

# **Predicting COVID-19 distribution in Morocco through a Markov chain and SIR model.**

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## **Abstract.**

Nowadays, Coronavirus, known also as covid-19, has set the alarm bells in all over the world. That virus arose from December 2019 in Wuhan, the capital city of Hubei province in Chinese Republic. It belongs to BetaCoronaviruses kind which causes respiratory infections.

Efforts have been made by health officials to preveue that cough, fever, shortness of breath, muscle aches, sore throat, Diarrhea, and headache are the main virus symptoms which shows up in the affected people within 14 days of the virus exposure, while the virus can rarely lead to severe respiratory problems, kidney failure or death. Scientifically, Coronavirus, like SARS, MERS, AIDS, and Ebola, is a zoonotic disease which the virus's protein spikes attach to ACE2 protein on the surface of cells(that protein plays normally a role in regulating the human blood pressure). But When the virus is attached to it, it sets off chemical changes that fruitfully agglutinate around both the cell and the virus, allowing the virus's RNA to enter the cell.

As of now, there is no specific treatment to prevent further spread of the virus. In this paper, we attempt to summarise and apply a stochastic model characterising the probability distribution of cases in Morocco by regions, with an estimated number of cases using SIR model, the thing that will help us to characterise the disease in Morocco so as to promote logical actions and to be more prepared for the next days.

Keywords.

Covid-19, Markov Chain, SIR

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## **Introduction.**

Coronavirus are a large family of viruses that can be pathogenic in animals or humans. We know that in humans, a lot of coronavirus can cause respiratory infections ranging from the common cold to more serious illnesses such as Middle east respiratory Syndrome(MERS) and severe acute respiratory syndrome (SARS),the last coronavirus that was discovered is responsible for Coronavirus disease 2019 (COVID-19).This new virus and disease was unknown before the outbreak in Wuhan China in December 2019 COVID-19 is Now pandemic and affects many countries around the world.One of those countries Morocco .From March 2, a first case confirmed by infection has been detected in Morocco .Today the number of confirmed cases is reached 7584 ,the number of cured cases amounts to 4969 with 88 new recoveries ,while the number of deaths stands at 202.In addition, the number of cases excluded after negative laboratory results amounts to 155 791.In this Context ,it's essential to take advantages of optimisation tools as well than from a published study regarding the spread of the virus COVID-19 in Mexico for the designer and to reproduced for the case of Morocco,For that reason we will follow the following plan :

we will start by phase I :for what we will Briefly explain the SIR model while setting some variants of the model.Then the application on the case of Morocco specifying the hypotheses considered and then specifying the approach adopted to adjust the parameters relating to the famous  $R_0$ .After that we will present for you phase II:that show the neighborhoods existing between different regions of Morocco ,and we will Take again the approach of the paper on Mexico for the calculation of the transition matrix.and finally we will move to phase III : for what we will Publish the results of the study,and Also we will finish our study by showing that we have a certain perspective.And in the end we will finish our paper by a conclusion and this is the fourth phase that contain the approach accomplished as well as the results obtained and most interesting axe for our group in order to continue on explaining this study .(see the Fig.1 and Fig.2)

## Model.

We will start by applying Markov Chain model which can help us to predict the probability distribution of Coronavirus in time in Moroccan population, for said chain we need the estimation of the infected population in given time, and all information that shall be known by the SIR (susceptible, infected, recovered cases) differential equation model of infections.

### SIR.

Models are a simplification of the world, and the SIR model is known to be the most popular model in the science of epidemiology. First let's define the SIR model and why we aborted its use and used a more complex and advanced version.

The SIR Model is based on three functions:  $S(t)$  (number of people susceptible on day  $t$ ),  $I(t)$  (number of people infected on day  $t$ ), (number of people recovered on day  $t$ ). We study the derivative of these functions, by introducing 5 more variables:  $N$  (total population),  $\beta$  (expected amount of people an infected person infects per day),  $D$  (number of days an infected person has and can spread the disease),  $\gamma$  (the proportion of infected recovering per day --  $\gamma = 1/D$ ),  $R_0$  (the total number of people an infected person infects --  $R_0 = \beta / \gamma$ )

Giving the following equations:

As we are aiming to approach reality, we need to have a model that is also closer to reality, therefore, we know that Many infectious diseases have an incubation period before being infectious during which the host cannot yet spread the disease. We'll call such individuals — and the whole compartment — Exposed.

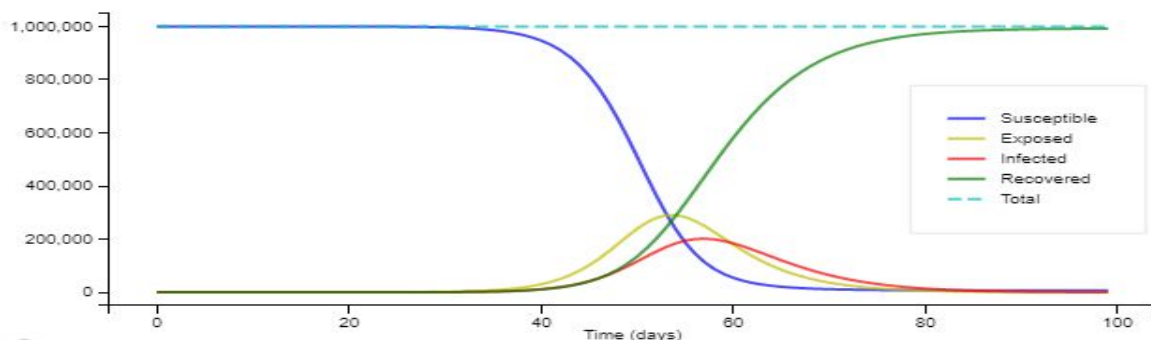
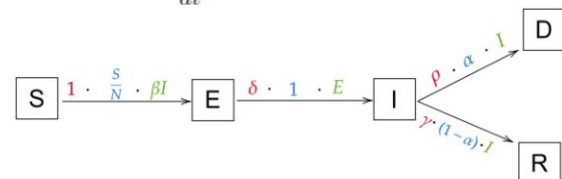
We should also take in consideration the dead compartment, to have an accurate representation of reality.

So now we are working with a modified equation system that looks as follow:

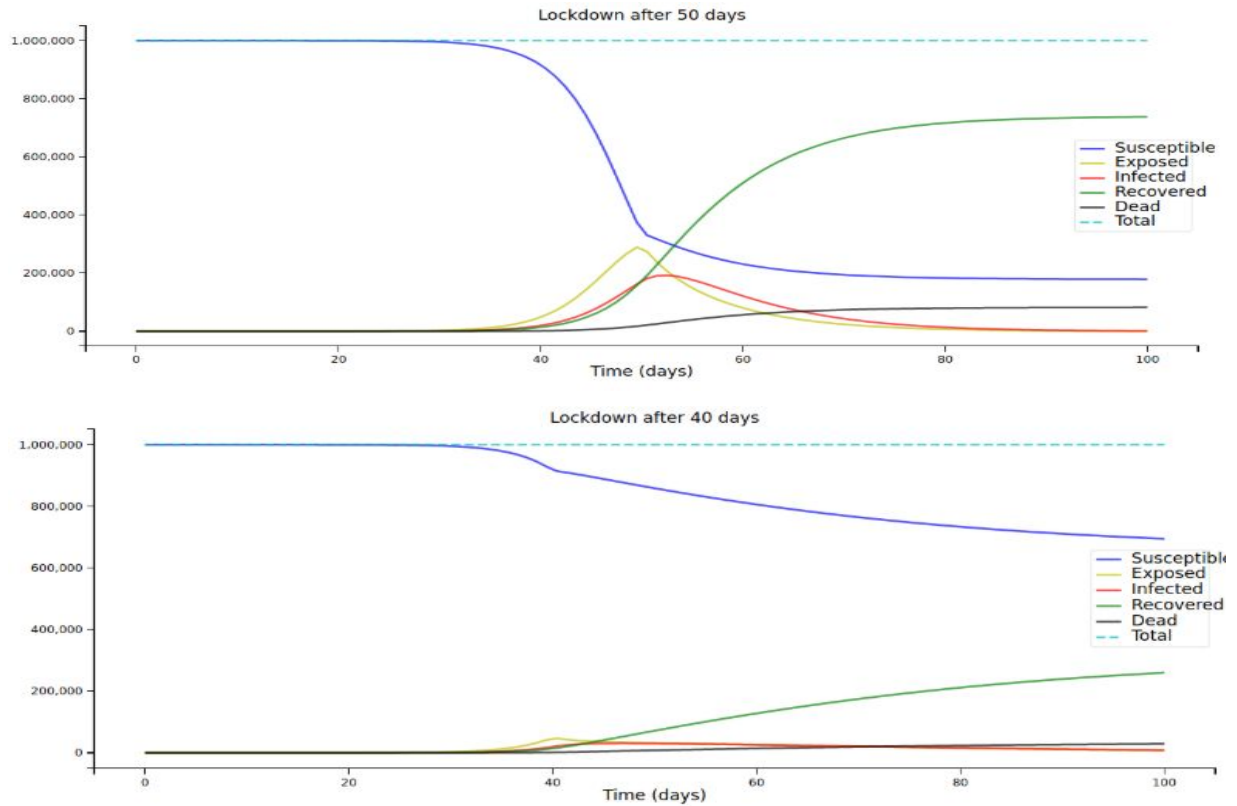
Now we have somewhat of a good model, but it could be better and to do so, we should put it to the test, let's simulate 2 epidemic with different  $R_0$ , and see the difference:

$$\begin{aligned}\frac{dS}{dt} &= -\beta \cdot I \cdot \frac{S}{N} \\ \frac{dI}{dt} &= \beta \cdot I \cdot \frac{S}{N} - \gamma \cdot I \\ \frac{dR}{dt} &= \gamma \cdot I\end{aligned}$$

$$\begin{aligned}\frac{dS}{dt} &= -\beta \cdot I \cdot \frac{S}{N} \\ \frac{dE}{dt} &= \beta \cdot I \cdot \frac{S}{N} - \delta \cdot E \\ \frac{dI}{dt} &= \delta \cdot E - (1 - \alpha) \cdot \gamma \cdot I - \alpha \cdot \rho \cdot I \\ \frac{dR}{dt} &= (1 - \alpha) \cdot \gamma \cdot I\end{aligned}$$



As we can easily recognize, the  $R_0$  has a major role in the spread of the disease, and for the most time we ignored it's time dependency, so maybe it's time reconsider that and what a better way then a simulation, this time we will change the value of  $R_0$  in the middle of an epidemic, first at the day 50 and then at the day 40, expressing a lockdown like simulation, as if we want to see if a lockdown was made 10 days in advance will it matter:



This simulation proves two points, first we should work with  $R_0$  dependent on time, second, 10 days earlier saves more than 60% of the population from being infected. We will be considering the next equation to define  $R_0$  from now on:

$$R_0(t) = \frac{R_{0_{start}} - R_{0_{end}}}{1 + e^{-k(-x+x_0)}} + R_{0_{end}}$$

Similarly to  $R_0$ , the fatality rate  $\alpha$  is probably not constant for most real diseases. It might depend on a variety of things; We'll focus on dependency on resources and age.

Now that we have figured out the model, we need to adapt it to fit the data of morocco, and to fit the COVID 19, epidemic.

As for Morocco it's fair to notice a new compartment of Critical, for individuals that need intensive care. This will allow us to model overflowing hospitals. Of course, only infected individuals can enter the critical state. From the critical state, they can either die or recover.

Now we're missing the rate of becoming critically ill after being infected, the rate of dying while being critically ill, and the rate of recovery while being critically ill. Reading through current estimates, we get the following numbers (we aggregated these from multiple sources):

Number of days from infected to critical: 12 ( $\rightarrow$ rate:  $1/12$ )

Number of days from critical to dead: 7.5 ( $\rightarrow$ rate:  $1/7.5$ )

Number of days from critical to recovered: 6.5 ( $\rightarrow$ rate:  $1/6.5$ )

There is one more detail to add to our model, that is beds availability, cause there has been lots of coverage on triage taking place in Italy and other highly impacted places, meaning that doctors have to choose who gets treated with the limited resources available.

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We finally get this revised model:

$$\frac{dS}{dt} = -\beta(t) \cdot I \cdot \frac{S}{N}$$

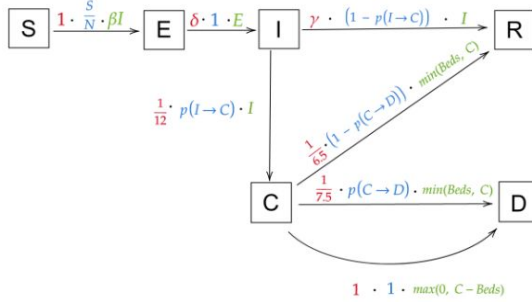
$$\frac{dE}{dt} = \beta(t) \cdot I \cdot \frac{S}{N} - \delta \cdot E$$

$$\frac{dI}{dt} = \delta \cdot E - \frac{1}{12} \cdot p(I \rightarrow C) \cdot I - \gamma \cdot (1 - p(I \rightarrow C)) \cdot I$$

$$\frac{dC}{dt} = \frac{1}{12} \cdot p(I \rightarrow C) \cdot I - \frac{1}{7.5} \cdot p(C \rightarrow D) \cdot \min(Beds(t), C) - \max(0, C - Beds(t)) - \frac{1}{6.5} \cdot (1 - p(C \rightarrow D)) \cdot \min(Beds(t), C)$$

$$\frac{dR}{dt} = \gamma \cdot (1 - p(I \rightarrow C)) \cdot I + \frac{1}{6.5} \cdot (1 - p(C \rightarrow D)) \cdot \min(Beds(t), C)$$

$$\frac{dD}{dt} = \frac{1}{7.5} \cdot p(C \rightarrow D) \cdot \min(Beds(t), C) + \max(0, C - Beds(t))$$



- $N$ : total population
- $\beta(t)$ : expected amount of people an infected person infects per day
- $\gamma$ : the proportion of infected recovering per day ( $\gamma = 1/D$ )
- $Ro\_start$  (parameter in  $Ro(t)$ )
- $Ro\_end$  (parameter in  $Ro(t)$ )
- $xo$  (parameter in  $Ro(t)$ )
- $k$  (parameter in  $Ro(t)$ )
- $s$  (parameter in  $Beds(t)$ )
- $Bedso$  (parameter in  $Ro(t)$ )
- $\delta$ : length of incubation period
- $p(I \rightarrow C)$ : probability of going from infected to critical
- $p(C \rightarrow D)$ : probability of dying while critical

Now that we have finished the preparation of our model, we just need to go through the data of Morocco about Covid19, and tune the parameters we don't know, to fit the model well;

The data was gathered from different resources, to be found in acknowledgment. Let's look at our model in comparison with the real world data:

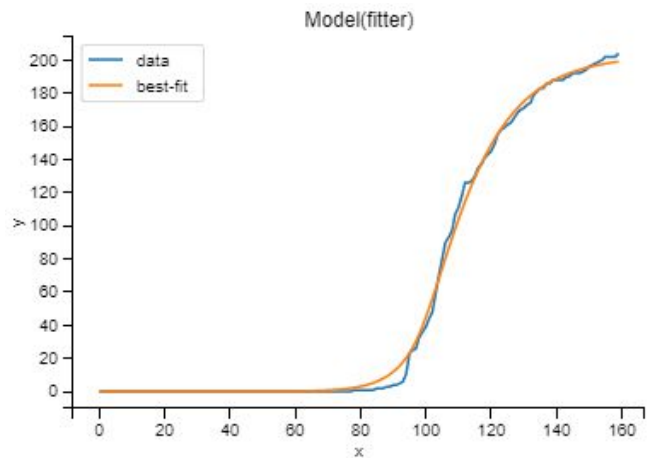
The model looks to fit the world's data well and as we have used the least square method to find our tuned variables, we can check how accurate it is:

chi-square 1775.13599

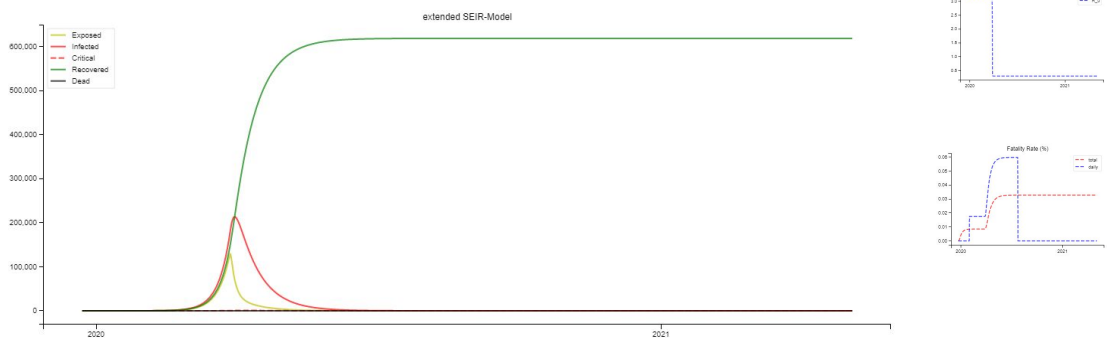
Akaike. 399.033360

Bayesian 420.559576

This translate that our model is fairly accurate, giving the lack of data,



Now, dat we have our model, and it's fit to the data of more than 90days data of Morocco under epidemic, we might run our predictions:



Our prediction is giving promising results, of a fatality rate &  $R_0$  strongly decreasing, and the patients never reaching the capacity limits.

## Discrete Markov chain.

This chain consists of 12 regions which correspond to administrative divisions in Moroccan kingdom. Thus  $E = \{ei : e \in F, i \in \mathbb{N}\}$  where  $F$  stands for the Moroccan territory, this set maps to  $S = \{s1, s2, \dots, s12\}$  of discrete states  $f: E \rightarrow S$  in a bijective fashion; let us call  $U$  this process, then  $T \subset U$  where  $T$  stands for the set of temporal parameters,  $T = \{tj | j \in \mathbb{N}\}$  where the  $j$ -th stands for the  $j$ -th day or  $[j] = [day]$ , i.e., the corresponding unit of the temporal parameter is the day. For now, let us establish the conditions of probability,  $\forall siRsk \exists pik \in \Omega$ , for every relationship existing between the  $i$ -th and  $k$ -th region, there exists an associated probability  $ik$  for the transition from the  $i$ -th towards the  $k$ -th state. To be more specific, if for example the  $i$ -th state interact with  $n$  different states, then the associated probability for every  $siRsk$  is  $pik = 1/n$ .

Using the graphic card below that shows Moroccan regions, we extract the transition matrix M, This matrix is shown in Fig.4(We did our stochastic matrix based on the numbers that existed in the geographic card shown in Fig.3) such as :

$$\sum_{i=1}^{12} P_{1n} = 1$$

$$M = \begin{pmatrix} 0.0 & 1/3 & 1/3 & 1/3 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 \\ 1/3 & 0.0 & 1/3 & 0.0 & 0.0 & 0.0 & 0.0 & 1/3 & 0.0 & 0.0 & 0.0 & 0.0 \\ 1/5 & 1/5 & 0.0 & 1/5 & 1/5 & 0.0 & 0.0 & 1/5 & 0.0 & 0.0 & 0.0 & 0.0 \\ 1/4 & 0.0 & 1/4 & 0.0 & 1/4 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 \\ 0.0 & 0.0 & 1/5 & 1/5 & 0.0 & 1/5 & 1/5 & 1/5 & 0.0 & 0.0 & 0.0 & 0.0 \\ 0.0 & 0.0 & 0.0 & 1/3 & 1/3 & 0.0 & 1/3 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 \\ 0.0 & 0.0 & 0.0 & 0.0 & 1/4 & 1/4 & 0.0 & 1/4 & 1/4 & 0.0 & 0.0 & 0.0 \\ 0.0 & 1/5 & 1/5 & 0.0 & 1/5 & 0.0 & 1/5 & 0.0 & 1/5 & 0.0 & 0.0 & 0.0 \\ 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 1/3 & 1/3 & 0.0 & 1/3 & 0.0 & 0.0 \\ 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 1/2 & 0.0 & 1/2 \\ 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 1/2 & 0.0 & 1/2 \\ 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 1.0 & 0.0 \end{pmatrix}$$

In our case, the initial vector of this process would be, according to the moroccan ministry of health reports, starting from the first case confirmed in 02/03/2020 to 13/03/2020 which the following cases are already confirmed: Casablanca, 3 cases (one case is a dead case latter); Marrakech, 3 cases; Fez, 1 case; Souss Massa, 1 case. So, the total amount of cases which can be described as the cardinality of the set of cases CA, here  $|CA|=8$  with the probabilities of the initial vector  $p_0$  for any given region are  $p_i = \text{\#cases} / |CA|$ . Considering the process we already have, the initial vector is:

$$p_0 = (0.0 \ 0.0 \ 1/8 \ 0.0 \ 0.0 \ 3/8 \ 3/8 \ 0.0 \ 1/8 \ 0.0 \ 0.0 \ 0.0)$$

(we apply the relation above to calculate probabilities. For instance, to calculate the probability of Casablanca-Settat, we divide the total cases of the region, which is 3, by the total of cases 8).

We have computed the distributions probabilities of covid-19 for the following dates: 14/03/2020, 15/03/2020, 16/03/2020, 17/03/2020, 18/03/2020 and 19/03/2020. We should note that the quarantine starts on 20 of March. So, we have selected those dates with consideration to be before launching the emergency state in Morocco in order to prevent if Markov chain has a good prediction on the model or not.

$$\begin{aligned} p_1 &= p_0 * M = (0.025 \ 0.025 \ 0.15 \ 0.24375 \ 0.09375 \ 0.16666667 \ 0.16041667 \ 0.09375 \ 0.04166667 \ 0.0) \\ p_2 &= p_0 M^{**2} = (0.0458 \ 0.0404 \ 0.135 \ 0.088 \ 0.1425 \ 0.1279 \ 0.14333 \ 0.13 \ 0.09458 \ 0.03125 \ 0.02083 \ 0) \\ p_3 &= (0.06255 \ 0.0682 \ 0.1053 \ 0.1134 \ 0.1535 \ 0.086 \ 0.128 \ 0.1363 \ 0.077 \ 0.0419 \ 0.0156 \ 0.010416) \\ p_4 &= (0.07218 \ 0.069 \ 0.1299 \ 0.101430 \ 0.1376 \ 0.091 \ 0.1126 \ 0.1325 \ 0.0804 \ 0.0336 \ 0.03138 \ 0.0078) \\ p_5 &= (0.0744 \ 0.07655 \ 0.1265 \ 0.1079 \ 0.1364 \ 0.081 \ 0.11125 \ 0.131 \ 0.0715 \ 0.0425 \ 0.025 \ 0.0157) \\ p_6 &= (0.0778 \ 0.0764 \ 0.1309 \ 0.1044 \ 0.133 \ 0.0821 \ 0.104 \ 0.1298 \ 0.0754 \ 0.037 \ 0.0369 \ 0.01231) \end{aligned}$$

Based on real statistics of our case, we had calculated  $p_{3r}$  and  $p_{6r}$  and we get:

$$\begin{aligned} p_{2r} &= (0.035 \ 0.0107 \ 0.39 \ 0.25 \ 0.071 \ 0.107 \ 0.035 \ 0.0 \ 0.0) \\ p_{6r} &= (0.049 \ 0.032 \ 0.196 \ 0.245 \ 0.033 \ 0.2786 \ 0.081 \ 0.0006 \ 0.016 \ 0.0) \end{aligned}$$

We observe, comparing between the previous predicted and real vectors, that the markov chain process predicts the model well in some regions when it doesn't in others.

By now, we had also applied the Markov chain model after the quarantine to prevent if this latter was really a good measure to take or not (so there is no interaction between regions what makes our stochastic matrix an identity matrix). We took the 20/03/2020 as the initial vector in this process (we have 86 cases) as follows:

$$P_0 = (0.081 \ 0.046 \ 0.23 \ 0.232 \ 0.023 \ 0.232 \ 0.081 \ 0.0 \ 0.07 \ 0.012 \ 0.0)$$

Now, we will compute the probability distributions of covid-19 for the following dates: 21/03/2020, 21/04/2020, 21/06/2020, 21/07/2020, 21/08/2020.

By calculating the other predicted vectors, we realise that they remain the same as the initial one. Let us now calculate some real vectors :

$$P1=(0.081 \ 0.046 \ 0.23 \ 0.232 \ 0.023 \ 0.232 \ 0.081 \ 0 \ 0.07 \ 0.012 \ 0 \ 0)$$

$$P2=(0.13 \ 0.04 \ 0.15 \ 0.087 \ 0.02 \ 0.26 \ 0.23 \ 0.048 \ 0.015 \ 0.0003 \ 0.0012 \ 0.0006)$$

We believe in the same conclusion we did before, the Markov Chain may be a good predictor in some areas while it can't be in others. This conclusion may lead us to think of other factors spreading such as temperature, no preventive measures and preparedness..etc.

### **Gather round.**

Inspiring from The CIDRAP team studies developing three scenarios for the development of COVID-19 over the next two years. The first scenario consists of predicting that the first pandemic wave will be followed by repetitive smaller, variant and consistent waves that will diminish in 2021 but depending on governments' prevention measures. The second one predicts an expecting wave by the end of 2020 before the virus appears in 2021 in smaller waves. The last scenario predicts an unclear pique appearing after the spring wave. This latter remains the optimistic version as the pique wouldn't require any mitigation measures.

As already mentioned, We can ask several questions to get an idea about factors influencing covid-19 spread like temperature effects and humidity as shown in Fig.5: a relative humidity of 80% or lower than 20%, most coronaviruses are still active after two days at a constant temperature of 20 degrees Celsius. At a constant temperature and relative humidity of 50%, less than 1% of the viruses survived after 2 days, the thing that can lead us to suspect temperature and humidity as major factors especially when the total cases were still in progress despite the confinement between regions. We also ask if the season influences the virus. So far, the change in infection rate might be due to the ways that people change their behavior with the seasons, going from being enclosed in offices and schools to opening windows and spending more time outdoors. (Getting more sunlight, which drives Vitamin D production and might enhance the immune system's defenses, might play a role, too.). In brief, Trusting in summer would be a complicated solution, because other respiratory infections, such as the flu and some colds, are largely seasonal. One more question should be asked is the influence of the treatment protocol adopted by the nation. The decision and protocols that each state takes for treating the situation of coronavirus play a big role in limiting the number of confirmed cases for which our state has taken a very good decision on the good time and those decisions contribute very well on reducing the number of deaths and confirmed cases .

### **Conclusion.**

In this scientific paper, we have applied from a published study regarding the spread of the virus COVID-19 in Mexico the two models Markov Chain and SIR for moroccan case with these two models we can say that Morocco did a great job when announcing the quarantine in very early time, because the total cases was diminishing until this day, and as Markov chain model and SIR model had predicted. Wetherver, the observed progression in cases numbers goes for sure to other factors that has not been proven yet which obviously people unconscious is the big part. Our team is interested, by computing both previous models, in predicting the virus spread in our country, particularly in each region, although the application of the early preventive measures taken.

### **acknowledgment.**

Predicting COVID-19 distribution in Mexico through a discrete and time-dependent Markov chain and an SIR-like model.

<https://duux.com/en/the-effects-of-temperature-and-humidity-on-covid-19-corona-virus/>

<https://www.wired.com/story/how-might-the-change-of-seasons-affect-covid-19/>

<https://towardsdatascience.com/infectious-disease-modelling-beyond-the-basic-sir-model-216369c584c4>

<https://towardsdatascience.com/infectious-disease-modelling-fit-your-model-to-coronavirus-data-2568e672dbc7>

[https://raw.githubusercontent.com/hf2000510/infectious\\_disease\\_modelling/master/data/](https://raw.githubusercontent.com/hf2000510/infectious_disease_modelling/master/data/)

<https://tinyurl.com/t59cgxn>

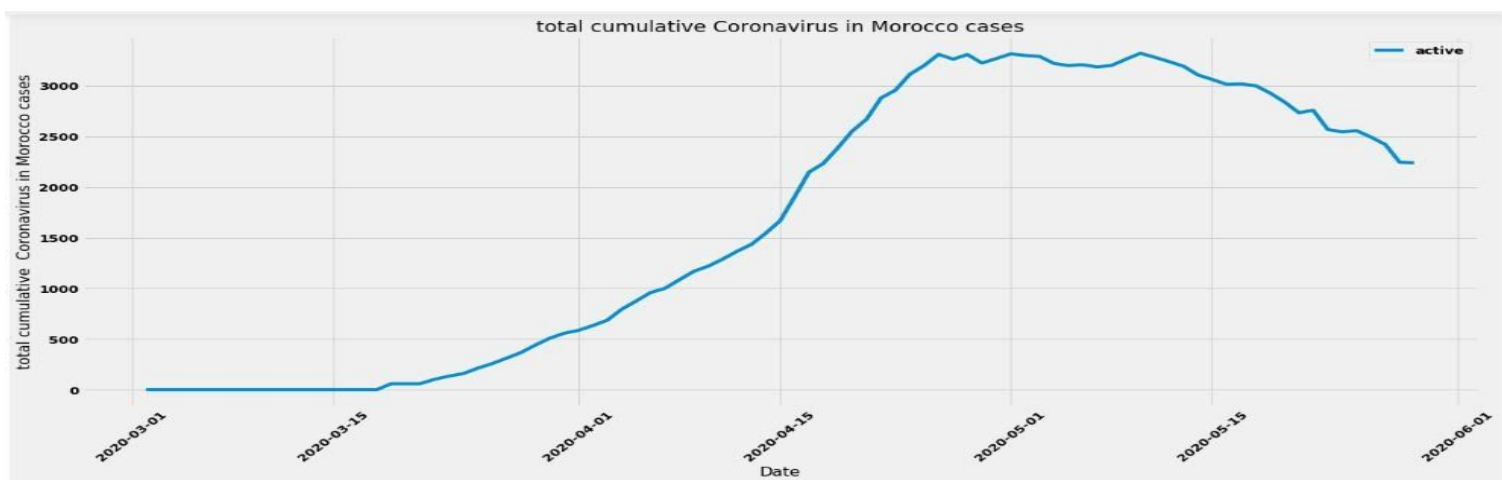


Fig.2 .A graph showing the total cumulative of active cases

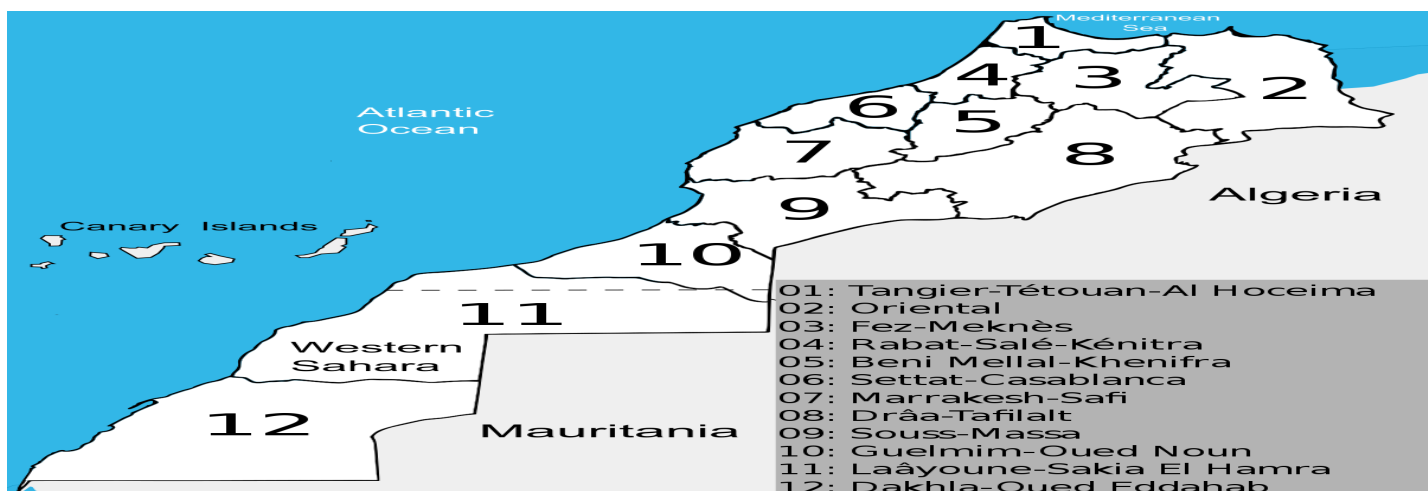


Fig.3 . The graph is showing the 12 regions of Moroccan territory with numbers which are based in the counting above.



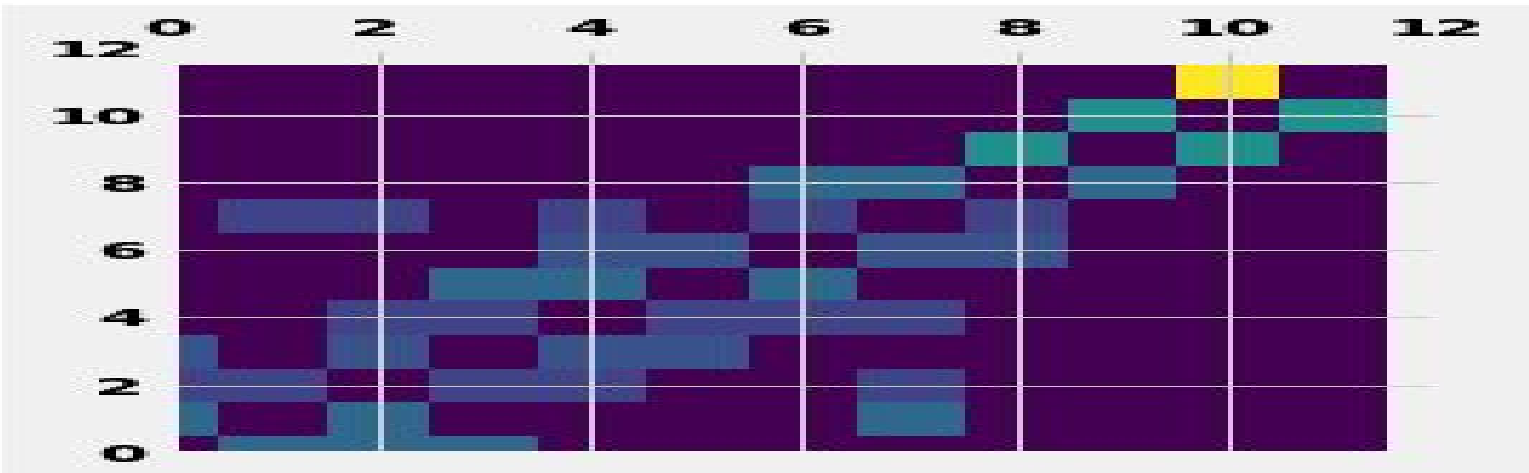


Fig.4 . A graph showing the stochastic matrix corresponding to the transition probabilities between regions

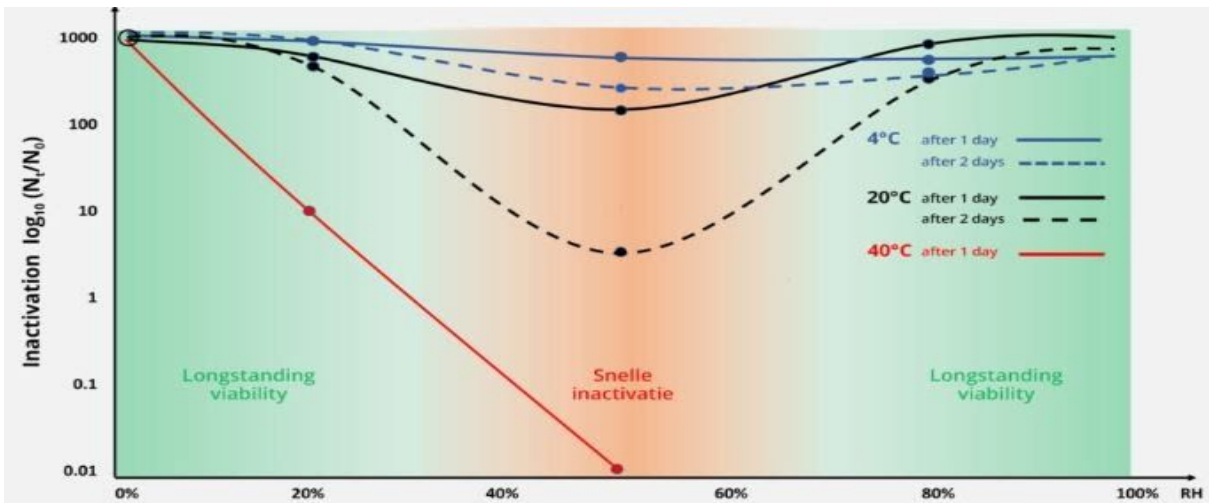


Fig.5 . temperature and humidity effects on Coronavirus spreading



