

On the Mixture and Non-Mixture Cure Fraction Models Based on Fréchet-Weibull Distribution with Application to Cancer Survival Data

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Abstract

Standard survival models do not perform well when clinical data contain a cured fraction of population who will never experience the event. To take care this, we establish mixture and non-mixture cure models based on the Fréchet-Weibull distribution (FWD) and estimate their maximum likelihood estimators. Evaluating these models on clinical data shows that both cure rate models significantly outperform the baseline FWD and Fréchet-Weibull Distribution, Non-Mixture Cure Models. Specifically, the Fréchet-Weibull Distribution, Mixture Cure Model (FWD-MCM) yields higher cure estimates, indicating superior suitability for modeling cured proportions. Clinically, Treatment Group I exhibited a higher cured fraction than Group II, a finding validated by Kaplan-Meier survival plots. Mounting cure parameter into the FWD model improves statistical fit and clinical insights for cohorts with long-term survivors. While this study considers a univariate model, extending the proposed framework to bivariate and multivariate contexts presents a key avenue for future research to account for multi-variable influences. For survival data with long-term survivors, implementing mixture cure models is recommended because of the empirical superiority of the Fréchet-Weibull mixture cure model (FWD-MCM) over its non-mixture counterpart and standard distribution.

Keywords: Fréchet-Weibull Distribution, Kaplan-Meier, Maximum Likelihood Estimation, Mixture Cure Model, Non-Mixture Cure Model.

Introduction

In lifetime data analysis, standard survival modeling methods assume that all subjects share the same susceptibility to the event of interest and will eventually experience it given a sufficiently long follow-up period. However, this assumption is highly violated in clinical populations that involve a heterogeneous mixture of susceptible (uncured) individuals who are at risk, and non-susceptible (cured) individuals who will not experience the event. If there exist such a cured fraction, standard survival models tend to be insufficient because they do not account for the possibility of long-term survival (Omer, et al., 2021). Modern therapy, particularly in oncology, have allowed a significant number of patients to achieve complete cure states, making cure models important statistical tools for analyzing these

groups of populations. This field of research originated with the pioneering work of Boag (1949).

Standard parametric survival models have been considered as models that lack the flexibility required to capture non-monotonic hazard shapes and complex lifetime characteristics. To address these limitations, many researchers have introduced modified parametric families, for example, the Log-Beta Weibull (Ortega et al., 2013), Generalized Gompertz (Swain et al., 2016), and Generalized Alpha Power Inverse Weibull Distributions (Basheer, 2019). More recently, hybrid and extended formulations such as the Modified Weibull–Fréchet (Abed, (2025) and Exponentiated Fréchet–Weibull distributions (Igiozee et al., 2026) have further advanced distributional flexibility. Parallel to these innovations, advances in targeted clinical therapies increasingly generate patient groups characterized by long-term survivors, where a distinct subpopulation is permanently cured while remaining individuals remain susceptible to relapse or mortality (Ieren and Umar (2025). In view of the above, mixture cure rate frameworks have seen rapid extension, Incorporating Proportional Hazards Formulations for Subgroup Analysis (Wang et al., 2025), Elastic Net Variable Selection for High-Dimensional Clinical Data (Ramalata et al., 2025), and Structural shifts from Classical Mixture to Matrix-Based Representations (Bladt & Yslas, 2026).

Research Questions

How effectively can a newly formulated family of flexible mixture and non-mixture cure rate models based on the Fréchet-Weibull Distribution (FWD) capture cured proportions without strict hazard assumptions, and which of these two frameworks provides a fundamentally superior statistical fit and practical utility when parameters are evaluated on clinical survival data?

Statement of the Problem.

Although advanced compound and generalized distributions offer superior fit compared to classical models (Mohammad, 2024), extensions involving the Weibull distribution applied specifically to cure rate modeling remain scarce in current literature. Furthermore, existing cure models typically rely on a single approach (either mixture or non-mixture) without adequately comparing their performance, leaving it unclear which framework is fundamentally superior.

There is a critical shortage of flexible, newly generalized parametric models—such as a manageable Fréchet-Weibull compound distribution, that can effectively model cure fractions without strict hazard assumptions, alongside a clear need to comprehensively evaluate both mixture/non-mixture frameworks. To accurately capture this cured proportion, this paper formulates a family of compound cure fraction models; Mixture and Non-Mixture cure fraction models, based on the Fréchet-Weibull Distribution (FWD).

Objectives of the Research

The aim of this research is to develop a robust and flexible mixture and non-mixture cure rate modeling frameworks using a compound probability distribution thereby providing a more adequate and practically applicable tool for analyzing survival data with cured fraction. This is achieved by mathematically formulating the models, deriving their parameter estimators using the method of maximum likelihood, and demonstrating their practical utility through the analysis of a clinical dataset.

Limitations of the Study

The study presents several notable methodological limitations. First, it is strictly restricted to a univariate framework, meaning it cannot account for scenarios influenced by multiple independent variables or capture complex bivariate and multivariate relationships. Second, the empirical evaluation of the mixture and non-mixture cure models on the leukemia dataset excludes patient covariates, which are often essential for explaining survival variability and subgroup dynamics. Finally, the practical application relies entirely on a complete dataset (Comprising of two groups: Group I ($n = 46$), Group II ($n = 45$), and a combined total of 91 patients) omitting the effects of censored or incomplete samples that commonly occur in real-world clinical survival data.

The remainder of this paper is structured as follows. Section 2 outlines the underlying methodology and mathematical framework of the proposed distributions. Section 3 details the parameter estimation process for both the mixture and non-mixture FWD cure models. Section 4 demonstrates the empirical application of these models using an acute lymphocytic leukemia (ALL) dataset and discussion of results. Ultimately, Section 5 offers a synthesis of the research findings, followed by Section 6, which presents actionable recommendations for future research.

Methodology

Fréchet-Weibull Distribution (FWD)

As established by Ieren et al., (2024), the mathematical characterization of the Fréchet-Weibull Distribution (FWD) is defined by its cumulative distribution function (CDF) and probability density function (PDF), expressed respectively in Equations (1) and (2):

$$F(x) = \exp \left\{ - \left(\frac{b}{\alpha} \right)^a x^{-a\beta} \right\} \quad (1)$$

and

$$f(x) = a\beta \left(\frac{b}{\alpha} \right)^a x^{-a\beta-1} \exp \left\{ - \left(\frac{b}{\alpha} \right)^a x^{-a\beta} \right\} \quad (2)$$

where $a, b, \alpha, \beta > 0$ are the parameters of the FWD. Similarly, the corresponding survival function (SF) and hazard function (HF) of FWD are given respectively as:

$$S(x) = 1 - F(x) = 1 - \exp \left\{ - \left(\frac{b}{\alpha} \right)^a x^{-a\beta} \right\} \quad (3)$$

and

$$h(x) = \frac{f(x)}{S(x)} = a\beta \left(\frac{b}{\alpha} \right)^a x^{-a\beta-1} \exp \left\{ - \left(\frac{b}{\alpha} \right)^a x^{-a\beta} \right\} \left(1 - \exp \left\{ - \left(\frac{b}{\alpha} \right)^a x^{-a\beta} \right\} \right)^{-1} \quad (4)$$

Mixture Cure Model

The foundational mixture cure model was introduced by Boag (1949) and subsequently formalized by Berkson and Gage (1952). Under this framework, the survival function of the entire population is modeled as a mixture of two distinct subpopulations: cured (non-susceptible) individuals and uncured (susceptible) individuals. Specifically, the overall cumulative distribution function is defined as:

$$F_t(t) = (1 - p)F(t) \quad (5)$$

and the survival function of T is

$$S_t = 1 - F_t(t) = 1 - (1 - p)F(t) \quad (6)$$

The corresponding density function of T is

$$f_T(t) = (1 - p)f(t) \quad (7)$$

where $f(t)$ represents the probability density function (PDF) of the uncured (susceptible) individuals, and $S(t)$ denotes the baseline survival function of the susceptible subpopulation. In this study, the baseline survival function is assumed to follow the proposed Fréchet-Weibull distribution (FWD). By substituting the baseline expressions from Equations (1), (2), and (3) of the proposed FWD, the cumulative distribution function (CDF), probability density function (PDF), survival function (SF), and hazard function (HF) for the population under the mixture cure formulation are obtained, respectively, as:

$$F(t) = (1 - P) \left(\exp \left\{ - \left(\frac{b}{\alpha} \right)^a t^{-a\beta} \right\} \right) \quad (8)$$

$$S(t) = P + (1 - P) \left(1 - \exp \left\{ - \left(\frac{b}{\alpha} \right)^a t^{-a\beta} \right\} \right) \quad (9)$$

$$f(t) = (1 - P) \left(\left(a\beta \left(\frac{b}{\alpha} \right)^a \right) t^{-a\beta-1} \exp \left\{ - \left(\frac{b}{\alpha} \right)^a t^{-a\beta} \right\} \right) \quad (10)$$

And

$$h(t) = \frac{f(t)}{S(t)} = \frac{(1-P) \left(\left(a\beta \left(\frac{b}{\alpha} \right)^a \right) t^{-a\beta-1} \exp \left\{ - \left(\frac{b}{\alpha} \right)^a t^{-a\beta} \right\} \right)}{P + (1-P) \left(1 - \exp \left\{ - \left(\frac{b}{\alpha} \right)^a t^{-a\beta} \right\} \right)} \quad (11)$$

Non-Mixture Cure Model

Proposed by Yakovlev et al. (1993), this model is formulated under the assumption that the number of carcinogenic cells surviving treatment—which may subsequently propagate to produce a detectable tumor—follows a Poisson distribution. Under this non-mixture (or promotion time) cure framework, the population survival function is defined as:

$$S_T(t) = P^{F(t)} \quad (12)$$

$$F_T(t) = 1 - P^{F(t)} \quad (13)$$

$$f_T(t) = -\ln(P)f(t)P^{F(t)} \quad (14)$$

and

$$h_T(t) = -\ln(P)f(t) \quad (15)$$

Where $f(t)$ and $F(t)$ are density function and distribution function from a baseline distribution.

By substituting g equations (1), (2) and (3) into equations (12), (13), (14), and (15), the CDF, PDF, SF and HF of the cured patients under non-mixture form are obtained respectively as;

$$F(t) = 1 - P^{\left(\exp\left\{-\left(\frac{b}{\alpha}\right)^a t^{-a\beta}\right\}\right)} \quad (16)$$

$$f(t) = -\ln(P)a\beta\left(\frac{b}{\alpha}\right)^a t^{-a\beta-1} \left(\exp\left\{-\left(\frac{b}{\alpha}\right)^a t^{-a\beta}\right\}\right) P^{\left(\exp\left\{-\left(\frac{b}{\alpha}\right)^a t^{-a\beta}\right\}\right)} \quad (17)$$

$$S(t) = P^{\left(\exp\left\{-\left(\frac{b}{\alpha}\right)^a t^{-a\beta}\right\}\right)} \quad (18)$$

and

$$h(t) = -\ln(P)a\beta\left(\frac{b}{\alpha}\right)^a t^{-a\beta-1} \left(\exp\left\{-\left(\frac{b}{\alpha}\right)^a t^{-a\beta}\right\}\right) \quad (19)$$

Estimation of Parameters of the Mixture and Non-mixture Models

The Likelihood function for cure models is defined by Boag (1949) as

$$L_i = \prod_{i=1}^n [(f(t_i))^{\delta_i} (S(t_i))^{1-\delta_i}] \quad (20)$$

Where $\delta_i = 1$ if failure is observed and $\delta_i = 0$ if the individual is alive.

Substituting the mixture density from Equation (10) and the mixture survival function from Equation (9) into the standard likelihood function presented in Equation (20) yields the log-likelihood function for the mixture cure model:

$$l = r \log(1 - P) + r \log a + r \log \beta + a r \log b - a r \log \alpha - r(a\beta + 1) \log(t_i) - r \left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} + \sum_{i=1}^n (1 - \delta_i) \log \left[P + (1 - P) \left(1 - \exp\left\{-\left(\frac{b}{\alpha}\right)^a t^{-a\beta}\right\}\right) \right] \quad (21)$$

Where, $r = \sum_{i=1}^n \delta_i$

Therefore, the maximum likelihood estimates for $\theta = (a, b, \alpha, \beta, P)$ denoted by

$\hat{\theta} = (\hat{a}, \hat{b}, \hat{\alpha}, \hat{\beta}, \hat{P})$ are obtained by differentiating l partially w.r.t. a, b, α, β , and P respectively as below;

$$\frac{\partial l}{\partial a} = \frac{r}{a} + r \log b - r \log \alpha - r \beta \log t_i - r \left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \left(\ln \left(\frac{b}{\alpha}\right) - \beta \ln(t_i) \right) - \sum_{i=1}^n (1 - \delta_i) \left[\frac{(1-P) \left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \left(\ln \left(\frac{b}{\alpha}\right) - \beta \ln(t_i) \right) \exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\}}{\left[P + (1-P) \left(1 - \exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\} \right) \right]} \right]$$

(22)

$$\frac{\partial l}{\partial b} = \frac{ar}{b} - rab^{a-1} \alpha^{-a} t_i^{-a\beta} \exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\} - \sum_{i=1}^n (1 - \delta_i) \left[\frac{(1-P) ab^{a-1} \alpha^{-a} t_i^{-a\beta} \exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\}}{\left[P + (1-P) \left(1 - \exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\} \right) \right]} \right] \quad (23)$$

$$\frac{\partial l}{\partial \alpha} = -\frac{ar}{\alpha} + ab^a \alpha^{-a-1} t_i^{-a\beta} - \sum_{i=1}^n (1 - \delta_i) \left[\frac{(1-P) ab^a \alpha^{-a-1} t_i^{-a\beta} \exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\}}{\left[P + (1-P) \left(1 - \exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\} \right) \right]} \right] \quad (24)$$

and

$$\frac{\partial l}{\partial P} = -\frac{r}{1-P} - \sum_{i=1}^n (1 - \delta_i) \left[\frac{1 - \exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\}}{\left[P + (1-P) \left(1 - \exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\} \right) \right]} \right] \quad (25)$$

Equating the above equations to zero (o) and solving for the solution of the non-linear system of equations produce the maximum likelihood estimates of parameters a , b , α , β , and P .

Also, substitution of the non-mixture density in equation (17) and the non-mixture survival function in equation (18) in the standard likelihood function in Equation (20) produces the likelihood for the long-term survivor non-mixture model as follows:

$$l = r \log[-\log(P)] + r \log a + r \log \beta + ar \log b - ar \log \alpha - r(a\beta + 1) \log t_i - r \left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} + \log(P) \sum_{i=1}^n \left[\exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\} \right] \quad (26)$$

$$r = \sum_{i=1}^n \delta_i$$

Therefore, the maximum likelihood estimates for $\theta = (a, b, \alpha, \beta, P)$ denoted by

$\hat{\theta} = (\hat{a}, \hat{b}, \hat{\alpha}, \hat{\beta}, \hat{P})$ are obtained by differentiating l partially w.r.t. a , b , α , β , and P respectively as below;

$$\frac{\partial l}{\partial a} = \frac{r}{a} + r \log \beta - r \log \alpha - r \beta \log t_i - r \left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \left(\ln \left(\frac{b}{\alpha}\right) - \beta \ln(t_i) \right) + \log(P) \left(\frac{b}{\alpha}\right)^a \sum_{i=1}^n \left[t_i^{-a\beta} \left(\ln \left(\frac{b}{\alpha}\right) - \beta \ln(t_i) \right) \left[\exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\} \right] \right]$$

(27)

$$\frac{\partial l}{\partial b} = \frac{ar}{b} - rab^{a-1}\alpha^{-a}t_i^{-a\beta} - \log(P)ab^{a-1}\alpha^{-a}\sum_{i=1}^n \left[t_i^{-a\beta} \exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\} \right] \quad (28)$$

$$\frac{\partial l}{\partial \alpha} = \frac{ar}{\alpha} + ab^a\alpha^{-a-1}t_i^{-a\beta} + \log(P)ab^a\alpha^{-a-1}\sum_{i=1}^n \left[t_i^{-a\beta} \exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\} \right] \quad (29)$$

$$\frac{\partial l}{\partial \beta} = \frac{r}{\beta} - ralogt_i + ar\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \ln(t_i) + \log(P)a\left(\frac{b}{\alpha}\right)^a \sum_{i=1}^n \left[t_i^{-a\beta} \ln(t_i) \exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\} \right]$$

(30)

and

$$\frac{\partial l}{\partial P} = \frac{r}{P \log(P)} + \frac{1}{P} \sum_{i=1}^n \left[\exp \left\{ -\left(\frac{b}{\alpha}\right)^a t_i^{-a\beta} \right\} \right] \quad (31)$$

Equating the above equations to zero (o) and solving for the solution of the non-linear system of equations produce the maximum likelihood estimates of parameters a , b , α , β , and P under Non-Mixture Cure Model.

Source of Data

To illustrate the empirical utility of the proposed models, this study utilizes a clinical leukemia dataset from a bone marrow transplant study conducted on patients with high-risk, refractory acute lymphoblastic leukemia (ALL). Originally compiled and analyzed by Kersey et al. (1987), this dataset is widely accessible via the smcure package in R (Cai et al., 2012) and has been subsequently analyzed by Cai (2013) and Omer et al. (2021). The cohort consists of 91 patients categorized into two treatment groups: Group 1 comprises 46 patients who underwent allogeneic bone marrow transplantation, while Group 2 includes 45 patients who received autologous bone marrow transplantation.

Discussion of Results

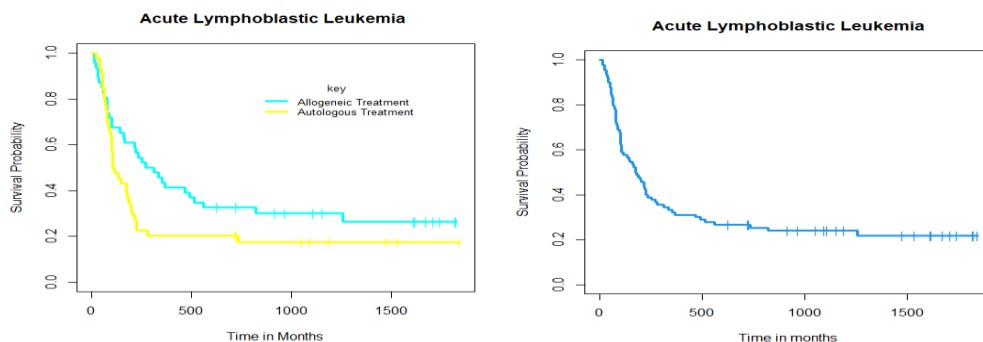


Figure 1: Kaplan-Meier estimates of overall survival and for each type of Treatment

This research utilized a secondary dataset comprising two groups: Group I ($n = 46$), Group II ($n = 45$), and a combined total of 91 patients. The empirical survival and hazard profiles of the cohort, estimated non-parametrically via the Kaplan–Meier survival curves for the acute

lymphoblastic leukemia (ALL) dataset are presented in Figure 1. Notably, the clear stabilization of both curves into a flat, horizontal plateau at the right tail of the distribution suggests the presence of a non-zero cure fraction across both treatment arms (allogeneic and autologous). This empirical pattern highlights the limitation of standard, non-cure survival models, which cannot adequately accommodate such long-term survivor fractions. As illustrated in the figure, the asymptotic survival plateau for the allogeneic transplantation cohort stabilizes at a higher level than that of the autologous cohort. This discrepancy indicates that patients undergoing allogeneic bone marrow transplantation exhibit a superior long-term survival probability compared to those receiving autologous transplants, suggesting a more pronounced therapeutic efficacy associated with the allogeneic protocol.

Table 1: MLEs of the Parameter with Standard errors, Z-value, Confidence Intervals (C. I.), P-value, AIC and BIC for Treatment Group I (46 Patients)

Parameter	Estimates	Standard Error	Z-value	C. I.	P-value	AIC	BIC
FWD	$\hat{\alpha} = 0.15252$	7.78780	0.0196	[-15.11157, 15.41661]	0.9844	827.2337	834.5482
	$\hat{\beta} = 0.58623$	10.2696	0.0571	[-19.54223, 20.71469]	0.9545		
	$\hat{a} = 1.19708$	20.97083	0.0571	[-39.90575, 42.29991]	0.9545		
	$\hat{b} = 2.56226$	4.19167	0.6113	[-5.65341, 10.77793]	0.5410		
FWDMM	$\hat{\alpha} = 0.043085$	0.066815	0.6448	[-0.08787, 0.17404]	0.5190	688.2794	697.4227
	$\hat{\beta} = 1.198306$	0.128025	9.3600	[0.94738, 1.44924]	2e-16 ***		
	$\hat{a} = 9.071999$	14.997518	0.6049	[-20.32314, 38.46713]	0.5452		
	$\hat{b} = 6.169875$	0.273333	22.5727	[5.63414, 6.70561]	2e-16 ***		
	$\hat{p} = 0.037046$	0.025125	1.4745	[-0.01220, 0.08629]	0.1404		
FWDNMCM	$\hat{\alpha} = 1.718e-02$	5.7225e-03	3.0026e+00	[0.00596, 0.02840]	0.002677 **	689.218	698.3612
	$\hat{\beta} = 1.2673$	1.2213e-01	1.0376e+01	[1.02793, 1.50667]	2.2e-16 ***		
	$\hat{a} = 7.2983$	5.6599e-05	1.2895e+05	[7.29819, 7.29841]	2.2e-16 ***		
	$\hat{b} = 8.0721$	2.2054e-05	3.6601e+05	[8.07206, 8.07214]	2.2e-16 ***		
	$\hat{p} = 0.0249$	2.5141e-02	9.8870e-01	[-0.02438, 0.07418]	0.322799		

* means significant at 5% level of significance

Table 1 presents the maximum likelihood estimates (MLEs), standard errors, Z-values, Confidence Intervals, P-values, and information criteria (AIC and BIC) for the

Fréchet-Weibull distribution (FWD), and the Fréchet-Weibull mixture cure model (FWDMM), fitted to treatment group I (46 Patients) of the ALL dataset. The estimation results indicate that the FWDMM exhibits marginally lower AIC and BIC values over the baseline FWD. This demonstrates that incorporating a cure parameter substantially improves model fit and explanatory power for this treatment cohort.

Table 2: MLEs of the Parameter with Standard errors, Z-value, Confidence Intervals (C. I.), P-value, AIC and BIC for Treatment Group II (45 Patients)

Parameter	Estimates	Standard Error	Z-value	C. I.	P-value	AIC	BIC
FWD	$\hat{\alpha} = 0.22955$	5.67042	0.0405	[-10.88447, 11.34357]	0.9677	830.2437	834.3704
	$\hat{\beta} = 0.81131$	5.39102	0.1505	[-9.75509, 11.37771]	0.8804		
	$\hat{a} = 1.40874$	9.36206	0.1505	[-16.94090, 19.75838]	0.8804		
	$\hat{b} = 9.37931$	0.45986	20.3958	[8.47798, 10.28064]	2e-16***		
FWDMM	$\hat{\alpha} = 0.068539$	0.104655	0.6549	[-0.13658, 0.27366]	0.5125	734.3673	743.2883
	$\hat{\beta} = 1.247442$	0.160713	7.7619	[0.93244, 1.56244]	8.3e15***		
	$\hat{a} = 6.658447$	11.134003	0.5980	[-15.16420, 28.48109]	0.5498		
	$\hat{b} = 7.062695$	0.259400	27.2271	[6.55427, 7.57112]	2.2e-16 ***		
	$\hat{p} = 0.031943$	0.021304	1.4994	[-0.00981, 0.07370]	0.1338		
FWDMMCM	$\hat{\alpha} = 0.021140$	0.036508	0.5790	[-0.05042, 0.09270]	0.5626	735.0298	743.9507
	$\hat{\beta} = 1.329516$	0.125914	10.5589	[1.08272, 1.57631]	2.2e-16 ***		
	$\hat{a} = 3.958071$	8.141474	0.4862	[-11.99922, 19.91536]	0.6269		
	$\hat{b} = 5.520210$	0.967697	5.7045	[3.62352, 7.41690]	1.167e-08 ***		
	$\hat{p} = 0.022380$	0.024765	0.9037	[-0.02616, 0.07092]	0.3662		

* means significant at 5% level of significance

Correspondingly, Table 2 presents the parameter estimates and goodness-of-fit metrics for the two models fitted to treatment group II (45 patients) of the ALL dataset. Based on the information criteria, the FWDMM yields the lowest AIC and BIC values. This pattern reinforces the finding that incorporating a cure parameter substantially improves model fit compared to the baseline FWD.

A comparative analysis of Tables 1 and 2 reveals that the estimated cured fraction is consistently higher for treatment group I than for group II, implying a superior survival probability for patients receiving the first treatment protocol. This empirical finding is visually corroborated by the Kaplan-Meier survival curves presented in Figure 1. These

findings align closely/confirm with prior literature in this domain (Kutal and Qinan, 2018; Lázaro et al., 2020; Omer et al., 2021).

Table 3: MLEs of the Parameter with Standard errors, Z-value, Confidence Intervals (C. I.), P-value, AIC and BIC for the entire ALL Dataset (91 Patients)

Parameter	Estimates	Standard Error	Z-value	C. I.	P-value	AIC	BIC
FWD	$\hat{\alpha} = 0.115607$	1.089407	0.1061	[-2.01963, 2.25084]	0.9155	833.2357	837.2329
	$\hat{\beta} = 0.670722$	2.020526	0.3320	[-3.28951, 4.63095]	0.7399		
	$\hat{a} = 1.249750$	3.764776	0.3320	[-6.12921, 8.62871]	0.7399		
	$\hat{b} = 2.667089$	0.083904	31.7873	[2.50264, 2.83154]	2e-16 ***		
FWDMMCM	$\hat{\alpha} = 3.797e-02$	9.8383e-03	3.8593e+00	[0.01869, 0.05725]	0.00011 ***	697.0336	709.5326
	$\hat{\beta} = 1.2357$	1.0151e-01	1.2173e+01	[1.03674, 1.43466]	2.2e-16 ***		
	$\hat{a} = 3.2489e+01$	3.5240e-05	9.2195e+05	[32.48893, 32.48907]	2.2e-16 ***		
	$\hat{b} = 1.9922e+01$	2.0897e-05	9.5335e+05	[19.92196, 19.92204]	2.2e-16 ***		
	$\hat{p} = 5.7469e-02$	2.6009e-02	2.2096e+00	[0.00649, 0.10845]	0.0271319 *		
FWDNMCM	$\hat{\alpha} = 1.7407e-02$	5.3581e-03	3.2488e+00	[0.00691, 0.02791]	0.001159 **	698.8292	711.3283
	$\hat{\beta} = 1.3499$	1.2326e-01	1.0952e+01	[1.10831, 1.59149]	2.2e-16 ***		
	$\hat{a} = 1.7004e+01$	1.1219e-05	1.5157e+06	[17.00398, 17.00402]	2.2e-16 ***		
	$\hat{b} = 1.7044e+01$	1.6677e-05	1.0220e+06	[17.04397, 17.04403]	2.2e-16 ***		
	$\hat{p} = 4.8017e-02$	2.9500e-02	1.6277e+00	[-0.00980, 0.10584]	0.103586		

* means significant at 5% level of significance

Table 3 presents the parameter estimates and model selection statistics for the FWD and FWDMMCM models fitted to the pooled ALL dataset (91 Patients). At the 5% significance level, all parameters are statistically significant in the FWDMMCM. Conversely, within the baseline FWD, only a single parameter (b) is statistically significant. The information criteria indicate that the FWDMMCM provides the optimal fit, yielding the lowest AIC and BIC values. This further confirms that accounting for a cured fraction markedly improves model performance when applied to the entire ALL cohort.

Conclusion

In summary, this study demonstrates that the estimated cured fraction is higher for treatment group I than for group II, indicating a superior probability of cure for patients in the former cohort. This finding is highly consistent with the empirical survival trajectories depicted in the Kaplan-Meier plots (Figure 1). Furthermore, the mixture model (FWDMM) yielded higher cure parameter estimates than the non-mixture model (FWDNMCM), suggesting its superior suitability for estimating the cured proportion in this context. Ultimately, both the mixture and non-mixture cure formulations outperform the baseline Fréchet-Weibull distribution (FWD) when analyzing data characterized by a cured fraction, highlighting the statistical and clinical importance of incorporating cure parameters into survival models.

Recommendations

1. For survival and lifetime data characterized by long-term survivors, the derivation and implementation of mixture cure models within this distributional framework are recommended. This recommendation is supported by the empirical superiority of the Fréchet-Weibull mixture cure model (FWDMM) over both its non-mixture counterpart and standard distributional models.
2. Given that this research is restricted to a univariate framework, it is recommended that future studies extend this work to bivariate or multivariate generalizations. Because real-world phenomena are frequently influenced by multiple covariates, such extensions would enable the formulation of parametric regression models capable of handling complex, multi-dimensional datasets.

References

- Abed, R. A. (2025). Modified Weibull-Fréchet distribution properties with application. *Iraqi Statisticians Journal*, 2(1), 195–216. <https://doi.org/10.62933/isj.v2i1.120>
- Basheer, A. M. (2019). Alpha power inverse Weibull distribution with reliability application. *Journal of Taibah University for Science*, 13(1), 423–432. <https://doi.org/10.1080/16583655.2019.1588488>
- Berkson, J. and Gage, R.P. (1952). Survival Curve for Cancer Patients following Treatment, *Journal of the American Statistical Association*, 47: 501–515.
- Bladt, M., & Yslas, J. (2026). Cure Models: From Mixture to Matrix Distributions. *arXiv preprint arXiv:2601.19774*. <https://doi.org/10.48550/arXiv.2601.19774>
- Boag, J. W. (1949). Maximum likelihood estimates of the proportion of patients cured by cancer therapy. *Journal of the Royal Statistical Society, Series B*, 11, 15–44.
- Cai, C. (2013). Advanced Methodology Developments in Mixture Cure Models. (Doctoral Dissertation). Retrieved from <https://scholarcommons.sc.edu/etd/544>
- Cai, Y., Li, Y., & Liu, X. (2012). Statistical analysis of tumor recurrence and cure rate models with Poisson distribution assumptions for residual cancer cells. *Journal of Mathematical Medicine and Statistics*, 15(3), 245–260.
- Ieren, et al. (2024). [A New Fréchet-G Family of Continuous Probability Distributions: Special Models, Properties, Simulation and Applications](#); *Journal of the Royal Statistical Society Nigeria Group (JRSS-NIG Group)*, Vol. 1 (1). PP. 46-71

- Ieren, T. G., & Umar, A. A. (2025). Cure fraction models based on a Lomax-exponential distribution with applications. *Royal Statistical Society Nigeria Local Group 2025 Conference Proceedings*, 446–455. <https://publications.funaab.edu.ng/index.php/RSS/article/view/1915>
- Igiozee, M., Afolabi, J. M., & Timothy, E. O. (2026). On development of Exponentiated Fréchet Weibull distribution: Properties and applications. *Frontline Professionals Journal*, 2(5), 35–46. <https://doi.org/10.5281/zenodo.14833215>
- Kersey, J. H. et al. (1987). Comparison of autologous and allogeneic bone marrow transplantation for treatment of high-risk refractory acute lymphoblastic leukemia. *New England Journal of Medicine*, 317(8), 461–467.
- Kutal, D. H., & Qinan, L. (2018). A non-mixture cure model for right-censored data with Fréchet distribution. *Stats*, 1(1), 176–188. <https://doi.org/10.3390/stats1010013>
- Lázaro, E., Armero, C., & Gómez-Rubio, V. (2020). Approximate Bayesian inference for mixture cure models. *TEST*, 29(3), 750–767. <https://doi.org/10.1007/s11749-019-00679-x>
- Mohammad, S. (2024). X-exponential-G Family of Distributions With Applications, *International Journal of Statistics and Probability* Vol. 13(1), 40–54. <https://doi.org/10.5539/ijsp.v13n1p40>
- Omer, M. E., Abu Bakar, M., Adam, M., & Mustafa, M. (2021). Utilization of a Mixture Cure Rate Model based on the Generalized Modified Weibull Distribution for the Analysis of Leukemia Patients. *Asian Pacific Journal of Cancer Prevention*, 22(4), 1045–1053. <https://doi.org/10.31557/apjcp.2021.22.4.1045>
- Ortega, E. M. M., Cordeiro, G. M., & Kattan, M. W. (2013). The log-beta Weibull Regression Model with Application to Predict Recurrence of Prostate Cancer. *Statistical Papers*, 54(1), 113–143. <https://doi.org/10.1007/s00362-011-0414-0>
- Ramalata, A., Adekpedjou, A., & Lesaoana, M. (2025). Variable selection in mixture cure models using elastic net penalty: Application to COVID-19 data. *PLOS ONE*, 20(5), e0320521. <https://doi.org/10.1371/journal.pone.0320521>
- Swain, P. K., Grover, G., & Goel, K. (2016). Mixture and non-mixture cure fraction models based on Generalized Gompertz Distribution under Bayesian Approach. *Tatra Mountains Mathematical Publications*, 66(1), 121–135. <https://doi.org/10.1515/tmmp-2016-0025>
- Wang, L., et al. (2025). A proportional hazards mixture cure model for subgroup analysis: Inferential method and an application to colon cancer data. *Journal of Personalized Medicine*, 9(1), 1. <https://doi.org/10.3390/jpm9010001>
- Yakovlev, A. Y. et al (1993). A stochastic model of tumor recurrence. In A. Y. Yakovlev & B. Asselain (Eds.), *Biometrical Aspects of Cancer Analysis* (pp. 58–82). Nova Science Publishers.