

Package ‘MsatAllele’

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Type Package

Title Visualizes the scoring and binning of microsatellite fragment sizes

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Description

The package contains functions to: 1) load ah files from Strand software and build a R data base; 2) plot different graphical displays of the fragment sizes obtained for each locus and their bins; 3) interact with graphs to sort the data base for a given locus and range, allowing to easily trace back a particular group of samples to its original Strand file; bin fragment size data into population genetics files. 4) From version 1.04 on, the user can set manually bin limits and write files combining the manual and automatic methods to bin alleles.

License GPL (>=2)

NeedsCompilation no

R topics documented:

MsatAllele-package	2
AlleleCum	3
AlleleHist	4
bin.limits	5
BinStat	6
DBase	7
DBZn	7
DefBinLim	8
get.allele	9
getpoints	10

InputFile 11

mark.bins 12

OrderByLocus 13

read.ah.file 14

read.frag.sizes 15

restrict.hist 16

STRandOUT 17

subdataBase 18

transDB 19

write.data 20

write.PG.file.all 21

write.PG.file.loc 22

Index 24

MsatAllele-package	<i>Visualizes and scores microsatellite alleles from electrophoresis fragment sizes</i>
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Description

The package contains functions to: 1) load ah files from Strand software and build a R data base; 2) plot different graphical displays of the fragment sizes obtained for each locus and their bins; 3) interact with graphs to sort the data base for a given locus and range, allowing to easily trace back a particular group of samples to its original Strand file; bin fragment size data into population genetics files. 5) From version 1.04 on, the user can set manually bin limits and write files combining the manual and automatic methods to bin alleles.

Details

Package: MsatAllele
Type: Package
Version: 1.05
Date: 2013-11-14
License: GPL (>=2)

The package contains functions to: 1) load ah files from Strand software and build a R data base; 2) plot different graphical displays of the fragment sizes obtained for each locus and their bins; 3) sort the data base for a given locus and range, allowing to easily trace back particular samples to its original Strand file; 4) write a population genetics input file from the data base. 5) Capacity to define bins manually is a new feature since MsatAllele 1.04

Author(s)

Filipe Alberto
Maintainer: Filipe Alberto <albertof@uwm.edu>

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

Examples

```
data(DBase)
AlleleHist(DBase,"BC-4",0.01,1)
subdataBase(DBase,"BC-4",227,233)
```

AlleleCum

Plots a cumulative allele size distribution

Description

This function plots a cumulative allele size distribution with number of observations on the x axis and allele size on the y axis. Each alternative allele bin is colored differently

Usage

```
AlleleCum(DataBase, loci,ymin=NULL,ymax=NULL, c1 = "black", c2 = "grey", ytsize = 1,
          psize = 1,pch=1)
```

Arguments

DataBase	A data base with loci and fragment size information
loci	The locus to be plotted
ymin	The minimum value in the allele size scale to plot
ymax	The maximum value in the allele size scale to plot
c1	color for the first allele and every other following ones
c2	color for the second allele and every other following ones
ytsize	Text size for the y axis in proportion of the default value of one
psize	Point size fin proportion of the default value of one
pch	Type of plotting symbol

Value

The function plots a cumulative allele size distribution for a given locus. The y scale can be restricted to a given interval of allele size. This plot is similar to the plots implemented in Flexibin and Allelogram programs

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

See Also

[AlleleHist](#), [restrict.hist](#)

Examples

```
data(DBase)
AlleleCum(DBase,"BC-4")
```

AlleleHist

Plots an histogram of microsatellite fragment sizes

Description

Plots an histogram of microsatellite fragment sizes obtained after the scoring of electrophoresis results

Usage

```
AlleleHist(DataBase, marker, limits=0.01, ticks=1)
```

Arguments

DataBase	A data base with loci and fragment size information
marker	The locus to be plotted
limits	The width of histogram classes
ticks	The interval between two consecutive tick marks on the x axis

Details

The generated plot is usefull to analyze the total variation of fragment sizes obtained for a given locus. It will allow the detection of range were 1bp mutation may have occurred

Value

An histogram with the frequency of the fragment sizes scored for a given locus in the data Base

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

See Also

[read.ah.file](#), [restrict.hist](#)

Examples

```
data(DBase)
AlleleHist(DBase, "BC-4", 0.01, 1)
```

bin.limits	<i>Writes the limits of bin classes and rounded bin codes</i>
------------	---

Description

Gets the bin information necessary to plot bin limits on the histogram of fragment sizes distribution

Usage

```
bin.limits(DBase, locus)
```

Arguments

DBase	A data base with loci and fragment size information
locus	The relevant locus

Value

A list with components

limits	The limits of each bin in bp with two decimals cases
bin	The bin codes

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

See Also

[write.PG.file.loc](#)

Examples

```
data(DBase)
bin.limits(DBase,"BC-4")
```

BinStat*Summary bin statistics*

Description

Writes a data frame with summary statistics for each bin of a given locus

Usage

```
BinStat(DataBase, loci)
```

Arguments

DataBase	A data base with loci and fragment size information
loci	The locus of interest

Details

This function writes to a table bin statistics: Bin code, number of observations, minimum size, maximum size, range, standard deviation, mean and median

Value

A data frame with bin summary statistics

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

Examples

```
data(DBase)
BinStat(DBase,"BC-4")
```

DBase	<i>A data base of the type used by this package</i>
-------	---

Description

A data base with fragment size information that can be created by the function transDB

Usage

```
data(DBase)
```

Format

A data frame with 691 observations on the following 5 variables.

Marker Genetic marker code

Sample Sample code

Fragment Fragment sizes scored

Date An entry field for the date

Plate An entry field for fragment analysis plate

Examples

```
data(DBase)
```

DBZn	<i>A data base of the type used by this package with Zostera noltii data</i>
------	--

Description

A data base with fragment size information that can be created by the function transDB

Usage

```
data(DBZn)
```

Format

A data frame with 3458 observations on the following 5 variables.

Marker Genetic marker code

Sample Sample code

Fragment Fragment sizes scored

Date An entry field for the date

Plate An entry field for fragment analysis plate

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

Examples

```
data(DBZn)
```

DefBinLim

Lets the user define bin limits

Description

This function lets the user define bin limits for a given locus by clicking on top of an [AlleleCum](#) graph

Usage

```
DefBinLim(marker,append2=NULL,alleles)
```

Arguments

marker	The name of the locus in the open AlleleCum graph
append2	A data.frame like the one produced by this function to where further bin limits may be appended
alleles	A numerical vector containing the allele labels for the alleles you want to provide limits

Details

Upon opening an AlleleCum graph and not being happy with MsatAllele automatic bin definition you can use this function to set bin limits to each allele. You need to set the lower limits for each bin in the AlleleCum (not only for those you want to change). If the locus has many alleles, making it hard to click on the lower limits of each allele, you can use this function sequentially making use of the parameter append2, and the ymin and ymax parameters in [AlleleCum](#) function. Remember to set append2 to the same object created in the first call to this function. Also remember to set the alleles argument to the new set of alleles.

Value

A data.frame with three columns, marker, alleles (the alleles argument provided) and LowerBin containing the lower bin limits set by the user

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

See Also

[AlleleCum](#)

Examples

```
data(DBase)
AlleleCum(DBase, "BC-4")
alleles.BC4<-c(222,224,226,228,230,232,234,236,240,242,244,247)
DefBinLim(DBase,append2=NULL,alleles=alleles.BC4)
```

get.allele	<i>Gets the allele code from an electrophoresis fragment size</i>
------------	---

Description

Rounds a fragment size with two decimal of a bp to an integer allele code

Usage

```
get.allele(RefDB, Marker, fragment)
```

Arguments

RefDB	A data base with loci and fragment size information
Marker	The locus to be plotted
fragment	The fragment size to round using the Data base distributions

Details

The algorithm implemented searches the database for all observed fragments within the interval set by -0.8 to + 0.8 bp of the fragment. It proceeds to detect breaks in the distribution of observed distribution to find the distribution where the fragment belongs. To get the allele code the median of that distribution is rounded to an iteger value

Value

An integer allele code

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles *Journal of Heredity*. 100(3):394,397

See Also

[write.PG.file.loc](#)

Examples

```
data(DBase)
get.allele(DBase, "BC-16", 142.54)
```

getpoints

Interacts with AlleleCum graph to list observations

Description

This function interacts with the graph created by AlleleCum, the user needs to click on the y axis intersections (allele size) of that graph to define the minimum and maximum values of the range of observations to list.

Usage

```
getpoints(Database, marker)
```

Arguments

Database	A data base with loci and fragment size information
marker	The locus to be sorted

Details

The user need to call the graphical display of [subdataBase](#) first and then use getpoints. You need to click select first the minimum value for the range of fragment sizes to list, by clicking somewhere on the plot area intersecting that y axis value, and then reposition the mouse cursor to the maximum limit value to list.

Value

DFrow	The row.name information for that fragment in the data base
Sample	The Sample code
Reading	The fragment size
Gel	The Strand file for that fragment

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

See Also

[subdataBase](#), [AlleleCum](#)

Examples

```
data(DBase)
AlleleCum(DBase,"BC-3")
getpoints(DBase,"BC-3")
```

InputFile	<i>A data matrix similar to the tab delimited text file such as needed to data input</i>
-----------	--

Description

A data table with the following fields: 1st column-sample name; 2nd column-Panel or test name (specific combination of loci in that sample); 3rd column-Locus name; 4th column-fragment size for first allele; 5th column-fragment size for 2nd allele.

Usage

```
data(InputFile)
```

Format

A data frame with 480 observations on the following 5 variables.

Sample.Name Sample names

Panel The panel or test (a group of loci used to genotype the sample)

Marker The loci's vector

Size.1 Fragment size for the first allele scored

Size.2 Fragment size for the second allele scored, homozygotes have the same value as the preceding item

Details

This table format can be easily generated from output files from peak calling software

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles *Journal of Heredity*. 100(3):394,397

Examples

```
data(InputFile)
```

mark.bins

Adds bin limits to histograms of fragment size distribution

Description

plots bin limits on top of the histogram of observed fragment sizes for a given locus

Usage

```
mark.bins(bins, text.size = 1, yscale = 5, offtext = 0.5)
```

Arguments

bins	A list of the type returned by <code>bin.limits</code> function
text.size	The size of text showing the bin codes
yscale	The height of the y axis
offtext	The offset tvalue for the text

Value

Lines and bin codes are added to the plot

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

Examples

```
data(DBase)
bins<-bin.limits(DBase,"BC-4")
mark.bins(bins)
```

OrderByLocus

A function to order the fragment size vector for a given locus

Description

Used by other functions to sort the fragment sizes

Usage

```
OrderByLocus(DataBase, marker)
```

Arguments

DataBase	A data base with loci and fragment size information
marker	The locus to be sorted

Value

An ordered fragment size vector for a given locus

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

See Also

[subdataBase](#), [AlleleHist](#)

Examples

```
data(DBase)
OrderByLocus(DBase, "BC-4")
```

read.ah.file	<i>Reads .ah files from Strand and creates a R data base</i>
--------------	--

Description

Reads .ah files from Strand and creates a R data base object with scored microsatellite fragment sizes

Usage

```
read.ah.file(ahfile, date, plate)
```

Arguments

ahfile	A export .ah file from Strand
date	A relevant date to be written on the data base
plate	A sample plate code to be written on the data base

Details

The Strand software exports scored fragment sizes in a .ah file. This function will read those files and create the R data base that will be used by this package

Value

Marker	Genetic marker code
Sample	Sample code
Read	Fragment size
Date	Date
Plate	Strand plate file

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

See Also

[AlleleHist](#), [restrict.hist](#), [subdataBase](#)

Examples

```
data(STRandOUT)
write.table(STRandOUT,"ah file simulated.txt",sep="\t",na="",quote=FALSE,col.names=FALSE,
            row.names=FALSE)
read.ah.file("ah file simulated.txt","25-2-2008","P1MX4MX5")
```

read.frag.sizes	<i>Reads tab delimited text files with input fragment sizes creates a R data base</i>
-----------------	---

Description

Reads input text files with continuous fragment size data and creates an R data base.

Usage

```
read.frag.sizes(in.file, date, plate)
```

Arguments

in.file	The name of the input file
date	A relevant date to be written on the data base
plate	A sample plate code to be written on the data base

Details

This functions reads tab delimited files with the following fields: 1st column-sample name; 2nd column-Panel or test name (specific combination of loci in that sample); 3rd column-Locus name; 4th column-fragment size for first allele; 5th column-fragment size for 2nd allele. Use NA to code absent data.

Value

Marker	Genetic marker code
Sample	Sample code
Read	Fragment size
Date	Date
Plate	Plate code

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

See Also

[read.ah.file](#), [AlleleCum](#), [subdataBase](#)

Examples

```
data(InputFile)
write.table(InputFile,"Input file.txt",sep="\t",na="",quote=FALSE,col.names=FALSE,row.names=FALSE)
read.frag.sizes("Input file.txt","25-2-2008","M1MpMetapop")
```

restrict.hist	<i>Plots an histogram of a restricted range of microsatellite fragment sizes</i>
---------------	--

Description

Plots an histogram of a restricted range microsatellite fragment sizes (i.e. zooming) obtained after the scoring of electrophoresis results

Usage

```
restrict.hist(DataBase, marker, MIN, MAX, limits=0.01, ticks=1 )
```

Arguments

DataBase	A data base with loci and fragment size information
marker	The locus to be plotted
MIN	The lower limit of the restricted range
MAX	The upper limit of the restricted range
ticks	The interval between two consecutive tick marks on the x axis
limits	The width of histogram classes

Details

Allows zooming up on the distribution of fragment sizes for a given locus. It is usefull to check closely for 1bp differentiated alleles, allowing to decide wwhich MIN and MAX to use on test.table and subdataBase functions

Value

A restricted range histogram

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

See Also

[AlleleHist](#), [subdataBase](#)

Examples

```
data(DBase)
restrict.hist(DBase, "BC-4", 228, 229, 0.01, 1)
```

STRandOUT

A table like the one exported in the Strand .ah file

Description

A table like the one exported in the Strand .ah file

Usage

```
data(STRandOUT)
```

Format

A data frame with 1440 observations on the following 10 variables.

- V1 A column with both sample code and number
- V2 The sample number, not sure what this means in the sequencer structure
- V3 A factor with the colors use for each marker
- V4 A factor with sample names
- V5 A factor with marker names
- V6 fragment sizes for the first allele scored
- V7 fragment sizes for the second allele scored, if any (i.e. homozygotes have nothing here)
- V8 Rounded allele codes, using the weird Strand algorithm
- V9 a logical vector
- V10 a logical vector

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles *Journal of Heredity*. 100(3):394,397

Examples

```
data(STRandOUT)
transDB(STRandOUT, "25-2-2008", "Plate1-MX4MX5")
```

subdataBase

Sorts the data base for a given locus and a restricted range

Description

This function can be used to see the information for the fragments observed in a given the range of a particular loci. It is usefull to trace back samples with strange sizes to their original Strand files

Usage

```
subdataBase(DataBase, marker, MIN=min(DataBase[,3]), MAX=max(DataBase[,3]))
```

Arguments

DataBase	A data base with loci and fragment size information
marker	The locus to be sorted
MIN	The lower limit of the restricted range
MAX	The upper limit of the restricted range

Details

Returns a list of observations from the data base for a given locus and range defined by the MIN and MAX allele sizes arguments, with default values equal to the minimum and maximum observations recorded in the data base

Value

~Describe the value returned If it is a LIST, use

DFrow	The row.name information for that fragment in the data base
Sample	The Sample code
Reading	The fragment size
Gel	The Strand file for that fragment

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles *Journal of Heredity*. 100(3):394,397

See Also

[AlleleHist](#), [AlleleCum](#)

Examples

```
data(DBase)
subdataBase(DBase, "BC-4", 228, 232)
```

transDB	<i>Creates a data base object in the form used by other functions in the package</i>
---------	--

Description

Creates a data base from an R object with structure identical to the .ah Strand export file

Usage

```
transDB(STRandOUT, data, corrida)
```

Arguments

STRandOUT	an R object with structure identical to the .ah Strand export file
data	the date entry field to be written in the data base
corrida	the plate code entry field to be written in the data base

Details

It is used internally to the read.ah.file function

Value

Marker	Genetic marker code
Sample	Sample code
Read	Fragment size
Date	Date
Plate	Strand plate file

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

Examples

```
data(STRandOUT)
transDB(STRandOUT, "25-2-2008", "P1MX4MX5")
```

write.data

Write multilocus genotype tables allowing to specify the use of manual or automatic binning methods

Description

Writes a multilocus genotype table from the data base allowing to specify for which loci should manual bin limits be used. In order to use manual defined bins you will need to use the function [DefBinLim](#) previously

Usage

```
write.data(DB,Mtable,file="MLG table")
```

Arguments

DB	A data base of the type used by this package, like the generated by transDB
Mtable	A data.frame with two columns Marker and Method, Marker contains the names of the markers in the Data base from where you want to write from; Method contains characters that can be "Alg" if you want to use the MsatAllele algorithm or the name of the data.frame returned by call to DefBinLim for the corresponding locus, if you want to use manually defined bin limits
file	the name of the file to output, don't use extensions. It defaults to "MLG table"

Details

Start by producing the data.frame Mtable that specifies which method to use when writting the multilocus genotypes. If you have previously defined manually bin limits you will need to provide the names of the objects that contain them in the second column of the Mtable argument (don't forget to use quotes). If you want to write all loci with the automatic method simply provide a second column filled with "Alg" for all loci.

Value

The function writes two files, with one and two columns per locus format.

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles *Journal of Heredity*. 100(3):394,397

See Also

[write.PG.file.loc](#), [write.PG.file.all](#)

Examples

```
data(DBase)
#In this example I am only using the automatic method
#To use manually defined bins replace the respective
# "Alg" by the name of the resulting obecjet from the
#DefBinLim function, don't forget to use quotes around
#the object name
MethodTab<-data.frame(Marker=unique(DBase$Marker),Method=c("Alg","Alg","Alg","Alg","Alg"))
write.data(DBase,Mtable=MethodTab)
```

write.PG.file.all	<i>Writes a file with the bin codes with one column per allele</i>
-------------------	--

Description

Writes a file in the working directory. Uses the information on the database to write a file in the appropriate format for most population genetics analysis software. The output format has one allele per column.

Usage

```
write.PG.file.all(DB, refDB = DB, outfile = "Population genetics file.txt")
```

Arguments

DB	A data base of the type used by this package, like the generated by transDB function
refDB	A larger data set for optimal reference during the allele coding
outfile	A name for the output file

Details

The algorithm implemented searches the database for all observed fragments within the interval set by -0.8 to + 0.8 bp of the fragment. It proceeds to detect breaks in the distribution of observed distribution to find the distribution where the fragment belongs. To get the allele code the median of that distribution is rounded to an integer value.

Value

A table is written into the working directory (.PG.txt file) with the first column having the sample names and every subsequent column the information for alleles. Alleles of a locus are given in two columns. There is also a file written with the counts for the number of fragments for each combination of locus and sample (AC.txt file), remember that there should be only a maximum of 2 for this value, otherwise the code will write the first two fragments scored to build the genotype

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles Journal of Heredity. 100(3):394,397

See Also

[write.PG.file.loc](#), [read.ah.file](#)

Examples

```
data(DBase)
write.PG.file.all(DBase)
```

write.PG.file.loc	<i>Writes a file with the bin codes with one column per locus</i>
-------------------	---

Description

Writes a file in the working directory. Uses the information on the database to write a file in the appropriate format for most population genetics analysis software. The output format has one locus per column.

Usage

```
write.PG.file.loc(DB, refDB = DB, outfile = "Population genetics file.txt")
```

Arguments

DB	A data base of the type used by this package, like the generated by transDB function
refDB	A larger data set for optimal reference during the allele coding
outfile	A name for the output file

Details

The algorithm implemented searches the database for all observed fragments within the interval set by -0.8 to + 0.8 bp of the fragment. It proceeds to detect breaks in the distribution of observed distribution to find the distribution where the fragment belongs. To get the allele code the median of that distribution is rounded to an integer value.

Value

A table is written into the working directory (.PG.txt file) with the first column having the sample names and every subsequent column the information for the loci. Both alleles of a locus are given in the same column (i.e. one column per locus). There is also a file written with the counts for the number of fragments for each combination of locus and sample (AC.txt file), remember that there should be only a maximum of 2 for this value, otherwise the code will write the first two fragments scored to build the genotype

Author(s)

Filipe Alberto

References

Alberto F. MsatAllele_1.0: an R package to visualize the binning of microsatellite alleles *Journal of Heredity*. 100(3):394,397

See Also

[write.PG.file.all](#), [read.ah.file](#)

Examples

```
data(DBase)
write.PG.file.loc(DBase)
```

Index

- * **IO**
 - read.ah.file, 14
 - read.frag.sizes, 15
 - write.PG.file.all, 21
 - write.PG.file.loc, 22
- * **aplot**
 - mark.bins, 12
- * **datasets**
 - DBase, 7
 - DBZn, 7
 - InputFile, 11
 - STRandOUT, 17
- * **hplot**
 - AlleleCum, 3
 - AlleleHist, 4
 - restrict.hist, 16
- * **manip**
 - bin.limits, 5
 - DefBinLim, 8
 - get.allele, 9
 - getpoints, 10
 - OrderByLocus, 13
 - subdataBase, 18
 - transDB, 19
 - write.data, 20
- * **package**
 - MsatAllele-package, 2
- * **univar**
 - BinStat, 6

AlleleCum, 3, 8, 9, 11, 16, 19

AlleleHist, 4, 4, 14, 15, 17, 19

bin.limits, 5, 12

BinStat, 6

DBase, 7

DBZn, 7

DefBinLim, 8, 20

get.allele, 9

getpoints, 10

InputFile, 11

mark.bins, 12

MsatAllele (MsatAllele-package), 2

MsatAllele-package, 2

OrderByLocus, 13

read.ah.file, 5, 14, 16, 22, 23

read.frag.sizes, 15

restrict.hist, 4, 5, 15, 16

STRandOUT, 17

subdataBase, 10, 11, 14–17, 18

transDB, 19, 20–22

write.data, 20

write.PG.file.all, 21, 21, 23

write.PG.file.loc, 5, 10, 21, 22, 22