

BOOTSTRAP RESAMPLING METHOD FOR ASSESSING MODEL ADEQUACY OF THE GOMPERTZ MODEL WITH RIGHT-CENSORED DATA

*(Kaedah Pensampelan Semula Butstrap untuk Menilai Kesesuaian Model Gompertz
dengan Data Tertapis ke Kanan)*

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ABSTRACT

Traditional Cox-Snell residuals are widely used for assessing goodness-of-fit in survival models, but they often perform inadequately in the presence of high censoring or small sample sizes, leading to poor model diagnostics. To address this limitation, this study extends the Gompertz parametric survival model by incorporating a single fixed covariate under right-censored data and proposes new modifications to the Cox-Snell residuals aimed at improving diagnostic accuracy. A comprehensive simulation study was conducted across varying levels of censoring and sample sizes, using maximum likelihood estimation to fit the model. Four novel residuals were developed by applying harmonic mean, geometric mean, bootstrap harmonic mean, and bootstrap geometric mean transformations to the standard Cox-Snell residuals. These modified residuals were evaluated using regression diagnostics consisting of intercept, slope, and R-squared values obtained from plots of the residuals against the cumulative hazard function. The findings show that the bootstrap-based residuals, particularly the bootstrap harmonic mean and bootstrap geometric mean, consistently provide better goodness-of-fit assessments than both the traditional Cox-Snell residuals and their non-bootstrap counterparts. These results highlight the potential of the proposed residuals to enhance model evaluation, especially in settings with substantial censoring or limited data.

Keywords: bootstrap; Gompertz model; right censored data; Cox-Snell residuals; survival analysis

ABSTRAK

Sisa Cox-Snell tradisional digunakan secara meluas untuk menilai kesesuaian model dalam model survival, tetapi ia sering menunjukkan prestasi yang tidak mencukupi jika terdapat penapisan yang tinggi atau saiz sampel yang kecil, yang membawa kepada diagnostik model yang lemah. Untuk mengatasi batasan ini, kajian ini melanjutkan model survival parametrik Gompertz dengan menggabungkan satu kovariat tetap di bawah data yang disensor kanan dan mencadangkan pengubahsuaian baharu pada sisa Cox-Snell yang bertujuan untuk meningkatkan ketepatan diagnostik. Satu kajian simulasi komprehensif telah dijalankan merentas pelbagai tahap sensor dan saiz sampel, menggunakan anggaran kebolehdjian maksimum untuk menyesuaikan model. Empat sisa novel telah dibangunkan dengan menggunakan min harmonik, min geometri, min harmonik butstrap, dan transformasi min geometri butstrap kepada sisa Cox-Snell standard. Sisaan yang diubah suai ini dinilai menggunakan diagnostik regresi yang terdiri daripada nilai pintasan, kecerunan, dan R-kuasa dua yang diperoleh daripada plot sisaan melawan fungsi bahaya kumulatif. Penemuan menunjukkan bahawa sisa berasaskan butstrap, terutamanya min harmonik butstrap dan min geometri butstrap, secara konsisten memberikan penilaian kesesuaian yang lebih baik berbanding kedua-dua sisa Cox-Snell tradisional dan yang tidak berasaskan butstrap. Keputusan ini menyerlahkan potensi sisa yang dicadangkan untuk meningkatkan penilaian model, terutamanya dalam tetapan dengan penapisan yang ketara atau data yang terhad.

Kata kunci: bootstrap; model Gompertz; data tertapis ke kanan; residu Cox-Snell; analisis kelangsungan hidup

1. Introduction

In survival analysis, assessing model adequacy is critical for ensuring the reliability of estimated survival probabilities and hazard rates. The Gompertz model, initially introduced by Benjamin Gompertz in 1825, has become a cornerstone in modeling mortality data due to its exponentially increasing hazard function, making it especially suitable for human aging and reliability studies. Despite its historical importance and frequent application in fields such as actuarial science, biostatistics, and epidemiology, less attention has been paid to the diagnostic evaluation of Gompertz models, particularly under censoring conditions. The Cox-Snell residual, a standard tool for model validation in survival analysis, is known to perform poorly when data are subject to right censoring. This study aims to address this gap by proposing improved versions of Cox-Snell residuals tailored for the Gompertz model in censored data settings. The most common type of censoring in survival analysis is the right censoring. As noted by Collett (2003), right censoring occurs when the survival time of an individual extends beyond the last known time that the individual is observed to be alive after entering the study. In other words, right censoring arises when some individuals experience the event of interest after the final observed time, such that the true event time is unobserved and lies to the right of the censoring time.

Over the past century, numerous studies have contributed to the theoretical and empirical advancement of the Gompertz model. Garg *et al.* (1970) examined the model's properties and compared parameter estimation techniques including least squares and maximum likelihood methods. Makany (1991) focused on the model's application to accretionary growth, while Chen (1997) derived exact confidence intervals and joint confidence regions for the model parameters. Wu *et al.* (2004) extended this by evaluating parameter estimation methods under complete and first-failure censored data.

Recent contributions have investigated the performance of the model in more complex settings. Lenart (2012) compared the method of moments with maximum likelihood estimation (MLE), finding MLE to be more accurate. Kiani and Arasan (2013) examined the model in the presence of time-dependent and fixed covariates under right-censored conditions, further comparing Wald and Jackknife confidence intervals. Dey *et al.* (2018) expanded this by exploring the model under multiple types of censoring: interval, right, left, and uncensored data.

In survival modeling, it is common to evaluate the adequacy of a fitted model using residual diagnostics, particularly the Cox-Snell residuals (Collett 2003). These residuals are expected to follow a unit exponential distribution when the model is correctly specified. However, as noted by Weissfeld and Schneider (1990), when censoring is present, Cox-Snell residuals deviate from this distribution, compromising their usefulness in detecting model misfit. This problem has led to the development of additional diagnostic tools, including martingale, deviance, and Schoenfeld residuals (Farrington 2000), as well as methods tailored for interval-censored data (Sparling *et al.* 2006; Sakurai & Hatori 2018).

Despite these advancements, few studies have addressed the diagnostic limitations of residuals specifically within the context of the Gompertz model under right-censored data. Moreover, current literature has not sufficiently investigated improvements or alternatives to Cox-Snell residuals tailored to the properties and challenges of the Gompertz model. While the Gompertz distribution has been widely studied with respect to parameter estimation, censoring

types, and covariate inclusion, there is a lack of focused research on model adequacy diagnostics particularly residual-based diagnostics under right-censored conditions. The standard Cox–Snell residuals, although commonly used, suffer from serious limitations in the presence of censoring. Specifically, they fail to approximate the unit exponential distribution, which reduces their effectiveness in evaluating model fit and identifying influential observations (Collett 2003; Weissfeld & Schneider 1990). While some work has been done on alternative residual types for other distributions or censoring schemes, little has been proposed or tested for enhancing Cox–Snell residuals within the Gompertz regression model. This leaves a notable methodological gap in survival model diagnostics.

The primary objective of this study is to evaluate the adequacy of the Gompertz regression model in the presence of right-censored data by addressing the known limitations of standard Cox–Snell residuals. Specifically, the study aims to investigate how varying levels of censoring and different sample sizes affect the performance of Cox–Snell residuals in assessing model fit. To overcome the diagnostic weaknesses inherent in the traditional approach particularly its deviation from the unit exponential distribution under censoring, this research proposes three modified forms of residuals: geometric mean-based, harmonic mean-based, and bootstrap-enhanced Cox–Snell residuals. These modifications are designed to improve the robustness, sensitivity, and accuracy of residual diagnostics. A simulation-based framework is employed to compare the performance of the proposed residuals against the standard and modified Cox–Snell residuals, using key diagnostic metrics such as the slope, intercept, and R-squared values of residual plots. Through this approach, the study seeks to identify which residual method provides the most reliable assessment of model adequacy under varying censoring scenarios, thereby offering a practical improvement in survival model diagnostics for Gompertz-distributed data.

2. Methodology

2.1. The Gompertz Model

The Gompertz distribution has been extensively studied and applied across various fields for more than a century. Its hazard function, defined as,

$$h(t; \gamma; \lambda) = \lambda \exp(\gamma t), t \geq 0, \lambda > 0, \gamma > 0, \quad (1)$$

reflects an exponentially increasing failure rate, where λ denotes the baseline mortality rate and γ represents the senescent component or aging component. The Gompertz distribution takes non-negative continuous random variables and exhibits an exponentially increasing hazard function (Wilson 1994). As shown by Kiani *et al.* (2012), the exponential distribution can be considered a special case of the Gompertz distribution when the senescent parameter γ approaches zero. These properties make the model particularly suited for describing life durations and survival probabilities, such as in:

$$S(t; \gamma; \lambda) = \exp \left[\frac{\lambda}{\gamma} (1 - e^{\gamma t}) \right], \quad (2)$$

and the corresponding probability density function:

$$f(t; \gamma; \lambda) = \lambda \exp(\gamma t) \times \exp \left[\frac{\lambda}{\gamma} (1 - e^{\gamma t}) \right]. \quad (3)$$

The effect of a covariate on the survival time of the i^{th} individual can be incorporated into the hazard function by letting the baseline hazard parameter λ be a function of the covariate, as follows:

$$\lambda = \exp(\beta'X). \quad (4)$$

For a dataset with covariate values x_i , where $i = 1, 2, \dots, n$, the hazard function for the i^{th} subject becomes:

$$h(t_i; \gamma; \lambda_i) = \lambda_i \exp(\gamma t_i), \quad (5)$$

where

$$\lambda_i = e^{\beta_0 + \beta_1 x_i}. \quad (6)$$

Thus, the hazard function for the Gompertz regression model can be written as:

$$h(t_i; x_i; \beta; \gamma) = e^{\beta_0 + \beta_1 x_i + \gamma t_i}. \quad (7)$$

The corresponding probability density function (PDF) and survival function are given by:

$$f(t_i; x_i; \beta; \gamma) = e^{\beta_0 + \beta_1 x_i + \gamma t_i + \frac{e^{\beta_0 + \beta_1 x_i}}{\gamma} (1 - e^{\gamma t_i})}, \quad (8)$$

$$S(t_i; x_i; \beta; \gamma) = e^{\left[\frac{e^{\beta_0 + \beta_1 x_i}}{\gamma} (1 - e^{\gamma t_i}) \right]}. \quad (9)$$

Let t_i represent the failure time and δ_i its censoring indicator for the i^{th} subject. The likelihood function for the full sample with both uncensored (observed) and right censored data is expressed as:

$$\begin{aligned} L(\beta; \gamma) &= \prod_{i=1}^n [f(t_i, x_i, \beta, \gamma)]^{\delta_{Ei}} [S(r_i, x_i, \beta, \gamma)]^{\delta_{Ri}} \\ &= \prod_{i=1}^n \left[\exp \left[\beta_0 + \beta_1 x_i + \gamma t_i + \frac{e^{\beta_0 + \beta_1 x_i}}{\gamma} (1 - e^{\gamma t_i}) \right] \right]^{\delta_{Ei}} \\ &\quad \left[\exp \left[\frac{e^{\beta_0 + \beta_1 x_i}}{\gamma} (1 - e^{\gamma t_i}) \right] \right]^{\delta_{Ri}} \end{aligned} \quad (10)$$

and the corresponding log-likelihood function is:

$$\ln[L(\beta; \gamma)] = \sum_{i=1}^n \delta_{Ei} \left[\beta_0 + \beta_1 x_i + \gamma t_i + \frac{e^{\beta_0 + \beta_1 x_i}}{\gamma} (1 - e^{\gamma t_i}) \right] +$$

$$\sum_{i=1}^n \delta_{Ri} \left[\frac{e^{\beta_0 + \beta_1 x_i}}{\gamma} (1 - e^{\gamma t_i}) \right]. \quad (11)$$

To evaluate the performance of the proposed residual diagnostics, a simulation study was conducted using $N = 1000$ replications for each configuration. The simulations involved sample sizes of $n = 30, 40, 50, 80$ and 100 . For each sample, covariate values x_i were generated independently from the standard normal distribution. The parameters values were set to $\beta_0 = -5$, $\beta_1 = 0.3$ and $\gamma = 0.5$, chosen to reflect realistic survival behavior with moderate covariate effect and increasing hazard over time.

Uniform random variables $u_i \sim U(0,1)$ were generated to simulate survival times t_i , and censoring times, c_i were drawn from an exponential distribution. The rate parameter μ of the exponential distribution was adjusted to produce six different censoring proportions: $cp = 0\%, 10\%, 20\%, 30\%, 40\%$ and 50% . The observed time for each individual was defined as: t_i if $t_i \leq c_i$ (event observed), and c_i if $t_i > c_i$ (right censored observation). Thus, the censoring proportion refers to the percentage of subjects in the sample whose survival time was censored due to the event not occurring before their censoring time. The true survival times were generated using the inverse transformation method applied to the Gompertz distribution:

$$t_i = \frac{1}{\gamma} \log \left[1 - \frac{\gamma \log(1-u_i)}{\lambda_i} \right] \quad (15)$$

Each simulation scenario represents a unique combination of sample size and censoring proportion, designed to evaluate how these two key factors affect the performance of Cox–Snell and the proposed residuals in assessing model adequacy. Varying the sample size from 30 to 100 allows for observing the behavior of residual diagnostics in small to moderate datasets, which are common in medical and actuarial studies. Simultaneously, increasing the censoring proportion from 0% to 50% reflects realistic situations where incomplete follow-up is common. These scenarios are crucial in determining whether the modified residuals maintain diagnostic accuracy and reliability under increasing data sparsity. By systematically analyzing combinations of sample size and censoring, the study offers robust evidence on the effectiveness and limitations of each residual method in practical applications.

3. Model Adequacy Checking

Cox-Snell (CS) residuals r_{Ci} , are widely used in survival data as a model adequacy procedure (Cox & Snell 1968). The model fit can be assessed by plotting the CS residuals against the cumulative hazard function in a log-cumulative hazard plot. If the model fits well, the CS residuals should follow an exponential distribution with parameter one, $\exp(1)$. A well fitting model is indicated by an intercept close to 0, and both the slope and R^2 values approaching 1. The Cox-Snell residual for the i^{th} individual, $i=1,2,\dots,n$ is defined as,

$$r_{Ci} = \hat{H}(t_i) = -\log(\hat{S}_i(t_i)) \quad (16)$$

However, CS residuals do not properly account for censored observations. Collet (2003) notes that CS residuals are biased when dealing with censored data, and the Modified Cox-Snell (MCS) residual was developed by Crowley and Hu (1977) to address this issue. Instead of adding unity censored observations (as in an exponential distribution), the MCS residual adds the median of the excess residual, $\Delta = \log(2) = 0.693$, to correct for censoring. The modified Cox-Snell residual is:

$$r_{MCI}^* = \begin{cases} r_{Ci}, & \text{for uncensored observations,} \\ r_{Ci} + 0.693, & \text{for censored observations.} \end{cases}$$

3.1 Modified Cox-Snell residuals using bootstrap method

In this study, we propose four modifications to the CS residuals, replacing the median adjustment in MCS residuals with the geometric mean (G), harmonic mean (H), and their bootstrap estimates to better capture the characteristics of censored data:

$$r_{GMCI}^* = \begin{cases} r_{Ci}, & \text{for uncensored observations,} \\ r_{Ci} + G, & \text{for censored observations.} \end{cases}$$

where G is the geometric mean of residuals that is appropriate for multiplicative structures. While, H is the harmonic mean of residuals that reduces influence of extreme large values. To evaluate these modifications, bootstrapping techniques were applied to compare residuals based on geometric and harmonic means. The bootstrap versions, denoted as BGMCS and BHMCS, use bootstrap resampling to estimate these means. Consequently, six types of residuals are included in the simulation study:

- 1) Cox-Snell Residuals (CS), r_{Ci} .
- 2) Modified Cox-Snell Residuals (MCS), r_{MCI}^* .
- 3) Geometric Mean Modified Cox-Snell Residuals (GMCS), r_{GMCI}^* .
- 4) Harmonic Mean Modified Cox-Snell Residuals (HMCS), r_{HMCI}^* .
- 5) Bootstrap Geometric Mean Modified Cox-Snell Residuals (BGMCS), r_{BGMCI}^* .
- 6) Bootstrap Harmonic Mean Modified Cox-Snell Residuals (BHMCS), r_{BHMCI}^* .

Right censoring alters the distribution of Cox–Snell residuals by increasing skewness and inflating extreme values associated with poorly estimated tail behavior. Since Cox–Snell residuals are constructed from cumulative hazard and survival functions with inherent multiplicative and reciprocal structure, arithmetic averaging can be overly sensitive to censoring effects. Geometric and harmonic mean adjustments mitigate this instability by operating on the log scale and down-weighting large residuals, respectively. However, censoring also induces nonstandard sampling distributions for these estimators, leading to finite-sample bias. Bootstrap resampling is therefore used to preserve the censoring mechanism while approximating the sampling distribution, resulting in more reliable and less biased estimates of the adjusted residual measures.

The bootstrap method is employed to provide more reliable and less biased estimates of the geometric and harmonic means, reducing variability inherent in small or skewed samples. This approach addresses limitations that simple means might not overcome, improving residual adjustment accuracy for censored observations. Using the geometric and harmonic means as replacements for the median in residual adjustments leverages their ability to better represent central tendency in skewed distributions, common in survival data residuals. This theoretically supports improved model fit assessment compared to using the median alone.

A plot of $\ln[-\ln(\hat{S}(r_{Ci}))]$ against $\ln(r_{Ci})$ should yield a linear line passing through the origin with a slope of one if the model fits well. These different residual modifications are compared to assess performance on both right-censored and uncensored data.

To compare performance, three selection criteria were used: intercept, slope and R^2 values from the plot of $\ln \left[-\ln \left(\hat{S}(r_{Ci}) \right) \right]$ against $\ln(r_{Ci})$. Residuals producing smaller ranges of these values closer to the ideal (intercept ~ 0 , slope and $R^2 \sim 1$) are preferred.

4. Simulation Results and Discussions

Table 1 and Figure 1 present the results from the simulation study. They show that as the proportion of right-censored data increases, the range of the intercept estimates decreases. However, this trend reverses as the sample size increases, suggesting a complex interaction between censoring and sample size. Overall, the results indicate that when proportion of censoring decreases, the intercept values tend to converge toward zero. This pattern is consistent across all six types of residuals analyzed. Among them, the HMCS residual consistently outperforms the others in terms of stability and performance.

Table 1: Range of intercept for various residual values

n	censoring proportion (%)	CS		MCS		GMCS		HMCS		BGMCS		BHMCS	
		min	max	min	max	min	max	min	max	min	max	min	max
30	0	-0.44	0.71	-0.44	0.71	-0.44	0.71	-0.44	0.71	-0.23	0.34	-0.23	0.34
	10	-0.51	0.71	-0.46	0.70	-0.50	0.70	-0.43	0.70	-0.28	0.35	-0.28	0.35
	20	-0.63	0.64	-0.64	0.54	-0.71	0.58	-0.63	0.61	-0.36	0.28	-0.36	0.28
	30	-0.67	0.42	-0.80	0.15	-0.93	0.29	-0.68	0.40	-0.72	0.14	-0.71	0.15
	40	-0.78	0.30	-1.23	-0.05	-1.05	0.12	-0.78	0.32	-0.91	-0.15	-0.91	-0.15
	50	-0.99	0.34	-1.61	-0.25	-1.31	0.07	-0.95	0.34	-1.24	-0.04	-1.24	-0.17
40	0	-0.56	0.26	-0.56	0.26	-0.56	0.27	-0.56	0.26	-0.25	0.27	-0.25	0.27
	10	-0.58	0.29	-0.60	0.26	-0.61	0.27	-0.60	0.28	-0.45	0.29	-0.45	0.29
	20	-0.57	0.29	-0.62	0.22	-0.61	0.22	-0.60	0.26	-0.54	0.21	-0.54	0.21
	30	-0.57	0.34	-0.68	0.17	-0.68	0.21	-0.66	0.27	-0.68	0.00	-0.86	0.00
	40	-0.64	0.28	-0.90	0.01	-0.82	0.17	-0.65	0.27	-0.91	-0.09	-0.97	-0.01
	50	-0.78	0.31	-1.30	0.00	-0.97	0.15	-0.75	0.30	-1.64	0.41	-1.60	-0.10
50	0	-0.32	0.33	-0.32	0.33	-0.32	0.33	-0.32	0.33	-0.33	0.38	-0.33	0.38
	10	-0.38	0.38	-0.40	0.27	-0.40	0.32	-0.38	0.36	-0.49	0.29	-0.49	0.29
	20	-0.42	0.39	-0.65	0.11	-0.53	0.26	-0.42	0.36	-0.71	0.13	-0.71	0.13
	30	-0.48	0.34	-0.69	0.00	-0.57	0.23	-0.42	0.34	-0.96	-0.01	-0.95	0.00
	40	-0.52	0.34	-0.75	-0.08	-0.73	0.11	-0.55	0.28	-1.16	-0.11	-1.15	-0.11
	50	-0.72	0.43	-1.33	-0.31	-0.98	0.20	-0.73	0.49	-1.27	0.16	-1.25	-0.33
80	0	-0.36	0.27	-0.36	0.27	-0.36	0.27	-0.36	0.27	-0.36	0.23	-0.36	0.23
	10	-0.46	0.27	-0.51	0.19	-0.52	0.22	-0.46	0.25	-0.69	0.07	-0.69	0.07
	20	-0.51	0.20	-0.70	0.00	-0.66	0.09	-0.52	0.16	-0.96	-0.07	-0.96	-0.07
	30	-0.67	0.17	-0.98	-0.14	-0.85	0.03	-0.66	0.16	-1.20	-0.19	-1.19	-0.19
	40	-0.81	0.08	-1.27	-0.31	-0.97	-0.06	-0.78	0.08	-1.50	0.08	-1.50	-0.39
	50	-0.95	-0.01	-1.41	-0.48	-1.08	-0.20	-0.89	0.01	-1.83	0.04	-1.82	-0.55
100	0	-0.22	0.24	-0.22	0.24	-0.22	0.24	-0.22	0.24	-0.39	0.22	-0.39	0.22
	10	-0.23	0.24	-0.27	0.22	-0.28	0.20	-0.25	0.24	-0.57	0.12	-0.56	0.12
	20	-0.30	0.32	-0.49	0.07	-0.41	0.19	-0.32	0.31	-0.76	0.02	-0.76	0.03
	30	-0.35	0.29	-0.54	0.01	-0.45	0.16	-0.41	0.29	-0.98	-0.06	-0.98	-0.06
	40	-0.49	0.24	-0.87	-0.10	-0.67	0.03	-0.52	0.23	-0.99	-0.14	-0.98	-0.14
	50	-0.68	0.19	-1.21	-0.29	-0.89	0.00	-0.68	0.20	-1.26	-0.12	-1.26	-0.36

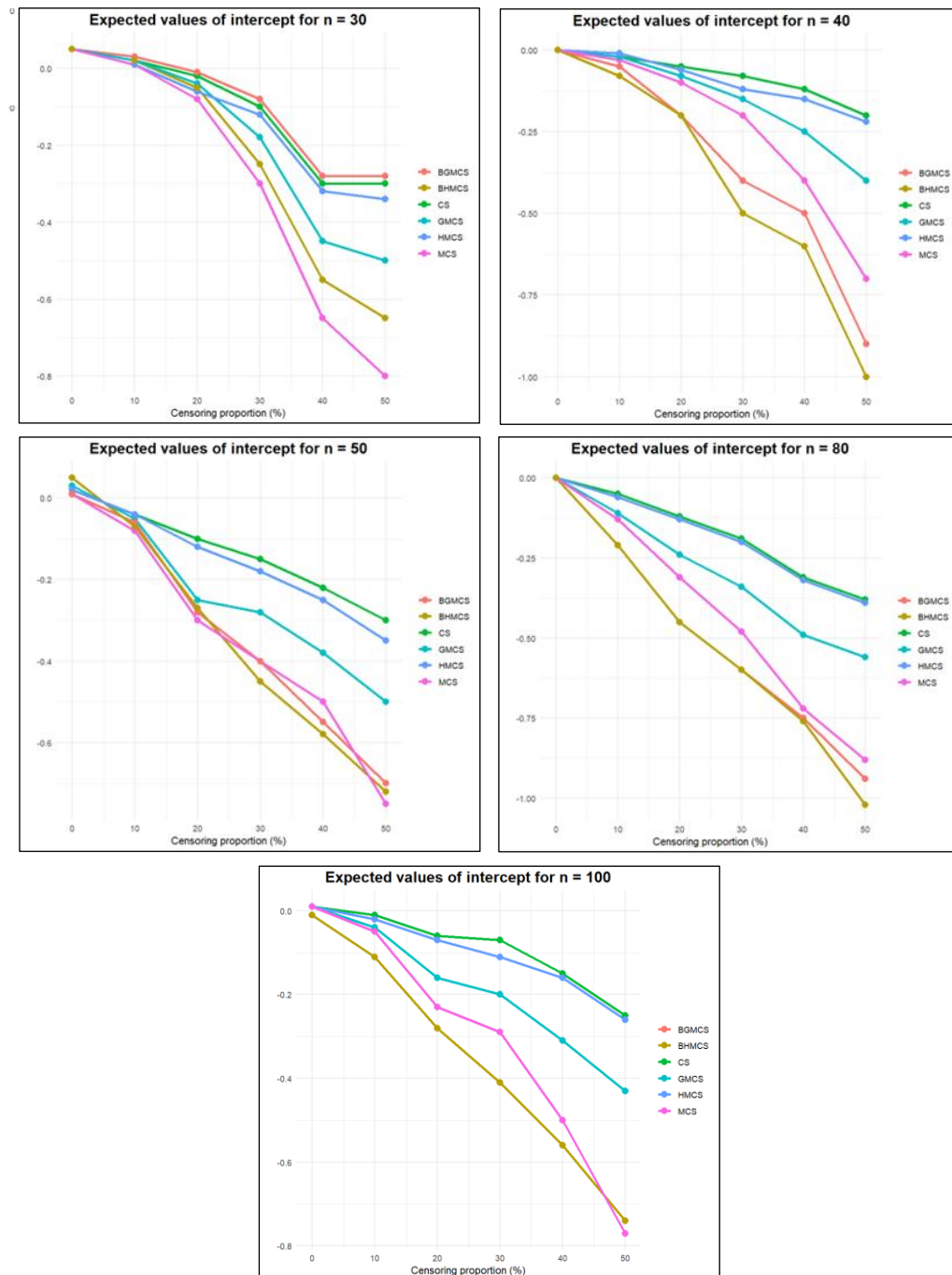


Figure 1: Comparison of residual values for estimated values of intercept

The findings from Table 2 and Figure 2 show that the range of slope estimates tends to increase as the censoring proportion increases. While the GMCS residual generally demonstrates better performance in terms of narrower slope ranges at larger sample sizes, this advantage is not consistent across all conditions. In scenarios with smaller sample sizes or higher censoring proportions, the performance differences between the six residuals diminish,

and in some cases, other residuals perform comparably to a or better than GMCS. These results highlight the importance of considering both sample size and censoring level when selecting a residual method, as no single approach consistently outperforms the others under all conditions

Table 2: Range of slope for various residual values

n	censoring proportion (%)	CS		MCS		GMCS		HMCS		BGMCS		BHMCS	
		min	max	min	max	min	max	min	max	min	max	min	max
30	0	0.452	1.167	0.452	1.167	0.452	1.167	0.452	1.167	0.600	1.334	0.600	1.334
	10	0.500	1.186	0.413	1.198	0.406	1.194	0.480	1.214	0.617	1.302	0.617	1.304
	20	0.524	1.143	0.417	1.147	0.468	1.176	0.535	1.272	0.581	1.273	0.582	1.281
	30	0.520	1.129	0.388	1.093	0.486	1.213	0.541	1.258	0.523	1.220	0.525	1.234
	40	0.525	1.285	0.413	1.354	0.553	1.600	0.572	1.309	0.517	1.327	0.521	1.328
	50	0.496	1.373	0.331	1.504	0.500	1.592	0.544	1.327	0.474	1.341	0.480	1.346
40	0	0.670	1.238	0.670	1.238	0.670	1.238	0.670	1.238	0.450	1.140	0.450	1.140
	10	0.668	1.213	0.668	1.221	0.668	1.216	0.668	1.221	0.446	1.141	0.446	1.141
	20	0.622	1.181	0.602	1.201	0.612	1.192	0.628	1.235	0.453	1.147	0.454	1.149
	30	0.606	1.206	0.575	1.207	0.602	1.221	0.591	1.230	0.465	0.969	0.449	1.065
	40	0.579	1.212	0.551	1.259	0.595	1.256	0.591	1.231	0.437	1.058	0.415	1.053
	50	0.564	1.178	0.508	1.255	0.599	1.264	0.555	1.180	0.381	1.237	0.385	1.416
50	0	0.510	1.176	0.510	1.176	0.510	1.176	0.510	1.176	0.637	1.183	0.637	1.183
	10	0.531	1.181	0.483	1.179	0.486	1.182	0.530	1.234	0.621	1.220	0.621	1.221
	20	0.573	1.197	0.477	1.185	0.502	1.196	0.575	1.253	0.599	1.191	0.599	1.193
	30	0.588	1.228	0.469	1.201	0.510	1.213	0.579	1.321	0.591	1.225	0.591	1.228
	40	0.591	1.276	0.461	1.309	0.506	1.326	0.588	1.305	0.569	1.163	0.570	1.167
	50	0.547	1.328	0.420	1.392	0.514	1.459	0.553	1.384	0.550	1.390	0.552	1.397
80	0	0.670	1.266	0.670	1.266	0.670	1.266	0.670	1.266	0.677	1.302	0.677	1.302
	10	0.669	1.365	0.661	1.364	0.662	1.357	0.675	1.386	0.659	1.274	0.659	1.275
	20	0.647	1.400	0.626	1.373	0.656	1.423	0.672	1.411	0.644	1.291	0.645	1.292
	30	0.617	1.339	0.605	1.436	0.661	1.444	0.649	1.377	0.595	1.290	0.596	1.294
	40	0.600	1.536	0.562	1.594	0.642	1.652	0.631	1.551	0.593	1.302	0.594	1.305
	50	0.585	1.454	0.549	1.622	0.667	1.613	0.655	1.474	0.581	1.776	0.538	1.782
100	0	0.674	1.187	0.674	1.187	0.674	1.187	0.674	1.187	0.613	1.165	0.613	1.165
	10	0.684	1.228	0.661	1.203	0.664	1.209	0.687	1.205	0.592	1.159	0.592	1.159
	20	0.660	1.244	0.634	1.188	0.657	1.203	0.684	1.262	0.564	1.162	0.564	1.162
	30	0.641	1.373	0.631	1.204	0.660	1.268	0.669	1.348	0.550	1.181	0.551	1.182
	40	0.636	1.340	0.609	1.293	0.674	1.354	0.673	1.431	0.529	1.203	0.530	1.205
	50	0.632	1.376	0.570	1.337	0.689	1.500	0.647	1.400	0.507	1.306	0.507	1.307

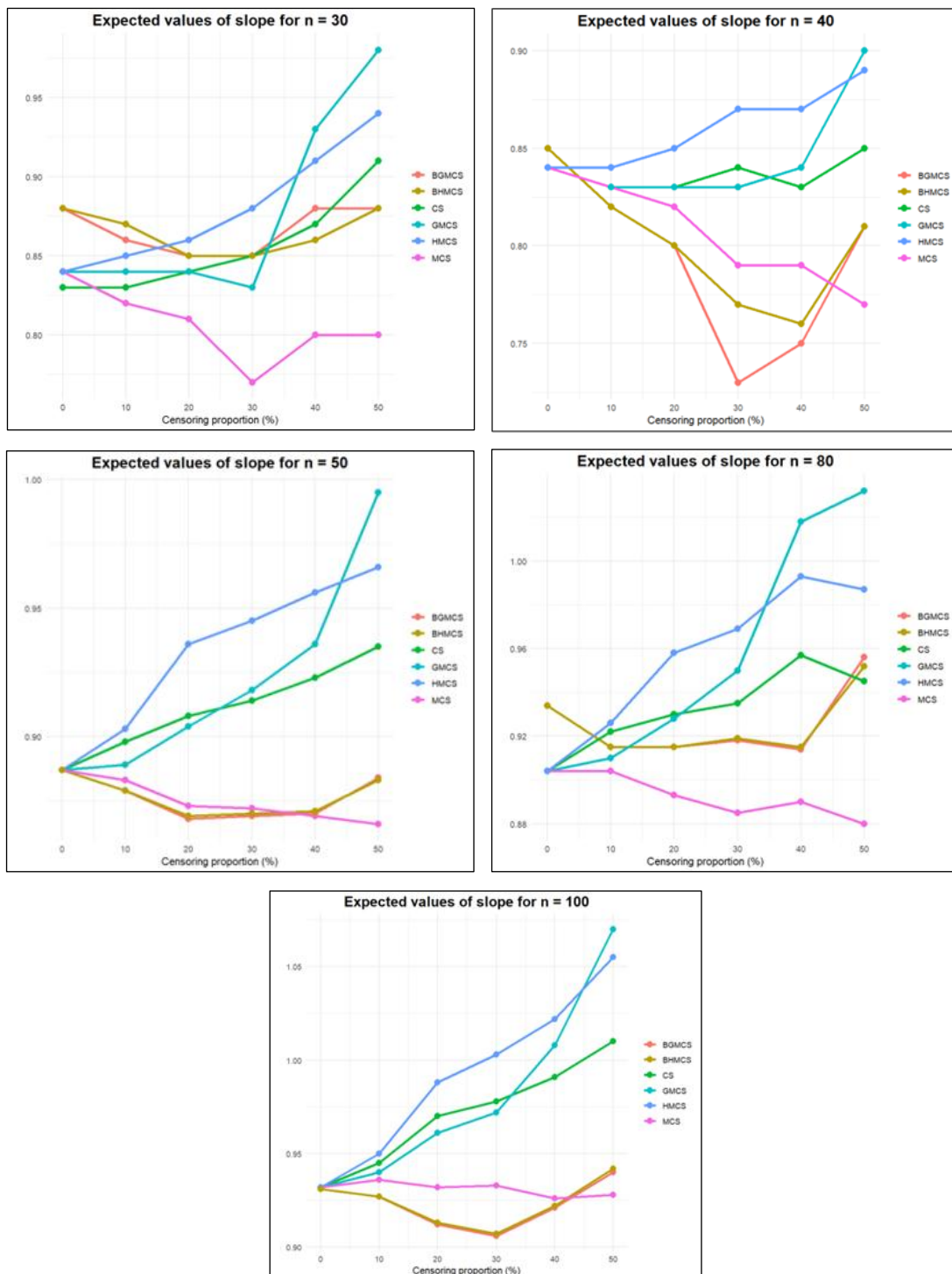


Figure 2: Comparison of residual values for estimated values of intercept

The results suggest that all residuals tend to perform more reliably in model diagnostics when the sample size is large and the censoring proportion is low. Among the six residuals studied, the proposed modifications of the Cox–Snell residual using bootstrap-based harmonic mean (BHMCS) approaches generally show improved performance in terms of reduced variability and closer adherence to theoretical expectations. However, these improvements are more evident under favorable conditions such as in larger sample sizes and lower censoring rates. In scenarios with small samples or high censoring, the performance gains are less pronounced, and other residuals may perform comparably. These findings indicate that while the HMCS and GMCS residuals are promising, their advantages are conditional and should be interpreted with caution. Further investigation is needed to evaluate their robustness under more extreme or complex data scenarios.

Table 3: R-square for various residual values

	censoring n proportion (%)	CS	MCS	GMCS	HMCS	BGMCS	BHMCS
30	0	0.698	0.698	0.698	0.698	0.962	0.962
	10	0.618	0.615	0.577	0.629	0.952	0.952
	20	0.682	0.536	0.499	0.681	0.966	0.966
	30	0.740	0.569	0.483	0.720	0.949	0.950
	40	0.730	0.611	0.511	0.759	0.932	0.936
	50	0.736	0.524	0.483	0.740	0.940	0.942
40	0	0.877	0.877	0.877	0.877	0.977	0.977
	10	0.889	0.889	0.889	0.882	0.969	0.969
	20	0.880	0.859	0.851	0.866	0.974	0.974
	30	0.889	0.825	0.795	0.864	0.922	0.965
	40	0.877	0.826	0.785	0.862	0.917	0.961
	50	0.828	0.738	0.709	0.823	0.883	0.889
50	0	0.768	0.768	0.769	0.768	0.956	0.956
	10	0.764	0.759	0.750	0.764	0.955	0.955
	20	0.811	0.742	0.688	0.808	0.947	0.948
	30	0.802	0.696	0.674	0.818	0.929	0.930
	40	0.815	0.691	0.655	0.808	0.926	0.927
	50	0.796	0.583	0.585	0.792	0.920	0.922
80	0	0.793	0.793	0.793	0.793	0.977	0.977
	10	0.791	0.774	0.773	0.787	0.968	0.968
	20	0.793	0.741	0.737	0.793	0.961	0.961
	30	0.788	0.707	0.707	0.794	0.954	0.954
	40	0.753	0.673	0.627	0.772	0.941	0.939
	50	0.739	0.644	0.622	0.761	0.933	0.934
100	0	0.907	0.907	0.907	0.907	0.979	0.979
	10	0.900	0.902	0.889	0.900	0.976	0.976
	20	0.915	0.873	0.870	0.914	0.976	0.976
	30	0.912	0.864	0.860	0.909	0.976	0.976
	40	0.887	0.830	0.801	0.901	0.958	0.958
	50	0.877	0.752	0.770	0.879	0.942	0.943

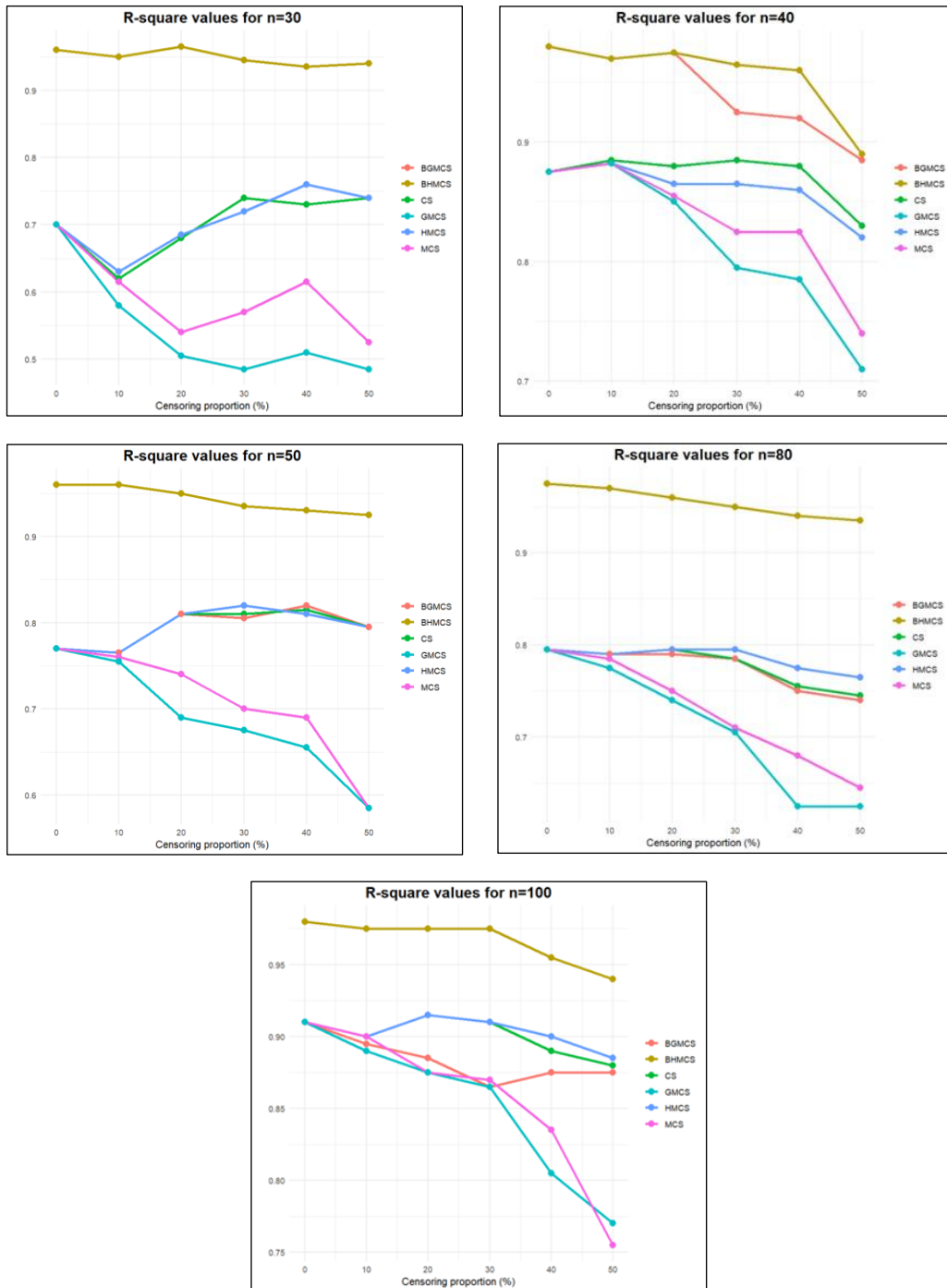


Figure 3: Comparison of residual values for R-square.

5. Conclusion

This study evaluated model adequacy in survival analysis by comparing six types of residuals, including two proposed modifications of the Cox–Snell residual: the bootstrapped geometric mean (BGMCS) and harmonic mean (BHMCS) residuals. Simulation results indicated that,

under favorable conditions specifically larger sample sizes and lower censoring proportions the GMCS and HMCS residuals exhibited modest improvements relative to traditional residuals. In these scenarios, intercept estimates approached zero and slope estimates neared one, consistent with improved model fit. However, as the proportion of censoring increased, variability in slope, intercept, and R-squared values also increased, diminishing the stability of all residuals.

Several limitations should be noted. The performance advantages of the proposed residuals were attenuated under small-sample or high-censoring conditions, and the analysis was restricted to specific simulation scenarios, without consideration of more complex survival models or real-world data. Future work should extend the evaluation of GMCS and HMCS residuals to broader modeling contexts, including applications involving real datasets, time-dependent covariates, and competing risks, and should investigate their statistical properties theoretically to better characterize robustness under varying conditions.

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