

Package ‘smsncut’

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Type Package

Title Optimal Diagnostic Cutoff Selection under Scale Mixtures of Skew-Normal Distributions

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Description Implements a parametric decision-theoretic framework for optimal diagnostic cutoff selection under the family of scale mixtures of skew-normal (SMSN) distributions, including the skew-normal (SN) and skew-t (ST) models as special cases. The optimal cutoff is defined by minimising a weighted misclassification risk that incorporates disease prevalence and asymmetric costs, leading to a likelihood-ratio equation that generalises the Youden criterion. Under a monotone likelihood ratio condition, existence, uniqueness, and global optimality of the cutoff are established. Asymptotic normality and a closed-form plug-in variance estimator are provided via the implicit function theorem and the multivariate delta method. Tools for model fitting, cutoff estimation, confidence intervals, the local identifiability diagnostic, and Monte Carlo simulation are included. The methodology is described in de Paula, Mouriño, and Dias Domingues (2026) [doi:10.48550/arXiv.2605.07829](https://doi.org/10.48550/arXiv.2605.07829).

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Author Renato de Paula [aut, cre] (ORCID:
<https://orcid.org/0000-0002-5835-5918>),
Helena Mouriño [aut],
Tiago Dias Domingues [aut]

Maintainer Renato de Paula <rrpaula@ciencias.ulisboa.pt>

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Contents

cutoff_admissible_interval	2
cutoff_boundary_check	3
cutoff_build_interval	4
cutoff_ci	5
cutoff_expand_interval_until_valid	6
cutoff_identifiability	7
cutoff_optimal	8
cutoff_phi	9
cutoff_risk	10
cutoff_variance	11
cutoff_youden	12
mc_one_rep	13
mc_run_all	14
mc_simulate_scenario	15
smsn_auc	16
smsn_cdf	17
smsn_density	17
smsn_fit	18
smsn_quantile	19
smsn_rdist	20
smsn_roc	20

Index	22
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cutoff_admissible_interval

Construct the admissible interval $[a, b]$

Description

Builds a compact admissible interval for cutoff optimisation from the $(\alpha/2, 1 - \alpha/2)$ quantiles of the fitted SMSN distributions (method "effective_support") or from extreme quantiles of the pooled observed sample (method "pooled_quantile").

Usage

```
cutoff_admissible_interval(
  theta0,
  theta1,
  family0,
  family1,
  method = c("effective_support", "pooled_quantile"),
  alpha = 0.01,
  x0 = NULL,
  x1 = NULL,
  probs = c(0.005, 0.995)
)
```

Arguments

theta0	Numeric vector. Parameters for group 0.
theta1	Numeric vector. Parameters for group 1.
family0	Character. Family for group 0.
family1	Character. Family for group 1.
method	Character. "effective_support" (default) or "pooled_quantile".
alpha	Numeric in (0, 1). Tail probability. Default 0.01.
x0	Numeric vector. Group-0 data (required for "pooled_quantile").
x1	Numeric vector. Group-1 data (required for "pooled_quantile").
probs	Numeric vector of length 2. Quantile probabilities for "pooled_quantile". Default c(0.005, 0.995).

Value

Named numeric vector c(a = ..., b = ...).

Examples

```
theta0 <- c(0, log(1), 1)
theta1 <- c(2, log(1), 1.5)
cutoff_admissible_interval(theta0, theta1, "SN", "SN")
```

cutoff_boundary_check *Verify boundary conditions of Proposition 5.7*

Description

Checks whether $\varphi(a; \theta) < 0$ and $\varphi(b; \theta) > 0$, which guarantees that the estimating equation $\varphi(c, \theta) = 0$ has a root inside (a, b) .

Usage

```
cutoff_boundary_check(
  a,
  b,
  theta0,
  theta1,
  family0,
  family1,
  lambda0,
  lambda1,
  pi0,
  pi1
)
```

Arguments

a	Numeric. Left endpoint of the admissible interval.
b	Numeric. Right endpoint.
theta0	Numeric vector. Unconstrained parameters for group 0.
theta1	Numeric vector. Unconstrained parameters for group 1.
family0	Character. Family for group 0 ("SN" or "ST").
family1	Character. Family for group 1 ("SN" or "ST").
lambda0	Positive numeric. Cost of a false positive.
lambda1	Positive numeric. Cost of a false negative.
pi0	Numeric in (0, 1). Prevalence of non-diseased.
pi1	Numeric in (0, 1). Prevalence of diseased.

Value

A list with components phi_a, phi_b, target_ratio, cond_a, cond_b, satisfied.

Examples

```
theta0 <- c(0, log(1), 1)
theta1 <- c(2, log(1), 1.5)
ab <- cutoff_admissible_interval(theta0, theta1, "SN", "SN")
cutoff_boundary_check(ab["a"], ab["b"], theta0, theta1, "SN", "SN",
  1, 1, 0.5, 0.5)
```

cutoff_build_interval *Build a padded search interval for cutoff root-finding*

Description

Constructs an interval $[a - \delta \cdot w, b + \delta \cdot w]$ where $[a, b]$ is the 0.5th–99.5th percentile effective support of the two fitted distributions and $w = b - a$ is its width. This mirrors the interval construction in the Monte Carlo study of de Paula et al. (2026).

Usage

```
cutoff_build_interval(theta, family0, family1, pad = 0.5)
```

Arguments

theta	Numeric vector: c(theta0, theta1).
family0	Character. Family for group 0.
family1	Character. Family for group 1.
pad	Non-negative numeric. Relative expansion factor δ . Default 0.

Value

Named numeric vector $c(a = \dots, b = \dots)$, or $c(a = NA, b = NA)$ if quantiles are non-finite.

Examples

```
theta <- c(0, log(1), 1, 2, log(1), 1.5) # theta0 then theta1, both SN
cutoff_build_interval(theta, "SN", "SN")
cutoff_build_interval(theta, "SN", "SN", pad = 0.5)
```

cutoff_ci	<i>Wald confidence interval for the optimal cutoff</i>
-----------	--

Description

Constructs a Wald-type $(1 - \alpha)$ confidence interval for c^* (equation (31) of de Paula et al., 2026):

$$\hat{c} \pm z_{1-\alpha/2} \sqrt{\hat{V}/n}.$$

Usage

```
cutoff_ci(c_star, V, n, conf_level = 0.95)
```

Arguments

c_star	Numeric. The plug-in optimal cutoff.
V	Numeric. Asymptotic variance from cutoff_variance .
n	Integer. Total sample size $n = n_0 + n_1$.
conf_level	Numeric in $(0, 1)$. Default 0.95.

Value

Named numeric vector $c(\text{lower}, \text{upper}, \text{length})$.

Examples

```
cutoff_ci(c_star = 1.6, V = 0.81, n = 400, conf_level = 0.95)
```

 cutoff_expand_interval_until_valid

Expand the search interval until boundary conditions hold

Description

Implements the additive interval-expansion strategy of de Paula et al. (2026, Section 6.1.1): starting from $\text{pad} = \text{pad_init}$, the padding is incremented by pad_step at each iteration until the boundary conditions $\varphi(a) < 0$ and $\varphi(b) > 0$ are satisfied, or max_iter attempts are exhausted.

Usage

```
cutoff_expand_interval_until_valid(
  theta,
  family0,
  family1,
  lambda0,
  lambda1,
  pi0,
  pi1,
  pad_init = 0,
  pad_step = 0.2,
  max_iter = 20L
)
```

Arguments

<code>theta</code>	Numeric vector: $c(\text{theta0}, \text{theta1})$.
<code>family0</code>	Character. Family for group 0.
<code>family1</code>	Character. Family for group 1.
<code>lambda0</code>	Positive numeric. Cost of a false positive.
<code>lambda1</code>	Positive numeric. Cost of a false negative.
<code>pi0</code>	Numeric in $(0, 1)$. Prevalence of non-diseased.
<code>pi1</code>	Numeric in $(0, 1)$. Prevalence of diseased.
<code>pad_init</code>	Initial padding. Default 0.
<code>pad_step</code>	Additive padding increment. Default 0.20.
<code>max_iter</code>	Maximum expansion attempts. Default 20.

Value

The output of [cutoff_boundary_check](#) for the final interval, augmented with `a`, `b`, `ok`, `pad`, and `iter`.

Examples

```
theta <- c(0, log(1), 1, 2, log(1), 1.5)
cutoff_expand_interval_until_valid(theta, "SN", "SN",
                                  lambda0 = 1, lambda1 = 1,
                                  pi0 = 0.5, pi1 = 0.5)
```

cutoff_identifiability

Local identifiability diagnostic

Description

Computes $|\partial_c \varphi(c^*, \theta^*)|$ at the optimal cutoff (Remark 5.14 of de Paula et al., 2026). Small values indicate a locally flat estimating equation, inflated asymptotic variance, and suggest using bootstrap confidence intervals instead of Wald intervals.

Usage

```
cutoff_identifiability(
  c_star,
  theta0,
  theta1,
  family0,
  family1,
  lambda0,
  lambda1,
  pi0,
  pi1
)
```

Arguments

c_star	Numeric. The optimal cutoff.
theta0	Numeric vector. Unconstrained parameters for group 0.
theta1	Numeric vector. Unconstrained parameters for group 1.
family0	Character. Family for group 0 ("SN" or "ST").
family1	Character. Family for group 1 ("SN" or "ST").
lambda0	Positive numeric. Cost of a false positive.
lambda1	Positive numeric. Cost of a false negative.
pi0	Numeric in (0, 1). Prevalence of non-diseased.
pi1	Numeric in (0, 1). Prevalence of diseased.

Value

Positive numeric scalar.

Examples

```
theta0 <- c(0, log(1), 1)
theta1 <- c(2, log(1), 1.5)
c_star <- cutoff_optimal(theta0, theta1, "SN", "SN", 1, 1, 0.5, 0.5)$cutoff
cutoff_identifiability(c_star, theta0, theta1, "SN", "SN", 1, 1, 0.5, 0.5)
```

cutoff_optimal	<i>Optimal diagnostic cutoff under SMSN distributions</i>
----------------	---

Description

Estimates the decision-theoretic optimal cutoff c^* as the minimiser of the weighted misclassification risk $R(c; \theta)$ over the admissible interval $[a, b]$ (Theorem 5.13 of de Paula et al., 2026). Under the monotone likelihood ratio condition, c^* is the unique root of $\varphi(c, \theta) = 0$, found by grid search followed by uniroot. If no root is found, optimize on R is used as fallback.

Usage

```
cutoff_optimal(
  theta0,
  theta1,
  family0,
  family1,
  lambda0,
  lambda1,
  pi0,
  pi1,
  interval = NULL,
  grid_length = 5000L
)
```

Arguments

theta0	Numeric vector. MLE for group 0.
theta1	Numeric vector. MLE for group 1.
family0	Character. Family for group 0.
family1	Character. Family for group 1.
lambda0	Positive numeric. Cost of a false positive.
lambda1	Positive numeric. Cost of a false negative.
pi0	Numeric in (0, 1). Prevalence of non-diseased.
pi1	Numeric in (0, 1). Prevalence of diseased.
interval	Numeric vector c(a, b). If NULL, computed via cutoff_admissible_interval .
grid_length	Integer. Grid resolution for sign-change search. Default 5000.

Value

A list with cutoff, risk, interval, and boundary.

Examples

```
theta0 <- c(0, log(1), 1)
theta1 <- c(2, log(1), 1.5)
res <- cutoff_optimal(theta0, theta1, "SN", "SN", 1, 1, 0.5, 0.5)
res$cutoff
```

cutoff_phi

Estimating equation phi(c, theta)

Description

Computes the derivative of the weighted misclassification risk with respect to the threshold (equation (15) of de Paula et al., 2026):

$$\varphi(c, \theta) = \lambda_1 \pi_1 f_1(c; \theta_1) - \lambda_0 \pi_0 f_0(c; \theta_0).$$

An interior minimiser satisfies $\varphi(c^*, \theta) = 0$, equivalently $\Lambda(c^*; \theta) = \lambda_0 \pi_0 / (\lambda_1 \pi_1)$.

Usage

```
cutoff_phi(c, theta0, theta1, family0, family1, lambda0, lambda1, pi0, pi1)
```

Arguments

c	Numeric scalar. Threshold value.
theta0	Numeric vector. Unconstrained parameters for group 0.
theta1	Numeric vector. Unconstrained parameters for group 1.
family0	Character. Family for group 0 ("SN" or "ST").
family1	Character. Family for group 1 ("SN" or "ST").
lambda0	Positive numeric. Cost of a false positive.
lambda1	Positive numeric. Cost of a false negative.
pi0	Numeric in (0, 1). Prevalence of non-diseased.
pi1	Numeric in (0, 1). Prevalence of diseased.

Value

Numeric scalar.

Examples

```
theta0 <- c(0, log(1), 1)
theta1 <- c(2, log(1), 1.5)
cutoff_phi(1.6, theta0, theta1, "SN", "SN", 1, 1, 0.5, 0.5)
```

cutoff_risk	<i>Weighted misclassification risk</i>
-------------	--

Description

Computes the expected weighted misclassification risk at threshold c (equation (13) of de Paula et al., 2026):

$$R(c; \theta) = \lambda_1 \pi_1 F_1(c; \theta_1) + \lambda_0 \pi_0 [1 - F_0(c; \theta_0)].$$

Usage

```
cutoff_risk(c, theta0, theta1, family0, family1, lambda0, lambda1, pi0, pi1)
```

Arguments

<code>c</code>	Numeric scalar. Threshold value.
<code>theta0</code>	Numeric vector. Unconstrained parameters for group 0.
<code>theta1</code>	Numeric vector. Unconstrained parameters for group 1.
<code>family0</code>	Character. Family for group 0 ("SN" or "ST").
<code>family1</code>	Character. Family for group 1 ("SN" or "ST").
<code>lambda0</code>	Positive numeric. Cost of a false positive.
<code>lambda1</code>	Positive numeric. Cost of a false negative.
<code>pi0</code>	Numeric in (0, 1). Prevalence of non-diseased.
<code>pi1</code>	Numeric in (0, 1). Prevalence of diseased.

Value

Numeric scalar.

Examples

```
theta0 <- c(0, log(1), 1)
theta1 <- c(2, log(1), 1.5)
cutoff_risk(1.5, theta0, theta1, "SN", "SN", 1, 1, 0.5, 0.5)
```

cutoff_variance	<i>Asymptotic variance of the plug-in cutoff estimator</i>
-----------------	--

Description

Computes the closed-form plug-in asymptotic variance of \hat{c} under separate SMSN maximum-likelihood fits (Theorem 5.13 and Proposition 5.15 of de Paula et al., 2026):

$$V = \frac{[\nabla_{\theta}\varphi]^{\top} \Sigma_{\text{sep}} [\nabla_{\theta}\varphi]}{[\partial_c \varphi]^2},$$

where $\Sigma_{\text{sep}} = n \cdot \text{blockdiag}(H_0^{-1}, H_1^{-1})$ and H_k is the Hessian of the negative log-likelihood for group k (equation (26)).

Usage

```
cutoff_variance(
  c_star,
  theta0,
  theta1,
  family0,
  family1,
  lambda0,
  lambda1,
  pi0,
  pi1,
  hess0,
  hess1,
  n0,
  n1,
  ridge = 1e-06
)
```

Arguments

c_star	Numeric. The plug-in optimal cutoff.
theta0	Numeric vector. MLE for group 0.
theta1	Numeric vector. MLE for group 1.
family0	Character. Family for group 0.
family1	Character. Family for group 1.
lambda0	Positive numeric. Cost of a false positive.
lambda1	Positive numeric. Cost of a false negative.
pi0	Numeric in (0, 1). Prevalence of non-diseased.
pi1	Numeric in (0, 1). Prevalence of diseased.

hess0	Numeric matrix. Hessian of the negative log-likelihood for group 0 at the MLE (from <code>smsn_fit</code>).
hess1	Numeric matrix. Hessian for group 1.
n0	Integer. Group-0 sample size.
n1	Integer. Group-1 sample size.
ridge	Numeric. Ridge added to each Hessian diagonal for numerical stability. Default 1e-6.

Value

Numeric scalar. The asymptotic variance V .

cutoff_youden	<i>Parametric Youden cutoff under SMSN distributions</i>
---------------	--

Description

Estimates the Youden cutoff c_Y as the maximiser of $J(c; \theta) = F_0(c; \theta_0) - F_1(c; \theta_1)$ over the admissible interval (equation (9) of de Paula et al., 2026), implemented via `optimize` on $J(c)$ directly.

Usage

```
cutoff_youden(
  theta0,
  theta1,
  family0,
  family1,
  interval = NULL,
  grid_length = 5000L
)
```

Arguments

theta0	Numeric vector. Parameters for group 0.
theta1	Numeric vector. Parameters for group 1.
family0	Character. Family for group 0.
family1	Character. Family for group 1.
interval	Numeric vector of length 2. If NULL, computed automatically.
grid_length	Number of grid points used in the search.

Value

Numeric scalar. The estimated Youden cutoff.

Examples

```
theta0 <- c(0, log(1), 1)
theta1 <- c(2, log(1), 1.5)
cutoff_youden(theta0, theta1, "SN", "SN")
```

mc_one_rep	<i>Run one Monte Carlo replication</i>
------------	--

Description

Run one Monte Carlo replication

Usage

```
mc_one_rep(
  theta0_true,
  theta1_true,
  family0,
  family1,
  c_true,
  lambda0,
  lambda1,
  pi0,
  pi1,
  n0,
  n1,
  flat_tol = 0.001,
  conf_level = 0.95
)
```

Arguments

theta0_true	True parameter vector for group 0.
theta1_true	True parameter vector for group 1.
family0	Family for group 0.
family1	Family for group 1.
c_true	True optimal cutoff.
lambda0	Cost of a false positive.
lambda1	Cost of a false negative.
pi0	Prevalence of group 0.
pi1	Prevalence of group 1.
n0	Sample size for group 0.
n1	Sample size for group 1.
flat_tol	Minimum admissible value of the identifiability diagnostic.
conf_level	Confidence level.

Value

A list describing the replication outcome.

mc_run_all	<i>Run all scenarios</i>
------------	--------------------------

Description

Run all scenarios

Usage

```
mc_run_all(  
  scenarios,  
  n_vec = c(200L, 400L, 1000L),  
  B = 2000L,  
  flat_tol = 0.001,  
  conf_level = 0.95,  
  seed = NULL  
)
```

Arguments

scenarios	Named list of scenarios.
n_vec	Vector of total sample sizes.
B	Number of replications.
flat_tol	Identifiability tolerance.
conf_level	Confidence level.
seed	Optional random seed.

Value

Named list of simulation outputs.

mc_simulate_scenario *Monte Carlo simulation for one scenario*

Description

Monte Carlo simulation for one scenario

Usage

```
mc_simulate_scenario(
  theta0_true,
  theta1_true,
  family0,
  family1,
  c_true,
  lambda0,
  lambda1,
  pi0,
  pi1,
  n0,
  n1,
  B = 2000L,
  flat_tol = 0.001,
  conf_level = 0.95,
  seed = NULL
)
```

Arguments

theta0_true	True parameter vector for group 0.
theta1_true	True parameter vector for group 1.
family0	Family for group 0.
family1	Family for group 1.
c_true	True optimal cutoff.
lambda0	Cost of a false positive.
lambda1	Cost of a false negative.
pi0	Prevalence of group 0.
pi1	Prevalence of group 1.
n0	Sample size for group 0.
n1	Sample size for group 1.
B	Number of replications.
flat_tol	Minimum admissible value of the identifiability diagnostic.
conf_level	Confidence level.
seed	Optional random seed.

Value

A list of Monte Carlo summary statistics.

smsn_auc	<i>Plug-in AUC estimator under SMSN distributions</i>
----------	---

Description

Approximates the AUC by the trapezoidal rule with h grid points (equation (13) of de Paula et al., 2026). The approximation error is $O(h^{-2})$; the default $h = 1000$ gives error $\approx 10^{-6}$.

Usage

```
smsn_auc(theta0, theta1, family0, family1, h = 1000L)
```

Arguments

theta0	Numeric vector. Parameters for group 0.
theta1	Numeric vector. Parameters for group 1.
family0	Character. Family for group 0.
family1	Character. Family for group 1.
h	Integer. Number of grid points. Default 1000.

Value

Numeric scalar in $[0, 1]$.

Examples

```
theta0 <- c(0, log(1), 1)
theta1 <- c(2, log(1), 1.5)
smsn_auc(theta0, theta1, "SN", "SN")
```

smsn_cdf	<i>CDF of an SMSN distribution</i>
----------	------------------------------------

Description

Evaluates the cumulative distribution function of a skew-normal (SN) or skew-t (ST) distribution at the unconstrained parametrisation $\theta = (\xi, \log \omega, \alpha)$ for SN, or $\theta = (\xi, \log \omega, \alpha, \log(\nu - 2))$ for ST.

Usage

```
smsn_cdf(x, theta, family = c("SN", "ST"))
```

Arguments

x	Numeric vector of evaluation points.
theta	Numeric vector of unconstrained parameters. Length 3 for SN, length 4 for ST.
family	Character string, either "SN" or "ST".

Value

Numeric vector of CDF values in $[0, 1]$.

Examples

```
theta_sn <- c(0, log(1), 1.5)
smsn_cdf(c(-1, 0, 1, 2), theta_sn, "SN")
```

smsn_density	<i>Density of an SMSN distribution</i>
--------------	--

Description

Evaluates the density of a skew-normal (SN) or skew-t (ST) distribution at the unconstrained parametrisation $\theta = (\xi, \log \omega, \alpha)$ for SN, or $\theta = (\xi, \log \omega, \alpha, \log(\nu - 2))$ for ST.

Usage

```
smsn_density(x, theta, family = c("SN", "ST"))
```

Arguments

x	Numeric vector of evaluation points.
theta	Numeric vector of unconstrained parameters. Length 3 for SN, length 4 for ST.
family	Character string, either "SN" or "ST".

Value

Numeric vector of density values.

Examples

```
theta_sn <- c(0, log(1), 1.5)
smsn_density(c(-1, 0, 1, 2), theta_sn, "SN")

theta_st <- c(0, log(1), 1.5, log(8 - 2))
smsn_density(c(-1, 0, 1, 2), theta_st, "ST")
```

smsn_fit

Fit an SMSN model by maximum likelihood

Description

Fits a skew-normal (SN) or skew-t (ST) distribution to a univariate sample by maximising the log-likelihood, using the unconstrained parametrisation $\theta = (\xi, \log \omega, \alpha)$ for SN or $\theta = (\xi, \log \omega, \alpha, \log(\nu - 2))$ for ST.

Usage

```
smsn_fit(x, family = c("SN", "ST"), maxit = 4000L, reltol = 1e-10)
```

Arguments

x	Numeric vector of observations. Non-finite values are removed.
family	Character string, either "SN" (default) or "ST".
maxit	Integer. Maximum number of iterations for optim. Default 4000.
reltol	Numeric. Relative convergence tolerance. Default 1e-10.

Details

The observed Fisher information matrix is computed via Richardson extrapolation as implemented in `numDeriv::hessian()`, which is critical for the reliability of the plug-in variance estimator \hat{V} in heavy-tailed models (de Paula et al., 2026, Section 6.2).

Value

A list with components:

par	MLE in unconstrained parametrisation θ .
hessian	Hessian of the negative log-likelihood at the MLE, computed by Richardson extrapolation.
logLik	Maximised log-likelihood.
family	Fitted family ("SN" or "ST").
convergence	Convergence code from optim (0 = success).

References

de Paula, R., Mouriño, H., and Dias Domingues, T. (2026). Parametric ROC analysis and optimal cutoff selection under scale mixtures of skew-normal distributions: a decision-theoretic framework with asymptotic inference. *arXiv:2605.07829*. doi:10.48550/arXiv.2605.07829.

Examples

```
set.seed(1)
x <- sn::rsn(200, xi = 0, omega = 1, alpha = 2)
fit <- smsn_fit(x, family = "SN")
fit$par
fit$convergence
```

smsn_quantile

Quantile function of an SMSN distribution

Description

Returns quantiles of a skew-normal (SN) or skew-t (ST) distribution at the unconstrained parametrisation $\theta = (\xi, \log \omega, \alpha)$ for SN, or $\theta = (\xi, \log \omega, \alpha, \log(\nu - 2))$ for ST.

Usage

```
smsn_quantile(prob, theta, family = c("SN", "ST"))
```

Arguments

prob	Numeric vector of probabilities in (0, 1).
theta	Numeric vector of unconstrained parameters. Length 3 for SN, length 4 for ST.
family	Character string, either "SN" or "ST".

Value

Numeric vector of quantiles.

Examples

```
theta_sn <- c(0, log(1), 1.5)
smsn_quantile(c(0.025, 0.5, 0.975), theta_sn, "SN")
```

 smsn_rdist

Random generation from an SMSN distribution

Description

Generates random observations from a skew-normal (SN) or skew-t (ST) distribution under the unconstrained parametrisation $\theta = (\xi, \log \omega, \alpha)$ for SN, or $\theta = (\xi, \log \omega, \alpha, \log(\nu - 2))$ for ST.

Usage

```
smsn_rdist(n, theta, family = c("SN", "ST"))
```

Arguments

n Integer. Number of observations.
theta Numeric vector of unconstrained parameters. Length 3 for SN, length 4 for ST.
family Character string, either "SN" or "ST".

Value

Numeric vector of length n .

Examples

```
set.seed(1)
theta_sn <- c(0, log(1), 1.5)
x <- smsn_rdist(100L, theta_sn, "SN")
hist(x, breaks = 20, main = "SN sample")
```

 smsn_roc

Parametric ROC curve under SMSN distributions

Description

Evaluates the parametric ROC curve at false positive rates r (equation (6) of de Paula et al., 2026):

$$\text{ROC}(r; \theta) = 1 - F_1(Q_0(1 - r; \theta_0); \theta_1).$$

Usage

```
smsn_roc(r, theta0, theta1, family0, family1)
```

Arguments

<code>r</code>	Numeric vector of false positive rates in $(0, 1)$.
<code>theta0</code>	Numeric vector. Parameters for group 0.
<code>theta1</code>	Numeric vector. Parameters for group 1.
<code>family0</code>	Character. Family for group 0.
<code>family1</code>	Character. Family for group 1.

Value

Numeric vector of true positive rates.

Examples

```
theta0 <- c(0, log(1), 1)
theta1 <- c(2, log(1), 1.5)
r <- seq(0.01, 0.99, by = 0.01)
plot(r, smsn_roc(r, theta0, theta1, "SN", "SN"), type = "l",
      xlab = "FPR", ylab = "TPR")
abline(0, 1, lty = 2)
```

Index

[cutoff_admissible_interval](#), [2](#), [8](#)
[cutoff_boundary_check](#), [3](#), [6](#)
[cutoff_build_interval](#), [4](#)
[cutoff_ci](#), [5](#)
[cutoff_expand_interval_until_valid](#), [6](#)
[cutoff_identifiability](#), [7](#)
[cutoff_optimal](#), [8](#)
[cutoff_phi](#), [9](#)
[cutoff_risk](#), [10](#)
[cutoff_variance](#), [5](#), [11](#)
[cutoff_youden](#), [12](#)

[mc_one_rep](#), [13](#)
[mc_run_all](#), [14](#)
[mc_simulate_scenario](#), [15](#)

[smsn_auc](#), [16](#)
[smsn_cdf](#), [17](#)
[smsn_density](#), [17](#)
[smsn_fit](#), [12](#), [18](#)
[smsn_quantile](#), [19](#)
[smsn_rdist](#), [20](#)
[smsn_roc](#), [20](#)