Package ‘sn’

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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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R topics documented:

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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 constitute 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 packages (`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](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/](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/](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


See Also

`package-overview`
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 $a + A^\top Y$.

Usage

```r
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 `makeSECdistr` or by `extractSECdistr` or by a previous call to these functions.
- **a**: a numeric vector with the length `ncol(A)`.
- **A**: a full-rank matrix with `nrow(A)` equal to the dimensionality $d$ 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 `ncol(A)` 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 $d=1$, in which case it indicates whether this object must be of class `SECdistrUv`.
- **comp**: a vector formed by a subset of `1:d` which indicates which components must be extracted from `object`, on denoting by $d$ its dimensionality.

Value

If `object` defines the distribution of a SEC random variable $Y$, `affineTransSECdistr` computes the distribution of $a + A^\top Y$ 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

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.

<p>| | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>[1]</td>
<td>sex</td>
<td>categorical, levels: female, male</td>
</tr>
<tr>
<td>[2]</td>
<td>sport</td>
<td>categorical, levels: B_Ball, Field, Gym, Netball, Row, Swim, T_400m, Tennis, T_Sprnt, W_Polo</td>
</tr>
<tr>
<td>[3]</td>
<td>RCC</td>
<td>red cell count (numeric)</td>
</tr>
<tr>
<td>[4]</td>
<td>WCC</td>
<td>white cell count (numeric)</td>
</tr>
<tr>
<td>[5]</td>
<td>Hc</td>
<td>Hematocrit (numeric)</td>
</tr>
<tr>
<td>[6]</td>
<td>Hg</td>
<td>Hemoglobin (numeric)</td>
</tr>
<tr>
<td>[7]</td>
<td>Fe</td>
<td>plasma ferritin concentration (numeric)</td>
</tr>
<tr>
<td>[8]</td>
<td>BMI</td>
<td>body mass index, weight/(height)^2 (numeric)</td>
</tr>
<tr>
<td>[9]</td>
<td>SSF</td>
<td>sum of skin folds (numeric)</td>
</tr>
<tr>
<td>[10]</td>
<td>Bfat</td>
<td>body fat percentage (numeric)</td>
</tr>
<tr>
<td>[12]</td>
<td>Ht</td>
<td>height, cm (numeric)</td>
</tr>
<tr>
<td>[13]</td>
<td>Wt</td>
<td>weight, kg (numeric)</td>
</tr>
</tbody>
</table>
Details
The data have been made publicly available in connection with the book by Cook and Weisberg (1994).

References

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

---

barolo

*Price of Barolo wine*

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:

<table>
<thead>
<tr>
<th>reseller</th>
<th>reseller code (factor with levels A, B, C, D)</th>
</tr>
</thead>
<tbody>
<tr>
<td>vintage</td>
<td>vintage year (numeric)</td>
</tr>
<tr>
<td>volume</td>
<td>content volume in centilitres (numeric)</td>
</tr>
<tr>
<td>price</td>
<td>price in Euro (numeric)</td>
</tr>
<tr>
<td>age</td>
<td>age in 2010 (numeric)</td>
</tr>
</tbody>
</table>

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


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

c 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)
### conditionalSECdistr

**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**


**See Also**

`dp2cp`, `summary.selm`, `selm` function, `selm-class`

**Examples**

```r
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**

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

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

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

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)

Confidence intervals for parameters of a selm-class object

Description

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

```r
## 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 `uniroot` 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.

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

**Author(s)**

Adelchi Azzalini
References


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

x  either a vector of length d, where d= length(alpha), or a matrix with d columns, giving the coordinates of the point(s) where the density or the distribution function must be evaluated.

xi  a numeric vector of length d representing the location parameter of the distribution; see ‘Background’. In a call to dmsn and pmsn, xi can be a matrix, whose rows represent a set of location parameters; in this case, its dimensions must match those of x.

Omega a symmetric positive-definite matrix of dimension (d,d); see ‘Background’.

alpha a numeric vector which regulates the slant of the density; see ‘Background’. Inf values in alpha are not allowed.
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 $\mathbf{x}_i$ 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


See Also
dsn, dmst, pmnorm, op2dp, cp2dp

Examples

```r
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

```r
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, ...)
rms(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

- `x`: for `dmst` and `dmsc`, this is either a vector of length d, where d=length(alpha), or a matrix with d columns, representing the coordinates of the point(s) where the density must be evaluated; for `pmst` and `pmsc`, only a vector of length d is allowed.
dmst

- **xi**: a numeric vector of length d representing the location parameter of the distribution; see ‘Background’. In a call to dmst or dmsc, xi can be a matrix, whose rows represent a set of location parameters; in this case, its dimensions must match those of x.

- **Omega**: a symmetric positive-definite matrix of dimension \((d,d)\); see Section ‘Background’.

- **alpha**: a numeric vector of length d which regulates the slant of the density; see Section ‘Background’. Inf values in alpha are not allowed.

- **nu**: a positive value representing the degrees of freedom of ST distribution; does not need to be integer. Default value is nu=Inf which corresponds to the multivariate skew-normal distribution.

- **dp**: a list with three elements named xi, Omega, alpha and nu, containing quantities as described above. If dp is specified, this prevents specification of the individual parameters.

- **n**: 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 pmst.

**Details**

Typical usages are

```r
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)
rms(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 dmsc) or a single probability (pmst and pmsc) or a matrix of random points (rmst and rmsc).
**Background**

The family of multivariate ST distributions is an extension of the multivariate Student’s t family, via the introduction of an 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 \( x_i \) and scale by \( \Omega \), when its diagonal terms are not all 1’s. When \( \nu=\infty \) the distribution reduces to the multivariate skew-normal one; see dmsn. Notice that the location vector \( x_1 \) 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, dmsc, pmsc and rmsc simply make a call to dmst, pmst, rmst with argument \( \nu \) set equal to 1.

**References**


**See Also**

dst, dsc, dmsn, dmt, makeSECDistr

**Examples**

```r
x <- seq(-4,4,length=15)
x1 <- 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), x1, Omega, alpha, 5)
rnd <- rmst(10, x1, Omega, alpha, 6)
p1 <- pmst(c(2,1), x1, Omega, alpha, nu=5)
p2 <- pmst(c(2,1), x1, 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**

```r
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 `makeSECdistr`; 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 `makeSECdistr`, except that family "ESN" is not implemented.

- **object**
  optionally, an S4 object of class SECdistrUv or SECdistrMv, as produced by `makeSECdistr` (default value: NULL). If this argument is not NULL, then family and dp must not be set.

- **cp.type**
  character string, which has effect only if family="ST" or "SC", otherwise a warning message is generated. Possible values are "proper", "pseudo", "auto", which correspond to the CP parameter set, their 'pseudo-cp' version and an automatic selection based on nu>4, where nu represents the degrees of freedom of the ST distribution.

- **upto**
  numeric value (in 1:length(dp), default=NULL) to select how many CP components are computed. Default value upto=NULL is equivalent to length(dp).

**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 ξ, Ψ, λ, 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 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


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 the 2nd and the 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")
cp3.back <- cp2dp(cp3, "ST")
#
\[ \text{dsc} \quad \text{Skew-Cauchy Distribution} \]

**Description**

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

**Usage**

\[
\begin{align*}
\text{dsc}(x, \text{xi} = 0, \omega = 1, \alpha = 0, \text{dp} = \text{NULL}, \text{log} = \text{FALSE}) \\
\text{psc}(x, \text{xi} = 0, \omega = 1, \alpha = 0, \text{dp} = \text{NULL}) \\
\text{qsc}(p, \text{xi} = 0, \omega = 1, \alpha = 0, \text{dp} = \text{NULL}) \\
\text{rsc}(n = 1, \text{xi} = 0, \omega = 1, \alpha = 0, \text{dp} = \text{NULL})
\end{align*}
\]

**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 \text{dsc} (default \text{FALSE}). When \text{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 \text{xi}, \omega and \alpha parameters or from the extended skew-normal if \tau\neq0.

**Details**

Typical usages are

\[
\begin{align*}
\text{dsc}(x, \text{xi}=0, \omega=1, \alpha=0, \text{log}=\text{FALSE}) \\
\text{dsc}(x, \text{dp}=, \text{log}=\text{FALSE}) \\
\text{psc}(x, \text{xi}=0, \omega=1, \alpha=0) \\
\text{psc}(x, \text{dp}=) \\
\text{qsc}(p, \text{xi}=0, \omega=1, \alpha=0) \\
\text{qsc}(x, \text{dp}=) \\
\text{rsc}(n=1, \text{xi}=0, \omega=1, \alpha=0) \\
\text{rsc}(x, \text{dp}=)
\end{align*}
\]
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


See Also

dst, dmsc

Examples

```r
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

```r
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 an 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.

Details

In version 1.6-2, the random number generation method for rsn has changed; the so-called transformation method (also referred to as the ‘additive representation’) has been adopted for all values of tau. Also, the code has been modified so that there is this form of consistency: provided set.seed() is reset similarly before calls, code like rsn(5, dp=1:3) and rsn(10, dp=1:3), for instance, will start with the same initial values in the longer sequence as in the shorter sequence.

References


See Also

Functions used by psn: T.Owen, biv.nt.prob
Related distributions: dmsn, dst, dmst

Examples

```r
df <- 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)
qu(1/10*(1:4), 0, 1, 5, 3, solver="RFB")
```

<table>
<thead>
<tr>
<th>dst</th>
<th>Skew-t Distribution</th>
</tr>
</thead>
</table>

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 (NA) 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

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-08, 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 an \( \alpha \) parameter which regulates skewness; when \( \alpha=0 \), the skew-\( t \) distribution reduces to the usual Student’s \( t \) distribution. When \( \nu=\infty \), 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 \texttt{dmst}.

Details

For evaluation of \( \text{pst} \), and so indirectly of \( \text{qst} \), four different methods are employed. Method 1 consists in using \texttt{pmst} with dimension \( d=1 \). Method 2 applies \texttt{integrate} to the density function \( \text{dst} \). Method 3 again uses \texttt{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 \texttt{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 \text{length}(x). If the default argument value \texttt{method=0} is retained, an automatic choice among the above four methods is made, which depends on the values of \( \nu, \alpha, \text{length}(x) \). The numerical accuracy of methods 1, 2 and 3 can be regulated via the \ldots argument, while method 4 is conceptually exact, up to machine precision.

If \( \text{qst} \) is called with \( \nu>1\times10^4 \), computation is transferred to \texttt{qsn}.

References


See Also

\texttt{dmst,dsn,dsc}

Examples

\begin{verbatim}
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)
\end{verbatim}
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 model.

Usage

extractSECdistr(object, name, compNames)

Arguments

- **object**: an object of class selm or mselm, as created by selm.
- **name**: an optional character string representing the name of the outcome distribution; if missing, a string is constructed from the object ingredients.
- **compNames**: 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 $x_1$ 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 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)
Description

Returns a quantile-based four-number summary of the input data

Usage

fournum(x, na.rm = TRUE, ...)

Arguments

x  
a numeric vector, maybe including NAs and +/-Inf. At least 8 not-NA values are required. It works with objects which can be coerced to vector.

na.rm  
logical; if TRUE, all NA and NaNs are dropped, before the statistics are computed.

...  
optional arguments passed to quantile

Details

Function quantile is used to compute 7 octiles of x, that is, quantiles of level (1:7)/8, denoted oct[1:7], and derive four summary quantities:

1. the median, which corresponds to oct[4],
2. the ‘(coefficient of) quartile deviation’ or semi-interquantile range: (oct[6] -oct[2])/2;

The term ‘coefficient of quartile deviation’ is adopted from the Encyclopedia of Statistical Sciences; see the reference below. What is called Galton-Bowley measure here is often named ‘Bowley’s measure’, but some sources attribute it to Francis Galton. For the Moors measure, see the reference below.

Value

a vector of length four containing the median, the quartile deviation, the Galton-Bowley measure and the Moors measure

Note

Computation of octiles makes real sense only if length(x) is substantially larger than 8. If x does not contain at least 8 values (excluding NAs), the function returns rep(NA, 4).

Author(s)

Adelchi Azzalini
References


See Also

quantile, fivenum, IQR

Examples

fournum(datasets::rivers)

<table>
<thead>
<tr>
<th>frontier</th>
<th>Simulated sample from a skew-normal distribution</th>
</tr>
</thead>
</table>

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)
galton_moors2alpha_nu  Mapping of the (Galton-Bowley, Moors) measures to the (alpha, nu) parameters of a ST distribution

Description

Given a pair of (Galton-Bowley, Moors) measures of skewness and kurtosis for a given sample, a pair of values \((alpha, nu)\) are found such that a skew-t (ST) distribution with these slant and tail-weight parameter has (Galton-Bowley, Moors) measures equal to the input values. This function is mainly intended for internal package usage.

Usage

galton_moors2alpha_nu(galton, moors, quick = TRUE, move.in = TRUE, verbose = 0, abstol = 1e-04)

Arguments

galton      a numeric value, representing a Galton-Bowley measure
moors       a numeric value, representing a Moors measure
quick       a logical value; if TRUE, a quick mapping is performed
move.in     if the input values \((galton, moors)\) are outside the feasible ST region, a suitable point within the feasible area is returned
verbose     a numeric value which regulates the amount of printed detail
abstol      the tolerance value of the mapping, only relevant is quick=FALSE

Details

For background information about the Galton-Bowley’s and the Moors measures, see the documentation of fournum. The working of the mapping by described in Azzalini and Salehi (2020).

Value

a named vector of length two, with one or more descriptive attributes

Note

This function is mainly intended for internal package usage. Specifically it is used by st.prelimFit.

Author(s)

Adelchi Azzalini
makeSECdistr

References


See Also

fournum, st.prelimFit

Examples

galton_moors2alpha_nu(0.5, 3, quick=FALSE) # input in the feasible area
galton_moors2alpha_nu(0.5, 3)     # very similar output, much more quickly
galton_moors2alpha_nu(0.5, 0.5) # input outside the feasible area

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 \( \text{family} \): 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 \( x_i \) (location), \( \omega \) (scale, positive) and \( \alpha \) (slant); see functions \( \text{dsn}, \text{dst}, \text{dsc} \) 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 \( x_i=dp[[1]] \) 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 \( x_i \) and \( \alpha \) must be of length \( \text{ncol}(\Omega) \). See also functions \( \text{dmsn}, \text{dmst} \) and \( \text{dmsc} \). The fourth component, when it exists, is a scalar with the same role as in the univariate case.

In the univariate case \( \alpha=\text{Inf} \) 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 \( \text{SECdistrUv} \); in the multivariate case, an object of class \( \text{SECdistrMv} \). See \( \text{SECdistrUv-class} \) and \( \text{SECdistrMv-class} \) 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 0 (or a vector of 0's, in the multivariate case), the distribution is of classical elliptical type.

The ESN distribution is included here as a members of the SEC class, with a very slight extension of the original definition of this class, since the only difference is the non-zero truncation point of the unobserved component of the \((d+1)\)-dimensional EC variable.

Author(s)

Adelchi Azzalini

References

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

```r
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

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

### Arguments

- `A` a (symmetric) square matrix.
- `v` a numeric vector such that `length(v)=n*(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 $v$=vech($M$) where $M$ is a symmetric numeric matrix, vech2mat($v$) performs the inverse operation and returns the original matrix $M$; this explain the requirement on length($v$). For a positive integer $n$, D=duplicationMatrix($n$) is a matrix of dimension ($n^2,n*(n+1)/2$) 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


Examples

```r
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

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

- **dp**
  a numeric vector (in the univariate case, for class SECdistrUv) or a list (in the multivariate case, for class SECdistrUv) 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 SECdistrUv or SECdistrMv.

- **object**
  an object of class SECdistrUv or SECdistrMv as created by `makeSECdistr` or `extractSECdistr`; if this argument is used, arguments dp and family must not be set, and *vice versa*.

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


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

```r
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
```

---

**overall**  
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 incapsulates a probability distribution and then certain operations can be be performed on such an object. These two schemes are described next.

Classical R scheme The following functions work similary to \{d,p,q,r\}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 trasformations. 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.

Additional material

Additional material is available in the section ‘User guides, package vignettes and other documentation’ accessible from the front page of the documentation. See especially the document `pkg_sn-intro.pdf`.

Author

Adelchi Azzalini.

Please send comments, error reports et cetera to the author, whose web page is [http://azzalini.stat.unipd.it/](http://azzalini.stat.unipd.it/).

References

plot.SECdistr

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

x
an object of class SECdistrUv or SECdistrMv.

range
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.

probs
a vector of probability values. In the univariate case, the corresponding quantiles
are plotted on the horizontal axis; it can be skipped by setting probs=NULL.
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: c(0.05,0.25,0.5,0.75,0.95) in the
univariate case, c(0.25,0.5,0.75,0.95) in the multivariate case.

npt
a numeric value or vector (in the univariate and in the multivariate case, re-
spectively) 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 exists, "auto" plots the proper mean if it exists,
otherwise it switches automatically to the pseudo-mean. See dp2cp 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 ingre-
dients.

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 rug 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


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 selm or mselm.
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 points, `panel.smooth` can be chosen
by `add.smooth = TRUE`.
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.
lables.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 `panel`
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 "mselm".
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 super-
imposed 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


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)
The distribution of the product of two jointly normal or t variables

Description

Consider the product \( W = X_1 X_2 \) from a bivariate random variable \((X_1, X_2)\) having joint normal or Student's t distribution, with 0 location and unit scale parameters. Functions are provided for the distribution function of \( W \) in the normal and the t case, and the quantile function for the t case.

Usage

\[
\begin{align*}
\text{pprodn2}(x, \rho) \\
\text{pprodt2}(x, \rho, \nu) \\
\text{qprodt2}(p, \rho, \nu, \text{tol}=1e-5, \text{trace}=0)
\end{align*}
\]

Arguments

- \( x \): a numeric vector
- \( p \): a numeric vector of probabilities
- \( \rho \): a scalar value representing the correlation (or the matching term in the t case when correlation does not exists)
- \( \nu \): a positive scalar representing the degrees of freedom
- \( \text{tol} \): the desired accuracy (convergence tolerance), passed to function \text{uniroot}
- \( \text{trace} \): integer number for controlling tracing information, passed on to \text{uniroot}

Details

Function \text{pprodt2} implements formulae in Theorem 1 of Wallgren (1980). Corresponding quantiles are obtained by \text{qprodt2} by solving the pertaining non-linear equations with the aid of \text{uniroot}, one such equation for each element of \( p \).

Function \text{pprodn2} implements results for the central case in Theorem 1 of Aroian et al. (1978).

Value

a numeric vector

Author(s)

Adelchi Azzalini

References


predict.selm

Predict method for selm-class objects

Description

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

Usage

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

Arguments

- `object`: an object of class `selm` as produced by a call to function `selm` with univariate response.
- `newdata`: an optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
- `param.type`: a character string with the required parameterization; it must be one of "CP", "DP", "pseudo-CP", or possibly their equivalent lowercase.
- `interval`: type of interval calculation among "none", "confidence", "prediction"; it can be abbreviated.
- `level`: tolerance/confidence level (default value is 0.95).
- `na.action`: function determining what should be done with missing values in `newdata`. The default is to predict NA.
- `...`: 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


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")
Arguments

fitted an object of class `selm` as produced by a call to function `selm` with univariate response.

called type a character string with the required parameterization; it must be either "CP" or "DP", or possibly their equivalent lowercase.

called name 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 `summary.selm(object,param.type)`.

called values 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 `selm`. See ‘Details’ for more information.

npt in case the vector or any of the vectors of argument param.values has length 2, an equally spaced grid of values is build with length equal to the corresponding component of npt. 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.

opt.control an optional list passed as argument control to optim to optimize the log-likelihood; see ‘Details’ for more information.

plot.it 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 level is marked on the plot; in the two-parameter case, the contour curves are labelled with approximate confidence levels. See however for more information.

log 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 param.name. This applies to omega and nu in the DP parameter set and to s.d. and gamma2 in the CP parameter set.

levels 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

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

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.

- **call** the calling statement
- `<param1>` values of the first parameter
- `<param2>` values of the second parameter (in the two-parameter case)
- `logLik` numeric vector or matrix of the profile log-likelihood values
- `confint` in the one-parameter case, the confidence interval
- `level` in the one-parameter case, the confidence level
- `deviance.contour` 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**

See Also

- `selm`, `summary.selm`
- `makeSECdistr` for the CP/DP parameterizations,
- `optim` for its control argument

Examples

```r
data(ais, package="sn")
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 distribution on `alpha`

Usage

```r
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 $\text{cov2cor}(\Omega)$. See ‘Details’ of \texttt{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 \textit{a posteriori} estimate in the stated sense.

As a simple illustration of this mechanism, function \texttt{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 $\alpha=+/-\infty$, this choice also penalizes $\alpha=0$ with $Q=\infty$, effectively removing $\alpha=0$ from the parameter space.

Starting from the code of function \texttt{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 \texttt{attr(Q,"der1")} and \texttt{attr(Q,"der2")}, depending on the input value \texttt{der}.

Author(s)

Adelchi Azzalini

References


See Also

\texttt{selm} function

Examples

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

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

Usage

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

Arguments

object an object of class "selm" or "msem" 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 msem-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

sd

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

x          a numeric vector, matrix or data frame.
na.rm      logical. Should missing values be removed?
...        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 obtained from an object generated by selm using the function extractSEDdistr.

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 = "SECdistrMv"): ...
v cov signature(object = "SECdistrMv"): ...

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)

mean(f10) # the mean value of the probability distribution
vcov(f10) # the variance-covariance matrix of the probability distribution

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 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
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,
     model = TRUE, x = FALSE, y = FALSE, contrasts = NULL, offset, ...)
```

**Arguments**

- **formula**: an object of class "formula" (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. "lm", 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-t and the skew-Cauchy family, respectively. See `makeSECdistr` 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 `data`, the variables are taken from `environment(formula)`, typically the environment from which `selm` 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 `length(weights)` must equal the number of observations. If not assigned, a vector of all 1's is generated.
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>subset</td>
<td>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>.</td>
</tr>
<tr>
<td>na.action</td>
<td>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.</td>
</tr>
<tr>
<td>start</td>
<td>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.</td>
</tr>
<tr>
<td>fixed.param</td>
<td>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 ( \alpha=0 ) to impose a symmetry condition of the distribution; the other is to set ( \nu=\text{&lt;value&gt;} ), to fix the degrees of freedom at the named (&lt;value&gt;) when <code>family=&quot;ST&quot;</code>, for instance <code>list(nu=3)</code>. See ‘Details’ for additional information.</td>
</tr>
<tr>
<td>method</td>
<td>a character string which selects the estimation method to be used for fitting. Currently, two options exist: &quot;MLE&quot; (default) and &quot;MPLE&quot;, corresponding to standard maximum likelihood and maximum penalized likelihood estimation, respectively. See ‘Details’ for additional information.</td>
</tr>
<tr>
<td>penalty</td>
<td>a character string which denotes the penalty function to be subtracted to the log-likelihood function, when <code>method=&quot;MPLE&quot;</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=&quot;MLE&quot;</code>, no penalization is applied and this argument has no effect.</td>
</tr>
<tr>
<td>model, x, y</td>
<td>logicals. If TRUE, the corresponding components of the fit are returned.</td>
</tr>
<tr>
<td>contrasts</td>
<td>an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code>.</td>
</tr>
<tr>
<td>offset</td>
<td>this can be used to specify an \textit{a priori} 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 <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.</td>
</tr>
<tr>
<td>...</td>
<td>optional control parameters, as follows.</td>
</tr>
<tr>
<td></td>
<td>• <code>trace</code>: a logical value which indicates whether intermediate evaluations of the optimization process are printed (default: FALSE).</td>
</tr>
<tr>
<td></td>
<td>• <code>info.type</code>: a character string which indicates the type of Fisher information matrix; possible values are &quot;observed&quot; (default) and &quot;expected&quot;. Currently, &quot;expected&quot; is implemented only for the SN family.</td>
</tr>
<tr>
<td></td>
<td>• <code>opt.method</code>: a character string which selects the numerical optimization method, among the possible values &quot;nlminb&quot;, &quot;Nelder-Mead&quot;, &quot;BFGS&quot;, &quot;CG&quot;, &quot;SANN&quot;. If <code>opt.method=&quot;nlminb&quot;</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>.</td>
</tr>
<tr>
<td></td>
<td>• <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>.</td>
</tr>
</tbody>
</table>

**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 near to 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 select 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 \(|\alpha| = \infty\) 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 \(\text{Qpenalty}\) 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 \(\text{makeSECdistr}\). In the univariate case \(\Omega = 1\), 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

\[
\text{anotherQ} \leftarrow \text{function}(alpha\_etc, nu = \text{NULL}, \text{der} = 0)
\]

with the following arguments.

- \(\text{alpha\_etc}\): 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 \(\text{cov2cor}(\Omega)\).
- \(\text{nu}\): degrees of freedom, only relevant if \(\text{family}="\text{ST}"\).
- \(\text{der}\): a numeric value which indicates the required order of derivation; if \(\text{der}=0\) (default value), only the penalty \(Q\) needs to be returned by the function; if \(\text{der}=1\), \(\text{attr}(Q,"\text{der1}\")\) must represent the first order derivative of \(Q\) with respect to \(\alpha\); if \(\text{der}=2\), also \(\text{attr}(Q,"\text{der2}\")\) 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 \(\text{der}>1\). Since \(\text{sn}\) imports functions \(\text{grad}\) and \(\text{hessian}\) from package \text{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 \textit{a posteriori} estimate in the stated sense. See \text{Qpenalty} for more information and an illustration.

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

\textbf{Value}

an S4 object of class \(\text{selm}\) or \(\text{mselm}\), depending on whether the response variable of the fitted model is univariate or multivariate; these objects are described in the \text{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 `nlminb` declare successful completion of a regular minimization problem at a point where the Hessian matrix is not positive-definite. An example of this sort is presented in the final portion of the examples below.

Author(s)

Adelchi Azzalini

References


**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", opt.method="Nelder-Mead")
summary(m)
summary(m, "DP")
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(alcohol,sugar)-1, family="ST", data=wines)
m5 <- selm(cbind(alcohol,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 the final passage of 'Cautionary notes' 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

---

**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-ellitically 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

<table>
<thead>
<tr>
<th>Function</th>
<th>Signature</th>
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</thead>
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<td>coef</td>
<td>signature(object = &quot;selm&quot;): ...</td>
</tr>
<tr>
<td>logLik</td>
<td>signature(object = &quot;selm&quot;): ...</td>
</tr>
<tr>
<td>plot</td>
<td>signature(x = &quot;selm&quot;): ...</td>
</tr>
<tr>
<td>show</td>
<td>signature(object = &quot;selm&quot;): ...</td>
</tr>
<tr>
<td>summary</td>
<td>signature(object = &quot;selm&quot;): ...</td>
</tr>
<tr>
<td>residuals</td>
<td>signature(object = &quot;selm&quot;): ...</td>
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<tr>
<td>fitted</td>
<td>signature(object = &quot;selm&quot;): ...</td>
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<tr>
<td>vcov</td>
<td>signature(object = &quot;selm&quot;): ...</td>
</tr>
<tr>
<td>weights</td>
<td>signature(object = &quot;selm&quot;): ...</td>
</tr>
<tr>
<td>profile</td>
<td>signature(fitted = &quot;selm&quot;): ...</td>
</tr>
<tr>
<td>confint</td>
<td>signature(object = &quot;selm&quot;): ...</td>
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<tr>
<td>predict</td>
<td>signature(object = &quot;selm&quot;): ...</td>
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</thead>
<tbody>
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<td>coef</td>
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<td>logLik</td>
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<td>vcov</td>
<td>signature(object = &quot;mselm&quot;): ...</td>
</tr>
<tr>
<td>weights</td>
<td>signature(object = &quot;mselm&quot;): ...</td>
</tr>
</tbody>
</table>

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 \texttt{selm} function, \texttt{plot.selm}, \texttt{summary.selm}, \texttt{dp2cp}

Examples

```r
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)
```

\textbf{Description}

A call to \texttt{selm} activates a call to \texttt{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

\begin{verbatim}
\texttt{selm.fit(x, y, family = "SN", start = NULL, w, fixed.param = list(),}
  \hspace{3.5em} offset = NULL, selm.control=list())
\texttt{sn.mple(x, y, cp = NULL, w, penalty = NULL, trace = FALSE, opt.method =}
  \hspace{3.5em} c("nlminb", "Nelder-Mead", "BFGS", "CG", "SANN"), control = list())
\texttt{st.mple(x, y, dp = NULL, w, fixed.nu = NULL, symmetr = FALSE, penalty = NULL,}
  \hspace{3.5em} trace = FALSE, opt.method = c("nlminb", "Nelder-Mead", "BFGS", "CG", "SANN"),
  \hspace{3.5em} control = list())
\texttt{msn.mle(x, y, start = NULL, w, trace = FALSE, opt.method = c("nlminb",}
  \hspace{3.5em} "Nelder-Mead", "BFGS", "CG", "SANN"), control = list())
\end{verbatim}
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-t and the skew-Cauchy family, respectively. See makeSECdistr 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 fixed.param=list(nu='value'), to fix the degrees of freedom at the named 'value' when family="ST". For instance list(nu=3). Setting fixed.param=list(nu=1) 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 a priori 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 offset 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 FALSE which suppresses printing.

- **fixed.nu**
  - a positive value to keep fixed the parameter nu of the ST distribution in the optimization process; with default value NULL, nu is estimated like the other parameters.

- **symmetr**
  - a logical flag indicating whether a constraint of symmetry is imposed on the slant parameter; default is symmetr=FALSE.

- **opt.method**
  - a character string which selects the optimization method within the set c("nlminb", "Nelder-Mead", "BFGS", "CG", "SANN"), the last four of these are "methods" of function optim.
selm.control a list whose components regulate the working of selm.fit; see ‘Details’ for their description;
ccontrol 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:

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

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.mple 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 $\alpha = 1$, 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


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")
Description

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

Usage

\[ \text{sn.cumulants}(\xi=0, \omega=1, \alpha=0, \tau=0, \text{dp=NULL}, n=4) \]
\[ \text{st.cumulants}(\xi=0, \omega=1, \alpha=0, \nu=\infty, \text{dp=NULL}, n=4) \]

Arguments

- \( \xi \) location parameters (numeric vector).
- \( \omega \) scale parameters (numeric vector, positive).
- \( \alpha \) slant parameters (numeric vector).
- \( \tau \) hidden mean parameter (numeric scalar).
- \( \nu \) degrees of freedom (numeric scalar, positive); the default value is \( \nu=\infty \) which corresponds to the skew-normal distribution.
- \( \text{dp} \) a vector containing the appropriate set of parameters. If \( \text{dp} \) is not NULL, the individual parameters must not be supplied.
- \( n \) maximal order of the cumulants. For \text{st.cumulants} and for \text{sn.cumulants} with \( \tau \neq 0 \) (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


See Also

dsn, dsn
Examples

```r
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))
```

### 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

```r
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, at.MLE=TRUE)
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, `sn.infoUv` is to be used, and these arguments are vectors. In the multivariate case, `sn.infoMv` is to be used and these arguments are lists. See `dp2cp` for their description.

- `x` an optional matrix which represents the design matrix of a regression model

- `y` a numeric vector (for `sn.infoUv` and `st.infoUv`) or a matrix (for `sn.infoMv` and `st.infoMv`) representing the response. In the SN case (for `sn.infoUv` and `sn.infoMv`), `y` can be missing, and in this case the expected information matrix is computed; otherwise the observed information is computed. In the ST case (for `st.infoUv` and `st.infoMv`), `y` is a required argument, since only the observed information matrix for ST distributions is implemented. See ‘Details’ for additional information.

- `w` an optional vector of weights (only meaningful for the observed information, hence if `y` is missing); if missing, a vector of 1’s is generated.

- `fixed.nu` an optional numeric value which declares a fixed value of the degrees of freedom, \(nu\). If not NULL, the information matrix has a dimension reduced by 1.
symmetr a logical flag which indicates whether a symmetry condition of the distribution is being imposed; default is symmetr=FALSE.

penalty a optional character string with the name of the penalty function used in the call to selm; see this function for its description.

norm2.tol for the observed information case, the Mahalanobis squared distance of the score function from 0 is evaluated; if it exceeds norm2.tol, a warning message is issued, since the ‘information matrix’ so evaluated may be not positive-definite. See ‘Details’ for additional information.

at.MLE a logical flag; if at.MLE=TRUE (default value), it generates a warning if the information matrix is not positive definite or an error if the observed information matrix is not evaluated at a maximum of the log-likelihood function.

Value
a list containing the following components:

dp, cp one of the two arguments is the one supplied on input; the other one matches the previous one in the alternative parametrization.

type the type of information matrix: "observed" or "expected".

info.dp, info.cp matrices of Fisher (observed or expected) information in the two parametrizations.

asyvar.dp, asyvar.cp inverse matrices of Fisher information in the two parametrizations, when available; See ‘Details’ for additional information.

aux 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 Mahalanobis 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


See Also
dsn, dmsn, dp2cp

Examples

```r
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")
infoO <- 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)
infoO <- sn.infoUv(cp=fit$cp, x=X, y=wines$alcohol)
```

---

**st.prelimFit**  
*Compute preliminary estimates for a linear model with \( ST \)-distributed error term*

**Description**

For a univariate or multivariate linear model where the error term is assumed to have skew-\( t \) (ST) distribution and the location parameter is a linear function of a set of explanatory values, the functions compute preliminary estimates to be used as initial values for a subsequent maximization of the likelihood function. These functions are mainly intended for internal package use.

**Usage**

```r
st.prelimFit(x, y, w, quick = TRUE, verbose = 0, max.nu = 30)
mst.prelimFit(x, y, w, quick = TRUE, verbose = 0, max.nu = 30)
```
Arguments

\begin{itemize}
\item \textbf{x} \hspace{1cm} \text{design matrix of numeric values. It may be missing; if present, the first column must contain all 1's.}
\item \textbf{y} \hspace{1cm} \text{vector of observations of length } n \text{, or a matrix with } n \text{ rows.}
\item \textbf{w} \hspace{1cm} \text{a vector of non-negative integer weights of length } n \text{; if missing, a vector of all 1's is generated.}
\item \textbf{quick} \hspace{1cm} \text{logical value which regulates whether a very quick estimate is produced (default value } \text{T} \text{RUE); see 'Details' for additional information.}
\item \textbf{verbose} \hspace{1cm} \text{an integer value which regulates the amount of messages printed out; default value is 0.}
\item \textbf{max.nu} \hspace{1cm} \text{threshold for the estimated degrees of freedom}
\end{itemize}

Details

The underlying methodology is the one presented by Azzalini and Salehi (2020). In its essence, it is based on the selection of parameter values achieving the best matching between certain quantile-based summaries of the ST distribution and the corresponding empirical quantities for the sample or, in the presence of explanatory variables, the same quantities computed from the residuals after fitting a median regression.

Argument quick selects whether the above-described matching is performed in a quick or in an accurate way. Since the output values of this function are intended to be only initial values for subsequent likelihood maximization, this explains the default option quick=\text{T} \text{RUE}.

Since the methodology hinges on some selected sample quantiles, it can occasionally be spoiled by poor behaviour of these basic quantiles, especially for small or moderate sample sizes. The more visible effect of such situation is a very large value of the estimated degrees of freedom, which then hampers rather than help a subsequent likelihood maximization. It is therefore appropriate to set an upper limit \text{max.nu} to this component.

Argument x may be missing. In this case, a one-column matrix with all elements 1 is created.

Value

A call to \text{st.prelimFit} returns a list with these components:

\begin{itemize}
\item \textbf{dp} \hspace{1cm} \text{a vector of estimates in the DP parameterization}
\item \textbf{residuals} \hspace{1cm} \text{a vector of residual values}
\item \textbf{logLik} \hspace{1cm} \text{the corresponding log-likelihood value}
\end{itemize}

A call to \text{mst.prelimFit} returns a list with these components:

\begin{itemize}
\item \textbf{dp} \hspace{1cm} \text{a list with the estimates in the DP parameterization}
\item \textbf{shrink.steps} \hspace{1cm} \text{the number of shrinking steps applied to the original estimate of the scale matrix to obtain an admissible matrix}
\item \textbf{dp.matrix} \hspace{1cm} \text{a numeric matrix formed by the component-wise DP estimates}
\item \textbf{logLik} \hspace{1cm} \text{the corresponding log-likelihood value}
\end{itemize}
Note

These functions are mainly intended to be called by `selm`, but they could be of interest for people developing their own procedures.

Author(s)

Adelchi Azzalini

References


See Also

`selm` and either `dst` or `dmst` for explanation of the DP parameters

Examples

data(barolo)
attach(barolo)
A75 <- (reseller=="A" & volume==75)
log.price <- log(price[A75], 10)
prelimFit <- st.prelimFit(y=log.price)
detach(barolo)
#
data(ais)
attach(ais)
prelim32 <- mst.prelimFit(y=cbind(BMI, LBM), x=cbind(1, Ht, Wt))
detach(ais)
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 dp2cp.

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 exists). 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**


**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**

```r
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)
```
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

**Summary.selm**

**Summary and Description**

**Summary**

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

**Description**

**Usage**

```r
## 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-ellitically contoured distributed (SEC) type.

- `logL`:
  - the maximized log-likelihood or penalized log-likelihood value

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

- `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 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


See Also

`selm` function, `selm` (and `mselm`) 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`
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 (not 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(\text{densities}).
symm-modulated-distr

n  an integer value (default: n=1) indicating the number of random numbers.
Omega  a symmetric positive-definite matrix which regulates the dependence structure of f0 and so of the final density.
range  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.
rpt  a numeric vector with two elements representing the number of equally-spaced points on each axis spanning the range described above; default value is rep(101,2).

... optional parameters regulating the function w and, for plot2D.SymmModulated only, graphical parameters to be supplied to function contour.

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 f0, such that f0(z) = f0(−z) for all z, and ‘modulate’ it in the form

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

where G0 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 f0 is now d-dimensional, while G0 is still univariate. The conditions f0(z) = f0(−z) and w(−z) = −w(z) refer to a d-dimensional vector z. Given a d × d symmetric positive-definite matrix Ω, we extract the square roots \( \omega \) of the diagonal element of Ω 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 f0(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 \(w <- \text{function}(z, \ldots)\) where \(\ldots\) 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 \(z = (x - x_i) / \omega\) 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


See Also

Distributions, Beta, TDist, dmnorm, dmt, contour
Examples

```r
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) 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**

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

**Arguments**

- **h**
  - a numeric vector. Missing values (NAs) and Inf are allowed.
- **a**
  - a numeric value. Inf is allowed.
- **jmax**
  - an integer scalar value which regulates the accuracy of the result. See Section ‘Details’ below for explanation.
- **cut.point**
  - 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 \( j_{\max} \) 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 \ feet. See the reference below for more information on function \( T(h, a) \).

Author(s)
Adelchi Azzalini and Francesca Furlan

References

See Also
psn

Examples
\[
\text{owen} \leftarrow \text{T.Owen}(1:10, 2)
\]

---

**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.

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

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


References


Examples

```r
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 Φ(x)) and its derivatives*

**Description**

The function \( \log(2 \Phi(x)) \) and its derivatives, including inverse Mills ratio.

**Usage**

```r
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 \( \mathcal{N}(0, 1) \) 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 \( \zeta(1, x) \) when \( x < -50 \) makes use of the asymptotic expansion (26.2.13) of Abramowitz and Stegun (1964).

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

References


Examples

```r
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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