

# Package ‘heteroplasmy’

June 1, 2021

**Title** Calculation of the standard error of the variance for heteroplasmy data

**Version** 0.0.0.9000

**Description** The package offers different methods to quantify uncertainty by calculating the standard errors of the variance of given data. The included functions are primarily aimed to heteroplasmy data, which are not assumed to follow a predefined distribution and the sample size is usually low. Included, there is a set of synthetic datasets to use, as well as real heteroplasmy data from mouse specimen, found in (xxx Iain's paper xxx) The code and the methods described in the package are used in the (xxx our report xxx), so please cite that work in case you use the heteroplasmy package.

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analyticVar	<i>Analytic calculation of the standard error of the variance</i>
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### Description

This function calculates analytically the standard error of the variance.

### Usage

```
analyticVar(data, normal = FALSE)
```

### Arguments

data	The input data in the form of a dataframe or matrix (which will be transformed into a dataframe). NA values are omitted.
normal	Parameter that indicates if the normal approximation should be used instead of the general formula from (Wilks, S. S. (1962).Mathematical Statistics). Default is FALSE.

### Value

The analytically derived standard error of the variance of data.

### Examples

```
# size of the sample
n=50
#generate a random sample of size n from a normal distribution
data_ex=rnorm(n,0.5,0.1)
analyticVar(data)

mouseData=readHeteroplasmyData("HB")
mouseData1 = mouseData[which(!is.na(mouseData[,1])),1]
analyticVar(mouseData1)
```

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bootstrapVar	<i>A bootstrap method to calculate the standard error of the variance</i>
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### Description

This function uses the bootstrap method to calculate the uncertainty of the variance of a given sample based on random resampling. The number of the resamples is a parameter (default is 1000) and along with the the "vanilla" version, we offer an optimized variation (using the **sigmaOpt** parameter) which has been seen to improve the precision of the calculation (see our report/paper). Given that the resampling methods underestimate the uncertainty and thus provide a biased estimation, we offer the the unbiased method as a default, although the user may change this option through the biased parameter for experimental purposes (they are strongly advised not to do for real problems with small samples).

**Usage**

```
bootstrapVar(
  data,
  nrep = 1000,
  biased = FALSE,
  corrected = FALSE,
  sigmaOpt = FALSE
)
```

**Arguments**

data	The input data in the form of a dataframe or matrix (which will be transformed into a dataframe). NA values are omitted.
nrep	The number of bootstrap resamples. Default is 1000. The higher the number of the samples, the better the bootstrap outcome.
biased	A logical parameter to indicate if the user wants the biased version. Resampling techniques always underestimate statistics like the variance or the standard error of it for small samples.
corrected	Simple correction with a factor of 2.61 that was experimentally found. It is included also in the case of sigmaOpt=TRUE
sigmaOpt	The outcome of the bootstrap resampling with a fitted sigmoid function $g(x)$ with four parameters. Derived through simulations on both real heteroplasmy data and various synthetic ones. Try the plotStdErrVar function in this package to observe it.

**Value**

The standard error of the variance of data.

**Examples**

```
# size of the sample
n=50
#generate a random sample of size n from a normal distribution
data_ex=rnorm(n,0.5,0.1)
bootstrapVar(data)

mouseData=readHeteroplasmyData("HB")
mouseData1 = mouseData[which(!is.na(mouseData[,1])),1]
bootstrapVar(mouseData1,sigmaOpt=TRUE)
```

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bootstrapVarCor

*The bootstrapVar function with default correction*


---

**Description**

This function is simply the bootstrapVar with the correction argument being TRUE. it is provided as a separate function for usability. The function can be used beyond heteroplasmy data, therefore one can use it to calculate the standard error of the variance for samples where other approaches may not fit, eg when the sample size is too small and/or the population distribution is not Gaussian (or not known at all).

**Usage**

```
bootstrapVarCor(data, nrep = 1000)
```

**Arguments**

data	The input data in the form of a dataframe or matrix (which will be transformed into a dataframe). NA values are omitted.
nrep	The number of bootstrap resamples. Default is 1000. The higher the number of the samples, the better the bootstrap outcome (see <a href="#">par</a> ).

**Value**

The analytically derived standard error of the variance of data.

**Author(s)**

Kostas and Iain, <us@example.com>

**References**

<https://en.wikipedia.org/>

**See Also**

[bootstrapVar](#)

**Examples**

```
# size of the sample
n=50
#generate a random sample of size n from a normal distribution
data_ex=rnorm(n,0.5,0.1)
bootstrapVarCor(data)

mouseData=readHeteroplasmyData("HB")
mouseData1 = mouseData[which(!is.na(mouseData[,1])),1]
bootstrapVarCor(mouseData1,nrep=10000)
```

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heteroplasmyShift

*Transformed heteroplasmy shift*

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**Description**

A numerical transformation of the heteroplasmy samples in order to work with the heteroplasmy shifts across diverse samples (e.g., due to time or different tissue samples). This transformation is used for comparing a heteroplasmy observation  $h$  to a reference value  $h_0$ . It corresponds to the formula:

$$\Delta h = \ln \left( \frac{h(h_0 - 1)}{h_0(h - 1)} \right)$$

**Usage**

```
heteroplasmyShift(h, h0)
```

**Arguments**

h	The heteroplasmy observation.
h0	The reference heteroplasmy value.

**Value**

The Transformed heteroplasmy shift.

**Author(s)**

Kostas and Iain, <us@example.com>

**References**

[Site or paper](#)

**See Also**

[readHeteroplasmyData](#)

**Examples**

```
# size of the sample
n=50
#generate a random sample of size n from a normal distribution
data_ex=rnorm(n,0.5,0.1)
heteroplasmyShift(data)

mouseData=readHeteroplasmyData("HB")
mouseData1 = mouseData[which(!is.na(mouseData[,1])),1]
heteroplasmyShift(mouseData1,nrep=10000)
```

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jackVar

*A jackknife method to compute the uncertainty of heteroplasmy data*

---

**Description**

Similarly to the main `bootstrapVar` function that implements the bootstrap method to measure the standard error of the variance, the jackknife technique is another resampling method that can be used for the same purpose. Unlike `bootstrapVar`, `jackVar` (and very jackknife method) is deterministic and doesn't rely on randomness, but instead it uses removals of the sample points, one each time to calculate different sub-samples of size  $(n-1)$ . Note that the size of the input data should be strictly greater than 1.

**Usage**

```
jackVar(data)
```

**Arguments**

**data** The input data in the form of a dataframe or matrix (which will be transformed into a dataframe). Its size should be  $\geq 2$ . NA values are omitted.

**Value**

The analytically derived standard error of the variance of data.

**Examples**

```
# size of the sample
n=50
#generate a random sample of size n from a normal distribution
data_ex=rnorm(n,0.5,0.1)
jackVar(data)

mouseData=readHeteroplasmyData("HB")
mouseData1 = mouseData[which(!is.na(mouseData[,1])),1]
jackVar(mouseData1)
## Not run:
#input data of size 1 will fail
data_ex=rnorm(1,0.5,0.1)
jackVar(data)

## End(Not run)
```

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mousedataHB	<i>HB oocyte heteroplasmy data.</i>
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**Description**

A dataset containing hetoplasmy values for the HB oocyte mouse lines. Each column corresponds to a different specimen. NA values have been added to make the number of rows equal. Please remove them after loading.

**Usage**

```
mousedataHB
```

**Format**

A data frame with 25 rows and 56 columns (TO FIX):

**price** price, in US dollars

**carat** weight of the diamond, in carats

**Source**

<http://www.example.info/>

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mousedataLE	<i>LE oocyte heteroplasmy data.</i>
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### Description

A dataset containing hetoplasmy values for the HB oocyte mouse lines. Each column corresponds to a different specimen. NA values have been added to make the number of rows equal. Please remove them after loading.

### Usage

```
mousedataLE
```

### Format

A data frame with 20 rows and 43 columns (TO FIX):

**price** price, in US dollars

**carat** weight of the diamond, in carats

### Source

<http://www.example.info/>

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plotStdErrVar	<i>An example plotting function</i>
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### Description

This function is used as a toy example on how to represent the data statistics regarding the variance of the sample. The mean variance and its standard error are depicted. Note that this is just an illustration to show that the analytic and the resampling approaches almost match each other.

### Usage

```
plotStdErrVar(  
  data,  
  functions = c("normalApr", "analytic", "bootstrap", "correctedBoot", "jackknife"),  
  ...  
)
```

### Arguments

**data** The input data in the form of a dataframe or matrix (which will be transformed into a dataframe).

**functions** Choose the subset of the functions you wish use for the calculation and subsequent plot of the standard error of the variance. You can use one or a combination of "normalApr", "analytic", "bootstrap", "correctedBoot", and "jackknife". For now, it outputs all of the aforementioned methods!

**Warning**

This is a plotting function just for demonstration purposes.

**Examples**

```
# size of the sample
n=50
#generate a random sample of size n from a normal distribution
data_ex=rnorm(n,0.5,0.1)
plotStdErrVar(data_ex)
```

---

readHeteroplasmyData    *A Function to read mouse heteroplasmy data (not finished!)*

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**Description**

This function allows you to read mouse heteroplasmy data from external files. Use with caution (for now).

**Usage**

```
readHeteroplasmyData(named = "HB")
```

**Arguments**

named                      Either "HB" or "LE".

**Value**

A dataframe containing mouse heteroplasmy data.

**Examples**

```
readHeteroplasmyData(named="LE")
```



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