

# Package ‘bootspcdens’

February 14, 2012

**Type** Package

**Title** Testing equality of spectral densities

**Version** 3.0

**Date** 2009-01-11

**Author** Tatjana Kinsvater

**Maintainer** Tatjana Kinsvater <tatjana.kinsvater@rub.de>

**Description** Bootstrap for testing the hypothesis that the spectral densities of a number  $m$ ,  $m \geq 2$ , not necessarily independent time series are equal

**Depends** MASS

**License** GPL ( $\geq 2$ )

**Repository** CRAN

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## Description

Bootstrap for testing the hypothesis that the spectral densities of a number  $m$ ,  $m \geq 2$ , not necessarily independent time series are equal. The returned value is "equal spectral densities" for equal spectral densities respectively "not equal spectral densities" for different spectral densities.

## Details

Package: bootspecdens  
 Type: Package  
 Version: 1.0  
 Date: 2009-01-11  
 License: GPL (>=2)

The package includes the function `specdens`. This function test with a bootstrap the hypothesis that the spectral densities of a number  $m$ ,  $m \geq 2$ , not necessarily independent time series are equal.

### Author(s)

Tatjana Kinsvater <tatjana.kinsvater@rub.de>  
 Maintainer: Tatjana Kinsvater <tatjana.kinsvater@rub.de>

### References

Dette,H. and Paparoditis,E. (2007) *Testing Equality Of Spectral Densities*.

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specdens

*Bootstrap for testing equality of spectral densities*

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### Description

Bootstrap for testing the hypothesis that the spectral densities of a number  $m$ ,  $m \geq 2$ , not necessarily independent time series are equal. The test is based on a appropriate L2-distance measure between the nonparametric estimated individual spectral density and an overall pooled spectral density, obtained using the whole set of time series. The returned value is "equal spectral densities" for equal spectral densities respectively "not equal densities" for different spectral densities.

### Usage

```
specdens(data, h, B, level)
```

### Arguments

<code>data</code>	Data is a $m \times n$ matrix. In each row the data of one time series considered, i.e. $m$ =number of time series and $n$ =number of observation.
<code>h</code>	A single number which represents the kernel bandwidth smoothing parameter.
<code>B</code>	The number of bootstrap replicates. This will be a single positive integer. Normally something like 1000 is used.
<code>level</code>	A single number in (0,1) represents the level of the test. Normally 0.05 is used.

### Value

The value returned is "equal spectral densities" for equal spectral densities respectively "not equal spectral densities" for different spectral densities. Furthermore the p-value is given.

**Author(s)**

Tatjana Kinsvater <tatjana.kinsvater@rub.de>

**References**

Dette, H. and Paparoditis ,E. (2007) *Testing Equality Of Spectral Densities*.

**Examples**

```
data(Nile)
data(WWWusage)
data<- matrix(c(Nile[1:20],WWWusage[1:20]), nrow=2, byrow=TRUE) #creates the data matrix with
  #the first 20 values of the
  #time series Nile and WWWusage
specdens(data, 0.2, 100, 0.05)
```

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