Package ‘ssmn’

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Type Package

Title Skew Scale Mixtures of Normal Distributions

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Imports mnormt, moments, truncdist, sn

Description Performs the EM algorithm for regression models using Skew Scale Mixtures of Normal Distributions.

License GPL (>= 2)

LazyData TRUE

NeedsCompilation no

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Description

It provides the density, distribution function, quantile function, random number generator, likelihood function, direct and EM algorithm for Maximum Likelihood estimators for a given sample, all this for regression models using Skew Scale Mixtures of Normal Distributions.

Details

Package: ssmn
Type: Package
Version: 1.0
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Author(s)

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References


See Also

ssmn

Examples

#See examples linked above.
Description

Data on 102 male and 100 female athletes collected at the Australian Institute of Sport.

Format

This data frame contains the following columns:

- **sex** (0 = male or 1 = female)
- **Ht** height (cm)
- **Wt** weight (kg)
- **LBM** lean body mass
- **RCC** red cell count
- **WCC** white cell count
- **Hc** Hematocrit
- **Hg** Hemoglobin
- **Fe** input description
- **BMI** body mass index, weight/(height)**2
- **SSF** sum of skin folds
- **Bfat** Percent body fat
- **sport** Sport

References


Examples

```r
# Load the data
library(ssmn)
data(ais)
attach(ais)

# Set the response y and covariate x
x1 <- cbind(1,SSF,Ht)
y    <- Bfat

# Fits a Skew Scale Mixtures of Normal Distributions to the data
fit.ssmn <- ssmn(y, x1, family="sn", method="EM", error = 1e-6, maxit=1000, show.envelope=FALSE)
```
ssmn

Skew Scale Mixtures of Normal Distributions

Description

It provides the density, distribution function, quantile function and random number generator for the Skew Scale Mixtures of Normal Distributions.

Usage

```r
dssmn(x, location=0, scale=1, shape=0, nu= 1, gama=1, dp=NULL, family="sn")
pssmn(q, location=0, scale=1, shape=0, nu= 1, gama=1, dp=NULL, family="sn")
qssmn(p, location=0, scale=1, shape=0, nu= 1, gama=1, dp=NULL, family="sn")
rssmn(n, location=0, scale=1, shape=0, nu= 1, gama=1, dp=NULL, family="sn")
```

Arguments

- `x` the response vector of length `n` where `n` is the total of observations.
- `q` vector of quantiles.
- `p` vector of probabilities.
- `n` number of observations.
- `location` parameter of location.
- `scale` parameter of scale.
- `shape` parameter of shape.
- `nu` degrees of freedom for "stn", "ssl" and "sep". For "scn", `nu` parameter is considered as proportion of outliers.
- `gama` factor scale, but only used by family "scn".
- `dp` vector of parameters.
- `family` Distribution family to be used in fitting ("sn", "stn", "ssl", "scn", "sep")
**ssmn.est**

*EM algorithm for Skew Scale Mixtures of Normal Distributions*

**Description**

Performs the EM algorithm and envelope for regression models using Skew Scale Mixtures of Normal Distributions

**Usage**

```r
ssmn(y, X, family="sn", method="EM", error = 1e-6, maxit=1000, show.envelope=FALSE)
envel(y,X, theta, family="sn", alpha=0.05)
```

**Arguments**

- **y** the response vector of length \( n \) where \( n \) is the total of observations.
- **X** the matrix of explanatory variables of dimension \( n \times (p + 1) \) where \( n \) is the total of observations and \( p \) is the number of variables.
- **family** its defines the distribution to be used: sn, stn, ssl, scn or sep.
- **method** the method to calculate the maximum likelihood estimates: EM algorithm or direct maximum likelihood estimates via Newton-Raphson.
- **maxit** Maximum number of iterations.
- **error** accuracy the convergence maximum error.
- **show.envelope** TRUE or FALSE. Indicates if envelope graph should be built for the fitted model. Default is FALSE.
- **alpha** 1 - alpha is level of confidence.
- **theta** Estimated parameter vector

**Value**

The function returns a list with 8 elements detailed as

- **iter** number of iterations.
- **theta** estimated parameter vector.
- **SE** Standard Error estimates.
- **table** Table containing the inference for the estimated parameters.
- **loglik** Log-likelihood value.
- **AIC** Akaike information criterion.
- **BIC** Bayesian information criterion.
- **time** processing time.
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