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MODELING OF EPIDEMICS-COVID-19 USING DIFFERENTIAL EQUATIONS

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Abstract: The study of epidemics since ancient times is an area that has aroused great interest; the history of humanity has been marked by major infections such as smallpox, the Black Death, measles, AIDS, cholera, Ebola and others. Humanity is being hit by epidemic outbreaks, which worries the World Health Organization due to the increase in the number of cases, with the Sars-CoV-2 coronavirus becoming a global pandemic on January 30, 2020. The same one that has captured the attention of The scientific community worldwide severe acute respiratory syndrome caused by the 2019-nCoV virus or Sars-CoV - 2, results in substantial morbidity and mortality. Coronaviruses can cause diseases in humans and animals, they are a large family of viruses, their impact on humans results in respiratory infections, the recently discovered coronavirus causes the COVID-19 disease.
To understand the dynamics of the epidemic allows us to design new measures that can be applied in order to combat the epidemiological outbreak, through mathematical modeling using differential equations as a tool used. to monitor the dynamics of the epidemiological behavior of Covid-19 in Ecuador. This research is developed through the explicit solution of the SIR model, and we model the development of short-term and more extensive epidemics such as COVID-19 in early stages and its best-known variants to predict the spread of infectious diseases in a population, both from the theoretical and computational point of view. Information about the Coronavirus was obtained from the Johns Hopkins University database.(Universidad Johns Hopkins, 2020)
Keywords: COVID-19, differential equations, deterministic, Susceptible (S), Infected (I), Retired (R)

INTRODUCTION

Humanity endured a new epidemic, a disease caused by a new type of coronavirus, which receives its name due to the vague resemblance to monarchical crowns when shown with an electron microscope. They are an extensive family of viruses that can cause diseases in human beings as well as animals. In humans they cause respiratory infections such as the common cold to more serious diseases such as Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS), the recently discovered one causing the coronavirus disease Covid-19. (Hernández Rodríguez, 2020)

In China, in December 2019, the first case of this new type of pneumonia was recorded in the city of Wuhan. The International Committee on Taxonomy of Viruses ICTV, in accordance with its terminology used, formally called Covid-19 the disease caused by the 2019-nCoV virus or SARS-CoV-2 (Peng et al., 2020), according to page data website: covid19.who.int/ of the World Health Organization (WHO), nearly 24,000,000 confirmed cases and more than 800,000 deaths have been reported worldwide(Gadbay & Edison Roberto, 2023)

In Ecuador, until May 19, 2022, it registers more than 873,609 infections and 35,613 deaths related to SARS-CoV-2. The first case was declared on February 29, 2020, a 71-year-old Ecuadorian resident in Spain, the citizen arrived in the country on February 14, 2020 from the Torrejón region of Spain, days later she presented symptoms of the disease(Gadbay & Edison Roberto, 2023)

(Vera Alcivar, 2020)In his research work "Modeling of COVID-19 in Ecuador", he uses the SIR model as a basis for the variants of the SEIR and SEIMR models in early stages, as well as a mathematical projection of cases that are not part of official figures.

(Manrique Abril, y otros, 2020)It does

this by applying the system of differential equations SIR compartmental model, where the population is classified into three states Susceptible (S), Infected (I) and recovered (R), the equation of the speed of variation of infected individuals is discretized, to guarantee the stability of the method, and to calibrate the model, it is done with tabulated data where the epidemic has already had a certain evolution.

It was presented a proposal for a mathematical model in differential equations using the generalized logistic curve or the (Villalobos Arias, 2020)Gompertz curve. Therefore, if you have the lower part of the Curve, that is, the first values of the curve, you can obtain the parameters of the curve, and obtain the complete curve. (Ballesteros, Blasco, & Gutierrez Sagredo, 2020)

It was applied Hamilton's equations to determine an exact closed-form solution of a modified SIR compartmental deterministic epidemiological model. In this model, the individuals S(t), R(t) are given as generalized logistic functions, while the individuals I(t) are found as a generalized logistic function multiplied by an exponential.

(Argueta, 2020)In the annexes he determines a resolution of his own authorship for the system of differential equations of the SIR compartmental deterministic epidemiological model, based on the initial conditions and the method of determinants.

(Sanz Garayalde, 2016)In his degree work he describes the importance of mathematical models that allow monitoring the epidemiological dynamics of a disease and allows establishing the durability of an epidemic, the number of infections.

Regarding Magro Garcia, in his research he adapts and applies the Be- CoDiS compartmental deterministic epidemiological model initially designed for Ebola to another disease, MERS. Obtaining very good results when estimating the magnitude of an epidemic, it is also recommended to consider the limitations of the mathematical model.

(Curth de Torres, 2015)From a scientific perspective, a mathematical model explains that it is the representative construction by contextualizing a certain part of the real world, with a specific objective. I also express "a mathematical model is the formal expression, through the use of mathematical language, of the relationships between the components of a system."(Curth de Torres, 2015, pág. 22).

García Piñera studies the SIR model through an explicit solution and its best-known variants to predict the spread of infectious diseases in a population, both from a theoretical and computational point of view, an epidemiological model introduced in 1927 by (Kermack & McKendrick, 1927).

Harko, Lobo, & Mak, they determine an exact parametric analytical solution for the (SIR) model, including births and deaths, described by a nonlinear system of differential equations, can be reduced to an Abel-type equation.

In the field of mathematical models there are countless classifications, such as Deterministic and Stochastic (Magro Garcia, 2016).(Pesco & Diambra, 2017)

The difference between these two models is very evident, because a deterministic model in the epidemiological field; a single individual causes a widespread epidemic, while the stochastic model is likely to cause the epidemic to die out depending on(Montesinos Lopez & Hernandez Suarez, 2007, págs. 218-226)

According to, (Ma & Xia, 2009) epidemiological modeling refers to compartmental deterministic dynamic models according to their epidemiological status, e.g. susceptible, infectious, recovered, etc. Where the interrelationship between compartments causes the population to become infected, progress, recover, migrate or die, these models

are specified using ED.

The (SIR) model was proposed in 1927 by Kermack and McKendrick (Kermack & McKendrick, 1927), (Baca¨er, 2012), (Brauer, Castillo Chavez, & Feng, 2019)and (Liu, Cao, Liang, & Chen, 2020), to explain the rapid rise and subsequent fall in the number of infected patients in epidemics such as the London plague (1665-1666) and Bombay (1906) or that of cholera in London (1865). It is called SIR because it is classified for the population into three possible "compartments".

METHODOLOGY

SIR MODEL

The deterministic model was created, where they considered a fixed population and classified it into three compartmental states such as: susceptible (S), infected (I) , removed (R) , hence the name of the model SIR.

$$\boxed{S(t)} \xrightarrow{\beta} \boxed{I(t)} \xrightarrow{\gamma} \boxed{R(t)}$$

Where:

$S(t)$ = Individuals susceptible to contracting the disease in time .

$I(t)$ = Individuals infected with the disease in time and who can infect the individuals in the group $S(t)$.

$R(t)$ = Removed Individuals, who can no longer be infected or transmit the disease, because they have been immunized or because they have died.

β = Infection cup.

y = Retirement mug.

N = S(t) + I(t) + R(t), Total population.

MODEL ASSUMPTIONS *SIR*

According to (Brauer et al., 2015, p. 6), the population is assumed to be constant, that is, births and deaths are not taken into account. in the time interval in which the epidemic occurs, then:

$$N = S(t) + I(t) + R(t)$$

- The transmission of the disease occurs through direct contact between people.
- When an individual is infected, he leaves the susceptible group and enters the infected group.
- Individuals in the I(t) compartment recover and acquire immunity from the disease or die, in both cases they move to the retired compartment.
- The transmission of the disease is assumed to be governed by the law of mass action between infected and susceptible, with the rate of new infections being proportional to the total number of contacts between susceptible and infected individuals. This assumption is reflected in the terms $-\beta.S(t).I$ and $\beta.S(t).I$

ORDINARY DIFFERENTIAL EQUATIONS OF THE SIR MODEL

MODEL FORMULATION

According to the law of mass action mentioned above, it stipulates the rate of variation of susceptible people who become infectious is proportional to the decrease in the product of susceptible individuals per infectious, thus we obtain the first equation that describes susceptible individuals.

$$S'(t) = -\beta.S(t)I(t)$$

Likewise: $S(t).I(\ )$ in the differential equation of infected individuals $I'(t)$ also represents the growth rate of infectious individuals by the law of mass action, in turn γ represents the growth rate of recovered individuals, then, $\gamma.I$ indicates the output of the infectious class, this way we obtain the differential equation for the infected.

$$I'(t) = -\beta.S(t) - \gamma.I(t)$$

The mathematical expression that describes the recovered individuals, and in turn represents the exit of the infectious compartment with a positive γ rate is:

$$R'(t) - \gamma . I(I)$$

From the previous hypotheses, the differential equations that govern the compartmental deterministic model known as the classic Kermack and McKendrick model were obtained. (Kermack & McKendrick, 1927), which are given by the differential equations:

$$\frac{dS}{dt} = -\beta . S(t) . I(t) \quad (1)$$

$$\frac{dS}{dt} = \beta . S(t) . I(t) - \gamma . I(t) \quad (2)$$

$$\frac{dR}{dt} = \gamma . I(t) \quad (3)$$

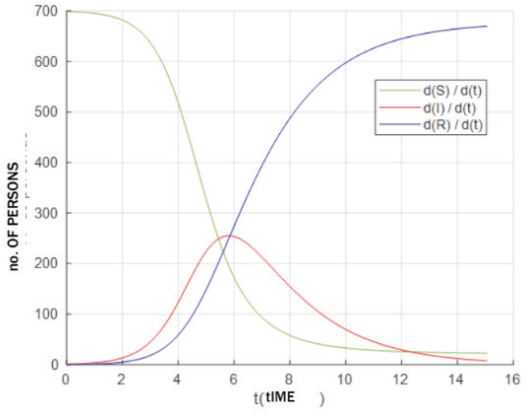

Figure 1 SIR model differential equation graph

At the beginning of the disease at time $t_0 = 0$, it will constitute the initial conditions, at this stage there will only be susceptible and infectious individuals, that is, there will be no recovered individuals, then, R 0 =0, that is, $_{the}$ total population will be given by the expression $N = S_0 + I\_0$, where β and γ represent the interaction rate of susceptible and infectious and the rate of individuals recovered from infection.

The main parameter used in epidemiology is the basic reproductive number $R_{0,}$ because this indicator allows us to analyze whether a disease will become an epidemic or disappear:

If $R_0 > 1$ an epidemic will occur.

If $R_0 < 1$ the disease will disappear.

The basic reproductive number is defined by:

$$R_0 = (\beta . S_0)/\gamma \quad (4)$$

Where:

R_0 = Basic reproductive number.

β= Infection rate.

γ= Withdrawal rate.

S_0 = Initial susceptible individuals.

ANALYTICAL STUDY SIR MODEL

Let's analyze and verify how he does in his research (García Piñera, 2014), in the event that an epidemic occurs, it must exist:

- There is a susceptible population, therefore: $S(t)>0, \forall\ t \geq 0$, in equation (1) we replace $a(t)=-\beta.I(t)$ continuous function in the interval [0.T], so:

$$S^{\wedge}{}'(t) = a(t).S(t)$$

Applying 3.4.1 similar PVI theorem $S'(t)$, we have that, $S(t)>0, \forall\ t \geq 0$

- Having at least one infected, then, $I(t)>0, \forall\ t>0$ in equation (2) we replace $a(t)=\beta.S(t)-\gamma$, continuous function in the interval $[0.T\ ]$, therefore: $I^{\wedge}{}'(t)=a(t).I(t)$ applying the similar PVI theorem S'(t), we have that, $I(t)>0, \forall\ t \geq 0$

- For there to be recovered individuals, the epidemic must have occurred, therefore, $R(t)>0 t \in (0,T]$ consequently $R\_0 \geq 0, \gamma . I > 0$ we $I(t) > \forall t \in (0,T]$ also know that $R'(t) = \gamma . 0$_ _

$$R(t)>0 t \in (0,T]$$

Likewise, since S(t)+I(t)+R(t)=N and also S(t),I(t),R(t)>0, ∀ t ∈ (0,T], then, S (t),I(t),R(t) < N, ∀ t ∈ (0,T].

Which shows that the solutions in the interval (0,T] always remain bounded, let us now examine that this same property is fulfilled

for ∀ t≥0. Applying boundedness theorem for integrals and the existence and uniqueness theorem, also taking as a condition initial t=T, we can deduce the existence and uniqueness of the solution in the interval [0,T+δ], then, the compartmental states belong to the interval of individuals of $0<S(t),I(t),R(t) < N, \forall t \in [T,T+\delta]$. By repeating the same process, the existence and uniqueness of the solution for the interval $(0, +\infty)$ can be proven by repeated application of the theorem of existence and uniqueness of the solution for the Cauchy problem, therefore, it concludes:

$$0 < S(t) < N, \forall t > 0 \quad (4)$$

$$0 < I(t) < N, \forall t > 0 \quad (5)$$

$$0 < R(t) < N, \forall t > 0 \quad (6)$$

Therefore, it can be established that the differential equations that make up the deterministic compartmental SIR model have a minimum or maximum depending on the sign of the differential equation such that (4), (5) and (6) ∈ I (0, N).

VALIDATION, CALIBRATION AND APPLICATION OF THE SIR MODEL WITH REAL DATA IN SHORT-TERM EPIDEMICS. INFLUENZA EPIDEMIC IN ENGLISH BOARDING SCHOOL 1978

On March 4, 1978, the British Medical Journal (Anonymous, 1978) published, according to the report provided, the outbreak of an influenza epidemic in a boarding school in the north of England, which housed 763 students.

The start of classes was on January 10. The students returned from their vacations that were in different parts of the world. A student returning from Hong Kong showed signs of elevated temperature from January 15 to 18. On January 22, three children were sick, the time they were sick was an average of 5-6 days. However, since the children were isolated in the infirmary, they spent perhaps around 2 days as infectious.

Additionally, as explained above, infected students were not removed from the population until 1 or 2 days after becoming infected. Therefore, not only were they contagious and they were infecting more students.

Date	Days	Infected	Recovered
01/18/1978	0	1	0
01/22/1978	1	3	0
01/23/1978	2	8	0
01/24/1978	3	25	0
01/25/1978	4	75	0
01/26/1978	5	227	9
01/27/1978	6	296	17
01/28/1978	7	258	105
01/29/1978	8	236	162
01/30/1978	9	192	176
01/31/1978	10	126	166
02/01/1978	11	71	150
02/02/1978	12	28	85
02/03/1978	13	11	47
02/04/1978	14	7	twenty

Table 1 Daily number of students infected with influenza

Note. From British Medical Journal, March 4, 1978 "Influenza in a Boarding " School "

CALCULATE AN INITIAL ESTIMATE OF THE INFECTION (β) AND WITHDRAWAL (Y) RATES

INFECTION RATE (β)

We will keep in mind that at an initial time t_0=0 there must be at least one infected person I_0=1 for an epidemic to start, likewise the recovery rate parameter is very small so it tends to zero γ→0, applying these conditions to equation (2) and solving for β we have:

$$I'(t) = \beta.S(t).I(t) - \gamma.I(t)$$

$$\beta = \frac{I'(t)}{S(t).I(t)} \quad (7)$$

We know that the derivative is equal to the tangent so I'(t) can be approximated by:

$$I'(t) \approx \frac{I(t)-I(t_0)}{t-t_0} \quad (8)$$

From table 1 we observe that after 1 day there are 3 infected out of a total of 763 students, therefore, $I(t_0)=1$, $I(t_1)=3$, replacing these data in equation (8) we will have :

Substitute $S_0=763-1$, $I_0=1$ and I^' (t)≈2 in equation (7) we obtain the value of β

$$\beta = \frac{I'(t)}{S_0.I_0}$$

$$\beta = \frac{2}{762*1}$$

$$\boldsymbol{\beta = 0.002625}$$

WITHDRAWAL CUP (Γ)

To estimate the recovery rate parameter we have two alternatives

Using equation (1) integrating S(t) and assuming that we know I(t) we have:

$$\frac{ds}{S(t)} = -\beta.I(t)dt$$

$$\int_{S_0}^{S} \frac{ds}{S} = -\beta \int_{t_0=0}^{t} I(S).ds$$

$$\ln\frac{S}{S_0} = -\beta \int_0^t I(S).ds$$

$$S(t) = S_0.e^{-\beta \int_0^t I(S).ds} \quad (9)$$

We consider t* the time that the function f(t) reaches its maximum value when its derivative is equal to zero, therefore, f^' (t^*)=0, applying equation (2) we will have I ^ ' (t^*)=0, then:

$$I'(t^*) = \beta.I(t^*).S(t^*) - \gamma.I(t^*)$$

$$0 = I(t^*)(\beta.S(t^*) - \gamma)$$

$$\gamma = \beta.S(t^*)$$

In equation (60) let us substitute t=t^* and multiply by β, then we have:

$$\beta.S(t^*) = \beta.S_0.e^{-\beta \int_0^{t^*} I(S).ds}$$

$$\gamma = \beta.S_0.e^{-\beta \int_0^{t^*} I(S).ds} \quad (10)$$

To calculate the integral that is the exponent of equation (10), we apply the compound trapezoid rule

$$\int_a^b f(x)dx \approx \frac{b-a}{n}\left(\frac{f(a)+f(b)}{2} + \sum_{i=1}^{n-1} f(x_i)\right)$$

In table 1 we can see that the maximum number of infected is after 6 days, therefore, $t_0=0$ and t^*=6, then, let us approximate the integral for n=6 where a=t_0 and b=t^ * the result being γ=0.5592

RESULTS

MODEL VALIDATION

Once the Infection (β)and Recovery (y)rates have been found, we are going to calibrate the model with the data in Table 1, considering a population of 500 individuals, comparing the results obtained when using the explicit analytical solution, with the solution obtained by numerical integration of the system. of differential equations of the SIR model given by the initial values S_0=499, I_0=1, R_0=0, as well as N = 500 and the infection and recovery rates obtained previously y=0.5592 y β=0.0026, for which we applied programming in Matlab according to (Cápsulas MultiON, 2020) and followed the following order:

- Numerical solution of the system of differential equations , (2) and (3) of the traditional SIR model in the time interval, 0 to 15 days, where $t \in [0, 15]$.
- Obtaining the parameter (u), applying the base equation in the interval $t \in [0, 15]$, by initial conditions we know that $t_0 = 0$, $R_0 = 0$, that is, at the beginning of the epidemic there will be no recovered

individuals and from the numerical solution we obtain $t_{15} = 15$, $R_{15}=398.16$, replacing we have for $t_0 = 0$, $u_0 = 1$, and for $t_{15} = 15$, $u_{15} = 0.1612$, by therefore u ∈ [1, 0.1612],

- Calculation of *S(u), I(u), R(u)* in the interval $u \in [1, 0.1612]$, applying the explicit solution given for the SIR model.
- Relationship of time (t) as a function of the parameter (u), applying the equation.
- We solve again the system of equations, (2) and (3) for the time obtained as a function of the parameter *u*.
- Graph of the numerical and explicit solution of the SIR model.
- Comparison of results obtained.

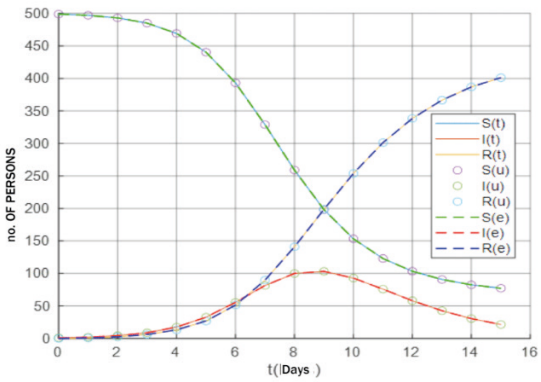

Figure 2 Joint solution of the SIR Model, numerical, parametric and explicit solution

Note. Where the Numerical solution is S(t), I((t) and R(t), parametric, S(u), I((u) and R(u) and explicit, S(e), I((e), R(e), it is also observed how the solutions follow the same trend.

To obtain **Figure** 2, the following parameters were applied, $S_0 = 499$, $I_0 = 1$ $R_0 = 0$ thus , $N = 500$, for a time interval of 15 days and the infection and recovery rates obtained previously $y = 0.5592$ y $\beta = 0.0026$.

In **Figure** 2 we can see the graphs, where the numerical solution represented by a solid line, the parametric solution represented by circles and the explicit solution represented by dashed lines, follow the same trend and overlap for both Susceptible, Infected and Recovered individuals, at the moment to execute the program developed in Matlab.

MODEL CALIBRATION

To calibrate the model, consider the total population, $N = 763$, $S0 = 762$, $I0 = 1$, $R0 = 0$, $\beta = 0.0026$, $y = 0.5592$, with these data, solve the system and obtain the solution and the joint graph of the real data represented by asterisks (*) from Table 1 of the number of students infected by influenza and the explicit parametric solution given by the proposed equations, then, the solution of the SIR model without adjustment is given:

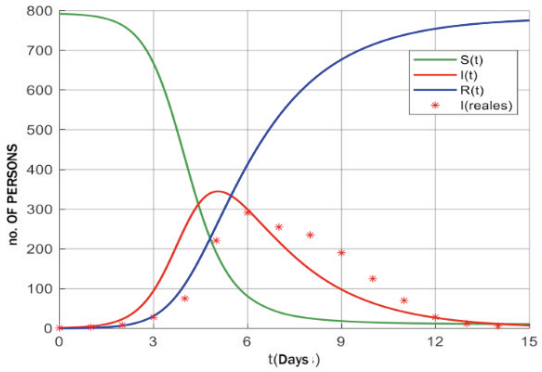

Figure **3** Explicit SIR model without adjustments versus real data from infected individuals

Note. Evolution of the 1978 English boarding school influenza epidemic.

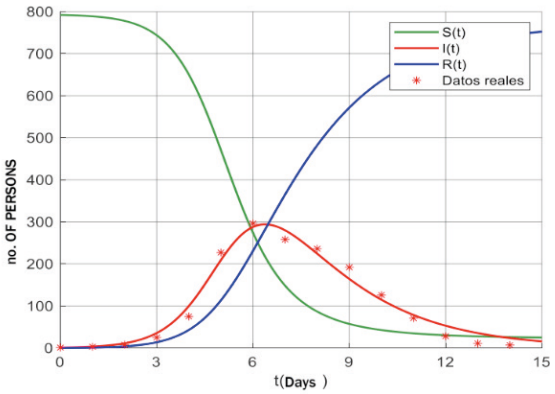

Figure **4** Explicit SIR model solution with fits versus actual infected data.

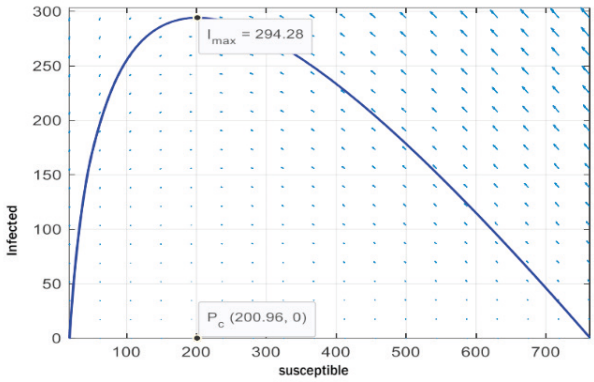

***Figure* 5** SI Phase Plan of the explicit SIR model of the influenza epidemic in an English boarding school in 1978

CONCLUSIONS

To validate the explicit solution, we proceeded to first solve the SIR model by applying numerical methods, solve the SIR model parametrically and finally solve the explicit solution of the SIR model. We proceeded to compare the graphs and numerical, parametric and exact solutions, resulting in minimal differences, therefore, the model was validated.

When applying the model to Epidemics of longer duration such as Covid- 19, and carrying out numerical and graphic research on databases from other countries, for intervals of two to three months, it can be observed that the data follows the trend of the model, therefore, is very useful to understand the development of the epidemic in early stages, for this it is important:

- The database is the product of a reliable registry, that there is agreement and there are no inconsistencies in them.
- The quality of parameter estimation depends largely on the quality of the data that the health system can provide.
- Understand and be able to interpret the parameters that govern this model.
- The basic reproductive number parameter R_0 is very important.
- The Covid-19 simulation time depends on the quality of the database.
- Being clear about the hypothesis of the SIR model establishes that recovered and deceased individuals are included within the compartment of retired individuals.

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