SMALLEST ORDER STATISTICS OF COVID-19

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Abstract

It is now known that the coronavirus-2019 can be transmitted through a variety of human mechanisms that include the disease can spread from person to person through small droplets from the nose or mouth which are spread when a person with COVID-19 coughs or exhales. Most of the behavior in the stochastic model for the expected time strongly depends on initial conditions. In this paper the expected time and variance of the estimated threshold level through two modes of transmission using three-parameter Generalized Rayleigh distribution has been derived in smallest order statistics for COVID-19.

Key words: Coronavirus-2019, COVID-19, Threshold, Three parameter Generalized Rayleigh distribution, Cumulative damage process, Survival function, Order Statistics.

Introduction:

COVID-19 infection is an infectious disease that is caused by the severe acute respiratory syndrome known as corona virus. While the virus was identified first in December 2019 in the city Wuhan, which is the capital of Hubei province in China, it now a global pandemic and has affected close to a million people. Many of the countries had made mild preparations knowing that the diseases would ultimately catch up with them due to inadequate information on its short and long-term effects.

In the paper a stochastic model to estimate expected time and its variance are obtain by using order statistics. A random sample '*n*' of inter arrival times can be taken and such values can be arranged in the increasing order of magnitude. This forms a sequence, which forms an order statistics. Using the probability distribution of the order statistics, the present model is developed. The random variable which indicates the inter arrival times between successive COVID-19 is such that it is distributed as that of an order statistics. The diseases are mostly spread through via respiratory droplets, which are produced whenever a person coughs or sneezes. In addition, an individual can also contract the virus through touching a contaminated place or surface before touching their face These model are discussed, taking the inter arrival times as follows smallest order statistics.

Model Description:

The aim of this paper is model the spread of COVID-19 thus enabling the government to make ready and proper preparations thus reducing India becoming another "hotbed" of COVID-19 virus deaths in India. In addition, the results from paper after stochastically

modeling of the virus spread help in making predictions on the potential effects thus assisting the response agency deal with inadequate hospital and infrastructure development for safety of India at large. This is to prevent any form unnecessary death that is likely to be experienced during the period.

Let v_t denote the number of registrations in the interval $(0,t)$. The study of these random variables has also been undertaken by two types of counters very recently when $H(x)$ follows the exponential law. In this case are identically distributed random variables whose distribution function.

In this paper, we will model the number of confirmed cases of infections of COVID-19 in India as a Generalized Rayleigh Distribution. The model follows as

It can be shown that

$$\text{Probability of}\left[\sum_{i=1}^{k} X_i < Y\right] = \int_{0}^{\infty} g_k(x)\bar{H}(x)\,dx$$

From the above equation model, we can note that is the confirmed cases of COVID-19 in India, where is the number of persons who made contact persons who have confirmed cases of the virus, is the number of daily flights to India from infected countries and is the error term, which is assumed to be independently and identically distributed and follows a GRD.

Let Y ~ Generalized Rayleigh Distribution (α, λ, μ)

$$\overline{H}(x) = e^{-\lambda(x-\mu)^2}$$

The parameter mean of the number of confirmed COVID-19 cases.

Hence

$$P\left[\sum_{i=1}^{k} X_i < Y\right] = \int_{0}^{\infty} g_k(x)\left[e^{-\lambda(x-\mu)^2}\right] = \left[g^* \lambda(1-\mu)^2\right]^k$$

Let $N(t)$ be the number of particles arriving in the counter in the interval $(0,t)$. Let $S_n = X_1 + X_2 + \ldots\ldots + X_n$ and $F_n(x)$ be the distribution function of S_n.

From Gurland. Then the survival function S(t) is

$$S(t) = P[T > t]$$

The cases of virus have a direct linear relationship since more contact persons means more people are likely to get infected hence measures such as social distancing. The model is given as;

$$= \sum_{k=0}^{\infty}\left[F_k(t) - F_{k+1}(t)\right]\left[g^* \lambda(1-\mu)^2\right]^k$$

$F_{n+1}(t)$ is the $(n+1)^{th}$ convolution of $F(t)$ with itself. Using the well known Renewal theory, one gets

$$L(t) = 1 - S(t)$$

$$L(t) = \left[1 - g^*\left(\lambda + \lambda\mu^2 - 2\lambda\mu\right)\right] \sum_{k=1}^{\infty} F_k(t) \left[1 - g^*\left(\lambda + \lambda\mu^2 - 2\lambda\mu\right)\right]^{k-1}$$

On simplification

Now Taking Laplace Stieltjes transform of $l(t)$, which is denoted by $l^*(s)$, we have

$$l^*(s) = \frac{\left[1 - g^*\left(\lambda + \lambda\mu^2 - 2\lambda\mu\right)\right] f^*(s)}{\left[1 - g^*\left(\lambda + \lambda\mu^2 - 2\lambda\mu\right) f^*(s)\right]} \quad \text{On simplification} \qquad \dots (1)$$

The p.d.f of the smallest order statistics is $f_{u_{(1)}}(t) = K\left[1 - F(t)\right]^{k-1} f(t)$

The Laplace Stieltjes transform the same is given by

$$f^*_{u_{(1)}}(t) = \int_0^{\infty} e^{-st} K\left[1 - F(t)\right]^{k-1} f(t)\, dt$$

Where the right hand side contains the nth iterated convolution. In the above discussion we have to restrict ourselves to the special case when is exponential.

Assuming that $f(t)$ follows $\exp(c)$, it can be shown that

$$f^*_{u_{(1)}}(s) = \frac{kc}{kc + s} \qquad \dots (2)$$

Substituting equation (2) in (1), we get

$$l^*(s) = \frac{\left[1 - g^*\left(\lambda + \lambda\mu^2 - 2\lambda\mu\right)\right]\dfrac{kc}{kc + s}}{\left[1 - g^*\left(\lambda + \lambda\mu^2 - 2\lambda\mu\right)\dfrac{kc}{kc + s}\right]}$$

$$E(T) = -\left.\frac{dl^* s}{ds}\right|_{s=0} \qquad \text{At} \qquad s = 0$$

$$E(T) = \frac{1}{kc\left[1 - g^*\left(\lambda + \lambda\mu^2 - 2\lambda\mu\right)\right]} \qquad \dots (3)$$

Let $\qquad g^*(.) \, \square \, \exp(\alpha)$

$$g^*(\lambda) = \frac{\alpha}{\alpha + \lambda},\, g^*2(\lambda\mu) = \frac{\alpha}{\alpha + 2\lambda\mu},\, g^*\left(\lambda\mu^2\right) = \frac{\alpha}{\alpha + \lambda\mu^2} \qquad \dots (4)$$

Then (4) in (3), we can get

$$E[T] = \frac{\begin{array}{l}\alpha^3 + \alpha^2\lambda + \alpha^2\lambda\mu^2 + 2\alpha^2\lambda\mu + \alpha\lambda^2\mu^2 \\ \qquad + 2\alpha\lambda^2\mu^3 + 2\alpha\lambda^2\mu + 2\lambda^3\mu^3\end{array}}{kc\lambda\left[\alpha^2 + \alpha^2\mu^2 - 2\alpha^2\mu + 2\alpha\lambda\mu^2 + 2\lambda^2\mu^3\right]}$$

….. (5)

$$E(T^2) = \frac{d^2 l * s}{ds^2}\bigg|_{s=0} \quad \text{At} \quad s = 0$$

$$E[T^2] = \frac{2}{(kc)^2\left[1 - g^*\left(\lambda + \lambda\mu^2 - 2\lambda\mu\right)\right]^2}$$

… (6)

Let $\quad g^*(.) \square \exp(\alpha)$

$$E(T^2) = \frac{2\left(\begin{array}{l}\alpha^3 + \alpha^2\lambda + \alpha^2\lambda\mu^2 + 2\alpha^2\lambda\mu + \alpha\lambda^2\mu^2 \\ \qquad + 2\alpha\lambda^2\mu^3 + 2\alpha\lambda^2\mu + 2\lambda^3\mu^3\end{array}\right)^2}{(kc)^2\lambda^2\left(2\lambda^2\mu^3 + 2\alpha\lambda\mu^2 + \alpha^2 + \alpha^2\mu^2 - 2\alpha^2\mu\right)^2}$$

Hence, the variance V (T) = E (T^2) – [Mean]

$$V[T] = \frac{\left(\begin{array}{l}\alpha^3 + \alpha^2\lambda + \alpha^2\lambda\mu^2 + 2\alpha^2\lambda\mu + \alpha\lambda^2\mu^2 \\ \qquad + 2\alpha\lambda^2\mu^3 + 2\alpha\lambda^2\mu + 2\lambda^3\mu^3\end{array}\right)^2}{(kc)^2\lambda^2\left(2\lambda^2\mu^3 + 2\alpha\lambda\mu^2 + \alpha^2 + \alpha^2\mu^2 - 2\alpha^2\mu\right)^2}$$

Case 1.

Illustrates the variations of mean and variance, at the value of k increases the mean time and its variance decreases. This is due to the fact that as k namely number of days in (0,t] decreases it means that the infection day are more frequent. It is easily seen from Fig. (1).
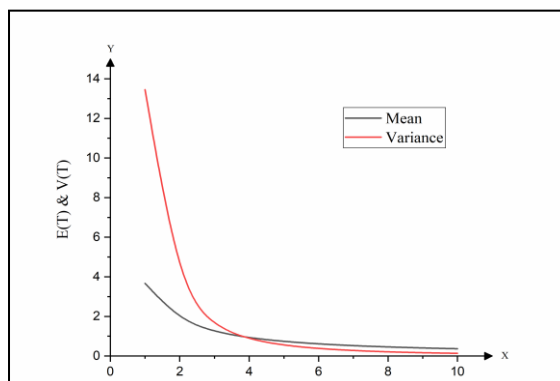
Case: 2

It is observed from the Fig (2), the contribution to the antigenic diversity threshold ' α ' which increases, then the mean time and its variance increases
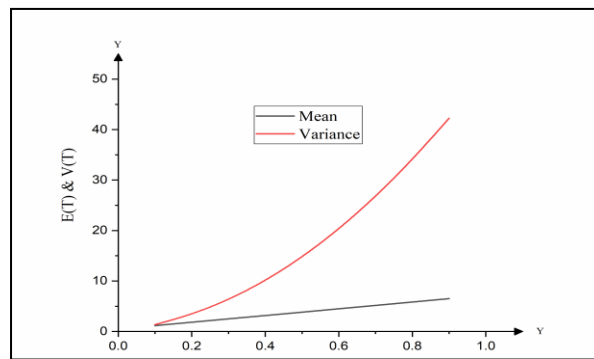
In terms of the degree of relationship between the number of people who made contact with other persons in India. The research has predicted the spread of COVID-19 where it is easy to see how it is likely to progress in the future. This is because the pandemic has been a threat to human beings globally.

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