

# Package ‘sn’

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**Title** The Skew-Normal and Related Distributions Such as the Skew-t

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**Imports** mnormt (>= 1.5-4), numDeriv, stats, grDevices, graphics, utils

**Description** Build and manipulate probability distributions of the skew-normal family and some related ones, notably the skew-t family, and provide related statistical methods for data fitting and model diagnostics, in the univariate and the multivariate case.

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 sn-package

*Package sn: development and brief overview*


---

## Description

The **sn** package provides facilities to define and manipulate probability distributions of the skew-normal (SN) family and some related ones, notably the skew- $t$  (ST) family, and to apply connected statistical methods for data fitting and diagnostics, in the univariate and the multivariate case.

## Development and basic facts

The first version of the package was written in 1997 (on CRAN since 1998); subsequent versions have evolved gradually up to version 0.4-18 in May 2013. In January 2014, version 1.0-0 has been uploaded to CRAN; this represented a substantial re-writing of the earlier ‘version 0.x’. Differences between the ‘version 0’ and the ‘version 1’ series are radical; they concern the core computational

and graphical part as well as the user interface. Since version 1.0-0, the S4 protocol for classes and methods has been adopted.

Broadly speaking, the available tools can be divided in two groups: the probability section and the statistics section. For a quick start, one could look at their key functions, `makeSECdistr` and `selm`, respectively, and from here explore the rest. In the probability section, one finds also functions `dsn`, `dst`, `dmsn` and others alike; these functions existed also in ‘version 0’ and their working is still very much the same (not necessarily so their code). Additional information on the current package structure and the set of commands is available in a more extended [overview](#) of the package.

The first instance of the ‘version 1’ series (that is, 1.0-0) has appeared at the same time when the companion book by Azzalini and Capitanio (2014) was published. Although the two projects are formally separate, they adopt the same notation, terminology and logical frame. This matching and the numerous references in the software documentation to specific sections of the book for background information should facilitate familiarizing with these tools.

Information on additional and on more recent change to the package is provided in NEWS file, accessible from the package documentation index page.

A word of explanation is appropriate about the numerous references to Azzalini and Capitanio (2014) in the documentation of the package. The reason why the documentation often refers to the monograph rather than to the original research papers is that the book provides a relatively informal summary of material which has been elaborated in a number of technical papers, sometimes very technical or with information on the point of interest mixed with other material. In other words, the motivation behind this policy is readability, not indulgence in self-citation. When one or a few original sources appeared to deliver the required information in a compact and accessible form, they have been cited directly. In any case, the quoted sections of the book include bibliographic notes which refer back to the original sources.

### Backward Compatibility of ‘version 1.x-y’

There is a partial backward compatibility of ‘version 1.x-y’ versus ‘version 0-4.18’. Some functions of the older version would work as before with virtually no change; a wider set arguments is now allowed. Functions `dsn`, `dst`, `dmsn` and alike fall in this category: in some cases, the names of the arguments have been altered, but they work as before if called with unnamed arguments; similar cases are `msn.mle`, `sn.cumulants` and `T.Owen`. Notice, however, that `msn.mle` and other fitting functions have effectively been subsumed into the more comprehensive fitting function `selm`.

A second group of functions will work with little or even minimal changes. Specific examples are functions `sn.mle` and `st.mle` which have become `sn.mple` and `st.mple`, with some additional arguments (again, one can achieve the same result via `selm`). Another example is constituted by the group of functions `dp.to.cp`, `cp.to.dp` and `st.cumulants.inversion`, which have been replaced by the more general functions `dp2cp` and `cp2dp`; one only needs to pay attention to conversion from 3rd and 4th order cumulants to their standardized form in connection with the replacement of `st.cumulants.inversion`.

Finally, some functions are not there any longer, with no similarly-working functions in the new version. This is the case of `sn.mle.grouped` and `st.mle.grouped` for maximum likelihood estimation from grouped data, that is, data recorded as intervals and corresponding frequencies.

### Requirements

R version 2.15-3 or higher, plus packages `mnormt`, `numDeriv`, `stats4` in addition to standard pack-

ages (**methods**, **graphics**, etc.)

### Version

The command `citation("sn")` indicates, among other information, the running version of the package. The most recent version of the package can be obtained from the web page: <http://azzalini.stat.unipd.it/SN> which also provides related material.

From the above-indicated web page, one can also obtain the package ‘sn0’ which is essentially the last ‘version 0’ (that is, 0.4-18) with suitable renaming of certain ingredients. This allows to have both the current and the old package installed at the same time.

### Author

Adelchi Azzalini.

Please send comments, error reports *et cetera* to the author, whose web page is <http://azzalini.stat.unipd.it/>.

### Licence

This package and its documentation are usable under the terms of the “GNU General Public License” version 3 or version 2, as you prefer; a copy of them is available from <https://www.R-project.org/Licenses/>.

While the software is freely usable, it would be appreciated if a reference is inserted in publications or other work which makes use of it. For the appropriate way of referencing it, see the command `citation("sn")`.

### References

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

### See Also

[package-overview](#)

---

affineTransSECdistr    *Affine transformations and marginals of a skew-elliptical distribution*

---

### Description

Given a multivariate random variable  $Y$  with skew-elliptical (SEC) distribution, compute the distribution of a (possibly multivariate) marginal or the distribution of an affine transformation  $a + A^T Y$ .

### Usage

```
affineTransSECdistr(object, a, A, name, compNames, drop=TRUE)
marginalSECdistr(object, comp, name, drop=TRUE)
```

**Arguments**

object	an object of class SECdistrMv which identifies the source random variable, as created by <a href="#">makeSECdistr</a> or by <a href="#">extractSECdistr</a> or by a previous call to these functions
a	a numeric vector with the length <code>ncol(A)</code> .
A	a full-rank matrix with <code>nrow(A)</code> equal to the dimensionality <code>d</code> of the random variable identified by object.
name	an optional character string representing the name of the outcome distribution; if missing, one such string is constructed.
compNames	an optional vector of length <code>ncol(A)</code> of character strings with the names of the components of the outcome distribution; if missing, one such vector is constructed.
drop	a logical flag (default value: TRUE), operating only if the returned object has dimension <code>d=1</code> , in which case it indicates whether this object must be of class SECdistrUv.
comp	a vector formed by a subset of <code>1:d</code> which indicates which components must be extracted from object, on denoting by <code>d</code> its dimensionality.

**Value**

If object defines the distribution of a SEC random variable  $Y$ , `affineTransSECdistr` computes the distribution of  $a + A'Y$  and `marginalSECdistr` computes the marginal distribution of the comp components. In both cases the returned object is of class SECdistrMv, except when `drop=TRUE` operates, leading to an object of class SECdistrUv.

**Background**

These functions implement formulae given in Sections 5.1.4, 5.1.6 and 6.2.2 of the reference below.

**References**

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

**See Also**

[makeSECdistr](#), [extractSECdistr](#), [SECdistrMv-class](#)

**Examples**

```
dp3 <- list(xi=1:3, Omega=toeplitz(1/(1:3)), alpha=c(3,-1,2), nu=5)
st3 <- makeSECdistr(dp3, family="ST", name="ST3", compNames=c("U", "V", "W"))
A <- matrix(c(1,-1,1, 3,0,-2), 3, 2)
new.st <- affineTransSECdistr(st3, a=c(-3,0), A=A)
#
st2 <- marginalSECdistr(st3, comp=c(3,1), name="2D marginal of ST3")
```

---

 ais

*Australian Institute of Sport data*


---

### Description

Data on 102 male and 100 female athletes collected at the Australian Institute of Sport, courtesy of Richard Telford and Ross Cunningham.

### Usage

```
data(ais)
```

### Format

A data frame with 202 observations on the following 13 variables.

[,1]	sex	categorical, levels: female, male
[,2]	sport	categorical, levels: B_Ball, Field, Gym, Netball, Row, Swim, T_400m, Tennis, T_Sprnt, W_Polo
[,3]	RCC	red cell count (numeric)
[,4]	WCC	white cell count (numeric)
[,5]	Hc	Hematocrit (numeric)
[,6]	Hg	Hemoglobin (numeric)
[,7]	Fe	plasma ferritin concentration (numeric)
[,8]	BMI	body mass index, $\text{weight}/(\text{height})^2$ (numeric)
[,9]	SSF	sum of skin folds (numeric)
[,10]	Bfat	body fat percentage (numeric)
[,11]	LBM	lean body mass (numeric)
[,12]	Ht	height, cm (numeric)
[,13]	Wt	weight, kg (numeric)

### Details

The data have been made publicly available in connection with the book by Cook and Weisberg (1994).

### References

Cook and Weisberg (1994), *An Introduction to Regression Graphics*. John Wiley & Sons, New York.

### Examples

```
data(ais, package="sn")
pairs(ais[,c(3:4,10:13)], col=as.numeric(ais[,1]), main = "AIS data")
```

---

barolo	<i>Price of Barolo wine</i>
--------	-----------------------------

---

### Description

A data frame with prices of bottles of Barolo wine and some auxiliary variables

### Usage

```
data(barolo)
```

### Format

A data frame with 307 observations on five variables, as follows:

reseller	reseller code (factor with levels A, B, C, D)
vintage	vintage year (numeric)
volume	content volume in centilitres (numeric)
price	price in Euro (numeric)
age	age in 2010 (numeric)

For six items, vintage is NA's and so also age. Three items have a non-standard volume of 50 cl.

### Details

The data have been obtained in July 2010 from the websites of four Italian wine resellers, selecting only quotations of Barolo wine, which is produced in the Piedmont region of Italy. The price does not include the delivery charge.

The data have been presented in Section 4.3.2 of the reference below, where a subset of them has been used for illustrative purposes. This subset refers to reseller "A" and bottles of 75cl.

### Source

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

### Examples

```
data(barolo)
attach(barolo)
f <- cut(age, c(0, 5, 6, 8, 11, 30))
table(volume, f)
plot(volume, price, col=as.numeric(f), pch=as.character(reseller))
legend(400, 990, col=1:5, lty=1, title="age class",
      legend=c("4-5", "6", "7-8", "9-11", "12-30"))
#
A75 <- (reseller=="A" & volume==75)
hist(log(price[A75]),10, col="gray85")
```

# see Figure 4.7 of the source

---

coef.selm                      *Coefficients of objects created by selm*

---

## Description

coef method for classes "selm" and "mselm".

## Usage

```
## S4 method for signature 'selm'
coef(object, param.type = "CP", ...)
## S4 method for signature 'mselm'
coef(object, param.type = "CP", vector=TRUE, ...)
```

## Arguments

object	an object of class "selm" or "mselm" as created by a call to function selm.
param.type	a character string which indicates the required type of parameter type; possible values are "CP" (default), "DP", "pseudo-CP" and their equivalent lower-case expressions.
vector	a logical value (default is TRUE) which selects a vector or a list format of the returned value
...	not used, included for compatibility with the generic method

## Value

a numeric vector or a list (the latter only for mselm-class objects if vector=FALSE)

## Note

The possible options of param.type are described in the documentation of [dp2cp](#); their corresponding outcomes differ by an additive constant only. With the "CP" option (that is, the 'centred parametrization'), the residuals are centred around 0, at least approximately; this is a reason for setting "CP" as the default option. For more information, see the 'Note' in the documentation of [summary.selm](#).

## Author(s)

Adelchi Azzalini

## References

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.



**See Also**

[dp2cp](#), [summary.selm](#), [selm](#) function, [selm-class](#)

**Examples**

```
data(wines, package="sn")
m5 <- selm(acidity ~ phenols + wine, family="SN", data=wines)
coef(m5)
coef(m5, "dp")
#
m12 <- selm(cbind(acidity, alcohol) ~ phenols + wine, family="SN", data=wines)
coef(m12)
coef(m12, "DP", vector=FALSE)
```

---

conditionalSECdistr     *Skew-normal conditional distribution*

---

**Description**

For a multivariate (extended) skew-normal distribution, compute its conditional distribution for given values of some of its components.

**Usage**

```
conditionalSECdistr(object, fixed.comp, fixed.values, name, drop = TRUE)
```

**Arguments**

object	an object of class <code>SECdistrMv</code> with <code>family="SN"</code> or <code>family="ESN"</code> .
fixed.comp	a vector containing a subset of <code>1:d</code> which selects the components whose values are to be fixed, if <code>d</code> denotes the dimensionality of the distribution.
fixed.values	a numeric vector of values taken on by the components <code>fixed.comp</code> ; it must be of the same length of <code>fixed.comp</code> .
name	an optional character string with the name of the outcome distribution; if missing, one such string is constructed.
drop	logical (default= <code>TRUE</code> ), to indicate whether the returned object must be of class <code>SECdistrUv</code> when <code>length(fixed.comp)+1=d</code> .

**Details**

For background information, see Section 5.3.2 of the reference below.

**Value**

an object of class `SECdistrMv`, except in the case when `drop=TRUE` operates, leading to an object of class `SECdistrUv-class`.

## References

Azzalini, A. and Capitanio, A. (2014). *The Skew-normal and Related Families*. Cambridge University Press, IMS Monographs series.

## See Also

[makeSECdistr](#), [SECdistrMv-class](#), [affineTransSECdistr](#)

## Examples

```
Omega <- diag(3) + outer(1:3,1:3)
sn <- makeSECdistr(dp=list(xi=rep(0,3), Omega=Omega, alpha=1:3), family="SN")
esn <- conditionalSECdistr(sn, fixed.comp=2, fixed.values=1.5)
show(esn)
```

---

confint.selm

*Confidence intervals for parameters of a selm-class object*

---

## Description

Computes confidence intervals for parameters in a selm-class object produced by selm fit when the response variable is univariate.

## Usage

```
## S3 method for class 'selm'
confint(object, parm, level=0.95, param.type, tol=1e-3, ...)
```

## Arguments

object	an object of class selm as produced by a call to function selm with univariate response.
parm	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
level	the confidence level required (default value is 0.95).
param.type	a character string with the required parameterization; it must be either "CP" or "DP" or "pseudo-CP", or possibly their equivalent lowercase.
tol	the desired accuracy (convergence tolerance); this is a parameter passed to <a href="#">uniroot</a> for computing the roots of the likelihood-based confidence interval for alpha.
...	not used, only there for compatibility reasons.

**Details**

A description of the methodology underlying `confint.selm` is provided in the technical note of Azzalini (2016). That document also explains why in certain cases an interval is not constructed and NA's are returned as endpoint.

**Value**

An invisible list whose components, described below, are partly different in the one- and the two-parameter cases.

<code>call</code>	the calling statement
<code>&lt;param1&gt;</code>	values of the first parameter
<code>&lt;param2&gt;</code>	values of the second parameter (in a two-parameter case)
<code>logLik</code>	numeric vector or matrix of the profile log-likelihood values
<code>confint</code>	in the one-parameter case, the confidence interval
<code>level</code>	in the one-parameter case, the confidence level
<code>deviance.contour</code>	in the two-parameter case, a list of lists whose elements identify each curve of the contour plot

**Author(s)**

Adelchi Azzalini

**References**

Azzalini, A. (2016). Derivation of various types of intervals from a `selm` object. Technical note distributed with the documentation of the R package `sn` in file [selm-intervals.pdf](#) within section 'User guide, package vignettes and other documentation'.

**See Also**

[selm](#), [summary.selm](#), [profile.selm](#),  
[makeSECdistr](#) for the CP/DP parameterizations,  
[uniroot](#) for its `tol` argument

**Examples**

```
data(ais)
m1 <- selm(log(Fe) ~ BMI + LBM, family = "sn", data = ais)
intervCP <- confint(m1)
intervDP <- confint(m1, param.type="DP")
confint(m1, parm=2:3)
confint(m1, parm=c("omega", "alpha"), param.type="DP")
```

dmsn

*Multivariate skew-normal distribution***Description**

Probability density function, distribution function and random number generation for the multivariate skew-normal (SN) distribution.

**Usage**

```
dmsn(x, xi=rep(0,length(alpha)), Omega, alpha, tau=0, dp=NULL, log=FALSE)
pmsn(x, xi=rep(0,length(alpha)), Omega, alpha, tau=0, dp=NULL, ...)
rmsn(n=1, xi=rep(0,length(alpha)), Omega, alpha, tau=0, dp=NULL)
```

**Arguments**

<code>x</code>	either a vector of length $d$ , where $d=\text{length}(\text{alpha})$ , or a matrix with $d$ columns, giving the coordinates of the point(s) where the density or the distribution function must be evaluated.
<code>xi</code>	a numeric vector of length $d$ representing the location parameter of the distribution; see ‘Background’. In a call to <code>dmsn</code> and <code>pmsn</code> , <code>xi</code> can be a matrix, whose rows represent a set of location parameters; in this case, its dimensions must match those of <code>x</code> .
<code>Omega</code>	a symmetric positive-definite matrix of dimension $(d, d)$ ; see ‘Background’.
<code>alpha</code>	a numeric vector which regulates the slant of the density; see ‘Background’. Inf values in <code>alpha</code> are not allowed.
<code>tau</code>	a single value representing the ‘hidden mean’ parameter of the ESN distribution; <code>tau=0</code> (default) corresponds to a SN distribution.
<code>dp</code>	a list with three elements, corresponding to <code>xi</code> , <code>Omega</code> and <code>alpha</code> described above; default value <code>FALSE</code> . If <code>dp</code> is assigned, individual parameters must not be specified.
<code>n</code>	a numeric value which represents the number of random vectors to be drawn.
<code>log</code>	logical (default value: <code>FALSE</code> ); if <code>TRUE</code> , log-densities are returned.
<code>...</code>	additional parameters passed to <code>pmnorm</code> .

**Details**

Typical usages are

```
dmsn(x, xi=rep(0,length(alpha)), Omega, alpha, log=FALSE)
dmsn(x, dp=, log=FALSE)
pmsn(x, xi=rep(0,length(alpha)), Omega, alpha, ...)
pmsn(x, dp=)
rmsn(n=1, xi=rep(0,length(alpha)), Omega, alpha)
rmsn(n=1, dp=)
```

Function `pmsn` makes use of `pmnorm` from package **mnormt**; the accuracy of its computation can be controlled via . . .

### Value

A vector of density values (`dmsn`) or of probabilities (`pmsn`) or a matrix of random points (`rmsn`).

### Background

The multivariate skew-normal distribution is discussed by Azzalini and Dalla Valle (1996). The  $(\Omega, \alpha)$  parametrization adopted here is the one of Azzalini and Capitanio (1999). Chapter 5 of Azzalini and Capitanio (2014) provides an extensive account, including subsequent developments.

Notice that the location vector  $\xi$  does not represent the mean vector of the distribution. Similarly,  $\Omega$  is not *the* covariance matrix of the distribution, although it is *a* covariance matrix. Finally, the components of  $\alpha$  are not equal to the slant parameters of the marginal distributions; to fix the marginal parameters at prescribed values, it is convenient to start from the OP parameterization, as illustrated in the ‘Examples’ below. Another option is to start from the CP parameterization, but notice that, at variance from the OP, not all CP sets are invertible to lend a DP set.

### References

- Azzalini, A. and Capitanio, A. (1999). Statistical applications of the multivariate skew normal distribution. *J.Roy.Statist.Soc. B* **61**, 579–602. Full-length version available at <http://arXiv.org/abs/0911.2093>
- Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.
- Azzalini, A. and Dalla Valle, A. (1996). The multivariate skew-normal distribution. *Biometrika* **83**, 715–726.

### See Also

[dsn](#), [dmst](#), [dmnorm](#), [op2dp](#), [cp2dp](#)

### Examples

```
x <- seq(-3,3,length=15)
xi <- c(0.5, -1)
Omega <- diag(2)
Omega[2,1] <- Omega[1,2] <- 0.5
alpha <- c(2,-6)
pdf <- dmsn(cbind(x, 2*x-1), xi, Omega, alpha)
cdf <- pmsn(cbind(x, 2*x-1), xi, Omega, alpha)
p1 <- pmsn(c(2,1), xi, Omega, alpha)
p2 <- pmsn(c(2,1), xi, Omega, alpha, abseps=1e-12, maxpts=10000)
#
rnd <- rmsn(10, xi, Omega, alpha)
#
# use OP parameters to fix marginal shapes at given lambda values:
op <- list(xi=c(0,1), Psi=matrix(c(2,2,2,3), 2, 2), lambda=c(5, -2))
```

```

rnd <- rmsn(10, dp=op2dp(op,"SN"))
#
# use CP parameters to fix mean vector, variance matrix and marginal skewness:
cp <- list(mean=c(0,0), var.cov=matrix(c(3,2,2,3)/3, 2, 2), gamma1=c(0.8, 0.4))
dp <- cp2dp(cp, "SN")
rnd <- rmsn(5, dp=dp)

```

---

dmst

---

*Multivariate skew-t distribution and skew-Cauchy distribution*


---

## Description

Probability density function, distribution function and random number generation for the multivariate skew-*t* (ST) and skew-Cauchy (SC) distributions.

## Usage

```

dmst(x, xi=rep(0,length(alpha)), Omega, alpha, nu=Inf, dp=NULL, log=FALSE)
pmst(x, xi=rep(0,length(alpha)), Omega, alpha, nu=Inf, dp=NULL, ...)
rmst(n=1, xi=rep(0,length(alpha)), Omega, alpha, nu=Inf, dp=NULL)
dmsc(x, xi=rep(0,length(alpha)), Omega, alpha, dp=NULL, log=FALSE)
pmsc(x, xi=rep(0,length(alpha)), Omega, alpha, dp=NULL, ...)
rmsc(n=1, xi=rep(0,length(alpha)), Omega, alpha, dp=NULL)

```

## Arguments

- |                    |   |
|--------------------|---|
| <code>x</code>     | for <code>dmst</code> and <code>dmsc</code> , this is either a vector of length <code>d</code> , where <code>d=length(alpha)</code> , or a matrix with <code>d</code> columns, representing the coordinates of the point(s) where the density must be evaluated; for <code>pmst</code> and <code>pmsc</code> , only a vector of length <code>d</code> is allowed. |
| <code>xi</code>    | a numeric vector of length <code>d</code> representing the location parameter of the distribution; see ‘Background’. In a call to <code>dmst</code> or <code>dmsc</code> , <code>xi</code> can be a matrix, whose rows represent a set of location parameters; in this case, its dimensions must match those of <code>x</code> .                                  |
| <code>Omega</code> | a symmetric positive-definite matrix of dimension $(d, d)$ ; see Section ‘Background’.  |
| <code>alpha</code> | a numeric vector of length <code>d</code> which regulates the slant of the density; see Section ‘Background’. <code>Inf</code> values in <code>alpha</code> are not allowed.  |
| <code>nu</code>    | a positive value representing the degrees of freedom of ST distribution; does not need to be integer. Default value is <code>nu=Inf</code> which corresponds to the multivariate skew-normal distribution.  |
| <code>dp</code>    | a list with three elements named <code>xi</code> , <code>Omega</code> , <code>alpha</code> and <code>nu</code> , containing quantities as described above. If <code>dp</code> is specified, this prevents specification of the individual parameters.   |
| <code>n</code>     | a numeric value which represents the number of random vectors to be drawn; default value is 1.  |

log                    logical (default value: FALSE); if TRUE, log-densities are returned.  
 ...                    additional parameters passed to pmt.

### Details

Typical usages are

```
dmst(x, xi=rep(0,length(alpha)), Omega, alpha, nu=Inf, log=FALSE)
dmst(x, dp=, log=FALSE)
pmst(x, xi=rep(0,length(alpha)), Omega, alpha, nu=Inf, ...)
pmst(x, dp=, ...)
rmst(n=1, xi=rep(0,length(alpha)), Omega, alpha, nu=Inf)
rmst(n=1, dp=)
dmsc(x, xi=rep(0,length(alpha)), Omega, alpha, log=FALSE)
dmsc(x, dp=, log=FALSE)
pmsc(x, xi=rep(0,length(alpha)), Omega, alpha, ...)
pmsc(x, dp=, ...)
rmsc(n=1, xi=rep(0,length(alpha)), Omega, alpha)
rmsc(n=1, dp=)
```

Function pmst requires [dmt](#) from package **mnormt**; the accuracy of its computation can be controlled via argument `....`

### Value

A vector of density values (dmst and dmisc) or a single probability (pmst and pmisc) or a matrix of random points (rmst and rmisc).

### Background

The family of multivariate ST distributions is an extension of the multivariate Student's  $t$  family, via the introduction of a  $\alpha$  parameter which regulates asymmetry; when  $\alpha=0$ , the skew- $t$  distribution reduces to the commonly used form of multivariate Student's  $t$ . Further, location is regulated by  $\xi$  and scale by  $\Omega$ , when its diagonal terms are not all 1's. When  $\nu=\text{Inf}$  the distribution reduces to the multivariate skew-normal one; see [dmsn](#). Notice that the location vector  $\xi$  does not represent the mean vector of the distribution (which in fact may not even exist if  $\nu \leq 1$ ), and similarly  $\Omega$  is not *the* covariance matrix of the distribution, although it is *a* covariance matrix. For additional information, see Section 6.2 of the reference below.

The family of multivariate SC distributions is the subset of the ST family, obtained when  $\nu=1$ . While in the univariate case there are specialized functions for the SC distribution, [dmisc](#), [pmisc](#) and [rmisc](#) simply make a call to [dmst](#), [pmst](#), [rmst](#) with argument  $\nu$  set equal to 1.

### References

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monograph series.

### See Also

[dst](#), [dsc](#), [dmsn](#), [dmt](#), [makeSECDistr](#)

**Examples**

```
x <- seq(-4,4,length=15)
xi <- c(0.5, -1)
Omega <- diag(2)
Omega[2,1] <- Omega[1,2] <- 0.5
alpha <- c(2,2)
pdf <- dmst(cbind(x,2*x-1), xi, Omega, alpha, 5)
rnd <- rmst(10, xi, Omega, alpha, 6)
p1 <- pmst(c(2,1), xi, Omega, alpha, nu=5)
p2 <- pmst(c(2,1), xi, Omega, alpha, nu=5, abseps=1e-12, maxpts=10000)
```

dp2cp

*Conversion between parametrizations of a skew-elliptical distribution***Description**

Convert direct parameters (DP) to centred parameters (CP) of a skew-elliptical distribution and *vice versa*.

**Usage**

```
dp2cp(dp, family, object = NULL, cp.type = "proper", upto = NULL)
cp2dp(cp, family)
dp2op(dp, family)
op2dp(op, family)
```

**Arguments**

dp	a vector (in the univariate case) or a list (in the multivariate case) as described in <a href="#">makeSECdistr</a> ; see ‘Background and Details’ for an extended form of usage.
cp	a vector or a list, in agreement with dp as for type and dimension.
op	a vector or a list, in agreement with dp as for type and dimension.
family	a character string with the family acronym, as described in <a href="#">makeSECdistr</a> , except that family "ESN" is not implemented.
object	optionally, an S4 object of class <code>SECdistrUv</code> or <code>SECdistrMv</code> , as produced by <a href="#">makeSECdistr</a> (default value: <code>NULL</code> ). If this argument is not <code>NULL</code> , then <code>family</code> and <code>dp</code> must not be set.
cp.type	character string, which has effect only if <code>family="ST"</code> or <code>"SC"</code> , otherwise a warning message is generated. Possible values are <code>"proper"</code> , <code>"pseudo"</code> , <code>"auto"</code> , which correspond to the CP parameter set, their ‘pseudo-CP’ version and an automatic selection based on <code>nu&gt;4</code> , where <code>nu</code> represents the degrees of freedom of the ST distribution.
upto	numeric value (in <code>1:length(dp)</code> ), default= <code>NULL</code> ) to select how many CP components are computed. Default value <code>upto=NULL</code> is equivalent to <code>length(dp)</code> .



## Value

For `dp2cp`, a matching vector (in the univariate case) or a list (in the multivariate case) of `cp` parameters. For `cp2dp` and `op2dp`, a similar object of `dp` parameters, provided the set of input parameters is in the admissible region. For `dp2op`, a similar set of `op` parameters.

## Background

For a description of the DP parameters, see Section ‘Details’ of `makeSECdistr`. The CP form of parameterization is cumulant-based. For a univariate distribution, the CP components are the mean value (first cumulant), the standard deviation (square root of the 2nd cumulant), the coefficient of skewness (3rd standardized cumulant) and, for the ST, the coefficient of excess kurtosis (4th standardized cumulant). For a multivariate distribution, there exists an extension based on the same logic; its components represent the vector mean value, the variance matrix, the vector of marginal coefficients of skewness and, only for the ST, the Mardia’s coefficient of excess kurtosis. The pseudo-CP variant provides an ‘approximate form’ of CP when not all required cumulants exist; however, this parameter set is not uniquely invertible to DP. The names of pseudo-CP components printed in summary output are composed by adding a `~` after the usual component name; for example, the first one is denoted `mean~`.

Additional information is provided by Azzalini and Capitanio (2014). Specifically, their Section 3.1.4 presents CP in the univariate SN case, Section 4.3.4 CP for the ST case and the ‘pseudo-CP’ version. Section 5.2.3 presents the multivariate extension for the SN distribution, Section 6.2.5 for the multivariate ST case. For a more detailed discussion, see Arellano-Valle & Azzalini (2013).

The OP parameterization is very similar to DP, from which it differs only for the components which regulate dispersion (or scatter) and slant. Its relevance lies essentially in the multivariate case, where the components of the slant parameter can be interpreted component-wise and remain unaffected if marginalization with respect to some other components is performed. In the multivariate SN case, the components of OP, denoted  $\xi, \Psi, \lambda$ , are associated to the expression of the density function (5.30) of Azzalini & Capitanio (2014); see pp.128–131 for more information. In the univariate case, the slant component of DP and the one of OP coincide, that is,  $\alpha = \lambda$ . Parameter  $\xi$  and other parameters which may exist with other families remain the same of the DP set. The term OP stands for ‘original parameterization’ since this is, up to a negligible difference, the parameterization adopted by Azzalini & Dalla Valle (1996).

## Details

While any choice of the components of DP or OP is admissible, this is not true for CP. An implication is that a call to `cp2dp` may fail with an error message `"non-admissible CP"` for certain input values. The most extreme case is represented by the SC family, for which CP never exists; hence it makes to sense to call `cp2dp` with `family="SC"`.

It is possible to call the functions with `dp` or `cp` having more components than those expected for a given family as described above and in `makeSECdistr`. In the univariate case, this means that `dp` or `cp` can be vectors of longer length than indicated earlier. This occurrence is interpreted in the sense that the additional components after the first one are regarded as regression coefficients of a `selm` model, and they are transferred unchanged to the matching components of the transformed parameter set; the motivation is given in Section 3.1.4 of Azzalini and Capitanio (2014). In the multivariate case, `dp[[1]]` and `cp[[1]]` can be matrices instead of vectors; the rows beyond the first one are transferred unchanged to `cp[[1]]` and `dp[[1]]`, respectively.

## References

Arellano-Valle, R. B. and Azzalini, A. (2013, available on-line 12 June 2011). The centred parameterization and related quantities of the skew- $t$  distribution. *J. Multiv. Analysis* **113**, 73-90.

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

Azzalini, A. and Dalla Valle, A. (1996). The multivariate skew-normal distribution. *Biometrika* **83**, 715–726.

## See Also

[makeSECdistr](#), [summary.SECdistr](#), [sn.cumulants](#),

the ‘Note’ at [summary.selm](#) for the reason why CP is the default parameterization in that function and in related ones,

the ‘Examples’ at [rmsn](#) for use of the CP parameterization

## Examples

```
# univariate case
cp <- dp2cp(c(1, 2222, 3333, 2, 3), "SN")
dp <- cp2dp(cp, "SN")
# notice that 2nd and 3rd component remain unchanged
#
# multivariate case
dp3 <- list(xi=1:3, Omega=toeplitz(1/(1:3)), alpha=c(-3, 8, 5), nu=6)
cp3 <- dp2cp(dp3, "ST")
dp3.back <- cp2dp(cp3, "ST")
#
op3 <- dp2op(dp3, "ST")
dp3back <- op2dp(op3, "ST")
```

---

dsc

*Skew-Cauchy Distribution*

---

## Description

Density function, distribution function, quantiles and random number generation for the skew-Cauchy (SC) distribution.

## Usage

```
dsc(x, xi = 0, omega = 1, alpha = 0, dp = NULL, log = FALSE)
psc(x, xi = 0, omega = 1, alpha = 0, dp = NULL)
qsc(p, xi = 0, omega = 1, alpha = 0, dp = NULL)
rsc(n = 1, xi = 0, omega = 1, alpha = 0, dp = NULL)
```

**Arguments**

x	vector of quantiles. Missing values (NAs) and Inf's are allowed.
p	vector of probabilities. Missing values (NAs) are allowed.
xi	vector of location parameters.
omega	vector of (positive) scale parameters.
alpha	vector of slant parameters.
dp	a vector of length 3 whose elements represent the parameters described above. If dp is specified, the individual parameters cannot be set.
n	sample size.
log	logical flag used in dsc (default FALSE). When TRUE, the logarithm of the density values is returned.

**Value**

density (dsc), probability (psc), quantile (qsc) or random sample (rsc) from the skew-Cauchy distribution with given xi, omega and alpha parameters or from the extended skew-normal if tau!=0

**Details**

Typical usages are

```
dsc(x, xi=0, omega=1, alpha=0, log=FALSE)
dsc(x, dp=, log=FALSE)
psc(x, xi=0, omega=1, alpha=0)
psc(x, dp= )
qsc(p, xi=0, omega=1, alpha=0)
qsc(x, dp=)
rsc(n=1, xi=0, omega=1, alpha=0)
rsc(x, dp=)
```

**Background**

The skew-Cauchy distribution can be thought as a skew- $t$  with tail-weight parameter  $\nu=1$ . In this case, closed-form expressions of the distribution function and the quantile function have been obtained by Behboodian *et al.* (2006). The key facts are summarized in Complement 4.2 of Azzalini and Capitanio (2014). A multivariate version of the distribution exists.

**References**

- Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-normal and Related Families*. Cambridge University Press, IMS Monographs series.
- Behboodian, J., Jamalizadeh, A., and Balakrishnan, N. (2006). A new class of skew-Cauchy distributions. *Statist. Probab. Lett.* **76**, 1488–1493.

**See Also**

[dst](#), [dmsc](#)

**Examples**

```
pdf <- dsc(seq(-5,5,by=0.1), alpha=3)
cdf <- psc(seq(-5,5,by=0.1), alpha=3)
q <- qsc(seq(0.1,0.9,by=0.1), alpha=-2)
p <- psc(q, alpha=-2)
rn <- rsc(100, 5, 2, 5)
```

dsn

*Skew-Normal Distribution***Description**

Density function, distribution function, quantiles and random number generation for the skew-normal (SN) and the extended skew-normal (ESN) distribution.

**Usage**

```
dsn(x, xi=0, omega=1, alpha=0, tau=0, dp=NULL, log=FALSE)
psn(x, xi=0, omega=1, alpha=0, tau=0, dp=NULL, engine, ...)
qsn(p, xi=0, omega=1, alpha=0, tau=0, dp=NULL, tol=1e-8, solver="NR", ...)
rsn(n=1, xi=0, omega=1, alpha=0, tau=0, dp=NULL)
```

**Arguments**

x	vector of quantiles. Missing values (NA's) and Inf's are allowed.
p	vector of probabilities. Missing values (NAs) are allowed
xi	vector of location parameters.
omega	vector of scale parameters; must be positive.
alpha	vector of slant parameter(s); +/- Inf is allowed. With psn, it must be of length 1 if engine="T.Owen". With qsn, it must be of length 1.
tau	a single value representing the 'hidden mean' parameter of the ESN distribution; tau=0 (default) corresponds to a SN distribution.
dp	a vector of length 3 (in the SN case) or 4 (in the ESN case), whose components represent the individual parameters described above. If dp is specified, the individual parameters cannot be set.
n	a positive integer representing the sample size.
tol	a scalar value which regulates the accuracy of the result of qsn, measured on the probability scale.
log	logical flag used in dsn (default FALSE). When TRUE, the logarithm of the density values is returned.
engine	a character string which selects the computing engine; this is either "T.Owen" or "biv.nt.prob", the latter from package mnormt. If tau != 0 or length(alpha)>1, "biv.nt.prob" must be used. If this argument is missing, a default selection rule is applied.

`solver` a character string which selects the numerical method used for solving the quantile equation; possible options are "NR" (default) and "RFB", described in the 'Details' section.

... additional parameters passed to `T.Owen`

### Value

density (`dsn`), probability (`psn`), quantile (`qsn`) or random sample (`rsn`) from the skew-normal distribution with given `xi`, `omega` and `alpha` parameters or from the extended skew-normal if `tau!=0`

### Details

Typical usages are

```
dsn(x, xi=0, omega=1, alpha=0, log=FALSE)
dsn(x, dp=, log=FALSE)
psn(x, xi=0, omega=1, alpha=0, ...)
psn(x, dp=, ...)
qsn(p, xi=0, omega=1, alpha=0, tol=1e-8, ...)
qsn(x, dp=, ...)
rsn(n=1, xi=0, omega=1, alpha=0)
rsn(x, dp=)
```

`psn` and `qsn` make use of function `T.Owen` or `biv.nt.prob`

In `qsn`, the choice `solver="NR"` selects the Newton-Raphson method for solving the quantile equation, while option `solver="RFB"` alternates a step of *regula falsi* with one of bisection. The "NR" method is generally more efficient, but "RFB" is occasionally required in some problematic cases.

### Background

The family of skew-normal distributions is an extension of the normal family, via the introduction of a `alpha` parameter which regulates asymmetry; when `alpha=0`, the skew-normal distribution reduces to the normal one. The density function of the SN distribution in the 'normalized' case having `xi=0` and `omega=1` is  $2\phi(x)\Phi(\alpha x)$ , if  $\phi$  and  $\Phi$  denote the standard normal density and distribution function. An early discussion of the skew-normal distribution is given by Azzalini (1985); see Section 3.3 for the ESN variant, up to a slight difference in the parameterization.

An updated exposition is provided in Chapter 2 of Azzalini and Capitanio (2014); the ESN variant is presented Section 2.2. See Section 2.3 for an historical account. A multivariate version of the distribution is examined in Chapter 5.

### References

- Azzalini, A. (1985). A class of distributions which includes the normal ones. *Scand. J. Statist.* **12**, 171-178.
- Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

**See Also**

Functions used by psn: [T.Owen](#), [biv.nt.prob](#)

Related distributions: [dmsn](#), [dst](#), [dmst](#)

**Examples**

```
pdf <- dsn(seq(-3, 3, by=0.1), alpha=3)
cdf <- psn(seq(-3, 3, by=0.1), alpha=3)
q <- qsn(seq(0.1, 0.9, by=0.1), alpha=-2)
r <- rsn(100, 5, 2, 5)
qsn(1/10^(1:4), 0, 1, 5, 3, solver="RFB")
```

---

 dst

*Skew-t Distribution*


---

**Description**

Density function, distribution function, quantiles and random number generation for the skew-*t* (ST) distribution

**Usage**

```
dst(x, xi=0, omega=1, alpha=0, nu=Inf, dp=NULL, log=FALSE)
pst(x, xi=0, omega=1, alpha=0, nu=Inf, dp=NULL, method=0, ...)
qst(p, xi=0, omega=1, alpha=0, nu=Inf, tol=1e-08, dp=NULL, method=0, ...)
rst(n=1, xi=0, omega=1, alpha=0, nu=Inf, dp=NULL)
```

**Arguments**

x	vector of quantiles. Missing values (NAs) are allowed.
p	vector of probabilities.
xi	vector of location parameters.
omega	vector of scale parameters; must be positive.
alpha	vector of slant parameters. With pst and qst, it must be of length 1.
nu	a single positive value representing the degrees of freedom; it can be non-integer. Default value is nu=Inf which corresponds to the skew-normal distribution.
dp	a vector of length 4, whose elements represent location, scale (positive), slant and degrees of freedom, respectively. If dp is specified, the individual parameters cannot be set.
n	a positive integer representing the sample size.
log	logical; if TRUE, densities are given as log-densities
tol	a scalar value which regulates the accuracy of the result of qsn, measured on the probability scale.

method            an integer value between 0 and 4 which selects the computing method; see ‘Details’ below for the meaning of these values. If method=0 (default value), an automatic choice is made among the four actual computing methods, depending on the other arguments.

...                additional parameters passed to integrate or pmst.

### Value

Density (dst), probability (pst), quantiles (qst) and random sample (rst) from the skew- $t$  distribution with given  $\xi$ ,  $\omega$ ,  $\alpha$  and  $\nu$  parameters.

### Details

Typical usages are

```
dst(x, xi=0, omega=1, alpha=0, nu=Inf, log=FALSE)
dst(x, dp=, log=FALSE)
pst(x, xi=0, omega=1, alpha=0, nu=Inf, method=0, ...)
pst(x, dp=, log=FALSE)
qst(p, xi=0, omega=1, alpha=0, nu=Inf, tol=1e-8, method=0, ...)
qst(x, dp=, log=FALSE)
rst(n=1, xi=0, omega=1, alpha=0, nu=Inf)
rst(x, dp=, log=FALSE)
```

### Background

The family of skew- $t$  distributions is an extension of the Student’s  $t$  family, via the introduction of a  $\alpha$  parameter which regulates skewness; when  $\alpha=0$ , the skew- $t$  distribution reduces to the usual Student’s  $t$  distribution. When  $\nu=\text{Inf}$ , it reduces to the skew-normal distribution. When  $\nu=1$ , it reduces to a form of skew-Cauchy distribution. See Chapter 4 of Azzalini & Capitanio (2014) for additional information. A multivariate version of the distribution exists; see `dmst`.

### Details

For evaluation of `pst`, and so indirectly of `qst`, four different methods are employed. Method 1 consists in using `pmst` with dimension  $d=1$ . Method 2 applies `integrate` to the density function `dst`. Method 3 again uses `integrate` too but with a different integrand, as given in Section 4.2 of Azzalini & Capitanio (2003), full version of the paper. Method 4 consists in the recursive procedure of Jamalizadeh, Khosravi and Balakrishnan (2009), which is recalled in Complement 4.3 on Azzalini & Capitanio (2014); the recursion over  $\nu$  starts from the explicit expression for  $\nu=1$  given by `psc`. Of these, Method 1 and 4 are only suitable for integer values of  $\nu$ . Method 4 becomes progressively less efficient as  $\nu$  increases, because the value of  $\nu$  determines the number of nested calls, but the decay of efficiency is slower for larger values of `length(x)`. If the default argument value `method=0` is retained, an automatic choice among the above four methods is made, which depends on the values of  $\nu$ ,  $\alpha$ , `length(x)`. The numerical accuracy of methods 1, 2 and 3 can be regulated via the `...` argument, while method 4 is conceptually exact, up to machine precision.

If `qst` is called with  $\nu > 1e4$ , computation is transferred to `qsn`.

## References

Azzalini, A. and Capitanio, A. (2003). Distributions generated by perturbation of symmetry with emphasis on a multivariate skew- $t$  distribution. *J.Roy. Statist. Soc. B* **65**, 367–389. Full version of the paper at <http://arXiv.org/abs/0911.2342>.

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-normal and Related Families*. Cambridge University Press, IMS Monographs series.

Jamalizadeh, A., Khosravi, M., and Balakrishnan, N. (2009). Recurrence relations for distributions of a skew- $t$  and a linear combination of order statistics from a bivariate- $t$ . *Comp. Statist. Data An.* **53**, 847–852.

## See Also

[dmst](#), [dsn](#), [dsc](#)

## Examples

```
pdf <- dst(seq(-4, 4, by=0.1), alpha=3, nu=5)
rnd <- rst(100, 5, 2, -5, 8)
q <- qst(c(0.25, 0.50, 0.75), alpha=3, nu=5)
pst(q, alpha=3, nu=5) # must give back c(0.25, 0.50, 0.75)
#
p1 <- pst(x=seq(-3,3, by=1), dp=c(0,1,pi, 3.5))
p2 <- pst(x=seq(-3,3, by=1), dp=c(0,1,pi, 3.5), method=2, rel.tol=1e-9)
```

---

extractSECdistr

*Extract the SEC error term from an object created by selm*

---

## Description

Given an object created by a call to `selm`, the function delivers the SEC distribution representing the stochastic term of the fitted distribution

## Usage

```
extractSECdistr(object, name, compNames)
```

## Arguments

<code>object</code>	an object of class <code>selm</code> or <code>mse1m</code> , as created by <a href="#">selm</a> .
<code>name</code>	an optional character string representing the name of the outcome distribution; if missing, a string is constructed from the object ingredients.
<code>compNames</code>	in the multivariate case, an optional vector of character strings with the names of the components of the error distribution; if missing, one such vector is constructed from the object ingredients.



**Value**

An object of class `SECdistrMv` or `SECdistrUv`, depending of the class of object.

**Details**

When the formula of the fitted model includes only the constant 1, the returned object represents the fitted SEC distribution. If the formula includes additional terms, the linear predictor is eliminated and the returned object corresponds to the error term of the model; hence the location parameter  $\xi$  in the DP parameterization is set to zero.

The returned object can be submitted to tools available for objects created by `makeSECdistr`, such as `summary.SECdistr`, `conditionalSECdistr` and and so on.

**See Also**

[selm](#), [makeSECdistr](#)

**Examples**

```
data(ais)
m2 <- selm(log(Fe) ~ 1, family="ST", data=ais, fixed=list(nu=8))
f2 <- extractSECdistr(m2)
show(f2)
#
m4 <- selm(cbind(BMI, LBM) ~ 1, family="SN", data=ais)
f4 <- extractSECdistr(m4)
mean(f4)
vcov(f4)
```

---

frontier

*Simulated sample from a skew-normal distribution*

---

**Description**

A sample simulated from the  $SN(0,1,5)$  distribution with sample coefficient of skewness inside the admissible range  $(-0.9952719, 0.9952719)$  for the skew-normal family but maximum likelihood estimate on the frontier of the parameter space.

**Usage**

```
data(frontier)
```

**Format**

A numeric vector of length 50.

**Source**

Generated by a run of `rsn(50, 0, 1, 5)`.

**Examples**

```

data(frontier, package="sn")
fit <- selm(frontier ~ 1)
plot(fit, which=2)
#
fit.p <- selm(frontier ~ 1, method="MPLE")
plot(fit.p, which=2)

```

---

makeSECdistr

*Build a skew-elliptically contoured distribution*


---

**Description**

Build an object which identifies a skew-elliptically contoured distribution (SEC), in the univariate and in the multivariate case. The term ‘skew-elliptical distribution’ is a synonym of SEC distribution.

**Usage**

```
makeSECdistr(dp, family, name, compNames)
```

**Arguments**

dp	a numeric vector (in the univariate case) or a list (in the multivariate case) of parameters which identify the specific distribution within the named family. See ‘Details’ for their expected structure.
family	a character string which identifies the parametric family; currently, possible values are: "SN", "ESN", "ST", "SC". See ‘Details’ for additional information.
name	an optional character string with the name of the distribution. If missing, one is created.
compNames	in the multivariate case, an optional vector of character strings with the names of the component variables; its length must be equal to the dimensionality of the distribution being generated. If missing and the first component of dp is a named vector, its names are used as compNames; otherwise the components are named "V1", "V2", ...

**Details**

If dp is a numeric vector, a univariate distribution is built. Alternatively, if dp is a list, a multivariate distribution is built. In both cases, the required number of components of dp depends on family: it must be 3 for "SN" and "SC"; it must be 4 for "ESN" and "ST".

In the univariate case, the first three components of dp represent what for the specific distributions are denoted xi (location), omega (scale, positive) and alpha (slant); see functions [dsn](#), [dst](#), [dsc](#) for their description. The fourth component, when it exists, represents either tau (hidden variable mean) for "ESN" or nu (degrees of freedom) for "ST". The names of the individual parameters are attached to the components of dp in the returned object.

In the multivariate case, `dp` is a list with components having similar role as in the univariate case, but `xi=dp[[1]]` and `alpha=dp[[3]]` are now vectors and the scale parameter `Omega=dp[[2]]` is a symmetric positive-definite matrix. For a multivariate distribution of dimension 1 (which can be created, although a warning message is issued), `Omega` corresponds to the square of `omega` in the univariate case. Vectors `xi` and `alpha` must be of length `ncol(Omega)`. See also functions [dmsn](#), [dmst](#) and [dmsc](#). The fourth component, when it exists, is a scalar with the same role as in the univariate case.

In the univariate case `alpha=Inf` is allowed, but in the multivariate case all components of the vector `alpha` must be finite.

### Value

In the univariate case, an object of class `SECdistrUv`; in the multivariate case, an object of class `SECdistrMv`. See [SECdistrUv-class](#) and [SECdistrMv-class](#) for their description.

### Background

For background information, see Azzalini and Capitanio (2014), specifically Chapters 2 and 4 for univariate cases, Chapters 5 and 6 for multivariate cases; Section 6.1 provides a general formulation of SEC distributions.

If the slant parameter `alpha` is  $\emptyset$  (or a vector of  $\emptyset$ 's, in the multivariate case), the distribution is of classical elliptical type.

Among the admissible families, the ESN distribution is not, strictly speaking, of SEC type, but it is nevertheless included because of its strong connection.

### Author(s)

Adelchi Azzalini

### References

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

### See Also

The description of classes [SECdistrUv-class](#) and [SECdistrMv-class](#)  
[plot.SECdistr](#) for plotting and [summary.SECdistr](#) for summaries

Related functions [dsn](#), [dst](#), [dsc](#), [dmsn](#), [dmst](#), [dp2cp](#)

Functions [affineTransSECdistr](#) and [conditionalSECdistr](#) to manipulate objects of class [SECdistrMv-class](#)

Function [extractSECdistr](#) to extract objects of class [SECdistrMv-class](#) and [SECdistrUv-class](#) representing the SEC distribution of a [selm](#) fit

## Examples

```
f1 <- makeSECdistr(dp=c(3,2,5), family="SN", name="First-SN")
show(f1)
summary(f1)
plot(f1)
plot(f1, probs=c(0.1, 0.9))
#
f2 <- makeSECdistr(dp=c(3, 5, -4, 8), family="ST", name="First-ST")
f9 <- makeSECdistr(dp=c(5, 1, Inf, 0.5), family="ESN", name="ESN,alpha=Inf")
#
dp0 <- list(xi=1:2, Omega=diag(3:4), alpha=c(3, -5))
f10 <- makeSECdistr(dp=dp0, family="SN", name="SN-2d", compNames=c("u1", "u2"))
#
dp1 <- list(xi=1:2, Omega=diag(1:2)+outer(c(3,3),c(2,2)), alpha=c(-3, 5), nu=6)
f11 <- makeSECdistr(dp=dp1, family="ST", name="ST-2d", compNames=c("t1", "t2"))
```

---

matrix-op

*vech and other matrix operators*

---

## Description

vech and other matrix operators

## Usage

```
vech(A)
vech2mat(v)
duplicationMatrix(n)
```

## Arguments

A	a (symmetric) square matrix.
v	a numeric vector such that $\text{length}(v) = n \cdot (n+1) / 2$ for some positive integer n.
n	a positive integer number; default is n=1.

## Value

a vector in case of vech, otherwise a matrix.

## Details

For a square matrix A, `vech(A)` returns the vector formed by the lower triangular portion of the matrix, including the diagonal; usually, this only makes sense for a symmetric matrix of numeric values. If  $v = \text{vech}(M)$  where M is a symmetric numeric matrix, `vech2mat(v)` performs the inverse operation and returns the original matrix codeM; this explain the requirement on `length(v)`. For a positive integer n, `D=duplicationMatrix(n)` is a matrix of dimension  $(n^2, n \cdot (n+1) / 2)$  such that `D %*% vech(M)` returns the vec-form of a symmetric matrix M of order n, that is, the vector

which stacks the columns of  $M$ ; for more information, see Section 3.8 of Magnus and Neudecker (1988).

### Author

Adelchi Azzalini; the original Octave code of `duplicationMatrix` is by Kurt Hornik.

### References

Magnus, Jan R. and Neudecker, Heinz (1988). *Matrix differential calculus with application in statistics and econometrics*. Wiley series in probability and statistics.

### Examples

```
M <- toeplitz(1:4)
v <- vech(M)
vech2mat(v) - M
D <- duplicationMatrix(ncol(M))
# D %*% vech(M) - as.vector(M)
```

---

modeSECdistr

*The mode of a skew-elliptically contoured (SEC) distribution*

---

### Description

Compute compute the mode of a univariate or multivariate SEC distribution.

### Usage

```
modeSECdistr(dp, family, object=NULL)
```

### Arguments

dp	a numeric vector (in the univariate case, for class <code>SECdistrUv</code> ) or a list (in the multivariate case, , for class <code>SECdistrUv</code> ) of parameters which identify the specific distribution within the named family.
family	a character string which identifies the parametric family among those admissible for classes <code>SECdistrUv</code> or <code>SECdistrMv</code> .
object	an object of class <code>SECdistrUv</code> or <code>SECdistrMv</code> as created by <a href="#">makeSECdistr</a> or <a href="#">extractSECdistr</a> ; if this argument is used, arguments <code>dp</code> and <code>family</code> must not be set, and <i>vice versa</i> .

### Value

a numeric vector

## Background

The mode is obtained through numerical maximization. In the multivariate case, the problem is reduced to a one-dimensional search using Propositions 5.14 and 6.2 of the reference below.

## References

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

## See Also

[makeSECdistr](#) and [extractSECdistr](#) for additional information and for constructing a suitable object,

[SECdistrUv-class](#) and [SECdistrMv-class](#) for methods `mean` and `vcov` which compute the mean (vector) and the variance (matrix) of the object distribution

## Examples

```
dp3 <- list(xi=1:3, Omega=toeplitz(1/(1:3)), alpha=c(3,-1,2), nu=5)
st3 <- makeSECdistr(dp3, family="ST", name="ST3", compNames=c("U", "V", "W"))
mode1 <- modeSECdistr(dp3, "ST")
mode2 <- modeSECdistr(object=st3) # the same of mode1
```

---

overview

*Package sn: overview of the package structure and commands*

---

## Description

The package provides facilities to build and manipulate probability distributions of the skew-normal and some related families, notably the skew-*t* family, and makes available related statistical methods for data fitting and model diagnostics, in the univariate and the multivariate case.

The package comprises two main sides; one side provides facilities for the pertaining probability distributions, the other one makes available statistical methods dealing with these distributions.

Underlying formulation, parameterizations of distributions and terminology are in agreement with the monograph of Azzalini and Capitanio (2014).

## Probability side

There are two layers of support for the probability distributions of interest. At the basic level, there exist functions which follow the classical R scheme for distributions. In addition, there exists facilities to build an object which encapsulates a probability distribution and then certain operations can be performed on such an object. These two schemes are described next.

**Classical R scheme** The following functions work similarly to  $\{d, p, q, r\}_{\text{norm}}$  and other R functions for probability distributions:

- skew-normal (SN): functions  $\{d, p, q, r\}_{sn}$  for the univariate case, functions  $\{d, p, r\}_{msn}$  for the multivariate case, where in both cases the ‘Extended skew-normal’ (ESN) variant form is included;
- skew- $t$  (ST): functions  $\{d, p, q, r\}_{st}$  for the univariate case, functions  $\{d, p, r\}_{mst}$  for the multivariate case;
- skew-Cauchy (SC): functions  $\{d, p, q, r\}_{sc}$  for the univariate case, functions  $\{d, p, r\}_{msc}$  for the multivariate case.

In addition to the usual specification of their parameters as a sequence of individual components, a parameter set can be specified as a single  $dp$  entity, namely a vector in the univariate case, a list in the multivariate case;  $dp$  stands for ‘Direct Parameters’ (DP).

Conversion from the  $dp$  parameter set to the corresponding Centred Parameters (CP) can be accomplished using the function  $dp2cp$ , while function  $cp2dp$  performs the inverse transformation.

In addition, one can introduce a user-specified density function using  $dSymmModulated$  and  $dmSymmModulated$ , in the univariate and the multivariate case, respectively. These densities are of the ‘symmetry-modulated’ type, also called ‘skew-symmetric’, where one can specify the base density and the modulation factor with high degree of flexibility. Random numbers can be sampled using the corresponding functions  $rSymmModulated$  and  $rmSymmModulated$ . In the bivariate case, a dedicated plotting function exists.

**SEC distribution objects** Function  $makeSECdistr$  can be used to build a ‘SEC distribution’ object representing a member of a specified parametric family (among the types SN, ESN, ST, SC) with a given  $dp$  parameter set. This object can be used for various operations such as plotting or extraction of moments and other summary quantities. Another way of constructing a SEC distribution object is via  $extractSECdistr$  which extracts suitable components of an object produced by function  $selm$  to be described below.

Additional operations on these objects are possible in the multivariate case, namely  $marginalSECdistr$  and  $affineTransSECdistr$  for marginalization and affine transformations. For the multivariate SN family only (but including ESN),  $conditionalSECdistr$  performs a conditioning on the values taken on by some components of the multivariate variable.

## Statistics side

The main function for data fitting is represented by  $selm$ , which allows to specify a linear regression model for the location parameter, similarly to function  $lm$ , but assuming a *skew-elliptical* distribution; this explains the name  $selm=(se+lm)$ . Allowed types of distributions are SN (but not ESN), ST and SC. The fitted distribution is univariate or multivariate, depending on the nature of the response variable of the posited regression model. The model fitting method is either maximum likelihood or maximum penalized likelihood; the latter option effectively allows the introduction of a prior distribution on the slant parameter of the error distribution, hence leading to a ‘maximum a posteriori’ estimate.

Once the fitting process has been accomplished, an object of class either  $selm$  (for univariate response) or  $mselm$  (for multivariate response) is produced. A number of ‘methods’ are available for these objects:  $show$ ,  $plot$ ,  $summary$ ,  $coef$ ,  $residuals$ ,  $logLik$  and others. For univariate  $selm$ -class objects, univariate and bivariate profile log-likelihood functions can be obtained; a  $predict$  method also exists. These methods are built following the S4 protocol; however, the user must not be concerned with the choice of the adopted protocol (unless this is wished).

The actual fitting process invoked via `selm` is actually performed by a set of lower-level procedures. These are accessible for direct call, if so wished, typically for improved efficiency, at the expense of a little additional programming effort. Similarly, functions to compute the Fisher information matrix are available, in the expected and the observed form (with some restrictions depending on the selected distribution).

The `extractSECdistr` function extracts the fitted SEC distribution from `selm`-class and `mselm`-class objects, hence providing a bridge with the probability side of the package.

### Author

Adelchi Azzalini.

Please send comments, error reports *et cetera* to the author, whose web page is <http://azzalini.stat.unipd.it/>.

### References

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

---

plot.SECdistr                      *Plotting methods for classes SECdistrUv and SECdistrMv*

---

### Description

Methods for classes `SECdistrUv` and `SECdistrMv`

### Usage

```
## S4 method for signature 'SECdistrUv'
plot(x, range, probs, main, npt = 251, ...)

## S4 method for signature 'SECdistrMv'
plot(x, range, probs, npt, landmarks = "auto",
     main, comp, compLabs, data = NULL, data.par = NULL, gap = 0.5, ...)
```

### Arguments

<code>x</code>	an object of class <code>SECdistrUv</code> or <code>SECdistrMv</code> .
<code>range</code>	in the univariate case, a vector of length 2 which defines the plotting range; in the multivariate case, a matrix with two rows where each column defines the plotting range of the corresponding component variable. If missing, a sensible choice is made.
<code>probs</code>	a vector of probability values. In the univariate case, the corresponding quantiles are plotted on the horizontal axis; it can be skipped by setting <code>probs=NULL</code> . In the multivariate case, each probability value corresponds to a contour level in each bivariate plot; at least one probability value is required. See ‘Details’ for further information. Default value: <code>c(0.05, 0.25, 0.5, 0.75, 0.95)</code> in the univariate case, <code>c(0.25, 0.5, 0.75, 0.95)</code> in the multivariate case.



npt	a numeric value or vector (in the univariate and in the multivariate case, respectively) to assign the number of evaluation points of the distribution, on an equally-spaced grid over the range defined above. Default value: 251 in the univariate case, a vector of 101's in the multivariate case.
landmarks	a character string which affects the placement of some landmark values in the multivariate case, that is, the origin, the mode and the mean (or its substitute pseudo-mean), which are all aligned. Possible values: "proper", "pseudo", "auto" (default), "". The option "" prevents plotting of the landmarks. With the other options, the landmarks are plotted, with some variation in the last one: "proper" plots the proper mean value, "pseudo" plots the pseudo-mean, useful when the proper mean does not exist, "auto" plots the proper mean if it exists, otherwise it switches automatically to the pseudo-mean. See <a href="#">dp2cp</a> for more information on pseudo-CP parameters, including pseudo-mean.
main	a character string for main title; if missing, one is built from the available ingredients.
comp	a subset of the vector 1:d, if d denotes the dimensionality of the multivariate distribution.
compLabs	a vector of character strings or expressions used to denote the variables in the plot; if missing, slot(object, "compNames") is used.
data	an optional set of data of matching dimensionality of object to be superimposed to the plot. The default value data=NULL produces no effect. In the univariate case, data are plotted using <a href="#">rug</a> at the top horizontal axis, unless if probs=NULL, in which case plotting is at the bottom axis. In the multivariate case, points are plotted in the form of a scatterplot or matrix of scatterplots; this can be regulated by argument data.par.
data.par	an optional list of graphical parameters used for plotting data in the multivariate case, when data is not NULL. Recognized parameters are: col, pch, cex. If missing, the analogous components of par() are used.
gap	a numeric value which regulates the gap between panels of a multivariate plot when d>2.
...	additional graphical parameters

### Value

an invisible list. In the univariate case the list has three components: the input object representing the distribution and two numeric vectors with the coordinates of the plotted density values. In the multivariate case, the first element of the list is the input object representing the distribution and all subsequent list elements are lists with components of the panels comprising the matrix plot; the elements of these sub-lists are: the vectors of x and y coordinates, the names of the variables, the density values at the (x,y) points, a vector of the density levels of the curves appearing in each panel plot, with the corresponding approximate probability content as a vector attribute.

### Details

For univariate density plots, probs are used to compute quantiles from the appropriate distribution, and these are superimposed to the plot of the density function, unless probs=NULL. In the multivariate case, each bivariate plot is constructed as a collection of contour curves, one curve for each

probability level; consequently, probs cannot be missing or NULL. The level of the density contour lines are chosen so that each curve circumscribes a region with the quoted probability, to a good degree of approximation; for additional information, see Azzalini and Capitanio (2014), specifically Complement 5.2 and p.179, and references therein.

### Methods

signature(x = "SECdistrUv") Plot an object x of class SECdistrUv.

signature(x = "SECdistrMv") Plot an object x of class SECdistrMv.

### Author(s)

Adelchi Azzalini

### References

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

### See Also

[makeSECdistr](#), [summary.SECdistr](#), [dp2cp](#)

### Examples

```
# d=1
f1 <- makeSECdistr(dp=c(3,2,5), family="SC", name="Univariate Skew-Cauchy")
plot(f1)
plot(f1, range=c(-3,40), probs=NULL, col=4)
#
# d=2
Omega2 <- matrix(c(3, -3, -3, 5), 2, 2)
f2 <- makeSECdistr(dp=list(c(10,30), Omega=Omega2, alpha=c(-3, 5)),
                  family="sn", name="SN-2d", compNames=c("x1", "x2"))
plot(f2)
x2 <- rmsn(100, dp=slot(f2,"dp"))
plot(f2, main="Distribution 'f2'", probs=c(0.5,0.9), cex.main=1.5, col=2,
      cex=0.8, complabs=c(expression(x[1]), expression(log(z[2]-beta^{1/3}))),
      data=x2, data.par=list(col=4, cex=0.6, pch=5))
```

---

plot.selm

*Diagnostic plots for selm fits*

---

### Description

Diagnostic plots for objects of class selm and mselm generated by a call to function selm

**Usage**

```

## S4 method for signature 'selm'
plot(x, param.type="CP", which = c(1:4), caption,
     panel = if (add.smooth) panel.smooth else points, main = "",
     ask = prod(par("mfcol")) < length(which) && dev.interactive(), ...,
     id.n = 3, labels.id = names(x@residuals.dp),
     cex.id = 0.75, identline = TRUE, add.smooth = getOption("add.smooth"),
     label.pos = c(4, 2), cex.caption = 1)

## S4 method for signature 'mselm'
plot(x, param.type="CP", which, caption,
     panel = if (add.smooth) panel.smooth else points, main = "",
     ask = prod(par("mfcol")) < length(which) && dev.interactive(), ...,
     id.n = 3, labels.id = names(x@residuals.dp),
     cex.id = 0.75, identline = TRUE, add.smooth = getOption("add.smooth"),
     label.pos = c(4, 2), cex.caption = 1)

```

**Arguments**

x	an object of class <code>selm</code> or <code>mselm</code> .
param.type	a character string which selects the type of residuals to be used for some of the plots; possible values are: "CP" (default), "DP", "pseudo-CP". The various type of residuals only differ by an additive term; see 'Details' for more information.
which	if a subset of the plots is required, specify a subset of 1:4; see 'Details' for a description of the plots.
caption	a vector of character strings with captions to appear above the plots.
panel	panel function. The useful alternative to <code>points</code> , <code>panel.smooth</code> can be chosen by <code>add.smooth = TRUE</code> .
main	title to each plot, in addition to the above caption.
ask	logical; if TRUE, the user is asked before each plot.
...	other parameters to be passed through to plotting functions.
id.n	number of points to be labelled in each plot, starting with the most extreme.
labels.id	vector of labels, from which the labels for extreme points will be chosen. NULL uses observation numbers..
cex.id	magnification of point labels.
identline	logical indicating if an identity line should be added to QQ-plot and PP-plot (default: TRUE).
add.smooth	logical indicating if a smoother should be added to most plots; see also <code>panel</code> above.
label.pos	positioning of labels, for the left half and right half of the graph respectively, for plots 1-3.
cex.caption	controls the size of caption.

## Details

The meaning of `param.type` is described in [dp2cp](#). However, for these plot only the first parameter component is relevant, which affects the location of the residuals; the other components are not computed. Moreover, for QQ-plot and PP-plot, DP-residuals are used irrespectively of `param.type`; see Section ‘Background’.

Values `which=1` and `which=2` have a different effect for object of class `"selm"` and class `"mse1m"`. In the univariate case, `which=1` plots the residual values versus the fitted values if  $p > 1$ , where  $p$  denotes the number of covariates including the constant; if  $p = 1$ , a boxplot of the response is produced. Value `which=2` produces an histogram of the residuals with superimposed the fitted curve, when  $p > 1$ ; if  $p = 1$ , a similar plot is generated using the response variable instead of the residuals. Default value for `which` is 1:4.

In the multivariate case, `which=1` is feasible only if  $p = 1$  and it displays the data scatter with superimposed the fitted distribution. Value `which=2` produces a similar plot but for residuals instead of data. Default value for `codewhich` is 2:4 if  $p > 1$ , otherwise `c(1, 3, 4)`.

Value `which=3` produces a QQ-plot, both in the univariate and in the multivariate case; the difference is that the squares of normalized residuals and suitably defined Mahalanobis distances, respectively, are used in the two cases. Similarly, `which=4` produces a PP-plot, working in a similar fashion.

## Background

Healy-type graphical diagnostics, in the form of QQ- and PP-plots, for the multivariate normal distribution have been extended to the skew-normal distribution by Azzalini and Capitanio (1999, section 6.1), and subsequently to the skew- $t$  distribution in Azzalini and Capitanio (2003). A brief explanation in the univariate SN case is provided in Section 3.1.1 of Azzalini and Capitanio (2014); see also Section 3.1.6. For the univariate ST case, see p.102 and p.111 of the monograph. The multivariate case is discussed in Section 5.2.1 as for the SN distribution, in Section 6.2.6 as for the ST distribution.

## Author(s)

Adelchi Azzalini

## References

- Azzalini, A. and Capitanio, A. (1999). Statistical applications of the multivariate skew normal distribution. *J.Roy.Statist.Soc. B* **61**, 579-602. Full-length version available at <http://arXiv.org/abs/0911.2093>
- Azzalini, A. and Capitanio, A. (2003). Distributions generated by perturbation of symmetry with emphasis on a multivariate skew  $t$  distribution. *J.Roy. Statist. Soc. B* **65**, 367-389. Full-length version available at <http://arXiv.org/abs/0911.2342>
- Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

## See Also

[selm](#), [dp2cp](#)

**Examples**

```

data(wines)
#
m10 <- selm(flavanoids ~ 1, family="SN", data=wines, subset=(wine=="Barolo"))
plot(m10)
plot(m10, which=c(1,3)) # fig 3.1 and 3.2(a) of Azzalini and Capitanio (2014)
#
m18 <- selm(acidity ~ sugar + nonflavanoids + wine, family="SN", data=wines)
plot(m18)
plot(m18, param.type="DP")
#
m28 <- selm(cbind(acidity, alcohol) ~ sugar + nonflavanoids + wine,
            family="SN", data=wines)
plot(m28, col=4)
#
data(ais)
m30 <- selm(cbind(RCC, Hg, Fe) ~ 1, family="SN", data=ais)
plot(m30, col=2, which=2)

```

predict.selm

*Predict method for selm-class objects***Description**

Predicted values based on a model object produced by `selm` with univariate response.

**Usage**

```

## S3 method for class 'selm'
predict(object, newdata, param.type = "CP",
        interval = "none", level = 0.95, na.action = na.pass, ...)

```

**Arguments**

<code>object</code>	an object of class <code>selm</code> as produced by a call to function <code>selm</code> with univariate response.
<code>newdata</code>	an optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
<code>param.type</code>	a character string with the required parameterization; it must be one of "CP", "DP", "pseudo-CP", or possibly their equivalent lowercase.
<code>interval</code>	type of interval calculation among "none", "confidence", "prediction"; it can be abbreviated.
<code>level</code>	tolerance/confidence level (default value is 0.95).
<code>na.action</code>	function determining what should be done with missing values in <code>newdata</code> . The default is to predict NA.
<code>...</code>	not used, only there for compatibility reasons.

## Details

Predicted values are obtained by evaluating the regression function in the dataframe `newdata` (which defaults to `model.frame(object)`). Setting `interval` other than "none" produces computation of confidence or prediction (tolerance) intervals at the specified level.

If `newdata` is omitted the predictions are based on the data used for the fit.

The action taken in case of missing data is regulated by argument `na.action`, along the lines of function `predict.lm`.

A detailed description of the methodology underlying `predict.selm` is available in the technical note of Azzalini (2016).

## Value

a vector of predictions (if `interval="none"`) or a matrix of predictions and bounds with column names `fit`, `lwr`, and `upr`, if `interval` is set.

## Author(s)

Adelchi Azzalini

## References

Azzalini, A. (2016). Derivation of various types of intervals from a `selm` object. Technical note distributed with the documentation of the R package `sn`, in file [selm-intervals.pdf](#) within section 'User guide, package vignettes and other documentation'.

## See Also

[selm](#), [summary.selm](#),

[makeSECdistr](#) for the CP/DP parameterizations,

[predict.lm](#) for usage of `na.action`

## Examples

```
data(barolo)
attach(barolo)
A75 <- (reseller=="A" & volume==75)
detach(barolo)
m3 <- selm(log(price, 10) ~ age, data=barolo[A75,], family="ST")
```

---

profile.selm	<i>Profile log-likelihood function of selm-class objects</i>
--------------	--

---

**Description**

One- or two-dimensional profile (penalized) log-likelihood function of a `selm` fit and corresponding confidence interval or regions

**Usage**

```
## S3 method for class 'selm'
profile(fitted, param.type, param.name, param.values, npt,
  opt.control = list(), plot.it = TRUE, log = TRUE, level,
  trace = FALSE, ...)
```

**Arguments**

<code>fitted</code>	an object of class <code>selm</code> as produced by a call to function <code>selm</code> with univariate response.
<code>param.type</code>	a character string with the required parameterization; it must be either "CP" or "DP", or possibly their equivalent lowercase.
<code>param.name</code>	either a single character string or a vector of two such terms with the name(s) of the parameter(s) for which the profile log-likelihood is required; these names must match those appearing in <code>summary.selm(object, param.type)</code> .
<code>param.values</code>	in the one-parameter case, a numeric vector with the values where the log-likelihood must be evaluated; in the two-parameter case, a list of two such vectors used to build a grid of coordinates of points. Their range must identify an interval or a rectangle which includes the MLE or MPLE obtained by <code>selm</code> . See 'Details' for more information.
<code>npt</code>	in case the vector or any of the vectors of argument <code>param.values</code> has length 2, an equally spaced grid of values is build with length equal to the corresponding component of <code>npt</code> . If the above condition is met but this argument is missing, a default choice is made, namely 51 or (26,26) in the one- or two-parameter case, respectively.
<code>opt.control</code>	an optional list passed as argument <code>control</code> to <code>optim</code> to optimize the log-likelihood; see 'Details' for more information.
<code>plot.it</code>	a logical value; if TRUE (default value), a plot is produced representing the deviance, which is described in 'Details' below. In the one-parameter case, a confidence interval of prescribed <code>level</code> is marked on the plot; in the two-parameter case, the contour curves are labelled with approximate confidence levels. See however for more information.
<code>log</code>	a logical value (default: TRUE) indicating whether the scale and tail-weight parameter (the latter only for the ST family) must be log-transformed, if case any of them occurs in <code>param.name</code> . This applies to <code>omega</code> and <code>nu</code> in the DP parameter set and to <code>s.d.</code> and <code>gamma2</code> in the CP parameter set.

level	a single probability value (in the one-parameter case) or a vector of such values (in the two-parameter case) for which the confidence interval or region is required; see ‘Details’ for more information.
trace	a logical value (default: FALSE) to activate printing of intermediate outcome of the log-likelihood optimization process
...	optional graphical parameters passed to the plotting functions.

### Details

For each chosen point of the parameter(s) to be profiled, the log-likelihood is maximized with respect to the remaining parameters. The optimization process is accomplished using the `optim` optimization function, with `method="BFGS"`. This step can be regulated by the user via `opt.control` which is passed to `optim` as `control` argument, apart from element `fnscale` whose use is reserved.

If the original fitted object included a fixed parameter value, this is kept fixed here. If the estimation method was "MPLE", that choice carries on here; in case the penalty function was user-defined, it must still be accessible.

For plotting purposes and also in the numerical output, the deviance function  $D$  is used, namely

$$D = 2 [\max(\log L) - \log L]$$

where  $L$  denotes the likelihood.

The range of `param.values` must enclose the maximum (penalized) likelihood estimates (MLE or MPLE) by an adequate extent such that suitable confidence intervals or regions can be established from standard asymptotic theory. If this condition does not hold, the function still proceeds, but no confidence interval or region is delivered. For the SN family and DP parameterization, the asymptotic theory is actually non-standard near the important point  $\alpha = 0$ , but the correspondence with the regular case of the CP parameterization, still allows to derive confidence regions using standard procedures; for more information on this point, see Section 3.1.6 of Azzalini and Capitanio (2014). When the MLE occurs on the frontier of the parameter space, a message is issued and no confidence interval is produced, while in the two-parameter case the plot is not labelled with probability values, but only with deviance levels.

### Value

An invisible list whose components, described below, are partly different in the one- and the two-parameter cases.

<code>call</code>	the calling statement
<code>&lt;param1&gt;</code>	values of the first parameter
<code>&lt;param2&gt;</code>	values of the second parameter (in the two-parameter case)
<code>logLik</code>	numeric vector or matrix of the profile log-likelihood values
<code>confint</code>	in the one-parameter case, the confidence interval
<code>level</code>	in the one-parameter case, the confidence level
<code>deviance.contour</code>	in the two-parameter case, a list of lists whose elements identify each curve of the contour plot



**Warnings**

- This function is experimental and changes in future versions of the package may occur. Users should not rely on the persistence of the same user interface or the same name(s).
- It is a known fact that, in some critical situations, peculiar outcomes are produced.

**Author(s)**

Adelchi Azzalini

**References**

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

**See Also**

[selm](#), [summary.selm](#),  
[makeSECdistr](#) for the CP/DP parameterizations,  
[optim](#) for its control argument

**Examples**

```
data(ais)
m1 <- selm(log(Fe) ~ BMI + LBM, family = "sn", data = ais)

pll <- profile(m1, "dp", param.name="alpha", param.val=c(-3,2))

profile(m1, "cp", param.name="gamma1", param.val=seq(-0.7, 0.4, by=0.1))

# in the next example, we reduce grid points to save execution time
pll <- profile(m1, "cp", param.name=c("(Intercept.CP)", "gamma1"),
  param.val=list(c(1.5, 4), c(-0.8, 0.5)), npt=c(11,16) )
```

---

Qpenalty

*Penalty function for log-likelihood of selm models*

---

**Description**

Penalty function for the log-likelihood of selm models when method="MPLE". Qpenalty is the default function; MPpenalty is an example of a user-defined function effectively corresponding to a prior distributio on alpha.

**Usage**

```
Qpenalty(alpha_etc, nu = NULL, der = 0)
```

```
MPpenalty(alpha, der = 0)
```

**Arguments**

alpha_etc, alpha	in the univariate case, a single value alpha; in the multivariate case, a two-component list whose first component is the vector alpha, the second one is matrix cov2cor(Omega).
nu	degrees of freedom, only required if selm is called with family="ST".
der	a numeric value in the set 0, 1, 2 which indicates the required number of derivatives of the function. In the multivariate case the function will only be called with der equal to 0 or 1.

**Details**

The penalty is a function of alpha, but its expression may depend on other ingredients, specifically nu and cov2cor(Omega). See 'Details' of [selm](#) for additional information.

The penalty mechanism allows to introduce a prior distribution  $\pi$  for  $\alpha$  by setting  $Q = -\log \pi$ , leading to a maximum *a posteriori* estimate in the stated sense.

As a simple illustration of this mechanism, function MPpenalty implements the 'matching prior' distribution for the univariate SN distribution studied by Cabras *et al.* (2012); a brief summary of the proposal is provided in Section 3.2 of Azzalini and Capitanio (2014). Note that, besides alpha=+/-Inf, this choice also penalizes alpha=0 with Q=Inf, effectively removing alpha=0 from the parameter space.

Starting from the code of function MPpenalty, a user should be able to introduce an alternative prior distribution if so desired.

**Value**

A positive number Q representing the penalty, possibly with attributes attr(Q, "der1") and attr(Q, "der2"), depending on the input value der.

**Author(s)**

Adelchi Azzalini

**References**

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

Cabras, S., Racugno, W., Castellanos, M. E., and Ventura, L. (2012). A matching prior for the shape parameter of the skew-normal distribution. *Scand. J. Statist.* **39**, 236–247.

**See Also**

[selm](#) function

**Examples**

```

data(frontier)
m2 <- selm(frontier ~ 1) # no penalty
m2a <- selm(frontier ~ 1, method="MPLE") # penalty="Qpenalty" is implied here
m2b <- selm(frontier ~ 1, method="MPLE", penalty="MPpenalty")

```

---

residuals.selm                      *Residuals and fitted values from selm fits*

---

**Description**

residuals and fitted methods for classes "selm" and "mselm".

**Usage**

```

## S4 method for signature 'selm'
residuals(object, param.type = "CP", ...)
## S4 method for signature 'mselm'
residuals(object, param.type = "CP", ...)
## S4 method for signature 'selm'
fitted(object, param.type = "CP", ...)
## S4 method for signature 'mselm'
fitted(object, param.type = "CP", ...)

```

**Arguments**

object	an object of class "selm" or "mselm" as created by a call to function selm.
param.type	a character string which indicates the required type of parameter type; possible values are "CP" (default), "DP", "pseudo-CP" and their equivalent lower-case expressions.
...	not used, included for compatibility with the generic method.

**Value**

a numeric vector (for selm-class objects) or a matrix (for mselm-class objects).

**Note**

The possible options of param.type are described in the documentation of [dp2cp](#); their corresponding outcomes differ by an additive constant only. With the "CP" option (that is, the 'centred parametrization'), the residuals are centred around 0, at least approximately; this is a reason for setting "CP" as the default option. For more information, see the 'Note' in the documentation of [summary.selm](#).

**Author(s)**

Adelchi Azzalini

## References

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

## See Also

[dp2cp](#), [summary.selm](#), [selm](#) function, [selm-class](#)

## Examples

```
data(wines, package="sn")
m5 <- selm(acidity ~ phenols + wine, family="SN", data=wines)
residuals(m5)
residuals(m5, "dp")
fitted(m5, "dp")
#
m12 <- selm(cbind(acidity, alcohol) ~ phenols + wine, family="SN", data=wines)
residuals(m12)
#
# see other examples at function selm
```

---

 sd

*Standard deviation*


---

## Description

The `sd` function from the **stats** is replaced by a new method in order to introduce a separate method to deal with objects of class `SECdistrUv`. The function `sd.default` is an alias of the original function `sd`.

## Usage

```
sd(x, ...)
## Default S3 method:
sd(x, na.rm = FALSE, ...)
```

## Arguments

<code>x</code>	a numeric vector, matrix or data frame.
<code>na.rm</code>	logical. Should missing values be removed?
<code>...</code>	further arguments passed to or from other methods.

## See Also

[sd](#), [SECdistrUv](#)

---

SECdistrMv-class      *Class "SECdistrMv"*

---

### Description

Multivariate skew-elliptically contoured distributions

### Objects from the Class

Objects can be created by a call to function `makeSECdistr`, when its argument `dp` is a list, or by a suitable transformation of some object of this class. They can also be obtained from an object generated by `selm` using the function `extractSECdistr`.

### Slots

**family**: a character string which identifies the parametric family; currently, possible values are: "SN", "ESN", "ST", "SC".

**dp**: a list of parameters; its length depends on the selected family.

**name**: a character string with the name of the multivariate variable; it can be an empty string.

**compNames**: a vector of character strings with the names of the component variables.

### Methods

**show** signature(object = "SECdistrMv-class"): ...

**plot** signature(x = "SECdistrMv-class"): ...

**summary** signature(object = "SECdistrMv-class"): ...

**mean** signature(x = "SECdistrUv"): ...

**vcov** signature(object = "SECdistrUv"): ...

### Note

See `makeSECdistr` for a detailed description of `family` and `dp`.

Note that here methods `mean` and `vcov` are not applied to data or to a fitted model, but to a *probability distribution* instead, of which they provide the mean (vector) value and the variance-covariance matrix. If methods `mean` and `vcov` are applied to a distribution for which the mean or the variance do not exist, a NULL value is returned and a warning message is issued.

### Author(s)

Adelchi Azzalini

### See Also

[SECdistrUv](#), [plot, SECdistrMv-method](#), [summary, SECdistrMv-method](#), [affineTransSECdistr](#), [marginalSECdistr](#), [extractSECdistr](#)

**Examples**

```

dp0 <- list(xi=1:2, Omega=diag(3:4), alpha=c(3, -5))
f10 <- makeSECdistr(dp=dp0, family="SN", name="SN-2D", compNames=c("x", "y"))
show(f10)
plot(f10)
summary(f10)
mean(f10) # the mean value of the probability distribution
vcov(f10) # the variance-covariance matrix of the probability distribution

```

---

SECdistrUv-class      *Class "SECdistrUv"*

---

**Description**

Univariate skew-elliptically contoured distributions

**Objects from the class**

Objects can be created by a call to function [makeSECdistr](#) when its argument `dp` is a vector. They can also be obtained from an object generated by `selm` using the function `extractSEDdistr`.

**Slots**

**family:** a character string which selects the parametric family; currently, possible values are: "SN", "ESN", "ST", "SC".

**dp:** a numeric vector of parameters; its length depends on the selected family.

**name:** a character string with name of the distribution.

**Methods**

**show** signature(object = "SECdistrUv"): ...

**plot** signature(x = "SECdistrUv"): ...

**summary** signature(object = "SECdistrUv"): ...

**mean** signature(x = "SECdistrUv"): ...

**sd** signature(object = "SECdistrUv"): ...

**Note**

See [makeSECdistr](#) for a detailed description of family and `dp`.

Unlike various other packages, methods `mean` and `sd` here are not targeted to data or to a fitted model, but to a *probability distribution* instead, of which they provide the mean value and the standard deviation. If these methods are applied to a distribution of which the mean or the variance do not exist, a NULL value is returned and a warning message is issued.

**Author(s)**

Adelchi Azzalini

**See Also**[SECdistrMv](#), [plot,SECdistrUv-method](#), [summary,SECdistrUv-method](#), [extractSECdistr](#)**Examples**

```
f2 <- makeSECdistr(dp=c(3, 5, -pi, 6), family="ST", name="My first ST")
show(f2)
plot(f2)
plot(f2, probs=c(1,5,9)/10)
plot(f2, range=c(-30,10), probs=NULL, col=2, main=NULL)
summary(f2)
mean(f2) # the mean value of the probability distribution
sd(f2) # the standard deviation of the distribution
```

selm

*Fitting linear models with skew-elliptical error term***Description**

Function `selm` fits a linear model with skew-elliptical error term. The term ‘skew-elliptical distribution’ is an abbreviated equivalent of skew-elliptically contoured (SEC) distribution. The function works for univariate and multivariate response variables.

**Usage**

```
selm(formula, family = "SN", data, weights, subset, na.action,
      start = NULL, fixed.param = list(), method = "MLE", penalty=NULL,
      offset, model = TRUE, x = FALSE, y = FALSE, ...)
```

**Arguments**

formula	an object of class " <code>formula</code> " (or one that can be coerced to that class): a symbolic description of the model to be fitted, using the same syntax used for the similar parameter of e.g. " <code>lm</code> ", with the restriction that the constant term must not be removed from the linear predictor.
family	a character string which selects the parametric family of SEC type assumed for the error term. It must be one of "SN" (default), "ST" or "SC", which correspond to the skew-normal, the skew- <i>t</i> and the skew-Cauchy family, respectively. See <a href="#">makeSECdistr</a> for more information on these families and the set of SEC distributions; notice that the family "ESN" listed there is not allowed here.
data	an optional data frame containing the variables in the model. If not found in <code>data</code> , the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>selm</code> is called.

weights	a numeric vector of weights associated to individual observations. Weights are supposed to represent frequencies, hence must be non-negative integers (not all 0) and <code>length(weights)</code> must equal the number of observations. If not assigned, a vector of all 1's is generated.
subset	an optional vector specifying a subset of observations to be used in the fitting process. It works like the same parameter in <code>lm</code> .
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the <code>na.action</code> setting of <code>options</code> . The 'factory-fresh' default is <code>na.omit</code> . Another possible value is <code>NULL</code> , no action.
start	a vector (in the univariate case) or a list (in the multivariate case) of initial DP values for searching the parameter estimates. See 'Details' about a choice of start to be avoided. If <code>start=NULL</code> (default), initial values are selected by the procedure.
fixed.param	a list of assignments of parameter values which must be kept fixed in the estimation process. Currently, there only two types of admissible constraint: one is to set <code>alpha=0</code> to impose a symmetry condition of the distribution; the other is to set <code>nu=&lt;value&gt;</code> , to fix the degrees of freedom at the named <code>&lt;value&gt;</code> when <code>family="ST"</code> , for instance <code>list(nu=3)</code> . See 'Details' for additional information.
method	a character string which selects the estimation method to be used for fitting. Currently, two options exist: <code>"MLE"</code> (default) and <code>"MPL"</code> , corresponding to standard maximum likelihood and maximum penalized likelihood estimation, respectively. See 'Details' for additional information.
penalty	a character string which denotes the penalty function to be subtracted to the log-likelihood function, when <code>method="MPL"</code> ; if <code>penalty=NULL</code> (default), a pre-defined function is adopted. See 'Details' for a description of the default penalty function and for the expected format of alternative specifications. When <code>method="MLE"</code> , no penalization is applied and this argument has no effect.
offset	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be <code>NULL</code> or a numeric vector of length equal to the number of cases. One or more <code>offset</code> terms can be included in the formula instead or as well, and if more than one are specified their sum is used.
model, x, y	logicals. If <code>TRUE</code> , the corresponding components of the fit are returned.
...	optional control parameters, as follows. <ul style="list-style-type: none"> <li>• <code>trace</code>: a logical value which indicates whether intermediate evaluations of the optimization process are printed (default: <code>FALSE</code>).</li> <li>• <code>info.type</code>: a character string which indicates the type of Fisher information matrix; possible values are <code>"observed"</code> (default) and <code>"expected"</code>. Currently, <code>"expected"</code> is implemented only for the SN family.</li> <li>• <code>opt.method</code>: a character string which selects the numerical optimization method, among the possible values <code>"nlminb"</code>, <code>"Nelder-Mead"</code>, <code>"BFGS"</code>, <code>"CG"</code>, <code>"SANN"</code>. If <code>opt.method="nlminb"</code> (default), function <code>nlminb</code> is called, otherwise function <code>optim</code> is called with <code>method</code> equal to <code>opt.method</code>.</li> <li>• <code>opt.control</code>: a list of control parameters which is passed on either to <code>nlminb</code> or to <code>optim</code>, depending on the chosen <code>opt.method</code>.</li> </ul>



## Details

By default, `selm` fits the selected model by maximum likelihood estimation (MLE), making use of some numerical optimization method. Maximization is performed in one parameterization, usually DP, and then the estimates are mapped to other parameter sets, CP and pseudo-CP; see [dp2cp](#) for more information on parameterizations. These parameter transformations are carried out transparently to the user. The observed information matrix is used to obtain the estimated variance matrix of the MLE's and from this the standard errors. Background information on MLE in the context of SEC distributions is provided by Azzalini and Capitanio (2014); see specifically Chapter 3, Sections 4.3, 5.2, 6.2.5–6. For additional information, see the original research work referenced therein as well as the sources quoted below.

Although the density function of SEC distributions are expressed using DP parameter sets, the methods associated to the objects created by this function communicate, by default, their outcomes in the CP parameter set, or its variant form pseudo-CP when CP does not exist; the 'Note' at [summary.selm](#) explains why. A more detailed discussion is provided by Azzalini and Capitanio (1999, Section 5.2) and Arellano-Valle and Azzalini (2008, Section 4), for the univariate and the multivariate SN case, respectively; an abridged account is available in Sections 3.1.4–6 and 5.2.3 of Azzalini and Capitanio (2014). For the ST case, see Arellano-Valle and Azzalini (2013).

There is a known open issue which affects computation of the information matrix of the multivariate skew-normal distribution when the slant parameter  $\alpha$  approaches the null vector; see p.149 of Azzalini and Capitanio (2014). Consequently, if a model with multivariate response is fitted with `family="SN"` and the estimate `alpha` of  $\alpha$  is at the origin or neary so, the information matrix and the standard errors are not computed and a warning message is issued. In this unusual circumstance, a simple work-around is to re-fit the model with `family="ST"`, which will work except in remote cases when (i) the estimated degrees of freedom `nu` diverge and (ii) still `alpha` remains at the origin.

The optional argument `fixed.param=list(alpha=0)` imposes the constraint  $\alpha = 0$  in the estimation process; in the multivariate case, the expression is interpreted in the sense that all the components of vector  $\alpha$  are zero, which implies symmetry of the error distribution, irrespectively of the parameterization subsequently adopted for summaries and diagnostics. When this restriction is selected, the estimation method cannot be set to "MPLE". Under the constraint  $\alpha = 0$ , if `family="SN"`, the model is fitted similarly to `lm`, except that here MLE is used for estimation of the covariance matrix. If `family="ST"` or `family="SC"`, a symmetric Student's  $t$  or Cauchy distribution is adopted.

Under the constraint  $\alpha = 0$ , the location parameter  $\xi$  coincides with the mode and the mean of the distribution, when the latter exists. In addition, when the covariance matrix of a ST distribution exists, it differs from  $\Omega$  only by a multiplicative factor. Consequently, the summaries of a model of this sort automatically adopt the DP parametrization.

The other possible form of constraint allows to fix the degrees of freedom when `family="ST"`. The two constraints can be combined writing, for instance, `fixed.param=list(alpha=0, nu=6)`. The constraint `nu=1` is equivalent to `family="SC"`. In practice, an expression of type `fixed.param=list(...)` can be abbreviated to `fixed=list(...)`.

Argument `start` allows to set the initial values, with respect to the DP parameterization, of the numerical optimization. However, there is a specific choice of `start` to be avoided. When `family="SN"`, do not set the shape parameter `alpha` exactly at 0, as this would blow-up computation of the log-likelihood gradient and the Hessian matrix. This is not due to a software bug, but to a known peculiar behaviour of the log-likelihood function at that specific point. Therefore, in the univariate

case for instance, do not set e.g. `start=c(12, 21, 0)`, but set instead something like `start=c(12, 21, 0.01)`.

Recall that, if one needs to fit a model forcing 0 asymmetry, typically to compare two log-likelihood functions with/without asymmetry, then the option to use is `fixed.param=list(alpha=0)`.

In some cases, especially for small sample size, the MLE occurs on the frontier of the parameter space, leading to DP estimates with `abs(alpha)=Inf` or to a similar situation in the multivariate case or in an alternative parameterization. Such outcome is regarded by many as unsatisfactory; surely it prevents using the observed information matrix to compute standard errors. This problem motivates the use of maximum penalized likelihood estimation (MPLE), where the regular log-likelihood function  $\log L$  is penalized by subtracting an amount  $Q$ , say, increasingly large as  $|\alpha|$  increases. Hence the function which is maximized at the optimization stage is now  $\log L - Q$ . If `method="MPLE"` and `penalty=NULL`, the default function `Qpenalty` is used, which implements the penalization:

$$Q(\alpha) = c_1 \log(1 + c_2 \alpha_*^2)$$

where  $c_1$  and  $c_2$  are positive constants, which depend on the degrees of freedom  $\nu$  in the ST case,

$$\alpha_*^2 = \alpha^\top \bar{\Omega} \alpha$$

and  $\bar{\Omega}$  denotes the correlation matrix associated to the scale matrix  $\Omega$  described in connection with `makeSECdistr`. In the univariate case  $\bar{\Omega} = 1$ , so that  $\alpha_*^2 = \alpha^2$ . Further information on MPLE and this choice of the penalty function is given in Section 3.1.8 and p.111 of Azzalini and Capitanio (2014); for a more detailed account, see Azzalini and Arellano-Valle (2013) and references therein.

It is possible to change the penalty function, to be declared via the argument `penalty`. For instance, if the calling statement includes `penalty="anotherQ"`, the user must have defined

```
anotherQ <- function(alpha_etc, nu = NULL, der = 0)
```

with the following arguments.

- `alpha_etc`: in the univariate case, a single value `alpha`; in the multivariate case, a two-component list whose first component is the vector `alpha`, the second one is matrix equal to `cov2cor(Omega)`.
- `nu`: degrees of freedom, only relevant if `family="ST"`.
- `der`: a numeric value which indicates the required order of derivation; if `der=0` (default value), only the penalty  $Q$  needs to be returned by the function; if `der=1`, `attr(Q, "der1")` must represent the first order derivative of  $Q$  with respect to `alpha`; if `der=2`, also `attr(Q, "der2")` must be assigned, containing the second derivative (only required in the univariate case).

This function must return a single numeric value, possibly with required attributes when is called with `der>1`. Since `sn` imports functions `grad` and `hessian` from package `numDeriv`, one can rely on them for numerical evaluation of the derivatives, if they are not available in an explicit form.

This penalization scheme allows to introduce a prior distribution  $\pi$  for  $\alpha$  by setting  $Q = -\log \pi$ , leading to a maximum *a posteriori* estimate in the stated sense. See `Qpenalty` for more information and an illustration.

The actual computations are not performed within `selm` which only sets-up ingredients for work of `selm.fit` and other functions further below this one. See `selm.fit` for more information.

**Value**

an S4 object of class `selm` or `mselm`, depending on whether the response variable of the fitted model is univariate or multivariate; these objects are described in the `selm` class.

**Cautionary notes**

The first of these notes applies to the stage *preceding* the use of `selm` and related fitting procedures. Before fitting a model of this sort, consider whether you have enough data for this task. In this respect, the passage below taken from p.63 of Azzalini and Capitanio (2014) is relevant.

“Before entering technical aspects, it is advisable to underline a qualitative effect of working with a parametric family which effectively is regulated by moments up to the third order. The implication is that the traditional rule of thumb by which a sample size is small up to ‘about  $n = 30$ ’, and then starts to become ‘large’, while sensible for a normal population or other two-parameter distribution, is not really appropriate here. To give an indication of a new threshold is especially difficult, because the value of  $\alpha$  also has a role here. Under this *caveat*, numerical experience suggests that ‘about  $n = 50$ ’ may be a more appropriate guideline in this context.”

The above passage referred to the univariate SN context. In the multivariate case, increase the sample size appropriately, especially so with the ST family. This is not to say that one cannot attempt fitting these models with small or moderate sample size. However, one must be aware of the implications and not be surprised if problems appear.

The second cautionary note refers instead to the outcome of a call to `selm` and related function, or the lack of it. The estimates are obtained by numerical optimization methods and, as usual in similar cases, there is no guarantee that the maximum of the objective function is achieved. Consideration of model simplicity and of numerical experience indicate that models with SN error terms generally produce more reliable results compared to those with the ST family. Take into account that models involving a traditional Student’s  $t$  distribution with unknown degrees of freedom can already be problematic; the presence of the (multivariate) slant parameter  $\alpha$  in the ST family cannot make things any simpler. Consequently, care must be exercised, especially so if one works with the (multivariate) ST family. Consider re-fitting a model with different starting values and, in the ST case, building the profile log-likelihood for a range of  $\nu$  values; function `profile.selm` can be useful here.

Details on the numerical optimization which has produced object `obj` can be extracted with `slot(obj, "opt.method")`; inspection of this component can be useful in problematic cases. Be aware that occasionally `optim` and `nlm` declare successful completion of a regular minimization problem at a point where the Hessian matrix is not positive-definite. Two cases of this sort are presented in the final portion of the examples below.

**Author(s)**

Adelchi Azzalini

**References**

- Arellano-Valle, R. B., and Azzalini, A. (2008). The centred parametrization for the multivariate skew-normal distribution. *J. Multiv. Anal.* **99**, 1362–1382. Corrigendum: **100** (2009), 816.
- Arellano-Valle, R. B., and Azzalini, A. (2013, available online 12 June 2011). The centred parametrization and related quantities for the skew- $t$  distribution. *J. Multiv. Anal.* **113**, 73–90.

Azzalini, A. and Capitanio, A. (1999). Statistical applications of the multivariate skew normal distribution. *J.Roy.Statist.Soc. B* **61**, 579–602. Full-length version available at <http://arXiv.org/abs/0911.2093>

Azzalini, A. and Arellano-Valle, R. B. (2013, available online 30 June 2012). Maximum penalized likelihood estimation for skew-normal and skew-*t* distributions. *J. Stat. Planning & Inference* **143**, 419–433.

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### See Also

- `selm`-class for classes "selm" and "mselm", `summary.selm` for summaries, `plot.selm` for plots, `residuals.selm` for residuals and fitted values
- the generic functions `coef`, `logLik`, `vcov`, `profile`, `confint`, `predict`
- the underlying function `selm.fit` and those further down
- the selection of a penalty function of the log-likelihood, such as `Qpenalty`
- the function `extractSECdistr` to extract the SEC error distribution from an object returned by `selm`
- the broad underlying logic and a number of ingredients are like in function `lm`

### Examples

```
data(ais)
m1 <- selm(log(Fe) ~ BMI + LBM, family="SN", data=ais)
print(m1)
summary(m1)
s<- summary(m1, "DP", cov=TRUE, cor=TRUE)
plot(m1)
plot(m1, param.type="DP")
logLik(m1)
coef(m1)
coef(m1, "DP")
var <- vcov(m1)
#
m1a <- selm(log(Fe) ~ BMI + LBM, family="SN", method="MPLE", data=ais)
m1b <- selm(log(Fe) ~ BMI + LBM, family="ST", fixed.param=list(nu=8), data=ais)
#
data(barolo)
attach(barolo)
A75 <- (reseller=="A" & volume==75)
logPrice <- log(price[A75],10)
m <- selm(logPrice ~ 1, family="ST")
summary(m)
plot(m, which=2, col=4, main="Barolo log10(price)")
# cfr Figure 4.7 of Azzalini & Capitanio (2014), p.107
detach(barolo)
#-----
# examples with multivariate response
#
```

```

m3 <- selm(cbind(BMI, LBM) ~ WCC + RCC, family="SN", data=ais)
plot(m3, col=2, which=2)
summary(m3, "dp")
coef(m3)
coef(m3, vector=FALSE)
#
data(wines)
m28 <- selm(cbind(chloride, glycerol, magnesium) ~ 1, family="ST", data=wines)
dp28 <- coef(m28, "DP", vector=FALSE)
pcp28 <- coef(m28, "pseudo-CP", vector=FALSE)
# the next statement takes a little more time than others
plot(m28)

#
m4 <- selm(cbind(alc, sugar)~1, family="ST", data=wines)
m5 <- selm(cbind(alc, sugar)~1, family="ST", data=wines, fixed=list(alpha=0))
print(1 - pchisq(2*as.numeric(logLik(m4)-logLik(m5)), 2)) # test for symmetry
#

# illustrate final passage of 'Warning' section above:
# the execution of the next selm command is known to produce warning messages
# although the optimizer declares successful convergence
m31 <- selm(cbind(BMI, LBM)~ Ht + Wt, family="ST", data=ais)
# Warning message...
slot(m31, "opt.method")$convergence # a 0 value indicates success
# the next case is similar
m32 <- selm(cbind(BMI, LBM)~ Ht + Wt, family="ST", data=ais, opt.method="BFGS")
# Warning message...
slot(m32, "opt.method")$convergence

```

---

selm-class

*Classes selm and mselm of objects created by function selm*


---

## Description

A successful call to function `selm` creates an object of either of these classes, having a structure described in section ‘Slots’. A set of methods for these classes of objects exist, listed in section ‘Methods’.

## Objects from the class

An object can be created by a successful call to function `selm`.

## Slots

**call:** the calling statement.

**family:** the parametric family of skew-elliptically contoured distributed (SEC) type.

`logL`: log-likelihood or penalized log-likelihood value achieved at the end of the maximization process.

`method`: estimation method ("MLE" or "MPLE").

`param`: estimated parameters, for various parameterizations.

`param.var`: approximate variance matrices of the parameter estimates, for various parameterizations.

`size`: a numeric vector with size of various components.

`fixed.param`: a vector of parameters which have been kept fixed in the fitting process, if any.

`residuals.dp`: residual values, for DP-type parameters.

`fitted.values.dp`: fitted values, for DP-type parameters.

`control`: a list with control parameters.

`input`: a list of selected input values.

`opt.method`: a list with details on the optimization method.

## Methods

<code>coef</code>	<code>signature(object = "selm"): ...</code>
<code>logLik</code>	<code>signature(object = "selm"): ...</code>
<code>plot</code>	<code>signature(x = "selm"): ...</code>
<code>show</code>	<code>signature(object = "selm"): ...</code>
<code>summary</code>	<code>signature(object = "selm"): ...</code>
<code>residuals</code>	<code>signature(object = "selm"): ...</code>
<code>fitted</code>	<code>signature(object = "selm"): ...</code>
<code>vcov</code>	<code>signature(object = "selm"): ...</code>
<code>weights</code>	<code>signature(object = "selm"): ...</code>
<code>profile</code>	<code>signature(fitted = "selm"): ...</code>
<code>confint</code>	<code>signature(object = "selm"): ...</code>
<code>predict</code>	<code>signature(object = "selm"): ...</code>

<code>coef</code>	<code>signature(object = "mselm"): ...</code>
<code>logLik</code>	<code>signature(object = "mselm"): ...</code>
<code>plot</code>	<code>signature(x = "mselm"): ...</code>
<code>show</code>	<code>signature(object = "mselm"): ...</code>
<code>summary</code>	<code>signature(object = "mselm"): ...</code>
<code>residuals</code>	<code>signature(object = "mselm"): ...</code>
<code>fitted</code>	<code>signature(object = "mselm"): ...</code>
<code>vcov</code>	<code>signature(object = "mselm"): ...</code>
<code>weights</code>	<code>signature(object = "mselm"): ...</code>

**Note**

See [dp2cp](#) for a description of possible parameter sets. When `logLik` is used on an object obtained using the MPLE estimation method, the value reported is actually the *penalized* log-likelihood.

**Author(s)**

Adelchi Azzalini

**See Also**

See also [selm](#) function, [plot.selm](#), [summary.selm](#), [dp2cp](#)

**Examples**

```
data(ais)
m1 <- selm(log(Fe) ~ BMI + LBM, family="SN", data=ais)
summary(m1)
plot(m1)
logLik(m1)
res <- residuals(m1)
fv <- fitted(m1)
#
data(wines, package="sn")
m2 <- selm(alcohol ~ malic + phenols, data=wines)
#
m12 <- selm(cbind(acidity, alcohol) ~ phenols + wine, family="SN", data=wines)
coef(m12)
cp <- coef(m12, vector=FALSE)
dp <- coef(m12, "DP", vector=FALSE)
plot(m12)
plot(m12, which=2, col="gray60", pch=20)
```

---

selm.fit

*Fitting functions for selm models*

---

**Description**

A call to `selm` activates a call to `selm.fit` and from here to some other function which actually performs the parameter search, among those listed below. These lower-level functions can be called directly for increased efficiency, at the expense of some more programming effort and lack of methods for the returned object.

**Usage**

```
selm.fit(x, y, family = "SN", start = NULL, w, fixed.param = list(),
        offset = NULL, selm.control=list())
```

```

sn.mple(x, y, cp = NULL, w, penalty = NULL, trace = FALSE, opt.method =
  c("nlminb", "Nelder-Mead", "BFGS", "CG", "SANN"), control = list())

st.mple(x, y, dp = NULL, w, fixed.nu = NULL, symmetr = FALSE, penalty = NULL,
  trace = FALSE, opt.method = c("nlminb", "Nelder-Mead", "BFGS", "CG", "SANN"),
  control = list())

msn.mle(x, y, start = NULL, w, trace = FALSE, opt.method = c("nlminb",
  "Nelder-Mead", "BFGS", "CG", "SANN"), control = list())

msn.mple(x, y, start = NULL, w, trace = FALSE, penalty = NULL,
  opt.method = c("nlminb", "Nelder-Mead", "BFGS", "CG", "SANN"),
  control = list())

mst.mple(x, y, start = NULL, w, fixed.nu = NULL, symmetr=FALSE,
  penalty = NULL, trace = FALSE,
  opt.method = c("nlminb", "Nelder-Mead", "BFGS", "CG", "SANN"),
  control = list())

```

## Arguments

x	a full-rank design matrix with the first column of all 1's.
y	a vector or a matrix of response values such that $NROW(y)=nrow(x)$ .
family	a character string which selects the parametric family of distributions assumed for the error term of the regression model. It must one of "SN" (default), "ST" or "SC", which correspond to the skew-normal, the skew- <i>t</i> and the skew-Cauchy family, respectively. See <a href="#">makeSECdistr</a> for more information on these families and the skew-elliptically contoured (SEC) distributions; notice that family "ESN" is not allowed here.
start, dp, cp	a vector or a list of initial parameter values, depending whether y is a vector or a matrix. It is assumed that cp is given in the CP parameterization, dp and start in the DP parameterization.
w	a vector of non-negative integer weights of length equal to $NROW(y)$ ; if missing, a vector of all 1's is generated.
fixed.param	a list of assignments of parameter values to be kept fixed during the optimization process. Currently, there is only one such option, namely <code>fixed.param=list(nu='value')</code> , to fix the degrees of freedom at the named 'value' when family="ST", for instance <code>list(nu=3)</code> . Setting <code>fixed.param=list(nu=1)</code> is equivalent to select family="SC".
penalty	an optional character string with the name of the penalty function of the log-likelihood; default value NULL corresponds to no penalty.
offset	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more <a href="#">offset</a> terms can be included in the formula instead or as well, and if more than one are specified their sum is used.
trace	a logical value which regulates printing of successive calls to the target function; default value is FALSE which suppresses printing.



<code>fixed.nu</code>	a positive value to keep fixed the parameter <code>nu</code> of the ST distribution in the optimization process; with default value <code>NULL</code> , <code>nu</code> is estimated like the other parameters.
<code>symmetr</code>	a logical flag indicating whether a constraint of symmetry is imposed on the slant parameter; default is <code>symmetr=FALSE</code> .
<code>opt.method</code>	a character string which selects the optimization method within the set <code>c("nlminb", "Nelder-Mead", "E"</code> , the last four of these are "methods" of function <code>optim</code> .
<code>selm.control</code>	a list whose components regulate the working of <code>selm.fit</code> ; see 'Details' for their description;
<code>control</code>	a list of control items passed to the optimization function.

### Details

A call to `selm` produces a call to `selm.fit` which selects the appropriate function among `sn.mple`, `st.mple`, `msn.mle`, `msn.mple`, `mst.mple`, depending on the arguments of the calling statement. In the adopted scheme for function names, `msn` refers to a multivariate skew-normal distribution and `mst` refers to a multivariate skew- $t$  distribution, while `mle` and `mple` refers to maximum likelihood and maximum penalized likelihood estimation, respectively. Of these functions, `sn.mple` works in CP space; the others in the DP space. In all cases, a corresponding mapping to the alternative parameter space is performed before exiting `selm.fit`, in addition to the selected parameter set.

The components of `selm.control` are as follows:

- `method`: the estimation method, "MLE" or "MPLE".
- `penalty`: a string with the name of the penalty function.
- `info.type`: a string with the name of the information matrix, "observed" or "expected"; currently fixed at "observed".
- `opt.method`: a character string which selects the optimization method.
- `opt.control`: a list of control parameters of `opt.method`.

Function `msn.mle`, for MLE estimation of linear models with SN errors, is unchanged from version 0.4-x of the package. Function `msn.mple` is similar to `msn.mle` but allows to introduce a penalization of the log-likelihood; when `penalty=NULL`, a call to `msn.mle` is more efficient. Functions `sn.mple` and `mst.mple` work like `sn.mle` and `mst.mle` in version 0.4-x if the argument `penalty` is not set or it is set to `NULL`, except that `mst.mple` does not handle a univariate response (use `st.mple` for that).

### Value

A list whose specific components depend on the named function. Typical components are:

<code>call</code>	the calling statement
<code>dp</code>	vector or list of estimated DP parameters
<code>cp</code>	vector or list of estimated CP parameters
<code>logL</code>	the maximized (penalized) log-likelihood
<code>aux</code>	a list with auxiliary output values, depending on the function
<code>opt.method</code>	a list produced by the numerical <code>opt.method</code>

## Background

Computational aspects of maximum likelihood estimation for univariate SN distributions are discussed in Section 3.1.7 of Azzalini and Capitanio (2014). The working of `sn.mle` follows these lines; maximization is performed in the CP space. All other functions operate on the DP space.

The technique underlying `msn.mle` is based on a partial analytical maximization, leading implicitly to a form of profile log-likelihood. This scheme is formulated in detail in Section 6.1 of Azzalini and Capitanio (1999) and summarized in Section 5.2.1 of Azzalini and Capitanio (2014). The same procedure is not feasible when one adopts MPLE; hence function `msn.mple` has to maximize over a larger parameter space.

When the SN family is fitted with the constraint  $\alpha=$ , this amounts to adopt a classical linear model with Gaussian distributional assumption. The corresponding MLE's are the same as those produced by `lm`, except that the denominator of the MLE variance (matrix) has the 'uncorrected' form. In the multivariate case, the covariance matrix of MLE is computed using expression (10) in Section 15.8 of Magnus and Neudecker (2007).

Maximization of the univariate ST log-likelihood is speeded-up by using the expressions of the gradient given by DiCiccio and Monti (2011), reproduced with inessential variants in Section 4.3.3 of Azzalini and Capitanio (2014).

The working of `mst.mple` is based on a re-parameterization described in Section 5.1 of Azzalini and Capitanio (2003). The expressions of the corresponding log-likelihood derivatives are given in Appendix B of the full version of the paper.

## Author(s)

Adelchi Azzalini

## References

- Azzalini, A. and Capitanio, A. (1999). Statistical applications of the multivariate skew normal distribution. *J.Roy.Statist.Soc. B* **61**, 579–602. Full-length version available at <http://arXiv.org/abs/0911.2093>
- Azzalini, A. and Capitanio, A. (2003). Distributions generated by perturbation of symmetry with emphasis on a multivariate skew *t* distribution. *J.Roy. Statist. Soc. B* **65**, 367–389. Full-length version available at <http://arXiv.org/abs/0911.2342>
- Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.
- DiCiccio, T. J. and Monti, A. C. (2011). Inferential aspects of the skew *t*-distribution. *Quaderni di Statistica* **13**, 1–21.
- Magnus, J. R. and Neudecker, H. (2007). *Matrix Differential Calculus with Applications in Statistics and Econometrics*, third edition. John Wiley & Sons.

## See Also

[selm](#) for a comprehensive higher level fitting function,  
[Qpenalty](#) for specification of a penalty function

**Examples**

```
data(wines, package="sn")
X <- model.matrix(~ phenols + wine, data=wines)
fit <- msn.mle(x=X, y=cbind(wines$acidity, wines$alcohol), opt.method="BFGS")
fit <- st.mple(x=X, y = wines$acidity, fixed.nu=4, penalty="Qpenalty")
```

sn-st.cumulants

*Cumulants of univariate skew-normal and skew-t distributions***Description**

Compute cumulants of univariate (extended) skew-normal and skew- $t$  distributions up to a given order.

**Usage**

```
sn.cumulants(xi=0, omega=1, alpha=0, tau=0, dp=NULL, n=4)
st.cumulants(xi=0, omega=1, alpha=0, nu=Inf, dp=NULL, n=4)
```

**Arguments**

<code>xi</code>	location parameters (numeric vector).
<code>omega</code>	scale parameters (numeric vector, positive).
<code>alpha</code>	slant parameters (numeric vector).
<code>tau</code>	hidden mean parameter (numeric scalar).
<code>nu</code>	degrees of freedom (numeric scalar, positive); the default value is <code>nu=Inf</code> which corresponds to the skew-normal distribution.
<code>dp</code>	a vector containing the appropriate set of parameters. If 0 <code>dp</code> is not <code>NULL</code> , the individual parameters must not be supplied.
<code>n</code>	maximal order of the cumulants. For <code>st.cumulants</code> and for <code>sn.cumulants</code> with <code>tau!=0</code> (ESN distribution), it cannot exceed 4.

**Value**

A vector of length `n` or a matrix with `n` columns, in case the input values are vectors.

**Background**

See Sections 2.1.4, 2.2.3 and 4.3.1 of the reference below

**Author(s)**

Adelchi Azzalini

## References

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

## See Also

[dsn](#), [dsn](#)

## Examples

```
sn.cumulants(omega=2, alpha=c(0, 3, 5, 10), n=5)
sn.cumulants(dp=c(0, 3, -8), n=6)
st.cumulants(dp=c(0, 3, -8, 5), n=6) # only four of them are computed
st.cumulants(dp=c(0, 3, -8, 3))
```

---

sn-st.info

*Expected and observed Fisher information for SN and ST distributions*

---

## Description

Computes Fisher information for parameters of simple sample having skew-normal (SN) or skew- $t$  (ST) distribution or for a regression model with errors term having such distributions, in the DP and CP parametrizations.

## Usage

```
sn.infoUv(dp=NULL, cp=NULL, x=NULL, y, w, penalty=NULL, norm2.tol=1e-06)
```

```
sn.infoMv(dp, x=NULL, y, w, penalty=NULL, norm2.tol=1e-06)
```

```
st.infoUv(dp = NULL, cp = NULL, x = NULL, y, w, fixed.nu = NULL,
  symmetr = FALSE, penalty = NULL, norm2.tol = 1e-06)
```

```
st.infoMv(dp, x = NULL, y, w, fixed.nu = NULL, symmetr = FALSE,
  penalty = NULL, norm2.tol = 1e-06)
```

## Arguments

dp, cp	direct or centred parameters, respectively; one of them can be a non-NULL argument. For the univariate SN distribution, <code>sn.infoUv</code> is to be used, and these arguments are vectors. In the multivariate case, <code>sn.infoMv</code> is to be used and these arguments are lists. See <a href="#">dp2cp</a> for their description.
x	an optional matrix which represents the design matrix of a regression model
y	a numeric vector (for <code>sn.infoUv</code> and <code>st.infoUv</code> ) or a matrix (for <code>sn.infoMv</code> and <code>st.infoMv</code> ) representing the response. In the SN case ( <code>sn.infoUv</code> and <code>sn.infoMv</code> ), <code>y</code> can be missing, and in this case the expected information matrix is computed; otherwise the observed information is computed. In the ST

	case ( <code>st.infoUv</code> and <code>st.infoMv</code> ), <code>y</code> is a required argument, since only the observed information matrix for ST distributions is implemented. See ‘Details’ for additional information.
<code>w</code>	an optional vector of weights (only meaningful for the observed information, hence if <code>y</code> is missing); if missing, a vector of 1’s is generated.
<code>fixed.nu</code>	an optional numeric value which declares a fixed value of the degrees of freedom, <code>nu</code> . If not NULL, the information matrix has a dimension reduced by 1.
<code>symmetr</code>	a logical flag which indicates whether a symmetry condition of the distribution is being imposed; default is <code>symmetr=FALSE</code> .
<code>penalty</code>	a optional character string with the name of the penalty function used in the call to <a href="#">selm</a> ; see this function for its description.
<code>norm2.tol</code>	for the observed information case, the Mahalanobis squared distance of the score function from 0 is evaluated; if it exceeds <code>norm2.tol</code> , a warning message is issued, since the ‘information matrix’ so evaluated may be not positive-definite. See ‘Details’ for additional information.

### Value

a list containing the following components:

<code>dp, cp</code>	one of the two arguments is the one supplied on input; the other one matches the previous one in the alternative parametrization.
<code>type</code>	the type of information matrix: "observed" or "expected".
<code>info.dp, info.cp</code>	matrices of Fisher (observed or expected) information in the two parametrizations.
<code>asyvar.dp, asyvar.cp</code>	inverse matrices of Fisher information in the two parametrizations, when available; See ‘Details’ for additional information.
<code>aux</code>	a list containing auxiliary elements, depending of the selected function and the type of computation.

### Details

In the univariate SN case, when `x` is not set, then a simple random sample is assumed and a matrix `x` with a single column of all 1’s is constructed; in this case, the supplied vector `dp` or `cp` must have length 3. If `x` is set, then the supplied vector of parameters, `dp` or `cp`, must have length `ncol(x)+2`. In the multivariate case, a direct extension of this scheme applies.

If the observed information matrix is required, `dp` or `cp` should represent the maximum likelihood estimates (MLE) for the given `y`, otherwise the information matrix may fail to be positive-definite and it would be meaningless anyway. Therefore, the squared Mahalobis norm of the score vector is evaluated and compared with `norm2.tol`. If it exceeds this threshold, this is taken as an indication that the supplied parameter list is not at the MLE and a warning message is issued. The returned list still includes `info.dp` and `info.cp`, but in this case these represent merely the matrices of second derivatives; `asyvar.dp` and `asyvar.cp` are set to NULL.

## Background

The information matrix for the the univariate SN distribution in the two stated parameterizations in discussed in Sections 3.1.3–4 of Azzalini and Capitanio (2014). For the multivariate distribution, Section 5.2.2 of this monograph summarizes briefly the findings of Arellano-Valle and Azzalini (2008).

For ST distributions, only the observed information matrix is provided, at the moment. Computation for the univariate case is based on DiCiccio and Monti (2011). For the multivariate case, the score function is computed using an expression of Arellano-Valle (2010) followed by numerical differentiation.

## References

- Arellano-Valle, R. B. (2010). The information matrix of the multivariate skew- $t$  distribution. *Metron*, **LXVIII**, 371–386.
- Arellano-Valle, R. B., and Azzalini, A. (2008). The centred parametrization for the multivariate skew-normal distribution. *J. Multiv. Anal.* **99**, 1362–1382. Corrigendum: **100** (2009), 816.
- Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.
- DiCiccio, T. J. and Monti, A. C. (2011). Inferential aspects of the skew  $t$ -distribution. *Quaderni di Statistica* **13**, 1–21.

## See Also

[dsn](#), [dmsn](#), [dp2cp](#)

## Examples

```
infoE <- sn.infoUv(dp=c(0,1,5))           # expected information
set.seed(1); rnd <- rsn(100, dp=c(0, 1, 3))
fit <- selm(rnd~1, family="SN")
info0 <- sn.infoUv(cp=coef(fit), y=rnd)  # observed information
#
data(wines)
X <- model.matrix(~ pH + wine, data=wines)
fit <- sn.mple(x=X, y=wines$alcohol)
infoE <- sn.infoUv(cp=fit$cp, x=X)
info0 <- sn.infoUv(cp=fit$cp, x=X, y=wines$alcohol)
```

---

summary.SECdistr

*Summary of a SEC distribution object*

---

## Description

Produce a summary of an object of class either "SECdistrUv" or "SECdistrMv", which refer to a univariate or a multivariate SEC distribution, respectively. Both types of objects can be produced by makeSECdistr.

**Usage**

```
## S4 method for signature 'SECdistrUv'
summary(object, cp.type = "auto", probs)
```

```
## S4 method for signature 'SECdistrMv'
summary(object, cp.type = "auto")
```

**Arguments**

object	an object of class "SECdistrUv" or "SECdistrMv".
cp.type	a character string to select the required variance of CP parameterization; possible values are "proper", "pseudo", "auto" (default). For a description of these codes, see <a href="#">dp2cp</a> .
probs	in the univariate case, a vector of probabilities for which the corresponding quantiles are required. If missing, the vector $c(0.05, 0.25, 0.50, 0.75, 0.95)$ is used.

**Details**

For a description of the DP, CP and pseudo-CP parameter sets included in the returned object, see [dp2cp](#).

The aux slot of the returned object includes other summary quantities, as described next. In the univariate case, the reported quantile-based measures of skewness and kurtosis refer to the Bowley and Moors measures, respectively; see Groeneveld (2006) and Moors (1988) for their specifications. In the multivariate case, the Mardia's measures of skewness and kurtosis are computed from the expressions given on p.153 and p.178 of Azzalini and Capitanio (2014).

In the univariate case, delta is a simple transformation of the slant parameter alpha; it takes values in  $(-1, 1)$ . In the multivariate case, delta is a vector with components of similar type; they correspond to the matching terms of the univariate components. The  $\alpha^*$  and  $\delta^*$  coefficients are univariate comprehensive summary quantities of slant; see pp.132-3 of Azzalini and Capitanio (2014) for their expressions. These quantities play an important role in SEC distributions; for instance, the Mardia's measures of multivariate skewness and kurtosis depend on the vector of slant parameters only via  $\delta^*$  or, equivalently, via  $\alpha^*$ .

The mode, which is unique for all these distributions, is computed by a numerical line search between the DP location and the CP location (or the pseudo-DP location, when the latter does exist). This line search is univariate also in the multivariate case, using Propositions 5.14 and 6.2 of Azzalini and Capitanio (2014); see also Problem 5.14.

The examples below illustrate how extract various components from aux and other slots of the returned object.

**Value**

A list with the following components:

family	name of the family within the SEC class, character
dp	DP parameters, a list or a vector
name	the name of the distribution, character string

compNames	in the multivariate case the names of the components, a character vector
cp	CP parameters, a list or a vector
cp.type	the name of the selected variant of the CP set
aux	a list with auxiliary ingredients (mode, coefficients of skewness and kurtosis, in the parametric and non-parametric variants, and more); see Section ‘Details’ for more information.

The list items `dp` and `cp` are vectors if `class(object)` is `SECdistrUv` (univariate distribution); they are lists if `class(object)` is `SECdistrMv` (multivariate distribution).

### Author(s)

Adelchi Azzalini

### References

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

Moors, I. J. A. (1988). A quantile alternative for kurtosis. *The Statistician* **37**, 25-32.

Groeneveld, R. A. (2006). Skewness, Bowley’s measures of. In volume **12**, 7771-3, of *Encyclopedia of Statistical Sciences*, 2nd edition, edited by Kotz et al. Wiley, New York.

### See Also

[makeSECdistr](#) for building a SEC distribution

[extractSECdistr](#) for extracting a SEC distribution from a [selm](#) fit

methods [mean](#) and [sd](#) for computing the mean and the standard deviation of `SECdistrUv-class` objects, methods [mean](#) and [vcov](#) for computing the mean vector and the variance matrix of `SECdistrMv-class` objects

[modeSECdistr](#) for computing the mode directly

### Examples

```
f3 <- makeSECdistr(dp=c(3,2,5), family="SC")
summary(f3)
s <- summary(f3, probs=(1:9)/10)
print(slotNames(s))
print(names(slot(s,"aux"))) # the components of the 'aux' slot
slot(s, "aux")$mode        # the same of modeSECdistr(object=f3)
slot(s, "aux")$q.measures  # quantile-based measures of skewness and kurtosis
#
dp3 <- list(xi=1:3, Omega=toeplitz(1/(1:3)), alpha=c(-3, 8, 5), nu=6)
st3 <- makeSECdistr(dp=dp3, family="ST", name="ST3", compNames=c("U", "V", "W"))
s <- summary(st3)
dp <- slot(s, "dp")        # the same of slot(st3, "dp")
slot(s, "cp")$var.cov     # the same of vcov(st3)
slot(s, "aux")$delta.star # comprehensive coefficient of shape
slot(s, "aux")$mardia     # Mardia's measures of skewness and kurtosis
```



```
#
dp2 <- list(xi=rep(0,2), Omega=matrix(c(2,2,2,4),2,2), alpha=c(3,-5), tau=-1)
esn2 <- makeSECdistr(dp=dp2, family="ESN", name="ESN-2d")
summary(esn2)
```

---

summary.SECdistrMv-class

*Classes* summary.SECdistrMv and summary.SECdistrUv

---

## Description

Summaries of objects of classes SECdistrMv and SECdistrUv

## Objects from the Class

Objects can be created by calls of type `summary(object)` when object is of class either "SECdistrMv" or "SECdistrUv".

## Slots

**family:** A character string which represents the parametric family of SEC type

**dp:** Object of class "list" or "vector" for "SECdistrMv" and "SECdistrUv", respectively

**name:** Object of class "character" with the name of distribution

**compNames:** For "SECdistrMv" objects, a character vector with names of the components of the multivariate distribution

**cp:** Object of class "list" or "vector" for "SECdistrMv" and "SECdistrUv", respectively

**cp.type:** a character string of the CP version

**aux:** A list of auxiliary quantities

## Methods

**show** signature(object = "summary.SECdistrMv"): ...

**show** signature(object = "summary.SECdistrUv"): ...

## Author(s)

Adelchi Azzalini

## See Also

[summary.SECdistrMv](#), [summary.SECdistrUv](#),

[makeSECdistr](#), [dp2cp](#)

summary.selm

*Summarizing selm fits***Description**

summary method for class "selm" and "mselm".

**Usage**

```
## S4 method for signature 'selm'
summary(object, param.type = "CP", cov = FALSE, cor = FALSE)

## S4 method for signature 'mselm'
summary(object, param.type = "CP", cov = FALSE, cor = FALSE)
```

**Arguments**

object	an object of class "selm" or "mselm" as created by a call to function selm.
param.type	a character string which indicates the required type of parameter type; possible values are "CP" (default), "DP", "pseudo-CP" and their equivalent lower-case expressions.
cov	a logical value, to indicate if an estimate of the variance and covariance matrix of the estimates is required (default: FALSE).
cor	a logical value, to indicate if an estimate of the correlation matrix of the estimates is required (default: FALSE).

**Value**

An S4 object of class summary.selm with 12 slots.

call:	the calling statement.
family:	the parametric family of skew-elliptically contoured distributed (SEC) type.
logL:	the maximized log-likelihood or penalized log-likelihood value
method:	estimation method ("MLE" or "MPL")
param.type:	a character string with the chosen parameter set.
param.table:	table of parameters, std.errors and z-values
fixed.param:	a list of fixed parameter values
resid:	residual values
control:	a list with control parameters
aux:	a list of auxiliary quantities
size:	a numeric vector with various lengths and dimensions
boundary:	a logical value which indicates whether the estimates are on the boundary of the parameter space

**Note**

There are two reasons why the default choice of `param.type` is CP. One is the the easier interpretation of cumulant-based quantities such as mean value, standard deviation, coefficient of skewness.

The other reason is more technical and applies only to cases when the estimate of the slant parameter  $\alpha$  of the SN distribution is close to the origin: standard asymptotic distribution theory of maximum likelihood estimates (MLE's) does not apply in this case and the corresponding standard errors are not trustworthy. The problem is especially severe at  $\alpha = 0$  but to some extent propagates to its vicinity. If  $d = 1$ , adoption of CP leads to MLE's with regular asymptotic distribution across the parameter space, including  $\alpha = 0$ . For  $d > 1$  and  $\alpha = 0$ , the problem is still unsolved at the present time, which is the reason why `selm` issues a warning message when the MLE is in the vicinity of  $\alpha = 0$ ; see 'Details' of `selm`. For background information, see Sections 3.1.4–6 and 5.2.3 of Azzalini and Capitanio (2014) and references therein.

This problem does not occur with the the SC and the ST distribution (unless its tail-weight parameter  $\nu$  diverges, that is, when we are effectively approaching the SN case).

**Author(s)**

Adelchi Azzalini

**References**

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

**See Also**

`selm` function, `selm` (and `mse1m`) class, `plot.selm`, `dp2cp`

**Examples**

```
data(wines, package="sn")
m5 <- selm(acidity ~ phenols + wine, family="SN", data=wines)
summary(m5)
summary(m5, "dp")
s5 <- summary(m5, "dp", cor=TRUE, cov=TRUE)
dp.cor <- slot(s5, "aux")$param.cor
cov2cor(vcov(m5, "dp")) # the same
#
# m6 <- selm(acidity ~ phenols + wine, family="ST", data=wines) # boundary!?!
#
m12 <- selm(cbind(acidity, alcohol) ~ phenols + wine, family="SN", data=wines)
s12 <- summary(m12)
coef(m12, 'dp')
coef(m12, "dp", vector=FALSE)
#
# see other examples at function selm
```

---

symm-modulated-distr *Symmetry-modulated distributions*

---

## Description

Symmetry-modulated distributions, univariate and multivariate, AKA skew-symmetric distributions

## Usage

```
dSymmModulated(x, xi=0, omega=1, f0, G0, w, par.f0, par.G0, odd="check",
  log=FALSE, ...)
rSymmModulated(n=1, xi=0, omega=1, f0, G0, w, par.f0, par.G0, odd="check", ...)
dmSymmModulated(x, xi, Omega, f0, G0, w, par.f0, par.G0, odd="check",
  log=FALSE, ...)
rmSymmModulated(n=1, xi, Omega, f0, G0, w, par.f0, par.G0, odd="check", ...)
plot2D.SymmModulated(range, npt=rep(101,2), xi=c(0,0), Omega, f0, G0, w,
  par.f0, par.G0, odd="check", ...)
```

## Arguments

x	a vector of coordinates where the density must be evaluated; for multivariate densities, evaluated by dmSymmModulated, a matrix is also allowed, each row representing a point.
xi	a numeric vector representing the location parameter; if must have length 1 for dSymmModulated and rSymmModulated, length 2 for plot2D.SymmModulated).
omega	a positive value representing the scale parameter.
f0	a character string denoting the symmetric density to be modulated; admissible values for dSymmModulated and dSymmModulated are "beta", "cauchy", "logistic" (or "logis"), "normal" (or "norm"), "t", "uniform"; for the other functions the possible values are "cauchy", "normal" (or "norm"), "t"; the meaning of the names is described in the 'Details' section.
G0	a character string denoting the symmetric distribution used in the modulating factor; admissible values are "beta", "cauchy", "logistic" (or "logis"), "normal" (or "norm"), "t", "uniform", with meaning described in the 'Details' section.
w	the name ( <i>not</i> as a character string) of a user-defined function which satisfies the condition $w(-z) = -w(z)$ for all $z$ ; see the 'Details' section for additional specifications.
par.f0, par.G0	parameters required by f0 and G0, when they are of type "beta" or "t", otherwise ignored.
odd	a character string, with possible values "check" (default), "assume", "force", for regulation of the behaviour about the condition that w is an odd function, as explained in the 'Details' section.
log	logical (default: FALSE); if TRUE, densities are given as log(densities).

<code>n</code>	an integer value (default: <code>n=1</code> ) indicating the number of random numbers.
<code>Omega</code>	a symmetric positive-definite matrix which regulates the dependence structure of <code>f0</code> and so of the final density.
<code>range</code>	a two-column matrix whose column-wise range is taken as the plotting intervals on the coordinated axes forming a bivariate grid of points over which the density is plotted.
<code>npt</code>	a numeric vector with two elements representing the number of equally-spaced points on each axis spanning the range described above; default value is <code>rep(101, 2)</code> .
<code>...</code>	optional parameters regulating the function <code>w</code> and, for <code>plot2D.SymmModulated</code> only, graphical parameters to be supplied to function <code>contour</code> .

**Value**

For `dSymmModulated`, `rSymmModulated` and `dmSymmModulated`, a numeric vector; for `dmSymmModulated` a matrix, unless `n=1`.

For `plot2D.SymmModulated` an invisible list containing the `x` and `y` coordinates forming the grid over which the density pdf has been evaluated for plotting.

**Background**

In the univariate case, start from symmetric density function  $f_0$ , such that  $f_0(z) = f_0(-z)$  for all  $z$ , and ‘modulate’ it in the form

$$f(z) = 2 f_0(z) G_0\{w(z)\}$$

where  $G_0$  is a univariate symmetric (about 0) distribution function and  $w(z)$  is a real-valued odd function, hence satisfying the condition  $w(-z) = -w(z)$ ; then  $f(z)$  is a proper density function which integrates to 1. A subsequent location and scale transformation applied to  $f(z)$  delivers the final density. Specifically, if  $Z$  denotes a univariate random variable with density  $f(z)$ , then the computed density pertains to the transformed variable

$$\xi + \omega Z.$$

In the multivariate case, the scheme is similar, with natural adaptation. Density  $f_0$  is now  $d$ -dimensional, while  $G_0$  is still univariate. The conditions  $f_0(z) = f_0(-z)$  and  $w(-z) = -w(z)$  refer to a  $d$ -dimensional vector  $z$ . Given a  $d \times d$  symmetric positive-definite matrix  $\Omega$ , we extract the square roots  $\omega$  of the diagonal element of  $\Omega$  and correspondingly obtain the scale-free matrix

$$\bar{\Omega} = \text{diag}(\omega)^{-1} \Omega \text{diag}(\omega)^{-1}$$

which is used to regulate the dependence structure of  $f_0(z)$  and so of  $f(z)$ . If  $Z$  is multivariate random variable with density  $f(z)$ , then the final distribution refers to

$$\xi + \text{diag}(\omega) Z$$

where  $\xi$  is a  $d$ -dimensional vector of location parameters.

This construction was put forward by Azzalini and Capitanio (2003). An essentially equivalent formulation has been presented by Wang et al. (2004). A summary account is available in Section 1.2 of Azzalini and Capitanio (2014); this includes, inter alia, an explanation of why the term ‘symmetry-modulated’ distributions is preferred to ‘skew-symmetric’ distributions.

Random number generation is based on expression (1.11a) of Azzalini and Capitanio (2014).

## Details

Functions `dSymmModulated` and `rSymmModulated` deal with univariate distributions, for computing densities and generating random numbers, respectively; `dmSymmModulated` and `rmSymmModulated` act similarly for multivariate distributions. For the bivariate case only, `plot2D.SymmModulated` computes a density over a grid of coordinates and produces a contour plot.

The distribution names used in `f0` and `G0` have, in the univariate case, the same meaning as described in the [Distributions](#) page, with the following exceptions, to achieve symmetry about 0: "uniform" denotes a uniform distribution over the interval  $(-1, 1)$ ; "beta" denotes the a symmetric Beta distribution with support over the interval  $(-1, 1)$  and a common value of the shape parameters.

In the multivariate case, the available options "normal" and "t" for `f0` refer to densities computed by `dmnorm` and `dmt` with 0 location and correlation matrix  $\bar{\Omega}$ , implied by  $\Omega$ . Argument `G0` has the same meaning as in the univariate case.

Options "beta" and "t" for `f0` and `G0` require the specification of a shape parameter, via the arguments `par.f0` and `par.G0`, respectively. For "beta" the parameter represents the common value of the shape parameters of [Beta](#); for "t", it represents `df` of [TDist](#) and `dmt`.

Function `w` must be of the form `w <- function(z, ...)` where `...` are optional additional parameters and `z` represents valued of the standardized form of the density; in the univariate case, `x` and `z` are related by  $z=(x-xi)/omega$  and an analogous fact holds in the multivariate setting. The function must satisfy the condition  $w(-z) = -w(z)$ . It is assumed that the function is vectorized and, in the multivariate case, it will be called with `z` representing a matrix with `d` columns, if `d` denotes the dimensionality of the random variable.

Argument `odd` regulates the behaviour with respect to the condition  $w(-z) = -w(z)$ . If its value is "assume", the condition is just assumed to hold, and no action is taken. If the value is "check" (default), a *limited* check is performed; namely, in case of densities, the check is at 0 and the supplied `x` points, while for random numbers the check is at 0 and the generated points. The value "force" ensures that the condition is satisfied by actually constructing a modified version of the user-supplied function `w`, such that the required condition is enforced.

## Author(s)

Adelchi Azzalini

## References

- Arellano-Valle, R. B., Gómez, H. W. and Quintana, F. A. (2004). A new class of skew-normal distributions. *Comm. Stat., Theory & Methods*, **58**, 111-121.
- Azzalini, A. and Capitanio, A. (2003). Distributions generated by perturbation of symmetry with emphasis on a multivariate skew-*t* distribution. *J.Roy. Statist. Soc. B* **65**, 367–389. Full version of the paper at <http://arXiv.org/abs/0911.2342>
- Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.
- Wang, J., Boyer, J. and Genton, M. G. (2004). A skew-symmetric representation of multivariate distributions. *Statistica Sinica*, **14**, 1259-1270.

## See Also

[Distributions](#), [Beta](#), [TDist](#), [dmnorm](#), [dmt](#), [contour](#)

**Examples**

```

x <- seq(2, 13, length=45)
wLinear <- function(z, lambda) lambda*z
y <- dSymmModulated(x, 5, 2, f0="normal", G0="normal", w=wLinear, lambda=3)
# the same of dsn(x, 5, 2, 3), up to negligible numerical differences
#
wSGN <- function(z, lambda) z*lambda[1]/sqrt(1 + lambda[2]*z^2)
y <- dSymmModulated(x, 5, 2, f0="normal", G0="normal", w=wSGN, lambda=c(3,5))
# SGN distribution of Arellano-Valle et al. (2004)
#
wST <- function(z, lambda, nu) lambda*z*sqrt((nu+1)/(nu+z^2))
y <- rSymmModulated(n=100, 5, 2, f0="t", G0="t", w=wST, par.f0=8, par.G0=9,
  lambda=3, nu=8)
# equivalent to rst(n=100, 5, 2, 3, 8)
#
wTrigs <- function(z, p, q) sin(z * p)/(1 + cos(z * q))
x <- seq(-1, 1, length=51)
y <- dSymmModulated(x, 0, 1, f0="beta", G0="logistic", w=wTrigs, par.f0=2,
  par.G0=NULL, p=5, q=0.5)
plot(x, y, type="l")
# univariate analogue of the bivariate distribution on pp.372-3 of
# Azzalini & Capitanio (2003)
#
range <- cbind(c(-3,3), c(-3,3))
wMvTrigs <- function(z, p, q) sin(z %*% p)/(1 + cos(z %*% q))
plot2D.SymmModulated(range, xi=c(0,0), Omega=diag(2), f0="normal", G0="normal",
  w=wMvTrigs, par.f0=NULL, par.G0=NULL, p=c(2,3), q=c(1,1), col=4)
# w(.) as in (1.6) of Azzalini & Capitanio (2014, p.4) and plot as in
# bottom-right panel of their Figure 1.1.

```

T.Owen

*Owen's function***Description**

Evaluates function  $T(h, a)$  studied by D.B.Owen

**Usage**

```
T.Owen(h, a, jmax=50, cut.point=8)
```

**Arguments**

<code>h</code>	a numeric vector. Missing values (NAs) and Inf are allowed.
<code>a</code>	a numeric value. Inf is allowed.
<code>jmax</code>	an integer scalar value which regulates the accuracy of the result. See Section 'Details' below for explanation.
<code>cut.point</code>	a scalar value which regulates the behaviour of the algorithm, as explained in Section 'Details' below (default value: 8).

**Details**

If  $a > 1$  and  $0 < h \leq \text{cut.point}$ , a series expansion is used, truncated after `jmax` terms. If  $a > 1$  and  $h > \text{cut.point}$ , an asymptotic approximation is used. In the other cases, various reflection properties of the function are exploited. See the reference below for more information.

**Value**

a numeric vector.

**Background**

The function  $T(h, a)$  studied by Owen (1956) is useful for the computation of the bivariate normal distribution function and related quantities, including the distribution function of a skew-normal variate; see `psn`. See the reference below for more information on function  $T(h, a)$ .

**Author(s)**

Adelchi Azzalini and Francesca Furlan

**References**

Owen, D. B. (1956). Tables for computing bivariate normal probabilities. *Ann. Math. Statist.* **27**, 1075-1090.

**See Also**

[psn](#)

**Examples**

```
owen <- T.Owen(1:10, 2)
```

---

wines

*Piedmont wines data*

---

**Description**

Data refer to chemical properties of 178 specimens of three types of wine produced in the Piedmont region of Italy.

**Usage**

```
data(wines)
```



**Format**

A data frame with 178 observations on the following 28 variables.

wine	wine name (categorical, levels: Barbera, Barolo, Grignolino)
alcohol	alcohol percentage (numeric)
sugar	sugar-free extract (numeric)
acidity	fixed acidity (numeric)
tartaric	tartaric acid (numeric)
malic	malic acid (numeric)
uronic	uronic acids (numeric)
pH	pH (numeric)
ash	ash (numeric)
alcal_ash	alcalinity of ash (numeric)
potassium	potassium (numeric)
calcium	calcium (numeric)
magnesium	magnesium (numeric)
phosphate	phosphate (numeric)
chloride	chloride (numeric)
phenols	total phenols (numeric)
flavanoids	flavanoids (numeric)
nonflavanoids	nonflavanoid phenols (numeric)
proanthocyanins	proanthocyanins (numeric)
colour	colour intensity (numeric)
hue	hue (numeric)
OD_dw	$OD_{280}/OD_{315}$ of diluted wines (numeric)
OD_fl	$OD_{280}/OD_{315}$ of flavanoids (numeric)
glycerol	glycerol (numeric)
butanediol	2,3-butanediol (numeric)
nitrogen	total nitrogen (numeric)
proline	proline (numeric)
methanol	methanol (numeric)

**Details**

The data represent 27 chemical measurements on each of 178 wine specimens belonging to three types of wine produced in the Piedmont region of Italy. The data have been presented and examined by Forina *et al.* (1986) and were freely accessible from the PARVUS web-site until it was active. These data or, more often, a subset of them are now available from various places, including some R packages. The present dataset includes all variables available on the PARVUS repository, which are the variables listed by Forina *et al.* (1986) with the exception of ‘Sulphate’. Moreover, it reveals the undocumented fact that the original dataset appears to include also the vintage year; see the final portion of the ‘Examples’ below.

**Source**

Forina, M., Lanteri, S. Armanino, C., Casolino, C., Casale, M. and Oliveri, P. v-PARVUS 2008: an extendible package of programs for explorative data analysis, classification and regression analysis.

Dip. Chimica e Tecnologie Farmaceutiche ed Alimentari, Università di Genova, Italia. Web-site (not accessible as of 2014): 'http://www.parvus.unige.it'

## References

Forina M., Armanino C., Castino M. and Ubigli M. (1986). Multivariate data analysis as a discriminating method of the origin of wines. *Vitis* **25**, 189–201.

## Examples

```
data(wines)
pairs(wines[,c(2,3,16:18)], col=as.numeric(wines$wine))
#
code <- substr(rownames(wines), 1, 3)
table(wines$wine, code)
#
year <- as.numeric(substr(rownames(wines), 6, 7))
table(wines$wine, year)
# coincides with Table 1(a) of Forina et al. (1986)
```

---

zeta

*Function  $\log(2\Phi(x))$  and its derivatives*

---

## Description

The function  $\log(2\text{pnorm}(x))$  and its derivatives, including inverse Mills ratio.

## Usage

```
zeta(k, x)
```

## Arguments

k                    an integer number between 0 and 5.  
 x                    a numeric vector. Missing values (NAs) and Infs are allowed.

## Details

For k between 0 and 5, the derivative of order k of  $\log(2\Phi(x))$  is evaluated, where  $\Phi(x)$  denotes the  $N(0, 1)$  cumulative distribution function. The derivative of order  $k=0$  refers to the function itself. If k is not integer, it is converted to integer and a warning message is generated. If  $k<0$  or  $k>5$ , NULL is returned.

## Value

a vector representing the k-th order derivative evaluated at x.

## Background

The computation for  $k > 1$  is reduced to the case  $k=1$ , making use of expressions given by Azzalini and Capitanio (1999); see especially Section 4 of the full-length version of the paper. The main facts are summarized in Section 2.1.4 of Azzalini and Capitanio (2014).

For numerical stability, the evaluation of  $\text{zeta}(1, x)$  when  $x < -50$  makes use of the asymptotic expansion (26.2.13) of Abramowitz and Stegun (1964).

$\text{zeta}(1, -x)$  equals  $\text{dnorm}(x)/\text{pnorm}(-x)$  (in principle, apart from the above-mentioned asymptotic expansion), called the *inverse Mills ratio*.

## References

Abramowitz, M. and Stegun, I. A., editors (1964). *Handbook of Mathematical Functions*. Dover Publications.

Azzalini, A. and Capitanio, A. (1999). Statistical applications of the multivariate skew normal distribution. *J.Roy.Statist.Soc. B* **61**, 579–602. Full-length version available at <http://arXiv.org/abs/0911.2093>

Azzalini, A. with the collaboration of Capitanio, A. (2014). *The Skew-Normal and Related Families*. Cambridge University Press, IMS Monographs series.

## Examples

```
y <- zeta(2, seq(-20, 20, by=0.5))
#
for(k in 0:5) curve(zeta(k,x), from=-1.5, to=5, col = k+2, add = k > 0)
legend(3.5, -0.5, legend=as.character(0:5), col=2:7, lty=1)
```

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