



A next generation probabilistic approach to analyze cancer patients data with inference and applications

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ABSTRACT

This study addresses the critical challenges faced in cancer care, particularly in predicting survival times for patients with lung cancer and acute myeloid leukemia. Despite recent advancements in medical science, existing models often fall short in accurately capturing disease progression, leading to less effective clinical decision-making, and compromised patient outcomes. The need for advanced predictive models is urgent to improve survival time forecasts and enhance treatment strategies. In response to this, we introduce a novel probabilistic approach, the New Weibull (NEWE) model, which is part of a newly generated class designed to model cancer patient data more effectively. Our methodology includes using seven well-known estimation methods, each rigorously evaluated for consistency through Monte Carlo simulation studies focused on key metrics such as absolute bias, mean square error, and mean relative error. The datasets analyzed include survival times for twenty acute myeloid leukemia patients, 121 breast cancer patients from 1929 to 1938, 33 patients with acute myelogenous leukemia, data from eighteen individuals who died from causes unrelated to cancer, and survival times of advanced lung cancer patients undergoing standard chemotherapy. The NEWE model outperformed competing models, particularly in Anderson-Darling, Cramer-von Mises, and Kolmogorov-Smirnov tests, with significantly higher p-values. These findings highlight the NEWE model's potential to transform predictive oncology by offering more precise survival time predictions, improving the quality of care and decision-making in cancer treatment.

1. Introduction

Cancer stands as a global health challenge with a significant impact across populations, affecting millions each year with its myriad forms. The World Health Organization (WHO [1]), along with other leading cancer research organizations, continuously emphasizes the importance of early detection, effective treatment, and ongoing research in improving outcomes for these diseases. The WHO's Global Action Plan for the Prevention and Control of Non-communicable Diseases underscores the importance of a multifaceted approach to cancer, encompassing prevention, early detection, research, and equitable access to treatment services. This plan serves as a blueprint for national

and international efforts to combat cancers like lung, breast, and AML, aiming to reduce the burden of these diseases and enhance patient survival and quality of life. In the battle against cancer, collaboration across disciplines and borders is essential. From the molecular biology of cancer cells to public health strategies for prevention and screening, the fight against lung cancer, breast cancer, and AML exemplifies the complex interplay of research, clinical practice, and policy. As we move forward, the integration of innovative treatments with comprehensive care models holds the promise of transforming cancer from a deadly disease to a manageable condition.

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1.1. Lung cancer

Lung cancer is the leading cause of cancer-related deaths worldwide, a status underscored by the WHO. It primarily results from tobacco use and exposure to carcinogens, including air pollution and occupational hazards. Despite advances in treatment, such as targeted therapy and immunotherapy, lung cancer's prognosis remains challenging, highlighting the urgent need for effective smoking cessation programs and early screening initiatives. Despite declining mortality rates, lung cancer remains the leading cause of cancer death in the U.S. Recent data shows mortality declines outpacing incidence drops among men (5.0 % vs. 2.6 %) and women (4.3 % vs. 1.1 %), with survival improving by 1.4 % annually. Geographic and racial disparities persist, emphasizing the need for targeted public health efforts (Kratzer et al. [2]).

1.2. Acute Myeloid Leukemia (AML)

AML, a type of blood cancer characterized by the rapid growth of abnormal white blood cells, poses significant treatment challenges. Research bodies emphasize the importance of genetic testing and precision medicine in developing targeted therapies for AML. Recent breakthroughs, including novel chemotherapeutic agents and stem cell transplantation techniques, offer hope for improved outcomes, yet the need for advancements in early detection and risk assessment remains critical. AML challenges include age-related incidence and poor outcomes, with preclinical successes not always translating to clinical therapies. This review explores advanced preclinical models for better understanding and drug testing in AML, highlighting 3D, on-chip technologies, and patient-derived samples for personalized approaches (Dozzo et al. [3]). MDREAM represents a significant advancement in personalized oncology, utilizing an ensemble-based approach that integrates comprehensive omics data with extensive drug testing results to predict AML treatment responses. This model has been meticulously trained and validated across multiple cohorts, demonstrating exceptional accuracy in forecasting drug efficacy. By employing a sophisticated algorithm that analyzes mutations, gene expression, and drug response data, MDREAM provides a nuanced understanding of AML's complex biological landscape. Its capability to generate reliable predictions, as evidenced by high confidence scores and a strong correlation with observed responses, positions MDREAM as a pivotal tool for clinicians. This approach not only facilitates the identification of optimal therapeutic strategies for individual patients but also enhances our grasp of AML's heterogeneity. Furthermore, MDREAM's comparative analysis with existing treatments like Midostaurin highlights its potential to recommend more effective alternatives, thereby opening new avenues for targeted therapy and contributing to the broader field of precision medicine in oncology (Trac et al. [4]). AML demonstrates notable heterogeneity, possibly due to differences in leukemic cell responses to cytokines. Our study, utilizing mathematical modeling, computer simulations, and patient data analysis, finds that cytokine-independent leukemic cell proliferation correlates with earlier relapses and inferior overall survival rates. We developed models for both cytokine-dependent and independent AML growth scenarios, enabling the classification of AML patients into groups with significantly different survival outcomes. These models also predict patient responses to external cytokine treatments, offering insights into why some patients experience blast crisis or remission without chemotherapy. This research provides a framework for tailoring treatment plans based on the cytokine dependence of leukemic cells, aiming to enhance patient prognosis and therapy effectiveness (Stiehl et al. [5]).

In the field of oncology, the utilization of probability models plays a pivotal role, primarily through the statistical analysis of extensive datasets that include demographic, clinical, and genetic patient information. These models enable healthcare professionals to tailor treatment plans more accurately for each patient, thereby enhancing the likelihood of favorable outcomes. Furthermore, probability models are

instrumental in assessing cancer-related risk factors and pinpointing populations at an elevated risk. This vital information facilitates the development and execution of strategies aimed at early detection and prevention, significantly boosting patient prognosis. For an in-depth understanding, the contributions of researchers like Alsolmi [6], Klakattawi [7], and Babaei et al. [8], Chakraborty and Tsokos [9], Rady et al. [10], Soto-Ortiz and Brody [11] and among others, provide valuable insights into the application and impact of these models in cancer research.

The last two decades have seen a significant increase in interest in constructing newly generated (G) classes of distributions. These advancements have deepened our comprehension of complex and asymmetrical random phenomena, applying this knowledge to solve practical issues. The emergence of new classes has heralded fresh research pathways, offering scholars novel exploratory opportunities. For additional exploration into this topic, the works of Gupta et al. [12], Marshall and Olkin [13], Eugene et al. [14], Alshawarbeh et al. [15], Cordeiro and de Castro [16], Gleaton and Lynch [17], Alzaatreh et al. [18], Bourguignon et al. [19], Al Mutairi et al. [20], Balogun et al. [21], Al Mutairi [22], Alghamdi and Abd El-Raouf [23], among others and many others, present a wealth of information on the development and application of these models in various fields, including cancer research. Their contributions highlight the ongoing innovation and potential that new-G families of probability models hold for advancing our understanding and management of cancer and other complex diseases.

More extended Weibull have been introduced as: Exponentiated generalized Weibull exponential distribution by Abonongo et al. [33], exponentiated generalized Weibull exponential distribution by AL-Dayian et al. [34], a new extension of the odd inverse Weibull-G family Abdelal et al. [35], enhancing stock price prediction accuracy by Abotaleb et al. [36], bivariate Weibull distribution based on copula function by El-Sherpieny et al. [37], Bayesian and non-Bayesian inference for inverse Weibull model by Al Mutairi et al. [38], and alpha-power Weibull distribution by Almetwally et al. [39].

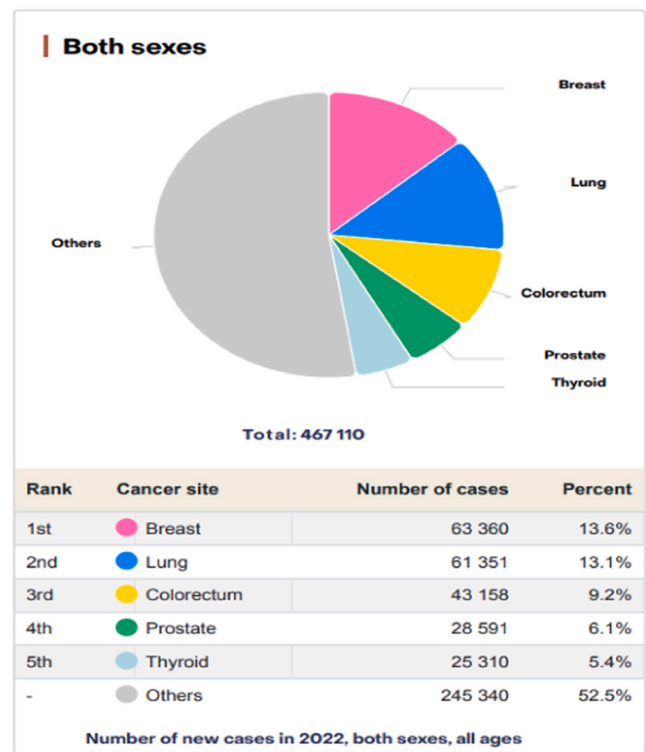


Fig. 1. Proportional distribution of new cancer cases for both sexes.

Fig. 1 presents a pie chart and an accompanying table that illustrate the distribution of new cancer cases by type, detailing the number of cases and the percentage share of each cancer. This combination provides a visual representation of the relative frequency of different cancers within a population. Fig. 2 highlights Age-Standardized Rates (ASR) for the incidence and mortality of various cancers, indicating the frequency of new diagnoses and deaths per 100,000 people. This information is essential for understanding the severity and lethal potential of each cancer type. Together, these graphs are instrumental in developing a comprehensive understanding of cancer's impact. Specifically, the bar chart in Fig. 2 underscores the urgency of addressing certain cancers due to their high mortality rates, while the pie chart in Fig. 1 highlights the most common cancers, emphasizing the need for significant medical and research attention due to their prevalence. Each graph offers unique insights that are critical for healthcare planning, resource allocation, and shaping public health strategies. Note that both graphs are sourced from the Global Cancer Observatory's Western Asia fact sheet, available at "<https://gco.iarc.who.int/media/globocan/factsheets/populations/922-western-asia-fact-sheet.pdf>."

Table 1 presents the Lung cancer and Leukemia details. Lung cancer has a high incidence and is the leading cause of cancer death, reflecting its severity and the challenges in treatment or late diagnosis. Leukemia has fewer new cases and deaths compared to lung cancer but remains a significant health concern. The cumulative risk percentages indicate an individual's likelihood over a lifetime of developing or dying from each cancer, with lung cancer posing a higher risk compared to leukemia. This information highlights the need for focused research, prevention, and treatment strategies for these cancers.

Research Gaps: The central focus of this study is to bridge a critical research gap in oncology by introducing a more advanced probabilistic model specifically designed to enhance the goodness-of-fit (GoF) for survival time data of cancer patients, particularly those suffering from lung cancer and acute myeloid leukemia. This need arises from the limitations of current predictive analytics in accurately modeling the complex nature of cancer progression and treatment responses. Despite advancements in medical science and technology, the variability and

uniqueness of each patient's disease trajectory presents significant challenges in predicting survival times with high precision. Traditional models often fall short in capturing the intricate dynamics of cancer, leading to suboptimal clinical decision-making and treatment planning. **Aims and Objectives:** This study has two main goals. The first is to rigorously evaluate the performance of seven classical estimation methods through detailed Monte Carlo simulations, emphasizing key metrics such as absolute bias, mean square error, and mean relative error. The second goal is to conduct a comparative analysis of the NEWWE model against existing models, specifically focusing on datasets for lung and acute myeloid leukemia patients. **Methodology:** To address these challenges and significantly enhance model outcomes, we developed the new Weibull model, known as the NEWWE model. The NEWWE model, a significant advancement within the newly generated (NE-G) class of models, offers a more effective method for modeling cancer patient data. Our methodology employs rigorous Monte Carlo simulation studies to evaluate the performance of seven classical estimation techniques, focusing on key metrics such as absolute bias, mean square error, and mean relative error. This approach not only highlights the NEWWE model's enhanced ability to accurately fit survival data but also demonstrates its potential to significantly improve the current landscape of predictive analytics in oncology. By focusing on improving the model's GoF, our research paves new pathways for both academic study and clinical practice, establishing the NEWWE model as a pivotal tool for developing highly precise treatment planning and management strategies. This innovative approach promises to revolutionize how oncologists predict survival times, making it an indispensable tool in the fight against cancer. **Contribution to the Scientific World:** This study makes a significant contribution to the scientific world by introducing a novel approach to probabilistic modeling that can enhance the accuracy and reliability of survival predictions in oncology. The NEWWE model's superior performance in GoF measures and its ability to manage complex datasets represent a substantial advancement over traditional models. By improving the precision of survival time estimates, this model facilitates more informed clinical decisions, leading to better patient outcomes. Furthermore, the methodology and findings from this study provide a valuable framework for future research, encouraging further exploration and development of probabilistic models tailored to the specific needs of different cancer types.

This study is designed into several sections: Section 2 focuses on the mathematical formulation of the newly generated class and the development of a special member within this class. Section 3 discussed statistical properties of the NEWWE distribution. Sections 4 and 5 discuss classical parameter estimation and simulation studies, respectively. Sections 6 and 7 describe predictive modeling and the interpretation of cancer data. Sections 8 and 9 illustrate competitor models and criteria for choosing statistical models. Finally, Sections 10, 11, 12, and 13 describe the discussion, conclusion, limitations, recommendations, and future recommendations of the study.

2. A new generated class

The mathematical formulation of cumulative distribution function (CDF, designated as $F|_T$) corresponding to probability density function (PDF, designated as $f|_T$) for the newly generated NE-G class is presented, respectively, as follows:

$$F|_T = \frac{\log[1 + G(t; \Omega)\{e^\alpha - 1\}]}{\alpha}, \quad (1)$$

$$f|_T = \frac{g(t; \Omega)\{e^\alpha - 1\}}{\alpha[1 + G(t; \Omega)\{e^\alpha - 1\}]}, \quad (2)$$

$$T|_u = G^{-1} \left[\frac{e^{\alpha U(t; \Omega)} - 1}{\alpha - 1} \right]. \quad (3)$$

Note that, $\alpha > 0$ represents the shape parameter, Ω is parametric

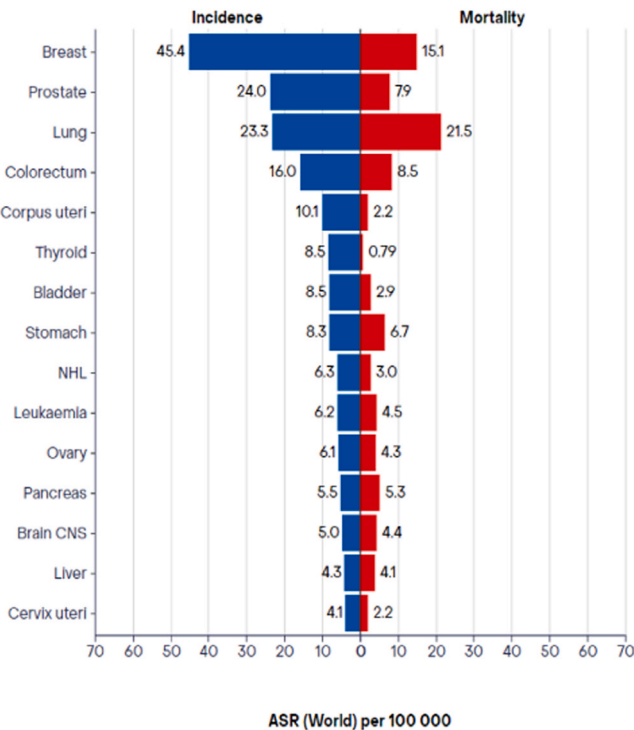


Fig. 2. Comparative incidence and mortality of common cancers (ASR per 100,000).

Table 1

Lung and Leukemia Cancer Statistics in Western Asia.

Cancer Type	New Cases (Number)	Rank (New Cases)	Cumulative Risk (%)	Deaths (Number)	Rank (Deaths)	Cumulative Risk (Deaths, %)
Lung	61,351	2	2.80	55,972	1	2.60
Leukemia	16,889	9	0.57	12,563	6	0.44

Source: Global Cancer Observatory's Western Asia fact sheet

space, $U \sim \text{uniform}(0, 1)$, indicating that U follows a uniform distribution, and $G(t; \Omega)$ is identified as the baseline model. The corresponding probability density function (PDF), $g(t; \Omega)$ is the derivative of $G(t; \Omega)$ with respect to t , denoted as $d[G(t; \Omega)]/dt$. Furthermore, as $\lim_{t \rightarrow 0} G(t; \Omega) = 0$ and $\lim_{t \rightarrow \infty} G(t; \Omega) = 1$. Hence, $\lim_{t \rightarrow -\infty} F|_T = 0$ and $\lim_{t \rightarrow +\infty} F|_T = 1$. Henceforth, the random variable T , following PDF, is now referred to as $T \sim \text{NE-G}(t; \Omega)$. To analyze data from lung and AML patients, we have selected the Weibull (WE) model, noted for its robustness and potential in medical research. This model, characterized by its CDF given by $G(t; \zeta, \phi) = \{1 - e^{-\zeta t^\phi}\}$, is distinguished for its precision in capturing survival patterns. Alongside, we explore the NEWE model, an esteemed representative of the innovative NEG-class, to uncover its strengths and contributions in enhancing our understanding of patient data. The mathematical formulations of the NEWE model's CDF and PDF, along with reliability measures such as the survival function (SF, designated as $SF|_T$) and hazard rate function (HrF, designated as $HrF|_T$), are presented as follows:

$$F|_T = \frac{\log \left[1 + \{1 - e^{-\zeta t^\phi}\} \{e^\alpha - 1\} \right]}{\alpha}, \quad (4)$$

$$f|_T = \frac{\phi \zeta (e^\alpha - 1) t^{\phi-1} e^{-\zeta t^\phi}}{\alpha [1 + \{1 - e^{-\zeta t^\phi}\} \{e^\alpha - 1\}]}, \quad (5)$$

$$SF|_T = \frac{\alpha - \log \left[1 + \{1 - e^{-\zeta t^\phi}\} \{e^\alpha - 1\} \right]}{\alpha}, \quad (6)$$

$$HrF|_T = \frac{\phi \zeta t^{\phi-1} e^{-\zeta t^\phi} (e^\alpha - 1)}{[1 + \{1 - e^{-\zeta t^\phi}\} \{e^\alpha - 1\}] [\alpha - \log \{1 + \{1 - e^{-\zeta t^\phi}\} \{e^\alpha - 1\}\}]}. \quad (7)$$

3. Statistical properties of the NEWE distribution

In this section, we explored various statistical properties of the NEWE distribution, including the expansion of the CDF and PDF, the quantile function, ordinary moments, and the moment generating function, Entropy measures, and order Statistics.

3.1. NEWE expansion

In this subsection, we present a series representation of the NEWE CDF. This is achieved by expanding the denominator of the CDF, as defined in Eq. (4), using a logarithmic series and exponential expansion

$$\left\{ \begin{array}{l} \log(1+x) = \sum_{d_1=1}^{\infty} (-1)^{d_1+1} \frac{x^{d_1}}{d_1}, \quad |x| < 1, \\ e^{-y} = \sum_{d_2=0}^{\infty} \frac{(-y)^{d_2}}{d_2!}, \quad 1 - e^{-y} = \sum_{d_2=1}^{\infty} \frac{y^{d_2}}{d_2!}, \quad y > 0 \\ (1-z)^n = \sum_{d_3=0}^{\infty} \binom{n}{d_3} (-1)^{d_3} z^{d_3}, \quad (1-z)^{-1} = \sum_{d_3=0}^{\infty} z^{d_3}, \quad |z| < 1 \end{array} \right. \quad (8)$$

Therefore, using Eq. (8) in the CDF (4)'s denominator yields

$$F|_T = \sum_{d_1=1}^{\infty} (-1)^{d_1+1} \{e^\alpha - 1\}^{d_1} \frac{\left(\sum_{d_2=1}^{\infty} \frac{\zeta^{d_2} t^{d_2 \phi}}{d_2!} \right)^{d_1}}{d_1}. \quad (9)$$

Therefore, using Eq. (8) in the PDF (5)'s denominator yields

$$f|_T = \frac{\phi}{\alpha} \sum_{d_3=0}^{\infty} \sum_{d_2=0}^{\infty} \binom{d_3}{d_2} (e^\alpha - 1)^{d_3+1} (-1)^{d_1+d_2+d_3} \frac{(1+d_2)^{d_1}}{d_1!} \zeta^{1+d_1} t^{\phi+d_1-1} \quad (10)$$

3.2. Quantile function

For random variable T has cdf of NEWE distribution, the quantile function $Q(p)$ is given by the relation

$$Q(p) = \inf \{ t \in R : F|_T \geq p \}$$

where $0 < p < 1$. This relation is used to find the quantile function of NEWE distribution as follows

$$Q(p) = \left[\frac{-1}{\zeta} \ln \left(1 - \frac{e^{\alpha p} - 1}{e^\alpha - 1} \right) \right]^{1/\phi}. \quad (11)$$

Because uniform random variables can be easily generated in most statistical software, the method described above is highly practical for generating NEWE random variates and can be easily implemented. Additionally, the quantile function in Eq. (11) can be used to calculate Bowley's skewness and Moors' kurtosis. Bowley's skewness, which is based on quartiles, is discussed in Kenney and Keeping (1962), and is given by

$$B_s = \frac{Q\left(\frac{3}{4}\right) - 2Q\left(\frac{2}{4}\right) + Q\left(\frac{1}{4}\right)}{Q\left(\frac{3}{4}\right) - Q\left(\frac{1}{4}\right)}$$

and the Moors' kurtosis, see Moors (1998), is given by

$$M_k = \frac{Q\left(\frac{7}{8}\right) - Q\left(\frac{5}{8}\right) + Q\left(\frac{3}{8}\right) - Q\left(\frac{1}{8}\right)}{Q\left(\frac{6}{8}\right) - Q\left(\frac{2}{8}\right)}$$

where $Q(\cdot)$ is the quantile function given by Eq. (11).

3.3. Moments

Moments play a crucial role in statistical analysis, especially in practical applications. They can be employed to examine key characteristics and properties of a distribution, such as dispersion, skewness, kurtosis, and central tendency. The r -th moment of the NEWE distribution, whose PDF is given in Eq. (8), can be determined as follows:

$$\mu'_r = \frac{\phi}{\alpha} \sum_{d_3=0}^{\infty} \sum_{d_2=0}^{\infty} \binom{d_3}{d_2} (e^\alpha - 1)^{d_3+1} (-1)^{d_1+d_2+d_3} \frac{(1+d_2)^{d_1}}{d_1!} \zeta^{1+d_1} \int_0^{\infty} t^{\phi+r+d_1-1} dt.$$

After simplification, the r^{th} moment of NEWE model is obtained as follows

$$\mu'_r = \frac{\phi}{\alpha} \sum_{d_3=0}^{\infty} \sum_{d_2=0}^{\infty} \times \sum_{d_1=0}^{\infty} \binom{d_3}{d_2} (e^{\alpha} - 1)^{d_3+1} (-1)^{d_1+d_2+d_3} \frac{(1+d_2)^{d_1}}{d_1} \frac{\zeta^{1+d_1}}{\phi + r + \phi d_1}.$$

The Bonferroni and Lorenz curves are significant examples of how the first incomplete moment can be applied. These curves have valuable

uses in fields such as economics, reliability analysis, and demographics.

3.4. Moment generating function

Moment generating functions (MGF) are valuable for various reasons, particularly in the analysis of sums of random variables. They offer an alternative approach to obtaining analytic results, compared to directly using the probability or cumulative distribution functions of the random variable. The MGF of T is given as follows

$$M_T(x) = \frac{\phi}{\alpha} \sum_{d_3=0}^{\infty} \sum_{d_2=0}^{\infty} \sum_{d_1=0}^{\infty} \binom{d_3}{d_2} (e^{\alpha} - 1)^{d_3+1} (-1)^{d_1+d_2+d_3} \frac{(1+d_2)^{d_1}}{d_1} \zeta^{1+d_1} \int_0^{\infty} e^{-xt} t^{\phi+\phi d_1-1} dt.$$

Table 2
Statistical properties of NEWE distribution with different values of parameters.

α	ζ	ϕ	Min	Mean	Var	CV	Max	Bs	Mk
0.5	0.4	0.35	0.0000	55.0799	48003.7539	3.9778	4111.5446	0.7748	3.2040
		1.2	0.0031	1.8067	2.5730	0.8878	11.3262	0.2299	1.2796
		2.05	0.0338	1.2877	0.4804	0.5383	4.1402	0.0931	1.2082
		2.9	0.0912	1.1584	0.2074	0.3931	2.7301	0.0348	1.2050
		3.75	0.1569	1.1044	0.1183	0.3114	2.1742	0.0025	1.2102
	1.2	0.35	0.0000	2.3867	90.1297	3.9778	178.1564	0.7748	3.2040
		1.2	0.0012	0.7232	0.4123	0.8878	4.5340	0.2298	1.2795
		2.05	0.0197	0.7535	0.1645	0.5383	2.4226	0.0932	1.2082
		2.9	0.0625	0.7931	0.0972	0.3931	1.8692	0.0347	1.2050
		3.75	0.1171	0.8240	0.0658	0.3114	1.6221	0.0027	1.2101
	2	0.35	0.0000	0.5545	4.8659	3.9778	41.3950	0.7749	3.2043
		1.2	0.0008	0.4725	0.1760	0.8878	2.9622	0.2299	1.2795
		2.05	0.0154	0.5873	0.0999	0.5383	1.8883	0.0932	1.2083
		2.9	0.0524	0.6650	0.0683	0.3931	1.5673	0.0348	1.2050
		3.75	0.1022	0.7190	0.0501	0.3114	1.4155	0.0027	1.2101
	2.8	0.35	0.0000	0.2120	0.7114	3.9777	15.8285	0.7753	3.2053
		1.2	0.0006	0.3570	0.1004	0.8878	2.2379	0.2299	1.2796
		2.05	0.0131	0.4984	0.0720	0.5383	1.6024	0.0931	1.2082
		2.9	0.0466	0.5922	0.0542	0.3931	1.3956	0.0347	1.2050
		3.75	0.0934	0.6573	0.0419	0.3114	1.2941	0.0026	1.2100
	3.6	0.35	0.0000	0.1034	0.1692	3.9776	7.7197	0.7738	3.2029
		1.2	0.0005	0.2895	0.0661	0.8878	1.8150	0.2298	1.2795
		2.05	0.0116	0.4409	0.0563	0.5383	1.4176	0.0932	1.2081
		2.9	0.0428	0.5430	0.0456	0.3931	1.2797	0.0347	1.2050
		3.75	0.0873	0.6147	0.0366	0.3114	1.2102	0.0027	1.2100
1.5	0.4	0.35	0.0000	37.3369	30595.8454	4.6848	3478.9716	0.8351	4.0313
		1.2	0.0019	1.4444	2.1264	1.0096	10.7876	0.2908	1.3415
		2.05	0.0255	1.1068	0.4449	0.6026	4.0238	0.1397	1.2205
		2.9	0.0747	1.0339	0.2040	0.4369	2.6756	0.0744	1.2023
		3.75	0.1344	1.0084	0.1208	0.3447	2.1406	0.0382	1.2010
	1.2	0.35	0.0000	1.6178	57.4454	4.6848	150.7465	0.8350	4.0314
		1.2	0.0008	0.5782	0.3408	1.0096	4.3184	0.2908	1.3415
		2.05	0.0149	0.6476	0.1523	0.6026	2.3545	0.1397	1.2204
		2.9	0.0511	0.7079	0.0956	0.4369	1.8319	0.0743	1.2025
		3.75	0.1002	0.7523	0.0672	0.3447	1.5970	0.0382	1.2010
	2	0.35	0.0000	0.3759	3.1013	4.6847	35.0263	0.8354	4.0314
		1.2	0.0005	0.3778	1.454	1.0096	2.8213	0.2907	1.3414
		2.05	0.0116	0.5048	0.0925	0.6026	1.8352	0.1397	1.2204
		2.9	0.0429	0.5935	0.0672	0.4369	1.5360	0.0745	1.2024
		3.75	0.0875	0.6565	0.0512	0.3447	1.3936	0.0381	1.2009
	2.8	0.35	0.0000	0.1437	0.4534	4.6846	13.3932	0.8345	4.0297
		1.2	0.0004	0.2854	0.0830	1.0096	2.1314	0.2908	1.3416
		2.05	0.0099	0.4284	0.0666	0.6026	1.5574	0.1398	1.2205
		2.9	0.0382	0.5285	0.0533	0.4369	1.3677	0.0743	1.2022
		3.75	0.0800	0.6001	0.0428	0.3447	1.2740	0.0381	1.2010
	3.6	0.35	0.0000	0.0701	0.1079	4.6843	6.5320	0.8312	4.0238
		1.2	0.0003	0.2315	0.0546	1.0096	1.7287	0.2909	1.3415
		2.05	0.0087	0.3790	0.0522	0.6026	1.3777	0.1397	1.2206
		2.9	0.0350	0.4846	0.0448	0.4369	1.2542	0.0743	1.2023
		3.75	0.0748	0.5612	0.0374	0.3447	1.1914	0.0381	1.2010

After simplification, the MGF of NEWWE model is obtained as follows

$$M_T(x) = \frac{\phi}{\alpha} \sum_{d_3=0}^{\infty} \sum_{d_2=0}^{\infty} \times \sum_{d_1=0}^{\infty} \binom{d_3}{d_2} (e^{\alpha} - 1)^{d_3+1} (-1)^{d_1+d_2+d_3} \frac{(1+d_2)^{d_1}}{d_1} \zeta^{1+d_1} \frac{\Gamma(\phi+\phi d_1)}{x^{\phi+\phi d_1}}.$$

Table 2 presents the statistical properties of the NEWWE distribution with varying parameters (α , ζ , and ϕ). The properties include minimum, maximum, mean, variance (Var), coefficient of variation (CV), skewness

$$f_{X_{(r)}}(x) = \phi \zeta \sum_{d=0}^{n-r} \sum_{d_3, d_2=0}^{\infty} \sum_{d_1=1}^{\infty} (-1)^{d_1+d_2+d_3+1} (e^{\alpha} - 1)^{d_1+d_3+1} \frac{r+d-1}{d_1 \alpha^{r+d}} \binom{d_1+d_3}{d_2} t^{\phi-1} e^{-\zeta t^{\phi}(1+d_2)}$$

(Bs), and kurtosis (Mk). The table highlights how the distribution's characteristics change with different parameter values, which provides insight into how the distribution's shape, spread, and tendencies vary. Such a detailed breakdown helps understand the impact of each parameter on the distribution's behavior in statistical modeling.

The results indicate that varying the parameters (α , ζ , and ϕ) significantly affects the statistical properties of the NEWWE distribution. As these parameters change, there is a noticeable variation in the mean, variance, skewness, and kurtosis values, suggesting that they influence the distribution's spread and shape. Higher values of α and ϕ seem to increase the distribution's central tendency and variability, while ζ affects the tail behavior. This flexibility makes the NEWWE distribution a suitable model for various statistical applications.

3.5. Entropy measures

The entropy of a random variable with probability density (12) is a measure of the uncertainty's fluctuation. A high entropy number suggests that the data is more unpredictable. The Rényi entropy, presented by Rényi (1960), is defined by

$$\Lambda(\vartheta) = (1 - \vartheta)^{-1} \log \left(\int_0^{\infty} (f|_T)^{\vartheta} dx \right), \vartheta \neq 1, \vartheta > 0.$$

To obtain $\Lambda(\vartheta)$ of the NEWWE distribution, we must obtain $(f|_T)^{\vartheta}$ by using the same expansions as given in (10), then

$$(f|_T)^{\vartheta} = \left(\frac{\phi}{\alpha} \sum_{d_3=0}^{\infty} \sum_{d_2=0}^{\infty} \sum_{d_1=0}^{\infty} \binom{d_3}{d_2} (e^{\alpha} - 1)^{d_3+1} (-1)^{d_1+d_2+d_3} \frac{(1+d_2)^{d_1}}{d_1} \zeta^{1+d_1} t^{\phi+\phi d_1-1} \right)^{\vartheta}$$

By using numerical analysis, you can solve this function.

3.6. Order statistics

Suppose $T_{(1)}, T_{(2)}, \dots, T_{(n)}$ be an ordered random sample of size n drawn from NEWWE distribution with CDF and PDF given by (4) and (5), respectively. The PDF of $T_{(r)}$ is given by:

$$f_{T_{(r)}}(t) = \sum_{d=0}^{n-r} \frac{(-1)^d}{B(r, n-r+1)} \binom{n-r}{d} [F|_T]^{r+d-1} f|_T.$$

Using Eq. (8), we get the PDF of r^{th} order statistic of the NEWWE distribution as follows:

The density function of the NEWWE order statistics can be written as a linear combination of the EXP-G density function with power parameter ϕ . For $r=1$, and $r=n$, the smallest order statistics $X_{(1)}$ and the largest order statistics $X_{(n)}$ of the NEWWE distribution are produced.

4. Classical parameter estimation

Determining the best method for estimating model parameters has historically been a challenging task for clinical practitioners and oncologists in the field of cancer research. To address this, the study's authors have utilized seven renowned classical estimation techniques. These methods, which include Maximum Likelihood (ML, designated as I_{ML}), Anderson-Darling (AD, designated as

II_{AD}), Cramer-von-Mises (CVM, designated as III_{CVM}), Maximum Product Spacing (MPS, designated as IV_{MPS}), Least Squares (LS, designated as V_{LS}), Right-Truncated Anderson-Darling (RTAD, designated as VI_{RTAD}), and Weighted Least Squares (WLS, designated as VII_{WLS}), are crucial in enhancing oncological studies. Each approach offers distinct advantages, significantly enriching the analysis and interpretation of cancer patient data with a more detailed and comprehensive understanding. By integrating these methodologies, researchers can better understand cancer behaviors and treatment responses, facilitating the development of more effective therapeutic strategies.

4.1. First maximum likelihood

The ML estimation technique is invaluable in cancer studies for its precision in parameter estimation within statistical models. It enhances the accuracy of predictions regarding treatment outcomes and survival rates, providing oncologists with reliable data to inform patient-specific therapeutic decisions and advancing personalized medicine in oncology.

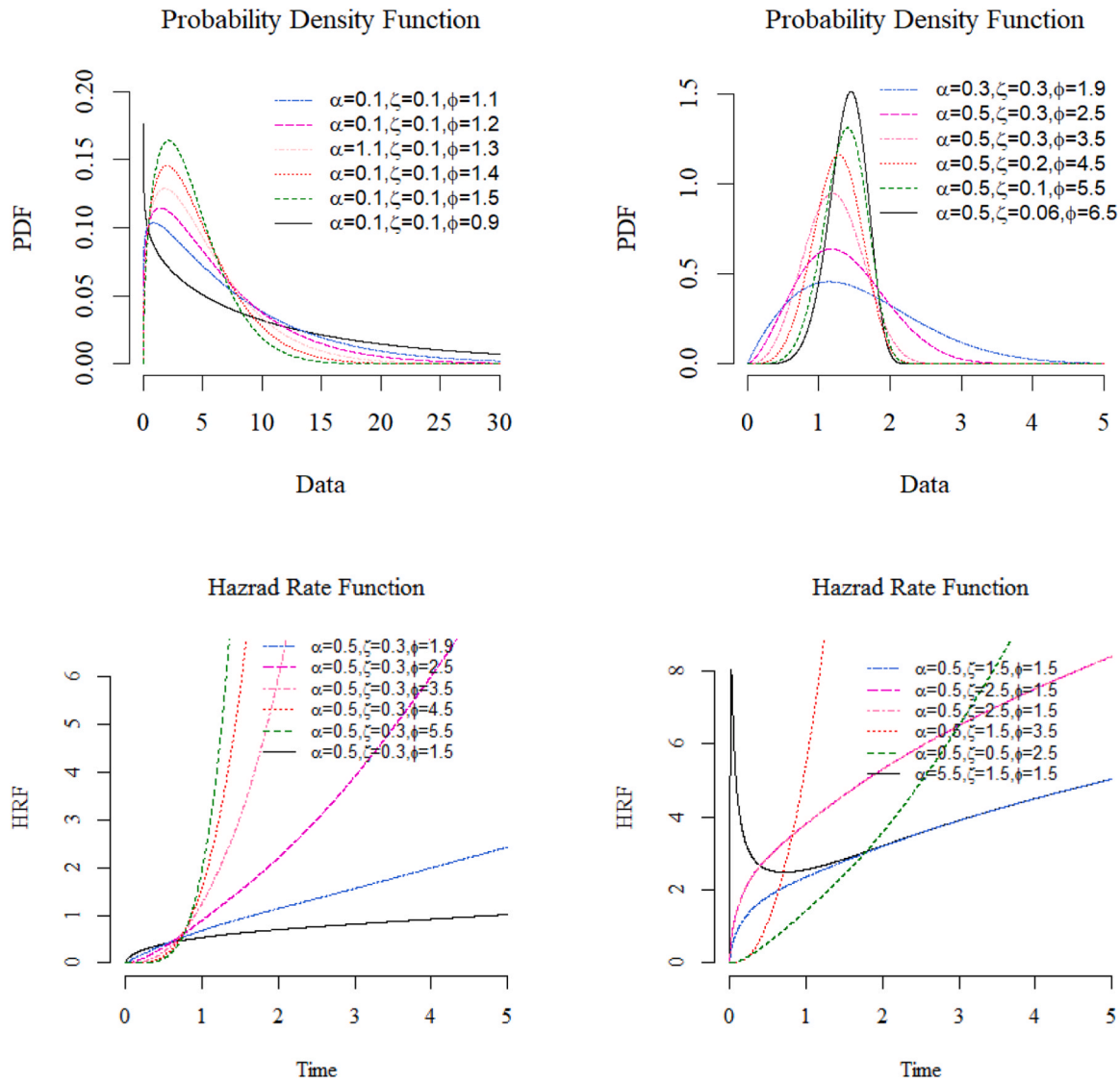


Fig. 3. Plots of the NEWWE model's PDF and HRF for various parameter combinations.

If $T_v \sim \text{NEWWE}(t_v; \zeta, \phi, \alpha)$, with $\zeta, \phi, \alpha > 0$, then the estimates $\hat{\zeta}, \hat{\phi}, \hat{\alpha}$ of the NEWWE model are derived through the minimization of the log-likelihood function symbolized by L_{IT} . The procedure is outlined as follows:

$$L_{IT} = \left[\begin{aligned} & n \log \zeta - n \log \alpha + n \log(e^\alpha - 1) + n \log \phi + (\phi - 1) \sum_{v=1}^n \log t_v - \\ & \zeta \sum_{v=1}^n t_v^\phi - \sum_{v=1}^n \log \left[1 + \{1 - e^{-\zeta t_v^\phi}\} \{e^\alpha - 1\} \right] \end{aligned} \right].$$

The mathematical expression for the partial derivatives of L_{IT} with respect to ζ, ϕ , and α are presented in detail below.

$$\frac{\partial L_{IT}}{\partial \zeta} = \frac{n}{\zeta} - \sum_{v=1}^n t_v^\phi + \sum_{v=1}^n \left[\frac{t_v^\phi \{e^\alpha - 1\} e^{-\zeta t_v^\phi}}{[1 + \{1 - e^{-\zeta t_v^\phi}\} \{e^\alpha - 1\}]} \right],$$

$$\frac{\partial L_{IT}}{\partial \phi} = \frac{n}{\phi} + \sum_{v=1}^n \log t_v - \zeta \sum_{v=1}^n t_v^\phi \log t_v - \sum_{v=1}^n \left[\frac{\zeta \{e^\alpha - 1\} t_v^\phi e^{-\zeta t_v^\phi} \log t_v}{[1 + \{1 - e^{-\zeta t_v^\phi}\} \{e^\alpha - 1\}]} \right],$$

$$\frac{\partial L_{IT}}{\partial \alpha} = -\frac{n}{\alpha} + \frac{ne^\alpha}{(e^\alpha - 1)} - \sum_{v=1}^n \left[\frac{e^\alpha \{1 - e^{-\zeta t_v^\phi}\}}{[1 + \{1 - e^{-\zeta t_v^\phi}\} \{e^\alpha - 1\}]} \right].$$

Fig. 3 presents the PDF and HRF plots of the NEWWE model for lung and AML cancer patients, providing vital information for individuals battling these conditions. The ability to interpret these plots is essential for understanding the overall survival outlook and the risk dynamics over time. The PDF offers a statistical expectation of survival times, informing the prognosis and aiding in treatment planning. Meanwhile, the HRF reveals the risk trajectory, enabling patients and clinicians to pinpoint periods of higher or lower risk throughout the disease's progression. These insights participate in making informed decisions about treatment strategies, monitoring schedules, and supportive care needs, with the goal of improving quality of life and potentially extending survival.

4.2. Second anderson-darling

The AD test is a robust statistical tool employed within cancer research to determine how well data aligns with specific distributions. By analyzing distributions of patient survival times or tumor sizes against theoretical models, oncologists and researchers can ascertain the suitability of various models, such as the Weibull or exponential, for cancer data analysis. The test's ability to detect differences in the tails of distributions is especially valuable for uncovering subtle variations in survival patterns, thereby facilitating the formation of precise

prognostic models and customized treatment plans.

If $Tv \sim \text{NEWWE}(t_v; \zeta, \phi, \alpha)$, where $\zeta, \phi, \alpha > 0$, then the estimates $\hat{\zeta}, \hat{\phi}, \hat{\alpha}$ of the NEWWE model are obtained by minimizing the following mathematical expression:

$$II_{AD} = -n - \frac{1}{n} - \sum_{v=1}^n [2v-1] [\log F_{v:nT} - \log(1 - F_{v:nT})].$$

4.3. Third Cramer-von-Mises

The CVM criterion stands as a robust statistical tool within cancer research, emphasizing the GoF for empirical data against theoretical models. By integrating the squared differences between the observed and expected CDFs, the CVM approach accurately quantifies the correspondence of survival data or treatment responses with specified distributions. This method is invaluable in the careful examination of cancer patient data, including survival rates and treatment outcomes, offering a comprehensive measure of fit those aids in the validation and refinement of predictive models. Through its application, researchers can better understand the effectiveness of treatments across different cancer types, driving forward the development of more tailored and effective intervention strategies.

If $Tv \sim \text{NEWWE}(t_v; \zeta, \phi, \alpha)$, where $\zeta, \phi, \alpha > 0$, then the estimates $\hat{\zeta}, \hat{\phi}, \hat{\alpha}$ of the NEWWE model are obtained by minimizing the following mathematical expression:

$$III_{CVM} = \frac{1}{12n} + \sum_{v=1}^n \left[\log F_{v:nT} - \frac{2v-1}{2n} \right] \Xi_m|_T = 0; m = 1, 2, 3.$$

4.4. Fourth maximum product spacing

The MPS approach is a sophisticated statistical method increasingly applied in cancer research for estimating distribution parameters. In the realm of cancer, especially for complex diseases such as lung cancer and AML, MPS can significantly enhance the precision of model estimates. This method aids in uncovering the complicated dynamics of cancer progression and treatment efficacy, facilitating the design of more personalized and effective therapeutic strategies.

If $Tv \sim \text{NEWWE}(t_v; \zeta, \phi, \alpha)$, where $\zeta, \phi, \alpha > 0$, then the estimates $\hat{\zeta}, \hat{\phi}, \hat{\alpha}$ of the NEWWE model are obtained by maximizing the following mathematical expression:

$$IV_{MPS} = \frac{1}{n+1} \sum_{v=1}^{n+1} [\log F_{v:nT} - F_{v-1:nT}].$$

4.5. Fifth least squares

The LS method is a foundational statistical tool in cancer research, used extensively for fitting models to observational data. In cancer studies, LS is particularly useful for analyzing the relationship between treatment effects and patient outcomes, including survival rates and response to therapy. This method provides a straightforward yet powerful way to identify patterns and make predictions, supporting the development of effective cancer treatments and improving prognostic assessments.

If $Tv \sim \text{NEWWE}(t_v; \zeta, \phi, \alpha)$, where $\zeta, \phi, \alpha > 0$, then the estimates $\hat{\zeta}, \hat{\phi}, \hat{\alpha}$ of the NEWWE model are obtained by minimizing the following mathematical expression:

$$V_{LS} = \sum_{v=1}^n \left[F_{v:nT} - \frac{v}{n+1} \right] \Xi_m|_T = 0; m = 1, 2, 3.$$

4.6. Sixth right-truncated anderson-darling

The RTAD method plays a crucial role in cancer research by

providing an accurate evaluation of survival distributions, particularly when dealing with right-censored data, a common scenario in survival studies. This technique fine-tunes the analysis of patient survival times, enabling researchers to account for individuals whose outcomes are not observed within the study period. By improving the precision of statistical models, RTAD ensures that survival patterns and associated risk factors are correctly captured across distinct types of cancer, aiding in the identification and development of effective treatment approaches.

If $Tv \sim \text{NEWWE}(t_v; \zeta, \phi, \alpha)$, where $\zeta, \phi, \alpha > 0$, then the estimates $\hat{\zeta}, \hat{\phi}, \hat{\alpha}$ of the NEWWE model are obtained by minimizing the following mathematical expression:

$$VI_{RTAD} = \frac{n}{2} - 2 \sum_{v=1}^n F_{v:nT} - \frac{1}{n} \sum_{v=1}^n [(2v-1) \log F_{n+1-jT}].$$

4.7. Seventh weighted least square

The WLS method is highly valuable in cancer research for its ability to refine the accuracy of statistical models by assigning different weights to data points based on their variance. This approach is particularly effective in addressing heteroscedasticity, where the variability in data points differs across the spectrum of measurements. In the context of cancer studies, WLS enhances the precision of analyses related to survival rates, treatment responses, and risk factors, ensuring that models are robust and reflective of the true dynamics observed in patient data. By leveraging WLS, researchers can derive more reliable insights, leading to the advancement of personalized medicine and the optimization of therapeutic strategies for cancer patients.

If $Tv \sim \text{NEWWE}(t_v; \zeta, \phi, \alpha)$, where $\zeta, \phi, \alpha > 0$, then the estimates $\hat{\zeta}, \hat{\phi}, \hat{\alpha}$ of the NEWWE model are obtained by minimizing the following mathematical expression:

$$VII_{WLS} = \frac{(n+1)(n+1)^2}{v(n-v+1)} \sum_{v=1}^n \left[F_{v:nT} - \frac{v}{n+1} \right] \Xi_m|_T = 0; m = 1, 2, 3.$$

Note that, $\Xi_1|_T = \frac{\partial}{\partial \zeta} \left[\frac{\log \left[1 + \frac{1 - e^{-\zeta \phi}}{\alpha} \right] \{e^\alpha - 1\}}{\alpha} \right]$, $\Xi_2|_T = \frac{\partial}{\partial \phi} \left[\frac{\log \left[1 + \frac{1 - e^{-\zeta \phi}}{\alpha} \right] \{e^\alpha - 1\}}{\alpha} \right]$, $\Xi_3|_T = \frac{\partial}{\partial \alpha} \left[\frac{\log \left[1 + \frac{1 - e^{-\zeta \phi}}{\alpha} \right] \{e^\alpha - 1\}}{\alpha} \right]$. The analytical expressions can be solved numerically, allowing for precise optimization of model parameters, crucial for data analysis in fields like epidemiology.

5. Simulation study

In this study, seven classical estimation techniques are employed, each demonstrating the property of consistency across various sample sizes ranging from 20 to 250. Their performance is rigorously assessed through extensive Monte Carlo simulation studies, utilizing standard metrics such as absolute bias $|AB|$, mean square error (MSE), and mean relative error (MRE). These simulations, conducted $N=1000$ times for each sample size and analyzed using the R software with the nlminb package, revealed a notable trend: as the sample size increased, the $|AB|$, MSE(s), and MRE(s) consistently decreased for all estimation techniques.

$$\begin{aligned} |AB|_{\hat{\phi}} &= \frac{1}{N} \sum_{q=1}^N (\hat{\phi}_q - \phi), \text{MSE}_{\hat{\phi}} = \frac{1}{N} \sum_{q=1}^N (\hat{\phi}_q - \phi)^2, \text{MRE}_{\hat{\phi}} \\ &= \frac{1}{N} \sum_{q=1}^N |\hat{\phi}_q - \phi| / \phi, \end{aligned}$$

where $\hat{\Phi} = (\hat{\zeta}, \hat{\phi}, \hat{\alpha})^T$. This pattern highlights the reliability and effectiveness of these methods in statistical analysis, supporting their value in

Table 3Classical estimates for ($\alpha = 2.50, \zeta = 1.50, \phi = 1.50$).

SS	Stat	Est	I_{ML}	II_{AD}	III_{CVM}	IV_{MPS}	V_{LS}	VI_{RTAD}	VII_{WLS}
20	AB	$\hat{\alpha}$	0.87870	1.20290	0.90800	0.65330	1.20630	0.76440	0.94690
		$\hat{\zeta}$	1.56880	0.59460	0.85450	0.79500	0.89640	0.44810	0.85570
		$\hat{\phi}$	0.87060	0.58930	0.73180	0.71140	0.70060	0.52090	0.77540
	MSE	$\hat{\alpha}$	1.70380	3.29920	1.89080	1.41480	2.79570	1.20190	2.15570
		$\hat{\zeta}$	5.10520	0.70420	1.22860	1.07910	1.33650	0.53290	1.32090
		$\hat{\phi}$	1.23900	0.45450	0.70970	0.70390	0.67150	0.36640	0.90020
	MRE	$\hat{\alpha}$	0.87000	1.19090	0.89900	0.64680	1.19430	0.75680	0.93750
		$\hat{\zeta}$	0.31310	0.11870	0.17060	0.15870	0.17890	0.08940	0.17080
		$\hat{\phi}$	0.25230	0.17080	0.21210	0.20620	0.20310	0.15100	0.22480
40	AB	$\hat{\alpha}$	0.91040	1.05180	0.64840	0.37790	0.85320	0.46900	1.04610
		$\hat{\zeta}$	0.76250	0.42880	0.49180	0.75690	0.73460	0.50450	0.52860
		$\hat{\phi}$	0.53920	0.46710	0.50730	0.54580	0.58960	0.58470	0.52940
	MSE	$\hat{\alpha}$	1.93440	2.56960	0.91820	0.32860	1.69630	0.42160	2.62030
		$\hat{\zeta}$	2.17340	0.38110	0.48430	0.94100	0.90140	0.52130	0.57230
		$\hat{\phi}$	0.68780	0.26710	0.35340	0.38230	0.49350	0.44360	0.39560
	MRE	$\hat{\alpha}$	0.90140	1.04130	0.64200	0.37420	0.84480	0.46430	1.03570
		$\hat{\zeta}$	0.15220	0.08560	0.09820	0.15110	0.14660	0.10070	0.10550
		$\hat{\phi}$	0.15630	0.13540	0.14700	0.15820	0.17090	0.16950	0.15350
80	AB	$\hat{\alpha}$	0.70040	0.87560	0.64470	0.38950	0.67560	0.41280	0.62610
		$\hat{\zeta}$	0.27470	0.41850	0.35760	0.53250	0.55760	0.31390	0.45480
		$\hat{\phi}$	0.53920	0.46710	0.50730	0.54580	0.58960	0.58470	0.52940
	MSE	$\hat{\alpha}$	1.58940	2.15400	1.08000	0.43890	1.16930	0.29040	0.85870
		$\hat{\zeta}$	0.20490	0.33010	0.30760	0.46880	0.51850	0.21030	0.35110
		$\hat{\phi}$	0.68780	0.26710	0.35340	0.38230	0.49350	0.44360	0.39560
	MRE	$\hat{\alpha}$	0.69350	0.86690	0.63830	0.38570	0.66890	0.40870	0.61990
		$\hat{\zeta}$	0.15220	0.08560	0.09820	0.15110	0.14660	0.10070	0.10550
		$\hat{\phi}$	0.08220	0.11480	0.10600	0.12090	0.13640	0.09520	0.11600
100	AB	$\hat{\alpha}$	0.69090	0.62830	0.49730	0.45070	0.55640	0.41040	0.78830
		$\hat{\zeta}$	0.65300	0.45530	0.52800	0.43370	0.36920	0.32240	0.38770
		$\hat{\phi}$	0.49230	0.39080	0.40180	0.35860	0.36090	0.32440	0.35600
	MSE	$\hat{\alpha}$	0.99400	1.01050	0.53910	0.66040	0.69040	0.25510	1.54980
		$\hat{\zeta}$	1.83830	0.32360	0.46580	0.33920	0.32510	0.22630	0.27180
		$\hat{\phi}$	0.62810	0.21290	0.25000	0.18380	0.23300	0.15580	0.17980
	MRE	$\hat{\alpha}$	0.68400	0.62210	0.49240	0.44620	0.55080	0.40640	0.78050
		$\hat{\zeta}$	0.13030	0.09090	0.10540	0.08660	0.07370	0.06430	0.07740
		$\hat{\phi}$	0.14270	0.11330	0.11650	0.10390	0.10460	0.09400	0.10320
150	AB	$\hat{\alpha}$	0.53330	0.60870	0.55460	0.34490	0.53510	0.39380	0.71060
		$\hat{\zeta}$	0.25660	0.34020	0.36260	0.35650	0.34510	0.31650	0.36100
		$\hat{\phi}$	0.25200	0.33180	0.29100	0.33620	0.30820	0.33400	0.34100
	MSE	$\hat{\alpha}$	0.92100	1.03690	0.79180	0.23080	0.86050	0.20480	1.47870
		$\hat{\zeta}$	0.13200	0.24230	0.28400	0.23470	0.25130	0.23740	0.25740
		$\hat{\phi}$	0.62810	0.21290	0.25000	0.18380	0.23300	0.15580	0.17980
	MRE	$\hat{\alpha}$	0.52800	0.60270	0.54910	0.34140	0.52980	0.38990	0.70360
		$\hat{\zeta}$	0.13030	0.09090	0.10540	0.08660	0.07370	0.06430	0.07740
		$\hat{\phi}$	0.07300	0.09620	0.08430	0.09740	0.08930	0.09680	0.09880
200	AB	$\hat{\alpha}$	0.52140	0.44490	0.94950	0.18840	0.46370	0.52800	0.50180
		$\hat{\zeta}$	0.19000	0.26800	0.35850	0.35410	0.34350	0.24580	0.25840
		$\hat{\phi}$	0.24230	0.27750	0.32800	0.23920	0.30340	0.26150	0.22360
	MSE	$\hat{\alpha}$	0.62690	0.53320	2.17560	0.05910	0.71280	0.50570	0.69430
		$\hat{\zeta}$	0.11230	0.14560	0.21110	0.21480	0.24850	0.16540	0.14220
		$\hat{\phi}$	0.09210	0.11610	0.13860	0.08690	0.13990	0.10480	0.07190
	MRE	$\hat{\alpha}$	0.51620	0.44050	0.94010	0.18650	0.45910	0.52280	0.49690
		$\hat{\zeta}$	0.13030	0.09090	0.10540	0.08660	0.07370	0.06430	0.07740
		$\hat{\phi}$	0.07020	0.08040	0.09510	0.06930	0.08790	0.07580	0.06480
250	AB	$\hat{\alpha}$	0.36280	0.44110	0.48470	0.15510	0.62300	0.36270	0.48360
		$\hat{\zeta}$	0.12320	0.25400	0.24050	0.18510	0.21140	0.14530	0.17130
		$\hat{\phi}$	0.13940	0.23420	0.22500	0.15070	0.20050	0.19440	0.17950
	MSE	$\hat{\alpha}$	0.30390	0.46200	0.68140	0.04800	0.91050	0.24190	0.62130
		$\hat{\zeta}$	0.03790	0.11310	0.11060	0.07360	0.09280	0.05040	0.07640
		$\hat{\phi}$	0.03070	0.08660	0.07690	0.04640	0.06110	0.05470	0.05020
	MRE	$\hat{\alpha}$	0.35920	0.43670	0.47990	0.15360	0.61680	0.35910	0.47880
		$\hat{\zeta}$	0.02460	0.05070	0.04800	0.03700	0.04220	0.02900	0.03420
		$\hat{\phi}$	0.04040	0.06790	0.06520	0.04370	0.05810	0.05630	0.05200

Table 4Classical estimates for ($\alpha = 2.10$, $\zeta = 2.50$, $\phi = 3.50$).

SS	Est	Par	I_{ML}	II_{AD}	III_{CVM}	IV_{MPS}	V_{LS}	VI_{RTAD}	VII_{WLS}
20	AB	$\hat{\alpha}$	2.14950	1.77000	1.70440	1.72250	1.89350	1.73100	1.73260
		$\hat{\zeta}$	1.22860	1.00150	1.40380	0.88670	0.85750	0.89690	1.16610
		$\hat{\phi}$	1.01370	0.90890	0.78640	0.81260	1.01070	0.83240	0.91890
	MSE	$\hat{\alpha}$	5.31390	3.72330	3.57830	3.78150	4.01830	3.77820	3.61950
		$\hat{\zeta}$	2.18990	1.56920	2.72780	1.16530	1.25510	1.30500	2.17390
		$\hat{\phi}$	1.23920	1.07620	0.90410	0.90210	1.26710	0.89060	1.10810
	MRE	$\hat{\alpha}$	1.02360	0.84290	0.81160	0.82030	0.90170	0.82430	0.82500
		$\hat{\zeta}$	0.49140	0.40060	0.56150	0.35470	0.34300	0.35880	0.46640
		$\hat{\phi}$	0.28960	0.25970	0.22470	0.23220	0.28880	0.23780	0.26250
	AB	$\hat{\alpha}$	1.66950	1.64710	1.81180	1.47260	1.90610	1.82610	1.79930
		$\hat{\zeta}$	0.96720	0.87180	0.83260	0.79090	0.90100	0.86400	0.74640
		$\hat{\phi}$	0.82370	0.76710	0.83810	0.74240	0.89090	0.81700	0.81720
40	AB	$\hat{\alpha}$	3.58380	3.51960	3.90710	3.13290	4.23680	3.96310	3.96580
		$\hat{\zeta}$	1.37830	1.14870	1.16740	0.93880	1.31380	1.00610	0.92590
		$\hat{\phi}$	0.98680	0.81970	0.93710	0.78000	0.98530	0.80840	0.85940
	MSE	$\hat{\alpha}$	0.79500	0.78430	0.86280	0.70130	0.90770	0.86960	0.85680
		$\hat{\zeta}$	0.38690	0.34870	0.33300	0.31640	0.36040	0.34560	0.29860
		$\hat{\phi}$	0.23530	0.21920	0.23950	0.21210	0.25450	0.23340	0.23350
	MRE	$\hat{\alpha}$	1.31910	1.78470	1.51820	1.58570	1.56130	1.50170	1.81850
		$\hat{\zeta}$	0.64320	0.72620	0.71930	0.62260	0.64070	0.57580	0.78360
		$\hat{\phi}$	0.82370	0.76710	0.83810	0.74240	0.89090	0.81700	0.81720
	AB	$\hat{\alpha}$	2.33620	3.62920	3.04830	3.56720	3.15880	3.13690	4.06880
		$\hat{\zeta}$	0.63070	0.73190	0.80750	0.56330	0.63040	0.51140	0.83090
		$\hat{\phi}$	0.98680	0.81970	0.93710	0.78000	0.98530	0.80840	0.85940
80	AB	$\hat{\alpha}$	0.62810	0.84990	0.72290	0.75510	0.74350	0.71510	0.86600
		$\hat{\zeta}$	0.38690	0.34870	0.33300	0.31640	0.36040	0.34560	0.29860
		$\hat{\phi}$	0.16370	0.20790	0.17930	0.21240	0.22850	0.18360	0.23060
	MSE	$\hat{\alpha}$	1.54080	1.26030	1.65490	1.07460	1.82580	1.40200	1.63260
		$\hat{\zeta}$	0.68120	0.58160	0.72870	0.51570	0.81900	0.68740	0.62700
		$\hat{\phi}$	0.70480	0.52730	0.76350	0.55180	0.71960	0.59690	0.72420
	MRE	$\hat{\alpha}$	3.10400	2.28550	3.38630	2.14640	3.81160	2.77240	3.25120
		$\hat{\zeta}$	0.62960	0.49170	0.79570	0.40520	0.83410	0.75790	0.55270
		$\hat{\phi}$	0.69840	0.40380	0.79810	0.49040	0.71870	0.50290	0.71810
	AB	$\hat{\alpha}$	0.73370	0.60020	0.78810	0.51170	0.86940	0.66760	0.77740
		$\hat{\zeta}$	0.27250	0.23260	0.29150	0.20630	0.32760	0.27500	0.25080
		$\hat{\phi}$	0.20140	0.15070	0.21810	0.15770	0.20560	0.17050	0.20690
150	AB	$\hat{\alpha}$	1.30800	1.39370	1.49240	1.02120	1.50830	1.67000	1.32320
		$\hat{\zeta}$	0.56320	0.55900	0.68170	0.48940	0.53830	0.65410	0.57310
		$\hat{\phi}$	0.53270	0.63050	0.63610	0.53830	0.68170	0.68960	0.59420
	MSE	$\hat{\alpha}$	2.37310	2.51850	2.69300	2.05560	2.88340	3.43510	2.33130
		$\hat{\zeta}$	0.48320	0.47090	0.67730	0.35470	0.40240	0.57940	0.55350
		$\hat{\phi}$	0.69840	0.40380	0.79810	0.49040	0.71870	0.50290	0.71810
	MRE	$\hat{\alpha}$	0.62280	0.66370	0.71070	0.48630	0.71820	0.79520	0.63010
		$\hat{\zeta}$	0.27250	0.23260	0.29150	0.20630	0.32760	0.27500	0.25080
		$\hat{\phi}$	0.15220	0.18010	0.18180	0.15380	0.19480	0.19700	0.16980
	AB	$\hat{\alpha}$	1.22350	1.21030	1.48790	0.61310	1.30770	1.57990	1.20960
		$\hat{\zeta}$	0.51660	0.52920	0.51270	0.41400	0.53740	0.59200	0.48170
		$\hat{\phi}$	0.53690	0.48200	0.69490	0.33140	0.60040	0.68450	0.52930
200	AB	$\hat{\alpha}$	2.04290	2.15870	2.98640	1.20440	2.34400	3.27370	2.04310
		$\hat{\zeta}$	0.38810	0.43730	0.42760	0.32850	0.48360	0.49020	0.34110
		$\hat{\phi}$	0.42410	0.39310	0.69120	0.24040	0.50560	0.68060	0.43470
	MSE	$\hat{\alpha}$	0.58260	0.57630	0.70850	0.29200	0.62270	0.75230	0.57600
		$\hat{\zeta}$	0.27250	0.23260	0.29150	0.20630	0.32760	0.27500	0.25080
		$\hat{\phi}$	0.15340	0.13770	0.19850	0.09470	0.17160	0.19560	0.15120
	MRE	$\hat{\alpha}$	1.01480	0.95770	1.34980	0.54670	1.33880	1.44610	1.10650
		$\hat{\zeta}$	0.42880	0.42840	0.50650	0.36910	0.54920	0.51110	0.43070
		$\hat{\phi}$	0.45020	0.39780	0.59820	0.31650	0.58190	0.63460	0.51920
	AB	$\hat{\alpha}$	1.54720	1.37800	2.41710	0.86440	2.40530	2.79290	1.77770
		$\hat{\zeta}$	0.28690	0.30990	0.38590	0.24400	0.48530	0.37240	0.30310
		$\hat{\phi}$	0.32120	0.27040	0.47320	0.18120	0.44650	0.60730	0.39630
250	AB	$\hat{\alpha}$	0.48320	0.45600	0.64280	0.26030	0.63750	0.68860	0.52690
		$\hat{\zeta}$	0.17150	0.17130	0.20260	0.14760	0.21970	0.20450	0.17230
		$\hat{\phi}$	0.12860	0.11370	0.17090	0.09040	0.16630	0.18130	0.14830

Table 5
Classical estimates for ($\alpha = 1.70, \zeta = 1.50, \phi = 2.25$).

SS	Est	Par	I_{ML}	II_{AD}	III_{CVM}	IV_{MPS}	V_{LS}	VI_{RTAD}	VII_{WLS}
20	AB	$\hat{\alpha}$	2.29890	1.77460	1.72660	1.84110	1.89200	1.55540	2.10250
		$\hat{\zeta}$	0.66090	0.61370	0.75750	0.58760	0.69760	0.72210	0.62310
		$\hat{\phi}$	0.82960	0.51250	0.56780	0.63200	0.71280	0.60950	0.69540
	MSE	$\hat{\alpha}$	6.36290	4.05150	4.07520	4.33080	4.77020	3.40210	5.32270
		$\hat{\zeta}$	0.65010	0.60600	1.18400	0.53080	0.78610	0.97630	0.58200
		$\hat{\phi}$	1.03040	0.45340	0.46500	0.53300	0.85410	0.65440	0.82440
	MRE	$\hat{\alpha}$	1.35230	1.04390	1.01560	1.08300	1.11300	0.91490	1.23680
		$\hat{\zeta}$	0.44060	0.40910	0.50500	0.39170	0.46510	0.48140	0.41540
		$\hat{\phi}$	0.36870	0.22780	0.25230	0.28090	0.31680	0.27090	0.30910
40	AB	$\hat{\alpha}$	1.79430	1.75370	2.05120	1.25320	1.95830	1.90060	1.51640
		$\hat{\zeta}$	0.60300	0.59530	0.64390	0.42650	0.57980	0.58680	0.50770
		$\hat{\phi}$	0.59690	0.57580	0.71340	0.43840	0.59190	0.63860	0.43540
	MSE	$\hat{\alpha}$	4.23670	3.92940	5.49620	2.27200	4.80120	4.67020	2.93650
		$\hat{\zeta}$	0.49210	0.51710	0.60670	0.26290	0.46300	0.45370	0.41730
		$\hat{\phi}$	0.55410	0.55600	0.73630	0.28220	0.54200	0.64950	0.31090
	MRE	$\hat{\alpha}$	1.05540	1.03160	1.20660	0.73720	1.15200	1.11800	0.89200
		$\hat{\zeta}$	0.40200	0.39680	0.42920	0.28430	0.38660	0.39120	0.33850
		$\hat{\phi}$	0.26530	0.25590	0.31710	0.19480	0.26300	0.28380	0.19350
80	AB	$\hat{\alpha}$	1.79930	1.72180	2.07560	1.03470	1.73550	1.58140	1.25450
		$\hat{\zeta}$	0.47900	0.51270	0.53370	0.38530	0.53140	0.56130	0.47360
		$\hat{\phi}$	0.59690	0.57580	0.71340	0.43840	0.59190	0.63860	0.43540
	MSE	$\hat{\alpha}$	4.37170	3.94990	5.15920	2.28000	3.81080	3.44140	2.45780
		$\hat{\zeta}$	0.27990	0.34420	0.37700	0.22940	0.39500	0.41830	0.35520
		$\hat{\phi}$	0.55410	0.55600	0.73630	0.28220	0.54200	0.64950	0.31090
	MRE	$\hat{\alpha}$	1.05840	1.01280	1.22100	0.60860	1.02090	0.93020	0.73790
		$\hat{\zeta}$	0.40200	0.39680	0.42920	0.28430	0.38660	0.39120	0.33850
		$\hat{\phi}$	0.24810	0.23220	0.28690	0.15350	0.23490	0.21480	0.17000
100	AB	$\hat{\alpha}$	1.55160	1.38650	1.62710	1.03790	1.53320	1.31030	1.48660
		$\hat{\zeta}$	0.50670	0.47390	0.51560	0.34860	0.48780	0.43070	0.46470
		$\hat{\phi}$	0.42140	0.38270	0.51550	0.37190	0.48520	0.37190	0.42320
	MSE	$\hat{\alpha}$	3.42840	2.77420	3.54620	2.03150	3.24180	2.13800	3.00540
		$\hat{\zeta}$	0.34200	0.33500	0.34740	0.18910	0.30430	0.26920	0.30440
		$\hat{\phi}$	0.32890	0.23680	0.45970	0.25600	0.39620	0.19870	0.27680
	MRE	$\hat{\alpha}$	0.91270	0.81560	0.95710	0.61050	0.90190	0.77070	0.87450
		$\hat{\zeta}$	0.33780	0.31590	0.34370	0.23240	0.32520	0.28710	0.30980
		$\hat{\phi}$	0.18730	0.17010	0.22910	0.16530	0.21560	0.16530	0.18810
150	AB	$\hat{\alpha}$	1.20790	1.66100	1.28330	1.18280	1.36960	1.41400	1.21470
		$\hat{\zeta}$	0.38280	0.49940	0.52240	0.35850	0.41700	0.45620	0.37310
		$\hat{\phi}$	0.34780	0.46540	0.31650	0.36230	0.45020	0.37380	0.36050
	MSE	$\hat{\alpha}$	2.24160	3.68430	2.15550	2.50340	2.72540	2.76210	2.13160
		$\hat{\zeta}$	0.22470	0.30850	0.39030	0.18900	0.23340	0.28040	0.20550
		$\hat{\phi}$	0.32890	0.23680	0.45970	0.25600	0.39620	0.19870	0.27680
	MRE	$\hat{\alpha}$	0.71060	0.97700	0.75490	0.69570	0.80560	0.83180	0.71450
		$\hat{\zeta}$	0.33780	0.31590	0.34370	0.23240	0.32520	0.28710	0.30980
		$\hat{\phi}$	0.15460	0.20680	0.14070	0.16100	0.20010	0.16620	0.16020
200	AB	$\hat{\alpha}$	1.04970	1.08950	1.35220	0.62840	1.34140	1.20770	0.95370
		$\hat{\zeta}$	0.39010	0.40560	0.44280	0.27050	0.52510	0.38510	0.35710
		$\hat{\phi}$	0.28950	0.32420	0.39390	0.22840	0.34910	0.36580	0.28270
	MSE	$\hat{\alpha}$	1.57190	1.97460	2.49150	1.10190	2.45640	2.28280	1.40150
		$\hat{\zeta}$	0.21910	0.23460	0.28790	0.13780	0.35010	0.23040	0.19110
		$\hat{\phi}$	0.14560	0.20820	0.22010	0.08940	0.20530	0.22230	0.12500
	MRE	$\hat{\alpha}$	0.61750	0.64090	0.79540	0.36960	0.78900	0.71040	0.56100
		$\hat{\zeta}$	0.33780	0.31590	0.34370	0.23240	0.32520	0.28710	0.30980
		$\hat{\phi}$	0.12870	0.14410	0.17510	0.10150	0.15510	0.16260	0.12560
250	AB	$\hat{\alpha}$	0.87300	1.01970	1.02580	0.52690	1.39440	1.29100	0.95510
		$\hat{\zeta}$	0.26400	0.33040	0.35950	0.23590	0.40970	0.44870	0.31670
		$\hat{\phi}$	0.26920	0.30250	0.30750	0.19160	0.42610	0.37790	0.28310
	MSE	$\hat{\alpha}$	1.27230	1.42890	1.52590	1.06520	2.80450	2.17780	1.31740
		$\hat{\zeta}$	0.11620	0.17000	0.19010	0.11870	0.22960	0.26690	0.14310
		$\hat{\phi}$	0.13280	0.13970	0.14380	0.09350	0.27980	0.21850	0.12700
	MRE	$\hat{\alpha}$	0.51350	0.59980	0.60340	0.30990	0.82020	0.75940	0.56180
		$\hat{\zeta}$	0.17600	0.22030	0.23970	0.15730	0.27310	0.29910	0.21110
		$\hat{\phi}$	0.11960	0.13440	0.13670	0.08520	0.18940	0.16800	0.12580

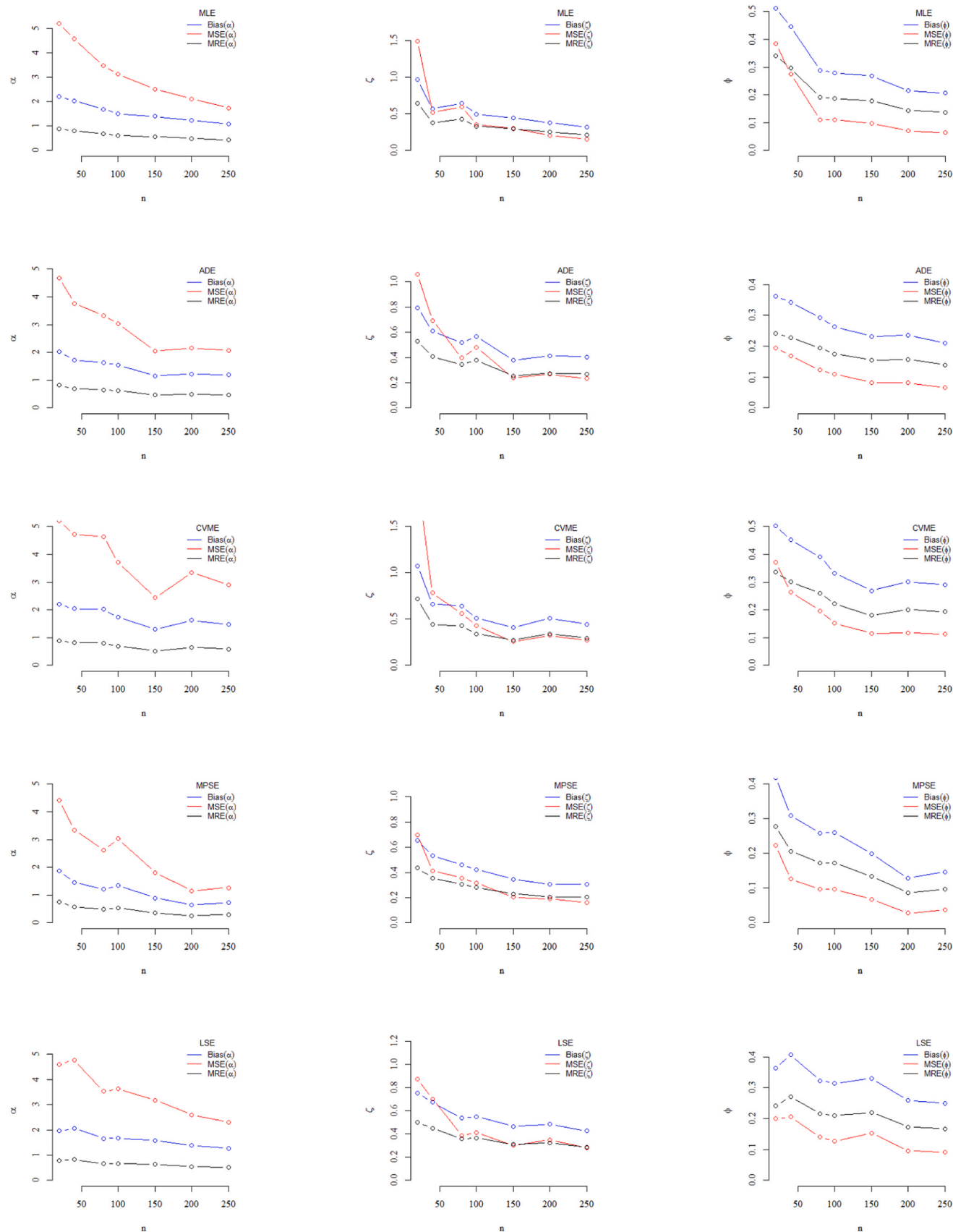


Fig. 4. Classical estimates plots of the NEWE model on simulated data for $(\alpha = 2.50, \zeta = 1.50, \phi = 1.50)$.

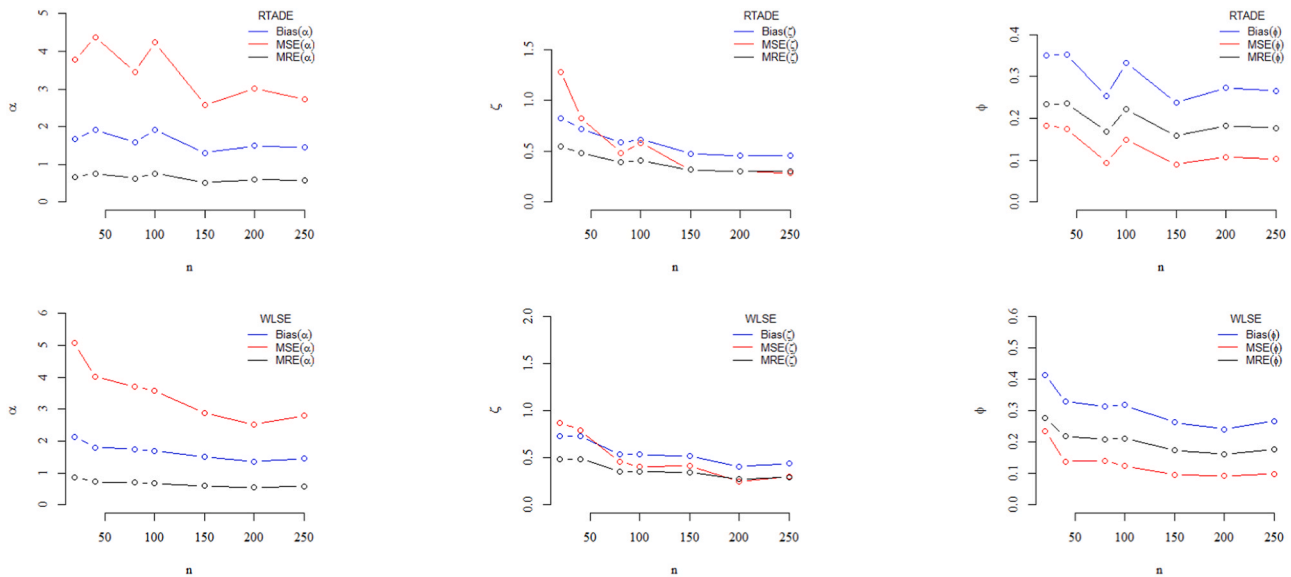


Fig. 4. (continued).

medical research and beyond. The results from Tables 3 to 5 and the accompanying visualizations in Figs. 4 to 6 provide a detailed evaluation of the performance of classical estimation techniques applied to the NEWE model. Table 3 focuses on absolute bias (AB), which measures the average deviation between the estimated and true parameter values. As expected, smaller sample sizes (e.g., $n = 20, 40$) exhibit higher biases, reflecting the challenge of achieving accurate parameter estimates with limited data. However, as the sample size increases, the AB decreases consistently across all methods, confirming the reliability and consistency of the estimators. Table 4 reports the mean square error (MSE), which accounts for both the bias and variability in the estimates. Higher MSEs at smaller sample sizes suggest greater variability in parameter estimates, but the values decline steadily as the sample size increases, indicating that the estimators perform more stably with larger datasets. Techniques like Maximum Product Spacing (MPS) and Maximum Likelihood Estimation (MLE) show lower MSEs even at smaller sample sizes, emphasizing their robustness across various conditions. Table 5 presents the mean relative error (MRE), which measures the proportionate deviation of the estimated parameters from their true values. In the early stages, methods such as Weighted Least Squares (WLS) display higher MREs, indicating greater sensitivity to smaller datasets. However, as the sample size grows, the MRE values for all techniques converge, confirming their asymptotic consistency and ability to provide reliable estimates as more data becomes available. The visualizations in Figs. 4 to 6 complement these findings by clearly illustrating how AB, MSE, and MRE values decrease as the sample size increases. Together, these results demonstrate that the estimation techniques are not only consistent but also adaptable to different data conditions, making them valuable tools for complex data analysis. For cancer researchers and clinicians working with survival data for diseases like lung cancer and AML, these insights highlight the NEWE model's potential to offer more accurate predictions and guide more effective treatment strategies.

6. Predictive modeling

The NEWE Model as a perspective in predictive modeling offers a compelling glimpse into advanced analytical techniques transforming cancer research. Within this context, the NEWE model emerges as a groundbreaking tool, uniquely capable of interpreting complex survival patterns among lung and AML patients. In Fig. 7, the PDF plots of the NEWE model, generated for a dataset covering 500 patients, illustrate its versatility in aligning with the diverse patterns of survival times

observed in lung cancer and AML patients. The model adeptly accommodates data trends ranging from pronounced skewness to perfect symmetry. This alignment is evidenced by the high KS p-values, nearing unity, which signal a strong correlation between the model predictions and actual patient outcomes. Such a robust fit highlights the NEWE model's capacity to effectively represent both the rapid disease progression often seen in certain lung cancer cases and the aggressive trajectory characteristic of AML. The appearance of symmetrical data trends further confirms the model's accuracy in forecasting the survival times of patients with more predictable disease progressions. The NEWE model's flexible and precise nature renders it an invaluable resource for clinicians and oncologists. It supports them in making accurate prognostic assessments, adapting treatment approaches to individual patient needs, and ultimately, enhancing the quality of care and survival prospects for individuals battling cancer.

In the United States for the year 2024, it is forecasted that there will be 2001,140 new cancer cases and more than 611,720 cancer-related deaths. Daily, this translates to nearly 5500 new cases and approximately 1680 deaths attributed to this pervasive illness. Figs. 8 and 9 offer a visual representation of various cancer statistics, with Fig. 8 detailing the estimated number of cancer-related deaths and Fig. 9 outlining the expected new cases of cancer for both men and women in 2024. These projections underscore the ongoing challenge cancer poses to public health and emphasize the urgent need for continued research, preventive measures, and effective treatment protocols. It's important to note that both graphs can be found on the American Cancer Society's website, and their data is further detailed in a document available at ["https://gco.iarc.who.int/media/globocan/factsheets/populations/922-western-asia-fact-sheet.pdf."](https://gco.iarc.who.int/media/globocan/factsheets/populations/922-western-asia-fact-sheet.pdf)

7. Interpretation of cancer data

To demonstrate the effectiveness and adaptability of the NEWE model in the interpretation of cancer data, a numerical study has been initiated, employing five lifetime datasets previously developed and analyzed by renowned researchers. The first dataset provided stands for the survival times in months for a cohort of 20 patients with acute myeloid leukemia, as documented in the study by Afify et al. [24]. The statistical analysis of survival times for 20 acute myeloid leukemia patients reveals a mean survival time of 2.1841 months, closely mirrored by the median survival time of 2.1695 months. This slight difference between the mean and median suggests a relatively symmetrical

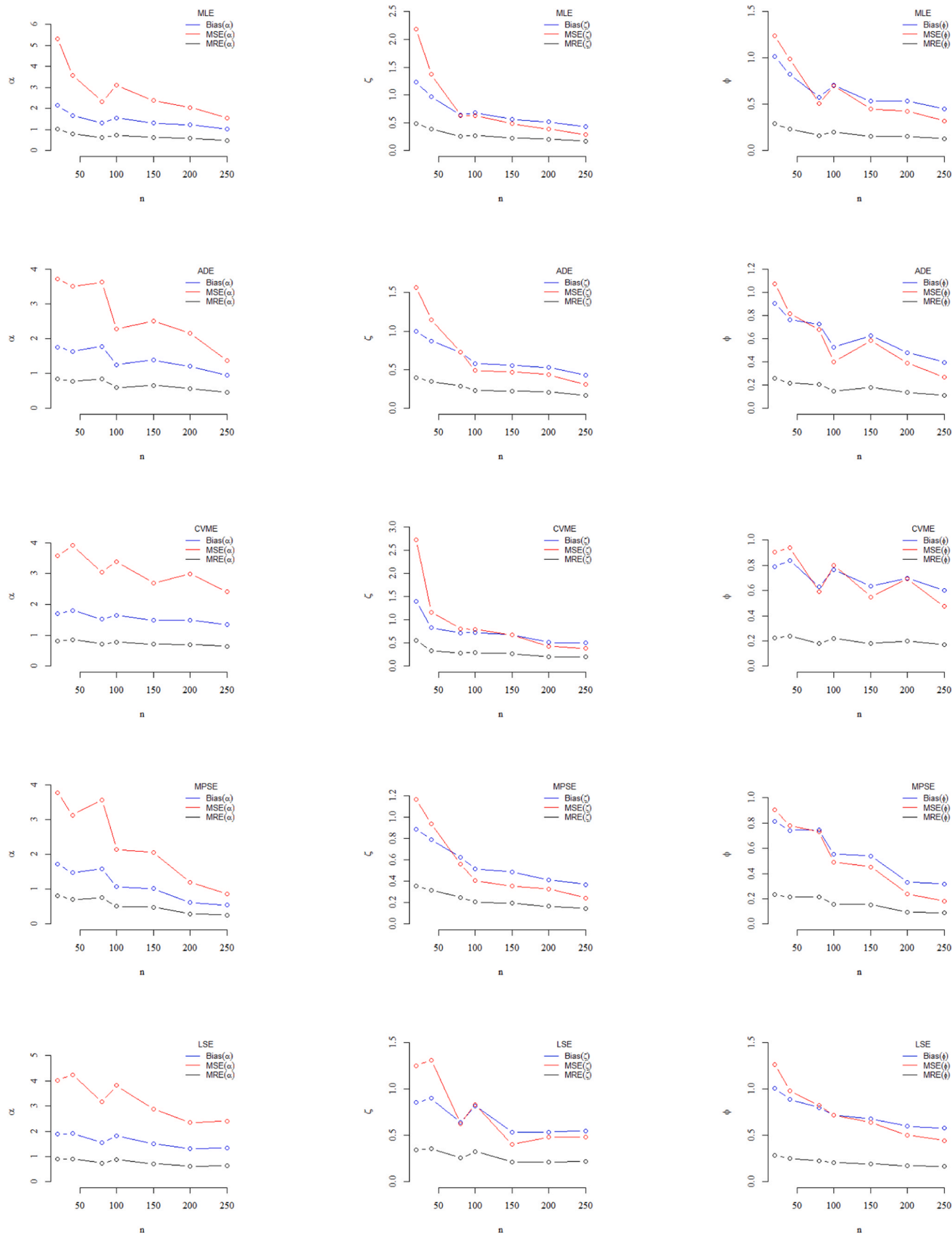


Fig. 5. Classical estimates plots of the NEWE model on simulated data for ($\alpha = 2.10, \zeta = 2.50, \phi = 3.50$).

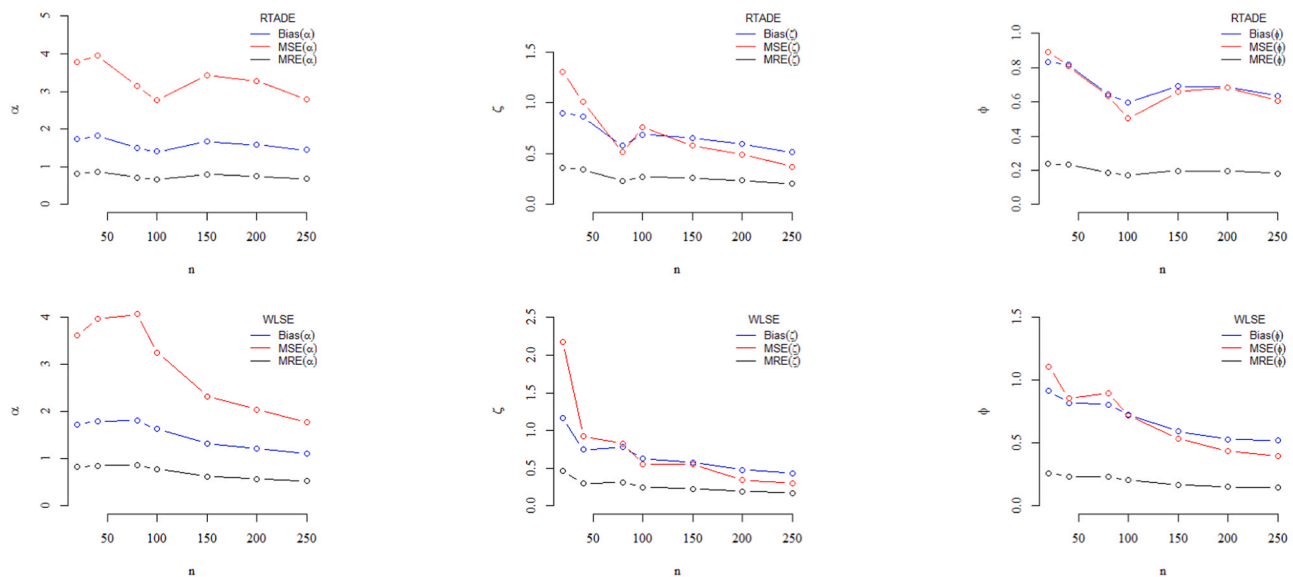


Fig. 5. (continued).

distribution of survival times around the central value, indicating consistency in the survival durations across this patient cohort. The standard deviation, calculated at 0.8396 months, alongside a variance of 0.7049, highlights moderate variability in survival times, suggesting that while some patients' survival times closely align with the average, others diverge more significantly, reflecting the heterogeneous nature of the disease's impact on patient outcomes. Furthermore, the skewness value of 0.1139 points to a marginally right-skewed distribution, implying a slight predominance of patients with survival times extending beyond the median, albeit not significantly. A kurtosis value of 2.6943 for survival times shows a distribution nearly matching a normal distribution, with a slightly flatter peak and thinner tails. This suggests a homogeneous pattern of survival times among patients, with few extreme outliers, and most values clustered around the mean.

The analysis of the second dataset, documenting the survival times of 121 breast cancer patients from 1929 to 1938 as reported by Lee [25], provides insightful observations on the survival patterns within this patient group. These statistics offer a comprehensive view of the patients' longevity after diagnosis, reflecting the historical context of breast cancer treatment and outcomes. The survival analysis of 121 breast cancer patients treated between 1929 and 1938, as reported by Lee (1992), yields significant insights into the patterns of survival during an era with different medical advancements than today. The mean survival time of 46.33 months, alongside a median of 40 months, reflects a substantial duration of survival given the period's medical context, showing that some patients experienced notably long lives post-diagnosis. The standard deviation and variance, at 35.13 months and 1244.464 respectively, highlight a wide variability in patient outcomes, emphasizing the personalized nature of the disease's progression and response to treatment. Furthermore, the distribution's skewness of 1.04 reveals a right-skewed pattern, suggesting that while many patients had survival times below the average, a notable number achieved significantly longer survival, pointing to a spectrum of disease behavior. The moderate kurtosis value of 3.40 shows a balanced distribution of survival times, with neither excessively heavy nor a light tail, suggesting a variety of patient experiences within the study cohort. Together, these statistics offer a detailed understanding of breast cancer survival rates in the early 20th century, highlighting the diversity of patient outcomes and providing a valuable historical benchmark for comparing with contemporary survival trends.

The third dataset, documenting the survival analysis of 33 patients with acute myelogenous leukemia from 1929 to 1938 by Feigl and Zelen

[26], reveals a mean survival time of 40.88 weeks and a median of 22 weeks. This shows a significant disparity in patient outcomes. The substantial standard deviation of 46.703 weeks and variance of 2181.172 reflect a wide variability in survival times, emphasizing the diverse responses to treatment or disease progression within the cohort. A skewness of 1.112 points towards a right-skewed distribution, suggesting that while many patients had relatively short survival times, a few experienced much longer survivals, contributing to the "bathtub" shape of the hazard rate function noted for this dataset. The kurtosis of 3.122 shows a distribution with a balance in the tails' weight, showing a slight tendency towards outlier survival times, yet not deviating significantly from a normal distribution. This detailed analysis highlights the complex survival patterns among leukemia patients, underscoring the variability and the need for individualized patient care strategies.

The fourth dataset, detailing the ages in months of 18 patients who died from causes other than cancer as studied by Boag [27], yields a mean age of approximately 67.81 months and a median age of 66.5 months. This slight difference between the mean and median suggests a relatively symmetrical distribution of ages at death. The standard deviation, at about 47.44 months, alongside a variance of 2250.14, shows a broad spread of ages, highlighting diverse patient ages within the dataset. The skewness, measured at 0.188, points to a distribution that is almost symmetrical, with a very slight lean towards older ages. The age distribution of patients dying from non-cancer causes, showed by a kurtosis value of 2.086, shows a slightly sharper peak than a normal distribution, suggesting mild variability with outliers, yet stays close to a typical pattern, reflecting diverse survival times among these patients.

The fifth dataset, concerning advanced lung cancer patients from a study by Lawless [28], who received "standard" chemotherapy treatments, provides a comprehensive look into their survival times, measured from the treatment onset. The mean survival time for these patients is approximately 101.76 days, with a median survival time of 56 days, showing a significant spread between the average and midpoint of the dataset. This discrepancy is further highlighted by a standard deviation of 110.81 days and a variance of 12,279.89, illustrating a wide range of survival times among the patients. The skewness value of 1.199 suggests a right-skewed distribution, showing that most patients had survival times shorter than the mean, with a few cases significantly exceeding it. The kurtosis value of 4.004 points to a distribution with a pronounced peak and heavier tails than a normal distribution, showing a notable number of outliers. This suggests that survival times vary widely, with some patients living significantly longer or shorter than the

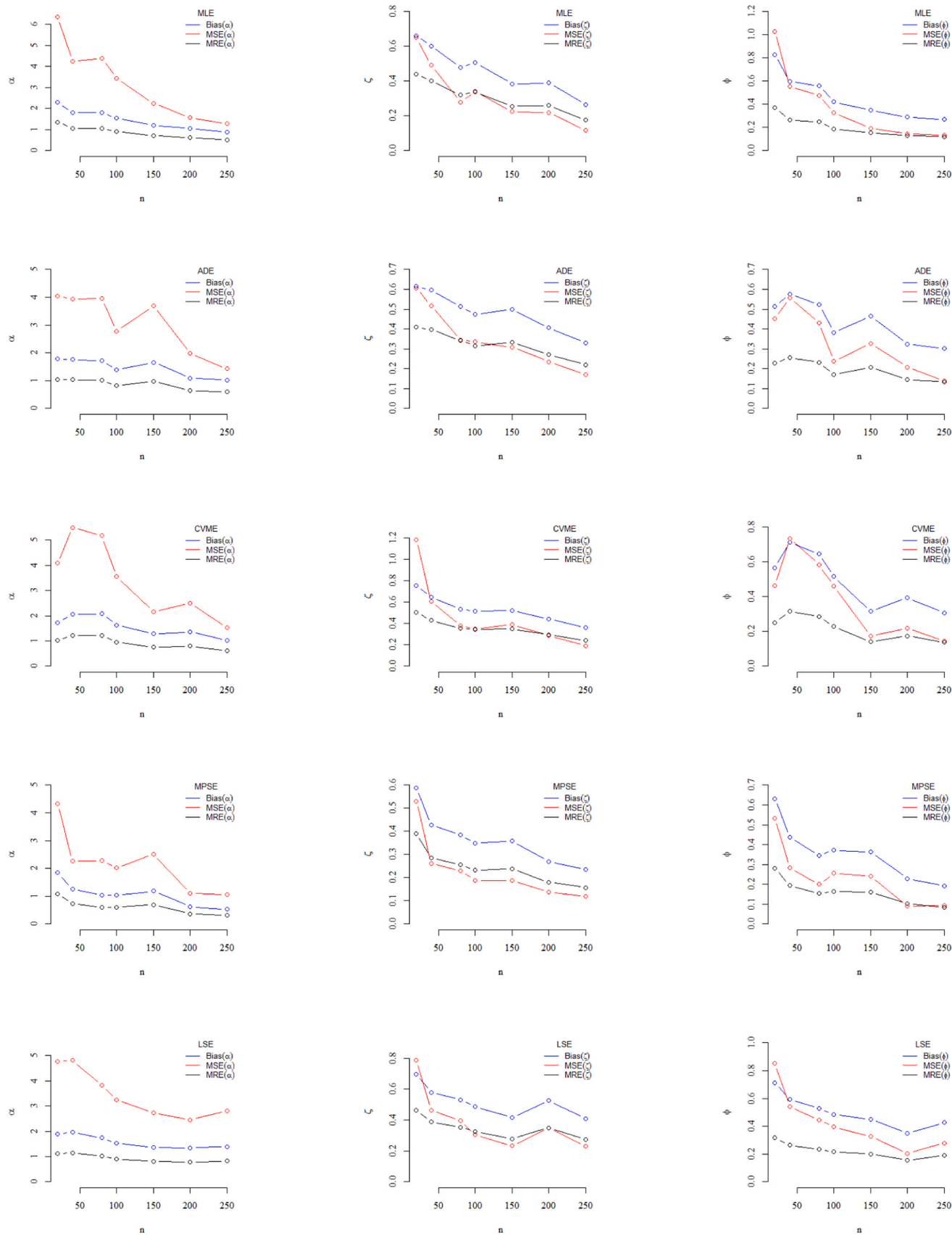


Fig. 6. Classical estimates plots of the NEWE model on simulated data for $(\alpha = 1.70, \zeta = 1.50, \phi = 2.25)$.

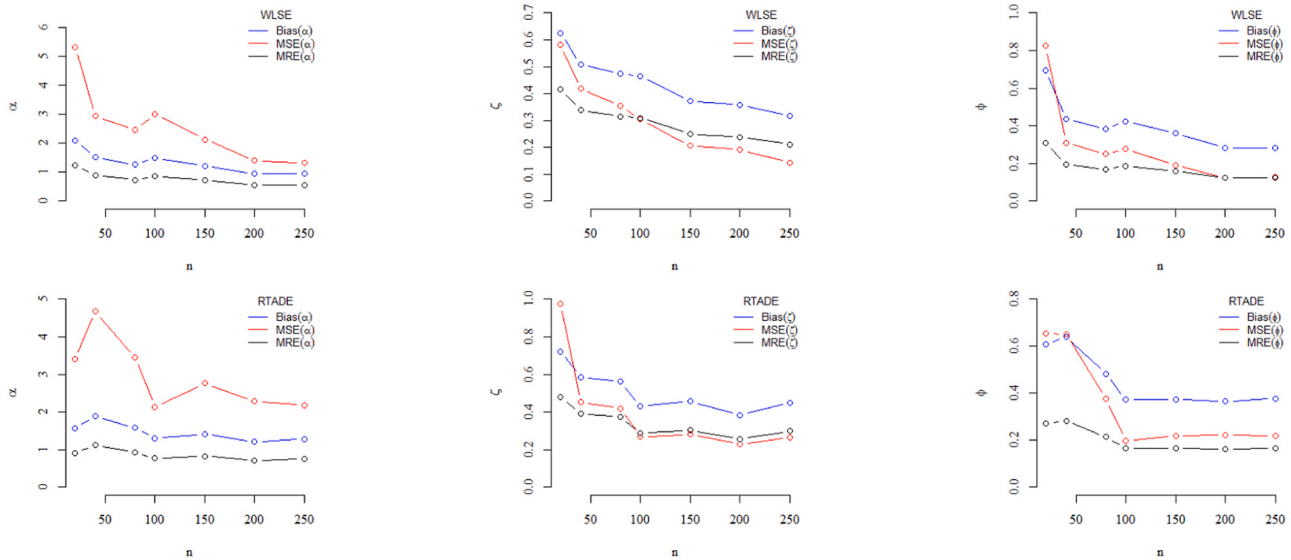


Fig. 6. (continued).

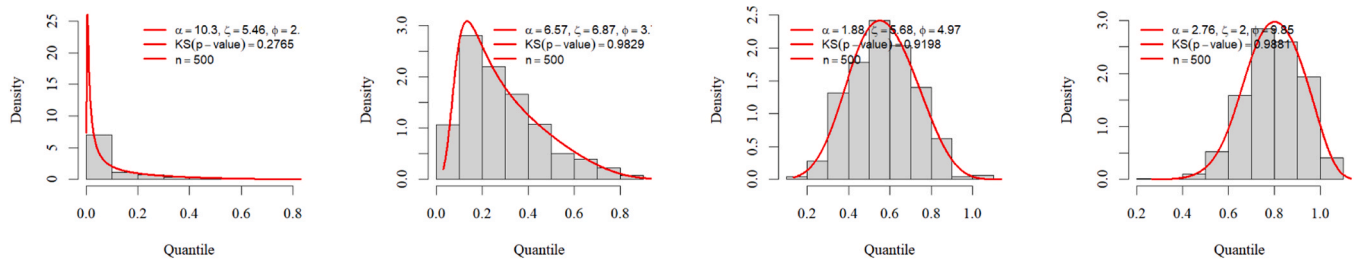


Fig. 7. The NEWWE model PDF plots with different parameter estimates and KS p-values for a sample size of 500.

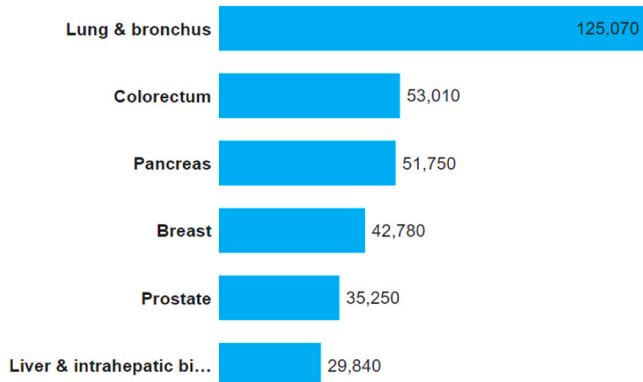


Fig. 8. Estimated cancer deaths for both sexes in 2024.

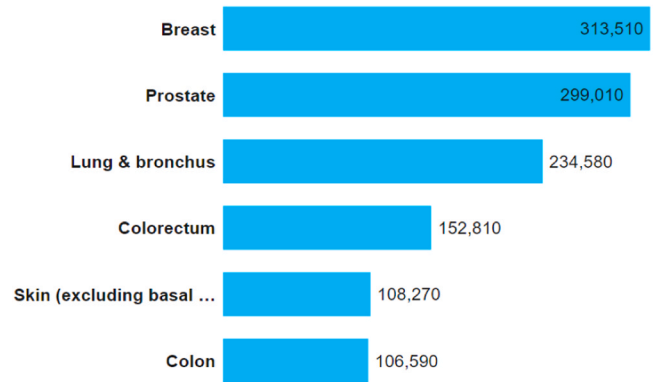


Fig. 9. New estimated cancer cases for both sexes in 2024.

median, reflecting diverse responses to chemotherapy in advanced lung cancer cases. For ease of the reader, note that all five datasets are provided in the Appendix

8. Competitor models

To illustrate the versatility and relevance of the NEWWE model within medical research, we conduct a comparative analysis against various high-profile classical models Lognormal (LN) model, known for its ability to model data skewed to the right, Exponentiated Weibull (EWE) model, which extends the flexibility of the Weibull model to accommodate varying hazard rates (Pal et al. [29]). The Weibull (WE) model, a

staple in reliability and survival analysis due to its ability to model different types of failure rates. Exponentiated Exponential (EEXP) model, which introduces an added parameter to the exponential model to provide a better fit for datasets with non-constant hazard rates (Nadarajah [30]). Nadarajah-Haghighi Exponential (NHEXP) model, designed to offer an enhanced fit for datasets exhibiting a heavy tail, typical in certain disease progression models (Nadarajah and Haghighi [31]). Inverse Weibull (IWE) model, adept at modeling life data where the hazard function may initially decrease before increasing, applicable in certain types of cancer studies. Alpha Exponential (AEXP) model, which is tailored to capture the first increasing and eventual decreasing hazard rate, applicable in various survival analysis scenarios (Mahdavi

Table 6
MLEs with fit statistics for 20 acute myeloid leukemia patient’s data.

Model	$\hat{\alpha}$	$\hat{\zeta}$	$\hat{\phi}$	CVME	ADE	K-S	P-Value
NEWE	−0.5878	0.1005	2.7536	0.0510	0.3059	0.1511	0.6964
EWE	0.0562	3.1052	0.9012	0.0525	0.3125	0.1526	0.6849
WE	0.0728	2.9236	-	0.0537	0.3160	0.1550	0.6663
EEXP	1.2260	7.9795	-	0.1191	0.6459	0.2184	0.2559
LN	0.6970	0.4359	-	0.1342	0.7247	0.2270	0.2181
IWE	2.6040	2.0648	-	0.2558	1.3707	0.2719	0.0850
NHEXP	0.0134	25.308	-	0.0598	0.3411	0.3546	0.0094
GEV	−0.5536	1.8874	-	0.1011	0.6669	0.3921	0.0028

Table 7
MLEs with fit statistics for 121 breast cancer patient’s data.

Model	$\hat{\alpha}$	$\hat{\zeta}$	$\hat{\phi}$	CVME	ADE	K-S	P-Value
NEWE	−0.1150	0.0066	1.2900	0.0539	0.4056	0.0586	0.8010
WE	0.0060	1.3058	-	0.0536	0.4014	0.0598	0.7791
EWE	0.0086	1.2336	1.0891	0.0545	0.4525	0.0659	0.6694
NHEXP	0.0064	2.4673	-	0.0728	0.5311	0.0712	0.5710
EEXP	0.0277	1.5169	-	0.0616	0.4289	0.0803	0.4158
LN	3.4657	1.0335	-	0.3185	2.0434	0.1261	0.0427
GEV	−0.1656	43.277	-	0.4449	2.9596	0.3834	<0.0001
IWE	6.8139	0.6660	-	1.1620	7.2144	0.2184	<0.0001

Table 8
MLEs with fit statistics for 33 acute myelogenous leukemia patient’s data.

Model	$\hat{\alpha}$	$\hat{\zeta}$	$\hat{\phi}$	CVME	ADE	K-S	P-Value
NEWE	9.4977	0.00003	2.1299	0.0571	0.3745	0.1220	0.7101
LN	2.8297	1.5119	-	0.1114	0.7030	0.1332	0.6021
EWE	0.14815	0.6221	1.4727	0.0952	0.6455	0.1365	0.5698
WE	0.0627	0.7765	-	0.0948	0.6509	0.1368	0.5676
EEXP	0.0188	0.6777	-	0.0966	0.6691	0.1382	0.5538
NHEXP	0.0998	0.4896	-	0.1002	0.6660	0.1393	0.5442
IWE	4.1873	0.6943	-	0.1601	0.9759	0.1490	0.4564
AEXP	0.2110	0.0169	-	0.0975	0.6643	0.1829	0.2198
GEV	0.8702	10.7692	-	0.1460	1.0134	0.3681	0.0003

Table 9
MLEs with fit statistics for 18 patient’s data.

Model	$\hat{\alpha}$	$\hat{\zeta}$	$\hat{\phi}$	CVME	ADE	K-S	P-Value
NEWE	−15.664	0.3946	0.7369	0.0358	0.2209	0.1456	0.8400
WE	0.0081	1.1340	-	0.1141	0.6754	0.1838	0.5776
EWE	0.0026	1.3359	0.6977	0.0992	0.5905	0.2054	0.4336
EEXP	0.0145	0.9814	-	0.1242	0.7322	0.2174	0.3625
LN	3.6455	1.5327	-	0.2628	1.5099	0.2698	0.1456
IWE	3.8193	0.4846	-	0.3978	2.2578	0.2770	0.1262
GEV	−0.4135	78.4691	-	0.0359	0.2976	0.3679	0.0153

Table 10
MLEs with fit statistics for lungs cancer patient’s data.

Model	$\hat{\alpha}$	$\hat{\zeta}$	$\hat{\phi}$	CVME	ADE	K-S	P-Value
NEWE	2.0659	0.0041	1.0768	0.0914	0.5967	0.1298	0.8712
EWE	0.4586	0.3892	5.5610	0.1079	0.6846	0.1472	0.7528
LN	3.9144	1.2982	-	0.1131	0.7087	0.1503	0.7299
NHEXP	0.0218	0.6425	-	0.0976	0.6366	0.1528	0.7109
WE	0.0183	0.8773	-	0.0922	0.6120	0.1624	0.6369
IWE	17.150	0.8699	-	0.1442	0.8691	0.1662	0.6075
EEXP	0.0086	0.8269	-	0.0906	0.6056	0.1701	0.5779
GEV	1.2874	15.072	-	0.1318	0.8143	0.3680	0.0068

and Kundu [32]). This comprehensive comparison underscores the NEWE model’s ability to provide a robust and adaptable framework for analyzing cancer data, positioning it as a competitive alternative to these well-established models. By assessing its performance compared to

such a diverse set of models, we highlight the NEWE model’s potential to address the subtle requirements of medical data analysis, offering researchers a powerful tool in their statistical arsenal.

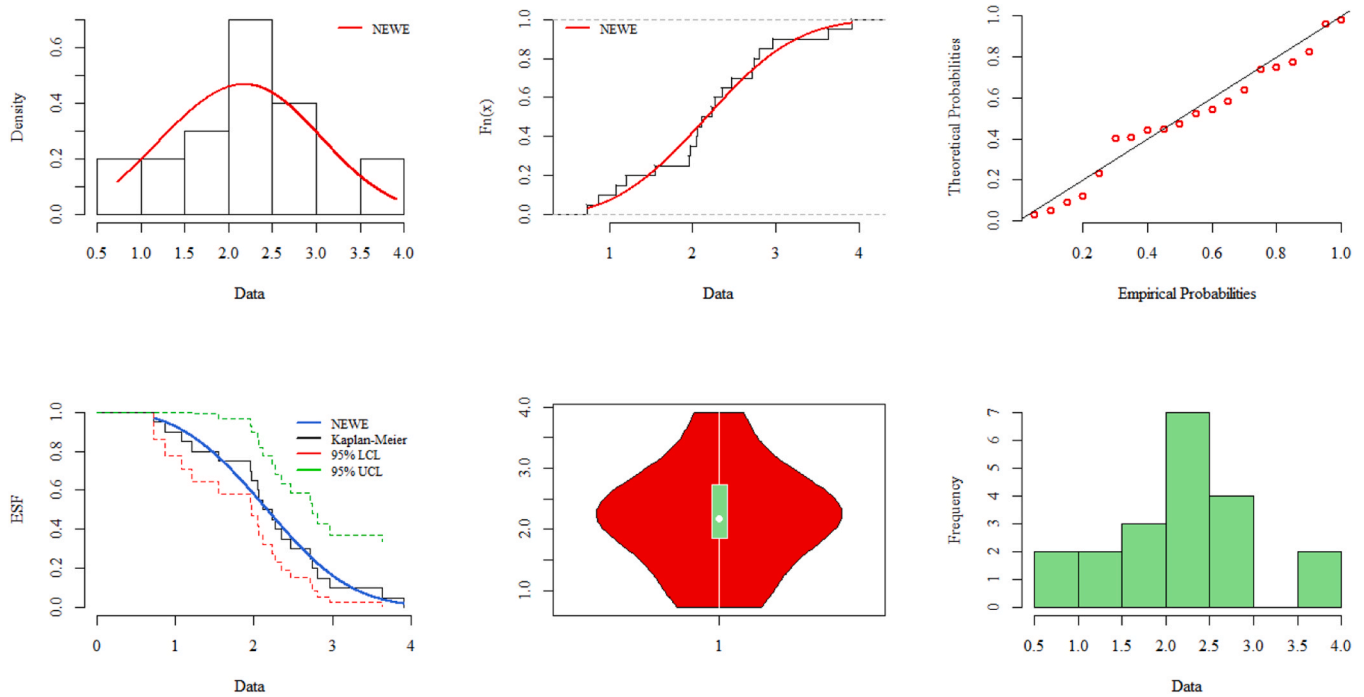


Fig. 10. Descriptive and fitted plots for 20 acute myeloid leukemia patient's data.

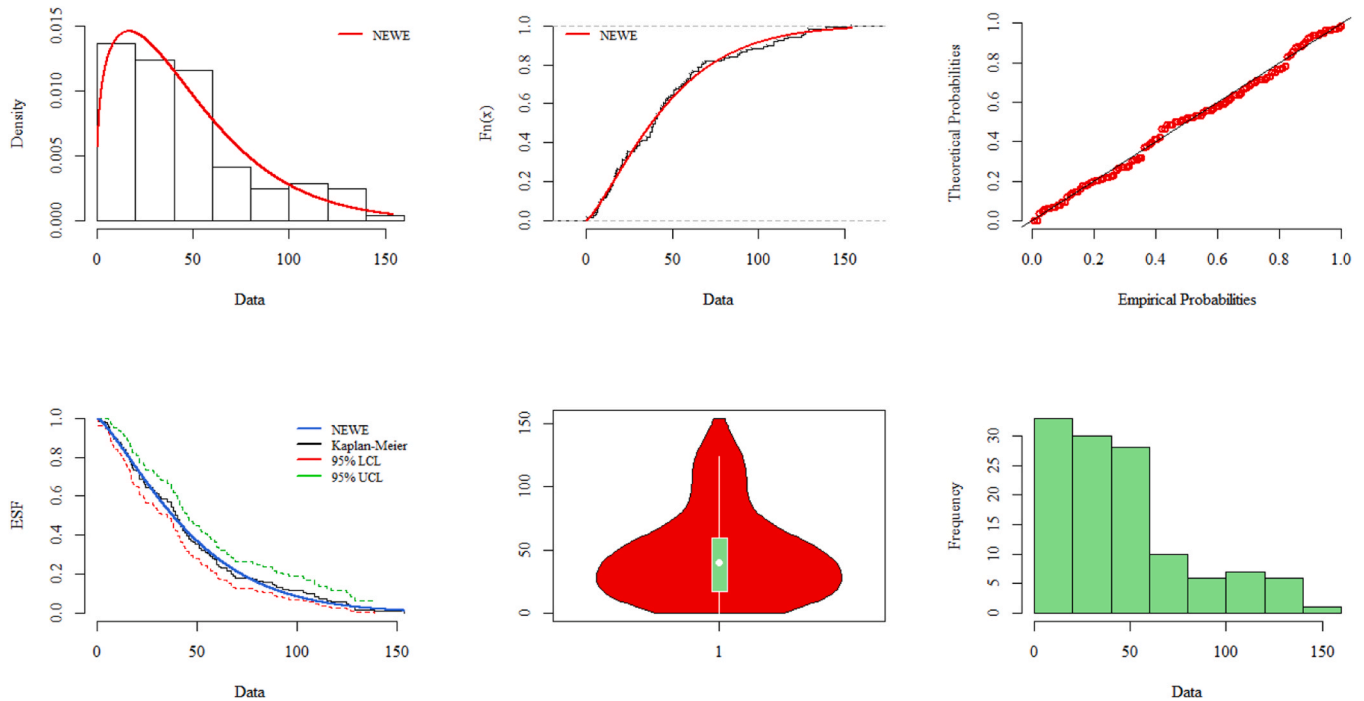


Fig. 11. Descriptive and fitted plots for 121 breast cancer patient's data.

9. Criteria for choosing statistical models

In this detailed analysis, we deploy a range of established fit statistics to evaluate model performance, specifically focusing on the Cramer-von Mises (CVM) test, Anderson-Darling (AD) test, and Kolmogorov-Smirnov (KS) test, along with their respective p-values. The calculation and interpretation of these fit statistics for the models under review are presented as follows:

For AD calculations, see subsection 3.2.

For CVM details, refer to subsection 3.3.

The KS statistic is defined as: $\text{Max}|F_{v,nT} - F_T|$, where $F_{v,nT}$ denotes the empirical CDF based on the sample data, F_T represents the theoretical CDF under consideration, and Max symbolizes the maximum absolute difference between $F_{v,nT}$ and F_T .

We base our evaluation strategy on the assumption that the best model will show the lowest fit statistics values and a relatively higher p-value for the KS test. The comprehensive data presented in [Tables 6 to 10](#) underpins the conclusion that the NEWWE model stands out as the

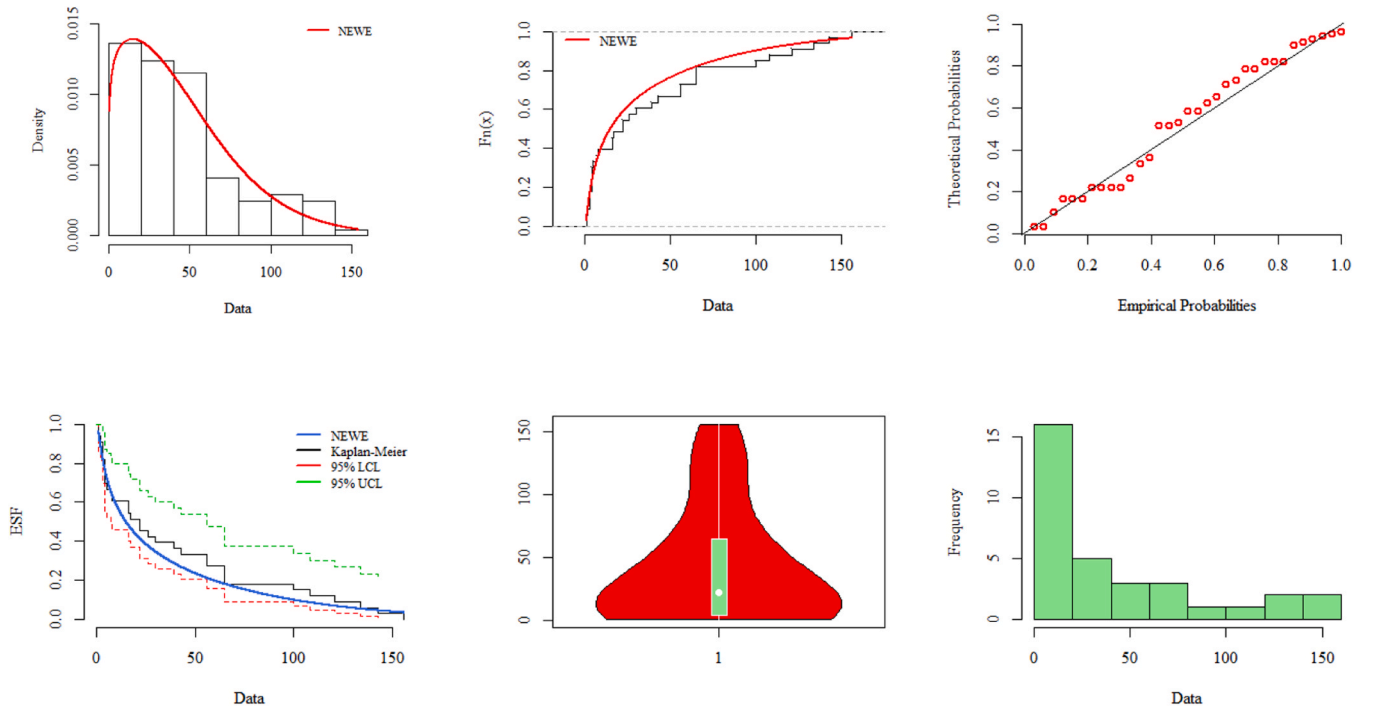


Fig. 12. Descriptive and fitted plots for 33 acute myelogenous leukemia patient's data.

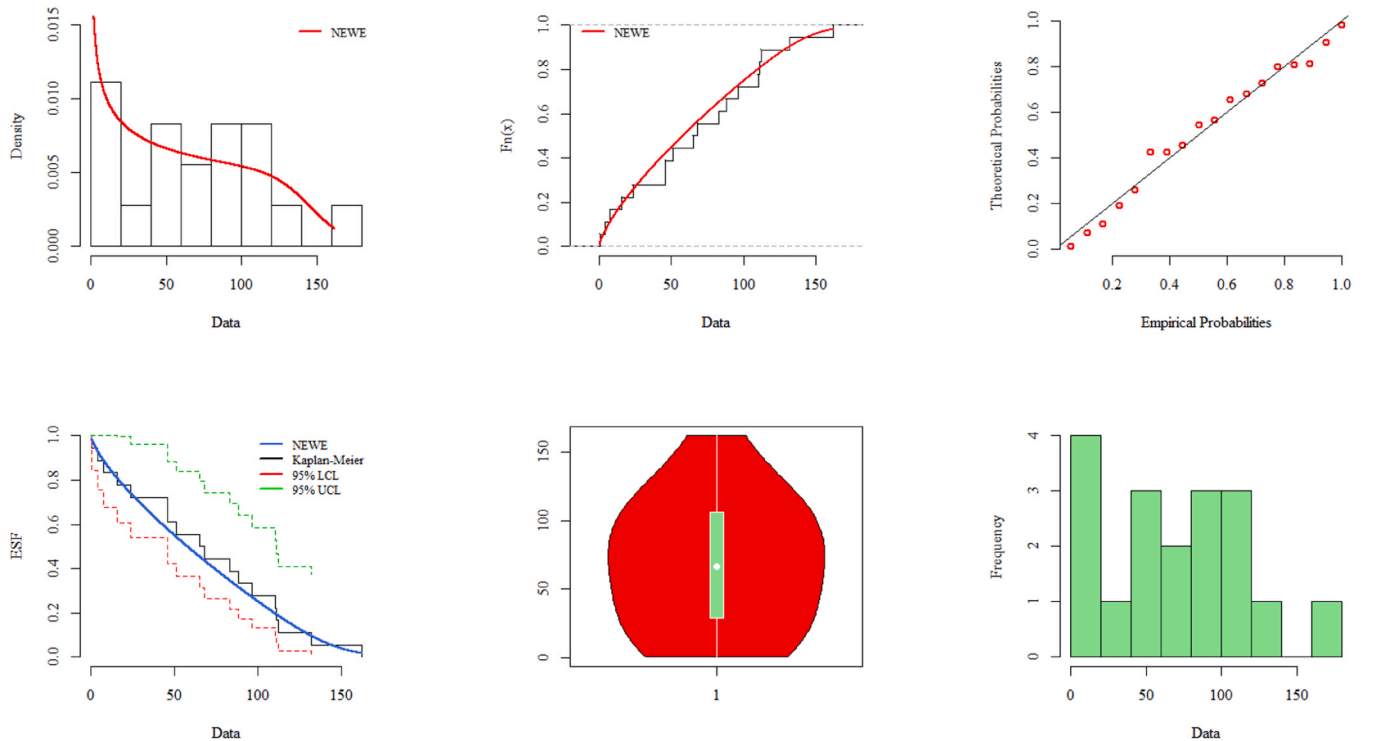


Fig. 13. Fitted and descriptive plots for 18 patients' data.

superior choice, surpassing its competitors with respect to MLEs and fit statistics performance. To enrich our quantitative analysis, Figs. 10 to 14 offer valuable visual enhancements. These figures highlight a comprehensive array of both descriptive and fitted plots. Descriptive plots such as histograms and violin plots provide a visual overview of the data's distribution. Additionally, fitted plots, including density, distribution, probability-probability (PP), and Kaplan-Meier survival plots, are

crucial for assessing the model's performance. These plots deliver crucial insights into how effectively the model captures and reflects the complexities of various datasets. They are essential tools for confirming the model's precision and adaptability in modeling the diverse and dynamic scenarios met in real-world cancer data analysis, demonstrating the model's robust applicability across different settings. It's important to note that the analysis conducted in this study weights the

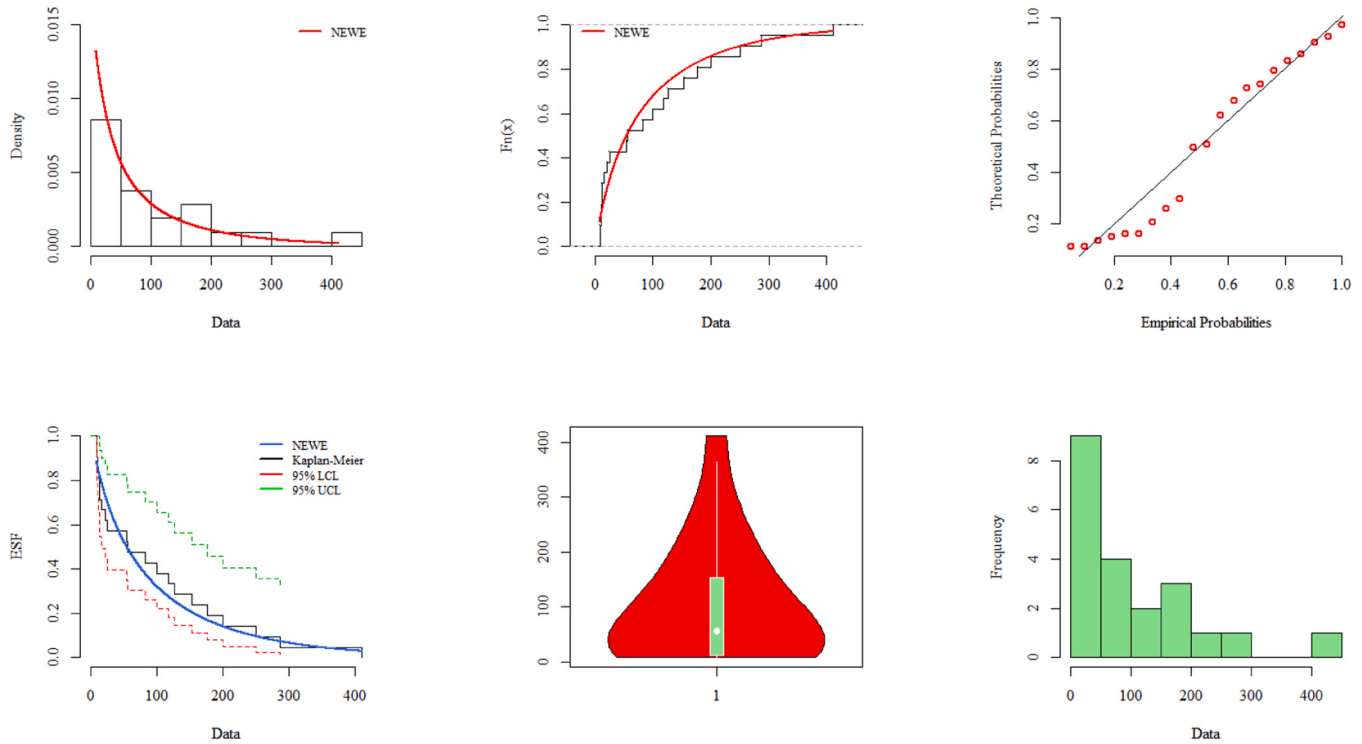


Fig. 14. Fitted and descriptive plots for lungs cancer patient's data.

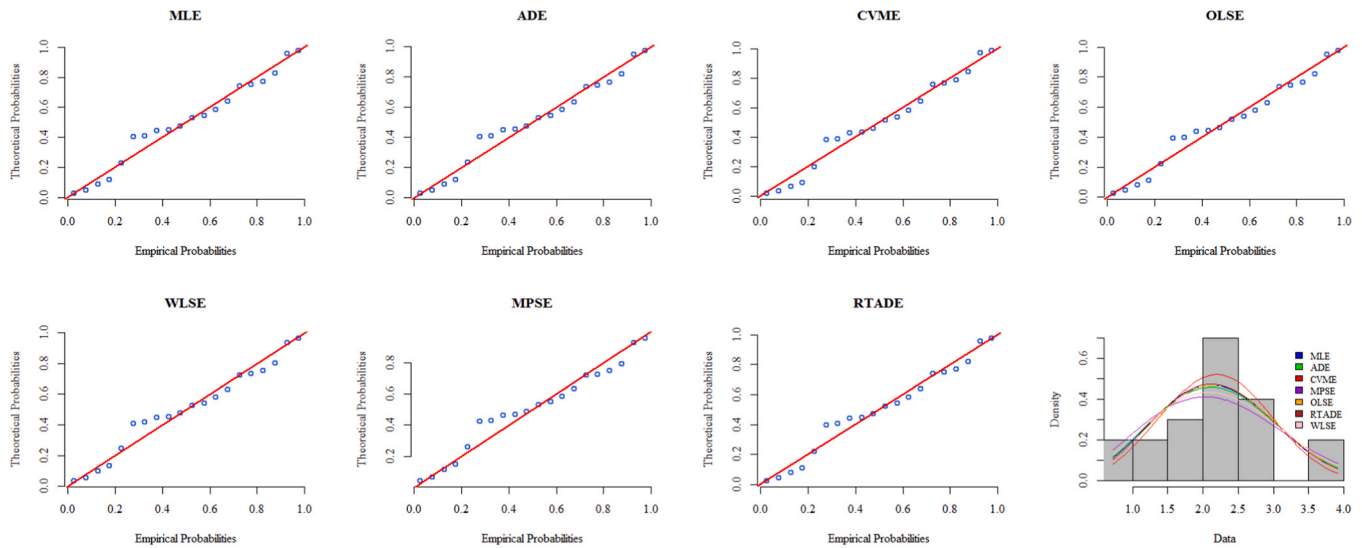


Fig. 15. The PP-plots and fitted density for 20 acute myeloid leukemia patient's data.

AdequacyModel package, designed specifically for use within the R statistical computing environment (<https://www.r-project.org/>). This package plays a pivotal role in easing the comprehensive analysis, underscoring the technical foundation upon which our findings are based.

Further in-depth analysis, supplemented by graphical representations found in Figs. 15 to 19. This phase involved applying various classical estimation techniques to figure out the most fitting method. The outcome of this analysis, summarized in Tables 11 to 15, was heavily influenced by the performance metrics of fit statistics. For the dataset including 20 patients with acute myeloid leukemia, the CVME approach was identified as the most effective method for parameter estimation. In contrast, analysis of the breast cancer dataset revealed

that MLE yielded the most correct results. For a group of 33 patients with acute myelogenous leukemia, the LSE method proved to be the most reliable. Among the data for 18 patients, the WLSE was distinguished as the foremost estimation technique. Lastly, for the lung cancer patient dataset, MLE was again found to be superior compared to other methods.

10. Discussion

The introduction of the Next Generation Weibull (NEWWE) model represents a significant advancement in the probabilistic analysis of cancer patient data. By comparing the NEWWE model against a range of classical models like the Lognormal (LN), Exponentiated Weibull (EWE),

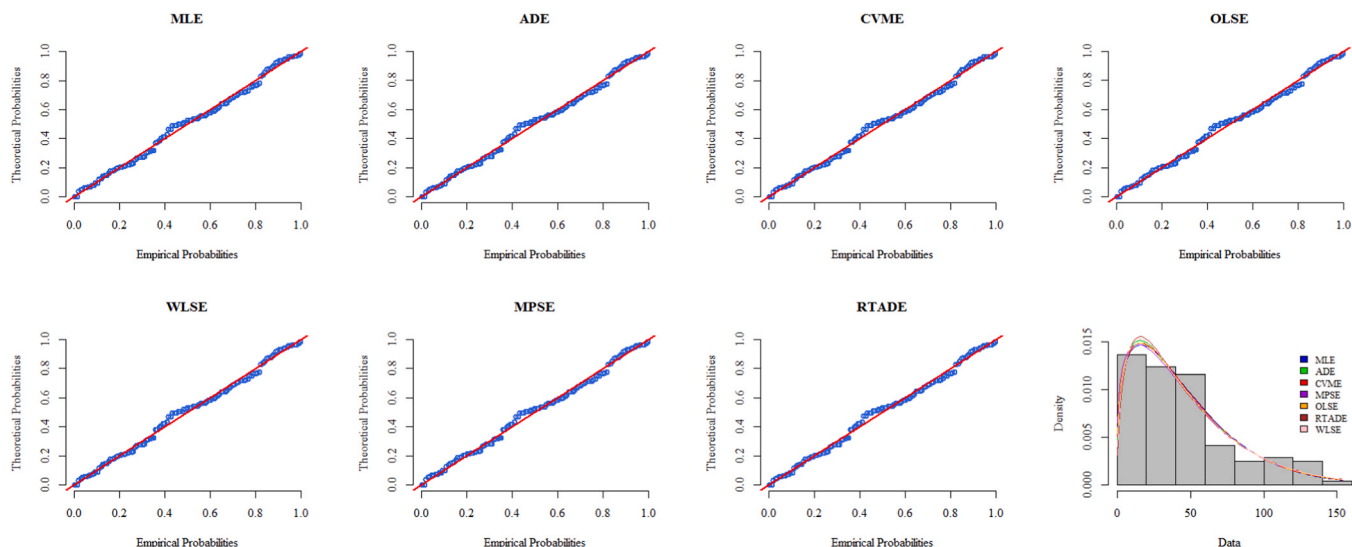


Fig. 16. The PP-plots and fitted density for 121 breast cancer patient's data.

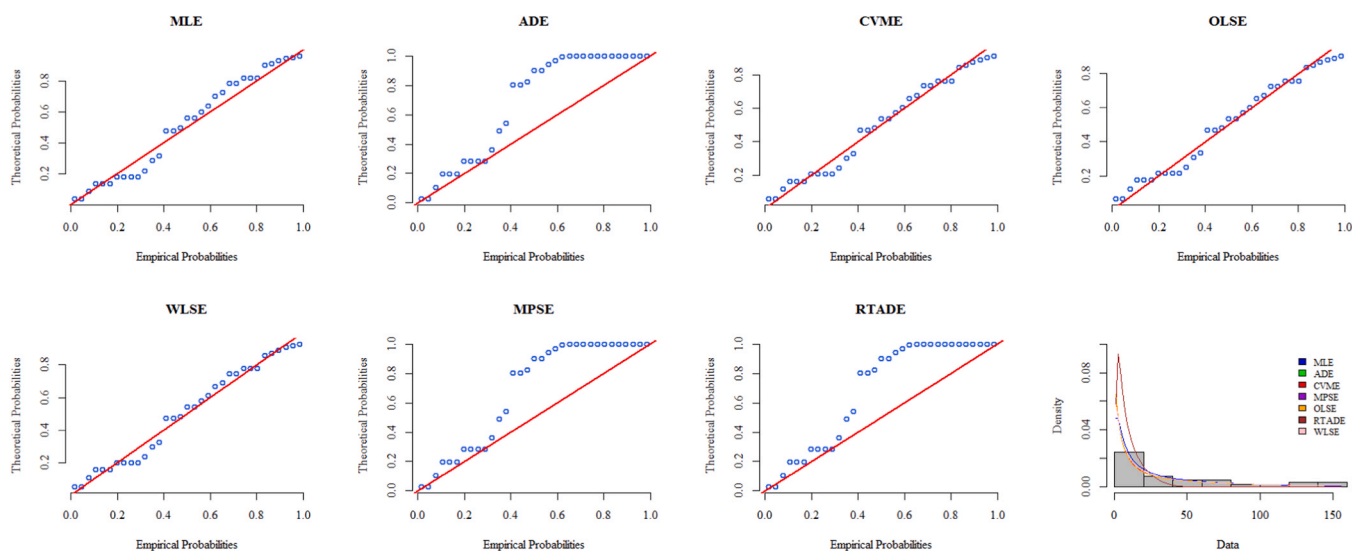


Fig. 17. The PP-plots and fitted density for 33 acute myelogenous leukemia patient's data.

and others, this study not only highlights its applicability across various datasets but also highlights its potential to offer more precise and adaptable solutions for modeling cancer survival data. The extensive use of classical estimation techniques and fit statistics further confirms the consistency and reliability of the NEWE model. One of the key findings of this study is the NEWE model's superior performance in fitting data for lung cancer and acute myeloid leukemia patients, as showed by lower values in fit statistics. This suggests that the NEWE model can effectively capture the complexities and nuances of cancer patient survival data, potentially leading to more correct survival time predictions. The inclusion of comprehensive graphical analyses further aids in understanding the model's fit and its implications for clinical decision-making. However, the study is not without limitations. The specificity of the NEWE model to the datasets analyzed raises questions about its universal applicability. Additionally, the reliance on high-quality data for effective model performance highlights the need for robust data collection and processing mechanisms. The focus on classical estimation techniques, while demonstrating consistency, may not fully capture the evolving nature of cancer progression and treatment responses, suggesting a potential area for methodological advancements.

11. Conclusion

The NEWE model appears as a strong tool in the arsenal of probabilistic models for analyzing cancer patient data, showing notable strengths in flexibility, adaptability, and precision. Its successful application to lung cancer and acute myeloid leukemia datasets, supported by rigorous statistical validation, sets the foundation for its potential wider use in oncology research and practice. To fully realize the potential of the NEWE model, future research should explore its applicability to other cancer types and incorporate advancements in estimation methodologies to keep pace with the evolving landscape of cancer treatment. Moreover, integrating the model into clinical settings requires collaborative efforts, technological support, and education for healthcare professionals and patients alike. Ultimately, the NEWE model holds promise for enhancing the precision of cancer survival predictions, guiding treatment decisions, and improving patient outcomes. Its development and validation represent a step forward in the ongoing quest to address the complexities of cancer through innovative statistical modeling, offering a glimpse into the future of personalized oncology and precision medicine.

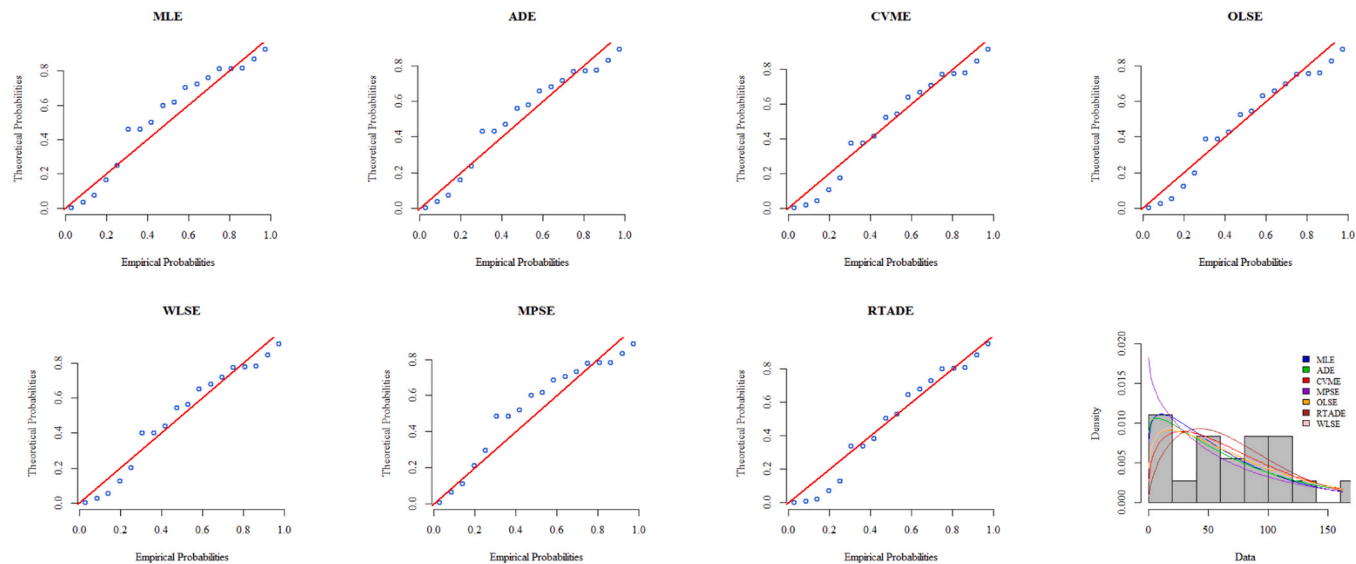


Fig. 18. The PP-plots and fitted density for 18 patient's data.

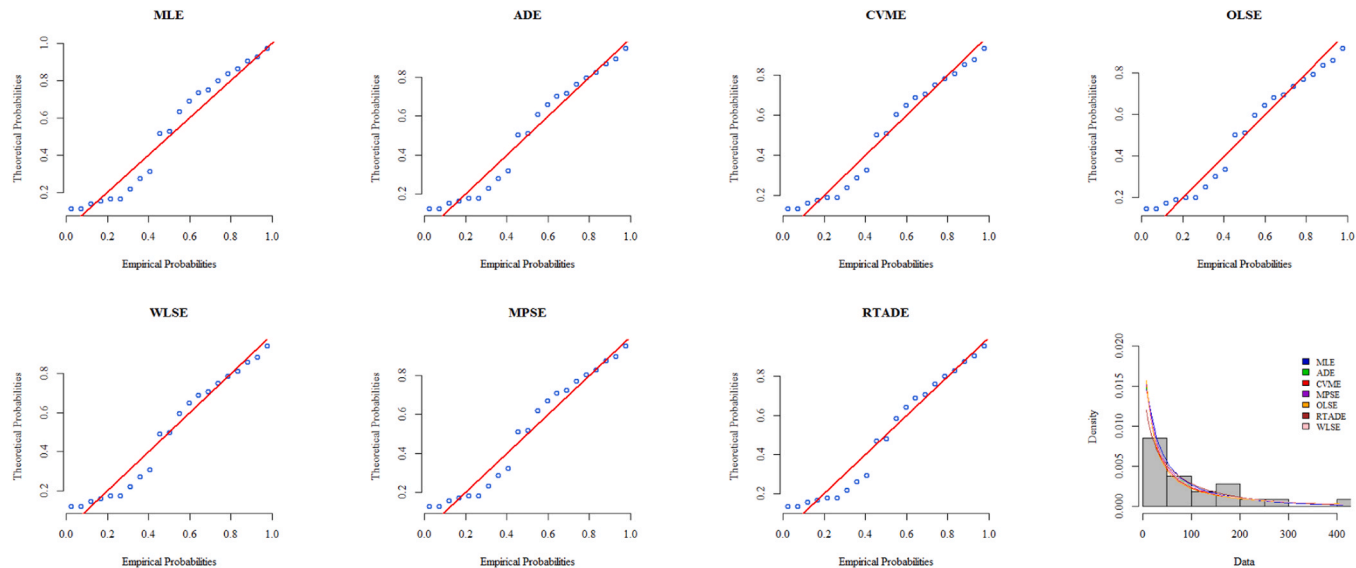


Fig. 19. The PP-plots and fitted density for lungs cancer patient's data.

Table 11
Classical estimates for 20 acute myeloid leukemia patient's data.

Statistics	MLE	ADE	CVME	MPSE	LSE	RTADE	WLSE
$\hat{\alpha}$	0.0010	0.0010	0.0010	0.0010	0.0010	0.3405	0.0010
$\hat{\tau}$	0.0728	0.0766	0.0525	0.1011	0.0688	0.0565	0.0865
$\hat{\phi}$	2.9240	2.8553	3.2910	2.5286	2.9592	3.0770	2.6986
CVME	0.0537	0.0544	0.0513	0.0582	0.0536	0.0554	0.0561
ADE	0.3161	0.3186	0.3093	0.3342	0.3157	0.3233	0.3255
KS	0.1550	0.1565	0.1306	0.1749	0.1449	0.1505	0.1617
KS-P-Value	0.6669	0.6552	0.8418	0.5174	0.7427	0.7010	0.6157

12. Limitations of study

While our research introduces the new Weibull (NEWE) model as a groundbreaking approach to modeling cancer patient data, it is important to acknowledge the inherent limitations that go with our findings. Firstly, the study's reliance on the NEWWE model, though advantageous for lung cancer and acute myeloid leukemia, might not be universally

applied across all cancer types. This specificity raises questions about the model's versatility and its adaptability to other complex diseases. Secondly, the effectiveness of the NEWWE model is deeply intertwined with the quality and comprehensiveness of the data it analyzes. In scenarios where data are sparse, incomplete, or biased, the model's performance could be significantly compromised, potentially affecting the reliability of survival time predictions. Moreover, the study's assessment

Table 12
Classical estimates for 121 breast cancer patient’s data.

Statistics	MLE	ADE	CVME	MPSE	LSE	RTADE	WLSE
$\hat{\alpha}$	0.0010	0.7056	0.2451	0.0010	0.2270	1.2648	0.8903
$\hat{\zeta}$	0.0060	0.0034	0.0049	0.0071	0.0053	0.0019	0.0029
$\hat{\phi}$	1.3058	1.3942	1.3387	1.2641	1.3187	1.4965	1.4227
CVME	0.0536	0.0553	0.0535	0.0532	0.0534	0.0600	0.0566
ADE	0.4013	0.3942	0.3950	0.3960	0.3939	0.4098	0.3980
KS	0.0599	0.0638	0.0620	0.0631	0.0622	0.0664	0.0653
KS-P-Value	0.7784	0.7089	0.7417	0.7212	0.7365	0.6593	0.6800

Table 13
Classical estimates for 33 acute myelogenous leukemia patient’s data.

Statistics	MLE	ADE	CVME	MPSE	LSE	RTADE	WLSE
$\hat{\alpha}$	5.0000	5.0000	5.0000	5.0000	5.0000	5.0000	5.0000
$\hat{\zeta}$	0.0014	0.0010	0.0023	0.0010	0.0026	0.0010	0.0020
$\hat{\phi}$	1.4132	2.2107	1.2116	2.2107	1.1681	2.2107	1.2618
CVME	0.0761	0.2600	0.0849	0.2600	0.0863	0.2600	0.0828
ADE	0.4987	1.7122	0.5483	1.7122	0.5560	1.7122	0.5362
KS	0.1236	0.4155	0.0970	0.4155	0.0966	0.4155	0.1042
KS-P-Value	0.6941	<0.0001	0.9152	<0.0001	0.9176	<0.0001	0.8664

Table 14
Classical estimates for 18 patients’ data.

Statistics	MLE	ADE	CVME	MPSE	LSE	RTADE	WLSE
$\hat{\alpha}$	0.0010	0.0010	0.0010	0.0010	0.0010	0.0010	0.0010
$\hat{\zeta}$	0.0081	0.0091	0.0030	0.0182	0.0051	0.0010	0.0047
$\hat{\phi}$	1.1340	1.0793	1.3232	0.9402	1.1977	1.5720	1.2274
CVME	0.1142	0.1209	0.1051	0.1305	0.1138	0.0901	0.1106
ADE	0.6755	0.7140	0.6241	0.7681	0.6740	0.5384	0.6553
KS	0.1839	0.1557	0.1258	0.2077	0.1261	0.1506	0.1237
KS-P-Value	0.5767	0.7755	0.9383	0.4194	0.9369	0.8092	0.9459

Table 15
Classical estimates for lungs cancer patient’s data.

Statistics	MLE	ADE	CVME	MPSE	LSE	RTADE	WLSE
$\hat{\alpha}$	3.5040	3.8776	4.1037	3.9080	4.3538	0.0010	3.8519
$\hat{\zeta}$	0.0010	0.0010	0.0010	0.0010	0.0010	0.0275	0.0010
$\hat{\phi}$	1.2908	1.2316	1.2036	1.2380	1.1764	0.7860	1.2203
CVME	0.0878	0.0914	0.0929	0.0907	0.0941	0.0935	0.0926
ADE	0.5700	0.5874	0.5943	0.5833	0.6001	0.6164	0.5938
KS	0.1200	0.1226	0.1326	0.1260	0.1451	0.1362	0.1200
KS-P-Value	0.9231	0.9104	0.8539	0.8928	0.7683	0.8307	0.9230

predominantly hinges on classical estimation techniques, which, while proven for consistency, may not fully capture the dynamic nature of cancer progression in the face of emerging treatment modalities and genetic variations. This limitation underscores the need for continuous refinement of estimation methodologies to keep pace with advancements in oncology. Additionally, the practical implementation of the NEWE model in clinical settings poses another challenge, needing a multifaceted approach that includes technological integration, healthcare professional training, and patient education. Lastly, our study’s findings, though promising, are subject to the constraints of simulation studies. Real-world applications and longitudinal studies are essential to confirming the model’s predictive accuracy and its impact on clinical outcomes. Addressing these limitations requires a collaborative effort among researchers, clinicians, and policymakers to enhance the model’s applicability, ensure the accuracy of cancer treatment predictions, and ultimately improve patient care.

13. Recommendations

To improve cancer care and patient outcomes, it is important for research organizations, governments, healthcare professionals, and policymakers to support the use of advanced models like the new Weibull (NEWE) model. This requires funding research and development to expand these models beyond lung cancer and acute myeloid leukemia to other cancer types. Collaboration between healthcare institutions and researchers is needed to smoothly integrate these models into practice. Health policies and treatment guidelines should reflect the insights provided by these models to improve early screening, targeted therapies, and personalized treatments. Educational institutions and professional organizations should train future healthcare professionals in probabilistic modeling and data analytics, so they are ready to apply these tools in real-world settings. Working across different fields can help develop better models that consider genetics, environment, and lifestyle factors. Involving patients in their treatment decisions with the help of these models ensures care is centered around their needs. Finally, global cooperation and data sharing between researchers and governments will

speed up the improvement and validation of these models, helping to advance cancer care and survival strategies. Following these recommendations will make cancer care more precise, personal, and effective, bringing us closer to a future where treatment is tailored to each patient's needs.

14. Future recommendations

Moving forward, efforts should focus on integrating time-dependent factors within the NEWE model to capture dynamic changes in patient conditions and treatment effects over time. Developing hybrid models by combining probabilistic approaches with machine learning techniques could further enhance prediction accuracy. Exploring applications across more diverse cancer types and incorporating competing risks models will provide deeper insights into patient outcomes. Bayesian frameworks could also be introduced for parameter estimation, adding flexibility and better uncertainty quantification, especially in smaller datasets. Robust methods for handling missing data, along with real-time data integration, will make these models more applicable in clinical practice. Personalizing treatment strategies through predictive models, coupled with interactive decision-support tools, will empower clinicians to improve patient care. These advancements, when pursued collectively, will significantly enhance cancer research and care, moving towards a future where predictions are more precise, treatments are more effective, and patient outcomes are optimized.

CRedit authorship contribution statement

M Yusuf: Formal analysis. **Anoop Kumar:** Methodology. **M. E Bakr:** Formal analysis. **Yusra A. Tashkandy:** Writing – original draft. **Mohammed A. Meraou:** Software. **M.M. Abd El-Raouf:** Formal analysis.

Declaration of Competing Interest

The authors declare that there are no conflict of interest.

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Appendix

The datasets mentioned below have been analyzed in the interpretation of cancer data section.

Application 1: These survival times are as follows: 2.226, 2.113, 3.631, 2.473, 2.720, 2.050, 2.061, 3.915, 0.871, 1.548, 2.746, 1.972, 2.265, 1.200, 2.967, 2.808, 1.079, 2.353, 0.726, and 1.958 months.

Application 2: The survival times for 121 breast cancer patients between the years 1929 and 1938 are as follows: 2:0.3, 0.3, 4.0, 5.0, 5.6, 6.2, 6.3, 6.6, 6.8, 7.4, 7.5, 8.4, 8.4, 10.3, 11.0, 11.8, 12.2, 12.3, 13.5, 14.4, 14.4, 14.8, 15.5, 15.7, 16.2, 16.3, 16.5, 16.8, 17.2, 17.3, 17.5, 17.9, 19.8, 20.4, 20.9, 21.0, 21.0, 21.1, 23.0, 23.4, 23.6, 24.0, 24.0, 27.9, 28.2, 29.1, 30.0, 31.0, 31.0, 32.0, 35.0, 35.0, 37.0, 37.0, 37.0, 38.0, 38.0, 38.0, 39.0, 39.0, 40.0, 40.0, 40.0, 41.0, 41.0, 41.0, 42.0, 43.0, 43.0, 43.0, 44.0, 45.0, 45.0, 46.0, 46.0, 47.0, 48.0, 49.0, 51.0, 51.0, 51.0, 52.0, 54.0, 55.0, 56.0, 57.0, 58.0, 59.0, 60.0, 60.0, 60.0, 61.0, 62.0, 65.0, 65.0, 67.0, 67.0, 68.0, 69.0, 78.0, 80.0, 83.0, 88.0, 89.0, 90.0, 93.0, 96.0, 103.0, 105.0, 109.0, 109.0, 111.0, 115.0, 117.0, 125.0, 126.0, 127.0, 129.0, 129.0, 139.0, 154.0.

Application 3: The survival times of the acute myelogenous leukemia patients dataset include the following values: 65, 156, 100, 134, 16, 108, 121, 4, 39, 143, 56, 26, 22, 1, 1, 5, 65, 56, 65, 17, 7, 16, 22, 3, 4, 2, 3, 8, 4, 3, 30, 4, and 43 weeks.

Application 4: The present dataset represents the ages (in months) of 18 patients who died from causes other than cancer, as described: 0.3, 4, 7.4, 15.5, 23.4, 46, 46, 51, 65, 68, 83, 88, 96, 110, 111, 112, 132, and 162.

Application 5: The survival time's data for advanced lung cancer patients undergoing chemotherapy treatments are as follows: 411, 126, 118, 82, 8, 25, 11, 54, 153, 16, 56, 21, 287, 10, 8, 12, 177, 12, 200, 250, 100.

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