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AN INFLATED PROBABILITY MODEL FOR INFECTION

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ABSTRACT

The present paper deals with the projected probability model in inflated form for the infection. There parameters of the model was estimated by suitable estimation technique. The suitability of the proposed model was tested by observed set of data. The study showed inflation trend or overdispersion in the case of community level, while delayed exponential increase in the case of preventive care towards infection. This research might be useful to elucidate strategy against infection in proper time.

Key wards: probability distribution, inflated estimation technique.

INTRODUCTION

A person infected with malaria may be re infected before recovering if bitten again by an infectious mosquito. Even third and higher order infections are possible (Brumpt, 1949). Here the best data available consist of planet studies are used for the present study, where blood samples were observed from a fixed set of individuals at discrete points in time (Johnson and Kutz, 1969). Both *Plasmodium vivax* and *Plasmodium falciparum* occur in abundance, but *Plasmodium falciparum* (the killer parasite) is accounting more as compared to eighties and nineties. Let us consider N objects and each subject is observed at discrete point of time in the interval (o,T). Let $f_x(x)$ be the probability function of infections, where x is a discrete random variable, representing the number of infections. Poission model in case of both method of moments and likelihood are good fit for both of the data sets (Clifford and Cohen, 1961).

Malaria is one of the most widespread diseases in the world today. Malaria is the most important parasitic disease in the world. It kills 3,000 children every day and more than one million each year. The majority of these deaths occur among children under five years of age and pregnant women

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is sub-saharan Africa Earlier about 80% of malaria disease was due to plasmodium vivax parasite. Now malaria disease due to Plasmodium falciparum is also increased. This is the most virulent of the four malaria parasites of humans. It is estimated that Plasmodium falciparum kills between 1.5 and 2.7 million children per year (Good 1999). Also women are at increased risk during pregnancy (Fried, 1998), Despite fifty years of world experience in malaria control more people are dying of malaria now (David and Elizabeth, 1998). Malaria is caused by the plasmodium parasite transmitted by the infective female Anopheles mosquito. So, the infected malaria patient can transmit the disease to many susceptible.

A person infected with malaria may be reinfected before recovering if bitten again by an infectious mosquito. Even third and higher order infections are possible. Two lines of evidence support these contentions. First individuals frequently harbor in their blood two or more of the four species of malaria parasite, which can infect humans (Sharma, 1995). Other evidence implicates multiple infections implicates multiple infections with a single species of parasite. The process of acquiring multiple infections of a single species called super infection was first modeled mathematically by the malariologist George Macdonald (1950). Macdonald- Dietz modeled (1970) describes the flow of infections through an individual as an infinite serve queue. The continuous observation of state is obviously practically impossible. Hence the best data available consist of panel studies are used to fit some probability models, where blood samples were observed from affixed set of individuals at discrete points.

Probability Model:Let α be the risk of infected population in the society in specific area and 1- α be the risk of no infections. Under this situation the proposed model takes the following inflated form (Nedelman, 1985):-

$$P[x=o] = 1 - \alpha, \quad k=o$$
$$P[X=k] = \frac{\alpha \theta^{k} (e^{\theta} - 1)^{-1}}{k!} \qquad k = 1, 2, 3, \dots$$

Where, θ denotes average infection in population. The above model has two parameters α and θ .

Estimation of Parameters: The proposed model has two parameters α and θ . The parameters are estimated with the help of Maximum likelihood method in following way.

A sample consisting of N observations of random variables x with probability function has been considered (Nedelman, 1985). The value chosen as estimates of and are those which maximize the expression

Now, taking logarithmic of above equation and partially differentiating w.r. to α and θ in term and equating to zero yield the estimating equation.

$$\frac{\partial \log L}{\partial \alpha} = -\frac{f_0}{1-\alpha} + \frac{f_1}{\alpha} + \frac{f-f_1-f_0}{\alpha} = 0 \qquad \dots (2)$$

$$\frac{\partial \log L}{\partial \alpha} = \frac{f_1 \left[-\theta e^{\theta} (e^{\theta} - 1)^{-2} + (e^{\theta} - 1)^{-1} \right]}{\theta (e^{\theta} - 1)^{-1}} + \frac{(f - f_1 - f_0) \left[\theta e^{\theta} (e^{\theta} - 1)^{-2} - (e^{\theta} - 1)^{-1} \right]}{\left[1 - \theta (e^{\theta} - 1)^{-1} \right]} = 0 \qquad \dots (3)$$

Now, solving the above two equation we get the value of α and θ as.

$$\alpha = \frac{f - f_0}{f}$$
$$\theta(e^{\theta} - 1)^{-1} = \frac{f_1}{f - f_0}$$

The second partial derivative of log L w.r. to α and we get as

$$\frac{\partial^2 \log L}{\partial \alpha^2} = -\frac{f_0}{(1-\alpha^2)} + \frac{f_1}{\alpha^2} + \frac{(f-f_1-f_0)}{\alpha^2} \qquad \dots (4)$$

Now before second partial derivative of log L and taking approximation at one place up to third term and then differentiating, we obtained as

$$\frac{\partial^2 \log L}{\partial \theta^2} = -f \left[-e^{2\theta} (e^{\theta} - 1)^{-2} + (e^{\theta} - 1)^{-1} e^{\theta} \right] - \frac{f_1}{\theta^2} +$$

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Now partial derivative of α and α respectively we get as,

$$\frac{\partial^2 \log L}{\partial \alpha \,\partial \theta} = \frac{\partial^2 \log L}{\partial \theta \,\partial \alpha} = 0 \frac{\partial^2 \log L}{\partial \alpha \,\partial \theta} = \frac{\partial^2 \log L}{\partial \theta \,\partial \alpha} = 0 \quad \dots (6)$$

Using the fact

 $E [f_0] = f (1-\alpha)$ $E [f_1] = f\alpha [\theta (e^{\theta} - 1)^{-1}]$ $E [f - f_0 - f_1] = f\alpha [1-\theta (e^{\theta} - 1)^{-1}]$ Where E denote for the expectation, The expected

Where E denote for the expectation, The expected value of second partial derivative of log L can be obtained as

$$\phi_{11} = \frac{E\left[-\frac{\partial^2 \log L}{\partial \alpha^2}\right]}{f} = \left[\frac{1}{1-\alpha} + \frac{1}{\alpha}\right] \qquad \dots (7)$$

$$\phi_{22} = \underbrace{\left[-\frac{\partial^{2} \log L}{\partial \theta^{2}}\right]}_{f} = \alpha \theta e^{\theta} (e^{\theta} - 1)^{2} \left[1 - e^{\theta} (e^{\theta} - 1)^{-1} + \frac{\alpha (e^{\theta} - 1)^{-1}}{\theta}\right] + \frac{\alpha \left[1 - \theta \left(e^{\theta} - 1\right)\right] \left[\frac{\theta^{2}}{2} + \theta + 1\right]}{\left[\frac{\theta^{2}}{2} + \theta\right]^{2}} \qquad \dots \dots \dots (8)$$

Therefore, by inverting the information matrix, expression for asymptotic variances of the estimates

can be obtained as :

$$V(\alpha)^{\hat{}} = \frac{1}{f} \left[\frac{\phi_{22}}{\phi_{11} \phi_{22} - \phi_{12}^2} \right] - \dots (11)$$
$$V(\theta)^{\hat{}} = \frac{1}{f} \left[\frac{\phi_{11}}{\phi_{11} \phi_{22} - \phi_{12}^2} \right] - \dots (12)$$

Here f_0 be Number of observation in zeroth cell f_1 – Number of observation in first cell. f – Total number of observations. – Observed Mean

Application: We used the data collected by the WHO in Garki, Nigeria in particular data of infection with Plasmodium falciparum only. The value of α from the Table (1) is 0.77 and Table (2) is 0.64. And the value of θ is 0.64 from Table (1) and 2.2045 from Table (2). The χ^2 shows that proposed model found to be better approximation to the both set of the observed data.

Table 1: Observed and expected values fromWHO in Garki, Nigeria (Source: Molineaux andGrammicia, 1980).

infants	infants	Values(M.L.E.)
7	7.13	
3	2.99	
5	4.95	=4.92
10	5.47	=0.77
4	10.13	=2.7975
1	10.53	=0.0082
0	0	=0.0013
1	Df=2	
N=31	N =31	
	infants 7 3 5 10 4 1 0 1 N=31	infants infants 7 7.13 3 2.99 5 4.95 10 5.47 4 10.13 1 10.53 0 0 1 Df=2 N=31 N=31

Table 2: Observed and expected values fromWHO in Garki, Nigeria (Source: Molineauxand Grammicia, 1980) .

Infections	Observed	Expected	Estimated
	infants	infants	Values
		(By M.L.E.)	
0	6	5.99	
1	3	3.01	= 5.65
2	1	3.31	= 0.77
3	3	2.43	= 2.7975
4	3	1.34	= 0.013
5	1	0.92	= 0.071

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Reference:

- **1.** Brumpt E (1949): The human parasites of the genus plasmodium, In Malariology, M.F. Boyed (ed.) 65-121.
- 2. Clifford A and Cohen Jr (1961): Estimating the Poisson parameter from samples that are truncated on the right. Technmetrics 3(3), 433-438.
- David N Nabarra and Elizabeth M Tayler (1998): The "Rall Back Malaria' campaign Science 280, 2067-68, Fried, Michal, Nosten,
- 4. Fried, Michel, Nosten Francois, Brockman Alan, BrabinBernad J and Duffy and Patrick E (1998):"Maternal Antibodies Block Malaria" Nature, 395, 851-852.
- 5. Johnson Norman L and Kotz, Samuel (1969): Discrete Distributions. Vol. 2, John Wiley and Sons New York.
- MacdenoldG(1950): The Epidemiology and Control of malaria London: Oxford University Press.
- 7. Molineaux L and Gramiccia G(1980): The Garki Project, World Health Organization.
- Nedelman J (1985): Some new thoughts about some old malaria model. Math. Biosci, 73, 159-182.
- 9. Nedelman J(1985): Estimation for a model of multiple malaria infections. Biometric 447-453.
- 10. Sharma HL(1995): Estimation of parameters involved in the distribution of the number of two types of children in a family, JISPS, 2, 1-14.

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