IOSR Journal of Mathematics (IOSR-JM)
e-ISSN: 2278-5728, p-ISSN: 2319-765X. Volume 12, Issue 1 Ver. IV (Jan. - Feb. 2016), PP 42-49
www.iosrjournals.org

Bivariate Stochastic Modeling For Spread Of Bacterial Diseases among Plants

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Abstract: *This study has proposed a stochastic model for assessment of control measures on the intensity of bacterial spread over the plants of different types as well as of different age groups in the same species of the plant. Deriving the stochastic differential equations through bivariate point processes is the core objective of the study. The developed differential equations are used for deriving several statistical measures based on the proposed parameters of bacteria growth, spread and loss. Sensitivity analysis is carried out for observing the patterns of statistical measures at changing values of one parameter and at fixed values of the remaining parameters.*

Keywords: *Bacterial Diseases, Bivariate Stochastic Processes, Stochastic Differential Equations.*

I. Introduction:

Studies on *bacteria*l diseases in plants have significant importance for farmers for making its control and regulating with optimal management approaches. They are responsible for huge damage to crops. It makes the attention and lot of human concern to curb the spread of these diseases. Knowing the dynamic behavior of bacterial diseases will help the agricultural agencies in designing the effective treatment protocols and intervention methods. Due to several explained and unexplained reasons, the influencing factors of bacteria spread among plants are stochastic rather than deterministic. Thus probabilistic tools need to be used to study bacterial transmission dynamics.

This study has proposed a stochastic model on the assessment of bacterial intensity spread over the plants. Stochastic differential equations approach as an application of bivariate point processes has been considered here. The steps in the study includes (i) formulation of postulates with suitable mix of plant pathology and mathematical biology assumptions, (ii) development of difference equations for bivariate stochastic processes, (iii) deriving the differential equations, (iv) getting the probability functions through transient state of equations, (v) deriving the mathematical relations of various statistical measures through generating functions and (vi) sensitivity analysis with numerical data sets for better understanding of model behaviour.

Evidence on reporting the literature on this research work reveals that it was initiated in the beginning of the 20th century as Kermack and McKendrick (1927) have introduced the mathematical theory of epidemics with deterministic model. The most important stochastic model from that era is that using the chain-binomial model on epidemiology by Reed and Frost (1928). Using stochastic simulation model, Xu and Ridout (2000) demonstrated the importance of initial epidemic conditions, especially the spatial pattern of initially infected plants and the relationships of spatio-temporal statistics with underlying biological and physical factors. The area of epidemic modeling has grown rapidly and a good overview of other important works can be found in Baily (1975); Anderson and Britton (2000). Hofmann et al. (2004) developed a stochastic model based on a Poisson branching process for analyzing surveillance data of infectious diseases that allows making forecasts of the future development of the epidemic. They estimated the model in a Bayesian context using Markov Chain Monte Carlo (MCMC) technique. Tirupathi Rao and Srinivasa Rao (2006), Tirupathi Rao et al., (2011, 2012, 2013) have developed several stochastic models on cancer growth using Poisson postulates and differential difference equations.

When an individual plant becomes infected, the pathogen moves through the latent stage to become infectious at a rate which is the inverse of mean latent period. Infected plants lose infectiousness and proceed into the removed or post-infectious stage at rate which is the inverse of mean infectious period (Segarra et al., 2001). Keeping the philosophy of epidemiology, cancer like disease spread, predicting the severity of disease with mathematical and stochastic models in the above reviewed literature, it has focused on stochastic modeling of infectious disease spread among the flora and fauna.

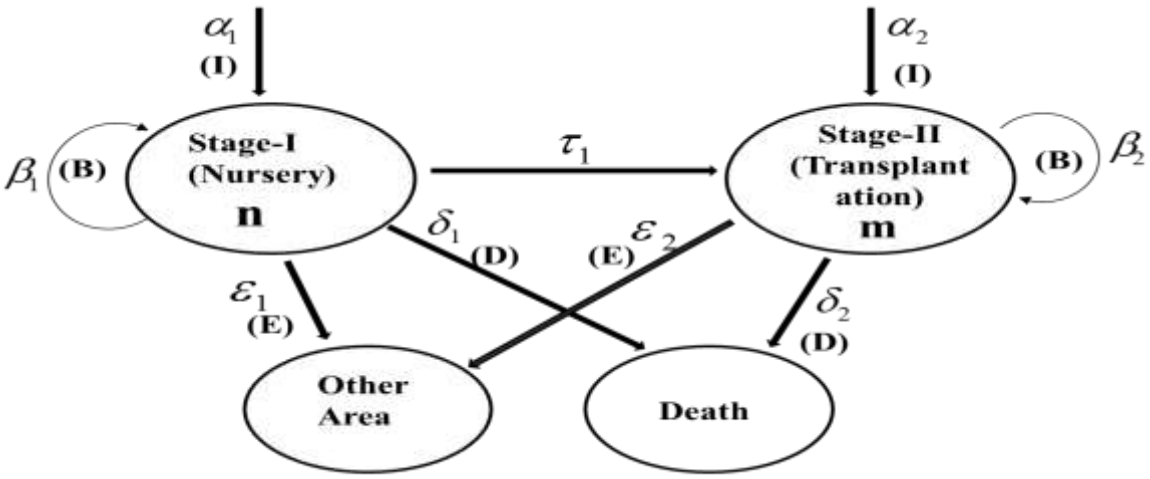
More specifically this work is on invasion and expansion of the infectious diseases among plants. The plant has different ages/ stages from seed germination to its crop yielding. It has different levels of vulnerabilities of exposing to diseases at different age groups. The plants at nursery stage and transplantation stage were considered in this model for observing the growth, loss and transition of disease causing bacteria. The motive of this study is to assess the intensity levels of bacterial accumulation in the unit area of plant. This

study will help in providing the indicators on lethality of bacteria so as the disease control management can be designed through interventions accordingly.

Bivariate stochastic model with Poisson postulates is the basis of this work. There are two stages of plant namely nursery and transplantation. Logging of bacteria on the plant at nursery stage may be due to either immigration from other plants or from some vector influencing mechanism. The accumulation of bacteria after its latency during nursery stage of the plant may be done due to its own growth on the existing host plant also. The similar mechanism can be observed on the plants of transplantation stage also. The dynamics of growth, loss and transition of the bacteria within same aged plant and between different aged plants will be observed simultaneously due to birth, death and migration processes of it.

Stochastic Model for *Bacteria*l Diseases among Plants:

The modeling activity is carried out under the assumptions of pathophysiology of bacterial diseases and the mathematical principles. As the transition of bacterial disease is purely random and influenced by complete chance factors, the developed model is categorized as stochastic model. The study his based on the assumptions and postulates of bivariate Poisson processes. The following diagram will explain the processes behind the construction of model in more detailed way.



Schematic Diagram for Spread of Bacterial Disease

Assumptions and Postulates of the model:

Let the events occurred in non-overlapping intervals of time are statistically independent. Let Δt be an infinitesimal interval of time. Initially, let there be 'n' units of bacteria in stage-I (nursery) and 'm' units of bacteria in stage-II (transplantation) at time 't'. Here one unit denotes the number of bacteria in a square area (mm^2). Let '$\alpha_1 \text{ and } \alpha_2$' be the rates of immigration of bacteria per unit time from external means to stage-I and stage-II respectively; $\beta_1 \text{ and } \beta_2$ are the rates of growth (birth) of bacteria per unit time in stage-I and stage-II respectively; τ_1 is the rate of transition of bacteria per unit time from stage-I to stage-II; $\varepsilon_1 \text{ and } \varepsilon_2$ are the rates of emigration of bacteria per unit time from stage-I and stage-II respectively to the other area; $\delta_1 \text{ and } \delta_2$ be the rates of loss (death) of bacteria per unit time in stage-I and stage-II respectively.

Assuming the above conditions the postulates of the model are as follows. The probability of (i) arrival of bacteria to the stage-I during Δt through immigration from external sources is $\alpha_1 \Delta t + o(\Delta t)$; (ii) arrival of bacteria to the stage-I during Δt through internal birth process provided there exits 'n' units of bacteria at time 't' is $n\beta_1 \Delta t + o(\Delta t)$; (iii) transition of bacteria from stage-I to stage-II during Δt provided there exits 'n' units of bacteria at time 't' in stage-I is $n\tau_1 \Delta t + o(\Delta t)$; (iv) emigration of bacteria from stage-I to other areas during Δt provided there exits 'n' units of bacteria at time 't' is $n\varepsilon_1 \Delta t + o(\Delta t)$; (v) death of bacteria in stage-I during Δt time provided there exits 'n' units of bacteria at time 't' in stage-I is $n\delta_1 \Delta t + o(\Delta t)$; (vi) arrival of bacteria to the stage-II during Δt through immigration from external sources is $\alpha_2 \Delta t + o(\Delta t)$; (vii)

arrival/growth of bacteria to the stage-II during Δt through internal birth process provided there exits 'm' units of bacteria at time 't' is $m\beta_2\Delta t + o(\Delta t)$; (viii) emigration of bacteria from stage-II to other areas during Δt provided there exits 'm' units of bacteria at time 't' is $m\varepsilon_2\Delta t + o(\Delta t)$; (ix) death of bacteria in stage-II during Δt provided there exits 'm' units of bacteria at time 't' is $m\delta_2\Delta t + o(\Delta t)$; (x) no arrival of bacteria to stage-I and stage-II from outside, no internal growth/birth of bacteria in stage-I and stage-II, no transition of bacteria from stage-I to stage-II, no emigration of bacteria from stage-I and stage-II to other areas and no death of bacteria in stage-I and stage-II during Δt is $1-\{\alpha_1 + n(\beta_1+\tau_1) + \alpha_2 + m\beta_2 + n(\varepsilon_1+\delta_1) + m(\varepsilon_2+\delta_2)\}.\Delta t + o(\Delta t)$; and (xi) occurrence of other than the above events during an infinitesimal interval of time Δt is $O(\Delta t)^2$.

Differential Equations of the Model:

Let $P_{n,m}(t)$ be the joint probability of existence of 'n' and 'm' *units of bacteria* in stage-I and stage-II respectively per unit time 't'.

$$\begin{aligned}P_{n,m}(t+\Delta t) = P_{n,m}(t)[1-\{\alpha_1 + n(\beta_1+\tau_1) + \alpha_2 + m\beta_2 + n(\varepsilon_1+\delta_1) + m(\varepsilon_2+\delta_2)\}.\Delta t + O(\Delta t)] \\ + P_{n,m-1}(t)\left[\{\alpha_2 + (\mathrm{m}-1)\beta_2\}\Delta t + O(\Delta t)\right] + P_{n,m+1}(t)[\{(m+1)(\varepsilon_2+\delta_2)\}.\Delta t + O(\Delta t)] \\ + P_{n-1,m}(t)[\{\alpha_1 + (\mathrm{n}-1)\beta_1\}\Delta t + O(\Delta t)] + P_{n+1,m}(t)[\{(\mathrm{n}+1)(\varepsilon_1+\delta_1)\}.\Delta t + O(\Delta t)] \\ + P_{n+1,m-1}(t)[\{(\mathrm{n}+1)\tau_1\}.\Delta t + O(\Delta t)] + P_{n\pm i,m\pm i}(t)[O(\Delta t)^2] \quad for\ i \geq 2\end{aligned}$$

$$\begin{aligned}\frac{d}{dt}P_{n,m}(t) = \left[-\{\alpha_1 + n(\beta_1+\tau_1) + \alpha_2 + m\beta_2 + n(\varepsilon_1+\delta_1) + m(\varepsilon_2+\delta_2)\}.P_{n,m}(t)\right] \\ + \left[\{\alpha_2 + (\mathrm{m}-1)\beta_2\}.P_{n,m-1}(t)\right] + [\{(m+1)(\varepsilon_2+\delta_2)\}.P_{n,m+1}(t)] \\ + [\{\alpha_1 + (\mathrm{n}-1)\beta_1\}P_{n-1,m}(t)] + [\{(\mathrm{n}+1)(\varepsilon_1+\delta_1)\}.P_{n+1,m}(t)] \\ + [\{(\mathrm{n}+1)\tau_1\}.P_{n+1,m-1}(t)] \quad for\ n,m \geq 1\end{aligned}$$

Other differential equations for n, m = 0,1 are

$$\frac{d}{dt}P_{0,0}(t) = -(\alpha_1+\alpha_2)P_{0,0}(t) + (\varepsilon_2+\delta_2)P_{0,1}(t) + (\varepsilon_1+\delta_1)P_{0,1}(t)$$

$$\frac{d}{dt}P_{0,1}(t) = -(\alpha_1+\alpha_2+\beta_2+\varepsilon_2+\delta_2)P_{0,1}(t) + (\alpha_2)P_{0,0}(t) + 2(\varepsilon_2+\delta_2)P_{0,2}(t) + (\varepsilon_1+\delta_1)P_{1,1}(t)$$

$$\frac{d}{dt}P_{1,0}(t) = -(\alpha_1+\beta_1+\tau_1+\alpha_2+\varepsilon_1+\delta_1)P_{1,0}(t) + (\varepsilon_2+\delta_2)P_{1,1}(t) + (\alpha_1)P_{0,0}(t) + 2(\varepsilon_1+\delta_1)P_{2,0}(t)$$

The initial conditions are $P_{n,m}(t) = 0$; for $n<N_0$; $m<M_0$; for $t=0$

and $P_{n,m}(t) = 1$; for $n=N_0$; $m=M_0$;

Using the boundary conditions and differential-difference equations, the probability generating function (p.g.f.) is,

$$p(x,y;t) = \sum_{n=0}^{\infty}\sum_{m=0}^{\infty} x^n y^m p_{n,m}(t)$$

Differentiating on both sides, we get

$$\frac{d}{dt}p(x,y;t) = \frac{d}{dt}\left(\sum_{n=0}^{\infty}\sum_{m=0}^{\infty} x^n y^m p_{n,m}(t)\right) = \sum_{n=0}^{\infty}\sum_{m=0}^{\infty} x^n y^m \frac{d}{dt}\left(p_{n,m}(t)\right)$$

The above equation can be solved by multiplying the differential-difference equation with $x^n y^m$ on both sides and summing over n, m from 0 to ∞ and using the approaches of cumulant generating function (c.g.f.).

$$\sum_{n=0}^{\infty}\sum_{m=0}^{\infty} x^n y^m \frac{d}{dt}\left(p_{n,m}(t)\right) =$$

$$= \sum_{n=0}^{\infty}\sum_{m=0}^{\infty} \left[\begin{array}{l} \left(-\{\alpha_1 + n(\beta_1+\tau_1) + \alpha_2 + m\beta_2 + n(\varepsilon_1+\delta_1) + m(\varepsilon_2+\delta_2)\} x^n y^m . P_{n,m}(t)\right) + \\ \left\{\alpha_2 + (\mathrm{m}-1)\beta_2\right\} x^n y^m . P_{n,m-1}(t) + \left\{(m+1)(\varepsilon_2+\delta_2)\right\} x^n y^m . P_{n,m+1}(t) + \\ \left\{\alpha_1 + (\mathrm{n}-1)\beta_1\right\} x^n y^m . P_{n-1,m}(t) + \left\{(\mathrm{n}+1)(\varepsilon_1+\delta_1)\right\} x^n y^m . P_{n+1,m}(t) + \\ \left\{(\mathrm{n}+1)\tau_1\right\} x^n y^m . P_{n+1,m-1}(t) \end{array}\right]$$

The statistical measures after solving the above differential equations using initial conditions and joint cumulant generating function are:

Expected number of *units of bacteria* in stage-I at time 't' is

$$m_{1,0}(t) = N_o . e^{At} \tag{2.2.1}$$

Expected number of *units of bacteria* in stage-II at time 't' is

$$m_{0,1}(t) = \frac{\tau_1 N_o . e^{At}}{(A-B)} + M_o . e^{Bt} \tag{2.2.2}$$

Variance of number of *units of bacteria* in stage-I at time 't' is

$$m_{2,0}(t) = \frac{-\left(2\alpha_1 + \beta_1 + \tau_1\right) N_o . e^{At}}{A} + C_o . e^{2At} \tag{2.2.3}$$

Variance of number of *units of bacteria* in stage-II at time 't' is

$$\begin{aligned} m_{0,2}(t) = {} & \frac{\tau_1 N_o . e^{At}}{(A-2B)} + \frac{\left(-J\tau_1 N_o . e^{Bt}\right)}{(A-B)(B)} + \frac{\left(-JM_o . e^{Bt}\right)}{(B)} + \frac{\left\{-2\tau_1(\alpha_2-\tau_1) N_o . e^{At}\right\}}{(A-2B)(B)} \\ & + \frac{\left(-2\alpha_1\tau_1^2 N_o . e^{At}\right)}{(A-B)(B)(A-2B)} + \frac{\left(2\alpha_1\tau_1 M_o . e^{Bt}\right)}{(A)(B)} + \frac{\left\{2\tau_1^2(2\alpha_1+\beta_1+\tau_1) N_o . e^{At}\right\}}{(A-2B)(A)(B)} \\ & + \frac{\tau_1^2 C_o . e^{2At}}{(A-B)^2} + \frac{D_o . e^{(A+B)t}}{(A-B)} + E_o . e^{2Bt} \end{aligned} \tag{2.2.4}$$

Covariance of number of *units of bacteria* in stage-I and stage-II at time 't' is

$$\begin{aligned} m_{1,1}(t) = {} & \frac{\left\{-(\alpha_2-\tau_1) N_o . e^{At}\right\}}{(B)} + \frac{\left(-\alpha_1\tau_1 N_o . e^{At}\right)}{(A-B)(B)} + \frac{\left(-\alpha_1 M_o . e^{Bt}\right)}{(A)} + \frac{\left\{\tau_1(2\alpha_1+\beta_1+\tau_1) N_o . e^{At}\right\}}{(A)(B)} \\ & + \frac{\left(\tau_1 C_o . e^{2At}\right)}{(A-B)} + D_o . e^{(A+B)t} \end{aligned} \tag{2.2.5}$$

Where

$A = \left[\beta_1 - (\tau_1 + \varepsilon_1 + \delta_1)\right];$

$B = \left[\beta_2 - (\varepsilon_2 + \delta_2)\right];$

$J = \left[2\alpha_2 + \varepsilon_2 + \delta_2\right]$

N_o, M_o are initial values and C_o, D_o, E_o are constants which can be evaluated.

II. Numerical Illustration:

In order to verify model behavior, a hypothetical numerical data set is obtained for various statistical measures from equations from 2.2.1 to 2.2.5, such as average number of bacteria units on first stage and second stage, variances of bacterial units in first and second stages and covariance between the number of bacterial units in first and second stages. While computing the values of $m_{10}(t)$, $m_{01}(t)$, $m_{20}(t)$, $m_{02}(t)$ and $m_{11}(t)$ with MATHCAD, it is considered for changing values one parameter and for the fixed parameters of the remaining parameters among α_1; β_1; τ_1; α_2; β_2; ε_1; δ_1; ε_2; δ_2; N_0; M_0; and t.

Table-3.1: Values of $m_{10}(t)$, $m_{01}(t)$, $m_{20}(t)$, $m_{02}(t)$ and $m_{11}(t)$ for changing and fixed values of α_1; β_1; τ_1; α_2; β_2; ε_1; δ_1; ε_2; δ_2; N_0; M_0; and t

α_1	β_1	τ_1	α_2	β_2	ε_1	δ_1	ε_2	δ_2	No	Mo	t	m_{10}	m_{01}	m_{20}	m_{02}	m_{11}
1	9	3	4	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
2	9	3	4	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**4.52E+04**	**1.66E+05**	**4.28E+04**
3	9	3	4	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**5.09E+04**	**1.83E+05**	**4.98E+04**
4	9	3	4	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**5.65E+04**	**1.99E+05**	**5.67E+04**
5	9	3	4	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**6.22E+04**	**2.15E+05**	**6.36E+04**
6	9	3	4	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**6.78E+04**	**2.31E+05**	**7.05E+04**
1	**9**	3	4	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	**9.5**	3	4	5	2	1	3	1	200	100	0.65	**1.95E+03**	**2.53E+03**	**7.04E+04**	**1.58E+05**	**5.78E+04**
1	**10**	3	4	5	2	1	3	1	200	100	0.65	**2.69E+03**	**2.88E+03**	**1.26E+05**	**1.83E+05**	**9.44E+04**
1	**10.5**	3	4	5	2	1	3	1	200	100	0.65	**3.73E+03**	**3.39E+03**	**2.26E+05**	**2.27E+05**	**1.56E+05**
1	**11**	3	4	5	2	1	3	1	200	100	0.65	**5.16E+03**	**4.06E+03**	**4.09E+05**	**2.97E+05**	**2.59E+05**
1	**11.5**	3	4	5	2	1	3	1	200	100	0.65	**7.14E+03**	**4.95E+03**	**7.43E+05**	**4.05E+05**	**4.36E+05**
1	9	**2.5**	4	5	2	1	3	1	200	100	0.65	**1.95E+03**	**2.14E+03**	**6.55E+04**	**9.98E+04**	**4.64E+04**
1	9	**2.75**	4	5	2	1	3	1	200	100	0.65	**1.65E+03**	**2.21E+03**	**5.09E+04**	**1.22E+05**	**4.09E+04**
1	9	**3**	4	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	**3.25**	4	5	2	1	3	1	200	100	0.65	**1.20E+03**	**2.41E+03**	**3.08E+04**	**1.88E+05**	**3.15E+04**
1	9	**3.5**	4	5	2	1	3	1	200	100	0.65	**1.02E+03**	**2.56E+03**	**2.40E+04**	**2.44E+05**	**2.76E+04**
1	9	**3.75**	4	5	2	1	3	1	200	100	0.65	**8.63E+02**	**2.78E+03**	**1.88E+04**	**3.32E+05**	**2.42E+04**
1	9	3	**4**	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	3	**5**	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.48E+05**	**3.72E+04**
1	9	3	**6**	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.47E+05**	**3.85E+04**
1	9	3	**7**	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.45E+05**	**3.98E+04**
1	9	3	**8**	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.43E+05**	**4.11E+04**
1	9	3	**9**	5	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.42E+05**	**4.23E+04**
1	9	3	4	**5**	2	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	3	4	**6**	2	1	3	1	200	100	0.65	**1.41E+03**	**2.58E+03**	**3.96E+04**	**5.64E+05**	**4.81E+04**
1	9	3	4	**7**	2	1	3	1	200	100	0.65	**1.41E+03**	**2.78E+03**	**3.96E+04**	**1.04E+06**	**5.30E+04**
1	9	3	4	**8**	2	1	3	1	200	100	0.65	**1.41E+03**	**2.87E+03**	**3.96E+04**	**2.04E+06**	**5.93E+04**
1	9	3	4	**9**	2	1	3	1	200	100	0.65	**1.41E+03**	**4.70E+02**	**3.96E+04**	**2.76E+06**	**8.87E+04**
1	9	3	4	**10**	2	1	3	1	200	100	0.65	**1.41E+03**	**3.54E+02**	**3.96E+04**	**3.03E+06**	**1.29E+05**
1	9	3	4	5	**1.5**	1	3	1	200	100	0.65	**1.95E+03**	**2.53E+03**	**6.79E+04**	**1.47E+05**	**5.60E+04**
1	9	3	4	5	**1.75**	1	3	1	200	100	0.65	**1.65E+03**	**2.40E+03**	**5.18E+04**	**1.49E+05**	**4.47E+04**
1	9	3	4	5	**2**	1	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	3	4	5	**2.25**	1	3	1	200	100	0.65	**1.20E+03**	**2.24E+03**	**3.03E+04**	**1.56E+05**	**2.89E+04**
1	9	3	4	5	**2.5**	1	3	1	200	100	0.65	**1.02E+03**	**2.22E+03**	**2.32E+04**	**1.70E+05**	**2.35E+04**
1	9	3	4	5	**2.75**	1	3	1	200	100	0.65	**8.63E+02**	**2.21E+03**	**1.78E+04**	**1.99E+05**	**1.92E+04**
1	9	3	4	5	2	**1**	3	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	3	4	5	2	**1.15**	3	1	200	100	0.65	**1.28E+03**	**2.26E+03**	**3.37E+04**	**1.53E+05**	**3.15E+04**
1	9	3	4	5	2	**1.3**	3	1	200	100	0.65	**1.16E+03**	**2.23E+03**	**2.87E+04**	**1.58E+05**	**2.77E+04**
1	9	3	4	5	2	**1.45**	3	1	200	100	0.65	**1.05E+03**	**2.22E+03**	**2.45E+04**	**1.67E+05**	**2.45E+04**
1	9	3	4	5	2	**1.6**	3	1	200	100	0.65	**9.52E+02**	**2.21E+03**	**2.09E+04**	**1.80E+05**	**2.16E+04**
1	9	3	4	5	2	**1.75**	3	1	200	100	0.65	**8.63E+02**	**2.21E+03**	**1.78E+04**	**1.99E+05**	**1.92E+04**
1	9	3	4	5	2	1	**3**	1	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	3	4	5	2	1	**3.15**	1	200	100	0.65	**1.41E+03**	**2.14E+03**	**3.96E+04**	**1.37E+05**	**3.46E+04**
1	9	3	4	5	2	1	**3.3**	1	200	100	0.65	**1.41E+03**	**1.99E+03**	**3.96E+04**	**1.30E+05**	**3.34E+04**
1	9	3	4	5	2	1	**3.45**	1	200	100	0.65	**1.41E+03**	**1.86E+03**	**3.96E+04**	**1.28E+05**	**3.23E+04**
1	9	3	4	5	2	1	**3.6**	1	200	100	0.65	**1.41E+03**	**1.75E+03**	**3.96E+04**	**1.25E+05**	**3.13E+04**
1	9	3	4	5	2	1	**3.75**	1	200	100	0.65	**1.41E+03**	**1.65E+03**	**3.96E+04**	**1.14E+05**	**3.03E+04**
1	9	3	4	5	2	1	3	**1**	200	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	3	4	5	2	1	3	**1.15**	200	100	0.65	**1.41E+03**	**2.14E+03**	**3.96E+04**	**1.37E+05**	**3.46E+04**
1	9	3	4	5	2	1	3	**1.3**	200	100	0.65	**1.41E+03**	**1.99E+03**	**3.96E+04**	**1.30E+05**	**3.34E+04**
1	9	3	4	5	2	1	3	**1.45**	200	100	0.65	**1.41E+03**	**1.86E+03**	**3.96E+04**	**1.28E+05**	**3.23E+04**
1	9	3	4	5	2	1	3	**1.6**	200	100	0.65	**1.41E+03**	**1.75E+03**	**3.96E+04**	**1.25E+05**	**3.13E+04**
1	9	3	4	5	2	1	3	**1.75**	200	100	0.65	**1.41E+03**	**1.65E+03**	**3.96E+04**	**1.14E+05**	**3.03E+04**
1	9	3	4	5	2	1	3	1	**200**	100	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	3	4	5	2	1	3	1	**205**	100	0.65	**1.44E+03**	**2.35E+03**	**4.05E+04**	**1.54E+05**	**3.68E+04**
1	9	3	4	5	2	1	3	1	**210**	100	0.65	**1.48E+03**	**2.41E+03**	**4.15E+04**	**1.57E+05**	**3.77E+04**
1	9	3	4	5	2	1	3	1	**215**	100	0.65	**1.51E+03**	**2.46E+03**	**4.25E+04**	**1.61E+05**	**3.86E+04**
1	9	3	4	5	2	1	3	1	**220**	100	0.65	**1.55E+03**	**2.51E+03**	**4.35E+04**	**1.65E+05**	**3.95E+04**
1	9	3	4	5	2	1	3	1	**225**	100	0.65	**1.58E+03**	**2.56E+03**	**4.45E+04**	**1.68E+05**	**4.03E+04**
1	9	3	4	5	2	1	3	1	200	**100**	0.65	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	3	4	5	2	1	3	1	200	**105**	0.65	**1.41E+03**	**2.31E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	3	4	5	2	1	3	1	200	**110**	0.65	**1.41E+03**	**2.32E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	3	4	5	2	1	3	1	200	**115**	0.65	**1.41E+03**	**2.33E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	3	4	5	2	1	3	1	200	**120**	0.65	**1.41E+03**	**2.34E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	3	4	5	2	1	3	1	200	**125**	0.65	**1.41E+03**	**2.35E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**
1	9	3	4	5	2	1	3	1	200	100	**0.65**	**1.41E+03**	**2.30E+03**	**3.96E+04**	**1.50E+05**	**3.59E+04**

α_1	β_1	τ_1	α_2	β_2	ε_1	δ_1	ε_2	δ_2	No	Mo	t	m_{10}	m_{01}	m_{20}	m_{02}	m_{11}
1	9	3	4	5	2	1	3	1	200	100	**0.75**	**1.90E+03**	**3.06E+03**	**7.52E+04**	**2.53E+05**	**7.41E+04**
1	9	3	4	5	2	1	3	1	200	100	**0.85**	**2.56E+03**	**4.08E+03**	**1.41E+05**	**4.31E+05**	**1.49E+05**
1	9	3	4	5	2	1	3	1	200	100	**0.95**	**3.46E+03**	**5.45E+03**	**2.63E+05**	**7.44E+05**	**2.94E+05**
1	9	3	4	5	2	1	3	1	200	100	**1.05**	**4.67E+03**	**7.29E+03**	**4.87E+05**	**1.30E+06**	**5.72E+05**
1	9	3	4	5	2	1	3	1	200	100	**1.15**	**6.30E+03**	**9.77E+03**	**8.97E+05**	**2.28E+06**	**1.10E+06**

III. Discussion And Analysis

3.1. Observations with changing values of immigrant bacterial growth rate to stage-I: From the above table it is observed that m_{10} and m_{01} are invariant functions of α_1; further m_{20} and m_{02} are increasing functions of α_1; and m_{11} is positive and increasing function of α_1. Hence it may conclude that the growth of bacteria through immigrations have no impact on the average sizes in each stage; the variances of both stages have increasing patterns with immigrated growth of bacteria; further there is a positive and increasing correlations between the sizes of bacteria in stage -I and stage-II, influenced by the arrivals through immigrations of bacteria from outside the plants group.

3.2. Observations with changing values of internal growth of bacteria in stage-I plants: It is observed that m_{10} and m_{01} are increasing functions of β_1; further m_{20} and m_{02} are increasing functions of β_1; and m_{11} is positive and increasing function of β_1. Hence it may conclude that there is a positive relation between average size of bacterial units in stage-I plants and the internal growth of bacteria in stage-I plants; positive relation between the internal growth rate of bacterial units in stage -I plants and the average size of bacteria in stage-II plants; the variances of bacterial units in both stage plants are positively related with the internal growth rate of bacteria in stage-I plants; Further, there is a positive and increasing correlation between the sizes of the bacterial units in stage-I and stage-II plants influenced with the internal growth rate of plants in stage-I.

3.3. Observations with changing values of transition of bacteria from stage-I plants:
It is observed that m_{10} and m_{01} are decreasing and increasing functions respectively of τ_1; m_{20} and m_{02} are decreasing and increasing functions respectively of τ_1; m_{11} is positive and decreasing function of τ_1. Hence it may conclude that there is a negative relation between average size of bacterial units in stage-I plants and the transition of bacteria from stage-I plants to stage-II; positive relation between the average size of bacteria in stage-II plants and transition rate of bacterial units from stage -I to stage-II plants; the variance of bacterial units in stage-I plants is negatively related and the variance of bacterial units in stage-I plants is positively related with the transition rate of bacteria from stage-I plants to stage-II; Further, there is a positive and decreasing correlation between the sizes of the bacterial units in stage-I and stage-II plants influenced with the transition rate of bacteria from stage-I plants to stage-II.

3.4. Observations with changing values of immigrant bacterial growth rate to stage-II plants:
It is observed that m_{10} and m_{01} are invariant functions of α_2; m_{20} and m_{02} are invariant and decreasing functions of α_2; m_{11} is positive and increasing function of α_2. Hence it may conclude that the growth of bacteria through immigration to stage-II have no impact on the average sizes in each stage; the variance of stage-I has no impact with immigrated growth of bacteria to stage-II; the variance of stage-II has decreasing pattern with immigrated growth of bacteria; further there is a positive and increasing correlations between the sizes of bacteria in stage -I and stage-II plants, influenced by the arrivals through immigrations of bacteria from outside the plants group.

3.5. Observations with changing values of internal growth of bacteria in stage-II plants:
It is observed that m_{10} and m_{01} are invariant and increasing functions respectively of β_2; m_{20} and m_{02} are invariant and increasing functions respectively of β_2; m_{11} is positive and increasing function of β_2; Hence it may conclude that there is no impact of the internal growth of bacteria in stage-II plants on average size of bacterial units in stage-I plants and it has positive relation with the average size of bacteria in stage-II plants; the variance of bacterial units in stage-I plants has no impact of the internal growth of bacteria in stage-II plants; the variance of bacterial units in stage-II plants is positively related with the internal growth rate of bacteria in stage-II plants; Further, there is a positive and increasing correlation between the sizes of the bacterial units in stage-I and stage-II plants influenced with the internal growth rate of plants in stage-II.

3.6. Observations with changing values of emigrant bacterial growth rate to stage-I plants:
It is observed that m_{10} and m_{01} are decreasing functions of ε_1; m_{20} and m_{02} are decreasing and increasing functions respectively of ε_1; m_{11} is positive and decreasing function of ε_1; Hence it may conclude that the loss of bacteria through emigrations from stage-I plants have negative relation with the average sizes of bacteria in each stage; the variance of bacterial units in stage-I plants is negatively related with the loss of bacteria in stage-I

plants; the variance of bacterial units in stage-II plants is positively related with the loss of bacteria in stage-I plants; further there is a positive and increasing correlations between the sizes of bacteria in stage -I and stage-II, influenced by the loss of bacteria from stage-I plants.

3.7. Observations with changing values of bacterial loss (death) rate in stage-I plants:
It is observed that m_{10} and m_{01} are decreasing functions of δ_1; m_{20} and m_{02} are decreasing and increasing functions respectively of δ_1; m_{11} is positive and decreasing function of δ_1; Hence it may conclude that the loss of bacteria due to death in stage-I plants have negative relation with the average sizes of bacteria in each stage; the variance of bacterial units in stage-I plants is negatively related with the loss (death) of bacteria in stage-I plants; the variance of bacterial units in stage-II plants is positively related with the loss (death) of bacteria in stage-I plants; further there is a positive and decreasing correlations between the sizes of bacteria in stage -I and stage-II plants, influenced by the loss (death) of bacteria from stage-I plants.

3.8. Observations with changing values of emigrant bacterial growth rate to stage-II plants:
It is observed that m_{10} and m_{01} are invariant and decreasing functions respectively of ε_2; m_{20} and m_{02} are invariant and decreasing functions respectively of ε_2; m_{11} is positive and decreasing function of ε_2; Hence it may conclude that the loss of bacteria through emigrations from stage-II plants has no impact on the average size of bacteria in stage-I plants; the loss of bacteria through emigrations from stage-II plants has negative relation with the average size of bacteria in stage-II plants; the variance of bacterial units in stage-I plants is not influenced by the loss of bacteria in stage-II plants; the variance of bacterial units in stage-II plants is negatively related with the loss of bacteria in stage-II plants; further there is a positive and decreasing correlations between the sizes of bacteria in stage -I and stage-II, influenced by the loss of bacteria from stage-II plants.

3.9. Observations with changing values of bacterial loss (death) rate in stage-II plants:
It is observed that m_{10} and m_{01} are invariant and decreasing functions respectively of δ_2; m_{20} and m_{02} are invariant and decreasing functions respectively of δ_2; m_{11} is positive and decreasing function of δ_2; Hence it may conclude that the loss of bacteria due to death in stage-II plants has no impact on the average size of bacteria in stage-I; the loss of bacteria due to death in stage-II plants have negative relation with the average size of bacteria in stage-II; the variance of bacterial units in stage-I plants is not influenced by the loss (death) of bacteria in stage-I plants; the variance of bacterial units in stage-II plants is negatively related with the loss (death) of bacteria in stage-II plants; further there is a positive and decreasing correlations between the sizes of bacteria in stage -I and stage-II, influenced by the loss (death) of bacteria from stage-II plants.

3.10. Observations with changing values of initial number of bacterial units in stage-I plants:
It is observed that m_{10} and m_{01} are increasing functions of N_0; m_{20} and m_{02} are increasing function of N_0; m_{11} is positive and increasing function of N_0. Hence it may conclude that there is a positive relation between the initial number of units of bacteria in stage-I and average size of bacterial units in each stage; the variances of bacterial units in both stage plants are positively related with the initial number of units of bacteria in stage-I plants; Further, there is a positive and increasing correlation between the sizes of the bacterial units in stage-I and stage-II plants influenced with the initial number of units of bacteria in stage-I.

3.11. Observations with changing values of initial number of bacterial units in stage-II plants:
It is observed that m_{10} and m_{01} are invariant and increasing functions respectively of M_0; m_{20} and m_{02} are invariant functions of M_0; m_{11} is invariant function of M_0. Hence it may conclude that there is no impact of initial number of bacteria in stage-II on average size of bacterial units in stage-I; positive relation between the initial number of units of bacteria in stage-II and average size of bacterial units in stage-II; the variances of bacterial units in both stage plants are not influenced by the initial number of units of bacteria in stage-II plants; Further, there is a no correlation between the sizes of the bacterial units in stage-I and stage-II plants influenced with the initial number of units of bacteria in stage-I.

3.12. Observations with changing values of time period:
It is observed that m_{10} and m_{01} are increasing functions of time t; m_{20} and m_{02} are increasing functions of time t; m_{11} is positive and increasing functions of time t. Hence it may conclude that there is a positive relation between average size of bacterial units in each stage and the time; the variances of bacterial units in both stage plants are positively related with the time. Further, there is a positive and increasing correlation between the sizes of the bacterial units in stage-I and stage-II plants influenced by the time.

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