

International Journal of Statistics and Applied Mathematics

ISSN: 2456-1452
 Maths 2022; 7(5): 135-141
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www.mathsjournal.com
 Received: 25-06-2022
 Accepted: 30-07-2022

M Ahajeeth
 Research Scholar, Department of
 Statistics, Annamalai
 University, Chidambaram, Tamil
 Nadu, India

R Kannan
 Professor, Department of
 Statistics, Annamalai
 University, Chidambaram, Tamil
 Nadu, India

Corresponding Author:
M Ahajeeth
 Research Scholar, Department of
 Statistics, Annamalai
 University, Chidambaram, Tamil
 Nadu, India

Generalized cure rate model based on Aradhana distribution

M Ahajeeth and R Kannan

Abstract

In this article, we propose a new two parametric survival model for the population of interest that consists long term survivors or immunes. The model is referred to as Aradhana cure rate model. The model is a mixture model that involved a component representing the proportion of immunes and a distribution representing the lifetimes of the susceptible population.

Keywords: Aradhana distribution, moments, maximum likelihood estimation, standard cure rate

Introduction

Over 5.8 million Indians die as a result of lung diseases, diabetes, cancer, stroke, and other diseases. The World Health Organization (WHO) estimates that heart disease accounts for roughly 1.7 million deaths in India each year. In this regard, the cure rate model is essential for studying Co-variates that are either correlated to short-term or long-term impacts, as well as for determining if new therapies improve or decrease the likelihood that patients will be permanently cured, respond to treatment, or survive. Progress in the treatment of cancer has led to a spate of statistical research to develop cure models. On overall survival or progression-free survival, many studies of cancer survival data are conducted (PFS). In these circumstances, cure models can be used to depict long-term survivors rather than cured patients since no patient can be "cured" of death. The heterogeneity between cancer patients who are long-term survivors and those who are not can be examined using cure models. Examining the survival curve is a simple approach to tell if a certain data collection contains a subset of long-term survivors. A cure model may be appropriate and helpful if the survival curve plateaus at the conclusion of the trial.

For data with survival trends, cure models can be a suitable alternate for the Cox proportional hazards models. First, when survival curves have plateaus at their tails, the proportional hazards assumption could be inaccurate. Second, it may be important to explicitly describe variation within a patient population unless a survival plot has a long plateau. We can look at the covariates that are connected to either short-term or long-term impacts using cure models. For instance, using cure models, we can determine whether a new treatment increases or decreases the likelihood of becoming a long-term survivor or improves or worsens survival for individuals who are not long-term survivors.

Mixture and Non - mixture models are the two main categories of cure models. As the name implies, mixture cure models clearly represent survival as a combination of two patient types: those who are cured and those who are not. Logistic regression is typically used to model the likelihood that a patient will recover. A survival model for patients who are not cured makes up the model's second element. The Weibull and the Cox models are two of the many alternatives available for this. A mixed cure model can be expressed as follows in textual form: Probability alive at time t = probability cured + probability not cured \times probability alive at time t if not cured.

In contrast to the mixed cure model, standard survival models like the Cox model do not make the assumption of two distinct populations. The mixture cure model has the advantage of allowing factors to have distinct effects on patients who have been healed against patients who have not been healed. Non-mixture cure models approach modelling survival uniquely.

It is possible to think of many non-mixture cure models as Cox proportional hazards models with a cure fraction. Non – Mixture Cure models can be expressed as,

$$\text{Probability alive time } t = \text{probability cured}^{1-S \times(t)},$$

where $1-S \times(t)$ is an exponent of the probability of being cured

$S \times(t)$ is a survival function.

Non - mixture cure models may fit some data better than mixture cure models and vice versa

Hassan *et al.* (2020) [1] developed a new generalization of Aradhana distribution named Weighted Aradhana Distribution with some properties and applications. Welday and Shanker (2018) [3] presented a new Generalized Aradhana Distribution which includes exponential and Aradhana as special case. Rashid *et al.* (2019) [12] proposed a new generalization Aradhana distribution named Weighted Aradhana Distribution compared with the existing Aradhana distribution and revealed that Weighted Aradhana gives better fit. Maryam *et al.* (2020) [4] proposed a new parameter distribution said Alpha Power Transformed Aradhana distribution compared with the other well-known distributions and found that Alpha Power Transformed Aradhana distribution gives a better fit. Developed a new distribution said to be a Quasi Poisson – Distribution by compounding a Poisson – distribution with a Quasi Aradhana distribution. Rashid *et al.* (2022) [10] presented a new named Exponentiated Aradhana distribution with two parameter validate with the existing two parameter distribution and disclosed that Exponentiated Aradhana distribution with two parameter gives the better fit. Rama Shanker (2016) [14] developed a new one parameter distribution named Aradhana distribution for modelling real life data sets. Shanker *et al.* (2018) [13] proposed a Size – Biased Poisson Aradhana distribution compared with Size – Biased Poisson distribution and Size – Biased Lindley distribution by contrast Size – Biased Poisson Aradhana distribution gives the better fit. Balogun *et al.* (2020) presented a model which is useful for estimating the cure rate model in a hospital setting or the prevalence of diseases in cross – sectional data. Nandini *et al.* (2010) [8] developed a New Generalized Exponential Cure Rate model when the population of interest contains long – term survivors or Immunes. Tsodikov *et al.* (2015) [2] appealing that bounded cumulative hazard model in cure estimation is better than the two component mixture models. Othus *et al.* (2012) Utilizing cure models as a statistical tool, research on multiple myeloma patients' survival was done. Studied and revealed that exponentiated weibull model and generalized modified weibull model is the better model in analysing leukemia patients. Othus *et al.* (2017) [5] reviewed the cure model and when it is appropriate for the use. They also analysed competing risks of myeloma patients using cure models. Shanker (2016) [14] suggested the Aradhana distribution life span model for multiple medical applications and estimated its shape, moments, stochastic ordering, generating function, skewness and other mathematical and statistical characteristics. The new Aradhana distribution is a single parameter life time distribution when compared to Lindley and exponential distributions has greater flexibility when handling life time data.

Mixture Cure Rate Model

Standard Aradhana Cure Rate Model

The Probability density function of Standard Aradhana Cure Rate Model is given by

$$f(t) = (1 - \pi)f_u(t)$$

$$f(t) = (1 - \pi) \left(\frac{\theta^3}{\theta^2 + 2\theta + 2} \right) (1 + t)^2 e^{-\theta t} t > 0, \theta > 0$$

$$f(t) = \frac{(1-\pi)\theta^3(1+t)^2 e^{-\theta t}}{(\theta^2+2\theta+2)} \tag{1}$$

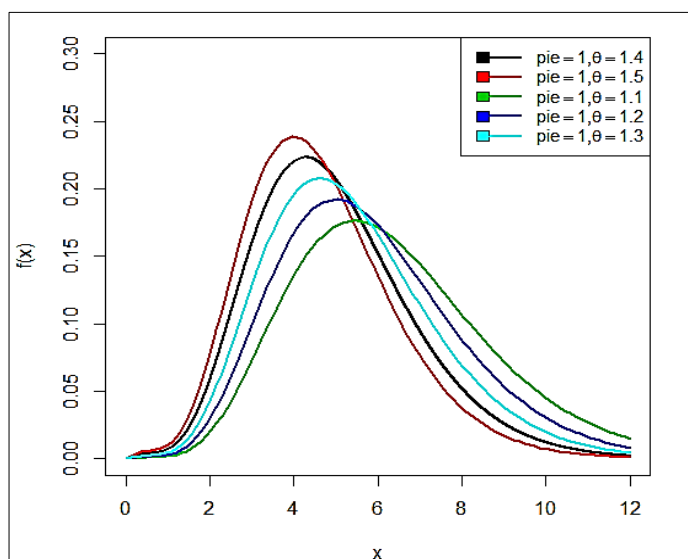


Fig 1: pdf plot generalized Aradhana cure rate model

The Cumulative distribution function of Standard Aradhana Cure Rate Model is given by

$$F(t) = (1 - \pi)F_u(t)$$

$$F(t) = (1 - \pi) \left\{ 1 - \left(1 + \frac{\theta t(\theta t + 2\theta + 2)}{\theta^2 + 2\theta + 2} \right) e^{-\theta t} \right\}$$

$$F(t) = \frac{(1-\pi) - (1-\pi) \left(\frac{(\theta^2 + 2\theta + 2) + \theta t(\theta t + 2\theta + 2)}{\theta^2 + 2\theta + 2} \right) e^{-\theta t}}{(\theta^2 + 2\theta + 2)}$$

$$F(t) = \frac{(1-\pi)(\theta^2 + 2\theta + 2) - (1-\pi)e^{-\theta t}((\theta^2 + 2\theta + 2) + \theta t(\theta t + 2\theta + 2))}{(\theta^2 + 2\theta + 2)} \tag{2}$$

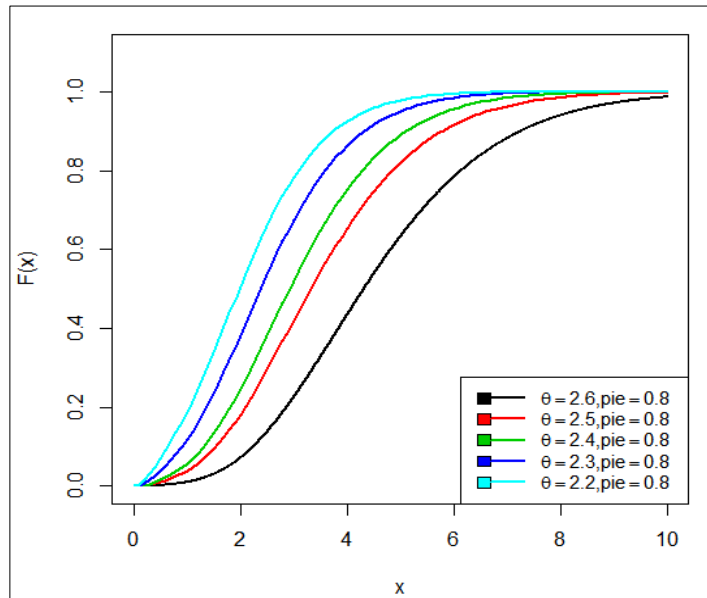


Fig 2: CDF plot Generalized Aradhana cure rate model

Survival Function

The Survival function of the Standard Aradhana Cure Rate model is given by

$$S(t) = \pi + (1 - \pi)S_u(t)$$

$$S(t) = \pi + (1 - \pi) \left(1 + \frac{\theta t(\theta t + 2\theta + 2)}{\theta^2 + 2\theta + 2} \right) e^{-\theta t}$$

$$S(t) = \pi + (1 - \pi) \left(\frac{(\theta^2 + 2\theta + 2) + \theta t(\theta t + 2\theta + 2)}{\theta^2 + 2\theta + 2} \right) e^{-\theta t}$$

$$S(t) = \left(\frac{\pi(\theta^2 + 2\theta + 2) + (1-\pi)((\theta^2 + 2\theta + 2) + \theta t(\theta t + 2\theta + 2))e^{-\theta t}}{(\theta^2 + 2\theta + 2)} \right)$$

(3)

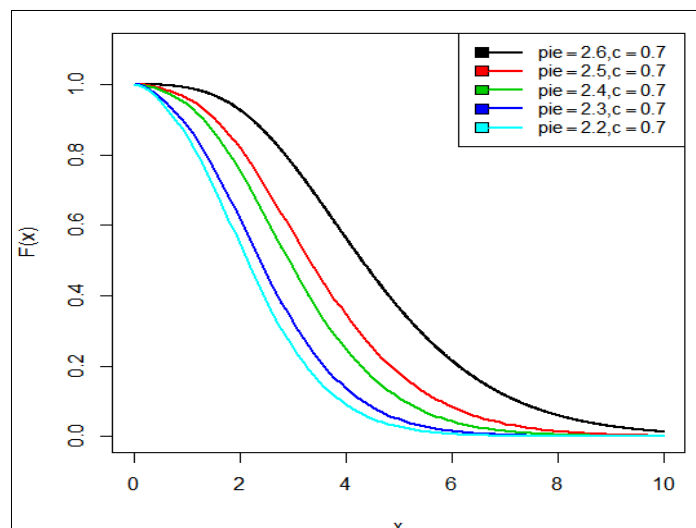


Fig 3: Survival Function of Generalized Aradhana cure rate model

Hazard Function

$$h(t) = \frac{(1-\pi)f_u(t)}{\pi+(1-\pi)S_u(t)}$$

$$h(t) = \frac{(1-\pi)\theta^3(1+t)^2 e^{-\theta t}}{(\pi(\theta^2+2\theta+2)+(1-\pi)((\theta^2+2\theta+2)+\theta t(\theta t+2\theta+2))e^{-\theta t}}$$

$$h(t) = \frac{\frac{(1-\pi)\theta^3(1+t)^2 e^{-\theta t}}{(\theta^2+2\theta+2)}}{\frac{\pi(\theta^2+2\theta+2)+(1-\pi)((\theta^2+2\theta+2)+\theta t(\theta t+2\theta+2))e^{-\theta t}}{(\theta^2+2\theta+2)}} \tag{4}$$

Parameter Estimation

Assume for each subject belongs to a random sample of size m, we observe the pair (t_j, d_j) , $j=1, 2, 3, \dots, m$ then the j^{th} subject contribution for the likelihood function can be given by

$$L_j = [f(t_j)]^{d_j} [S(t_j)]^{1-d_j} \tag{5}$$

$$L_j = [(1 - S)f_u(t_j)]^{d_j} [S + (1 - S)S_u(t_j)]^{1-d_j} \tag{6}$$

where d_j is a censoring indicator variable which is defined as

$$d_j = \begin{cases} 1, & \text{event of interest occurs} \\ 0, & \text{censoring} \end{cases}$$

Maximum Likelihood Estimation

$$L_j = \left[\frac{(1-\pi)(\theta^3(1+t_j)^2) e^{-\theta t_j}}{\theta^2+2\theta+2} \right]^{d_j} \left[\pi + (1-\pi) \left(1 + \frac{\theta t_i(\theta t_i+2\theta+2)}{\theta^2+2\theta+2} \right) e^{-\theta t_i} \right]^{1-d_j} \tag{7}$$

The log – likelihood

$$\log L = d_j \left\{ \sum_{j=1}^n \log(1-\pi) + \log \theta^3 + \log(1-t_j)^2 - \theta t_i - \log(\theta^2 + 2\theta + 2) \right\} +$$

$$(1-d_j) \left\{ \sum_{j=1}^n \log \pi + \log(1-\pi) - \theta t_j + \log \theta t_i + \log(\theta t_i + 2\theta + 2) - \log(\theta^2 + 2\theta + 2) \right\}$$

$$\log L = \log(1-\pi) \sum_{j=1}^n d_j + 3 \log \theta \sum_{j=1}^n d_j + \sum_{j=1}^n d_j \log(1+t_j)^2 + \log \pi \sum_{j=1}^n (1-d_j) - \theta \sum_{j=1}^n d_j t_j$$

$$- \log(\theta^2 + 2\theta + 2) \sum_{j=1}^n d_j + \log(1-\pi) \sum_{j=1}^n (1-d_j) - \theta \sum_{j=1}^n t_i (1-d_j) + \sum_{j=1}^n (1-d_j) \log(\theta^2 + 2\theta + 2) \sum_{j=1}^n (1-d_j)$$

Differentiating by π and θ we get

$$\frac{\partial \log L}{\partial \pi} = \frac{-1}{(1-\pi)} \sum_{j=1}^n d_j + \frac{1}{\pi} \sum_{i=1}^n (1-d_j) - \sum_{j=1}^n \frac{(1-d_j)}{(1-\pi)} = 0$$

$$\rightarrow \frac{-\sum d_j}{(1-\pi)} + \sum_{j=1}^n \frac{(1-d_j)}{\pi} - \sum_{j=1}^n \frac{(1-d_j)}{(1-\pi)} = 0$$

$$\rightarrow -\pi \sum_{j=1}^n d_j + \sum_{j=1}^n (1-d_j) (1-\pi) - \pi \sum_{j=1}^n (1-d_j) = 0$$

$$\rightarrow -\pi \sum_{j=1}^n d_j + (n - \sum d_j)(1-\pi) - \pi(n - \sum d_j) - \pi \sum_{j=1}^n d_j + n - n\pi - \sum d_j + \pi \sum d_j - n\pi + \pi \sum d_j = 0$$

$$\rightarrow n - n\pi - \sum d_j - n\pi + \pi \sum d_j = 0$$

$$\rightarrow n - 2n\pi - \sum d_j + \pi \sum d_j = 0$$

$$\rightarrow n - \sum d_j - \pi(2n - \sum d_j) = 0$$

$$\rightarrow n - \sum d_j = \pi(2n - \sum d_j)$$

$$\frac{\lambda}{\pi} = \frac{2n(1-\frac{1}{2}\bar{d})}{-n(1-\frac{1}{n}\sum d_j)}$$

$$\frac{\lambda}{\pi} = \left(\frac{2\left(1 - \frac{\bar{d}}{2}\right)}{1 - \bar{d}} \right) \tag{8}$$

$$\frac{\partial \log L}{\partial \theta} = \frac{3 \sum d_j}{\theta} - \sum_{j=1}^n t_j d_j - \sum_{j=1}^n d_j \frac{(2\theta+2)}{(\theta^2+2\theta+2)} - \sum_{j=1}^n (1 - d_j)t_j + \sum_{j=1}^n \frac{(1-d_j)(t_j+2)}{\theta t_j+2\theta+2} - \sum_{j=1}^n (1 - d_j) \frac{(2\theta+2)}{(\theta^2+2\theta+2)} = 0 \tag{9}$$

Generalized Cure Rate Model

The probability density function of Aradhana distribution is given by,

$$f(x; \theta) = \left(\frac{\theta^3}{\theta^2+2\theta+2} \right) (1 + x)^2 e^{-\theta x} \tag{10}$$

And the survival function is specified as,

$$S(x, \theta) = \left(1 + \frac{\theta x(\theta x+2\theta+2)}{\theta^2+2\theta+2} \right) e^{-\theta x} \tag{11}$$

Standard Cure Rate Model

The Standard Cure Rate Model is given by

$$S(t) = \pi + (1 - \pi)S_u(t) \tag{12}$$

Where,

$S_u(t)$ is the survival function of the susceptible population which may be assumed to follow a lifetime distribution.

π and $(1 - \pi)$ is a parameters of Standard Cure Rate model.

π : Probability of patients with a infectious disease and possible co – infection being a long term survivor.

$(1 - \pi)$: Probability of being susceptible.

The probability density function of Standard Cure Rate Model is given by

$$f(t) = (1 - \pi)f_u(t) \tag{13}$$

By this study, a modified model was developed using bounded cumulative hazard function a non – mixture model. The modified model is referred to as Generalized Cure Rate model with survival function and is given below as,

The survival function of the Generalised cure rate model can be specified as,

$$S(t) = \{\pi + (1 - \pi)S_u(t)\}^{1-d_i} \{\pi + (1 - \pi)S_u(t)\}^{d_i} \tag{14}(15)$$

Where,

$$\pi = \exp(-\theta) \text{ and } (1 - \pi) = (1 - \exp(-\theta))$$

θ is the mean number of occurrences of the disease. Equation 3 is used for patients with single infectious diseases and equation 4 is used for patients with co – infectious diseases.

d_i is the type of disease introduced.

Using equation 11 in equation 12 we get,

$$S(t) = \left\{ \pi + (1 + \pi) \left(1 + \frac{\theta t+2\theta+2}{\theta^2+2\theta+2} \right) e^{-\theta t} \right\}^{1-d_i} \left\{ e^{-\theta} + (1 - e^{-\theta}) \left(1 + \frac{\theta t+2\theta+2}{\theta^2+2\theta+2} \right) e^{-\theta} \right\}^{d_i} \tag{15}$$

Where,

θ = mean number of occurrences of the diseases.

The individual patient’s contribution to the likelihood function is given by

$$l_c = \left[\log \prod_{i=1}^n \{f_u(t_i)(1 - \pi)\}^{c_i} \right]^{\alpha_i} \left[\{\pi\}^{1-c_i} \{(1 - \pi)(1 - S_u(t))\}^{1-\alpha_i} \right]^{1-d_i} \tag{16}$$

$$\left[\log \prod_{i=1}^n \{f_u(t_i)(1 - \pi)\}^{c_i} \right]^{\alpha_i} \left[\{\pi\}^{1-c_i} \{(1 - \pi)(1 - S_u(t))\}^{c_i} \right]^{1-\alpha_i} \tag{16}$$

Assuming that $(\alpha_i, c_i, t_i, d_i)$ is the observed data of size n, where t_i is the survival time of the i^{th} patient, α_i denotes the censoring indicator variable. ($i=1, 2, 3 \dots n$)

$\alpha_i = 0 \rightarrow \text{UncensoredData}$
 $\alpha_i = 1 \rightarrow \text{CensoredData}$
 $C_i \rightarrow \text{CureIndicatorVariable}$
 $C_i = 0 \rightarrow \text{ForCuredPatient}$
 $C_i = 1 \rightarrow \text{ForIncuredPatient}$
 $d_i \rightarrow \text{DiseaseIndicator}$
 $d_i = 0 \rightarrow \text{ForSingleDisease}$
 $d_i = 1 \rightarrow \text{ForCo - infectedDisease}$

Parameter Estimation

The individual patients contribution to the likelihood function is given by,

$$\begin{aligned}
 L = & \sum_{i=1}^{m_1} (1 - d_i) C_i \alpha_i [3 \log \theta - \log(\theta^2 + 2\theta + 2) + \log(1 + t_i)^2 - \theta t_i + \log(1 - e^{-\theta})] + \sum_{i=1}^{m_1} (1 - d_i) (1 - \alpha_i) \\
 & \{C_i [\log(1 - e^{-\theta}) + \log \theta t_i + \log(\theta t_i + 2\theta + 2) - \theta t_i - \log(\theta^2 + 2\theta + 2)]\} + \sum_{i=1}^{m_1} [(1 - d_i)(1 - \alpha_i)](1 - C_i)(\theta) \\
 & + \sum_{i=1}^{m_2} d_i C_i \alpha_i [3 \log \theta - \log(\theta^2 + 2\theta + 2)] + \log(1 + t_i)^2 - \theta t_i + \log(1 - e^{-\theta}) + \sum_{i=1}^{m_2} d_i (1 - \alpha_i)(1 - C_i)(-\theta) \\
 & + \sum_{i=1}^{m_2} C_i d_i (1 - \alpha_i) [\log(1 - e^{-\theta})] + \log \theta t_i + \log(\theta t_i + 2\theta + 2) - \theta t_i - \log(\theta^2 + 2\theta + 2) \tag{17}
 \end{aligned}$$

The solution of $\frac{\partial l}{\partial \theta} = 0$,

The desired estimates of θ , where,

$$\frac{\partial l}{\partial \theta} = \sum_{i=1}^{m_1} (1 - d_i) \left\{ \alpha_i C_i \left(3/\theta - \frac{2\theta+2}{\theta^2+2\theta+2} - t_i + \frac{e^{-\theta(-1)}}{1-e^{-\theta}} + (1 - (i)(-1)) + (1 - \alpha_i) C_i \frac{e^{-\theta(-1)}}{1-e^{-\theta}} + \frac{t_i}{\theta t_i} + \left(\frac{t_i+2}{\theta t_i+2\theta+\theta} \right) - t_i - \frac{2\theta+2}{\theta^2+2\theta+2} \right) \right\}$$

$$\sum_{i=1}^{m_2} \left\{ d_i \alpha_i C_i \left[3/\theta - \frac{2\theta+2}{\theta^2+2\theta+2} - t_i - \frac{e^{-\theta(-1)}}{1-e^{-\theta}} + \frac{1}{\theta} + \left(\frac{t_i+2}{\theta t_i+2\theta+2} \right) - t_i - \frac{2\theta+2}{\theta^2+2\theta+2} \right] - (1 - C_i) + \left(\frac{(1-\alpha_i)C_i}{1-e^{-\theta}} \right) \right\} = 0 \tag{18}$$

m_1 is the sample of patients with a single disease and m_2 is the sample of patients with co – infected diseases.

Data Analysis

This section demonstrates the performance of existing models to the newly generated model with the help of real life data that consists of the patients suffering from many diseases.

Data set 1

We have taken the data set consisting remission time of 128 bladder cancer patients to demonstrate the performance of the proposed model Generalised Aradhana Cure rate model. The data were also studied by Zeal *et al.* Lee and Wang.

3.7, 3.11, 4.42, 3.28, 3.75, 2.96, 3.39, 3.31, 3.15, 2.76, 3.19, 1.59, 2.17, 3.51, 1.84, 1.61, 1.57, 1.89, 2.41, 3.09, 2.43, 2.53, 2.81, 3.31, 2.35, 2.77, 2.68, 2.00, 1.17, 2.17, 0.39, 2.79, 1.08, 2.88, 2.73, 2.87, 2.95, 2.67, 4.20, 2.85, 2.55, 2.17, 2.97, 3.68, 0.81, 1.69, 3.68, 4.70, 2.03, 2.82, 2.50, 1.47, 3.22, 3.15, 3.33, 2.56, 2.59, 2.83, 1.36, 1.84, 5.56, 1.12, 5.56, 1.12, 2.48, 2.03, 1.61, 2.05, 3.60, 3.11, 1.69, 4.19, 3.39, 3.22, 2.38, 1.92, 0.98, 1.59, 1.73, 1.71, 1.18, 4.38, 0.85, 3.65, 1.41, 3.27, 1.57, 1.87, 5.08, 2.93, 2.48, 3.56, 2.81, 2.74, 4.91, 3.19, 1.22, 2.97, 1.25, 2.55, 1.80, 2.12.

Data set 2

The first real data set is a subset of the data reported by Bekker *et al.* (2000), which corresponds to the survival times (in years) of a group of patients given chemotherapy treatment alone. The data consisting of survival times (in years) or 45 patients is given in table.

0.047, 0.115, 0.121, 0.132, 0.164, 0.197, 0.203, 0.260, 0.282, 0.296, 0.334, 0.395, 0.458, 0.466, 0.501, 0.507, 0.529, 0.534, 0.540, 0.641, 0.644, 0.696, 0.841, 0.863, 1.099, 1.219, 1.271, 1.326, 1.447, 1.485, 1.553, 1.581, 1.589, 2.178, 2.343, 2.416, 2.444, 2.825, 2.830, 3.578, 3.658, 3.743, 3.978, 4.033, 4.033.

In order to compare models, we use goodness of fit criterion to evaluate the performance of the models. The formulae are mentioned below

$$AIC = 2P - 2 \log L, BIC = P \log n - 2 \log L, AICC = AIC + \frac{2P(P+1)}{n-P-1}$$

Where,

AIC: Akaike Information Criterion is used to compare different possible models and determine which one is the best fit for the data.

BIC: Bayesian Information Criterion (BIC) is a metric that is used to compare the Goodness of fit of different regression models.

AICC: Akaike Information Criterion Corrected (AICC) is the corrected version of AIC. The correction is for finite sample sizes. A Corrected AIC for regression models containing a mix of random and fixed predictors is derived.

P is the number of parameters of the model, n is a sample size and $-2 \log L$ is the maximized value of the log-likelihood function and are shown in the below tables.

Table 1: Remission times (in weeks) for Bladder Cancer Patients

Model	Parameter	S.E	-2log L	AIC	BIC	AICC
Aradhana Cure Rate Model	$\hat{\theta}= 1.845782$ $\hat{\pi}= 0.001000$	$\hat{\theta}= 0.17889$ $\hat{\pi}= 0.081509$	34.3221	72.6442	76.2575	72.7402
Power Akash Cure Rate Model	$\hat{\alpha}= 0.95198$ $\hat{\theta}= 1.49633$	$\hat{\alpha}= 0.08714$ $\hat{\theta}= 0.14222$	116.5399	120.5399	124.1532	120.6359
Exponential Cure Rate Model	$\hat{\theta}= 0.74509$	$\hat{\theta}= 0.11107$	116.4819	118.4819	120.2886	118.5136

Table 2: Group of patients getting chemotherapy (in years)

Model	Parameter	S.E	-2log L	AIC	BIC	AICC
Aradhana Cure Rate Model	$\hat{\theta}= 1.84423$ $\hat{\pi}= 0.00100$	$\hat{\theta}= 0.151742$ $\hat{\pi}= 0.07679$	26.98263	49.96525	44.75491	50.25096
Power Akash Cure Rate Model	$\hat{\alpha}= 1.08049$ $\hat{\theta}= 0.86477$	$\hat{\alpha}= 0.06394$ $\hat{\theta}= 0.06493$	144.7026	148.7026	153.9129	148.9883
Exponential Cure Rate Model	$\hat{\theta}= 0.38293$	$\hat{\theta}= 0.03829$	191.9773	193.9773	196.5825	194.0703

Conclusion

In this present study, a new two parameter survival model has been introduced and the model is known as Generalized Aradhana cure rate model. The Generalized Aradhana cure rate model is a mixture model having two parameters obtained from the standard cure rate model provided by Boag (1949). The properties of the model has been obtained. The method of maximum likelihood technique is established to determine the parameters of the proposed model. The effectiveness of the model is examined by using a real life data. The results from the study signify that Generalized Aradhana cure rate model provides better fit for considered data.

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