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A simple mathematical model for corona virus disease

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Abstract

In this paper we develop mathematical model for awareness coronavirus disease 2019. This model takes in account of special characteristic to decreases infection of coronavirus disease for social distance awareness. In different situation how can it decrease the chain of infection person? It has been observed that the infected person. It has observed that the infected person chain depend on social distance and lockdown.

Key words: novel corona virus, human history, societies, pandemic.

Introduction

The human history shaped our societies and cultures of infection diseases. Pandemic was an outbreak of human kind of history. In the human history pandemic has decimated societies and wiped out entire population. In the real history pandemic have been closely examined throughout the lens of humanities in the history of medicine. Plagues have affected the group of society in the world and first angle went to poured out his bowl on the earth and harmful painful sores upon the people. There have been recorded in western history of pandemics that each snapped our societies. The initial symptoms of the plague were headache, conjunctivitis rash covering the body and fever. Generally the infected persons would die by eight days. The plague impacts of the Roman Empire weaking its military and super mace.

The real plague pandemic oriented in mid sixth century A.D. Plague spread quickly throughout the Roman and exchange the infections of goods. The disease progressed rapidly infected and person died within day. Many people died painfully when these buboes gangrened.

From the experience of ancient cultures that medieval societies observed the connection between the passage of time and symptoms after a period of observation. They started necessary isolation. This period is called quarantine. Twenty first century the influenza virus had an encre outbreak in the world. The deadly H_1,M_1 strain of influenza virus had spread to every curner of the world within one month. The mortality rate of Spanish flu ranged between 10 to 20 percent. Many scientists were either affected by the flu. Pandemic was also first one where the longering could be observed.

HIV/AIDS is a slowly progressive pandemic that bringing new challenges for every group. High mortality the initial expansion of HIV was marked among gay population. HIV affected 0.79 percent people globally.

The novel coronavirus disease covid-19 has spread Wuhan city in china in December 2019 and spread all over the world. China has faced enormus pressure from Chinese people from around the globe to end the use of wildlife as a resources. February 24, 2020 the Chinese government ban on the trade and food. The trade of wild animals for medicine in china. The WHO said that there currently no cure covid-19. Some medicines pain relievers and cough syrup can treat some of the symptoms in this disease.

The new coronavirus has effected acute respiration syndrome. In advance biology coronavirus have greater understanding of their capacity and emergence of new diseases. The coronavirus having spike, membrane and protein. The genome of coronaviruses is linear single standard RNA molecules of positive polarity. The genetics of coronavirus have been studies natural variants, host range mutants, passed virus and viruses selected for temperature sensitivity.

Coronavirus has been spread in air travel so thousands of people are dying by coronavirus in the all over the world.

In this infection patient with fever dry cough, headache, hypoxemia and dyspain's[1,2]. Death may be result for failure of respiratory[3]. This unknown infection transmitted from person to person quickly. This infection has spread from China to all over world[4]. According to WHO report about 4 percent infected peoples have been died. Death may be result of progressive from respiratory failure[5].

The purpose of this paper is to develop a mathematical model to decreases the chain of coronavirus infected persons.

Method: Covid-19 data was collected for the published literature. We introduce the social approach of modeling is important tools for decision that can be useful for human diseases.

Mathematical formulation of the model

The detail some of the model outputs will be performed. This model are of relevance studies in particularly in the real world. In this model influence of the people by corona virus is dynamic.

Let N(t) be the total infected people at time t, the rate of change;

$$\frac{dN}{dt} = N(I - S - L) \qquad (1)$$

Similarly chain rate and Death rate are;

$$\frac{dC}{dt} = C(I - S - L) \qquad (2)$$

And

$$\frac{dD}{dt} = D(H - S - L) \qquad (3)$$

Where $I = infected\ person$

$C = chain\ of\ infection\ person$

$S = social\ distance$

$L = lockdown\ perition$

$D = death\ of\ person$

$H = high\ infected\ person$

With boundary condition

$$\left.\begin{array}{ll} N = N_0 & at\ time\ t \\ C = C_0 & at\ time\ \ t \\ D = D_0 & at\ \ time\ t \end{array}\right] \qquad (4)$$

Solution of the problem

Integrating equation (1) with boundary conditions (4) , we get

$$N = N_0 e^{(I-S-L)t} \qquad (5)$$

Similarly integrating equation (2) & (3), applying the boundary condition;

$$C = C_0 e^{(I-S-L)t} \qquad (6)$$

And

$$D = D_0\ e^{(H-S-L)t} \qquad (7)$$

Result

The present paper proposes a more realistic model of explaining the infected person from coronavirus. The infected person chain of infected person has been examined social distance and lockdown. From equation (5) it is clear that the total infected person depends on social distance and hardly lockdown. Similarly from equation (6) it is also clear that the chain of infected person totally depend upon social distance and lockdown. For high infected case social distance and lockdown is meaningless. It depend the immunity of the person.

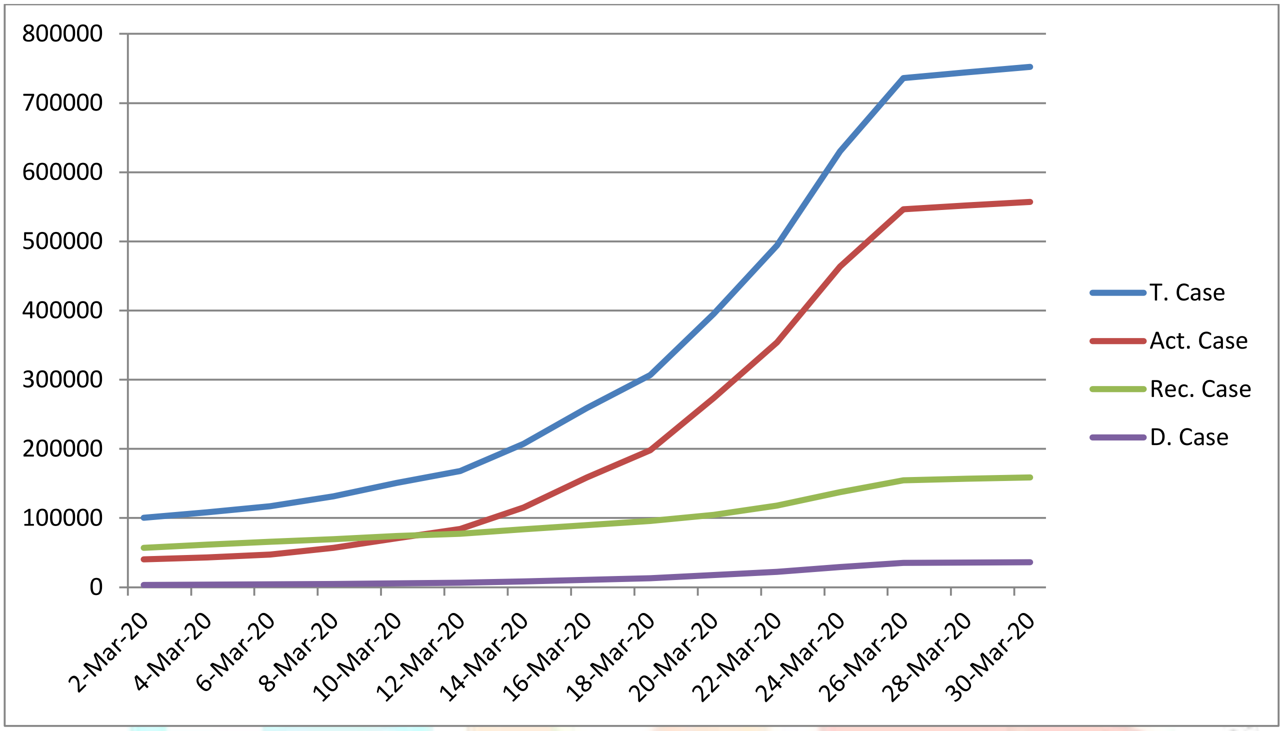
Discussion

From the graph of united state it has been observed that social distance and lockdown position in this country is not maintained in proper time. So the total infected person and dead person graph is very high. Which is very dangerous of humanity of that country? From graph of United Kingdom it has been observed that the social distance and lockdown decision take by their country government late so the graph of infected person and death rate very high. It has been observed that the infected chain is increasing rapidly in those countries. Infected person chain broken by social distance and lockdown. When infected chain is not broken then corona virus problem is much serious in world for living humanity.

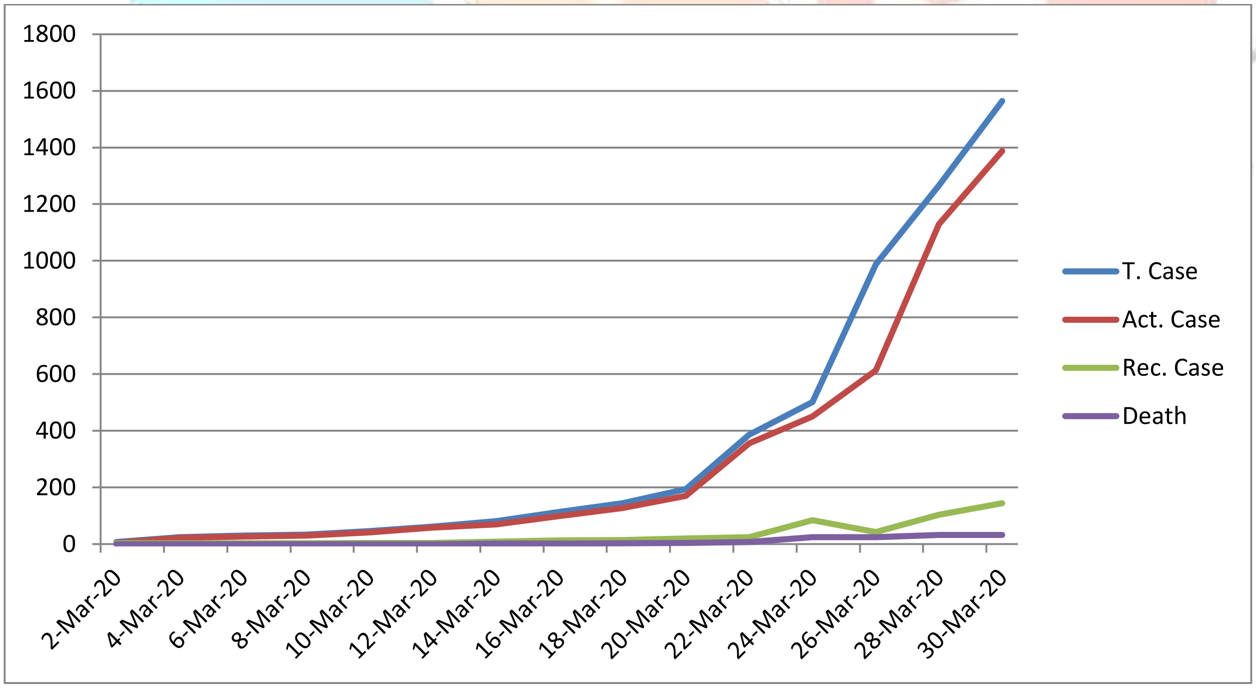
From Indian person infected graph it is clear that Indian government is taking suitable decision in proper time. In this decision Indian government hardly maintained lockdown in whole country and maintained social distance in proper time. In this way the graph of Indian infected person is very law in compare to the other countries of world. Indian government is taking good decision of human life.

Finally it has been observed that the whole world is catchingup Indian lockdown decision and try to control the chain of infected person.

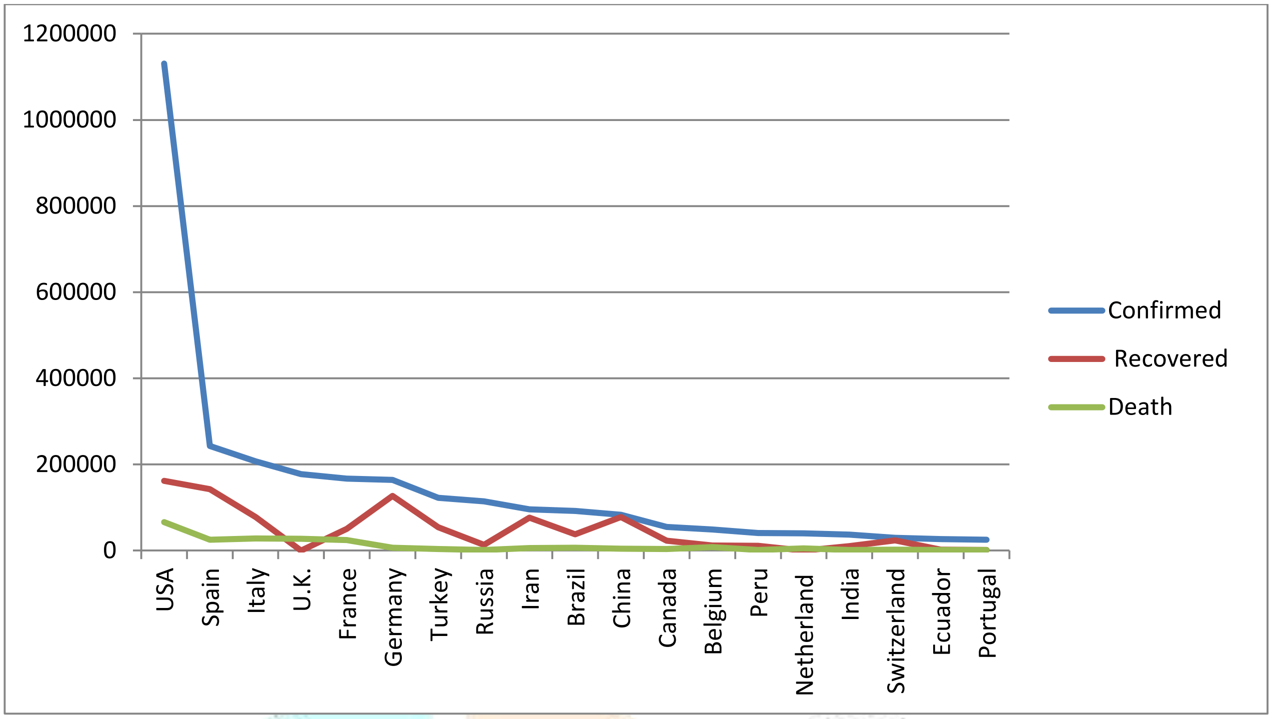
From this model it is also clear that the infected person and chain of infected person depends on social distance and lockdown. Those countries do not maintained social distance properly then graph of infected person and death rate will be very high.



Graph of Corona Cases in World Fig. (1.1)



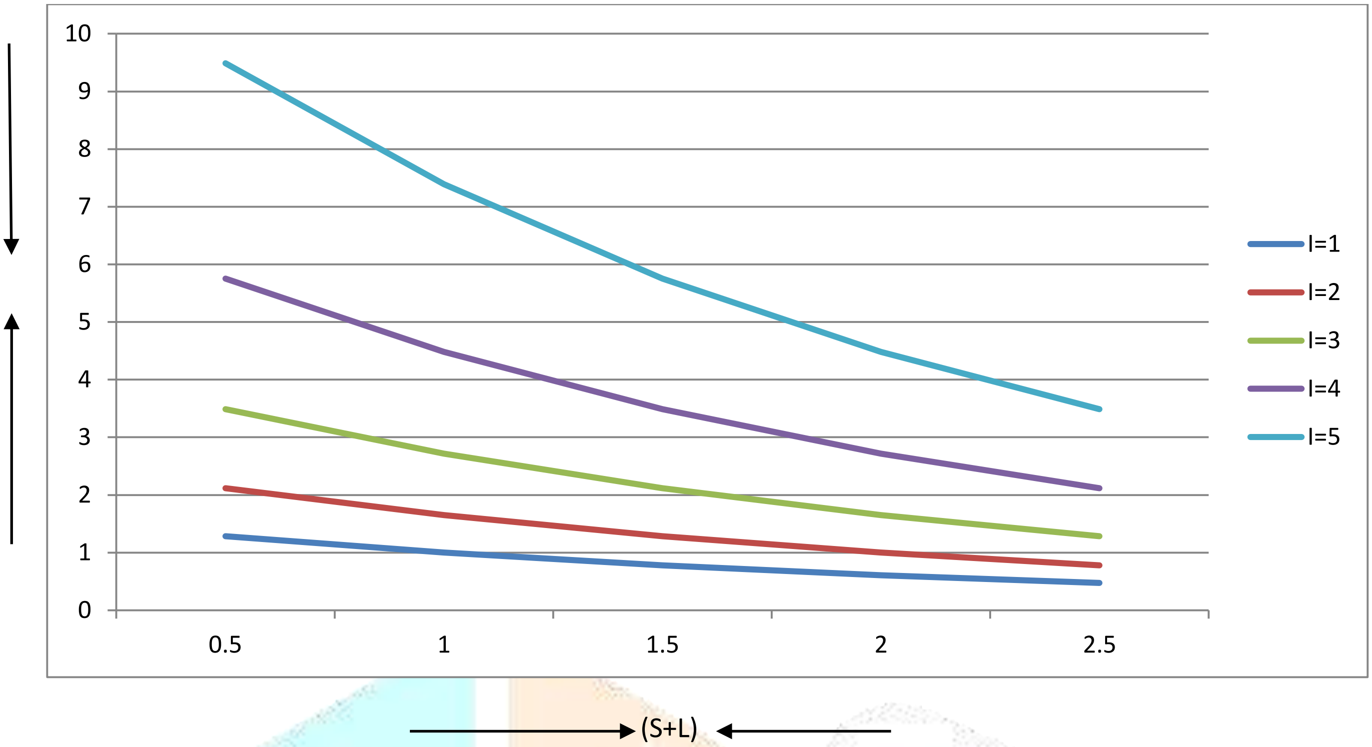
Graph of Corona Cases in IndiaFig. (1.2)



Corona cases in India comparing other Countries at 2 May 2020 Fig. (1.3)

Variation of total infected person for different value of N_0=1 , t= 0.5

(S+L) \ I	1	2	3	4	5
0.5	1.2840	2.1170	3.4903	5.7546	9.4877
1.0	1.0000	1.6487	2.7183	4.4817	7.3890
1.5	0.7788	1.2840	2.1170	3.4903	5.7546
2.0	0.6065	1.0000	1.6487	2.7183	4.4817
2.5	0.4724	0.7788	1.2840	2.1170	3.4903

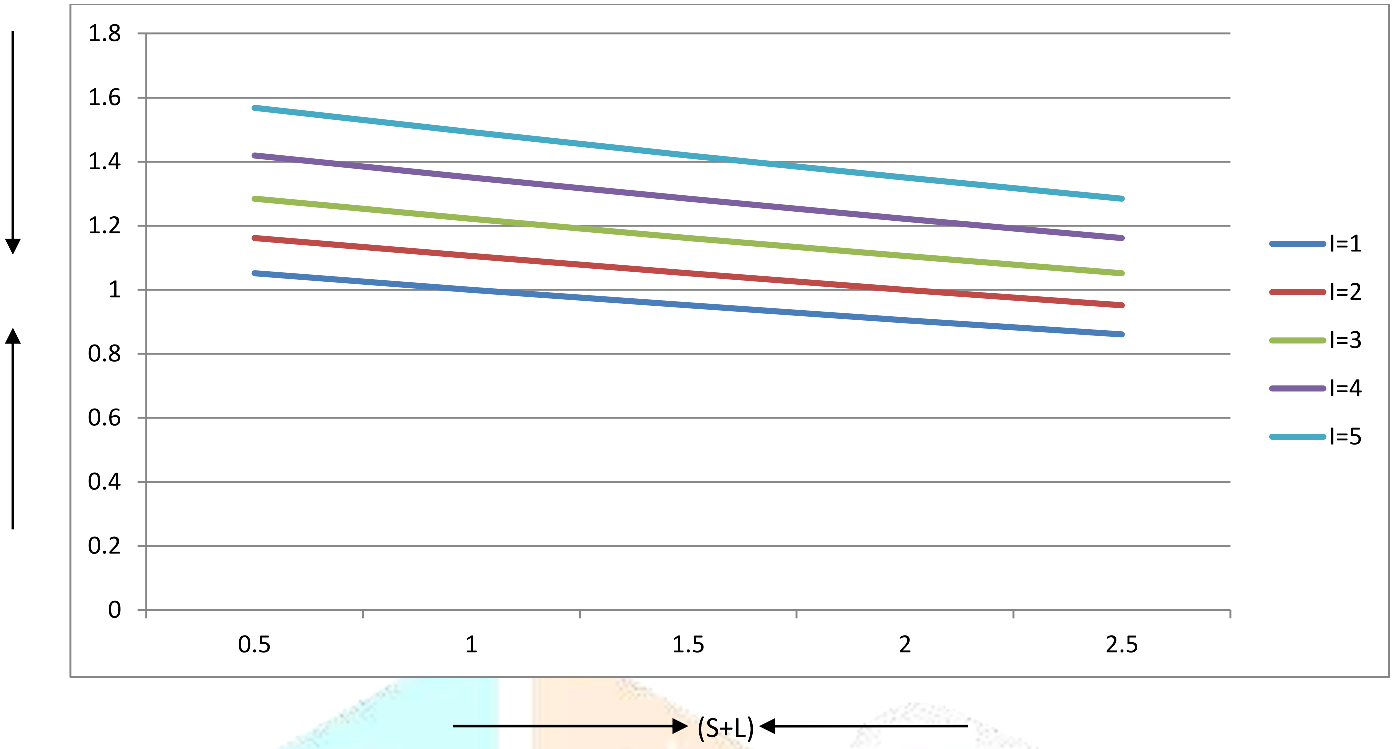


Variation of total infected person for different value of N_0=1 , t= 0.5

Fig. (1.4)

Variation of infected person for different value of C_0=1 , t= 0.1

I (S+L)	1	2	3	4	5
0.5	1.6487	1.1618	1.2840	1.4190	1.5683
1.0	1.0000	1.1052	1.2214	1.3499	1.4918
1.5	0.9512	1.0512	1.1618	1.2840	1.4190
2.0	0.9048	1.0000	1.1052	1.2214	1.3499
2.5	0.8607	0.9512	1.0512	1.1618	1.2840



Variation of infected person for different value of $C_0=1$, t= 0.1

Fig. (1.5)

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