Covid 19 pandemic and have been retrieved in [5]. These interventions correspond to 53 relative weekly variations of the mobility, with a reference value of 1 for the first week of the report, which correspond to the 9-th week of 2020.

4.3 Generating diverse pandemics

In order to evaluate the performances of my models on a wide range of pandemics, a training set of pandemics was generated. A huge diversity of pandemics is needed to determine the most consistent model. It is so relevant to identify the key parameters that generate this diversity. As Covasim has a very huge set of inputs parameters, a first subset of key parameters was identified: the spread parameters and the severity parameters. The severity parameters are the 4 parameters that correspond to the probability for an agent to get from a compartment to another (for instance from infected to crictical). The spread parameters are 9 parameters that represent the distribution of probability of the time spend by an agent in a compartment (such as infected, crictical...) once he entered it. This set of 13 parameters is then noted as S. This distribution is a log-normal distribution, but the spread-parameters correspond to the mean of this log-normal distribution All the parameters have a default value of 1, which corresponds to keeping the reference value. I decided to select 4 parameters and to make them vary in $[0.5, 1, 2]$, leading to a set of 81 pandemics. To select the 4 parameters that generated the most diversity, different diversity metrics were computed.

Let Y_1 , $Y_2 \in \mathbb{R}^n$ be two time series of n days representing the number of hospitalized in two pandemics, and Y' and Y'' the first and second derivatives of Y.

Let :

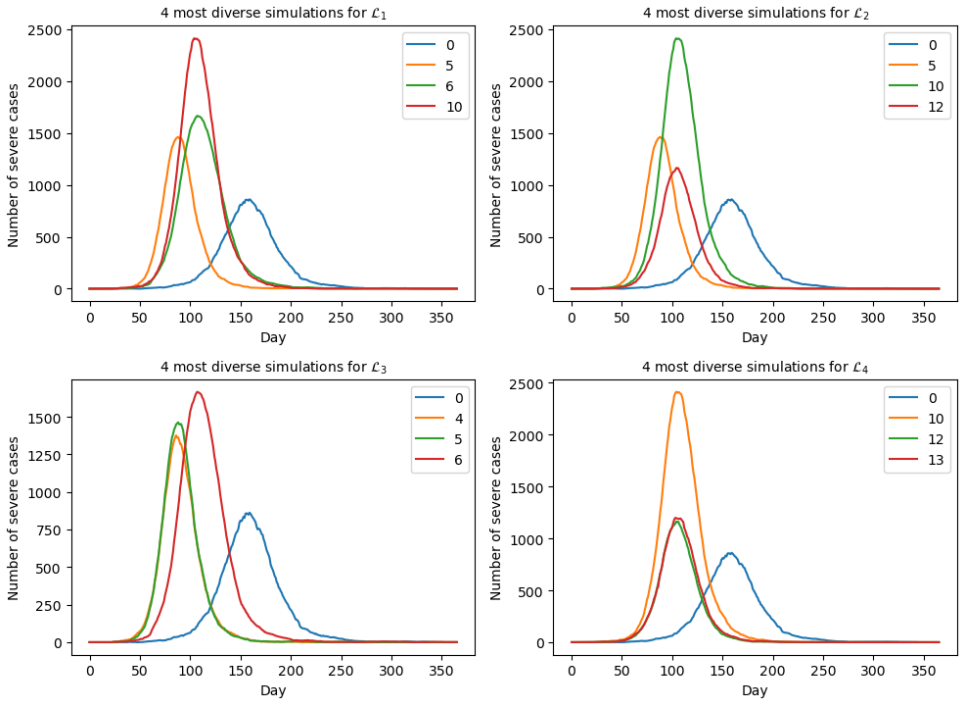


Figure 1: 4 most diverse pandemics according to each norm.

$\mathcal{L}_1(Y_1, Y_2) = \|Y_1 - Y_2\|_{L_1}$

$\mathcal{L}_2(Y_1, Y_2) = \|(\frac{max(Y_1)}{max(Y_2)}; \frac{max(Y_1')}{max(Y_2')}; \frac{max(Y_1'')}{max(Y_2'')}, \|\tilde{Y_1} - \tilde{Y_2}\|_{L_1}, \|\tilde{Y_1'} - \tilde{Y_2'}\|_{L_1}, \|\tilde{Y_1''} - \tilde{Y_2''}\|_{L_1})\|_{L_2}$

$\mathcal{L}_3 = \mathcal{W}(\tilde{Y_1} - \tilde{Y_2})$, with $\mathcal{W}$ the Wasserstein distance.

$\mathcal{L}_4(Y_1, Y_2) = \|(\frac{max(Y_1)}{max(Y_2)}; \frac{max(Y_1')}{max(Y_2')}; \frac{max(Y_1'')}{max(Y_2'')}, \mathcal{W}(\tilde{Y_1} - \tilde{Y_2}), \mathcal{W}(\tilde{Y_1'} - \tilde{Y_2'}), \mathcal{W}(\tilde{Y_1''} - \tilde{Y_2''}))\|_{L_2}$

To determine which measure to use, I generated 14 pandemics. Each pandemic but the last one has default parameters except one of them which was doubled. The last pandemic has only default parameters.

For each norm $\mathcal{L}_k$, I determined s, the subset of 4 pandemics that maximized the following quantity:

$$\mathcal{L}_k(S) = \sum_{i,j \in s, i \neq j} \mathcal{L}_k(Y_i, Y_j)$$

The 4 most diverse pandemics (in the subset of 14 pandemics generated) according to each norm are shown in the Fig.1. As "diversity" is not countable, a human choice was necessary to choose the most relevant norm. According to Fig. 1, I decided to select $\mathcal{L}_2$. But, keeping the parameters `[0, 5, 10, 12]` would not be accurate, as the parameters were changed independently, and the diversity did not take into account the correlation between some of them.

Finding the parameters that maximise the $\mathcal{L}_2$ diversity is equivalent to solve the following problem :

$s_{opt} = \underset{s \subset S, |s|=4}{argmax} \mathcal{L}(s)$, with $\mathcal{L}(s) = \sum_{p_1,p_2 \in \mathcal{P}_g(s)} \mathcal{L}_2(p_1, p_2)$, and $\mathcal{P}_g(s)$ the set of the 81 pandemics generated with the 4 parameters of s.

However, generating a pandemic with `Covasim` is time consuming, and it is not possible to compute the diversity of each set of 4 parameters s included in S (the set of all 13 parameters).

A MCMC algorithm [3] was then implemented, to perform a clever grid search on the different subsets $s \subset S$ of parameters. The MCMC algorithm is a method which is used to sample from a distribution that can't be directly sampled. The main idea is to construct a Markov Chain whose stationary distribution is the objective distribution.

Let $\mathcal{S} = \{s \subset S; |s| = 4\}$ be the support of the target distribution, which is, in our case, the set of all the 715 combinations of the 4 parameters among the 13 different possible, and let π be the target distribution on $\mathcal{S}$. $\forall s \in \mathcal{S}, \pi(s) = \frac{\mathcal{L}(s)}{\sum_{s \in \mathcal{S}} \mathcal{L}(s)}$. π is not directly computable as it is too time consuming to compute the denominator. We suppose that $\forall s \in \mathcal{S}, \mathcal{L}(s) > 0$. It is a reasonable assumption, as $\mathcal{L}(s) = 0$ means that the 81 pandemics generated are strictly identical.

For each $s = [a, b, c, d] \in \mathcal{S}$, let $ne(s)$ be the set of the neighbours of s, i.e the set of all the elements of $\mathcal{S}$ who have only one parameter different from s. For instance, $[0, 3, 9, 12] \in ne([0, 3, 10, 12])$, but $[0, 3, 9, 12] \notin ne([0, 3, 8, 10])$.

Let U_n be a sequence of independent uniform random variables on $[0, 1]$ and $\forall s \in \mathcal{S}$, let $U_n^{ne(s)}$ be a sequence of independent uniform random variables on $ne(s)$. Let $s_0 \in \mathcal{S}$ and let S_n be the random sequence defined as follow :

$$\begin{cases} S_0 = s_0 \\ \forall n \in \mathbb{N}, \alpha_n = \dfrac{\mathcal{L}(U_n^{ne(S_n)})}{\mathcal{L}(S_n)} \\ \forall n \in \mathbb{N}, S_{n+1} = U_n^{ne(S_n)} \mathbb{1}_{\{U_n < \alpha_n\}} + S_n \mathbb{1}_{\{U_n > \alpha_n\}} \end{cases}$$

This formula means that at each iteration, a neighbourgh of S_n is uniformly selected among all the neighbours of S_n (it is $U_n^{ne(S_n)}$). The Markov Chain moves to this neighbourgh if the value of $\mathcal{L}(U_n^{ne(S_n)})$ is higher than the value of the function $\mathcal{L}(S_n)$ at the current state. If the new value of $\mathcal{L}$ is smaller, the Markov Chain moves with a probability that is equal to the ratio of the two values. This way of moving on the different subsets prevents to be stucked in a local maxima but avoids exploring dummies areas, in which the diversity is very small.
As S_{n+1} is a function of S_n and of other independent random variables, the sequence S_n is a homogenous Markov Chain.

The transition matrix of this Markov Chain is the following:

$$K(s,s') : \begin{cases} 0 \text{ if } s' \notin ne(s) \text{ and } s' \neq s \\ \dfrac{1}{Card(ne(s))} = \dfrac{1}{36} \text{ if } s' \in ne(s) \text{ and } \dfrac{\mathcal{L}(s')}{\mathcal{L}(s)} > 1 \text{ and } s' \neq s \\ \dfrac{1}{36} \times \dfrac{\mathcal{L}(s')}{\mathcal{L}(s)} \text{ if } s' \in ne(s) \text{ and } \dfrac{\mathcal{L}(s')}{\mathcal{L}(s)} \leq 1 \text{ and } s' \neq s \\ 1 - \displaystyle\sum_{s' \in \mathcal{S}, s' \neq s} K(s,s') \text{ if } s' = s \end{cases}$$

Let $(s,s') \in \mathcal{S}^2$. Let us suppose that $s' \neq s$, that $s' \in ne(s)$, and that $\mathcal{L}(s) < \mathcal{L}(s')$ (the other case is symmetric).

$$\begin{aligned} \pi(s)K(s,s') &= \frac{\mathcal{L}(s)}{\sum_{s \in \mathcal{S}} \mathcal{L}(s)} \times \frac{1}{36} \quad \text{as } \mathcal{L}(s) < \mathcal{L}(s') \\ &= \frac{\mathcal{L}(s)}{\sum_{s \in \mathcal{S}} \mathcal{L}(s)} \times \frac{1}{36} \times \frac{\mathcal{L}(s')}{\mathcal{L}(s')} \\ &= \frac{\mathcal{L}(s')}{\sum_{s \in \mathcal{S}} \mathcal{L}(s)} \times \frac{1}{36} \times \frac{\mathcal{L}(s)}{\mathcal{L}(s')} \\ &= \pi(s')K(s',s) \end{aligned}$$

Indeed, each subset s has 36 neighbourgh, as there are 13 parameters and one can replace each parameter of s by any of the 9 others.

If $s' \notin ne(s)$, then $s \notin ne(s')$ and $K(s,s') = 0$. We directly have $\pi(s)K(s,s') = 0 = \pi(s')K(s',s)$.

Thus, π is **reversible** for K.

Let $(s,s') \in \mathcal{S}^2$. Let us note (a,b,c,d) and (a',b',c',d') the elements of s and s'. We note :
$s_1 = [a',b,c,d]$
$s_2 = [a',b',c,d]$
$s_3 = [a',b',c',d]$

$$
\begin{aligned}
\mathbb{P}(S_{n+4} = s' | S_n = s) &\geqslant \mathbb{P}(S_{n+4} = s' \cap S_{n+3} = s_3 \cap S_{n+2} = s_2 \cap S_{n+1} = s_1 | S_n = s) \\
&\geqslant \mathbb{P}(S_{n+4} = s' | S_{n+3} = s_3 \cap S_{n+2} = s_2 \cap S_{n+1} = s_1 \cap S_n = s) \\
&\qquad \times \mathbb{P}(S_{n+3} = s_3 \cap S_{n+2} = s_2 \cap S_{n+1} = s_1 | S_n = s) \text{ (Baye' s Formula)} \\
&\geqslant \mathbb{P}(S_{n+4} = s' | S_{n+3} = s_3) \\
&\qquad \times \mathbb{P}(S_{n+3} = s_3 \cap S_{n+2} = s_2 \cap S_{n+1} = s_1 | S_n = s) \text{ (by Markov's property)} \\
&\vdots \\
&\geqslant \mathbb{P}(S_{n+4} = s' | S_{n+3} = s_3) \times \mathbb{P}(S_{n+3} = s_3 | S_{n+2} = s_2) \times \mathbb{P}(S_{n+2} = s_2 | S_{n+1} = s_1) \\
&\qquad \times \mathbb{P}(S_{n+1} = s_1 | S_n = s) \text{ (by Markov's property)} \\
&\geqslant (\frac{1}{36})^4 \times min(1, \frac{\mathcal{L}(s')}{\mathcal{L}(s)}) \times min(1, \frac{\mathcal{L}(s_3)}{\mathcal{L}(s_2)}) \times min(1, \frac{\mathcal{L}(s_2)}{\mathcal{L}(s_1)}) \times min(1, \frac{\mathcal{L}(s_1)}{\mathcal{L}(s)}) \\
&> 0
\end{aligned}
$$

Thus, S_n is **irreducible**.

A Markov chain of transition matrix P on the support $\mathcal{S}$ is said to be *aperiodic* if:
$\forall s \in \mathcal{S}, \forall s' \in \mathcal{S}, \exists N \in \mathbb{N},$ s.t $\forall n > N, P(s, s')^n > 0$ [1]

First, note that $\forall s \in \mathcal{S}$, s is a local minimum (i.e if $\forall s' \in ne(s), \mathcal{L}(s') > \mathcal{L}(s)$) if and only if $K(s, s) = 0$

Thus, if s is not a local minimum, then $K(s, s) > 0$. Moreover, $\forall s \in \mathcal{S}, \forall s' \in ne(s)$, if $s \neq s'$, then $K(s, s') \neq 0$

Let $(s, s') \in \mathcal{S}^2$.

- If s' is not a local minimum,
  $\forall n > 4, \mathbb{P}(S_n = s' | S_0 = s) \geqslant \mathbb{P}(S_4 = s' | S_0 = s) \times K(s', s')^{n-4} > 0$

- If s' is a local minimum, $\forall s^* \in ne(s')$, s^* is not a local minimum and $K(s^*, s^*) \neq 0$.
  $\forall n > 5, \mathbb{P}(S_n = s' | S_0 = s) \geqslant \mathbb{P}(S_3 = s^* | S_0 = s) \times K(s^*, s^*)^{n-4} \times K(s^*, s') > 0$

Thus S_n is an **aperiodic** Markov Chain.

Finally, according to the **Theorem 5.5** from [1], as S_n is irreducible and aperiodic, as π is the stationary distribution, and as $\mathcal{S}$ is countable, S_n converges in distribution to π.

The most probable set that will be sampled by S_n is the one that maximises the diversity. I implemented this MCMC algorithm to maximise $\mathcal{L}_2$ on $\mathcal{S}$. The first value of the sequence was a clever starting point: the four parameters that maximized $\mathcal{L}_2$ on the 14 pandemics generated earlier (Fig.1). After 200 iterations, the set of parameters that maximised the diversity was `[2, 4, 9, 10]` , which correspond to the parameters `[sym2sev, asym2rec, rel_symp_prob,`

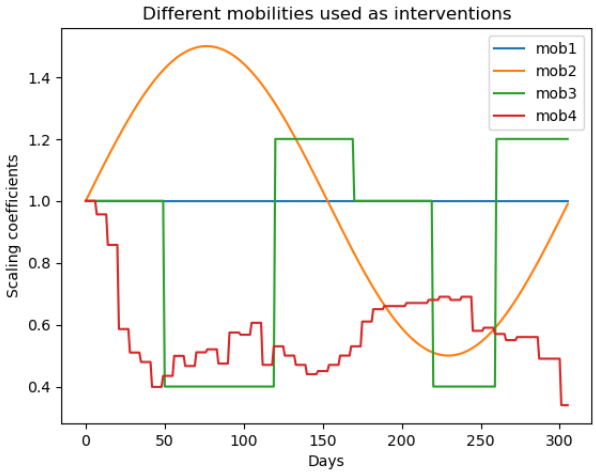


Figure 2: Mobility reports.

`rel_severe_prob]`. They correspond respectively to the mean of the log-normal distribution representing the time spent in the compartment 'symptomatic' before moving into the compartment 'severe', the mean of the log-normal distribution representing the time spent in the compartment 'asymptomatic' before moving into the compartment 'recovered', to the scale factor for proportion of symptomatic cases and to the scale factor for proportion of symptomatic cases that become severe. (see [9]). The $\mathcal{L}_2$- diversity increased from 62353 to 93553.

To create the most diverse set possible, I used 4 different mobilities reports (Fig.2), corresponding to constant mobility, annual variations, lockdown scenario and the reports from Vasträffik from [5]. These time-varying mobilities enabled us to model more complex behaviours of the pandemics. I finally modelled 324 pandemics. Indeed each of the 4 parameters was scaled among 3 values : `[0.5, 1, 2]` and the 4 mobilities reports were used.

5 Models

In this study, let us define a model h_θ as a function h defined on $\mathbb{N}$, with parameters θ and trained on the data $\mathcal{D}$. In the training phase, $\hat{\theta}$, an estimator of θ is computed from $\mathcal{D}$, and used for the prediction. I deisgned two types of models: the first type correspond to models which are only trained on the time series we want to predict (the number of hospitalized in our case), and the second type of models are trained on the time series we want to predict, but also on other time series that can be relevant to forecast the number of hospitalized (the mobility and the number of infected). All of these models were implemented in Python, and are available on the Github repository provided with this report (2). During the training or predicting phase, the computation sometimes fails (for instance, when the matrix is non-invertible for the linear regression model). The model then outputs the value of the moving average model (see 5.3), which can be interpreted as a naive output when the computation fails.

Task of a model:

Each model h is given :

1. A training set $\mathcal{D}$ of size n.
2. A reach of prediction r
3. A confidence threshold α

And outputs:

1. A prediction $\hat{Y}_{n+r}$
2. A $(1-\alpha)$ confidence interval on the prediction, $I_{\alpha,n+r}$

The model will train on the data $\mathcal{D}$ to compute $\hat{\theta}$ the parameter estimator and the output $\hat{Y}_{n+r} = h_{\hat{\theta}}(n+r)$.

5.1 The SIRH model

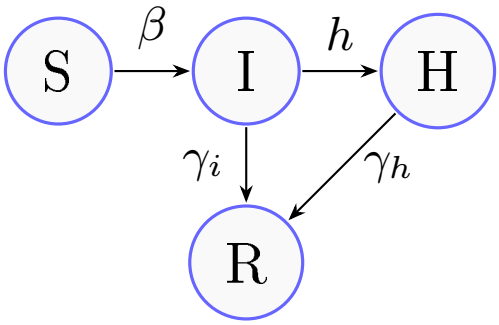


Figure 3: Scheme of the SIRH model

The SIRH model (Fig.3) is an extension of the classic compartemental SIR (Susceptible-Infectious-Recovered) model used to describe the spread of infectious diseases. In the SIRH model, a fourth compartment, "H" for "Hospitalized," is added. Each compartment corresponds to the number of person in the state of health of the compartment. The evolution of the number of person in each compartment is described by a system of ordinary differential equations:

$$\begin{cases} \frac{dS}{dt} = -\beta \frac{SI}{N} \\ \frac{dI}{dt} = \beta \frac{SI}{N} - \gamma_i I - hI \\ \frac{dR}{dt} = \gamma_i I + \gamma_h h \\ \frac{dH}{dt} = hI - \gamma_h H \end{cases} \tag{1}$$

At $t = 0$, the values of (S_0, I_0, R_0, H_0) are fixed to $(10^6 - 1, 1, 0, 0,)$. As the system of equation can't be directly solved, we use a Euler method to solve it.

To train this model, we minimize the least squares error between the curve of the number of hospitalized observed to the curve of the number of hospitalized of the training data with respect

to $\theta = (\beta, \gamma_i, \gamma_h, h)$. I implemented some variations of the model in which γ_i, γ_h or both were fixed to the value 0.2 (see the Table.1). This value of 0.2 seems arbitrairy but corresponds to an expected value of recovery of 5 days and sometimes helps the curve fit function to converge, as the computations sometimes fails to optimize on the 4 parameters.

	γ_i	γ_h
SIRH1	0.2	0.2
SIRH2	0.2	free
SIRH3	free	0.2
SIRH4	free	free

Table 1: Difference between the SIRH models

In the prediction phase, an r day SIRH simulation is launched, with the parameter $\hat{\theta}$ computed during the training phase. The initial values for S and I correspond to the last value of the fit of the training phase. The initial value for H corresponds to the last value of $\mathcal{D}$, the training data. The initial value of R is fixed by the previous values as the equation $S_t + I_t + R_t + H_t = N$ is always true. The confidence interval of the prediction is computed thanks to a linearization and the use of the delta-method (see 5.7)

An SIRH model of the second type was implemented. It has the same structure but uses the mobility data and the number of infected to be more precise. The idea is the same, but there are two differences :

- β varies with the time as a linear combination of the mobility : $\beta_t = a + b \times m_t$ (which is inspired from [5])
- The data is fitted to both the number of hospitalized and the number of infected.

To write it more formally, let $H_\theta(t)$ and $I_\theta(t)$ be the number of hospitalized and infected at time t in the SIRH model with parameters θ. Let $Y_{H,t}$ and $Y_{I,t}$ be the number of hospitalized and infected at time t in the data. We have :

$$\hat{\theta} = \underset{\theta \in \mathbb{R}^5}{\operatorname{argmin}} \sum_{t=1}^{n} \left(\frac{H_\theta(t) - Y_{H,t}}{\max\limits_{t \in \{1,\dots,n\}}(Y_{H,t})}\right)^2 + \left(\frac{I_\theta(t) - Y_{I,t}}{\max\limits_{t \in \{1,\dots,n\}}(Y_{I,t})}\right)^2$$

With $\theta = (a, b, \gamma_i, \gamma_h, h)$ and m_t the mobility at time t. The normalization factors enables to prevent the optimization to focus on the number of infected, which is bigger than the number of hospitalized. During my first tries, I hadn't normalized the data and the curve of the infected was almost perfectly fitted to the curve of the SIRH model, but the curve of the hospitalized was flat. Once again, a variation of the SIRH model was implemented, in which the value of γ_h and γ_i is fixed to 0.2. SIRH multi 1 refer to the model in which γ_h and γ_i are free and SIRH multi 2 refer to the model in which γ_h and γ_i are fixed to 0.2.

5.2 ARIMA and VAR models

The ARIMA and VAR models are used for time-series forecasting and have outperformed many models in pandemic forecasting (see [10] and [16]). The $ARIMA(p, d, q)$ model is the sum of an $AR(p)$ and a $MA(q)$ model applied on the time series differentiated d times. It follows the

equation :
$Y_t^d = \alpha + \sum_{i=1}^{p} \beta_{t-i}\, Y_{t-i}^d \; + \; \sum_{j=1}^{q} \phi_{t-j}\, \epsilon_{t-j}$
where Y_t^d is the time series at time t, d is the order of the differentiation, α is a constant, p is the order of the autoregressive part, q is the order of the moving average part and ϵ_{t-j} is the difference between the prediction of the model and the real value at time $t-j$.
The coefficient are estimated through maximum likelihood estimation. This method is implemented in the `statsmodels` library, which directly provides prediction and confidence intervals. I realized a grid search on a single pandemic to identify the combination of parameters that would optimize the prediction accuracy. I found an optimal value for $p = 3, d = 0, q = 3$.

The VAR model is a multi-dimensional AR model, in which different variables are predicted. It so corresponds to a second type model. This model exploits the correlation between variables and the value of the parameters of a VAR have physical sense as they can be interpreted to find correlations between variables. Let $Y_{1,t}, ..., Y_{k,t}$ be the times series (in our case, $k = 3$ and they correspond to the number of hospitalized, the number of infected and the mobility data).

$$VAR(p): \begin{pmatrix} Y_{1,t} \\ Y_{2,t} \\ \vdots \\ Y_{k,t} \end{pmatrix} = \begin{pmatrix} c_1 \\ c_2 \\ \vdots \\ c_k \end{pmatrix} + \begin{pmatrix} \phi_{11,1} & \phi_{12,1} & \cdots & \phi_{1k,1} \\ \phi_{21,1} & \phi_{22,1} & \cdots & \phi_{2k,1} \\ \vdots & \vdots & \ddots & \vdots \\ \phi_{k1,1} & \phi_{k2,1} & \cdots & \phi_{kk,1} \end{pmatrix} \begin{pmatrix} Y_{1,t-1} \\ Y_{2,t-1} \\ \vdots \\ Y_{k,t-1} \end{pmatrix}$$
$$+ \cdots + \begin{pmatrix} \phi_{11,p} & \phi_{12,p} & \cdots & \phi_{1k,p} \\ \phi_{21,p} & \phi_{22,p} & \cdots & \phi_{2k,p} \\ \vdots & \vdots & \ddots & \vdots \\ \phi_{k1,p} & \phi_{k2,p} & \cdots & \phi_{kk,p} \end{pmatrix} \begin{pmatrix} Y_{1,t-p} \\ Y_{2,t-p} \\ \vdots \\ Y_{k,t-p} \end{pmatrix} + \begin{pmatrix} \epsilon_{1,t} \\ \epsilon_{2,t} \\ \vdots \\ \epsilon_{k,t} \end{pmatrix}$$

Again, the $\phi_{i,j,k}$ and c_i are estimated through maximum likelihood estimation with the `statsmodel` library. The confidence intervals are also directy provided by the library.

5.3 The moving average model

A mere moving average model was also implemented. It returns a constant prediction that correspond to the mean of the 7 past days. The confidence intervals are computed by assuming that the predictions follow a normal distribution of variance equal to the variance of the 7 last data-points. This model is used as a baseline, indeed, a model that does not manage to outperform the moving average model would not be useful.

5.4 Exponential regression

An exponential regression model was implemented. It corresponds to fitting the data of the number of hospitalized (Y_t) to the function $E_{a,b,c}(t) = a \times e^{bt} + c$. The value of $\theta = (a, b, c)$ is computed through a least square minimization method. The confidence interval on the prediction is estimated with the same method as SIRH (see 5.7).

An exponential regression of the second type was also implemented:
The data of the number of hospitalized is fitted to the function $E_{a,b,c,d,e}(t) = a \times e^{bm_{t-i} + ct + d \times inf_{t-j}} + e$.

m_t is the mobility data at time t and inf_t is the number of infected at time t. The value of $\theta = (a, b, c, d, e)$ is computed through a least square method. The optimal value of the time lag i and j is optimized during the training phase through a grid search among all the values between 0 and 14. The confidence interval on the prediction is estimated with the same method as SIRH (see 5.7).

5.5 Machine learning models

In order to implement machine learning regressors, I converted the time-series $Y_{t,t\in\{1,...n\}}$ in a training set (X_i, Y_i) such that :
$\forall i \in \{21, ..., n\}, X_i = (Y_{i-1}, Y_{i-2}, ..., Y_{i-20})$.

I have then trained and optimized both regressors : the linear and the bayesain regressors, which were the only one that did not output absurd results on the `scikit-learn` models among : linear regression, bayesian regression, Gradient boosting regressor, Random Forest regressor and SVR. The Bayesian ridge model was implemented with the default prior of the `scikit-learn` library (a gamma distribution with shape parameter 10^{-6} and scale parameter 10^{-6}). The confidence interval for the linear regression prediction was computed as follow :
Let us suppose that the data follows a linear regression model : $Y = X\beta + \epsilon$, with $Y \in \mathbb{R}^n$, $X \in \mathbb{R}^{n\times d}$, $\beta \in \mathbb{R}^d$ and $\epsilon \sim \mathcal{N}(0, \sigma^2)$. The least square estimator of β is $\hat{\beta} = (X^T X)^{-1} X^T Y$. If we have new data $\tilde{X} \in \mathbb{R}^{1\times d}$ that we want to predict, the prediction is :

$$\begin{aligned}\tilde{Y} &= \tilde{X}\hat{\beta} \\ &= \tilde{X}(X^T X)^{-1} X^T Y \\ &= \tilde{X}(X^T X)^{-1} X^T (X\beta + \epsilon) \\ &= \tilde{X}\beta + \tilde{X}(X^T X)^{-1} X^T \epsilon.\end{aligned}$$

$\tilde{Y}$ follows a normal distribution of expected value $\tilde{X}\beta$ and variance $\tilde{X}(X^T X)^{-1}\tilde{X}^T\sigma^2$.
The confidence interval on bayesian regression was directly computed with the variance of the parameters given by the scikit-learn library and the delta method.

5.6 Ensemble model

It has been showned (see [2] and [14]), that ensemble models, which combine the outputs of many models, can outperform by far individual models. I have implemented an ensemble model which is a linear combination of the outputs of the 13 models described above, with the exponential models removed. The weights of this model were found my minimizing the least-squared error between the prediction of the ensemble model and the real value of the number of hospitalized on a train set of approximately 80% of the pandemic generated. They are represented in the Fig.4. As the ensemble model only outputs a single value without confidence intervals, it is only evaluated with the RMSE metric.

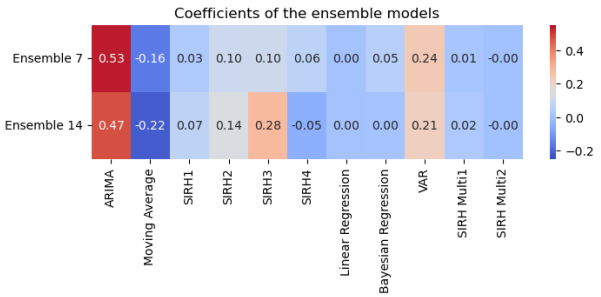


Figure 4: Weights of the ensemble models

5.7 Computing confidence intervals on the prediction

In this section, we prove the formula used for in the code to compute the confidence intervals. The following proof is inspired from [15] and [12]. I have assembled individuals proofs from these two articles to get the final results. Some notations and steps are identical to what we can find in the paper and are explicitely cited.
This problem is a non linear regression problem. The proof is made of three steps. First, we linearize the problem around the solution to get back to a linear regression problem. Then, we show that the estimator of the linear regression problem is asymptotically normal. Finally, we use the delta-method to obtain the asymptotic normality of the non linear regression estimator .

Assumption:

We suppose that the data of the pandemic observed follows the model h, of parameter $\theta^* \in \mathbb{R}^d$. Let Y_i, $i = 1, \dots, n$ be the number of hospitalized at each day. We suppose that: $Y_i = h_{\theta^*}(i) + \epsilon_i$, with $\epsilon_i \sim \mathcal{N}(0, \sigma^2)$, iid, and independent from all the other variables. The objective is to estimate θ^*. We use $\hat{\theta}$, the least square estimator of θ^* as an estimator of θ^*:

$$\hat{\theta} = \underset{\theta \in \mathbb{R}^d}{\operatorname{argmin}} \sum_{i=1}^{n} (Y_i - h_\theta(i))^2$$

This problem is a non-linear regression problem on the regressors i. We also suppose that h_θ is differentiable. Finally, we suppose that

$$\exists A_0 \in \mathbb{R}^{1 \times d}, \frac{1}{n} \sum_{i=1}^{n} \nabla_\theta h_{\theta^*}(i) \nabla_\theta h_{\theta^*}(i)^T \underset{n \to +\infty}{\to} A_0^T A_0. \tag{2}$$

STEP 1 :

Let:

$$Y = \begin{pmatrix} Y_1 \\ \vdots \\ Y_n \end{pmatrix}$$
$$h_\theta = \begin{pmatrix} h_\theta(1) \\ \vdots \\ h_\theta(n) \end{pmatrix}$$

We have:

$$\hat{\theta} = \underset{\theta \in \mathbb{R}^d}{\operatorname{argmin}} \|Y - h_\theta\|^2$$

Now, if θ is close enough to θ^*, we can write (from [15]):

$$\forall i \in \{1, ..., n\} : h_\theta(i) = h_{\theta^*}(i) + (\theta - \theta^*)^T \nabla_\theta h_{\theta^*}(i)$$

which leads to:

$$\hat{\theta} = \underset{\theta \in \mathbb{R}^d}{\operatorname{argmin}} \left\| Y - h_{\theta^*} - (\theta - \theta^*)^T \nabla_\theta h_{\theta^*} \right\|^2$$

Let us define (from [15]):

$$\tilde{Y} = Y - h_{\theta^*}$$
$$\beta = \theta - \theta^*$$
$$\hat{\beta} = \theta - \hat{\theta}$$

and let us define the matrix $A \in \mathbb{R}^{n \times d}$ such that $\forall i \in \{1, ..., n\}, \forall j \in \{1, ..., d\}, A_{i,j} = \frac{dh_{\theta^*}}{d\theta_j}(i)$. ([15])

The previous problem can be re-written as:

$$\hat{\beta} = \underset{\beta \in \mathbb{R}^d}{\operatorname{argmin}} \left\| \tilde{Y} - A\beta \right\|^2$$

This is now a linear regression problem on the regressors $\nabla_\theta h_{\theta^*}(i)$.

STEP 2 :

Let us solve this problem in the general case.

Let $(A_i, \tilde{Y}_i)$ be the observations. In our case, $A_i = (\nabla_\theta h_{\theta *}(i))^T$, the rows of A, and is a fixed quantity. Let us assume that $\tilde{Y}_i = A_i \beta^* + \epsilon'_i$, with $\epsilon'_i \sim \mathcal{N}(0, \sigma'^2)$.

The solution of this problem is explicitly (from [12]):

$$\hat{\beta} = (A^T A)^{-1} A^T \tilde{Y}$$

This least-square estimator is unbiased:

$$\mathbb{E}[\hat{\beta}] = \beta^*$$

$$\hat{\beta} = \left(\sum_{i=1}^{n} A_i^T A_i\right)^{-1} \times \left(\sum_{i=1}^{n} A_i^T \tilde{Y}_i\right)$$

$$\hat{\beta} = \frac{n}{n}\left(\sum_{i=1}^{n} A_i^T A_i\right)^{-1} \times \left(\sum_{i=1}^{n} A_i^T \tilde{Y}_i\right)$$

$$\hat{\beta} = \left(\frac{1}{n}\sum_{i=1}^{n} A_i^T A_i\right)^{-1} \times \left(\frac{1}{n}\sum_{i=1}^{n} A_i^T \tilde{Y}_i\right)$$

Let us denote, with the notations from [12]:

$$\hat{D} = \frac{1}{n}\sum_{i=1}^{n} A_i^T A_i, \quad \text{and} \quad \hat{\delta} = \left(\frac{1}{n}\sum_{i=1}^{n} A_i^T \tilde{Y}_i\right)$$

We have:

$$\hat{\beta} = \hat{D}^{-1}\hat{\delta}$$

$$\hat{D} \underset{a.s}{\to} D, \text{ with } D = \mathbb{E}[A_i^T A_i] = A_0^T A_0 \text{ (cf Hyp 2)}$$

$\hat{\delta}$ is the empirical mean of random variables independent but non identically distributed. We therefore cannot use the Kolmogorov's Strong Law of Large Numbers. There exists a law of large number for independent and non identically distributed random variables, which asserts that (see Therom 12 from [18]):

Theorem 1. *Let (X_k) be a sequence of independent random variables such that:*

1. *For all $k \geq 1$, $\mathbb{E}(X_k^2) < +\infty$;*
2. *There exists an increasing sequence (a_k) of strictly positive real numbers tending to infinity, such that*
$$\sum_{k=1}^{+\infty} \frac{\mathrm{Var}(X_k)}{a_k^2} < +\infty.$$

Then, $\frac{S_n - \mathbb{E}S_n}{a_n}$ converges almost surely to 0. If additionally $a_n^{-1}\mathbb{E}S_n \to m$, then $\frac{S_n}{a_n}$ converges almost surely to m.

Let $i \in \{1, ..., n\}$.

$X_i = A_i^T \tilde{Y_i} = A_i^T A_i \beta^* + A_i^T \epsilon_i'$.
The random values X_i are independent random variables.
$\forall i \in \{1, ...n\}, \mathbb{E}[X_i^2] = \mathbb{E}[X_i]^2 + A_0^T A_0 \sigma'^2 < +\infty$.

$\sum_{i=1}^{\infty} \frac{Var(X_i)}{i^2} = \sum_{i=1}^{\infty} \frac{A_0^T A_0 \sigma'^2}{i^2} = A_0^T A_0 \sigma'^2 \sum_{i=1}^{\infty} \frac{1}{i^2} < +\infty$.

Moreover, $\frac{1}{n} \sum_{i=1}^{n} \mathbb{E}[X_i] = \frac{1}{n} \sum_{i=1}^{n} A_i^T A_i \beta^* = \frac{\beta^*}{n} \sum_{i=1}^{n} A_i^T A_i \underset{n \to \infty}{\to} \beta^* A_0^T A_0$ (see 2).

Therefore, with Theorem 1, we have : $\frac{1}{n} \sum_{i=1}^{n} A_i^T \tilde{Y_i} \underset{a.s}{\to} \beta^* A_0^T A_0$

$$\hat{\delta} \underset{a.s}{\to} \delta = A_0^T A_0 \beta^*$$

$\hat{\beta} = \hat{D}^{-1} \hat{\delta} \underset{a.s}{\to} D^{-1} \delta$, as the following function ϕ is continuous:

$$\phi : \begin{cases} \mathcal{GL}_n(\mathbb{R}) & \to & \mathcal{GL}_n(\mathbb{R}) \\ M & \mapsto & M^{-1} \end{cases}$$

Now, let us show that $\hat{\beta}$ is asymptotically normal (proof from [12]):

$$\begin{aligned}
\sqrt{n}(\hat{\beta} - \beta^*) &= \sqrt{n}(\hat{D}^{-1}\hat{\delta} - \beta^*) \\
&= \sqrt{n}(\hat{D}^{-1}\hat{\delta} - \hat{D}^{-1}\hat{D}\beta^*) \\
&= \sqrt{n}\hat{D}^{-1}(\hat{\delta} - \hat{D}\beta^*) \\
&= \sqrt{n}\hat{D}^{-1}\left(\frac{1}{n}\sum_{i=1}^{n} A_i^T \tilde{Y_i} - \frac{1}{n}\sum_{i=1}^{n} A_i^T A_i \beta^*\right) \\
&= \frac{\sqrt{n}}{n}\hat{D}^{-1}\left(\sum_{i=1}^{n} A_i^T (\tilde{Y_i} - A_i\beta^*)\right) \\
&= \frac{1}{\sqrt{n}}\hat{D}^{-1}\left(\sum_{i=1}^{n} A_i^T \epsilon_i\right)
\end{aligned}$$

This line is made of two terms. Let's show that each one of them converges in law.

$$\begin{aligned}
\frac{1}{\sqrt{n}}\left(\sum_{i=1}^{n} A_i^T \epsilon_i'\right) &= \sqrt{n}\left(\frac{1}{n}\sum_{i=1}^{n} A_i^T \epsilon_i'\right) \\
&= \sqrt{n}\left(\frac{1}{n}\sum_{i=1}^{n} A_i^T \epsilon_i' - 0\right) \\
&\xrightarrow{\mathcal{L}} \mathcal{N}(0, \mathrm{Var}(A_i^T \epsilon_i))
\end{aligned}$$

Yet, as ϵ_i and A_i are independent, and $\mathbb{E}[A_i^T \epsilon_i'] = 0$, $\mathrm{Var}(A_i^T \epsilon_i) = \mathbb{E}[A_i^T A_i \epsilon_i^2] = \mathbb{E}[A_i^T A_i]\sigma'^2 = A_0^T A_0 \sigma'^2$.

Finally, $\frac{1}{\sqrt{n}}\left(\sum_{i=1}^{n} A_i^T \epsilon_i'\right) \xrightarrow{\mathcal{L}} \mathcal{N}(0, D\sigma'^2)$.

On the other hand, $\hat{D}^{-1} \xrightarrow{\mathcal{L}} D^{-1}$, which is constant.
Finally, with Slutsky, we obtain that:

$$\begin{aligned}\sqrt{n}(\hat{\beta} - \beta^*) &\xrightarrow{\mathcal{L}} D^{-1}\mathcal{N}(0, D\sigma'^2) \\ &\xrightarrow{\mathcal{L}} \mathcal{N}(0, D^{-1}(D\sigma'^2)(D^{-1})^T) \\ &\xrightarrow{\mathcal{L}} \mathcal{N}(0, D^{-1}D\sigma'^2(D^{-1})^T) \\ &\xrightarrow{\mathcal{L}} \mathcal{N}(0, \sigma'^2 D^{-1}) \\ &\xrightarrow{\mathcal{L}} \mathcal{N}(0, \sigma'^2(A_0^T A_0)^{-1})\end{aligned}$$

Let's get back to the first problem:
As $\beta^* = 0$ and $\hat{\beta} = \hat{\theta} - \theta^*$, we have:

$$\sqrt{n}(\hat{\theta} - \theta^*) \xrightarrow{\mathcal{L}} \mathcal{N}(0, \sigma^2(A_0^T A_0)^{-1})$$

and,

$$\hat{\theta} \sim \mathcal{N}(\theta^*, \frac{\sigma^2}{n}(A_0^T A_0)^{-1})$$

As a partial conclusion, we have that $\hat{\theta}$ is asymptotically normal.
STEP 3 :

Let Σ be the covariance matrix estimated from the computation of $\hat{\theta}$.
As $\hat{\theta}$ is asymptotically normal, we can apply the delta-method:

$$\sqrt{n}(\hat{\theta} - \theta^*) \xrightarrow{\mathcal{L}} \mathcal{N}(0,\ \Sigma)$$

$$\sqrt{n}(h_{\hat{\theta}} - h_{\theta^*}) \xrightarrow{\mathcal{L}} \mathcal{N}(0, \nabla_\theta h_\theta^T \Sigma \nabla_\theta h_\theta)$$

And finally:

$$h_{\hat{\theta}} \to \mathcal{N}(h_{\theta^*}, \frac{1}{n}\nabla_\theta h_\theta^T \Sigma \nabla_\theta h_\theta)$$

By estimating $\frac{1}{n}\Sigma$ from `curve_fit`, we can compute the confidence interval of the prediction with the quantiles of the normal distribution. The gradient of h_θ is approximated through numerical approximation:
$\nabla_\theta h_\theta[i] \simeq \frac{h_{\theta + d\theta_i} - h_\theta}{dt}$, with $dt = 0.0001$.

$$d\theta_i = \begin{pmatrix} \theta_0 \\ \theta_1 \\ \vdots \\ \theta_{i-1} \\ \theta_i + dt \\ \theta_{i+1} \\ \vdots \\ \theta_n \end{pmatrix}$$

6 Results and discussion

Metrics

Two metrics were used to assess the performance of the models. The first metric is the Weighted Interval Score (WIS), which is a metric commonly used in forecast evaluation (see [2] or [11]).

Let α be in $]0, 1[$. Let $\hat{y}$ be the prediction of the model and y the real value. Let $[l, u]$ be the $(1 - \alpha)$ confidence interval of the prediction. We define the Interval Score (IS) as :
$IS_\alpha([l, u], \hat{y}, y) = \frac{2}{\alpha} \times (\mathbb{1}_{\{y<l\}}(l - y) + \mathbb{1}_{\{y>u\}}(y - u) + (u - l))$.
This metric is made of three terms: a term of overprediction that punishes a model predicting a confidence interval which is above the real value, a term of underprediction that punishes a model whose confidence interval is under the real value, and a term of range, that punishes too wide confidence intervals.
Let $(\alpha_k)_{k\in\{1,...,K\}} \in]0, 1[^K$ The WIS is defined as follow.

$WIS([l, u], \hat{y}, y) = \sum_{k=0}^{K} w_k IS_{\alpha_k}([l, u], \hat{y}, y)$, with $(w_k)_{k\in\{1,...,K\}} \in \mathbb{R}_+^K$ weights chosen by the user.

According to previous literature ([2]), I decided to set
$(\alpha_k)_{k\in\{1,...,K\}} = [0.02, 0.05, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9]$ and $\forall k \in \{1, ..., K\}, w_k = \frac{\alpha_k}{2}$
One can notice that the WIS does not take into account the point prediction, but focuses on confidence interval accuracy.

The second metric chosen is the Root Mean Square Error ($RMSE$). With the same notations as above, we define the $RMSE$ as follow :
$RMSE([l, u], \hat{y}, y) = \sqrt{(y - \hat{y})^2}$
This metric focuses on the point prediction, and does not take into account the confidence intervals.

The models were tested on all the 324 pandemics, on 14 data points different (at days 20, 40, 60, ..., 280). For each individual point, the models were trained on the previous days of the pandemic. A 7 and 14 days ahead prediction was asked, and $[0.02, 0.05, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9]$

confidence-intervals were computed. The WIS and the RMSE of these predictions were then computed. For the analysis of the results, I decided to remove the points for which the number of hospitalized was below 100, as both point classification and model predictions were irrelevant at this period of the pandemic. Moreover, it is senseless to assess the performances of the models during the period in which there is no pandemic, as the interesting models are the ones that can predict the number of hospitalized during the waves. Not removing those points would lead to biaised results, as they represent 44% of the dataset, and we would have concluded that the best model is the one that performs well when there is no pandemic.

6.1 Point classification

In order to compare the performance of the models at different point of the pandemic, I have classified the points in six categories : *stable, increase, big increase, decrease, big decrease*. The R_{eff} number was used for the point classification. This number is easily available from the Covasim simulation. R_{eff} represents the expected number of people that an infected person will infect. For a pandemic $X_{i,i\in[1,\dots,n]}$ of reproduction number $R_{i,i\in[1,\dots,n]}$, and a day $d \in [1,\dots,n]$, the classification is made according the following rule :

- if $X[d]<100$:
  classification = "no pandemic"
- Elif $R[d] < 0.5$:
  classification = "big decrease"
- Elif $R[d] < 0.8$:
  classification = "decrease"
- Elif $R[d] < 1.2$:
  classification = "stable"
- Elif $R[d] < 3$:
  classification = "increase"
- Else :
  classification = "big increase"

The values of the thresholds were chosen by hand. As the model are tested on the days [20, 40, 60, ..., 280], we labelled all of these points with the function described above. It resulted that among all those 4536 points, 698 were classified as 'big decrease', 579 as 'decrease', 388 as 'stable', 752 as 'increase', 132 as 'big increase', and 1987 as 'no pandemic'.

6.2 Evaluation of the models

The models described above were tested on 14 points of each of the 324 pandemics generated, when the pandemic was significant (i.e when more than 0.01% of the population was hospitalized, in our case when the value of the number of hospitalized was above 100). For each point, two

predictions were made: a 7-days ahead and a 14-days ahead. Each prediction was evaluated thanks to WIS and RMSE (see 6), and then ranked according to the performances of other models. The points of evaluation were also classified in one of the following categories : 'big increase', 'increase', 'stable', 'decrease' and 'big decrease', based on the value of the reproductive number at this time of the pandemic (see :6.1 for more details). It is then possible to get global information on the rankings of the models. For instance, if the loss and the reach of prediction is fixed, we can look at the distribution of rankings of all the models for a type of point (to see the best model for a type of point), as in Fig.5. This distribution of rankings of the model can

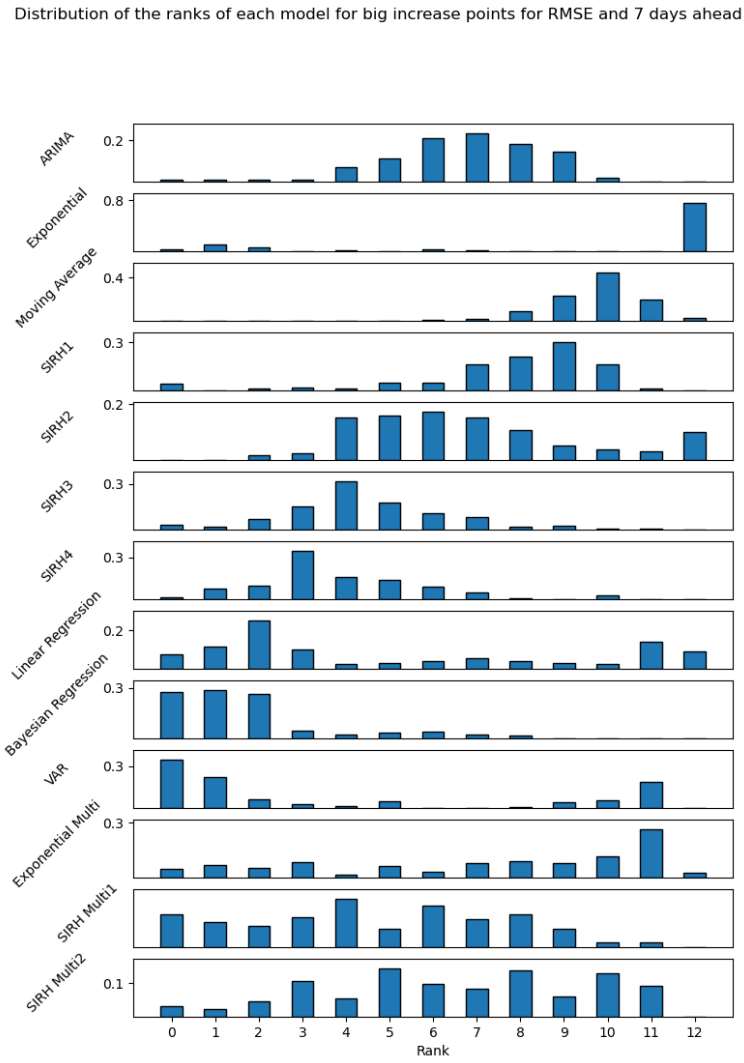


Figure 5: Distribution of rankings of the models for big increase points for 7-days ahead predictions and RMSE loss

be summed up in one single value : the expected value of the rank of a model (see Fig.6), which enables to get the idea of the best model for this type of point, this loss, and this prediction range on a more compact figure.

This new number loses information (for instance on bimodal rankings distribution) but enables to enlight the expected performance of a model. For each loss and range of prediction, the expected rank of the models for each type of point can be vizualized on the same figure, which enables to have a global look of the performances of the models.(Fig.7)

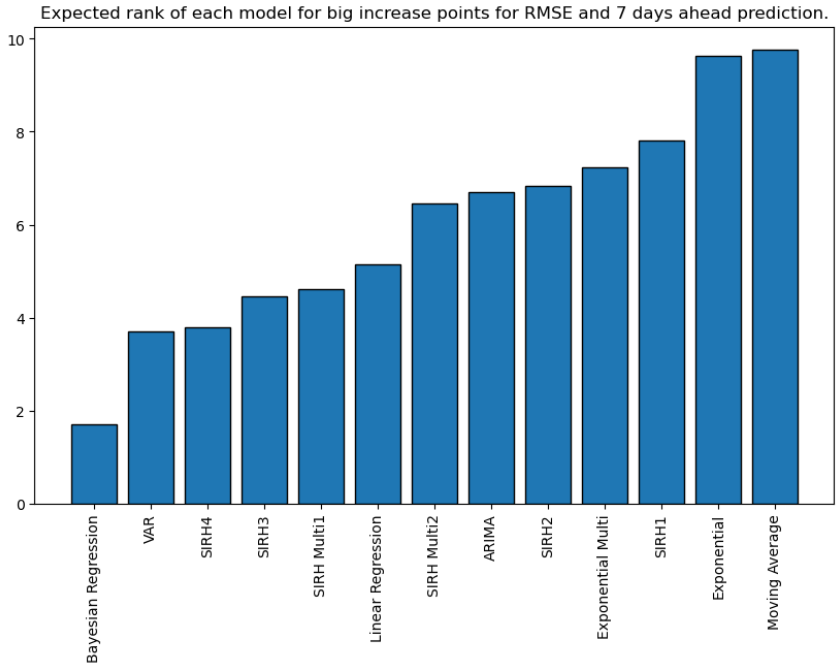


Figure 6: Expected rank of the models for big increase points for 7-days ahead predictions and RMSE loss

The other heatmaps corresponding to RMSE for 14 days ahead prediction and WIS for 7 and 14 days ahead predictions can be found in the appendix (7). Some general interpretations can be made on these results. I noticed that regressors performances dropp from 7-days ahead to 14-days ahead. The family of the SIRH model does slightly better for long terms predictions than for short term ones. The ARIMA performance dropps from 7-days ahead to 14-days ahead predictions. The exponential models are very bad and almost always the last ones.

6.3 The Ensemble model

The performance of the ensemble models have to be separated from the performances of the other models. Indeed, as the ensemble models were trained on a part of the pandemics, they can't be evaluated on the whole set of outbreaks. The performances discussed in this part refer to the same evaluation as above, but only for the RMSE loss and on a test set that represent 20% of the pandemics. The performances of these two models are showned in the two figure below (Fig.8a and Fig.8b)

The distribution of the ranks of the ensemble model is almost always on the left side of the x-axis. It is a very consistent model, and almost always in the top models. The heatmaps of expected ranks on all type of points enables to see how consistent is the ensemble model (Fig.9b and Fig.9a) compared to the other models.

From these figures, we can see that the ensemble model is rarely the best, but never the last model. Indeed, for a loss, a type of point and a prediction range, one can look at the best models in terms of expected rank. For instance, on the Figure.6, one can see that the top 3 models are Bayesian Regression, VAR and SIRH4. On the train set, the Ensemble model is the only model that appears in all top-6 models for all types of points, all losses and all prediction ranges.

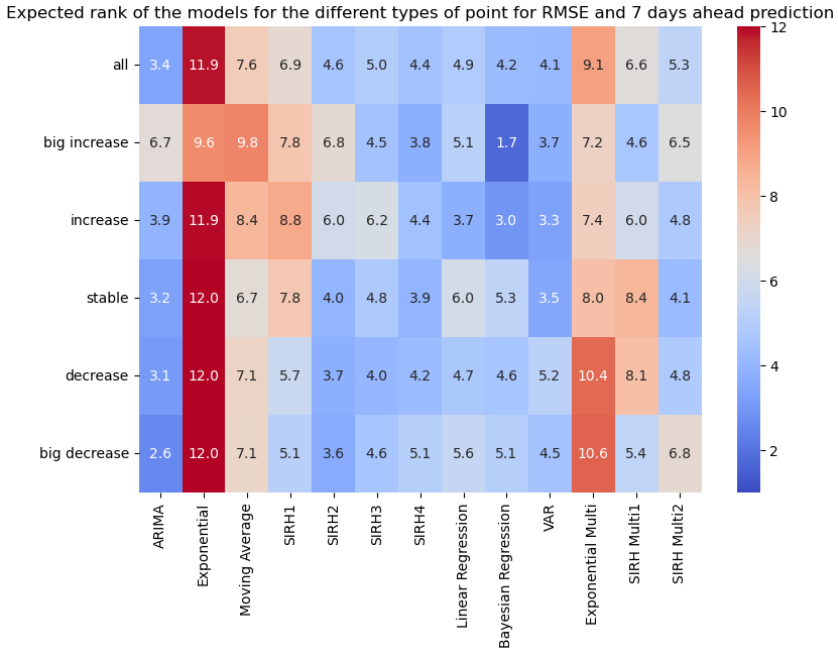


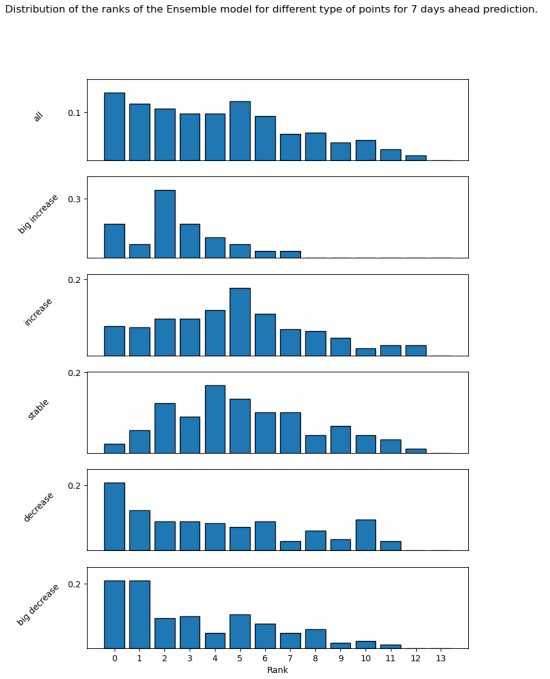
Figure 7: Expected rank of the models for each type of point for 7-days ahead predictions and RMSE loss. For instance, the Bayesian Regression has an average ranking of 1.7 on all the 'big increase' points of the 324 pandemics generated

Its consistency allows for accurate predictions and helps avoiding outlier predicted values that sometimes appear on the other good models (such as VAR and ARIMA).

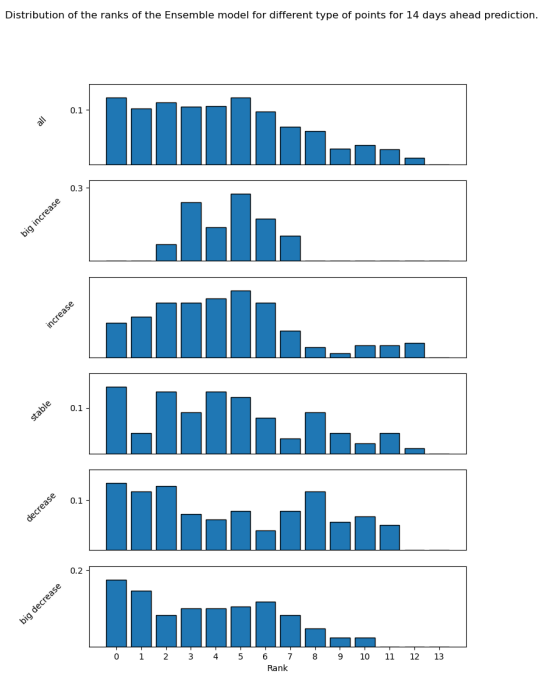
6.4 Summary of Key Findings

This method enabled us to assess the consistency of the different models that were implemented. Indeed, comparing the models on a set of diverse pandemics enlighted the most consistent with the different pandemics. Moreover, the classification of the models with the type of points leads to the determination of the phase of the pandemics in which each model is the best, and on the other hand to assess which model is the best for a R_{eff} given. This result is promising, as the reproduction number is a quantity oftenly estimated by the stakeholders during a pandemic. The interpretation based on the heatmaps Fig.10, Fig.7 and Fig.12 and Fig.11 show the following results :

- Arima and VAR are very performant models in terms of expected ranking. They are the two best models for 7-days ahead predictions and in the top 4 models for the 14-days ahead predictions.
- Adding information with the mobility and the number of infected is not beneficial for the models. We observe almost always a poorest performance of the models of the second type compared to their equivalent model of the first type (VAR / Arima and SIRH Multi / SIRH). Only the exponential multi outperforms the mere exponential model, but as they both perform pretty bad, this result is not interesting.

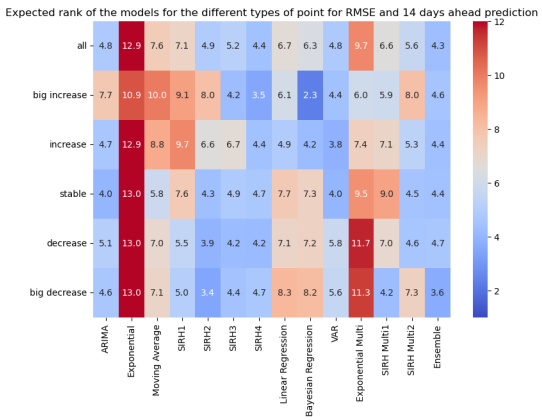


(a) Expected rank of the ensemble model for each type of point for 7-days ahead predictions and RMSE loss

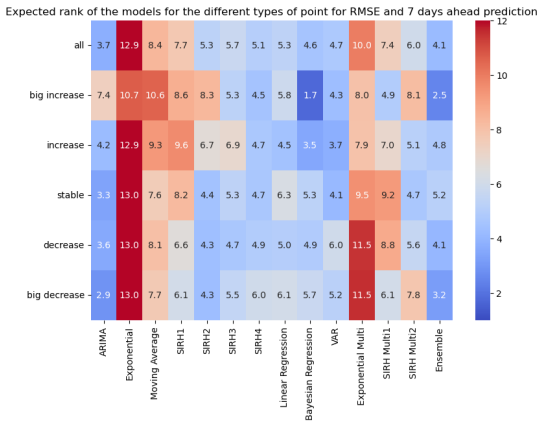


(b) Expected rank of the ensemble model for each type of point for 14-days ahead predictions and RMSE loss

Figure 8: Comparison of expected ranks for 7-days and 14-days ahead predictions



(a) Expected rank of all the models for each type of point for 14-days ahead predictions



(b) Expected rank of all the models for each type of point for 7-days ahead predictions

Figure 9: Expected rank of all the models for each type of point and RMSE loss on the test set for 7-days and 14-days ahead predictions

- The autoregressive models (Bayesian and Linear Regression, ARIMA and VAR) perform best for short term predictions rather than long term ones. On the other hand, the SIRH models, which have a phyisical meaning and try to fit the data to an understandable model perform better for long term predictions. This is also observed in the coefficients of the ensemble model (see Fig. 4). Indeed, the ensemble model put more weight on the VAR and Arima models for short term predictions and more on the SIRH models for long terms predictions.

- The difference of ranking between the models is more pronounced when we rank them with RMSE rather than WIS. This might be due to the fact that the confidence intervals are not well calibrated and that the real value always land out of it.

- The Moving Average model is not the worst model and is often ranked between 6 and 8. This might be due to the fact that as the curve of the number of hospitalized is continuous, the mean never diverge too much from the real value, while other models might misinterpret the trend of the curve and land far away from the real value.

- The Exponential models are almost always the last models, except for big increase points that are almost always at the very beginning of the pandemic. the fact that the beginning of a pandemic looks like an exponential curve is also showed with the SIRH model, when the number of infected is very small.

- The Ensemble model performs quite well. I noticed that it is very rarely the best model for a type of point, while other models almost always have some points on which they make the best prediction. On the other hand, it is never the last, and has a very consistent ranking: it is the only model that appears in all top-6 models for all types of points, all losses and all prediction ranges.

6.5 Test on real data

I have also tested the models on real data from the Covid-19 pandemic in Sweden. The data of the number of hospitalized individuals was taken from the website Our World in data, the data of the number of infected was taken from the website Worldometers, and the mobility used was the mobility from the Västraffik reports ([5]). I aknowledge that the mobility reports from Västraffik only concern the region of Västra Götaland, and that the mobility of the whole country would have been more relevant, but it is a good approximation, as the mitigation measures were at the state level in Sweden. The models were tested each 20 days from the 2nd of March to the 7th of December 2020. For each of these points, the models were trained on the data from the beginning of the pandemic to the day before the prediction, and outputed a 7-days ahead and a 14-days ahead prediction. As I wanted to compare the models with the ensemble model, I have decided to assess their performances with the RMSE and not the WIS. For each point prediction, the models were ranked according to the RMSE between the prediction and the real value. The rankings are shown on fig 14 in the appendix. The predictions of the models are plotted with the real data on fig 15. I noticed similar results to what was observed on the synthetized set for Arima, VAR, Bayesian and Linear regressors. The performance of the ensemble model is

quite disappointing during the period between the 20th of July and the 8th of October. This "flat" period was probably not present in the set on which the ensemble model was optimized, as the real-world data is probably much more complex than the data generated with Covasim. Moreover, the Ensemble model puts lots of weight on the VAR model (see fig 4), which might be very sensitive to the errors in the data, as it takes into account the number of infected and the mobility. However, event if the ensemble model is not well-ranked, it lands not far from the real value, the other models being a little closer than him.

6.6 Comparison with Previous Research

The very good performance of both VAR and ARIMA models is consistent with previous research. [10] and [16] both assess the performance of the ARIMA model in terms of regional or national prediction accuracy. The interpretation of the coefficients of the ARIMA model enables to have information on the inherent parameters of the pandemic, or to discover links between the different regions of a country. The consistency of the ensemble model has been shown in many previous studies (see [2], [19] and [14]), who also observe that their ensemble model outperformed any individual model. They also observe the fact that the ensemble model is very consistent: rarely the best, but never the last, allowing to produce robust forecasts. In [13], the authors compared several model to understand they key features that enabled a model to make long term predictions. These features are : " *(1) capturing the physics of transmission (instead of using black-box models); (2) projecting human behavioral reactions to an evolving pandemic; and (3) resetting state variables to account for randomness not captured in the model before starting projection.*" These findings are consistent with the results that I have observed. Indeed, I have showed that the SEIR model (capturing the physics of transmission and resetting state) performances increase from 7-days ahead to 14-days ahead predictions, while black-box models (such as Arima or VAR), are less performant for long terms prediction. This has to be qualified, as the "long term predictions" of this report refer to a 14-days ahead prediction, while the study [13] get interested to predictions up to 14-weeks reach.

The methodology of point classification has not be found in any other paper of the literature. Some studies assess the performance of the models during different times of a pandemic (see [7]), but this systematic point classification based on the reproduction number was not found.

6.7 Practical Implications

This study might be useful when facing a new pandemic. As the value of the R_{eff} is often estimated by the researchers during a pandemic, it could be used to decide which type of model to use during the current pandemic.

6.8 Limitations

During my researchs, I didn't take into account the impact of uncertainity of the data on the models. Indeed, the Covasim library provided a daily data of high quality and without any noise, but real-life data is often full of mistakes, of missing values or of time-lag in the reports ([6]). It would be interesting to measure the robustness of the models with respect to these imperfections

to assess if the models can still make good predictions, and to focus on the robustness of the ensemble model. Moreover, the models of the second type used the number of infected to predict the number of hospitalized. This quantity is not directy accessible and is often estimated with tests, which could lead to huge variations in the predicted values. Finally, the models were only tested on outbreaks generated with Covasim, which might lead to a bias in the results, despite the effort to create a diverse set of pandemics.

Conclusion

During my internship, I have tried to reproduce previous results on the consistency of autoregressive and ensemble models, but also to assess the robustness of some models with the evaluation on a huge set of diverse pandemics, which has never been before. The methodology for point classification is also a new way to compare model performnce, that might be useful during real outbreaks, as the reproduction number a popular quantity, which is often estimated. The results of the autoregressive and ensemble models are promising, as many aspects of previous research have been highlighted once again. Future research on the consticency of models with error in the data might complete this one, by assessing that the observed robustness of the model is not only due to the quality of the data.

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7 Appendix

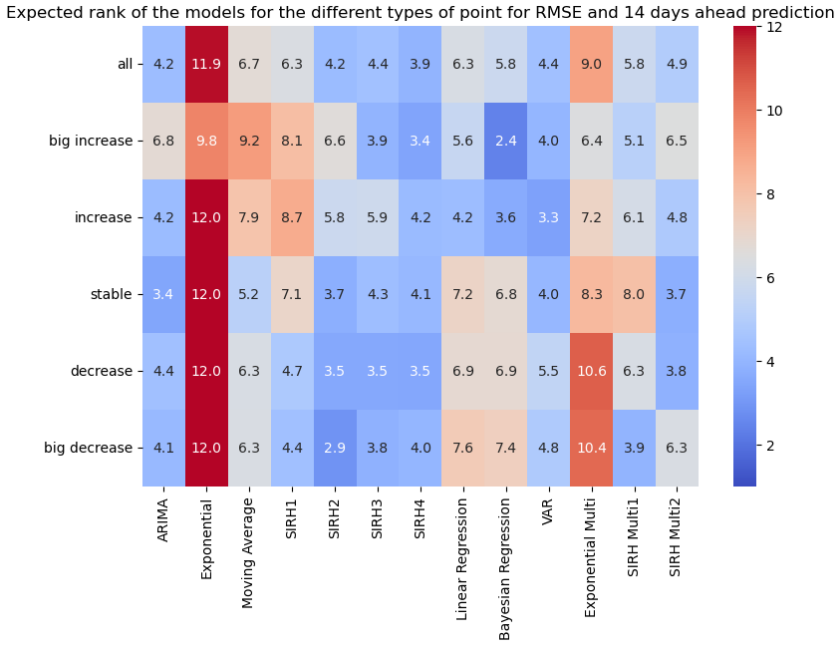


Figure 10: Expected rank of the models for each type of point for 14-days ahead predictions and RMSE loss

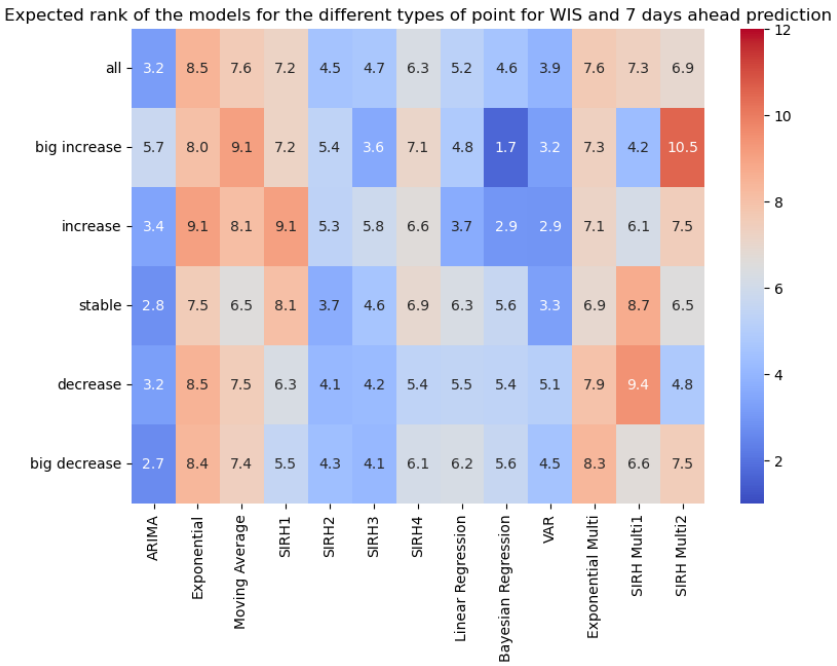


Figure 11: Expected rank of the models for each type of point for 7-days ahead predictions and WIS loss

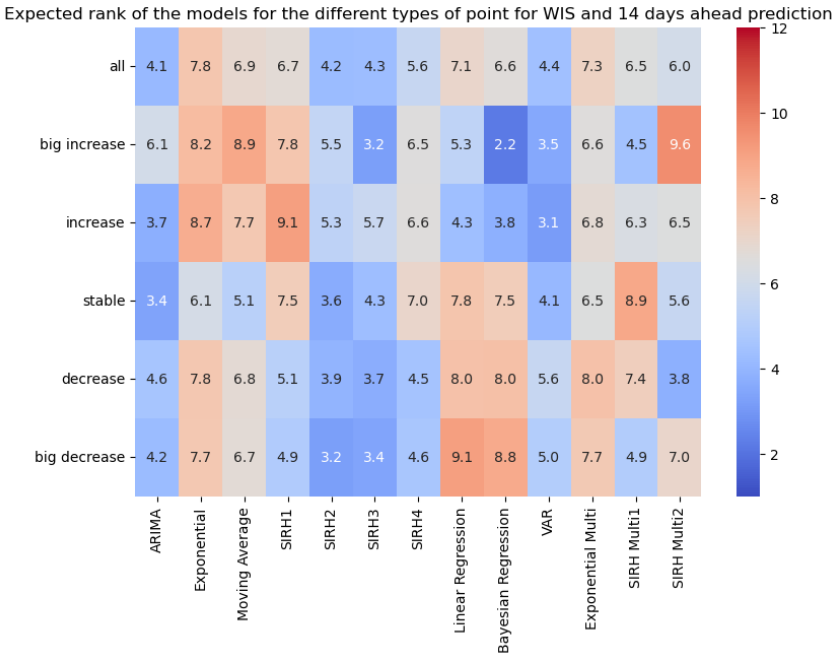


Figure 12: Expected rank of the models for each type of point for 14-days ahead predictions and WIS loss

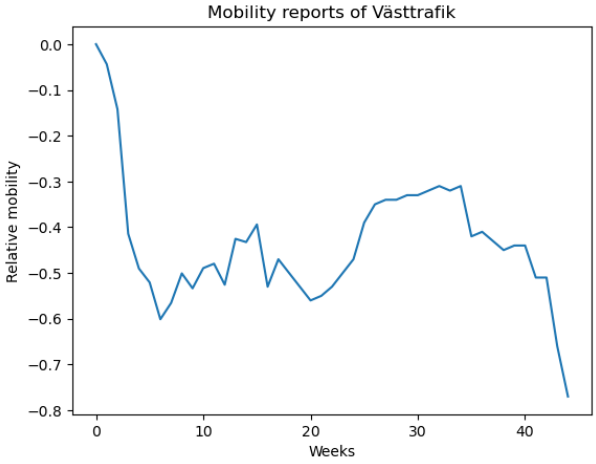
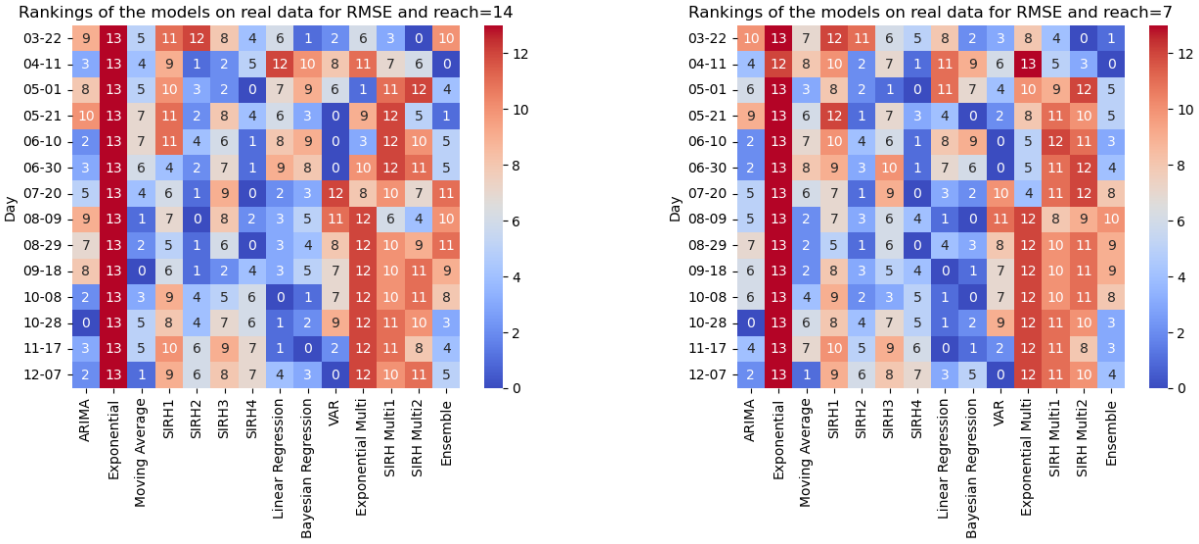


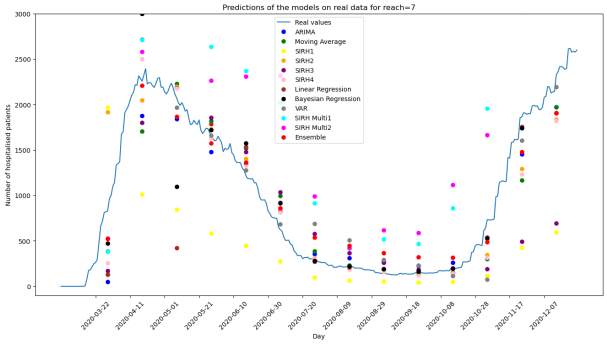
Figure 13: Mobility reports.



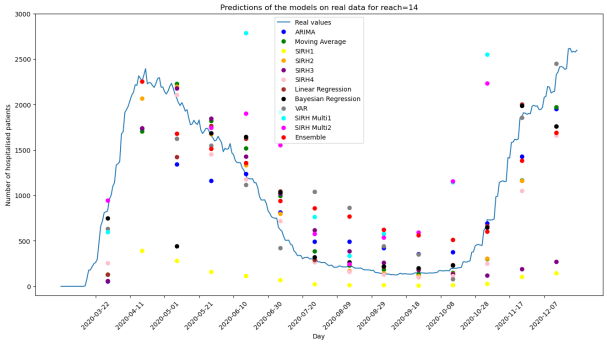
(a) Rankings for 7-days ahead predictions

(b) Rankings for 14-days ahead predictions

Figure 14: Rankings of the models during the Covid-19 pandemic in Sweden



(a) Predictions 7-days ahead



(b) Predictions 14-days ahead

Figure 15: Predictions of the models during the Covid-19 pandemic in Sweden. The y-axis was cut at 3000.