Package ‘retimes’

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Functions to identify the peak of a probability density distribution using a Gaussian kernel estimator (kernestim), a fixed-width histogram estimator (histestim), and a distance density estimator (distestim).

Usage

kernestim(x, smoothing = NULL)
histestim(x, smoothing = NULL)
distestim(x, smoothing = NULL)

Arguments

x Vector of data.
smoothing Smoothing parameter, also named bandwidth. If the argument is defined as NULL, the smoothing parameter will be calculated from the data (see details).

Details

The functions kernestim and histestim implement two well-known methods to estimate the density of an empirical distribution (see Van Zandt, 2000, for their application in RT analysis). The functions can be used to find the value corresponding to the peak of an empirical distribution.

The function kernestim center a Gaussian density over each observation and identifies the value with the greater density.

The function histestim divides the data in bins, starting from the lower to the higher value of data. The function searches the bin with the higher data frequency. The peak of the distribution is identified calculating the mean of the data into the bin.

The function distestim is an experimental method which mixes the two previous techniques. Around each data point (pivot), an interval \([x_i - h/2, x_i + h/2]\) is built, where \(h\) is the smoothing parameter. The function searches the interval (bin) with the higher data frequency. The output value is the weighted average of the values into the selected bin, in which each observation is weighted on the basis of the distance from the pivot. If bins with equal densities are found, the bin presenting the smallest deviance from the pivot is chosen.

For the Gaussian kernel estimator, the smoothing parameter is calculated using the Silverman’s method (Silverman, 1986). Differently, using histogram and distance estimators, the smoothing parameter is calculated as: \((Q_{0.975} - Q_{0.025})/\sqrt{n}\), where \(Q_p\) are the quantiles for \(\alpha = 0.05\) and \(n\) is the sample dimension.

Value

The value at which the peak of density is located.
**Author(s)**

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**References**


**Examples**

```r
x <- rexgauss(1000, mu=500, sigma=100, tau=250)
k <- kernestim(x); k
h <- histestim(x); h
d <- distestim(x); d
plot(density(x))
segments(k,0,k,1,col="red")
segments(h,0,h,1,col="blue")
segments(d,0,d,1,col="green")
```

---

**exgauss**

*Ex-Gaussian Distribution*

**Description**

Density function, parameter estimation by moments and random variable generation for the ex-Gaussian distribution.

**Usage**

```r
dexgauss(q, mu = 0, sigma = 1, tau = 1)
mexgauss(x, n = length(x))
rexgauss(n, mu = 0, sigma = 1, tau = 1, positive = TRUE)
```

**Arguments**

- `x,q` Vector of reaction times.
- `n` Number of observations.
- `mu,sigma,tau` Parameters of the ex-Gaussian distribution.
- `positive` Logical: imposes the generation of a vector containing only positive values.
Details

The function `mexgauss` implements the method of moments to estimate the parameters of an ex-Gaussian distribution as described by Heathcote (1996).

Author(s)

Davide Massidda <davide.massidda@humandata.it>

References


Luce, R. D. (1986). Response times: their role in inferring elementary mental organization. New York: Oxford University Press.

See Also

`timefit`

Examples

```r
# Vector of reaction times from Heathcote (1996):
RT <- c(474.688, 506.445, 524.081, 530.672, 530.869, 566.984, 582.311, 582.940, 603.574, 792.358)
mexgauss(RT)
```

```
    skew
Skewness Index
```

Description

Calculate the skewness index of an empirical distribution.

Usage

`skew(x)`

Arguments

- `x` Vector of data.

Details

The skewness measures the asymmetry of a probability distribution. If a positive skewness identifies a greater right tail, a negative skewness is symptom of a greater left tail of the distribution.

The skewness is calculated as: \( k_3/k_2^{1.5} \), where \( k_2 \) and \( k_3 \) are respectively the second and the third moment of the distribution.
**Value**

The skewness index.

**Author(s)**

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**Examples**

```r
# Vector of reaction times from Heathcote (1996):
RT <- c(474.688, 506.445, 524.081, 530.672, 530.869, 566.984, 582.311, 582.940, 603.574, 792.358)
skew(RT)
```

---

**Description**

Parameter estimation for reaction time distributions using the maximum likelihood method. Currently, the function works only for the ex-Gaussian probability distribution.

**Usage**

```r
timefit(x, iter = 0, size = length(x), replace = TRUE,
       plot = FALSE, start = NULL, ...)
```

**Arguments**

- `x` Vector of reaction times, in milliseconds or seconds.
- `iter` if `iter > 0`, the estimation is performed by bootstrap resampling. For each iteration, a sub-sample with a positive skewness will be extracted from the original sample, and distribution parameters will be estimated on resampled data.
- `size` Sample dimension to use in resampling, when the bootstrap is active.
- `replace` Logical: specifies if the resampling must be performed with replacement.
- `plot` Logical: if TRUE, it shows the data distribution (continuous line) and the estimated distribution (dashed line). Furthermore, when the bootstrap is used, the histogram of each parameter distribution is shown.
- `start` Vector containing starting values (in order: `mu`, `sigma` and `tau`) for the optimization routine. As default, the method of moments is used to estimate initial parameters. If the bootstrap is active, the argument will be ignored (starting values will be calculated on each bootstrapped sample using the method of moments).
- `...` Further arguments for the optimization routine. Arguments will be passed to the `optim` function: see the `optim` documentation for further details.
Details

The function `timefit` estimates ex-Gaussian parameters by maximum likelihood, using the `optim` function. As default, the Simplex method (Nelder-Mead) is applied to find the minimum of the objective function.

The function implements a bootstrap approach to identify distribution parameters. The bootstrap is useful especially working on small samples. The implemented method identifies $\mu$ and $\sigma$ using a gaussian kernel estimator (see Van Zandt, 2000, for details). Since small samples often present problems of convergence for $\sigma$, for this parameter only the values included a theoretical plausible range are considered. This range is defined by:

$$\sqrt{\frac{\min(x - M)^2}{n - 1}} \leq \sigma \leq S$$

where $M$ and $S$ are respectively the mean and the standard deviation of data. When $\mu$ and $\sigma$ are identified, $\tau$ is chosen within the bootstrapped values, according to the maximum likelihood criterion.

Value

An object of class `timefit`. The operator `@` should be used to extract the values from the slots of the output object.

- `@x`: vector of data.
- `@samples`: bootstrapped samples.
- `@par`: estimated parameters.
- `@bootPar`: bootstrapped parameters.
- `@bootValue`: log-likelihood of bootstrapped parameters.
- `@sigmaValid`: not rejected (TRUE) and rejected (FALSE) values for $\sigma$.
- `@start`: starting values.
- `@logLik`: log-likelihood of estimated parameters.
- `@AIC`: Akaike Information Criterion.
- `@BIC`: Bayesian Information Criterion.

Note

The methods `plot`, `logLik`, `AIC` and `BIC` are available.

Author(s)

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References


Luce, R. D. (1986). Response times: their role in inferring elementary mental organization. New York: Oxford University Press.


See Also

exgauss, density-estim, skew

Examples

```r
# Vector of reaction times from Heathcote (1996):
RT <- c(474.688, 506.445, 524.081, 530.672, 530.869,
       566.984, 582.311, 582.940, 603.574, 792.358)
RTfit <- timefit(RT); RTfit

# Bootstrap testing with simulated data (m=500, s=100, t=250):
x1 <- c(451.536, 958.612, 563.538, 505.735, 1266.825,
        860.663, 457.707, 268.679, 587.303, 669.594)
fit1a <- timefit(x1); fit1a
fit1b <- timefit(x1, iter=1000); fit1b

x2 <- c(532.474, 525.185, 1499.471, 480.732, 631.752,
        672.419, 322.341, 571.356, 428.832, 680.848)
fit2a <- timefit(x2, plot=TRUE); fit2a
fit2b <- timefit(x2, iter=1000, plot=TRUE); fit2b
```

## End(Not run)
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