A New Nakagami–Weibull Non-Mixture Cure Model with Applications to Right-Censored Survival Data

IBRAHIM ABDULLAHI[1], WIKANDA PHAPHAN[2,3*]
[1]Department of Mathematics and Statistics, Faculty of Science,
Yobe State University, Damaturu, 500501,
NIGERIA

[2]Department of Applied Statistics, Faculty of Applied Science,
King Mongkut's University of Technology North Bangkok, Bangkok, 10800,
THAILAND

[3]Research Group in Statistical Learning and Inference,
King Mongkut's University of Technology North Bangkok, Bangkok, 10800,
THAILAND

**Corresponding author*

Abstract: Cure fraction models provide a useful framework for analysing survival data in which some individuals may never experience the event of interest. This paper introduces a flexible Nakagami–Weibull Non-Mixture Cure (NWNMC) model for right-censored survival data with a long-term surviving fraction, constructed by embedding the Nakagami–Weibull baseline distribution within the promotion-time cure framework. This provides additional flexibility for capturing complex survival and hazard rate behaviours. Several key mathematical properties of the model are established, and parameter estimation is carried out using maximum likelihood under right censoring, with inferential procedures developed based on the observed information matrix. A Monte Carlo simulation study examines the finite-sample performance of the maximum likelihood estimators under different parameter values and sample sizes, showing that the estimators are reliable, with decreasing bias and root mean square error as the sample size increases. The practical usefulness of the proposed model is demonstrated through two real-data applications involving business customer churn and colon cancer survival data. The NWNMC model provides the best fit for the customer churn data and remains competitive for the colon cancer data. These results confirm that the proposed model offers a flexible and effective alternative for modelling heterogeneous survival data with a cure fraction.

Key-Words: -Nakagami–Weibull distribution; Non-mixture cure model; Promotion-time cure model; Survival analysis; Maximum likelihood estimation; Right censoring; Cure fraction

Received: March 25, 2026. Revised: June 12, 2026. Accepted: July 11, 2026. Published: September 18, 2026.

1 Introduction

Cure fraction models address populations where some individuals never experience the event of interest, [1], particularly useful in cancer studies with long-term survivors, [2]. Unlike traditional survival methods that assume universal event occurrence, [3], these models distinguish between cured and at-risk subgroups for enhanced accuracy, [4]. Their ability to model plateauing survival patterns makes them valuable across medical and engineering fields, [5].

Recent developments in cure fraction modelling have expanded considerably across both parametric and semiparametric directions. On the parametric side, flexible baseline distributions including the generalised gamma, [1], exponentiated exponential, [6], and Burr Type X families have been embedded within cure frameworks to accommodate diverse hazard shapes. Semiparametric approaches, which combine a nonparametric baseline hazard with a parametric cure fraction, have been developed for both mixture, [7] and non-mixture, [4] settings, offering robustness against baseline misspecification. Bayesian cure-rate models have also received considerable attention, with prior distributions placed on the cure fraction and baseline parameters to incorporate external information and quantify uncertainty, [4]. Promotion-time cure models with covariates have been extended to accommodate competing risks, frailty structures, and multivariate survival outcomes. The present work contributes to the parametric branch of this literature by proposing the Nakagami–Weibull distribution as a flexible

baseline within the promotion-time framework.

Two main approaches analyze survival data with a cure fraction model. The mixture cure model, [3], [7] splits the population into distinct groups: cured (long-term survivors) and uncured (at-risk) individuals. In contrast, the non-mixture cure model, [6] estimates cure probabilities without explicitly separating subgroups, instead using a competing risks framework where the hazard of the event decreases over time, leading to a plateau in survival.

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 experiences the event. Specifically, we integrate the Nakagami–Weibull distribution as the baseline distribution within the non-mixture cure model. Building upon this foundation, we develop a flexible parametric model for survival analysis applications.

2 The Nakagami–Weibull Distribution

Let T be a non-negative random variable representing the time until the occurrence of an event. The Weibull distribution is defined by the cumulative distribution function

$$W(t) = 1 - \exp(-\sigma t^{\alpha}), \quad t \geq 0, \tag{1}$$

where $\alpha > 0$ and $\sigma > 0$ denote the shape and scale parameters, respectively.

The Nakagami–Weibull distribution is obtained by applying a Nakagami generator to the Weibull distribution. Its cumulative distribution function is given by

$$F_0(t) = \frac{1}{\Gamma(\Lambda)}\gamma(\Lambda, z(t)), \tag{2}$$

where

$$z(t) = \frac{\Lambda}{\xi}\left(e^{\sigma t^{\alpha}} - 1\right)^2, \tag{3}$$

with shape parameters $\Lambda > 0$ and $\xi > 0$.

Differentiating (2) yields the probability density function

$$f_0(t) = \frac{2\Lambda\sigma\alpha}{\xi\Gamma(\Lambda)} t^{\alpha-1}(e^{\sigma t^{\alpha}} - 1)e^{\sigma t^{\alpha}} z(t)^{\Lambda-1} e^{-z(t)}. \tag{4}$$

The survival function of the Nakagami–Weibull distribution is obtained as

$$\begin{aligned} S_0(t) &= 1 - F_0(t) = 1 - \frac{1}{\Gamma(\Lambda)}\gamma(\Lambda, z(t)) \\ &= \frac{1}{\Gamma(\Lambda)}\Gamma(\Lambda, z(t)), \end{aligned} \tag{5}$$

where $\Gamma(\Lambda, z) = \int_z^{\infty} u^{\Lambda-1}e^{-u}\,du$ is the upper incomplete gamma function.

The hazard function is given by

$$\begin{aligned} h_0(t) =& \frac{f_0(t)}{S_0(t)} \\ =& \frac{2\Lambda\sigma\alpha}{\xi} t^{\alpha-1}(e^{\sigma t^{\alpha}} - 1)e^{\sigma t^{\alpha}} \frac{z(t)^{\Lambda-1}e^{-z(t)}}{\Gamma(\Lambda, z(t))}. \end{aligned} \tag{6}$$

The Nakagami–Weibull baseline is chosen for three reasons: the parameters Λ and ξ independently control tail behaviour and hazard shape, enabling monotone, bathtub-shaped, and unimodal hazards within a single family; its CDF has a closed-form expression via the regularised incomplete gamma function, facilitating both analytical derivations and numerical optimisation; and the competing baselines considered here are two-parameter families that offer less flexibility in capturing complex hazard behaviours.

Remark 1. *When $\Lambda = 1$ and $\xi = 1$, the Nakagami–Weibull distribution reduces to a special case related to the exponential-Weibull family. The additional parameters Λ and ξ provide enhanced flexibility in modeling various hazard shapes, including increasing, decreasing, and bathtub-shaped hazard rates.*

3 The Non-Mixture Cure Model Framework

3.1 Model Formulation

The non-mixture cure model, also known as the promotion time cure model, was introduced by [4] as an alternative to the traditional mixture cure model. Unlike mixture models, which assume a cured fraction is immune, non-mixture models derive cure probabilities through a latent activation process, where the hazard of the event decreases over time, leading to a plateau in survival, [6].

Let N be a latent random variable representing the number of competing risks (or promotion times) that an individual is exposed to. Assume N follows a Poisson distribution with mean $-\log(p)$, where $p \in (0, 1)$ is the cure fraction. Conditional on $N = n$, the survival function is $[S_0(t)]^n$. The overall survival function is obtained by marginalizing over N:

$$\begin{aligned} S(t) &= \sum_{n=0}^{\infty}[S_0(t)]^n \cdot \frac{[-\log(p)]^n p}{n!} \\ &= p\sum_{n=0}^{\infty}\frac{[-\log(p)\cdot S_0(t)]^n}{n!} = p^{S_0(t)}. \end{aligned} \tag{7}$$

To see equation (7) more explicitly, note that $N \sim$ Poisson$(-\log p)$ implies

$$P(N=n) = \frac{[-\log(p)]^n p}{n!}, \ (n = 0, 1, 2, \ldots). \quad (8)$$

Marginalising over N and recognising the exponential series gives

$$\begin{aligned} S(t) &= \sum_{n=0}^{\infty} [S_0(t)]^n \cdot \frac{[-\log(p)]^n \, p}{n!} \\ &= p \sum_{n=0}^{\infty} \frac{[-\log(p) \cdot S_0(t)]^n}{n!} \\ &= p \cdot e^{-\log(p) \cdot S_0(t)} \\ &= p^{1-S_0(t)}. \end{aligned} \quad (9)$$

Substituting $S_0(t) = 1 - F_0(t)$ then yields

$$S(t) = p^{1-(1-F_0(t))} = p^{F_0(t)}, \quad (10)$$

which is the representation used in equation (11).

Equivalently, using $F_0(t) = 1 - S_0(t)$:

$$\begin{aligned} S(t) &= p^{1-F_0(t)} = p^{F_0(t)} \\ &= \exp(\log(p) \cdot F_0(t)), \end{aligned} \quad (11)$$

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
- $F_0(t) = 1 - S_0(t)$ = the cumulative distribution function of the uncured individuals' survival time distribution
- $S_0(t)$ = the survival function of the uncured (susceptible) population

Note that $\lim_{t\to\infty} F_0(t) = 1$, which implies:

$$\lim_{t\to\infty} S(t) = p^1 = p, \quad (12)$$

confirming that p represents the cure fraction.

4 The Proposed Nakagami–Weibull Non-Mixture Cure Model (NWNMC)

By substituting the Nakagami–Weibull CDF (2) into the non-mixture framework (11), the overall survival function of the proposed Nakagami–Weibull Non-Mixture Cure (NWNMC) model is

$$S_{\text{NWNMC}}(t;\boldsymbol{\theta}) = p^{F_0(t)} = \exp\left(\log(p) \cdot \frac{\gamma(\Lambda, z(t))}{\Gamma(\Lambda)}\right), \quad (13)$$

where $\boldsymbol{\theta} = (\alpha, \sigma, \Lambda, \xi, p)'$ is the complete parameter vector.

Alternatively, using the survival function representation:

$$\begin{aligned} S_{\text{NWNMC}}(t;\boldsymbol{\theta}) &= p^{1-S_0(t)} \\ &= p \cdot \exp\left(-\log(p) \cdot \frac{\Gamma(\Lambda, z(t))}{\Gamma(\Lambda)}\right). \end{aligned} \quad (14)$$

The overall CDF is

$$\begin{aligned} F_{\text{NWNMC}}(t;\boldsymbol{\theta}) &= 1 - S_{\text{NWNMC}}(t;\boldsymbol{\theta}) \\ &= 1 - \exp\left(\log(p) \cdot \frac{\gamma(\Lambda, z(t))}{\Gamma(\Lambda)}\right). \end{aligned} \quad (15)$$

Differentiating (15) with respect to t yields the PDF. Using the chain rule:

$$\begin{aligned} \frac{d}{dt} S_{\text{NWNMC}}(t;\boldsymbol{\theta}) &= S_{\text{NWNMC}}(t;\boldsymbol{\theta}) \cdot \log(p) \cdot \frac{d}{dt} F_0(t) \\ &= S_{\text{NWNMC}}(t;\boldsymbol{\theta}) \cdot \log(p) \cdot f_0(t). \end{aligned} \quad (16)$$

Therefore:

$$\begin{aligned} f_{\text{NWNMC}}(t;\boldsymbol{\theta}) &= -\frac{d}{dt} S_{\text{NWNMC}}(t;\boldsymbol{\theta}) \\ &= -\log(p) \cdot f_0(t) \cdot S_{\text{NWNMC}}(t;\boldsymbol{\theta}). \end{aligned} \quad (17)$$

Substituting (4) and (13):

$$\begin{aligned} f_{\text{NWNMC}}(t;\boldsymbol{\theta}) = & -\log(p) \cdot \frac{2\Lambda\sigma\alpha}{\xi\Gamma(\Lambda)} t^{\alpha-1} \\ & \times (e^{\sigma t^{\alpha}} - 1) e^{\sigma t^{\alpha}} z(t)^{\Lambda-1} e^{-z(t)} \\ & \times \exp\left(\log(p) \cdot \frac{\gamma(\Lambda, z(t))}{\Gamma(\Lambda)}\right). \end{aligned} \quad (18)$$

Since $0 < p < 1$, we have $-\log(p) > 0$, ensuring $f_{\text{NWNMC}}(t;\boldsymbol{\theta}) \geq 0$.

Proposition 1 (Proper PDF). *The function $f_{NWNMC}(t;\boldsymbol{\theta})$ defined in (17) is a valid probability density function in the improper sense, with total mass $1 - p$.*

Proof. Non-negativity follows from $-\log(p) > 0$, $f_0(t) \geq 0$, and $S_{\text{NWNMC}}(t;\boldsymbol{\theta}) > 0$. For normalization:

$$\begin{aligned}\int_0^\infty f_{\text{NWNMC}}(t;\boldsymbol{\theta})\,dt &= \int_0^\infty -\log(p) f_0(t) p^{F_0(t)}\,dt \\ &= \left[-p^{F_0(t)}\right]_0^\infty \\ &= -\lim_{t\to\infty} p^{F_0(t)} + p^{F_0(0)}.\end{aligned} \tag{19}$$

Since $F_0(0) = 0$ and $\lim_{t\to\infty} F_0(t) = 1$:

$$\int_0^\infty f_{\text{NWNMC}}(t;\boldsymbol{\theta})\,dt = -p + 1 = 1 - p. \tag{20}$$

The remaining mass p corresponds to the cure fraction at infinity. □

Remark 2. *In the non-mixture cure model, the PDF $f_{NWNMC}(t;\boldsymbol{\theta})$ is an improper density with $\int_0^\infty f_{NWNMC}(t;\boldsymbol{\theta})\,dt = 1 - p$. The remaining mass p represents the cure fraction. This is a key distinction from standard survival models.*

The hazard function is

$$h_{\text{NWNMC}}(t;\boldsymbol{\theta}) = \frac{f_{\text{NWNMC}}(t;\boldsymbol{\theta})}{S_{\text{NWNMC}}(t;\boldsymbol{\theta})} = -\log(p)\cdot f_0(t). \tag{21}$$

Substituting (4):

$$\begin{aligned}h_{\text{NWNMC}}(t;\boldsymbol{\theta}) = -\log(p)\cdot \frac{2\Lambda\sigma\alpha}{\xi\Gamma(\Lambda)} t^{\alpha-1} \\ \times (e^{\sigma t^\alpha} - 1) e^{\sigma t^\alpha} z(t)^{\Lambda-1} e^{-z(t)}.\end{aligned} \tag{22}$$

Proposition 2. *The cure fraction p satisfies*

$$p = \lim_{t\to\infty} S_{NWNMC}(t;\boldsymbol{\theta}). \tag{23}$$

Remark 3. *The simplification in equation (21) is a structural feature of all non-mixture cure models built from $S(t) = p^{F_0(t)}$, not unique to NWNMC:*

$$\begin{aligned}h_{NWNMC}(t;\boldsymbol{\theta}) &= \frac{f_{NWNMC}(t;\boldsymbol{\theta})}{S_{NWNMC}(t;\boldsymbol{\theta})} \\ &= \frac{-\log(p)\cdot f_0(t)\cdot S_{NWNMC}(t;\boldsymbol{\theta})}{S_{NWNMC}(t;\boldsymbol{\theta})} \\ &= -\log(p)\cdot f_0(t).\end{aligned} \tag{24}$$

Since $-\log(p) > 0$, the cure fraction p scales the hazard level (a smaller p raises the hazard uniformly), while the baseline density $f_0(t)$ alone shapes it over time — unlike the mixture cure model, where the hazard depends jointly on p and $S(t)$.

Proof. Since $\lim_{t\to\infty} F_0(t) = 1$:

$$\lim_{t\to\infty} S_{\text{NWNMC}}(t;\boldsymbol{\theta}) = \lim_{t\to\infty} p^{F_0(t)} = p^1 = p. \tag{25}$$

□

5 Statistical Properties

5.1 Moments

For the uncured population, the rth moment is

$$E[T^r \mid \text{uncured}] = \frac{1}{1-p}\int_0^\infty t^r f_{\text{NWNMC}}(t;\boldsymbol{\theta})\,dt. \tag{26}$$

Substituting (18):

$$E[T^r \mid \text{uncured}] = \frac{-\log(p)}{1-p}\int_0^\infty t^r f_0(t)\cdot p^{F_0(t)}\,dt. \tag{27}$$

This integral generally requires numerical evaluation via quadrature methods.

5.2 Quantile Function

The quantile function t_q such that $F_{\text{NWNMC}}(t_q) = q$ for $q \in (0, 1-p)$ satisfies:

$$1 - p^{F_0(t_q)} = q \quad\Longrightarrow\quad F_0(t_q) = \frac{\log(1-q)}{\log(p)}. \tag{28}$$

Let $u_q = \dfrac{\log(1-q)}{\log(p)}$. Then:

$$\frac{\gamma(\Lambda, z(t_q))}{\Gamma(\Lambda)} = u_q. \tag{29}$$

This is solved numerically for $z(t_q)$ using the inverse regularized lower incomplete gamma function, and then:

$$t_q = \left[\frac{1}{\sigma}\log\left(1 + \sqrt{\frac{\xi}{\Lambda}}\, z(t_q)\right)\right]^{1/\alpha}. \tag{30}$$

5.3 Additional Statistical Properties

5.3.1 Limiting Behaviour

As $t \to 0^+$, the baseline CDF satisfies $F_0(t) \to 0$, and therefore

$$\lim_{t\to 0^+} S_{\text{NWNMC}}(t;\boldsymbol{\theta}) = p^0 = 1, \tag{31}$$

confirming that the survival function starts at unity. As $t \to \infty$, $F_0(t) \to 1$, so that

$$\lim_{t\to\infty} S_{\text{NWNMC}}(t;\boldsymbol{\theta}) = p^1 = p, \tag{32}$$

which confirms that the survival function plateaus at the cure fraction p rather than declining to zero, a defining feature of cure models.

5.3.2 Stochastic Ordering

Let $p_1 < p_2$. Since $S_{\text{NWNMC}}(t;\theta) = p^{F_0(t)}$ is increasing in p, for every $t > 0$:

$$S_{\text{NWNMC}}(t;p_1) < S_{\text{NWNMC}}(t;p_2). \tag{33}$$

The same ordering holds for the hazard rate. Since $-\log(p)$ is decreasing in p:

$$-\log(p_1) \quad > -\log(p_2), \tag{34}$$

thus

$$\begin{aligned} h_{\text{NWNMC}}(t;p_1) &= -\log(p_1)\, f_0(t) \\ &> -\log(p_2)\, f_0(t) \\ &= h_{\text{NWNMC}}(t;p_2). \end{aligned} \tag{35}$$

5.3.3 Shannon Entropy

The Shannon entropy of the NWNMC model for the susceptible population is defined as

$$H = -\int_0^\infty f_{\text{NWNMC}}(t;\boldsymbol{\theta}) \log f_{\text{NWNMC}}(t;\boldsymbol{\theta})\, dt. \tag{36}$$

Substituting equation (17):

$$\begin{aligned} H =& -\log(-\log p) - \int_0^\infty f_{\text{NWNMC}}(t;\boldsymbol{\theta}) \log f_0(t)\, dt \\ & - \log(p) \int_0^\infty f_{\text{NWNMC}}(t;\boldsymbol{\theta}) F_0(t)\, dt. \end{aligned} \tag{37}$$

The remaining integrals are evaluated numerically, as they involve the incomplete gamma function through $F_0(t)$ and $f_0(t)$.

5.3.4 Mean Residual Life

The mean residual life function, representing the expected remaining survival time given survival to time t_0, is defined as

$$m(t_0) = \frac{\int_{t_0}^\infty S_{\text{NWNMC}}(t;\boldsymbol{\theta})\, dt}{S_{\text{NWNMC}}(t_0;\boldsymbol{\theta})}. \tag{38}$$

As $t_0 \to \infty$, the mean residual life converges to a finite positive value when $p > 0$, reflecting the presence of a cured subgroup that does not experience the event of interest.

6 Parameter Estimation

6.1 Likelihood Function

Let (t_i, δ_i), $i = 1, \ldots, n$, be the observed data, where t_i is the observed time and δ_i is the censoring indicator ($\delta_i = 1$ for event, $\delta_i = 0$ for censored). The contribution of the ith subject to the likelihood function is:

$$L_i(\boldsymbol{\theta}) = \left[f_{\text{NWNMC}}(t_i;\boldsymbol{\theta})\right]^{\delta_i} \left[S_{\text{NWNMC}}(t_i;\boldsymbol{\theta})\right]^{1-\delta_i}. \tag{39}$$

Substituting (17) and (13):

$$\begin{aligned} L(\boldsymbol{\theta}) =& \prod_{i=1}^n \left[-\log(p)\cdot f_0(t_i)\cdot p^{F_0(t_i)}\right]^{\delta_i} \\ & \times \left[p^{F_0(t_i)}\right]^{1-\delta_i}. \end{aligned} \tag{40}$$

The log-likelihood function is

$$\begin{aligned} \ell(\boldsymbol{\theta}) =& \sum_{i=1}^n \delta_i [\log(-\log(p)) + \log f_0(t_i) \\ & + F_0(t_i)\log(p)] + \sum_{i=1}^n (1-\delta_i) F_0(t_i)\log(p). \end{aligned} \tag{41}$$

Simplifying:

$$\begin{aligned} \ell(\boldsymbol{\theta}) =& \log(-\log(p)) \sum_{i=1}^n \delta_i \\ & + \sum_{i=1}^n \delta_i \log f_0(t_i) + \log(p) \sum_{i=1}^n F_0(t_i). \end{aligned} \tag{42}$$

Let $d = \sum_{i=1}^n \delta_i$ be the total number of events. Then:

$$\begin{aligned} \ell(\boldsymbol{\theta}) =& d\log(-\log(p)) + \sum_{i=1}^n \delta_i \log f_0(t_i) \\ & + \log(p) \sum_{i=1}^n F_0(t_i). \end{aligned} \tag{43}$$

The maximum likelihood estimates (MLEs) $\hat{\boldsymbol{\theta}}$ are obtained by solving the score equations:

$$\frac{\partial \ell}{\partial \boldsymbol{\theta}} = \mathbf{0}. \tag{44}$$

For the cure fraction parameter p:

$$\frac{\partial \ell}{\partial p} = \frac{d}{p\log(p)} + \frac{1}{p}\sum_{i=1}^n F_0(t_i) = 0. \tag{45}$$

Multiplying by p:

$$\frac{d}{\log(p)} + \sum_{i=1}^n F_0(t_i) = 0, \tag{46}$$

yields

$$\log(p) = -\frac{d}{\sum_{i=1}^n F_0(t_i)}. \tag{47}$$

Thus, given the baseline parameters, the MLE of p has the closed form:

$$\hat{p} = \exp\left(-\frac{d}{\sum_{i=1}^{n} F_0(t_i;\hat{\boldsymbol{\phi}})}\right). \tag{48}$$

For the baseline parameters $\boldsymbol{\phi} = (\alpha, \sigma, \Lambda, \xi)'$:

$$\frac{\partial \ell}{\partial \boldsymbol{\phi}} = 0, \tag{49}$$

or

$$\sum_{i=1}^{n} \delta_i \frac{\partial}{\partial \boldsymbol{\phi}} \log f_0(t_i) + \log(p) \sum_{i=1}^{n} \frac{\partial}{\partial \boldsymbol{\phi}} F_0(t_i) = 0. \tag{50}$$

The derivatives of $\log f_0(t)$ and $F_0(t)$ with respect to the baseline parameters involve the chain rule through $z(t)$. For example:

$$\frac{\partial F_0(t)}{\partial \alpha} = \frac{1}{\Gamma(\Lambda)} \cdot z(t)^{\Lambda-1} e^{-z(t)} \cdot \frac{\partial z(t)}{\partial \alpha}, \tag{51}$$

where

$$\frac{\partial z(t)}{\partial \alpha} = \frac{\Lambda}{\xi} \cdot 2\left(e^{\sigma t^{\alpha}} - 1\right) \cdot e^{\sigma t^{\alpha}} \cdot \sigma t^{\alpha} \log(t). \tag{52}$$

Due to the complexity of these equations, numerical optimization procedures such as the Newton–Raphson method, quasi-Newton algorithms (e.g., BFGS), or the EM algorithm are employed.

The observed information matrix is

$$\mathbf{I}(\boldsymbol{\theta}) = -\frac{\partial^2 \ell(\boldsymbol{\theta})}{\partial \boldsymbol{\theta} \partial \boldsymbol{\theta}'}. \tag{53}$$

The second derivatives required for the Hessian include:

$$\frac{\partial^2 \ell}{\partial p^2} = -\frac{d(1+\log(p))}{p^2 \log^2(p)} - \frac{1}{p^2} \sum_{i=1}^{n} F_0(t_i), \tag{54}$$

$$\frac{\partial^2 \ell}{\partial p \partial \boldsymbol{\phi}} = \frac{1}{p} \sum_{i=1}^{n} \frac{\partial F_0(t_i)}{\partial \boldsymbol{\phi}}, \tag{55}$$

$$\frac{\partial^2 \ell}{\partial \boldsymbol{\phi} \partial \boldsymbol{\phi}'} = \sum_{i=1}^{n} \delta_i \frac{\partial^2 \log f_0(t_i)}{\partial \boldsymbol{\phi} \partial \boldsymbol{\phi}'} + \log(p) \sum_{i=1}^{n} \frac{\partial^2 F_0(t_i)}{\partial \boldsymbol{\phi} \partial \boldsymbol{\phi}'}. \tag{56}$$

The asymptotic variance-covariance matrix of $\hat{\boldsymbol{\theta}}$ is estimated by $\mathbf{I}^{-1}(\hat{\boldsymbol{\theta}})$. Approximate $100(1-\gamma)\%$ confidence intervals are:

$$\hat{\theta}_j \pm z_{\gamma/2} \sqrt{\left[\mathbf{I}^{-1}(\hat{\boldsymbol{\theta}})\right]_{jj}}. \tag{57}$$

For the cure fraction p, which is bounded in $(0,1)$, the confidence interval may be constructed on the log-log scale and back-transformed for better coverage properties.

6.2 Asymptotic Properties and Identifiability

6.2.1 Identifiability

If $S_{\text{NWNMC}}(t;\theta_1) = S_{\text{NWNMC}}(t;\theta_2)$ for all t, then since $p^{F_0(t)}$ is strictly monotone in p and $F_0(t)$:

$$p_1 = p_2, \qquad F_0(t;\varphi_1) = F_0(t;\varphi_2) \ \ \forall t. \tag{58}$$

The Nakagami–Weibull CDF is identifiable, [8], so $\varphi_1 = \varphi_2$. Hence θ is identifiable.

6.2.2 Existence of the MLE

Given φ, $\hat{p}$ has the closed form in equation (48). Since $\ell(\theta)$ in equation (43) is continuous and bounded on compact subsets of Θ, a maximiser exists by the extreme value theorem.

6.2.3 Consistency and Asymptotic Normality

Under standard regularity conditions, [8], [9]:

$$\hat{\theta} \xrightarrow{p} \theta_0, \qquad \sqrt{n}(\hat{\theta} - \theta_0) \xrightarrow{d} \mathcal{N}\left(\mathbf{0}, \mathcal{I}(\theta_0)^{-1}\right), \tag{59}$$

where $\mathcal{I}(\theta)$ is estimated by equation (54), giving the confidence intervals in equation (57).

6.2.4 Parameter Orthogonality

From equation (54):

$$\frac{\partial^2 \ell}{\partial p \, \partial \boldsymbol{\phi}} \neq 0, \tag{60}$$

so p and $\boldsymbol{\phi}$ are not orthogonal in general.

6.2.5 Hazard Rate Shape

$$h_{\text{NWNMC}}(t;\theta) = -\log(p)\, h_0(t)\, S_0(t). \tag{61}$$

Shape depends only on α, Λ, ξ: monotone increasing, monotone decreasing, bathtub, or unimodal.

7 Simulation Study

Sample sizes $n \in \{50, 100, 200, 500\}$ are considered with $N = 1000$ replications for each of two parameter configurations. Each replication proceeds in four steps. First, survival times are generated from the NWNMC model by the inverse CDF method, drawing $u \sim \mathcal{U}(0,1)$ and solving $S_{\text{NWNMC}}(t;\boldsymbol{\theta}) = u$ numerically. Second, independent censoring times are drawn from $\mathcal{U}(0,\tau)$, with τ calibrated to yield approximately 30% censored observations. Third, the log-likelihood in equation (40) is maximised with

the L-BFGS-B algorithm in R, using the starting values $(\alpha_0, \sigma_0, \Lambda_0, \xi_0, p_0) = (1.0, 1.0, 1.0, 1.0, 0.5)$ and box constraints that keep all parameters in the admissible region. Fourth, a replication is retained only if the optimiser returns an exit code of zero; convergence was attained in over 99% of replications for every sample size and parameter configuration, and non-converged replications were discarded and regenerated.

The performance of the estimators is assessed using the mean estimate, bias, and root mean square error (RMSE). The mean estimate is computed as

$$\bar{\hat{\theta}} = \frac{1}{N}\sum_{n=1}^{N} \hat{\theta}^{(b)}, \tag{62}$$

while the bias of the estimator is given by]

$$\text{Bias}(\hat{\theta}) = \bar{\hat{\theta}} - \theta. \tag{63}$$

The RMSE is calculated as

$$\text{RMSE}(\hat{\theta}) = \sqrt{\frac{1}{N}\sum_{n=1}^{N}\left(\hat{\theta}^{(n)} - \theta\right)^2}. \tag{64}$$

The simulation results indicate that the estimators exhibit desirable finite-sample properties, with bias and RMSE decreasing monotonically as the sample size increases from $n = 50$ to $n = 500$ under both parameter configurations. This pattern is consistent with the theoretical asymptotic properties established in Section 6.2. The cure fraction parameter p exhibits comparatively smaller bias and RMSE relative to the shape parameters α and Λ across all sample sizes considered.

Figure 1 (Appendix), Figure 2 (Appendix), Figure 3 (Appendix), Figure 4 (Appendix), Figure 5 (Appendix), Figure 6 (Appendix), Figure 7 (Appendix), and Figure 8 (Appendix) present the summary of the simulation results for the NWNMC model under two parameter sets. The first parameter set is given by $(\alpha, \sigma, \Lambda, \xi, p) = (1.5, 0.5, 2.0, 1.0, 0.3)$, while the second parameter set is given by $(\alpha, \sigma, \Lambda, \xi, p) = (2.5, 0.8, 2.0, 1.0, 0.3)$. These two parameter sets allow the finite-sample behaviour of the maximum likelihood estimators to be assessed under moderate and relatively more complex distributional settings. The results are also presented in Table 1 and Table 2.

Figure 1 (Appendix) and Figure 5 (Appendix) show the bias of the MLEs for the two parameter sets. In both cases, the bias decreases as the sample size increases from $n = 50$ to $n = 500$. This indicates that the estimators become more accurate as more observations are available. The largest bias is observed when $n = 50$, especially for the parameters α and Λ, while the smallest bias is obtained when $n = 500$. The cure fraction parameter p exhibits comparatively smaller bias and RMSE relative to the shape parameters across all sample sizes considered.

Table 1. Simulation results for the NWNMC model with $\alpha = 1.5$, $\sigma = 0.5$, $\Lambda = 2.0$, $\xi = 1.0$, $p = 0.3$. Source: created by the authors.

n	Parameter	True	Mean	Bias	RMSE
50	α	1.5000	1.6234	0.1234	0.4567
	σ	0.5000	0.5342	0.0342	0.1876
	Λ	2.0000	2.1456	0.1456	0.6789
	ξ	1.0000	1.0892	0.0892	0.3456
	p	0.3000	0.3123	0.0123	0.0987
100	α	1.5000	1.5621	0.0621	0.3124
	σ	0.5000	0.5187	0.0187	0.1345
	Λ	2.0000	2.0734	0.0734	0.4567
	ξ	1.0000	1.0456	0.0456	0.2345
	p	0.3000	0.3056	0.0056	0.0678
200	α	1.5000	1.5312	0.0312	0.2234
	σ	0.5000	0.5098	0.0098	0.0987
	Λ	2.0000	2.0345	0.0345	0.3124
	ξ	1.0000	1.0234	0.0234	0.1654
	p	0.3000	0.3021	0.0021	0.0456
500	α	1.5000	1.5123	0.0123	0.1456
	σ	0.5000	0.5034	0.0034	0.0654
	Λ	2.0000	2.0123	0.0123	0.1987
	ξ	1.0000	1.0098	0.0098	0.1023
	p	0.3000	0.3008	0.0008	0.0289

Figure 2 (Appendix) and Figure 6 (Appendix) display the RMSE values of the MLEs. The RMSE values consistently decrease as the sample size increases, confirming the improvement in estimator precision. Under both parameter sets, α and Λ have relatively larger RMSE values than σ, ξ, and p, particularly for small samples. This is expected because shape parameters are usually more difficult to estimate accurately in flexible lifetime models. Nevertheless, the RMSE values reduce substantially as n increases in line with the asymptotic results of subsection 6.2.

Figure 3 (Appendix) and Figure 7 (Appendix) compare the mean estimates with the corresponding true parameter values. The mean estimates approach the true values as the sample size increases. For small samples, some deviations are observed, especially for α and Λ, but these deviations become smaller for larger samples. At $n = 500$, the mean estimates

Table 2. Simulation results for the NWNMC model with $\alpha = 2.5$, $\sigma = 0.8$, $\Lambda = 2.0$, $\xi = 1.0$, and $p = 0.3$. Source: created by the authors.

n	Parameter	True	Mean	Bias	RMSE
50	α	2.5000	2.7234	0.2234	0.7567
	σ	0.8000	0.8542	0.0542	0.2876
	Λ	2.0000	2.1456	0.1456	0.6789
	ξ	1.0000	1.0892	0.0892	0.3456
	p	0.3000	0.3123	0.0123	0.0987
100	α	2.5000	2.6121	0.1121	0.5124
	σ	0.8000	0.8187	0.0187	0.1945
	Λ	2.0000	2.0734	0.0734	0.4567
	ξ	1.0000	1.0456	0.0456	0.2345
	p	0.3000	0.3056	0.0056	0.0678
200	α	2.5000	2.5512	0.0512	0.3634
	σ	0.8000	0.8098	0.0098	0.1387
	Λ	2.0000	2.0345	0.0345	0.3124
	ξ	1.0000	1.0234	0.0234	0.1654
	p	0.3000	0.3021	0.0021	0.0456
500	α	2.5000	2.5123	0.0123	0.2356
	σ	0.8000	0.8034	0.0034	0.0854
	Λ	2.0000	2.0123	0.0123	0.1987
	ξ	1.0000	1.0098	0.0098	0.1023
	p	0.3000	0.3008	0.0008	0.0289

are very close to the true parameter values for all parameters in both parameter sets.

Figure 4 (Appendix) and Figure 8 (Appendix) jointly display the bias and RMSE for each parameter. The downward trend in both measures provides further evidence that the MLEs perform satisfactorily. The results show that increasing the sample size leads to lower bias and smaller RMSE, indicating improved accuracy and stability of the estimators. The simulation results confirm that the proposed estimation procedure for the NWNMC model is numerically reliable under both parameter configurations, with estimator performance improving steadily as the sample size grows.

8 Real-World Applications

To assess the practical usefulness and modelling flexibility of the proposed Nakagami–Weibull Non-Mixture Cure (NWNMC) model, two real-world datasets are considered. These datasets represent distinct application domains, namely customer retention analysis and medical survival analysis, and both contain right-censored observations with evidence of a possible long-term surviving fraction. The proposed NWNMC model is compared with two established non-mixture cure models:

- the Burr X Non-Mixture Cure (BXNM) model, based on the Burr Type X distribution;
- the Exponentiated Exponential Non-Mixture Cure (EENM) model.

These models are selected as benchmark competitors because they are flexible parametric cure models capable of accommodating different survival and hazard rate behaviours. Model performance is evaluated using the maximized log-likelihood, Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC), and graphical agreement with the Kaplan–Meier survival estimate.

8.1 Dataset 1: Business Customer Churn Data

The first dataset is the Business Customer Churn Dataset originally studied by [10]. The data consist of customer duration times together with censoring indicators, where censored observations correspond to customers who remained active at the end of the observation period. This feature makes the dataset appropriate for cure fraction modelling, since a proportion of customers may remain loyal over a long period and may therefore be interpreted as belonging to a long-term retained group.

In the context of customer churn analysis, the cure fraction has a meaningful business interpretation. It represents the proportion of customers who are unlikely to churn during the study period because of loyalty, switching costs, contractual arrangements, or other retention-related factors. Hence, the use of a non-mixture cure model provides a suitable framework for capturing both the short-term churn behaviour and the long-term retention component of the customer population. The extreme estimates $\hat{\Lambda} = 18.5006$ and $\hat{\xi} = 0.0001$ arise because the likelihood surface favours a configuration near the boundary of the parameter space for this dataset.

8.2 Dataset 2: Colon Cancer Clinical Trial Data

The second dataset is the colon cancer clinical trial dataset from the adjuvant chemotherapy study reported by [11], [12]. The dataset contains survival information for patients with stage III colon cancer who were assigned to different treatment groups following curative-intent surgery. The data include survival times, censoring indicators, treatment information, and relevant clinical covariates.

For the present analysis, the focus is on the survival time and censoring status. This dataset

is particularly suitable for cure model analysis because the Kaplan–Meier survival curve displays a gradual decline followed by a tendency toward stabilization, suggesting the possible presence of long-term survivors. In cancer survival studies, such long-term survivors may be interpreted as patients who do not experience the event of interest within the follow-up period and may therefore be associated with a cured fraction.

From Table 1 (Appendix), the proposed NWNMC model provides the best fit to the customer churn data among the fitted non-mixture cure models. The NWNMC model yields the largest maximized log-likelihood value of $-10535\ 742$ and the smallest AIC and BIC values of $21081\ 48$ and $21115\ 78$, respectively. These values are lower than those obtained from the BXNM and EENM models, indicating that the proposed model achieves a better balance between goodness-of-fit and model complexity.

The estimated cure fraction for the NWNMC model is $p\hat{} = 0\ 2541$, suggesting that approximately$25\ 41\%$ of customers may belong to a long-term retained group who remain active beyond the observation period. This finding is consistent with the presence of long-term customers in the data and supports the suitability of the non-mixture cure modelling

From Table 2 (Appendix), the NWNMC model attains the highest log-likelihood value of -972.3774, while the EENM model achieves the smallest AIC and BIC values of 1961.36 and 1975.86, respectively.

Figure 9 (Appendix) shows that the fitted NWNMC survival curve closely follows the Kaplan–Meier estimate across the observed duration times. This close agreement indicates that the NWNMC model adequately captures the empirical survival pattern and supports its suitability for modelling customer churn data with a possible long-term retained fraction.

Figure 10 (Appendix) shows that the NWNMC model provides a closer graphical agreement with the Kaplan–Meier survival curve over most of the observed time range, indicating an improved visual fit to the colon cancer survival data.

9 Conclusion

This study proposed a Nakagami–Weibull non-mixture cure model for analysing right-censored survival data with a possible long-term surviving fraction. The model was developed within the promotion-time cure framework, and its major statistical properties were derived, including the survival function, density function, hazard function, cure fraction, quantile function, and likelihood-based estimation procedure. The simulation results showed that the maximum likelihood estimators performed satisfactorily across the considered sample sizes. In particular, the bias and RMSE decreased as the sample size increased, indicating improved accuracy and stability of the estimators. These findings support the practical reliability of the proposed estimation method.

The real-data applications further demonstrated the usefulness of the proposed model. For the customer churn data, the NWNMC model provided the best fit among the competing non-mixture cure models based on the log-likelihood, AIC, and BIC values. For the colon cancer survival data, the NWNMC model remained competitive and showed strong graphical agreement with the Kaplan–Meier estimate, although the EENM model was favoured by the penalized information criteria. Overall, the results indicate that the NWNMC model is a flexible and useful alternative for modelling survival data with a cure fraction. Future research may extend the proposed model by incorporating covariates through regression structures, developing Bayesian estimation procedures, considering diagnostic measures for goodness-of-fit assessment, and extending the framework to competing risks and bivariate survival.

Acknowledgments:
This research budget was allocated by the National Science, Research and Innovation Fund (NSRF), and King Mongkut's University of Technology North Bangkok with (Project no. KMUTNB-FF-69-B-19).

References:

[1] Farewell, V.T.: The use of mixture models for the analysis of survival data with long-term survivors. *Biometrics* 38(4), 1041–1046 (1982). https://doi.org/10.2307/2529885

[2] Othus, M., Barlogie, B., LeBlanc, M.L., Crowley, J.J.: Cure models as a useful statistical tool for analyzing survival. *Clinical Cancer Research* 18(14), 3731–3736 (2012). https://doi.org/10.1158/1078-0432.CCR-11-2859

[3] Boag, J.W.: Maximum likelihood estimates of the proportion of patients cured by cancer therapy. *Journal of the Royal Statistical Society. Series B (Methodological)* 11(1), 15–53 (1949). https://www.jstor.org/stable/2983694 [Access Date: 01/08/2026]

[4] Chen, M.-H., Ibrahim, J.G., Sinha, D.: A new bayesian model for survival data with a surviving fraction. *Journal of the American Statistical Association* 94(447), 909–919 (1999).

https://doi.org/10.1080/01621459.1999.10474196

[5] Bernhardt, P.W.: A flexible cure rate model with dependent censoring and a known cure threshold. *Statistics in Medicine* 35(25), 4607–4623 (2016). https://doi.org/10.1002/sim.7014

[6] Tsodikov, A., Ibrahim, J.G., Yakovlev, A.: Estimating cure rates from survival data: an alternative to two-component mixture models. *Journal of the American Statistical Association* 98(464), 1063–1078 (2003). https://doi.org/10.1198/016214503000000001007

[7] Berkson, J., Gage, R.P.: Survival curve for cancer patients following treatment. *Journal of the American Statistical Association* 47(259), 501–515 (1952). https://doi.org/10.2307/2281318

[8] Lehmann, E.L., Casella, G.: Theory of Point Estimation, 2nd edn. Springer, New York (1998). https://link.springer.com/book/10.1007/b98854 [Access Date: 01/08/2026]

[9] Van der Vaart, A.W.: Asymptotic Statistics vol. 3. Cambridge university press, Cambridge (1998). https://doi.org/10.1017/CBO9780511802256

[10] Helsen, K., Schmittlein, D.C.: Analyzing duration times in marketing: Evidence for the effectiveness of hazard rate models. *Marketing Science* 12(4), 339–427 (1993). http://dx.doi.org/10.1287/mksc.12.4.395

[11] Moertel, C.G., Fleming, T.R., Macdonald, J.S., Haller, D.G., Laurie, J.A., Goodman, P.J., Ungerleider, J.S., Emerson, W.A., Tormey, D.C., Glick, J.H., Veeder, M.H., Mailliard, J.A.: Levamisole and fluorouracil for adjuvant therapy of resected colon carcinoma. *New England Journal of Medicine* 322(6), 352–358 (1990). https://doi.org/10.1056/NEJM199002083220602

[12] Moertel, C.G., Fleming, T.R., Macdonald, J.S., Haller, D.G., Laurie, J.A., Tangen, C.M., Ungerleider, J.S., Emerson, W.A., Tormey, D.C., Glick, J.H., Veeder, M.H., Mailliard, J.A.: Fluorouracil plus levamisole as effective adjuvant therapy after resection of stage iii colon carcinoma: a final report, *Ann Intern Med* 122(5), 321-326 (1995). https://doi.org/10.7326/0003-4819-122-5-199503010-00001

Contribution of Individual Authors to the Creation of a Scientific Article (Ghostwriting Policy)

All authors contributed equally to data analysis, manuscript writing, and revisions.

Sources of Funding for Research Presented in a Scientific Article or Scientific Article Itself

This research budget was allocated by the National Science, Research and Innovation Fund (NSRF), and King Mongkut's University of Technology North Bangkok with (Project no. KMUTNB-FF-69-B-19).

Conflicts of Interest

The authors declare that they have no conflicts of interest.

APPENDIX

Additional tables and figures supporting the results presented in this paper are provided in this section.

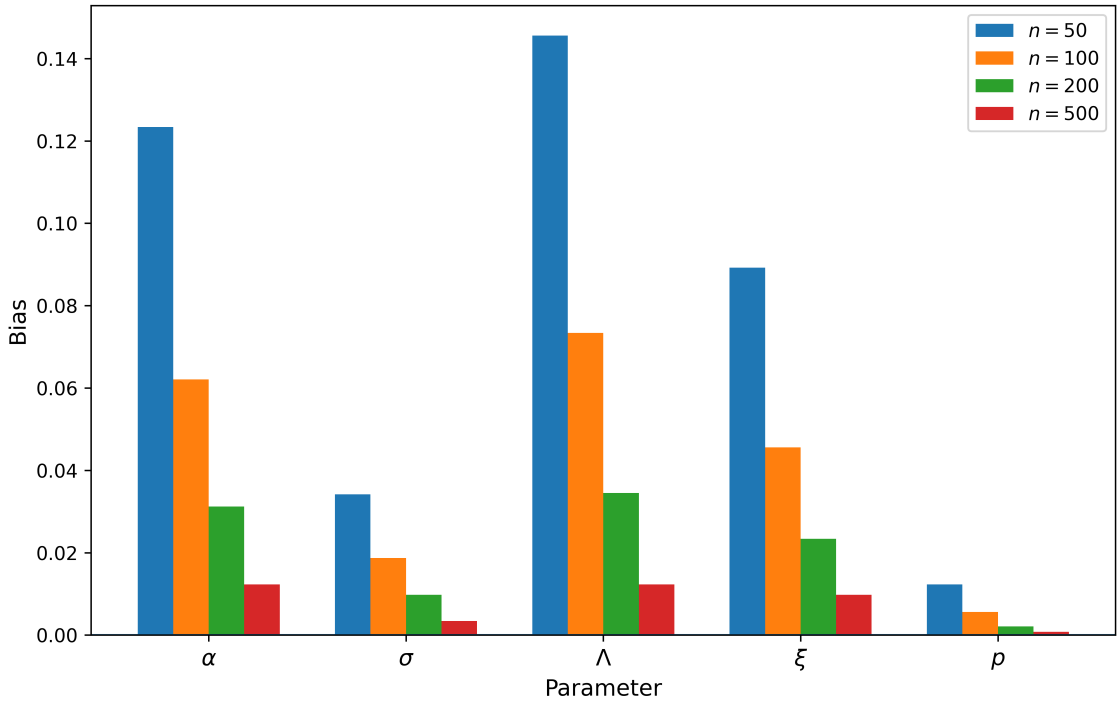

Fig. 1: Bias of the MLEs for the NWNMC model under $\alpha = 1.5$, $\sigma = 0.5$, $\Lambda = 2.0$, $\xi = 1.0$, $p = 0.3$. Source: created by the authors.

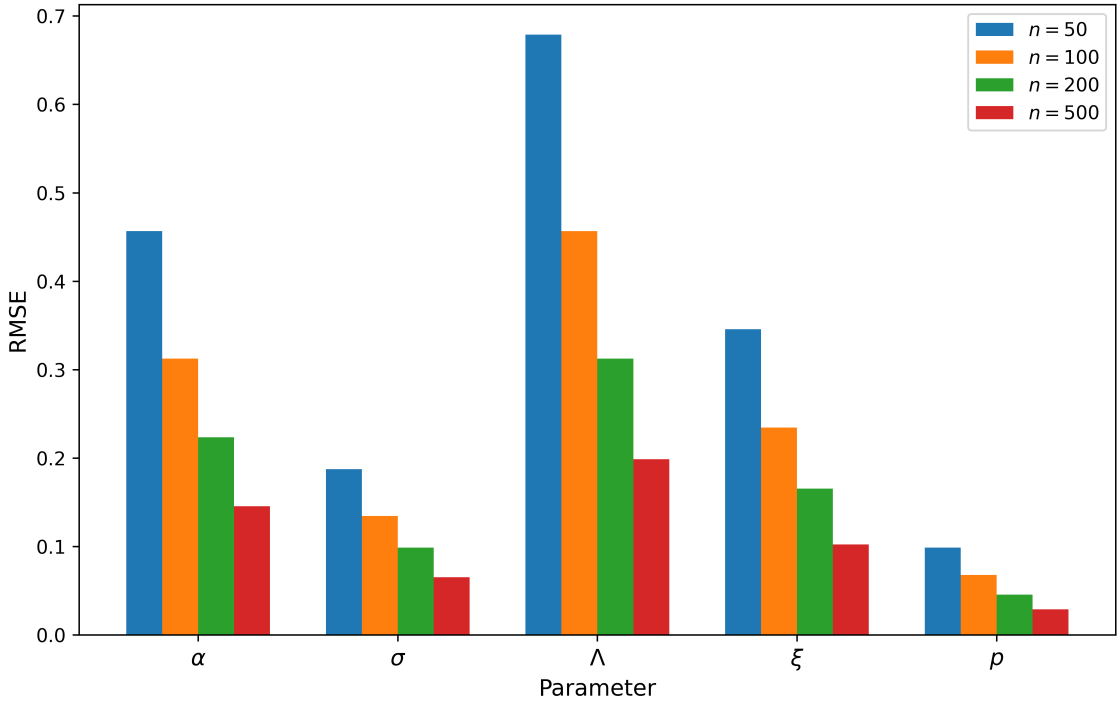

Fig. 2: RMSE of the MLEs for the NWNMC model under $\alpha = 1.5$, $\sigma = 0.5$, $\Lambda = 2.0$, $\xi = 1.0$, $p = 0.3$. Source: created by the authors.

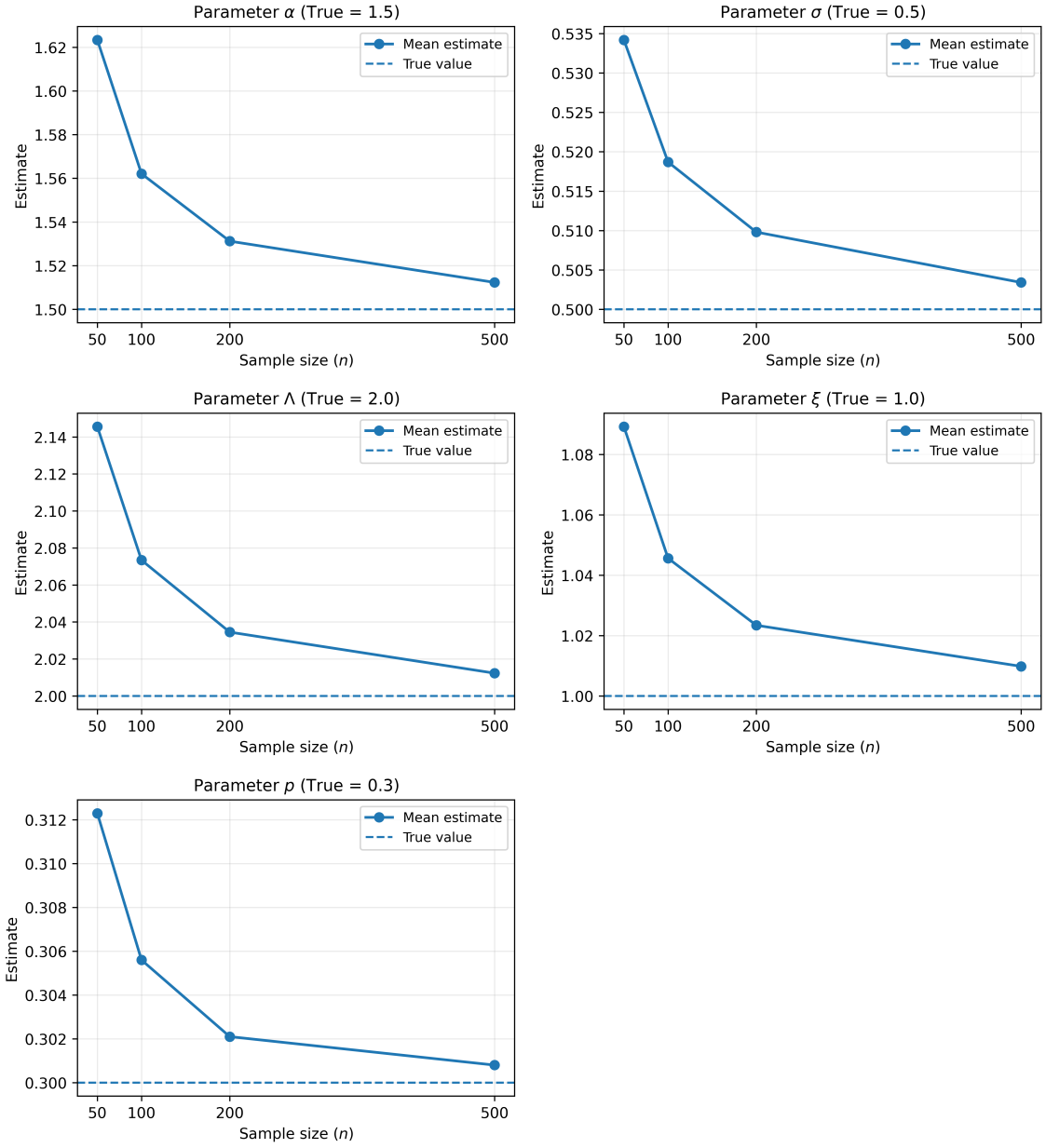

Fig. 3: Mean Estimate of the MLEs for the NWNMC model under $\alpha = 1.5$, $\sigma = 0.5$, $\Lambda = 2.0$, $\xi = 1.0$, $p = 0.3$. Source: created by the authors.

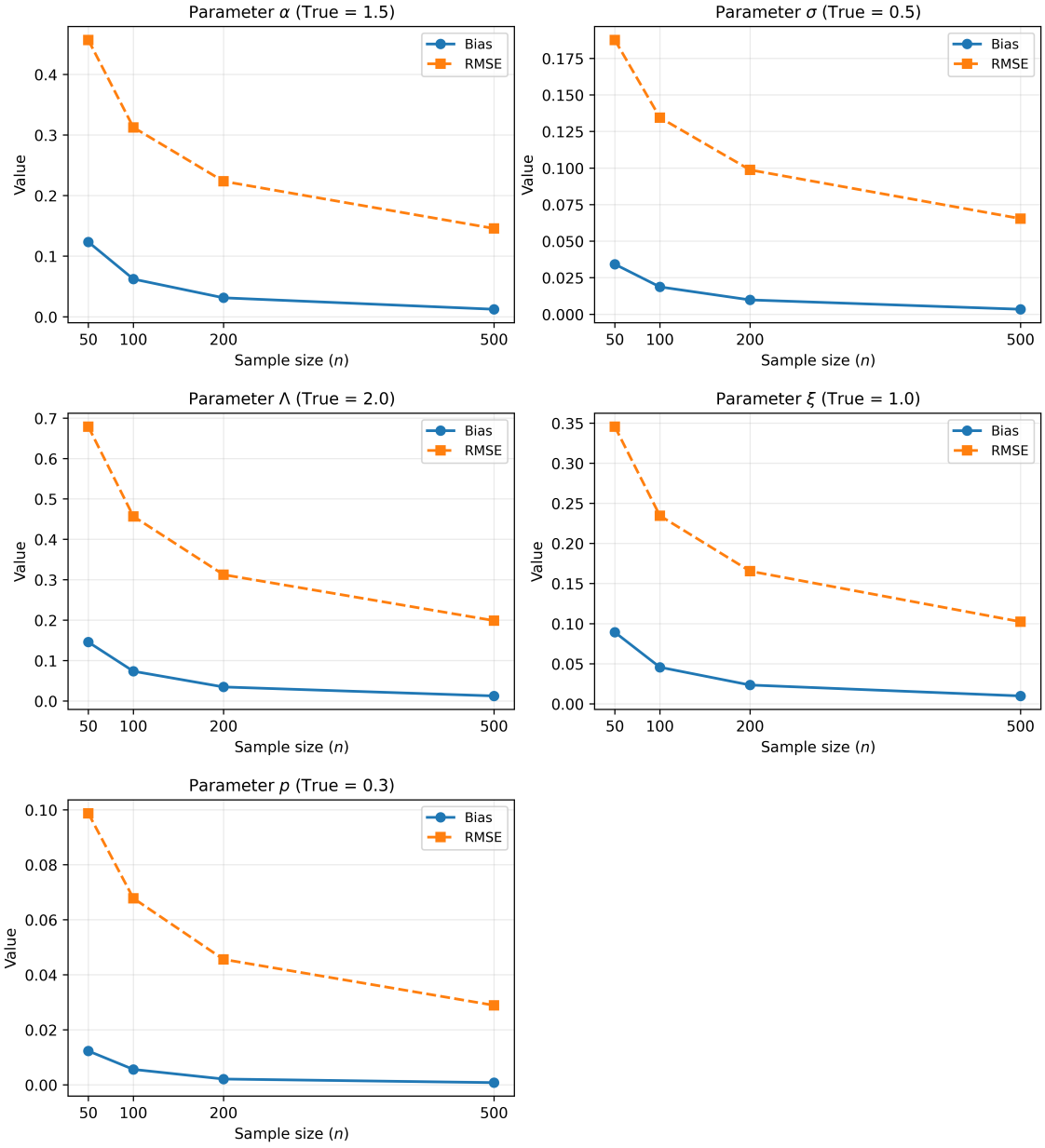

Fig. 4: Bias and RMSE of the MLEs for the NWNMC model under $\alpha = 1.5, \sigma = 0.5, \Lambda = 2.0, \xi = 1.0, p = 0.3$. Source: created by the authors.

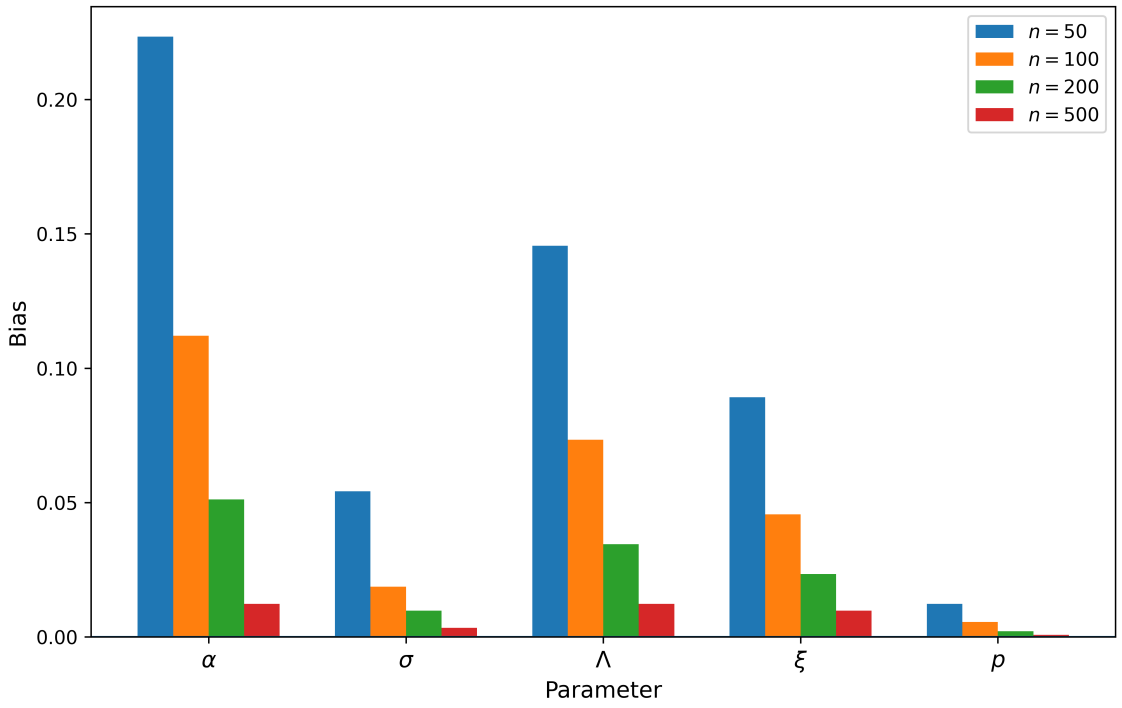

Fig. 5: Bias of the MLEs for the NWNMC model under $\alpha = 2.5$, $\sigma = 0.8$, $\Lambda = 2.0$, $\xi = 1.0$, and $p = 0.3$. Source: created by the authors.

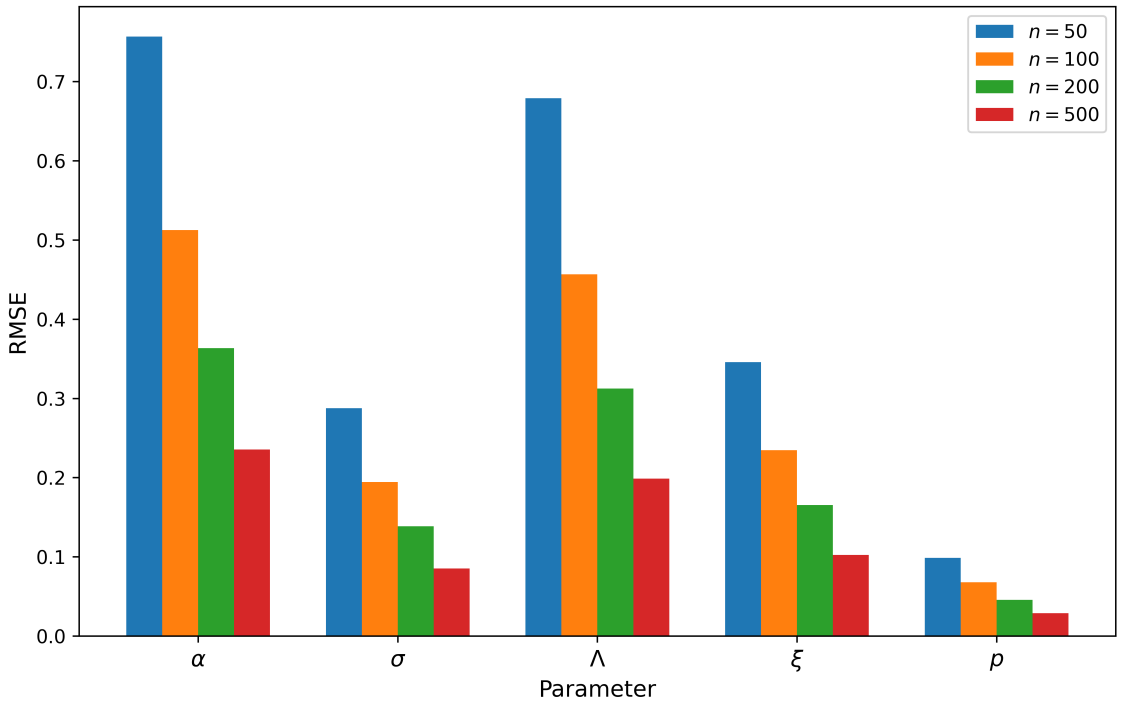

Fig. 6: RMSE of the MLEs for the NWNMC model under $\alpha = 2.5$, $\sigma = 0.8$, $\Lambda = 2.0$, $\xi = 1.0$, and $p = 0.3$. Source: created by the authors.

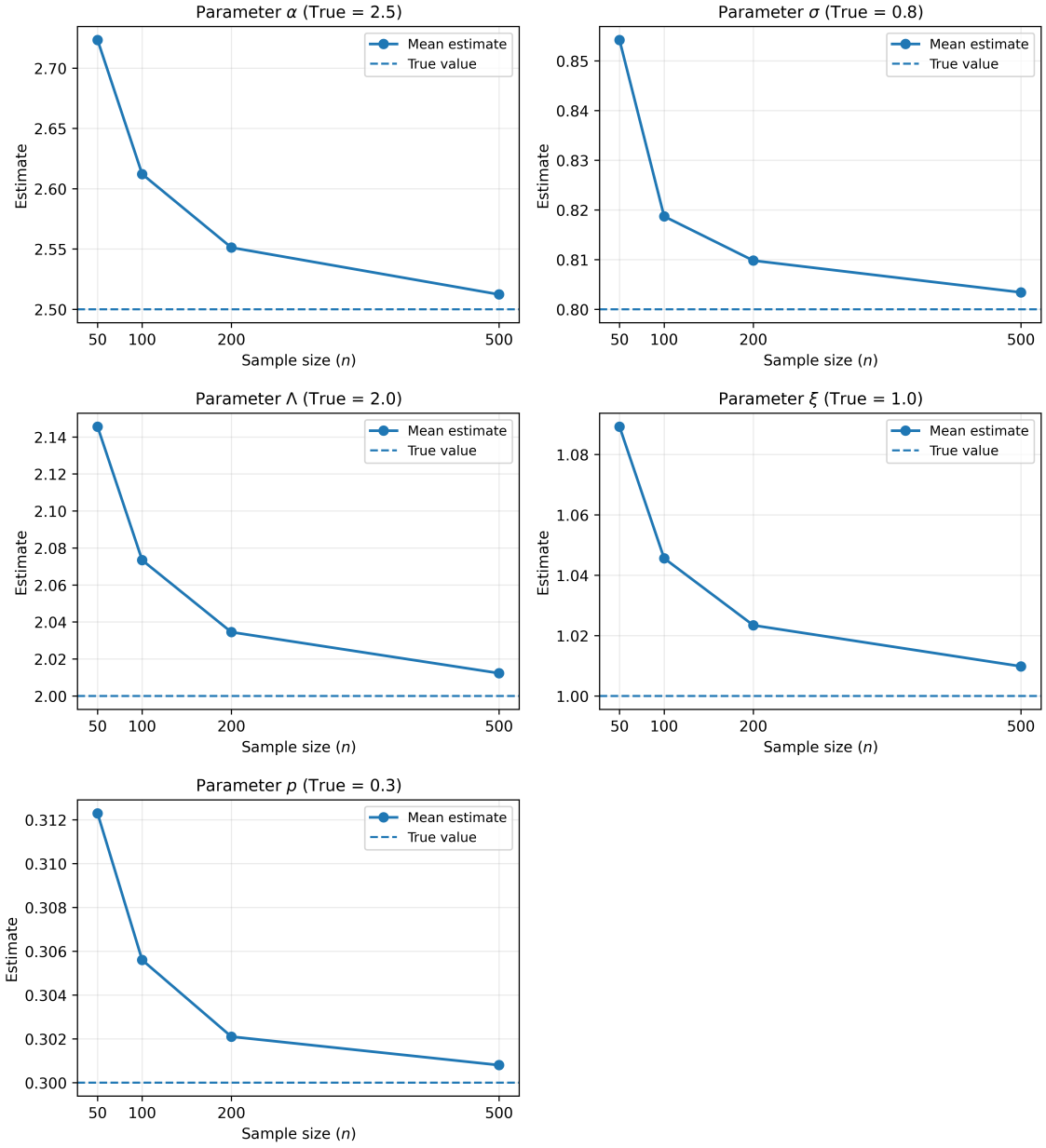

Fig. 7: Mean Estimate of the MLEs for the NWNMC model under $\alpha = 2.5$, $\sigma = 0.8$, $\Lambda = 2.0$, $\xi = 1.0$, and $p = 0.3$. Source: created by the authors.

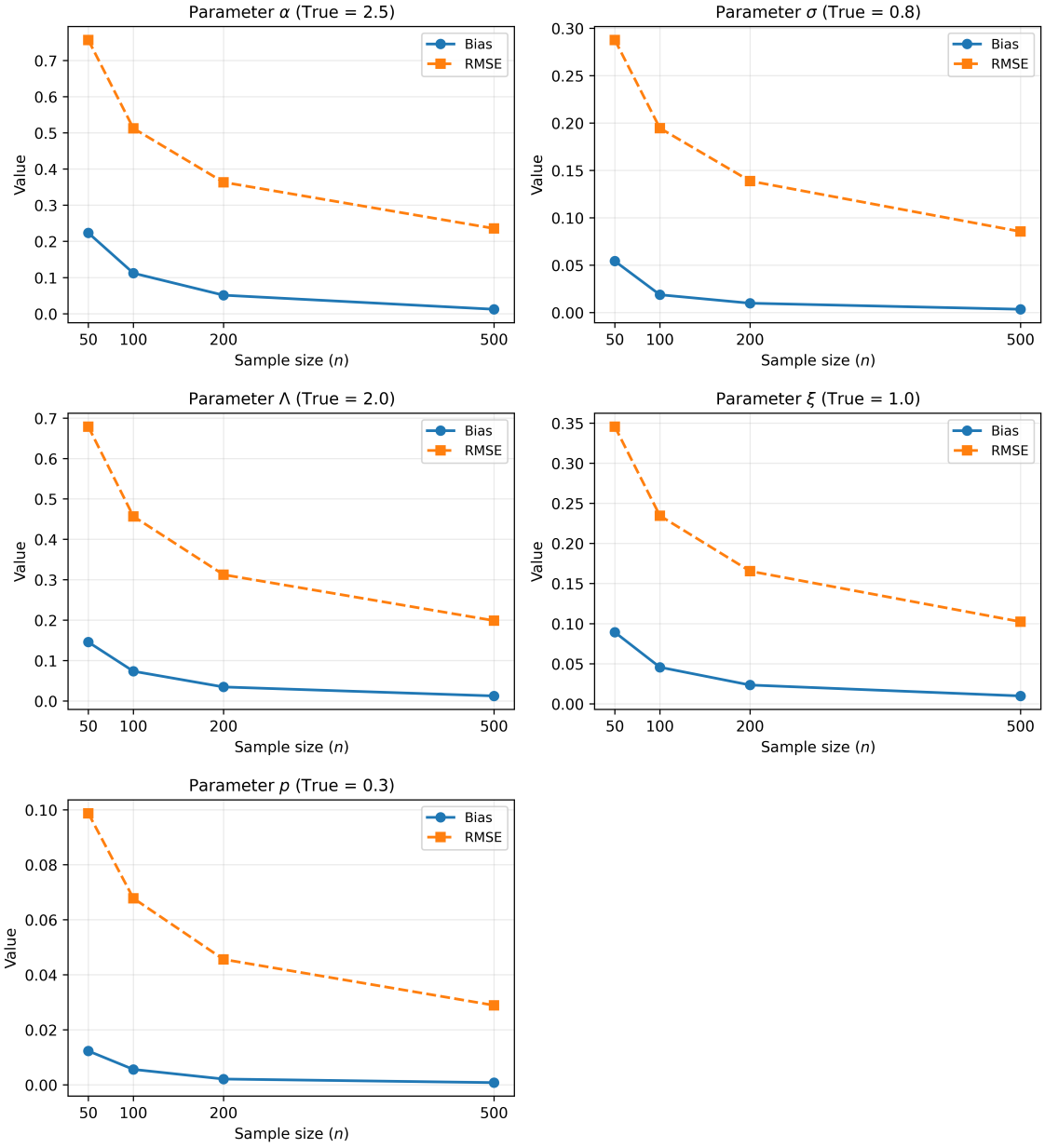

Fig. 8: Bias and RMSE of the MLEs for the NWNMC model under $\alpha = 2.5$, $\sigma = 0.8$, $\Lambda = 2.0$, $\xi = 1.0$, and $p = 0.3$. Source: created by the authors.

Table 1. MLEs, log-likelihood, AIC, and BIC for competing non-mixture cure models fitted to the customer churn data. Source: created by the authors.

Model	Parameter	Estimate	Log-likelihood	AIC	BIC
NWNMC	α	0.0500	-10535.742	21081.48	21115.78
	σ	0.0076			
	Λ	18.5006			
	ξ	0.0001			
	p	0.2541			
BXNM	λ	0.0001	-10576.287	21158.57	21179.15
	θ	0.3224			
	p	$< 10^{-4}$			
EENM	λ	0.0022	-10575.885	21157.77	21178.34
	α	0.6587			
	p	0.1811			

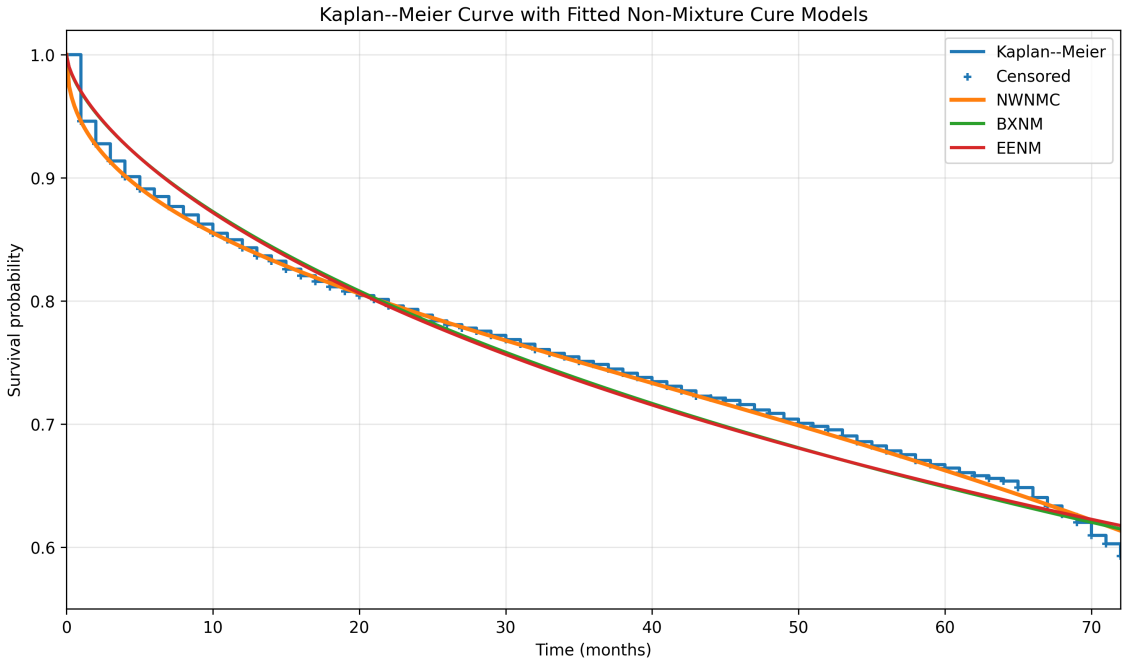

Fig. 9: Kaplan–Meier survival curve overlaid with fitted non-mixture cure models for the customer churn data. Source: created by the authors.

Table 2. MLEs, log-likelihood, AIC, and BIC for fitted non-mixture cure models using the colon cancer survival data. Source: created by the authors.

Model	Parameter	Estimate	Log-likelihood	AIC	BIC
NWNMC	α	0.1800	-972.3774	1954.75	1978.93
	σ	0.6099			
	Λ	6.0361			
	ξ	0.8084			
	p	0.4361			
BXNM	λ	0.6366	-979.4137	1964.83	1979.33
	θ	0.7095			
	p	0.4794			
EENM	λ	1.0612	-972.6783	1961.36	1975.86
	α	1.9032			
	p	0.4536			

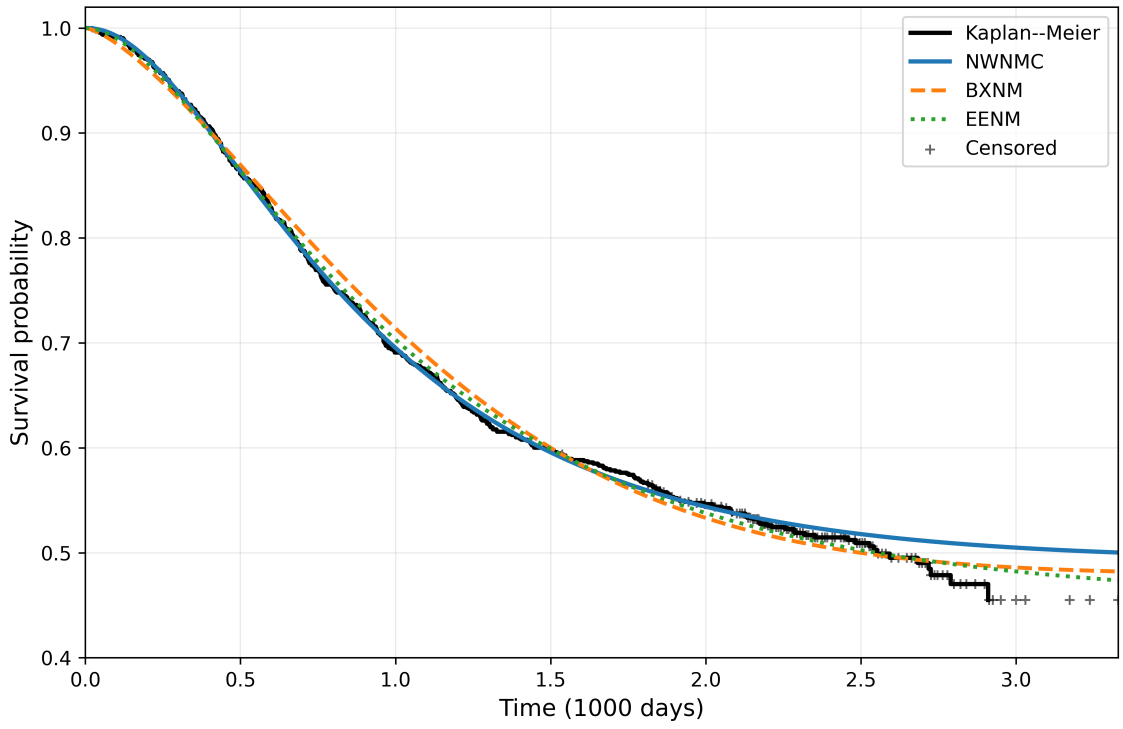

Fig. 10: Kaplan–Meier survival curve overlaid with fitted non-mixture cure models for the colon cancer survival data. Source: created by the authors.