Total time on testbased goodnessoffit statistics for the reciprocal property in fatiguelife models

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Abstract

We propose a total-time-on-test (TTT)-based procedure for assessing reciprocal symmetry in positive data, a structural property shared by generalized Birnbaum–Saunders distributions. Under this property, division of a positive random variable by its median produces the same distribution as its reciprocal, which is equivalent to symmetry on the logarithmic scale. The procedure compares the normalized empirical TTT curves of the observations and their reciprocals through supremum- and grid-area-based statistics, capturing local and overall discrepancies between the curves. Exact scale invariance makes the observed statistics independent of the unknown scale parameter. Under suitable smoothness and finite-second-moment conditions, the paired difference between the empirical curves has a Gaussian limit at the square-root sample-size rate on fixed probability intervals bounded away from the endpoints, while preserving the dependence between each observation and its reciprocal. Because endpoint behavior may invalidate a full-curve asymptotic approximation, the full-curve statistics are calibrated directly by numerically stable parametric Monte Carlo simulation under fitted Birnbaum–Saunders or Birnbaum–Saunders-t reference models. Simulations and applications to four lifetime and claim data sets illustrate the performance and interpretation of the procedure. The resulting calibrations are model-specific diagnostics, and nonrejection of reciprocal symmetry should not be interpreted as confirmation of the complete fitted distribution.

Keywords: Birnbaum–Saunders distribution; log-symmetry; model-calibrated diagnostic; paired empirical process; reciprocal symmetry; total time on test.

1 Introduction

The Birnbaum–Saunders distribution was originally introduced as a probabilistic model for material fatigue and failure times by Birnbaum and Saunders [7–9]. Since then, it has been used in several areas involving positive and potentially skewed observations, including reliability, survival analysis, environmental studies, insurance, and finance. A broad account of its theoretical properties, inferential methods, extensions, and applications is provided by Balakrishnan and Kundu [5].

The classical Birnbaum–Saunders construction begins with a standard normal variable and applies a monotone transformation that produces a positive random variable. The resulting model contains a shape parameter, which controls skewness and dispersion, and a scale parameter, which also corresponds to the median of the distribution. Generalized Birnbaum–Saunders models extend this construction by replacing the normal generator with another continuous distribution that is symmetric around zero [10, 11]. This broader class includes models with lighter or heavier tails and therefore allows greater flexibility in applications. An important example is the Birnbaum–Saunders-t distribution, which uses a Student-t generator and can accommodate observations that are more extreme than those expected under the classical model [4, 14].

Despite their different generators, all generalized Birnbaum–Saunders models based on symmetric generators share a fundamental structural property. Once the random variable is divided by its scale, the standardized variable has the same distribution as its reciprocal. This property is known as reciprocal symmetry. On the logarithmic scale, it is equivalent to ordinary symmetry around the logarithm of the scale parameter [2, 16].

Reciprocal symmetry is therefore a necessary property of every generalized Birnbaum–Saunders model generated from a symmetric distribution. However, it is not exclusive to that family. The lognormal distribution and many other positive log-symmetric distributions also satisfy the same condition. Consequently, a procedure based only on reciprocal symmetry cannot determine whether the classical Birnbaum–Saunders model, the Birnbaum–Saunders-t model, or another log-symmetric distribution provides the best description of the data.

This distinction is essential for both interpretation and calibration. A reciprocal-symmetry procedure evaluates one structural feature of a fitted model rather than the complete distributional specification. It should therefore be regarded as a property-specific diagnostic and not as an omnibus goodness-of-fit test. In particular, nonrejection only indicates that the data do not provide sufficient evidence against reciprocal symmetry under the chosen calibration. It does not establish that every feature of the fitted model is correct.

The same distinction applies to the reference distribution used to calculate critical values and Monte Carlo tail probabilities. The finite-sample distribution of a reciprocal-symmetry statistic depends on more than the symmetry property itself. It can vary with the shape, tail behavior, and other features of the underlying distribution. Accordingly, a calibration generated from a fitted Birnbaum–Saunders model is specific to that model and its estimated parameters. A calibration generated from a fitted Birnbaum–Saunders-t model is similarly specific to the selected heavy-tailed reference. Neither calibration automatically provides a test with a common significance level over the full class of log-symmetric distributions.

The present article investigates reciprocal symmetry through the normalized total-time-on-test transform. The total-time-on-test curve was developed as a graphical and analytical tool for studying lifetime distributions and failure-rate behavior [1]. It summarizes the cumulative exposure accumulated up to successive population or sample quantiles. Because it depends on the entire ordered sample rather than on a small collection of moments, it can reveal systematic distributional differences that may not be visible through conventional summary measures.

Our approach compares the normalized total-time-on-test curve calculated from the original observations with the corresponding curve calculated from their reciprocals. Under reciprocal symmetry, the original variable and its reciprocal agree in distribution after

an appropriate rescaling. Since the normalized total-time-on-test transform is invariant under positive scale changes, the two population curves must then coincide. A persistent separation between the empirical curves provides evidence against reciprocal symmetry.

Two complementary discrepancy measures are considered. The maximum-gap statistic records the greatest vertical distance between the empirical curves and is therefore sensitive to a pronounced local departure. The grid-area statistic averages the absolute differences across the empirical probability grid and is designed to capture departures that are smaller at individual locations but extend over a broader portion of the distribution. The two statistics emphasize different aspects of the discrepancy and should be interpreted as related but distinct diagnostics.

A key property of the procedure is its exact scale invariance. Multiplying every observation by the same positive constant does not alter a normalized total-time-on-test curve. The curve based on the reciprocals is equally unaffected because the common reciprocal scale also cancels during normalization. It follows that the observed discrepancy between the two curves does not depend on the unknown scale parameter.

This fact has several practical consequences. Most importantly, the scale parameter does not need to be estimated in order to calculate either observed statistic. The same discrepancy is obtained from the raw observations, from observations standardized by the sample median, or from observations standardized by any other positive common value. The observed statistics are therefore identical under classical Birnbaum–Saunders and Birnbaum–Saunders-t reference analyses. What changes between these analyses is not the empirical discrepancy but the Monte Carlo distribution used to assess its magnitude.

The article also establishes a population identification result. Under suitable regularity and integrability conditions, equality of normalized total-time-on-test curves implies equality of the corresponding distributions up to a positive scale transformation. When one of the distributions is the reciprocal image of the other, equality of the normalized curves therefore characterizes reciprocal symmetry. This result provides the population foundation for comparing the two empirical curves.

The large-sample analysis requires particular care because the two empirical curves are not constructed from independent samples. Each original observation is deterministically paired with its own reciprocal. Any asymptotic argument must preserve this dependence. Treating the two curves as though they came from independent data would produce an incorrect covariance structure and could lead to invalid limiting distributions.

Under appropriate smoothness assumptions and finite-second-moment conditions, the paired difference between the empirical total-time-on-test curves converges, after multiplication by the square root of the sample size, to a centered Gaussian process. This result is established on fixed probability intervals that remain separated from both endpoints. Restricting the asymptotic theory in this way avoids irregular behavior associated with extreme empirical quantiles and extreme order statistics.

The endpoint restriction is especially important for unbounded and heavy-tailed distributions. Near the lower and upper ends of the probability range, quantile derivatives may become unstable, and a small number of extreme observations can have a substantial effect on the empirical curve. For this reason, the article does not claim a general full-curve Gaussian approximation under weak assumptions. Instead, the large-sample theory is formulated for trimmed probability intervals, where the required regularity conditions can be stated and verified more transparently.

The asymptotic distributions of the trimmed maximum and area discrepancies are then obtained from the limiting paired process. No linear differentiability of the absolute-value or

supremum operations at the null function is required. Once convergence of the underlying process has been established, the corresponding limits follow from the continuity of these operations on the relevant function space.

The numerical analysis nevertheless uses the complete empirical curves because endpoint behavior may itself contain diagnostically relevant information. Rather than relying on an unverified asymptotic approximation over the entire probability range, the full-curve statistics are calibrated directly through parametric Monte Carlo simulation. This approach reproduces the finite-sample calculation of the statistic under the fitted reference distribution and therefore avoids extending the trimmed Gaussian theory beyond the conditions under which it is justified.

Numerical stability is particularly important for heavy-tailed Birnbaum–Saunders-t models. Direct evaluation of the usual positive transformation can suffer from severe cancellation when the simulated generator takes a large negative value. The Monte Carlo algorithm therefore uses an equivalent exponential representation based on the inverse hyperbolic sine transformation. This representation preserves the reciprocal structure while providing stable numerical values across a much wider range of simulated observations.

Moment conditions must also be distinguished carefully. For a heavy-tailed Birnbaum–Saunders-t distribution, existence of the population normalized total-time-on-test curve requires a finite first moment. The square-root sample-size Gaussian theory requires stronger conditions, including a finite second moment. As a result, some parameter values may allow the population curve to be defined while failing to satisfy the assumptions needed for the stated Gaussian limit. The theoretical and simulation sections therefore separate these two requirements.

The Monte Carlo results are interpreted within this model-specific framework. The study examines the ability of the statistics to detect selected departures from log-symmetry. It also includes a log-symmetric distribution outside the Birnbaum–Saunders family in order to show that reciprocal symmetry and parametric model calibration are different issues. A distribution may satisfy the structural null condition while producing rejection rates that differ from the nominal level when critical values are generated from a misspecified reference model.

The empirical applications consider four data sets involving lifetime or claim observations. For each data set, the same observed reciprocal-symmetry discrepancies are examined under classical Birnbaum–Saunders and Birnbaum–Saunders-t calibrations. Differences between the resulting Monte Carlo tail probabilities reflect differences between the fitted reference distributions rather than differences in the observed statistics. When the two calibrations lead to different conclusions, the result should be reported as calibration sensitivity and not as direct proof that one of the two complete models is correct.

The proposed procedure should therefore be used as one component of a broader model-assessment strategy. Reciprocal symmetry is necessary for the generalized Birnbaum–Saunders models considered here, but it does not assess all aspects of their generator, tail behavior, or parametric form. Model selection between the classical and heavy-tailed versions requires additional evidence, such as likelihood comparisons, residual analysis, probability plots, or complementary goodness-of-fit procedures.

The remainder of the article is organized as follows. Section 2 reviews the classical and generalized Birnbaum–Saunders constructions and explains their reciprocal-symmetry property. Section 3 introduces the population and empirical total-time-on-test transforms and defines the two discrepancy statistics. Section 4 presents the trimmed large-sample theory and the finite-sample Monte Carlo calibration. Section 5 reports the numerical

investigation. Section 6 discusses the four data examples. Finally, Section 7 summarizes the main findings, limitations, and appropriate interpretation of the proposed diagnostic.

2 Birnbaum–Saunders models and reciprocal symmetry

2.1 Classical and generalized constructions

Let X have a continuous cumulative distribution function (CDF) G and probability density function (PDF) g, both symmetric about zero. For $\alpha > 0$ and $\beta > 0$, define

$$T = \beta \left\{ \frac{\alpha X}{2} + \sqrt{1 + \left(\frac{\alpha X}{2}\right)^2} \right\}^2 = \beta \exp\left\{ 2 \operatorname{asinh}\left(\frac{\alpha X}{2}\right) \right\}. \tag{1}$$

The second expression is algebraically equivalent to the first and is numerically more stable, especially for large negative values of X. We write $T \sim \mathrm{GBS}(\alpha, \beta; G)$. When $G = \Phi$, the standard normal CDF, $T \sim \mathrm{BS}(\alpha, \beta)$; when G is the Student-t CDF with ν degrees of freedom, we write $T \sim \text{BS-}t(\alpha, \beta, \nu)$.

For $t > 0$, set

$$\xi(t; \alpha, \beta) = \frac{1}{\alpha}\left(\sqrt{\frac{t}{\beta}} - \sqrt{\frac{\beta}{t}} \right). \tag{2}$$

The transformation in (1) is strictly increasing in X, so

$$F_T(t) = G\{\xi(t; \alpha, \beta)\}, \tag{3}$$
$$f_T(t) = g\{\xi(t; \alpha, \beta)\}\, \xi'(t; \alpha, \beta), \tag{4}$$

where

$$\xi'(t; \alpha, \beta) = \frac{t + \beta}{2\alpha\sqrt{\beta}\, t^{3/2}}. \tag{5}$$

Consequently, the hazard function is

$$h_T(t) = \frac{g\{\xi(t; \alpha, \beta)\}\, \xi'(t; \alpha, \beta)}{1 - G\{\xi(t; \alpha, \beta)\}}, \qquad t > 0. \tag{6}$$

For the classical BS model, $g = \phi$ and $G = \Phi$. Equation (6), rather than a rational expression in square roots, is the correct BS/GBS hazard formula.

Because $G(0) = 1/2$, $F_T(\beta) = 1/2$ and β is the median. Moreover,

$$\log(T/\beta) = 2 \operatorname{asinh}(\alpha X/2),$$

and the right-hand side is an odd function of the symmetric variable X. Hence $\log(T/\beta)$ is symmetric about zero.

Proposition 2.1 (Reciprocal property)**.** *For the model in* (1)*,*

$$\frac{T}{\beta} \overset{d}{=} \frac{\beta}{T}, \qquad \textit{equivalently} \qquad T \overset{d}{=} \frac{\beta^2}{T}.$$

Thus $T^{-1} \sim \mathrm{GBS}(\alpha, \beta^{-1}; G)$.

Proof. Replacing X by $-X$ in (1) takes T/β to its reciprocal. Since $X \overset{d}{=} -X$, the two transformed variables have the same distribution. □

The normalized TTT transform used below requires a finite mean. From (1), symmetry of X gives

$$\mathbb{E}(T) = \beta \left\{ 1 + \frac{\alpha^2}{2} \mathbb{E}(X^2) \right\}, \tag{7}$$

whenever $\mathbb{E}(X^2) < \infty$. For $X \sim t_\nu$, this requires $\nu > 2$ and

$$\mathbb{E}(T) = \beta \left\{ 1 + \frac{\alpha^2 \nu}{2(\nu - 2)} \right\}.$$

A finite second moment of T requires $\mathbb{E}(X^4) < \infty$, hence $\nu > 4$ for the standard Student-t generator. These distinctions are essential: at $\nu \leq 2$ the normalized population TTT curve is not defined, and at $2 < \nu \leq 4$ the root-n Gaussian theory in Section 4 does not apply, although a finite-sample statistic and direct Monte Carlo calibration can still be computed.

3 TTT transform and reciprocal-symmetry statistics

3.1 Population TTT transform

Let Y be a positive random variable supported on $(0, \infty)$ with continuous CDF F, survival function $\bar{F} = 1 - F$, quantile function

$$Q_F(u) = \inf\{y : F(y) \geq u\}, \qquad 0 < u < 1,$$

and finite mean

$$\mu_F = \mathbb{E}(Y) = \int_0^\infty \bar{F}(y)\, \mathrm{d}y.$$

The normalized TTT transform is

$$\mathcal{T}_F(u) = \frac{1}{\mu_F} \int_0^{Q_F(u)} \bar{F}(y)\, \mathrm{d}y, \qquad 0 \leq u \leq 1, \tag{8}$$

with $\mathcal{T}_F(0) = 0$ and $\mathcal{T}_F(1) = 1$. Writing the denominator as an integral up to $F^{-1}(1)$ is potentially ambiguous for unbounded support; the mean representation in (8) is the appropriate definition.

Proposition 3.1 (Scale invariance)**.** *For every constant $c > 0$, the normalized TTT transform of cY equals that of Y:*

$$\mathcal{T}_{cY}(u) = \mathcal{T}_Y(u), \qquad 0 \leq u \leq 1.$$

Proof. The quantile and mean of cY are $cQ_F(u)$ and $c\mu_F$, respectively. A change of variable in the numerator of (8) multiplies it by the same factor c. □

Thus

$$\mathcal{T}_{T/\beta} = \mathcal{T}_T, \qquad \mathcal{T}_{\beta/T} = \mathcal{T}_{1/T}. \tag{9}$$

The discrepancy between the two curves is exactly independent of β, not merely asymptotically invariant.

The normalized TTT transform determines a continuous distribution on $(0, \infty)$ up to scale. To state this precisely, assume that the quantile function is absolutely continuous. By changing variables $y = Q_F(v)$ in (8),

$$\mathcal{T}_F(u) = \frac{1}{\mu_F} \int_0^u (1 - v) Q'_F(v) \, \mathrm{d}v,$$

so $\mathcal{T}'_F(u) = (1 - u)Q'_F(u)/\mu_F$ almost everywhere.

Proposition 3.2 (Characterization up to scale)**.** *Let Y_1 and Y_2 satisfy the preceding regularity conditions and have finite positive means. Then*

$$\mathcal{T}_{Y_1} = \mathcal{T}_{Y_2} \quad \Longleftrightarrow \quad Y_2 \overset{d}{=} cY_1 \text{ for some } c > 0.$$

If additionally $\mathbb{E}(T) + \mathbb{E}(T^{-1}) < \infty$, then

$$\mathcal{T}_T = \mathcal{T}_{1/T} \quad \Longleftrightarrow \quad \text{there exists } \beta > 0 \text{ such that } T/\beta \overset{d}{=} \beta/T.$$

In that case,

$$\beta^2 = \frac{\mathbb{E}(T)}{\mathbb{E}(T^{-1})}. \tag{10}$$

Proof. If the TTT transforms are equal, their derivatives imply $Q'_{F_1}(u)/\mu_{F_1} = Q'_{F_2}(u)/\mu_{F_2}$ almost everywhere. Integration from zero gives $Q_{F_2}(u) = cQ_{F_1}(u)$ with $c = \mu_{F_2}/\mu_{F_1}$. The converse follows from Proposition 3.1. Taking $Y_1 = T$ and $Y_2 = T^{-1}$ yields $T^{-1} \overset{d}{=} cT$. Setting $\beta = c^{-1/2}$ gives the reciprocal property, and taking expectations gives (10). □

3.2 Empirical TTT curves and discrepancy statistics

Let $y_1, \ldots, y_n$ be positive observations, with order statistics $y_{(1)} \le \cdots \le y_{(n)}$ and $y_{(0)} = 0$. Define

$$H_{n,k} = \sum_{j=1}^{k} (n - j + 1)\{y_{(j)} - y_{(j-1)}\} = \sum_{j=1}^{k} y_{(j)} + (n - k)y_{(k)}, \tag{11}$$

for $k = 1, \ldots, n$. Since $H_{n,n} = \sum_{i=1}^{n} y_i$, the empirical normalized TTT curve is specified on the grid by

$$\mathcal{T}_n(k/n) = \frac{H_{n,k}}{H_{n,n}}, \qquad \mathcal{T}_n(0) = 0, \tag{12}$$

and is linearly interpolated between grid points.

Let $\mathcal{T}_n^{\iota}$ be the empirical TTT curve computed from the reciprocal observations y_i^{-1}, and write

$$\Delta_n(u) = \mathcal{T}_n(u) - \mathcal{T}_n^{\iota}(u), \qquad a_{n,k} = |\Delta_n(k/n)|, \quad k = 0, \ldots, n.$$

Both endpoint gaps vanish: $a_{n,0} = a_{n,n} = 0$. Let $\mathcal{A}_n$ denote the piecewise-linear interpolation of the absolute *grid* gaps $(k/n, a_{n,k})$. For a trimming constant $0 \le \varepsilon < 1/2$, define

$$D_{\infty,n}^{(\varepsilon)} = \sup_{\varepsilon \le u \le 1-\varepsilon} \mathcal{A}_n(u), \tag{13}$$

$$D_{A,n}^{(\varepsilon)} = \int_{\varepsilon}^{1-\varepsilon} \mathcal{A}_n(u) \, \mathrm{d}u. \tag{14}$$

For the full curves, $\varepsilon = 0$, $D_{\infty,n}$ equals the usual supremum of $|\Delta_n|$, because a piecewise-linear function attains the maximum of its absolute value at a cell endpoint. Moreover,

$$D_{A,n} = \frac{1}{n} \sum_{k=1}^{n-1} a_{n,k}. \tag{15}$$

Thus $D_{A,n}$ is exactly the trapezoidal integral of the interpolated absolute grid gaps $\mathcal{A}_n$. It is not, in general, the exact value of $\int_0^1 |\Delta_n(u)| \, \mathrm{d}u$: if the signed difference crosses zero inside a grid cell, that continuous-curve integral requires splitting the cell at the crossing. The numerical tables and applications use the source-consistent grid-area statistic in (15), now labelled explicitly as $D_{A,n}$.

The structural population target is

$$H_{\mathrm{RS}} : \ \exists\, \beta > 0 \text{ such that } T/\beta \overset{d}{=} \beta/T, \qquad H_{\mathrm{RS}}^{c} : \ \text{no such } \beta \text{ exists.} \tag{16}$$

Under Proposition 3.2, the population TTT discrepancy vanishes exactly on H_{RS}. In a sample, large values describe departure from that feature. Attaching a tail probability additionally requires a reference distribution. When the Monte Carlo law is generated from a fitted family $M_{\widehat{\theta}}$, the inferential reference is the parametric hypothesis $H_M : F \in \{M_\theta : \theta \in \Theta\}$, for which reciprocal symmetry is only a necessary implication. Such a calibration is not a level-controlled test uniformly over the larger class H_{RS}.

Since the integration interval has length at most one,

$$D_{A,n}^{(\varepsilon)} \le (1 - 2\varepsilon) D_{\infty,n}^{(\varepsilon)}.$$

Therefore, smaller numerical reference values for $D_{A,n}$ are a mathematical consequence of the definitions and do not, by themselves, establish greater power or sensitivity.

Remark 3.3 (Scope of inference)**.** *At the population level, failure of reciprocal symmetry rules out every GBS model with a symmetric generator. Under a fitted parametric reference, however, an unusually large discrepancy provides evidence against that parametric reference through a necessary reciprocal feature; it need not reject reciprocal symmetry relative to every possible log-symmetric distribution. Conversely, a nonrejection does not establish a complete BS or BS-t fit, because distributions with different symmetric generators share the same property. Full model checking should additionally assess the transformed generator $\xi(T; \widehat{\alpha}, \widehat{\beta})$, for example by a bootstrap-calibrated Anderson–Darling or probability-integral-transform diagnostic [6, 15].*

4 Large-sample theory and calibration

4.1 Paired empirical-process limit

Owing to scale invariance, assume under H_0 that $Y = T/\beta$ and hence $Y \overset{d}{=} Y^{-1}$. Let F and f denote the CDF and PDF of Y, let Q_F be its quantile function, and let $\mu = \mathbb{E}(Y)$. For a perturbation h of F, the Hadamard derivative of the TTT functional in (8), at an interior probability u, is

$$\dot{\mathcal{T}}_F[h](u) = -\frac{1}{\mu} \left[\int_0^{Q_F(u)} h(t) \, \mathrm{d}t + \frac{1-u}{f\{Q_F(u)\}} h\{Q_F(u)\} - \mathcal{T}_F(u) \int_0^{\infty} h(t) \, \mathrm{d}t \right]. \tag{17}$$

The second term is the contribution from the perturbed quantile; omitting it gives an incorrect derivative.

Let F_n and F_n^ι be the empirical CDFs of Y_i and Y_i^{-1}, respectively. The two empirical distributions are not independent: they are built from the same observations. Under H_0,

$$\sqrt{n}\{F_n(t) - F_n^\iota(t)\} = \frac{1}{\sqrt{n}} \sum_{i=1}^{n} \Big[\mathbf{1}(Y_i \le t) - \mathbf{1}(Y_i^{-1} \le t)\Big].$$

Its Gaussian limit, denoted $\mathbb{H}_F$, has covariance kernel

$$K_F(s,t) = \mathbb{E}\Big([\mathbf{1}(Y \le s) - \mathbf{1}(Y^{-1} \le s)][\mathbf{1}(Y \le t) - \mathbf{1}(Y^{-1} \le t)]\Big). \tag{18}$$

For continuous reciprocal-symmetric F, this can also be written as

$$K_F(s,t) = 2F(s \wedge t) - \mathbb{P}(t^{-1} \le Y \le s) - \mathbb{P}(s^{-1} \le Y \le t), \tag{19}$$

where an interval probability is defined as zero when its lower endpoint exceeds its upper endpoint. This kernel is symmetric in s and t and contains the cross-dependence induced by reciprocation.

Theorem 4.1 (Weak limit of the paired TTT process)**.** *Fix $0 < \varepsilon < 1/2$. Assume that:*

(i) Y is positive, continuous, and $Y \overset{d}{=} Y^{-1}$;

(ii) f is continuous and bounded away from zero on $[Q_F(\varepsilon), Q_F(1-\varepsilon)]$;

(iii) $\mathbb{E}(Y^2 + Y^{-2}) < \infty$.

Then, in $\ell^\infty([\varepsilon, 1-\varepsilon])$,

$$\sqrt{n}\,\{\mathcal{T}_n - \mathcal{T}_n^\iota\} \;\rightsquigarrow\; \mathbb{Z}_F, \qquad \mathbb{Z}_F(u) = \dot{\mathcal{T}}_F[\mathbb{H}_F](u), \tag{20}$$

where $\mathbb{Z}_F$ is a centered Gaussian process with a version having uniformly continuous sample paths on the trimmed interval.

Proof. On the trimmed interval, the quantile map is Hadamard differentiable with derivative $-h\{Q_F(u)\}/f\{Q_F(u)\}$. Differentiating the numerator and denominator of (8) gives (17). Equivalently, the plug-in TTT transform admits the uniform asymptotic linearization

$$\sqrt{n}\{\mathcal{T}_{F_n}(u) - \mathcal{T}_F(u)\} = \frac{1}{\sqrt{n}} \sum_{i=1}^{n} \psi_u(Y_i) + o_p(1),$$

with ψ_u given in (21), uniformly for $u \in [\varepsilon, 1-\varepsilon]$. The same expansion for F_n^ι has summand $\psi_u(Y_i^{-1})$. Under conditions (ii)–(iii), the class of paired influence functions has an envelope bounded by a constant multiple of $1 + Y + Y^{-1}$ and is Donsker; its $L^2(P)$ semimetric is continuous in u. The functional central limit theorem therefore gives the Gaussian limit with covariance stated below. Finally, the empirical curves used in (12) linearly interpolate the plug-in values on a mesh of width $1/n$. Condition (ii) implies that the maximum interior quantile spacing is $o_p(n^{-1/2})$, so this interpolation changes the process by $o_p(1)$ after multiplication by $\sqrt{n}$. This proves (20); see van der Vaart and Wellner [17]. □

An equivalent covariance representation uses the influence function

$$\psi_u(x) = -\frac{1}{\mu}\left[\int_0^{Q_F(u)} \{\mathbf{1}(x \le t) - F(t)\}\,\mathrm{d}t + \frac{1-u}{f\{Q_F(u)\}}\{\mathbf{1}(x \le Q_F(u)) - u\}\right.$$

$$+ \mathcal{T}_F(u)(x-\mu)\Big]. \tag{21}$$

Then

$$\mathrm{Cov}\{\mathbb{Z}_F(u), \mathbb{Z}_F(v)\} = \mathbb{E}\left[\{\psi_u(Y) - \psi_u(Y^{-1})\}\{\psi_v(Y) - \psi_v(Y^{-1})\}\right].$$

This is the covariance of the TTT-difference process, not merely the covariance of the two empirical CDFs.

Corollary 4.2 (Limits of the distance statistics)**.** *Under the assumptions of Theorem 4.1,*

$$\sqrt{n}\, D^{(\varepsilon)}_{\infty,n} \xrightarrow{d} \sup_{\varepsilon \le u \le 1-\varepsilon} |\mathbb{Z}_F(u)|, \tag{22}$$

$$\sqrt{n}\, D^{(\varepsilon)}_{A,n} \xrightarrow{d} \int_{\varepsilon}^{1-\varepsilon} |\mathbb{Z}_F(u)|\, \mathrm{d}u. \tag{23}$$

Proof. Set $Z_n = \sqrt{n}\{\mathcal{T}_n - \mathcal{T}_n^{\iota}\}$. Theorem 4.1 gives $Z_n \rightsquigarrow \mathbb{Z}_F$ in the supremum norm, with a continuous version of the limit on the trimmed interval. Consequently, Z_n is asymptotically uniformly equicontinuous. On each mesh cell, the difference between the linear interpolation of the endpoint values $|Z_n(k/n)|$ and the absolute value of the linear interpolation of Z_n is bounded by the oscillation of Z_n on that cell. Since the mesh is $1/n$, this bound is $o_p(1)$ uniformly. Hence $\sqrt{n}\,\mathcal{A}_n \rightsquigarrow |\mathbb{Z}_F|$ in $\ell^\infty([\varepsilon, 1-\varepsilon])$. The supremum and integral maps are Lipschitz continuous on this space, so the asserted limits follow from the continuous mapping theorem. No claim that the absolute-value map is linearly Hadamard differentiable at zero is needed. □

Remark 4.3 (Endpoint qualification)**.** *Theorem 4.1 and Corollary 4.2 are stated for a fixed $\varepsilon > 0$. They do not by themselves justify $\sqrt{n}$ scaling for the untrimmed statistics with $\varepsilon = 0$. Near zero and one, quantile derivatives can be unbounded and extreme order statistics can dominate, especially for unbounded or heavy-tailed distributions. The full-curve statistics reported below are therefore treated as finite-sample statistics and calibrated directly by Monte Carlo.*

Remark 4.4 (Heavy-tailed BS-t models)**.** *For a standard Student-t generator, the population TTT transform requires $\nu > 2$, whereas Theorem 4.1 requires $\nu > 4$. Results reported below for $2 < \nu \le 4$ are finite-sample Monte Carlo calibrations only. The case $\nu \le 2$ is excluded because the normalized population TTT transform has an infinite denominator.*

4.2 Model-specific Monte Carlo calibration

The limit distribution depends on F and is not distribution-free. For a fitted parametric reference $M_{\widehat{\theta}}$, we therefore use a plug-in parametric Monte Carlo calibration:

1. Fit the reference model and obtain the shape/tail estimate $\widehat{\theta}$. The fitted scale can be set to one because of Proposition 3.1.
2. For $b = 1, \ldots, B$, generate a sample of size n from $M_{\widehat{\theta}}$ and compute $D^{(b)}_{\infty,n}$ and $D^{(b)}_{A,n}$.
3. Estimate the upper $1-\gamma$ critical value by the corresponding empirical quantile. For an observed statistic D^{obs}, compute the model-conditional Monte Carlo tail area

$$\widehat{p}_M = \frac{1 + \sum_{b=1}^{B} \mathbf{1}\{D^{(b)} \ge D^{\mathrm{obs}}\}}{B+1}. \tag{24}$$

The quantity $\widehat{p}_M$ is reported below as a plug-in Monte Carlo p-value, but its interpretation is explicitly conditional on the fitted parametric reference. It is neither distribution-free over H_{RS} nor an exact finite-sample composite-null p-value, because parameter-estimation uncertainty is not reproduced. A full refitting bootstrap can be used when the raw data and fitting routine are available.

For numerical stability, samples from (1) are generated as

$$T = \exp\{2\,\mathrm{asinh}(\alpha X/2)\} \tag{25}$$

with $\beta = 1$. Direct evaluation of $\left(\alpha X/2 + \sqrt{1 + (\alpha X/2)^2}\right)^2$ can suffer catastrophic cancellation for large negative X, especially under heavy-tailed generators.

The fitted model enters the procedure only through calibration. By (9), the observed $D_{\infty,n}$ and $D_{A,n}$ are identical under BS and BS-t fits to the same data. Different decisions arise because the fitted reference distributions, and therefore their critical values or p-values, differ.

5 Simulation study

All reported simulations use $B = 10{,}000$ replications, significance level $\gamma = 0.05$, and the stable generation formula (25). Critical values are linearly interpolated empirical 0.95 quantiles. The base random seed is 20260714. For a reported rejection proportion, the binomial Monte Carlo standard error is at most $1/(2\sqrt{B}) = 0.005$. The values are Monte Carlo estimates and should be regenerated by the accompanying script when the design or software changes.

5.1 BS critical values

Table 1 reports 95% critical values for the full-curve statistics under $T \sim \mathrm{BS}(\alpha, 1)$. The scale is fixed at one without loss of generality. For moderate α, the critical values decrease roughly at a root-n rate. This empirical pattern must not be confused with a theorem for the untrimmed supremum: Corollary 4.2 applies only on fixed trimmed intervals. Larger α produces greater dispersion and larger finite-sample critical values.

Table 1: Monte Carlo 95% critical values for the supremum $D_{\infty,n}$ and grid-area $D_{A,n}$ under $T \sim \mathrm{BS}(\alpha, 1)$ ($B = 10{,}000$).

	$\alpha = 0.1$		$\alpha = 0.5$		$\alpha = 1.0$		$\alpha = 1.5$		$\alpha = 2.0$	
n	D_∞	D_A	D_∞	D_A	D_∞	D_A	D_∞	D_A	D_∞	D_A
25	0.0981	0.0195	0.1929	0.0856	0.3114	0.1407	0.4094	0.1719	0.4693	0.1853
50	0.0938	0.0141	0.1590	0.0624	0.2351	0.1054	0.3070	0.1266	0.3568	0.1372
75	0.0904	0.0116	0.1426	0.0495	0.1974	0.0872	0.2568	0.1026	0.2989	0.1108
100	0.0880	0.0101	0.1304	0.0438	0.1710	0.0750	0.2240	0.0889	0.2644	0.0971
150	0.0850	0.0082	0.1181	0.0358	0.1407	0.0608	0.1856	0.0743	0.2178	0.0789
200	0.0825	0.0071	0.1112	0.0312	0.1232	0.0533	0.1637	0.0651	0.1920	0.0690

5.2 Birnbaum–Saunders-t critical values

Tables 2 and 3 report finite-sample critical values for Student-t generators. The $\nu = 2$ setting in the source table is omitted because the normalized population TTT functional has an infinite denominator; an empirical statistic still exists at a fixed sample size, but it is outside the population formulation and has nonstandard behavior. Values for $\nu = 3$ and $\nu = 4$ remain useful as direct finite-sample calibrations, but they are outside the finite-second-moment conditions of Theorem 4.1. Their convergence need not follow a root-n Gaussian approximation and can be slow or nonmonotone.

Table 2: Monte Carlo 95% critical values under $T \sim$ BS-$t(1, 1, \nu)$ ($B = 10{,}000$).

	$\nu = 3$		$\nu = 4$		$\nu = 6$		$\nu = 10$	
n	D_∞	D_A	D_∞	D_A	D_∞	D_A	D_∞	D_A
25	0.6070	0.2926	0.5004	0.2446	0.4167	0.2040	0.3616	0.1721
50	0.5533	0.2548	0.4273	0.2026	0.3270	0.1572	0.2731	0.1289
75	0.5342	0.2392	0.3867	0.1866	0.2841	0.1369	0.2290	0.1089
100	0.5151	0.2297	0.3595	0.1728	0.2538	0.1230	0.2029	0.0963
150	0.4828	0.2080	0.3240	0.1527	0.2133	0.1034	0.1662	0.0781
200	0.4649	0.1980	0.2956	0.1361	0.1908	0.0919	0.1490	0.0694

Table 3: Monte Carlo 95% critical values under $T \sim$ BS-$t(0.1, 1, \nu)$ ($B = 10{,}000$).

	$\nu = 3$		$\nu = 4$		$\nu = 6$		$\nu = 10$	
n	D_∞	D_A	D_∞	D_A	D_∞	D_A	D_∞	D_A
25	0.3241	0.0632	0.2446	0.0434	0.1758	0.0292	0.1406	0.0244
50	0.3453	0.0464	0.2714	0.0309	0.1922	0.0217	0.1418	0.0176
75	0.3676	0.0409	0.2861	0.0258	0.1990	0.0179	0.1431	0.0140
100	0.3756	0.0367	0.2923	0.0224	0.2039	0.0156	0.1447	0.0124
150	0.3694	0.0307	0.2977	0.0186	0.2103	0.0129	0.1427	0.0102
200	0.3805	0.0284	0.3065	0.0160	0.2119	0.0111	0.1479	0.0089

For fixed α, smaller ν generally produces larger critical values because rare extreme observations have a stronger effect on the normalized TTT curve and on its reciprocal. The raw critical values of the grid-area statistic D_A and the supremum statistic D_∞ should not be compared as if they were on a common scale. Power comparisons require a common set of alternatives and separate calibration of each statistic.

5.3 Rejection probabilities under selected distributions

Table 4 uses the BS critical values at $n = 100$ and $\alpha = 1$, namely 0.1710 for D_∞ and 0.0750 for D_A. The table is a cross-calibration scope study rather than an omnibus power comparison or a size study for the composite reciprocal-symmetry class. In particular, a

lognormal distribution is log-symmetric and therefore satisfies reciprocal symmetry after scaling by its median. Its low rejection rate under this particular BS reference is consistent with the property-specific nature of the statistic, but nominal level 0.05 is not guaranteed for every reciprocal-symmetric distribution under BS critical values.

Table 4: Monte Carlo rejection probabilities at nominal level 0.05 using BS$(1, 1)$ critical values, with $n = 100$ and $B = 10{,}000$.

Distribution	Parameterization	Log-symmetric?	Reciprocal-symmetric?	D_∞	D_A
Exponential	rate 1	No	No	0.9890	0.9892
Gamma	shape 2, scale 1	No	No	0.6613	0.7783
Inverse Gaussian	mean 2, shape 1	No	No	0.4231	0.4059
Lognormal	log-mean -0.25, log-SD $\sqrt{0.5}$	Yes	Yes	0.0129	0.0342
Weibull	shape 1.5, scale 2	No	No	0.9092	0.9526

The strong rejection rates for the exponential and Weibull cases reflect pronounced log-asymmetry. The moderate rates for the gamma and inverse Gaussian cases show that finite-sample power depends on the form and location of the asymmetry. The lognormal result is not evidence of diagnostic failure: it is structurally reciprocal-symmetric but lies outside the specific BS family. Because the calibration is BS-specific, this single cross-rejection probability must not be interpreted as a general size result for all log-symmetric distributions. An omnibus BS goodness-of-fit study must include an additional generator-sensitive statistic.

6 Applications to positive lifetime and claim data

The source analysis considered four data sets: two guinea-pig survival samples (`survpig43` and `survpig66`), one fatigue-life sample (`psi21`), and one insurance-claim sample (`amount1`); see [3, 9, 12–14]. The raw data and fitting code were not included with the supplied LaTeX file. Accordingly, the sample sizes, fitted parameters, and observed statistics in Table 5 are retained from the source analysis, while the model-conditional plug-in Monte Carlo p-values were independently recalculated from those reported parameter values using $B = 30{,}000$ replications and the stable generator (25).

Because of scale invariance, each data set has one observed pair $(D_{\infty,n}, D_{A,n})$, shared by its BS and BS-t rows. Only the calibration changes. The reported BS-t degrees of freedom are treated as fixed fitted values for calibration.

Table 5: Reported parameter estimates and observed TTT statistics, with independently recalculated model-conditional plug-in Monte Carlo p-values ($B = 30{,}000$); interpretations use level 0.05.

Data set	Model	n	$\widehat{\alpha}$	$\widehat{\beta}$	$\widehat{\nu}$	D_∞	p_∞	D_A	p_A	Interpretation
`survpig43`	BS	72	0.7039	140.82	–	0.1537	0.039	0.0946	0.005	Both < 0.05
	BS-t	72	0.4800	141.72	4	0.1537	0.202	0.0946	0.130	Neither < 0.05
`survpig66`	BS	72	0.7600	77.53	–	0.1068	0.287	0.0496	0.207	Neither < 0.05
	BS-t	72	0.6103	77.45	5	0.1068	0.464	0.0496	0.417	Neither < 0.05
`psi21`	BS	101	0.3101	1336.38	–	0.2585	< 0.001	0.0361	0.011	Both < 0.05
	BS-t	101	0.2704	1336.56	9	0.2585	0.012	0.0361	0.034	Both < 0.05
`amount1`	BS	542	0.8440	6592.41	–	0.1059	< 0.001	0.0525	< 0.001	Both < 0.05
	BS-t	542	0.5089	6633.74	3	0.1059	0.260	0.0525	0.320	Neither < 0.05

For `survpig43`, both discrepancies are atypical under the fitted BS reference but neither is atypical under the more variable BS-t reference. This does not prove that the BS-t model fits every aspect of the data; it states only that the observed reciprocal-TTT discrepancy is not unusually large under that fitted calibration. For `survpig66`, neither model-conditional tail area is below 0.05 under either reference.

For `psi21`, both discrepancies are atypical under both fitted references. For `amount1`, both are atypical under the fitted BS reference, whereas neither is atypical under the heavy-tailed BS-t reference with $\nu = 3$. Since $\nu = 3$ lies outside the finite-second-moment regime, this conclusion is based exclusively on direct finite-sample Monte Carlo calibration, not on the root-n theorem.

The two statistics are reported as separate model-conditional diagnostics. If a single combined decision rule is desired, it must be prespecified and calibrated jointly, for example by applying a bootstrap to $\max\{D_{\infty,n}/c_\infty, D_{A,n}/c_A\}$ or by controlling multiplicity. No unqualified statement that a model is "accepted" is warranted from nonrejection.

7 Conclusions

We developed mathematically coherent, model-calibrated TTT diagnostics for reciprocal symmetry of distributions supported on $(0, \infty)$. The normalized TTT curves of a variable and its reciprocal coincide exactly when their distributions agree up to scale; this is equivalent to log-symmetry about some center. The empirical discrepancy is exactly scale invariant and therefore does not depend on an estimate of the median parameter β.

On every fixed interval bounded away from zero and one, the discrepancy statistics have stochastic order $n^{-1/2}$, yielding $\sqrt{n}$ rather than n normalization. The limiting Gaussian process is obtained by applying the derivative of the TTT functional to a paired empirical process that retains the dependence between Y_i and Y_i^{-1}. Trimmed supremum and grid-area limits then follow from the continuous mapping theorem. No full-curve root-n claim is made without additional endpoint conditions; the reported untrimmed statistics are calibrated directly by Monte Carlo. For BS-t models, a finite population TTT transform requires $\nu > 2$, and the stated root-n Gaussian theory requires $\nu > 4$.

The procedure is intentionally property-specific. It is sensitive to departures from log-symmetry but cannot distinguish among different log-symmetric generators. Because the reference law is model-specific, neither rejection nor nonrejection should be interpreted as a distribution-free decision over the entire reciprocal-symmetry class. In particular, nonrejection must be supplemented by a generator-sensitive, bootstrap-calibrated goodness-of-fit analysis before concluding that a BS or BS-t model is adequate. Further work should develop calibration for censored data, joint combinations with omnibus statistics, and asymptotic theory for heavy-tailed regimes with infinite variance.

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Competing interests

The authors declare no financial or non-financial competing interests directly or indirectly related to this work.

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