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A NON-MIXTURE CURE MODEL BASED ON THE MARSHALL-OLKIN BURR TYPE X DISTRIBUTION

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ABSTRACT

In the study and analysis involving time-to-event data, models that incorporate individuals who remain event-free indefinitely are known as cure models (long-term survival model). These are primarily categorized into mixture cure models and non-mixture cure models. In this paper, we employed the Marshall–Olkin Burr Type X (MOBX) distribution as the baseline, specifically for the non-mixture cure model (NM) framework. We formulated the overall survival functions for the proposed MOBXNM, derive essential statistical properties, and estimated parameters via maximum likelihood estimation. A simulation study was carried out to evaluate the accuracy of these estimates. The model is then applied to Business Customer Churn Dataset and compared against established cure models, using AIC, BIC, and log-likelihood criteria for assessment. Findings indicated that the proposed model offers a superior fit and more accurately represents survival trends.

Keywords: Non-Mixture Cure Model, Time-to-event data, Marshall-Olkin Distribution, Burr Type X Distribution,

1. INTRODUCTION

Cure fraction models address populations where some individuals never experience the event of interest (Farewell, 1982), particularly useful in cancer studies with long-term survivors (Othus *et al*., 2012). Unlike traditional survival methods that assume universal event occurrence (Boag, 1949), these models distinguish between cured and at-risk subgroups for enhanced accuracy (Peng & Xu, 2022). Their ability to model plateauing survival patterns makes them valuable across medical and engineering fields (Rodrigues *et al*., 2022). Two main approaches analyze survival data with a cure fraction model. **The** mixture cure model (Boag, 1949; Berkson & Gage, 1952) splits the population into distinct groups: cured (long-term survivors) and uncured (at-risk) individuals. In contrast, the **non-mixture cure model** (Tsodikov *et al*., 2003) estimated cure probabilities without explicitly separating subgroups, instead using a competing risks framework.

In this study, we employ a non-mixture cure (promotion time) model framework, which assumes the event occurrence follows a competing risks process where a fraction of the population never experienced the event. Specifically, we integrated the Marshall-Olkin Burr Type X (MOBX) distribution proposed by Jamal *et al*. (2017) as the baseline distribution within the non-mixture cure model (NM). Building

upon this foundation, we develop a four-parameter Marshall-Olkin Burr X non-mixture cure model (MOBXNM) for survival analysis applications.

1.1 Marshall-Olkin Burr X (MOBX) Distribution (MOBX)

The Marshall-Olkin (MO) distribution family effectively models sudden failures from external shocks but shows limited hazard shape flexibility (Marshall & Olkin, 1997). Similarly, the Burr Type X (BX) distribution primarily handles monotonic hazard rates, struggling with bathtub-shaped patterns (Raqab & Kundu, 2005). To address these constraints, Jamal *et al*. (2017) developed the MOBX distribution by merging both approaches. This hybrid model captured both gradual deterioration processes and shock-induced failures while accommodating diverse hazard rate shapes. The MOBX extension particularly suits systems subject to multiple failure mechanisms. Its enhanced flexibility makes it valuable for reliability analysis across various medical and engineering applications. The cumulative distribution function, probability density function and survival function of MOBX by Jamal *et al*, (2017) are defined (for $x > 0$) by;

$$G_{MOBX}(x;\lambda,\theta,\alpha) = \frac{\left(1-e^{-(\lambda x)^2}\right)^{\theta}}{\alpha+(1-\alpha)\left(1-e^{-(\lambda x)^2}\right)^{\theta}} \tag{1}$$

$$g_{MOBX}(x;\lambda,\theta,\alpha) = \frac{2\alpha\theta\lambda^2 x e^{-(\lambda x)^2}\left(1-e^{-(\lambda x)^2}\right)^{\theta-1}}{\left[\alpha+(1-\alpha)\left(1-e^{-(\lambda x)^2}\right)^{\theta}\right]^2} \tag{2}$$

$$S_{MOBX}(x;\lambda,\theta,\alpha) = \frac{\alpha\left[1-\left(1-e^{-(\lambda x)^2}\right)^{\theta}\right]}{\alpha+(1-\alpha)\left(1-e^{-(\lambda x)^2}\right)^{\theta}} \tag{3}$$

Where; $\theta, \alpha > 0$: shape parameters and $\lambda > 0$: scale parameter.

2. THE NON-MIXTURE CURE MODEL

The non-mixture cure model, also known as the promotion time cure model, was used by Chen *et al*. (1999) as an alternative to the traditional mixture cure model (Berkson & Gage, 1952). Unlike mixture models, which assumed a cured fraction is immune, non-mixture models derived cure probabilities through a latent activation process, where the hazard of the event decreases over time, leading to a plateau in survival (Tsodikov *et al*., 2003). Researchers extended these models to incorporate covariates, improving their applicability in clinical and epidemiological studies. Recent advancements include flexible parametric (Farewell, 2008) and machine learning adaptations (Li *et al*., 2023), enhancing predictive accuracy. Critics like Othus *et al*. (2017) caution about identifiability issues, while others (Amico & Van Keilegom, 2018) highlighted robustness in long-term survival estimation. Today, non-mixture models are widely used in cancer research and reliability analysis, with ongoing debates about

their assumptions versus mixture models (Andersson *et al*., 2011). The overall survival function of non-mixture cure model is given by;

$$S(t) = P^{F_0(t)} = \exp\left(\ln pF_0(t)\right) \quad (4)$$

Where; $S(t)$: The overall survival function at time t, accounting for both cured and uncured individuals, $p \in [0,1]$: The proportion of individuals who are "cured" and will never experience the event, $F_o(t) = 1 - S_o(t)$: The cumulative distribution function (CDF) of the uncured individuals' survival time distribution, $S_o(t)$: is the survival function of the uncured (susceptible) population

However, the standard MOBX distribution lacks explicit accommodation for cure fractions in survival analysis especially when dealing with time-to-event data. In non-mixture cure modeling, failures occur through competing risks processes, where some individuals remain event-free indefinitely (Chen *et al*., 1999). By adapting the MOBX within this framework, we model the underlying failure process while accounting for those who will never experience the event. This approach differs from mixture models by avoiding population segmentation into cured/uncured subgroups (Tsodikov, 2002). The resulting MOBX non-mixture cure model better represents scenarios where immunity develops through competing risks rather than distinct subpopulations. This proves particularly useful for modeling cancer remission or ultra-reliable systems where failure becomes impossible after certain thresholds.

3. RELATED WORKS

In cure fraction modeling, a primary objective is to establish flexible baseline distributions that can accurately model the susceptible individuals within a heterogeneous population. Addressing this need for flexibility, Khan *et al*. (2013) developed Exponentiated Exponential cure models incorporating covariates, which were estimated via the EM algorithm to improve parameter estimation efficiency. Building on the idea of flexible parametric modeling, Ibrahim *et al*. (2014) proposed a log-normal baseline non-mixture cure model that accommodates various censoring types, offering a robust parametric framework for survival data analysis. Further advancements were made by Mazucheli *et al*. (2015), who introduced Burr XII-based mixture and non-mixture cure models, demonstrating superior model fit for cancer survival data compared to conventional approaches. Expanding the non-mixture framework, Rodrigues *et al*. (2018) incorporated a frailty term into the latent risk model and employed Bayesian estimation to capture individual heterogeneity in survival outcomes. In a related effort to enhance distributional flexibility. Usman et al. (2021) developed a survival model based on the Nadarajah Haghighi distribution to analyze right-censored data with long-term survivors. Their model provided a flexible framework for accurately estimating survival probabilities in the presence of a cured fraction. Madaki *et al*. (2022) proposed the Beta Kumaraswamy Burr Type X (Beta Kum-BX) distribution, which extends the Kumaraswamy-G family and broadens its applicability across various modeling contexts. More recently, Su *et al*. (2022) introduced a pseudo-observation-based variable selection approach within cure models, facilitating efficient analysis of high-dimensional covariates under both mixture and non-mixture settings

Madaki *et al*. (2023) proposed both mixture and non-mixture cure models based on the beta-Weibull distribution within a Bayesian framework. Their approach effectively handled censored survival data

while incorporating covariates, thereby demonstrating greater flexibility in modeling long-term survivors. Similarly, Puziol *et al*. (2023) developed a Bayesian non-mixture cure rate model using the discrete Burr XIII distribution, which successfully captured complex survival patterns in cardiovascular heart failure data. Extending research in non-mixture modeling, Safari *et al*. (2024) introduced a product-limit estimator for the conditional survival function where cure status is only partially known, improving estimation accuracy in semi-parametric contexts. In a related development, Yakubu *et al*. (2024) proposed the Weibull-Exponentiated Exponential distribution to construct both mixture and non-mixture cure fraction models for analyzing right-censored survival data. Using larynx and stomach cancer datasets, their study demonstrated the applicability of the proposed models, with parameter estimation carried out via the maximum likelihood method, also Aliyu and Usman (2025) extended the Nadarajah Haghighi distribution to formulate a non-mixture cure fraction model incorporating covariates for right-censored medical data. The proposed approach demonstrated strong applicability and improved fit in real-life survival analysis contexts.

4. METHODOLOGY

Let T be a random variable indicating the time until the occurrence of a particular event, and let t > 0, represent a specific observed value. The formulation in Equation (4) corresponds to the traditional non-mixture cure model initially proposed by Boag (1949) and later expanded by Berkson and Gage (1952). Within this framework, the survival function defines the likelihood that the event has not occurred by time t, with p representing the fraction of individuals considered cured or long-term survivors. The survival function can be referred to equation (4), for the non-mixture model. The probability density function of T is given by

$$g(t)=\frac{d}{dx}G(t)=\frac{d}{dx}(1-S(t))=-\frac{d}{dx}S(t) \tag{5}$$

Where, $G(t)=1-S(t)$, we should take note that $\lim_{t\to\infty}G(t)=1$ simply implies that $\lim_{t\to\infty}G(t)=p$. And the contribution of the ith subject for the likelihood function is given as:

$$L_i=\prod_{i=1}^{n}\left[\left(h(t_i)\right)^{\delta_i}\cdot\left(S(t_i)\right)\right]=\prod_{i=1}^{n}\left[\left((-\ln p)\,f_o(t_i)\right)^{\delta_i}\cdot\left(S(t_i)\right)\right] \tag{6}$$

Where; the hazard function, $h(t)=\frac{g(t)}{S(t)}$, can be interpreted as the risk of an event immediate after time t conditional on surviving up until time t.
Where g(t), is the pdf of the non-mixture cure model and S(t) is the overall survival function.

5. MOBX NON-MIXTURE CURE FRACTION MODEL (MOBXNM)

Using the MOBX distribution as the baseline within a non-mixture cure model helps characterize the survival behavior of individuals who are not cured. The overall survival function is then constructed by applying a power transformation to the baseline, incorporating the cure fraction. By substituting Equation [3] into Equation [4], the resulting model for MOBXNM is expressed as follows;

$$S_{MOBXNMCM}(x;\lambda,\theta,\alpha,p)=P^{\left(\frac{\left(1-e^{-(\lambda x)^2}\right)^{\theta}}{\alpha+(1-\alpha)\left(1-e^{-(\lambda x)^2}\right)^{\theta}}\right)} \quad (7)$$

Where; $\theta,\alpha>0$: shape parameters and $\lambda>0$: scale parameter, P: the proportion of the population that is cured (0 < P < 1),

5.1 The CDF, PDF and Hazard Function of MOBXNM

The cdf, pdf and hazard function of MOBXNM are respectively given as;

$$G_{MOBXNMCM}(x;\lambda,\theta,\alpha,p)=1-P^{\left(\frac{\left(1-e^{-(\lambda x)^2}\right)^{\theta}}{\alpha+(1-\alpha)\left(1-e^{-(\lambda x)^2}\right)^{\theta}}\right)} \quad (8)$$

$$g_{MOBXNMCM}(x;\lambda,\theta,\alpha,p)=-\ln p\cdot S_{MOBXNMCM}(x;\lambda,\theta,\alpha,p)\cdot\frac{2\theta\alpha\lambda^2 xe^{-(\lambda x)^2}\left(1-e^{-(\lambda x)^2}\right)^{\theta-1}}{\left[\alpha+(1-\alpha)\left(1-e^{-(\lambda x)^2}\right)^{\theta}\right]^2} \quad (9)$$

$$h_{MOBXNMCM}(x;\lambda,\theta,\alpha,p)=-\ln p\cdot\frac{2\theta\alpha\lambda^2 xe^{-(\lambda x)^2}\left(1-e^{-(\lambda x)^2}\right)^{\theta-1}}{\left[\alpha+(1-\alpha)\left(1-e^{-(\lambda x)^2}\right)^{\theta}\right]^2} \quad (10)$$

5.2 Parameter Estimation of MOBXNM using MLE

The likelihood and the log-likelihood of the MOBXNMCM are respectively given as;

$$L_{MOBXMCM}(\lambda,\theta,\alpha,P)=\prod_{i=1}^{n}\left[h_{MOBXNMCM}(\lambda,\theta,\alpha,P)\right]^{\delta_i}\cdot S_{MOBXNMCM}(\lambda,\theta,\alpha,P) \quad (11)$$

$$\ell_{MOBXMCM}(\lambda,\theta,\alpha,P)=\sum_{i=1}^{n}\left(\left[\delta_i\log(-\ln p)\,f_{MOBX}(x_i)+\log(S_{MOBXCM}(x_i)\right]\right) \quad (12)$$

6. SIMULATION STUDY

This section evaluates the performance of the developed cure model MOBXNM model through a simulation study using varying sample sizes (n = 20, 50, 100, 200, 500) and fixed parameter values. The use of different sample sizes allows for examining how the model behaves under small to large datasets.

Table 1: Estimates, Bias and RMSE of MOBXNM for the four model Parameter Values

n	Properties	$\lambda = 2.0$	$\theta = 2.0$	$\alpha = 1.2$	$p = 0.7$
20	Estms	2.7042	12.4594	347.9204	0.5491
	Bias	0.7042	10.4594	346.7204	-0.1509
	RMSE	1.5250	32.8272	2592.7974	0.2598
50	Estms	2.5601	4.5816	35.3085	0.6478
	Bias	0.5601	2.5816	34.1085	-0.0522
	RMSE	1.0410	7.7596	142.2821	0.2051
100	Estms	2.2643	2.6721	15.2374	0.7016
	Bias	0.2643	0.6721	14.0374	0.0016
	RMSE	0.9458	1.9672	76.2393	0.1291
150	Estms	2.1643	2.2471	5.0557	0.6915
	Bias	0.1643	0.2471	3.8554	-0.0085
	RMSE	0.9072	1.3599	9.7607	0.1008
200	Estms	2.0337	2.1325	2.5320	0.6926
	Bias	0.0337	0.1325	1.3320	-0.0074
	RMSE	0.7725	0.7441	3.8571	0.0032

From Table 1, the simulation results for the Marshall-Olkin Burr Type X Non-Mixture Cure Model (MOBXNM) demonstrated that parameter estimates improve with increasing sample size. At $n = 20$, α is highly overestimated (347.92 vs. 1.2) with a large RMSE (2592.80), and other parameters show notable bias. As the sample size increases to 50 and 100, estimation accuracy improves, though α remains unstable. By $n = 150$, all parameters show reduced bias and RMSE. At $n = 500$, estimates are close to true values ($\lambda = 2.03$, $\theta = 2.13$, $\alpha = 2.53$, $p = 0.69$) with minimal RMSE. The results confirm the consistency of parameter estimates. Larger samples are especially crucial for stable estimation of α.

7. ANALYSIS AND DISCUSSION OF RESULTS

To demonstrate the practical application of MOBXNM, we analyzed the Business Customer Churn Dataset by Helsen & Schmittlein (1993), which records the duration (in days) until churn for a cohort of subscription service users. Each observation includes the time until churn and a status indicator, where 1 denotes churn and 0 indicates continued subscription. For this study, we focused on modeling the churn behavior to evaluate long-term subscriber retention and identify the presence of a cured (loyal) customer segment.

Table 2. MLEs, Log-likelihood, AIC and BIC of all the competing Non-Mixture Cure models for 200 number of Business Customer Churn datasets**.**

Models	Parameter	Estimates	Log-likelihood	AIC	BIC
MOBXNM	λ	0.0054	-951.086	1910.17	1923.36
	θ	1.5062			
	α	1.0310			
	p	0.2027			
BXNM	λ	0.0033	-959.159	1924.32	1934.21
	θ	0.3070			
	p	0.0031			
EENM	λ	0.0045	-961.165	1925.03	1935.32
	α	0.3179			
	p	0.0038			
BXIINM	k	0.0098	-1071.97	2157.94	2167.83
	c	2.1659			
	p	0.0010			

In table 2, the model fit results show that **MOBXNM** is the best-fitting model, with the highest log-likelihood (-951.09) and the lowest AIC (1910.17) and BIC (1923.36). This indicated that, the model captures the survival pattern and cure fraction most accurately. **BXIINM** performed poorly, with the highest AIC and BIC, overestimating survival. **BXNM** and **EENM** had almost identical estimates and moderate fits but lag behind MOBXNM. The visual fit in the Kaplan-Meier plot in figure 1, supports our model to be the overall, MOBXNM offered the most reliable and realistic model fit.

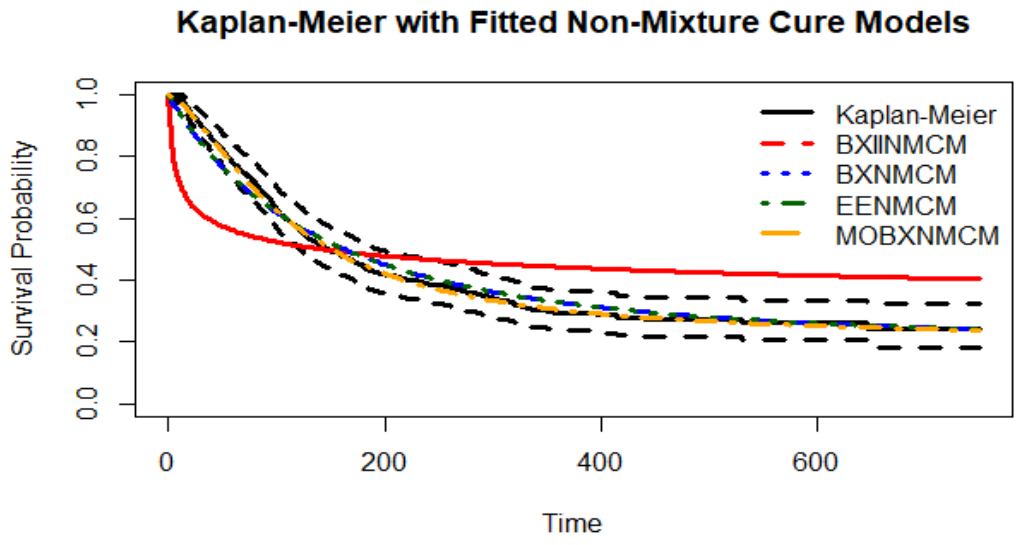

Figure 1: plot of Kaplan-Meier survival curve overlaid of the Non-mixture cure models with the fits of the MLEs for the data.

In figure 1, The Kaplan-Meier plot with overlaid model curves illustrates the comparative fit of the four non-mixture cure models. The **MOBXNM** curve (orange) aligns closely with the Kaplan-Meier curve, especially in the tail, indicating a good fit and realistic cure fraction. In contrast, the **BXIINM** (red) curve diverges significantly, overestimating survival at later times. Both **BXNM** and **EENM** (blue and green) track the data moderately well but do not match the precision of MOBXNM. This visual pattern supports the statistical results, where MOBXNM achieved the best log-likelihood and lowest AIC/BIC. Thus, MOBXNM provides the most accurate and credible model fit to the survival data.

7. CONCLUSION

In this study, we introduced a new non-mixture cure model based on the Marshall-Olkin Burr Type X distribution (MOBXNM) and applied it to business customer churn data. The model showed the best statistical performance with the highest log-likelihood and lowest AIC/BIC, while its survival curve closely aligned with the Kaplan-Meier estimate, especially in the tail, effectively capturing long-term subscribers. Competing models such as BXIINM and BXNM offered poorer and moderate fits and less realistic cure estimates respectively. Given these results, we recommend the MOBXNM as a reliable tool for churn analysis where customer retention includes a cured (loyal) segment. Its flexibility makes it particularly suitable when established models fail to capture long-term retention patterns perfectly. Researchers and analysts should consider this model for similar churn or survival-type data. Further extensions with covariates and validations on diverse datasets are encouraged to enhance its applicability and robustness.

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