A STUDY OF TB PATIENTS THROUGH STOCHASTIC MODEL

Elizabeth Sangeetha T[1], P. Pandiyan[2] R. K. Radha[3] M Meganathan[4*]

[1]Research scholar, Department of Statistics, Annamalai University, Annamalai Nagar, Tamil Nadu, India.

[2]Professor of Statistics, Department of Statistics, Annamalai University, Annamalai Nagar, Tamil Nadu, India

[3]Assistant Professor, Department Of Statistics, Presidency College Chennai

[4]Associate Professor, Department of Pharmacology, AVMC&H, Pondocherry

Corresponding author : subashstat@gmail.com.

ABSTRACT

An attempt is made here to compute the verge point of a Tuberculosis patient who has been infected with Mycobacterium Tuberculosis using a statistical model. Many studies with various families of distribution had already been investigated. When a patient becomes sick, the threshold level drops, which can be shown in the model to indicate the model's goodness of fit. Even if subsequent interactions are separate, it is possible that they become increasingly effective in inflicting damage. When the total cumulative damage exceeds a certain threshold, a component exposed to shocks that hurt the element is likely to fail.The projected survival of the human system will approach the threshold if the survival does not accrue the increase in shock, which is the inter-arrival time. The conversation was read as follows: when the infection period lengthens, the patient's survival time diminishes. Finally, we use a real-world dataset to demonstrate the analytical findings and the model's utility.

KEYWORDS: Distribution, Mycobacterium Tuberculosis, Threshold and infection.

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INTODUCTION

Tuberculosis (TB) is still a significant global pathological condition that claims the lives of one million people every year. TB is more common in communities with socioeconomic problems, but it is not limited to them. TB is most common in the world's poorest countries that don't appear to be developed, particularly where populations are overcrowded and in countries influenced by war. The most common cause of large-scale population displacement is conflict, which frequently leads to relocation to makeshift settlements such as camps. Factors such as deficient sickness and overcrowding in camp settings make these populations more vulnerable to tuberculosis infection. The causes of tubercle bacillus (MTB) infection in humans are exceedingly diverse. Some people appear to be able to get rid of the infection on their own, either with or without Mtb-specific T cell enlargement. In many others, the disease is suppressed but not cured, leaving a latent Mtb infection (LTBI) that could take years, if not decades, to become active.Mtb infection can proceed to active health in the most vulnerable patients without a long period of latency.Though a small percentage of the world's population is infected with MTB, it is well recognized that the majority of infections do not induce TB disease and that 90 to 95 percent of infections do not result in death. As a result, affordable TB models should include latent TB patients, such as those reported by S.Bowong and J. J. Tewa (2009), E.G.Nicholson et al., (2015), and G.Li and Z. Jin (2005). These applied math models have supplied valuable information in the study of tuberculosis transmission processes. However, the majority of models ignore the impact of intervention methods on the transmission dynamics of tuberculosis.

Regardless of existing control strategies, the global burden of tuberculosis has increased over time. Vaccines such as BacilleCalmette-Guerin (BCG) and the World Health Organization's direct observation therapy strategy (DOTS), which focuses on discovering cases and administering short-course therapy, are among these strategies, according to C.Colijn, T. Cohen, and M. Murray (2006). World Health Organization (WHO), confirmed around 1.8 million people died in 2007 as a result of 14 million illnesses, the majority of which occurred in developing nation. In Africa, 8.8 million new tuberculosis infections occurred in 2003, resulting in 1.7 million fatalities (WHO, 2010).The Western Pacific Regions and South-East Asia accounted for around 56% of the 9 million TB infections diagnosed in 2013. An extra 25% came from Africa, which had the highest mortality and infection rates in relation to population size. China and India together accounted for around 11% and 24% of all cases, respectively (WHO, 2010).

This distribution is more adaptable for modeling lifespan data, particularly in terms of dependability and hazard rate forms, which include decreasing, increasing, and upside down bathtub shaped hazard rates. Through Exponentiated Exponential Binomial Distribution (EEBD), a statistical model for the estimated time for Mycobacterium Tuberculosis patients to reach the threshold level is obtained. Study on information on estimated time to threshold of HIV and Tuberculosis, is seenin Ahmed Al Kuwaiti et al., (2018).

BACKGROUND

Tuberculosis is one of the infectious illnesses that have plagued humanity for centuries. Bacillus bacteria cause it, with Mycobacterium tuberculosis being the most prevalent pathogenic organism Cadmus.S (2006). Coughing, laughing, talking, sneezing, and singing all produce infectious aerosolized droplet nuclei that spread the bacterium. The patient's infectiousness determines the potential to produce infectious aerosolized droplet nuclei, with a sputum smear positive patient being the most infectious (Dooley S.W 1992).According to the WHO, 2 billion people, or one-third of the world's population, are afflicted with the bacteria that causes tuberculosis, Mycobacterium tuberculosis. In 2012, tuberculosis killed 1.4 million people worldwide, making it the leading infectious cause of death (WHO, 2012).

EEBD is a novel continuous distribution created by combining exponentiated exponential and binomial distributions. The capacity to predict lifetime data with increasing, decreasing, and upside-down bathtub shaped failure rates is provided by this distribution. Furthermore, the compounded zero-truncated binomial distribution is over distributed. Gupta and Kundu (1999) investigated an exponentiated exponential model that was built using a fixed sample size and the distribution of a maximum of independent exponential random variables. Karlis (2009) and Kus (2007) looked at the exponential-Poisson distribution recently.This distribution is more adaptable for modeling lifespan data, particularly in terms of dependability and hazard rate forms, which include decreasing, increasing, and upside down bathtub shaped hazard rates.

Table 1: Application of Stochastic modelsusing TB diseases

Author(s) (years)	Disease	Contribution
GetachewTeshome Tilahun (2020)	Dynamics of TB by incorporating vaccination of newly born babies	Modeling the dynamics of tuberculosis by including immunization of newborn newborns into a stochastic model. In this model, the overall population is separated into four compartments: susceptible S(t), infected I(t), vaccinated infants V(t), and recovered R(t). The deterministic technique is used to express and assess the produced model first.
N. B. J. Tchatchambe et.al., (2020)	Banana Bunchy Top Virus	The goal of this study was to create BBTV-free plantain seedlings from infected banana plants.

Aliyu Abba and S. Athithan (2020)	Extended nonlinear deterministic model of TB by considering the effect of case-detection and its treatment to a Stochastic Differential Equation Model (SDE).	We are deriving and extending a non-linear deterministic mathematical model of tuberculosis with emphasis on case detection and treatment into its equivalent stochastic model. By revising the analysis in the deterministic method, different Equilibrium in the model were found using convenient technique and analyzed their condition for stability and reproduction number were computed.
M. Mbokoma and S.C. OukouomiNoutchie (2017)	Transmission of the M. tuberculosis and infection of TB	Tuberculosis infection that incorporates both fast and slow progressions, efficient chemoprophylaxis (given only to individuals who are in a latent stage of infection) and therapeutic treatments was considered.
Kipruto, H et.al., (2013)	Kenyan TB epidemic model however with varying time periods	Susceptible Infective (SI), Susceptible Infective and Recovered (SIR) and Susceptible Exposed Infective and Recovered (SEIR) models were considered.

DATA PREPARATION AND CLEANING

The development of TB is examined in this article using data from people with age group ranged from less than 14, 15-24, 25-34, 35-44, 45-54, 55-64 and above 65+. Patients with all kinds of primary TB illness are included in the study. Nine nominal variables (Coughing for three weeks or more, Coughing up blood or mucus, Chest pain or pain with breathing or coughing, Unintentional weight loss, Fatigue, Fever, Night sweats, Chills, Loss of appetite) and nine numerical variables (Age groups, Sex, Risk factors, Measure, Unit, Best, Low, High, and ISO number) were found in a population of 7286 people. Tuberculosis can also damage other organs in the body, such as the kidneys, spine, and brain.When tuberculosis affects organs other than your lungs, the signs and symptoms differ. Tuberculosis in the spine, for example, can cause back discomfort, while tuberculosis of the kidneys can produce blood in the urine. The goal is to look at the factors that influence the outcomes and progression of Mycobacterium Tuberculosis patients, with a particular focus on age-related risk factors.

METHODOLOGY

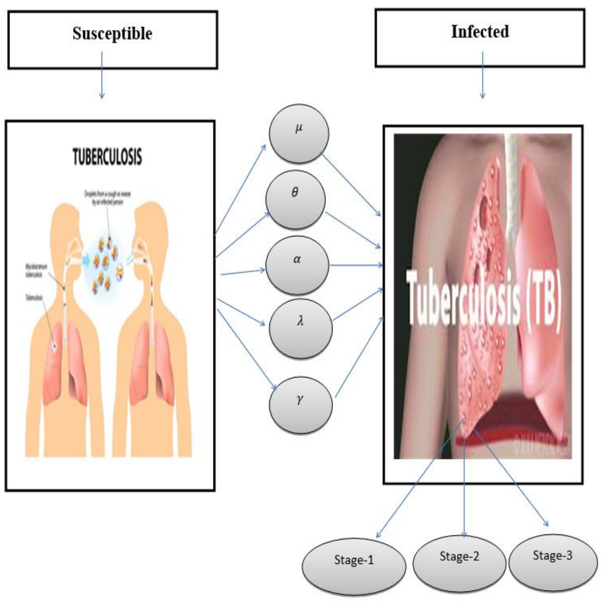

Figure 1: State-flow diagram describing each parameter's influence on the state of a node.

In our opinion, the model development is done with six parameters affecting Mycobacterium Tuberculosis: c- Age groups, r- Sex, μ- stands for Low, θ- for Best, and λ- for High. Where the number of virulent entities is minimal, or when anxiety in transmission, recovery, fatalities, or the environment influences the epidemic outcome, theoretical modeling of epidemics is required. Individual changes such as automated transmission, healing, and deaths are linked to uncertainty. Environmental uncertainty is defined as volatility connected to the environment, such as circumstances at terrestrial or marine sites.

MODEL DESCRIPTION AND SOLUTION

In general, the EEBD with parameter θ is followed by the threshold Y. It can be demonstrated that,

$$P(x<y)=\int_0^\infty g_k(x)\bar{H}(x)$$

$$=\int_0^\infty g_k(x)\left(1-\frac{\theta}{1-\theta^{-1}}\sum_{r=0}^{n}(-1)^r\binom{\alpha}{r}e^{-\lambda rx}\right)dx$$

We acquire the threshold distribution as a result of simplification in equation (1)

$$=[g^*(1)]^k-\frac{\theta}{1-\theta^{-1}}\sum_{r=1}^{\alpha}(-1)^r\binom{\alpha}{r}[g^*(\lambda r)]^k \qquad \dots(1)$$

The probability that the cumulative threshold will fail only after time t is given by the survival function.$S(t)=P(T>t)=$ Probability that the total damage survives beyond t .

$$=\sum_{k=0}^{\infty}\mathrm{P}\{\text{there are exactly k decisions in }(0,\mathrm{t}]*\mathrm{P}\ (\text{the total cumulative threshold }(0,\mathrm{t}]\}$$

The role of survival $S(t)$ is the chance of a person surviving for a certain amount of time t. The renewal process has also revealed that

$$P(T>t)=\sum_{k=0}^{\infty}F_k(t)P(X_i<y)$$

$$=\sum_{k=0}^{\infty}[F_k(t)-F_{k+1}(t)]\left[(g^*(1))^k-\frac{\theta}{1-\theta^{-1}}\sum_{r=1}^{n}(-1)^r\binom{\alpha}{r}[g^*(\lambda r)]^k\right]$$

$$=\sum_{k=0}^{\infty}[F_k(t)-F_{k+1}(t)](g^*(1))^k-\left[\frac{\theta}{1-\theta^{-1}}\sum_{k=0}^{\infty}\sum_{r=1}^{n}(-1)^r\binom{\alpha}{r}[g^*(\lambda r)]^k[F_k(t)-F_{k+1}(t)]\right]$$

We obtain the following equation (2) from the simplified renewal process:

$$=1-(1-g^*(1))\sum_{k=1}^{\infty}F_k(t)\,(g^*(1))^{k-1}-\frac{\theta}{1-\theta}+\sum_{k=1}^{\infty}\sum_{r=1}^{n}(-1)^{r+1}\binom{\alpha}{r}\frac{\theta}{1-\theta^{-1}}(1-g^*(\lambda r))F_k(t)(g^*(\lambda r))^{k-1} \qquad \dots(2)$$

Now, the life time is given by; $P(T<t)=L(t)=$ the distribution function of life time (t)

It can be proven that, using the convolution theory for Laplace transforms, $F_0(t)=1$ and on simplification we derive equation (3)

$$=(1-g^*(1))\sum_{k=1}^{\infty}F_k(t)\,(g^*(1))^{k-1}+\frac{\theta}{1-\theta^{-1}}+\sum_{k=1}^{\infty}\sum_{r=1}^{n}(-1)^{r+1}\binom{\alpha}{r}\frac{\theta}{1-\theta^{-1}}(1-g^*(\lambda r))F_k(t)(g^*(\lambda r))^{k-1}$$

$$=(1-g^*(1))\sum_{k=1}^{\infty}F_k(t)\,(g^*(1))^{k-1}+\frac{\theta}{1-\theta^{-1}}+\frac{\theta}{1-\theta^{-1}}\sum_{k=1}^{\infty}\sum_{r=1}^{n}(-1)^{r+1}\binom{\alpha}{r}(1-g^*(\lambda r))^{k-1}F_k(t)(g^*(\lambda r))^{k-1} \qquad \dots(3)$$

It may be demonstrated using the Laplace-Stieltjes transform that

$$l^*(s)=\frac{[(1-g^*(1))f^*(s)]}{[1-g^*(1)f^*(s)]}+\frac{\theta}{1-\theta^{-1}}\sum_{r=1}^{n}(-1)^{r+1}\binom{\alpha}{r}\frac{[(1-g^*(\lambda r))f^*(s)]}{[1-g^*(\lambda r)f^*(s)]}$$

Let c denote the inter-arrival time, which follows an exponential relationship with the parameter as observed in equation (5)

Now $f^*(s) = \left(\frac{c}{c+s}\right)$, substituting in the above equation (4) we get,

$$= \frac{\left[\left(1-g^*(1)\right)\frac{c}{c+s}\right]}{\left[1-g^*(1)\frac{c}{c+s}\right]} + \frac{\theta}{1-\theta^{-1}}\sum_{r=1}^{\alpha}(-1)^{r+1}\binom{\alpha}{r}\frac{\left[\left(1-g^*(\lambda r)\right)\frac{c}{c+s}\right]}{\left[1-g^*(\lambda r)\frac{c}{c+s}\right]}$$

$$= \frac{[(1-g^*(1))c]}{[c+s-g^*(1)c]} + \frac{\theta}{1-\theta^{-1}}\sum_{r=1}^{n}(-1)^{r+1}\binom{\alpha}{r}\frac{[(1-g^*(\lambda r))c]}{[c+s-g^*(\lambda r)c]}$$

Finding the expected value,

$$E(T) = \frac{-d}{ds}l^*(s)/s = 0$$

$$= \left[\frac{1}{c[1-g^*(1)]} + \frac{\theta}{1-\theta^{-1}}\sum_{r=1}^{n}(-1)^{r+1}\binom{\alpha}{r}\frac{1}{c[1-g^*(\lambda r)}\right] \quad \ldots (6)$$

$$g^*(1)\ follows\ \frac{1}{\mu} g^*(\lambda r)\ follows\ \frac{\mu}{\mu+2r}$$

$$E(T) = \frac{1}{c\left[1-\frac{1}{\mu}\right]} + \frac{\theta}{1-\theta^{-1}}\sum_{r=1}^{n}(-1)^{r+1}\binom{\alpha}{r}\frac{1}{c\left[1-\frac{\mu}{\mu+\lambda r}\right]}$$

The Expected life time of the Mycobacterium Tuberculosis patients

$$E(T) = \frac{\mu}{c[\mu-1]} + \frac{\theta}{1-\theta^{-1}}\sum_{r=1}^{n}(-1)^{r+1}\binom{\alpha}{r}\frac{\mu+\lambda r}{c[\lambda r]}$$

RESULTS

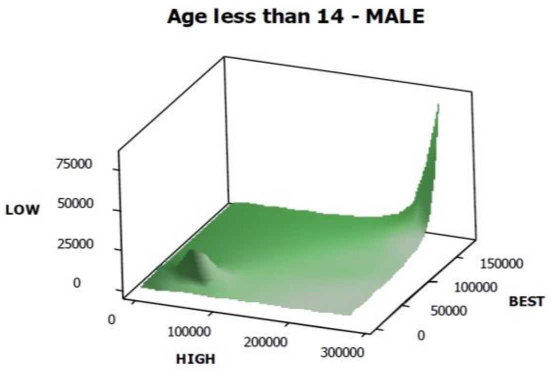

Figure 1. BEST estimate of TB patients threshold of male age group under 14

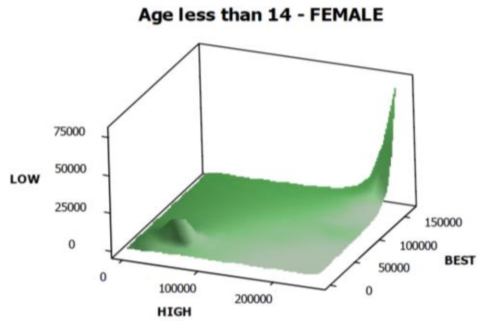

Figure 2. BEST estimate of TB patients threshold of female age group under 14

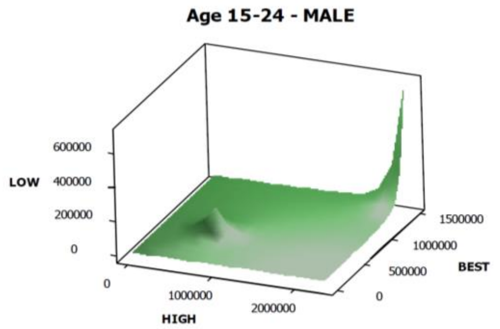

Figure 3. BEST estimate of TB patients threshold of male with age group 15-24

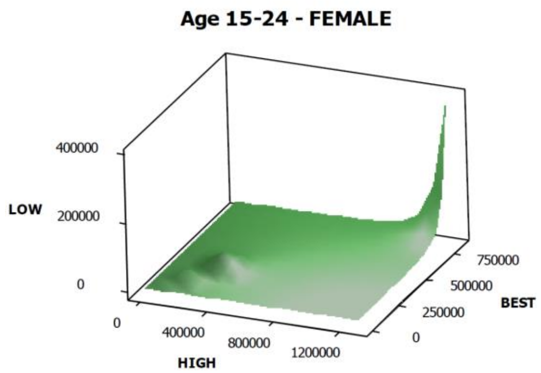

Figure 4. BEST estimate of TB patients threshold of female with age group 15-24

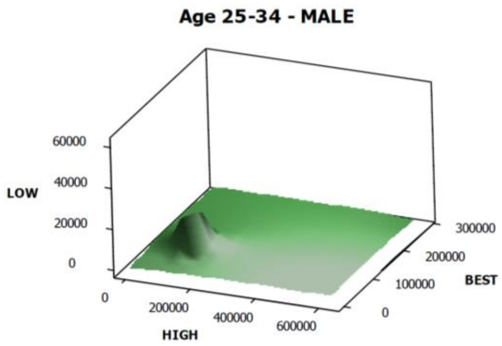

Figure 5. BEST estimate of TB patients threshold of male with age group 25-34

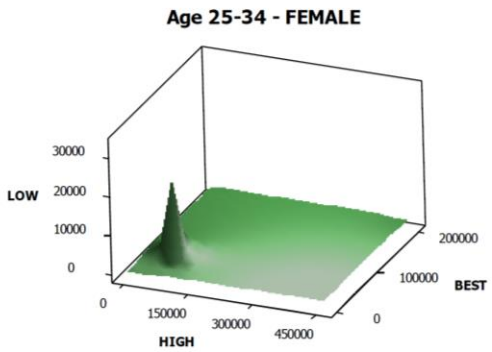

Figure 6. BEST estimate of TB patients threshold of female with age group 25-34

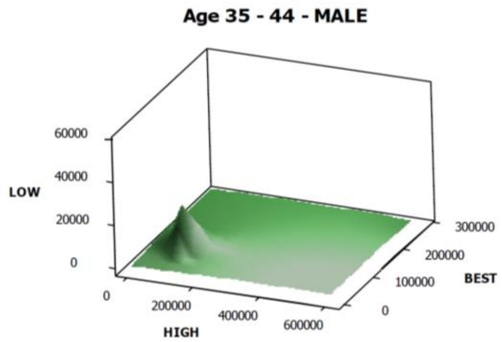

Figure 7. BEST estimate of TB patients threshold of male with age group 35-44

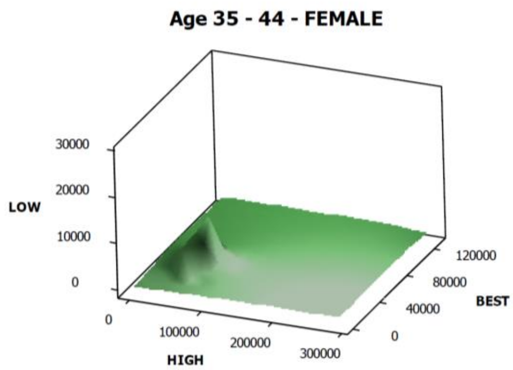

Figure 8. BEST estimate of TB patients threshold of female with age group 35-44

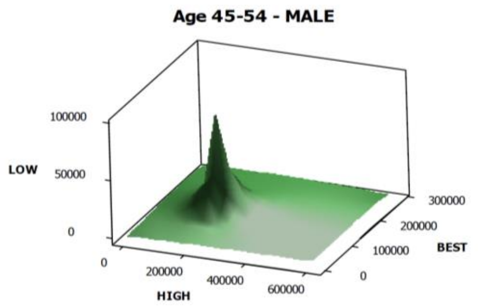

Figure 9. BEST estimate of TB patients threshold of male with age group 45-54

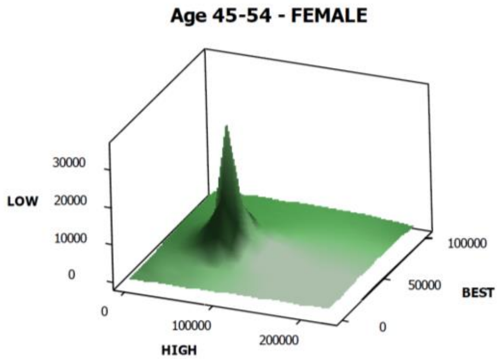

Figure 10. BEST estimate of TB patients threshold of female with age group 45-54

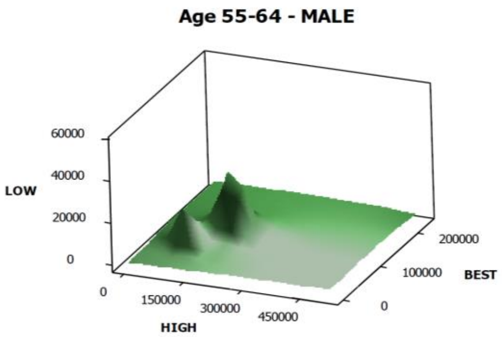

Figure 11. BEST estimate of TB patients threshold of male with age group 55-64

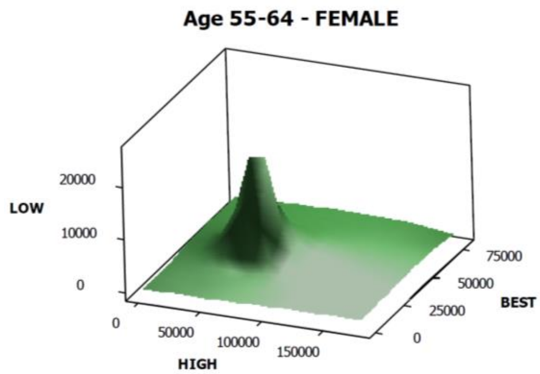

Figure 12. BEST estimate of TB patients threshold of female with age group 55-64

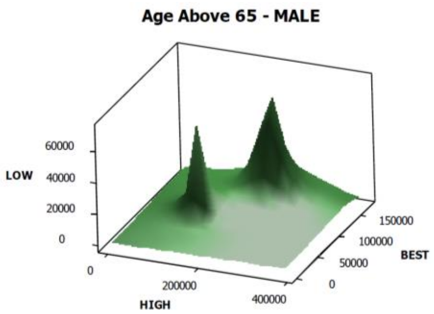

Figure 13. BEST estimate of TB patients threshold of male with age group above 65

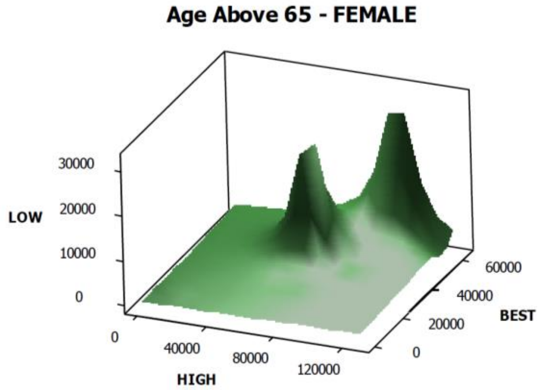

Figure 14. BEST estimate of TB patients threshold of female with age group above 65

The age group of male Figure 1 and female Figure 2 TB patients was observed between the BEST, Low, and High thresholds. As seen in Figures 1 and 2, there was no difference between male and female patients. This means that there is no gender difference.

Male Figure 3 and female Figure 4 patients were observed between the BEST, Low, and High thresholds in the 15-24 age group. As can be seen, there is a distinction between male and female patients. This demonstrates that there is a gender divide among infected threshold TB patients in the age group 15-24. Male infected patients are at a higher risk than female infected people.

Between the BEST, Low, and High thresholds were seen for male Figure 5 and female Figure 6 individuals in the 25-34 age group. As can be seen, there is a distinction between male and female patients. This demonstrates that there is a gender difference in the infection threshold TB patients in the age range 25-34. Male infected patients are at a higher risk than female infected people.

Between the BEST, Low, and High thresholds were seen for male Figure 7 and female Figure 8 individuals in the 35-44 age group. As can be seen, there is a distinction between male and female patients. This demonstrates that there is a gender divide among infected threshold TB patients in the age group 35-44. Male infected patients are at a higher risk than female infected people.

Between the BEST, Low, and High thresholds were seen for male Figure 9 and female Figure 10 individuals in the 45-54 age range. As can be seen, there is a distinction between male and female patients. This demonstrates that there is a gender difference in the infection threshold TB patients in the age group 45-54. Male infected patients are at a higher risk than female infected people.

Between the BEST, Low, and High thresholds were seen for male Figure 11 and female Figure 12 individuals in the 55-64 age range. As can be seen, there is a distinction between male and female patients. This suggests that there is a gender difference in the infection threshold TB patients in the age range 55-64. Male infected patients are at a higher risk than female infected people.

Patients in the 65+ age group were observed between the BEST, Low, and High thresholds for male Figure 13 and female Figure 14. As can be seen, there is a distinction between male and female patients. This demonstrates that there is a gender difference in the infection threshold TB patients over the age of 65. Male infected patients are at a higher risk than female infected people.

CONCLUSION

We provide a new generalization of the Exponentiated exponential Binomial distribution in this paper. The suggested distribution incorporates the four-parameter Exponentiated exponential Binomial distribution. Some mathematical properties are derived, as well as an estimate of the predicted time of Mycobacterium Tuberculosis patients. We feel that the subject distribution can be applied to a variety of situations. We anticipate that our work will be used as a reference and will aid future research in the field.

REFERENCES

1. Ahmed Al Kuwaiti, R. Vinoth, Arun Vijay Subbarayalu, SivasankarPrabaharan, Palanivel R.M, Goparaju Anumolu. (2018), "Computing the Infection Period of HIV and TB Patient through Non-deterministic model", *International Journal of Computational and Theoretical Statistics*, Vol. 5 (1), 15-18.
2. Aliyu Abba and S. Athithan. (2020). "A Stochastic Approach of Tuberculosis Model with Effects of Case Detection and Treatment." *Published by A.R Publisher in Proceedings of International Conference on Applied Mathematics & Computational Sciences*. pp.7-19.
3. C.Colijn, T. Cohen and M. Murray. (2006) "Mathematical models of tuberculosis: accomplishments and future challenges", *Proc. Natl. Aca. Sci*. Vol.103, pp. 1-28.
4. Cadmus S, Palmer S, Okker M, Dale J, Gover K, . (2006). "Molecular analysis of human and bovine tubercle bacilli from a local setting in Nigeria." *Journal of clinical microbiology,* Vol.44, pp.29–34.
5. Dooley S.W.; Villarino M.E, Lawrence M, Salinas L, Amil S, Rullan J.V, Jarvis W.R, Bloch A.B, Cauthen G.M. (1992). "Nosocomial transmissions of tuberculosis in a hospital unit for HIV-infected patients". *Journal of the American Medical Association.*; Vol.267, pp.2632-2634.
6. E.G.Nicholson, A.M.Geltemeyer and K.C.Smith, (2015). "Practice guideline for treatment of latent tuberculosis infection in children", *Journal of Pediatric Health Care*, Vol.29, pp.302–307.
7. G.Li and Z. Jin, (2005). "Global stability of a seir epidemic model with infectious force in latent, infected and immune period", *Chaos, Solitons & Fractals*, Vol.25, pp.1177–1184.
8. GetachewTeshomeTilahun, Melisew Tefera Belachew and ZinabuGebreselassie. (2020). "Stochastic model of tuberculosis with vaccination of newborns."*Advances in differential equations*. Vol.658, pp.1-24.
9. Gupta, R., Kundu, D., (1999). "Generalized exponential distributions". *Aust. N. Z. J. Stat.* Vol.41 (2), pp.173–188.
10. Karlis, D., (2009). "A note on the exponential Poisson distribution: a nested EM algorithm". *Comput. Statist. Data Anal*. Vol.53 (4), pp.894–899.
11. Kipruto, H, Mung'atu, J, Ogila, K, Adem, A, Mwalili, S, Kibuchi, E, Masini E, Kiplimo Rand Ong'ang'o JR. (2013). "An Application of Deterministic and Stochastic Processes to Model Evolving Epidemiology of Tuberculosis in Kenya." *International Journal of Science and Research*. Vol.4, No. 9, pp.1663-1671.
12. Kus, C., (2007). "A new lifetime distribution". *Comput. Statist. Data Anal*. Vol.51 No. (9), pp.4497–4509.
13. M. Mbokoma and S.C. OukouomiNoutchie (2017). "Mathematical analysis of a stochastic tuberculosis model." *Journal of Analysis and Applications*. Vol. 15, No.1, pp.21-50.
14. N. B. J. Tchatchambe, N. Ibanda, G. Adheka, O. Onautshu, R. Swennen and D. Dhed'a (2020). "Production of banana bunchy top virus (BBTV)-free plantain plants by in vitro culture."*African Journal of Agricultural Research*. Vol. 15(3), pp. 361-366.
15. S.Bowong and J. J. Tewa, (2009). "Mathematical analysis of a tuberculosis model with differential infectivity", *Communications in Nonlinear Science and Numerical Simulation*, Vol.14, pp. 4010–4021.
16. WHO. Global tuberculosis report. Geneva: World Health Organization, (2012).
17. World Health Organization, Tuberculosis Fact sheet. www.who.org, 2010.