

Age Prediction for COVID-19 Suspects and Contacts in Villa Clara Province, Cuba

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Abstract

The COVID-19 pandemic affecting planet Earth has had a peculiar development in Cuba. The objective of the research consisted in modeling by means of the methodology of the Regressive Objective Regression (ROR) two parameters/variables (age and number of contacts) inherent to the SARS-CoV-2 pandemic causing the COVID-19, during the year 2020 and so far in 2021 in Villa Clara province, Cuba. Mathematical models were obtained by means of the ROR methodology that explain their behavior, being able to extract information from a white noise, which made it possible to make a long-term prognosis of contact cases, which can be estimated up to 13 steps ahead, allowing to take measures in clinical services, and thus avoid and decrease the number of deaths and complications in patients, since patients can be detected and treated with medication faster. The age of suspects can also be estimated using the ROR methodology, where the trend of age was increasing for contact cases, where all variables were significant, indicating that there is an increasing tendency for cases to decrease if control measures are increased. It is concluded that COVID-19, despite being a new disease, can be followed by means of mathematical modeling ROR, a better management of the pandemic, so we hope that this prognosis can help in decision making for the prediction age, suspects and contacts of COVID-19 in the Villa Clara province and Cuba.

Keywords: COVID-19; Age; Prognosis; Objective Regression Regression (ORR); Suspects

Introduction

The struggle between man and infectious diseases dates back to the very beginning of civilization [1]. Throughout history, mankind has suffered the scourge of an infinite number of entities with varied etiological diversity (viral, bacterial and parasitic), which have delayed the advance of the American tropics for centuries and spread death and disability among millions of the planet's inhabitants [1-4].

The increase in re-emerging and emerging diseases in recent decades has greatly complexified the epidemiological picture at the planetary level [3,5,6], where several epidemic and pandemic outbreaks have been evident, with marked repercussions on human and animal health [7-10]. It should be kept in mind that this increase in infectious entities has not been, nor is it something casual, but rather, consequences of human mismanagement of ecosystems [4,10,11].

The current situation that the planet is experiencing, due to the new coronavirus, is one more effect, derived from the bad behavior of anthropogenic activity, accumulated over thousands of years [11-13].

Coronaviruses belong to the Coronaviridae family and can cause respiratory and digestive diseases in both birds and mammals, including humans, in which they can cause illnesses ranging from the common cold to more severe conditions such as bronchitis, bronchiolitis and pneumonia [14,15]. The most frequent symptoms are respiratory [15,16]; fever is present at onset (occurs in more than 90% of cases), followed by dry cough (70%). Muscle aches (myalgias), headache, feeling of fatigue or tiredness (40%) and digestive symptoms such as vomiting or diarrhea are also frequent at the onset of symptoms [17,18]. Less frequent seems to be sore throat. Because other respiratory illnesses may present with similar symptoms, it is important for the patient to report possible contacts with ill persons or persons who have been in areas identified as having a high frequency of coronavirus [18,19]. Monitoring and communication with the medical team is essential to detect respiratory distress early [17,19].

The new coronavirus (2019-nCoV) identified on December 31, 2019 in Wuhan, China, currently officialized as SARS-CoV-2, produces COVID-19. In addition, this virus is the first of its family to be declared a pandemic by the World Health Organization (WHO) on March 11, 2020 [20]. Global epidemiological studies of coronavirus (CoV) over 15 years have shown that bats in Asia, Europe, Africa, America and Australia harbor a wide variety of viruses, which harbor and spread these infectious agents quite easily, increasing their ability to transmit [21-23]. According to the Research Group Mathematical Models in Science and Technology: Development, Analysis, Numerical Simulation and Control (MOMAT) of the Institute of Interdisciplinary Mathematics of the Complutense University of Madrid, Spain, the application of the Be-CoDiS (Between-Countries Disease Spread) model in the analysis of the COVID-19 pandemic numerically projects that this viral phenomenon will be present until July 2020 in the world [22-24]. Therefore, it is important to estimate the trend in the behavior of the epidemiological curve of the COVID-19 pandemic.

Objective of the Study

The objective of the research consisted in modeling by means of the methodology of the Regressive Objective Regression (ROR) two parameters/variables (age and number of contacts) inherent to the SARS-CoV-2 pandemic causing the COVID-19, from January 1st to January 20th, 2021 in Villa Clara province, Cuba.

Materials and Methods

Study area

The research was carried out in Villa Clara province, which is located in the center of the country (Figure 1), it is politically and administratively conformed by 13 municipalities, being its provincial capital, Santa Clara, which at the same time constitutes the head municipality. It has geographical limits, to the west with the province of Matanzas, to the south with the provinces of Cienfuegos and Sancti Spiritus and to the north, with the waters of the Caribbean Sea.

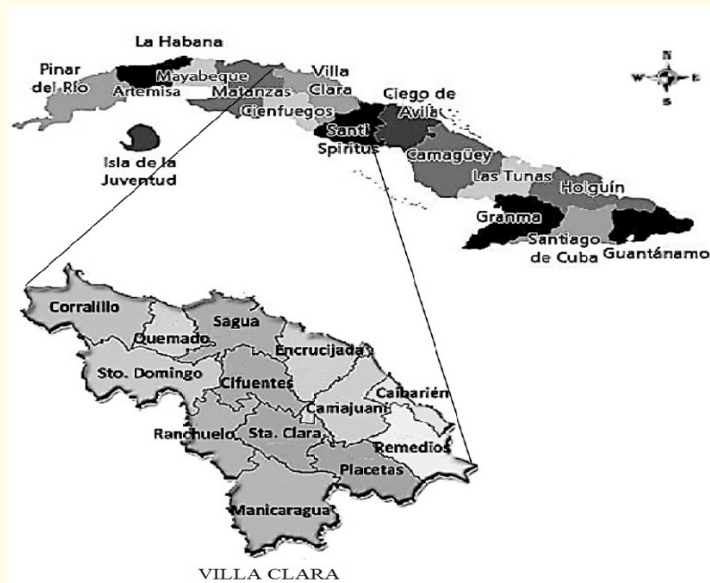


Figure 1: Political-administrative map of Cuba and Villa Clara province.

Research details

The research consisted in modeling by means of the Objective Regressive Regression (ORR) methodology the variables (age and contacts of cases) inherent to the SARS-CoV-2 pandemic causing the COVID-19 in Villa Clara province, so that prognostic models could be made for both variables. We worked with two databases: one for the age variable and the other for case contacts. In the case of age, we worked with a total of 247 cases during the period from January 1 to 12, 2021, which allowed us to make the prognosis of this variable from January 13 to 20, 2021. For case contacts, the database included 957 cases.

The prognosis was performed with the use of the Regressive Objective Regression (ROR) methodology that has been implemented on different variables such as viruses and bacteria circulating in Villa Clara province [25-28].

The objective regressive regression (ORR) methodology

The objective regressive modeling (ROR) is based on a combination of Dummy variables with ARIMA modeling, where only two Dummy variables are created and the trend of the series is obtained, it requires few cases to be used and allows to use also, it has given better results than ARIMA in some variables, such as the modeling of HIV, viral etiology/arbovirolosis entities and parasitic entities [26-30].

In the ROR methodology, dichotomous variables DS, DI and NoC are created in a first step, where:

NoC: Number of cases in the base,

DS = 1, if NoC is odd; DI = 0, if NoC is even, when DI = 1, DS = 0 and vice versa.

Subsequently, the module corresponding to the Regression analysis of the statistical package SPSS version 19.0 (IBM Company) is executed, specifically the ENTER method where the predicted variable and the ERROR are obtained.

Then the autocorrelograms of the variable ERROR are obtained, paying attention to the maximum of the significant partial autocorrelations PACF. The new variables are then calculated according to the significant Lag of the PACF. Finally, these regressed variables are included in the new regression in a process of successive approximations until a white noise in the regression errors is obtained.

All the analysis was carried out with the help of the SPSS statistical package, Version 19, from IBM.

Results and Discussion

The age of COVID-19 suspects in Villa Clara province is a random variable belonging to a white noise (Figure 2), where there is no information in previous steps to predict the future behavior of the series, however, we know that by means of the ROR methodology [25,30,31] information can be extracted from the base to predict.

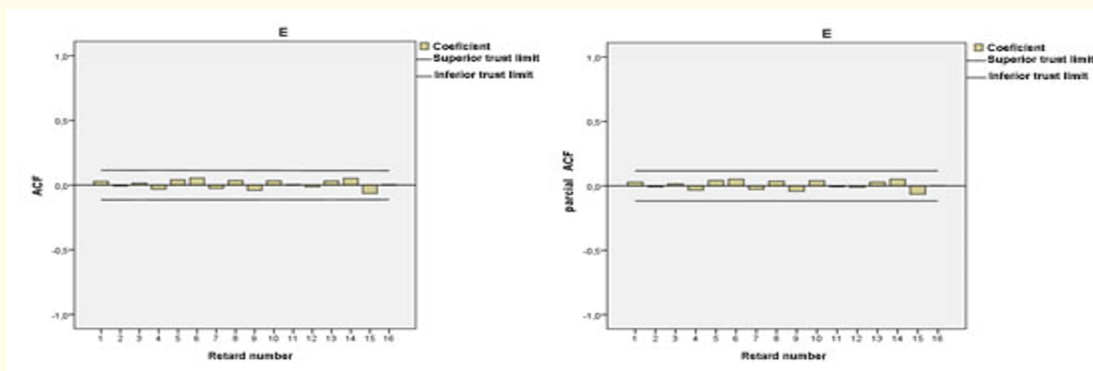


Figure 2: White noise for the age of Covid-19 suspects in Villa Clara.

Next, an ROR model to predict the age of the next Covid-19 suspects in Villa Clara, where we hope that this model can bring some clarity to the personnel who have to interview the confirmed ones, since it predicts the age of the next suspects.

Two models are obtained, the correlations of the predicted age with the actual age (Table 1).

		Age	Model_1	Model_2
Age	Correlation of Pearson	1	.812**	.862**
	Sig. (bilateral)		.000	.000
	N	247	47	43
Model_1	Correlation of Pearson	.812**	1	.898**
	Sig. (bilateral)	.000		.000
	N	47	52	48
Model_2	Correlation of Pearson	.862**	.898**	1
	Sig. (bilateral)	.000	.000	
	N	43	48	48

Table 1: Correlations of age with predicted values.

** : The Correlation is significative in the level 0,01 (2 tails).

As can be seen, model 2 presents better results than model 1, although we will present both results.

Table 2 shows the results for the next six days according to model 1.

Model 1			
	Date of report	Age	Unstandardized Predicted Value
1	13-JAN-2021	.	.
2	14-JAN-2021	.	22.74944
3	15-JAN-2021	.	.
4	16-JAN-2021	.	24.47470
5	17-JAN-2021	.	.
6	18-JAN-2021	.	33.65015
7	19-JAN-2021	.	.
8	20-JAN-2021	.	.
Total	N	8	3
a. Limited for the firsts 100 cases.			

Table 2: Case summaries for model 1(a).

Table 3 shows the results for the next six days, according to model 2.

Model 2			
	Date of report	Age	Unstandardized Predicted Value
1	13-JAN-2021	.	.
2	14-JAN-2021	.	7.67973
3	15-JAN-2021	.	.
4	16-JAN-2021	.	44.27944
5	17-JAN-2021	.	.
6	18-JAN-2021	.	51.89210
7	19-JAN-2021	.	.
8	20-JAN-2021	.	.
Total	N	8	3
a. Limited for the firsts 100 cases.			

Table 3: Cases summaries for model 2 (a).

In table 4, model 2 predicts the age of the suspects, for a period of six days after the last base data. The lags are lags of age. As can be seen, the tendency of this model is to increase in age, although none of the variables is significant, they all contribute variance to the model.

Model 2						
Model	B	Coefficients no standard		Coefficients standard	t	Sig.
		Error standard	Beta			
1	DS	-125.367	169.779	-2.089	-.738	.477
	DI	-140.682	168.720	-2.899	-.834	.424
	Tendencia	.190	.374	1.371	.506	.624

Step270	-9.396	39.165	-.038	-.240	.815
Lag29E	.399	.327	.436	1.220	.250
Lag30E	.581	.341	.565	1.702	.120
Lag14E	.085	.356	.088	.238	.816
Lag31E	.316	.320	.339	.987	.347
Lag63E	-.028	.280	-.035	-.102	.921
Lag23E	.619	.362	.692	1.712	.118
Lag86E	.059	.247	.074	.239	.816
Lag70E	-.055	.303	-.066	-.183	.858
Lag10E	.067	.344	.071	.196	.849
Lag15E	.415	.353	.453	1.177	.266
Lag56E	.523	.350	.643	1.494	.166
Lag34E	-.534	.349	-.562	-1.533	.156
Lag37E	.014	.239	.015	.059	.954
Lag17E	.151	.331	.169	.457	.657
Lag55E	.261	.264	.312	.988	.346
Lag25E	-.337	.246	-.380	-1.369	.201
Lag26E	-.405	.280	-.421	-1.445	.179
Lag38E	-.087	.340	-.097	-.256	.803
Lag22E	.630	.362	.704	1.738	.113
Lag40E	-.069	.344	-.079	-.200	.845
Lag8E	.041	.331	.043	.125	.903
Lag6E	-.291	.407	-.281	-.715	.491
Lag147E	.079	.209	.093	.377	.714
Lag145E	.502	.376	.622	1.336	.211
Lag177E	-.173	.240	-.202	-.724	.486
Lag196E	-.145	.321	-.164	-.452	.661
Lag245E	-.159	.213	-.208	-.749	.471
Lag206E	.356	.373	.397	.953	.363
Lag213E	.163	.212	.208	.769	.460
Coefficients (a, b)					
a. Dependent variable: Age					
b. Regression lineal by means origin					

Table 4: Tendency of this model 2 predicts the age and suspects.

A model (Table 5) and forecast of the case contact variable was also performed obtaining the following model that explains 96.4% of the variance with an error of 6.99 cases indicating that it is a good model [25,31,32].

Model	R	R cuadrado ^b	R squared right	Error standard of the estimation	Durbin-Watson
1	.964 ^a	.929	.926	6.990	1.713
a. Predictors: Step941, Step491, Step348, Step265, Step216, Step165, Step164, Step24, Step551, Step713, Step163, Step490, Step36, Step719, Step580, Step284, Step283, Step236, Step261, Step290, Step61, Step31, Step226, Step225, Step224, Step262, NoC, Lag13CC, DI, DS					
b. For regression through the origin (the model without intercept), R-squared measures the proportion of the variability in the dependent variable about the origin explained by the regression. This CANNOT be compared to R-squared for models that include an intercept.					
c. Dependent variable: Contact of case					
d. Regression lineal by means origin					

Table 5: Summaries of model (c, d).

In table 6, model 3 for contact cases, all variables are significant, the trend is negative, indicating that each time there is a tendency for cases to decrease, as long as control measures increase [29,31-33]. This model depends on contact cases with 13 lags (Lag13CC), so we can be 13 steps ahead of the disease in the future, and thus better disease control [33-36].

Model 3						
Model	B	Coefficient no standard		Coefficient standard	t	Sig.
		Error standard	Beta			
1	DS	11.517	.671	.317	17.161	.000
	DI	11.026	.668	.305	16.516	.000
	Tendency	-.006	.001	-.124	-5.594	.000
	Step262	415.510	7.004	.607	59.327	.000
	Step224	199.938	7.005	.292	28.540	.000
	Step225	173.333	7.005	.253	24.743	.000
	Step226	174.068	7.005	.254	24.848	.000
	Lag13CC	.059	.012	.061	5.092	.000
	Step31	112.302	7.017	.164	16.003	.000
	Step61	22.997	7.014	.034	3.279	.001
	Step290	85.550	7.003	.125	12.216	.000
	Step261	118.785	7.006	.174	16.955	.000
	Step236	36.977	7.036	.054	5.256	.000
	Step283	47.959	7.003	.070	6.848	.000
	Step284	49.169	7.004	.072	7.020	.000
	Step580	35.610	7.000	.052	5.087	.000
	Step719	55.382	7.004	.081	7.907	.000
Step36	38.179	7.019	.056	5.439	.000	
Step490	33.515	7.000	.049	4.788	.000	
Step163	30.338	7.008	.044	4.329	.000	

Step713	30.347	7.004	.044	4.333	.000
Step551	31.716	7.000	.046	4.531	.000
Step24	25.676	7.020	.038	3.657	.000
Step164	29.826	7.011	.044	4.254	.000
Step165	29.399	7.010	.043	4.194	.000
Step216	27.368	7.006	.040	3.907	.000
Step265	24.976	7.004	.037	3.566	.000
Step348	25.235	7.001	.037	3.604	.000
Step491	31.901	7.001	.047	4.557	.000
Step941	24.343	7.014	.036	3.471	.001
Coefficients ^{a,b}					
a. Dependent variable: Case contact					
b. Linear regression through the origin					

Table 6: Analysis of the contacts of cases by means model 3.

The long-term prognosis is shown in figure 3. The mean is 6.2 contacts. The highest value should occur for case number 961 with 7.37 cases.

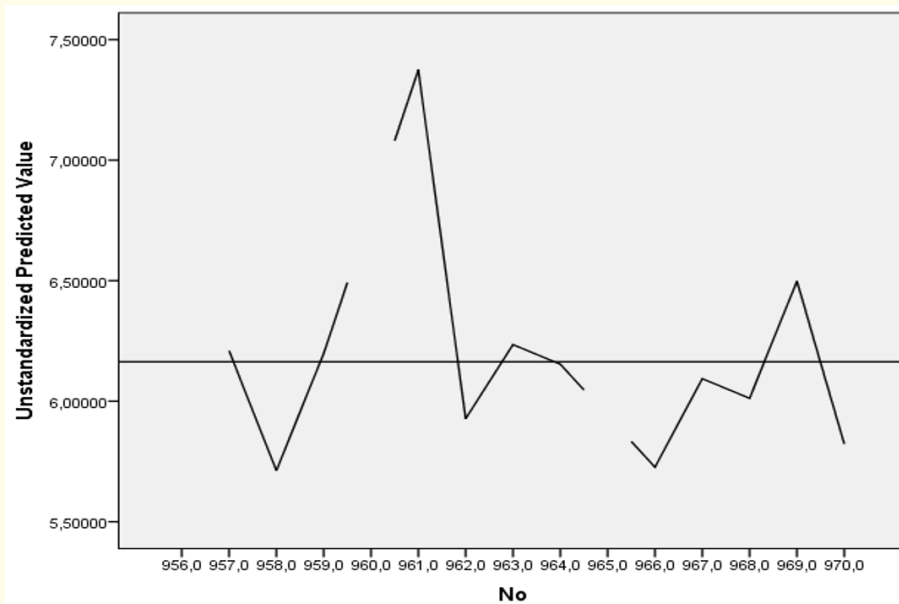


Figure 3: Predicted value of contact cases from case 957.

Conclusion

The age of suspects can be estimated using the ROR methodology, so we hope that this prognosis can help in decision making and the search for COVID-19 suspects in the Villa Clara province. The long-term prognosis of contact cases can estimate up to 13 steps forward, where the age trend is increasing. For contact cases, all variables are significant, the trend is negative, indicating that each time there is a tendency for cases to decrease with increasing control measures.

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