Package ‘CAnD’

April 12, 2022

Type Package

Title Perform Chromosomal Ancestry Differences (CAnD) Analyses

Version 1.26.0

Date 2016-01-20

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Imports methods, ggplot2, reshape

Suggests RUnit, BiocGenerics, BiocStyle

Description Functions to perform the CAnD test on a set of ancestry proportions. For a particular ancestral subpopulation, a user will supply the estimated ancestry proportion for each sample, and each chromosome or chromosomal segment of interest. A p-value for each chromosome as well as an overall CAnD p-value will be returned for each test. Plotting functions are also available.

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biocViews Genetics, StatisticalMethod, GeneticVariability, SNP

git_url https://git.bioconductor.org/packages/CAnD

git_branch RELEASE_3_14

git_last_commit b8a49be

git_last_commit_date 2021-10-26

Date/Publication 2022-04-12

R topics documented:

`ancestries` *Sample Chromosomal Proportions of Ancestral Subpopulations to Use for CAnD Testing*

Description

This dataset provides simulated ancestral proportions by chromosomes for 50 samples. The samples are assumed to have three different ancestral proportions, denoted by `Euro_`, `Afr_` and `Asian_`. Furthermore, these proportions are included as averages across each chromosome 1-22 and the X chromosome.

Usage

```
ancestries
```

Format

A data.frame containing 50 rows and 70 columns:

IID	unique sample id
Euro_AA	simulated proportion European ancestry on each chromosome, where `AA` ranges from 1-22, X
Afr_AA	simulated proportion African ancestry on each chromosome, where `AA` ranges from 1-22, X
Asian_AA	simulated proportion Asian ancestry on each chromosome, where `AA` ranges from 1-22, X

Value

A character value of the name of the dataset.

`barPlotAncest` *Create a Barplot of Ancestry Proportion Estimates for Every Sample and a Given Chromosome or Chromosomal Region*

Description

Plots ancestry proportion estimates for each sample

Usage

```
barPlotAncest(set, order = TRUE, title = "", xlab = "Sample",
  ylab = "Ancestry Proportion", ...)
```

Arguments

`set`	A `data.frame` with columns of the proportion ancestry for a given chromosome or chromosomal region, and one row per sample (bar).
`order`	A `logical` argument determining whether the samples should be ordered in increasing proportion of the first ancestry. Default is TRUE.
`title`	A character string containing the title of the plot. Default is "", a blank title.
`xlab`	A character vector with the label for the x-axis on the plot. Default is `Sample`.
`ylab`	A character vector holding the label for the y-axis on the plot. Default is `Ancestry Proportion`.
`...`	Further arguments to be passed to the plotting methods, such as graphical parameters.

Details

Creates a barplot of ancestry proportions for each sample for a given chromosome or chromosomal region.

Value

Creates a plot.

Author(s)

Caitlin McHugh `<mchughc@uw.edu>`

Examples

```
data(ancestries)
chr1 <- ancestries[,c("Euro_1","Afr_1","Asian_1")]
#barPlotAncest(chr1,title="Chr 1 Ancestry Proportions")
```

`BonfCorr-methods` ~~ *Methods for Function* `BonfCorr` ~~

Description

This function returns whether the Bonferroni multiple testing correction was applied in calculating the final p-values by chromosome/chromosomal segment.

Usage

```
BonfCorr(object)
```

Arguments

`object`	An object of type `CAnDResult`

Value

A logical indicator of whether the Bonferroni multiple testing correction was used.

Methods

Defined methods include:

Returns the whether the Bonferroni multiple testing correction was applied in calculating the final p-values for a `CAnD` object

Author(s)

`signature(object = "CAnD")` Caitlin McHugh

See Also

`CAnDResult`-class

Examples

```
data(ancestries)
BonfCorr( CAnD(ancestries[,c(2:5)]) )
```

`calc_combP` *Calculate the Combined CAnD Test Statistic P-value*

Description

Calculate the combined CAnD test statistic p-value on a set of ancestry proportions estimated for a particular ancestral subpopulation of interest

Usage

```
calc_combP(chrAncest)
```

Arguments

`chrAncest`	A data.frame holding the ancestral proportions; each row corresponds to a sample and each column corresponds to a chromosomal/chromosomal segment ancestry proportion. Note: only include the proportions for one ancestral population at a time.

Value

A `vector` of length two where 'statistic' is the combined CAnD statistic and 'pvalue' is it's corresponding p-value, where the combined statistic is combined over all chromosomes/chromosomal segments included in `chrAncest`.

Author(s)

Caitlin McHugh <`mchughc@uw.edu`>

References

McHugh, C., Brown, L., Thornton, T. Detecting heterogeneity in population structure across the genome in admixed populations. Genetics, 2016.

Examples

```
data(ancestries)
euroCols <- grep("Euro",colnames(ancestries))
euro <- ancestries[,euroCols]
res <- calc_combP(euro)
res
```

`CAnD` *Peform the CAnD Test*

Description

Perform the CAnD test on a set of ancestry proportions estimated for a particular ancestral subpopulation of interest

Usage

```
CAnD(chrAncest, bonfCorr = TRUE)
```

Arguments

`chrAncest`	A data.frame holding the ancestral proportions; each row corresponds to a sample and each column corresponds to a chromosomal/chromosomal segment ancestry proportion. Note: only include the proportions for one ancestral population at a time.
`bonfCorr`	A logical argument indicating whether the p-value should be corrected for multiple testing using Bonferroni correction. The default is `TRUE`.

Value

A `CAnDResult` object holding the p-value for each chromosome/chromosomal segment, the overall CAnD p-value, the CAnD statistic and whether the Bonferroni multiple testing correction was used.

Author(s)

Caitlin McHugh <`mchughc@uw.edu`>

References

McHugh, C., Brown, L., Thornton, T. Detecting heterogeneity in population structure across the genome in admixed populations. Genetics, 2016.

Examples

```
data(ancestries)
euroCols <- grep("Euro",colnames(ancestries))
euro <- ancestries[,euroCols]
res <- CAnD(euro)
res
```

`CAnDResult-class` *Class* `"CAnDResult"`

Description

Objects of this class store results from running CAnD methods.

Objects from the Class

Objects can be created by calls of `nonParam_CAnD` or `CAnD`.

Slots

- `test`: Object of class `"character"`, the type of CAnD test performed
- `pValues`: Object of class `"numeric"`, the p-values for each chromosome/chromosomal segment tested
- `overallStatistic`: Object of class `"numeric"`, the overall CAnD test statistic for the set
- `overallpValue`: Object of class `"numeric"`, the overall p-value for the set
- `BonfCorr`: Object of class `"logical"`, whether Bonferroni multiple testing correction was applied to the p-values for each chromosome/chromosomal segment tested

Methods

No methods defined with class "CAnDResult" in the signature.

Author(s)

Caitlin McHugh

Examples

```
showClass("CAnDResult")
```

`getDiffMatrices` *Calculate the Mean Ancestry Proportion Excluding Each Chromosome/Chromosomal Segment in Turn*

Description

A helper function to calculate the mean ancestry proportion for a given subpopulation, excluding each chromosome/chromosomal segment in turn.

Usage

```
getDiffMatrices(chrAncest, diff = TRUE)
```

Arguments

`chrAncest`	A data.frame holding the ancestral proportions; each row corresponds to a sample and each column corresponds to a chromosomal/chromosomal segment ancestry proportion. Note: only include the proportions for one ancestral population at a time.
`diff`	A logical argment indicating whether the difference between the pooled mean and the chromosomal mean should be returned, or whether simply the pooled mean should be returned.

Details

This function calculates the mean ancestry proportion of a given subpopulation excluding each chromosome in turn.

Value

A matrix of chromosomal ancestry differences.

Author(s)

Caitlin McHugh `<mchughc@uw.edu>`

`overallpValue-methods` ~~ *Methods for Function* `overallpValue` ~~

Description

This function returns the CAnD test p-value from performing a CAnD test on a set of ancestral proportions.

Usage

```
overallpValue(object)
```

Arguments

`object`	An object of type `CAnDResult`

Value

The CAnD p-value.

Methods

Defined methods include:

Returns the CAnD test p-value from applying the CAnD test to a set of ancestral proportions for a `CAnD` object

Author(s)

`signature(object = "CAnD")` Caitlin McHugh

See Also

`CAnDResult`-class

Examples

```
data(ancestries)
overallpValue( CAnD(ancestries[,c(2:5)]) )
```

`overallStatistic-methods`

~~ Methods for Function `overallStatistic` ~~

Description

This function returns the calculated CAnD test statistic from applying the CAnD test to a set of ancestral proportions.

Usage

```
overallStatistic(object)
```

Arguments

`object`	An object of type `CAnDResult`

Value

The CAnD test statistic stored in the object.

Methods

Defined methods include:

Returns the statistic calculated from performing the CAnD test on a set of ancestral proportions for a `CAnD` object

Author(s)

`signature(object = "CAnD")` Caitlin McHugh

See Also

`CAnDResult`-class

Examples

```
data(ancestries)
overallStatistic( CAnD(ancestries[,c(2:5)]) )
```

`plotPvals` *Create a Plot of P-Values for Each Chromosome or Chromosomal Region*

Description

Plots CAnD p-values for each chromosome/chromosomal region

Usage

```
plotPvals(set, title = "", xlab = "Chromosome", ylab = "-log10(PValue)",
  ...)
```

Arguments

`set`	An object of class `CAnDResult`.
`title`	A character string containing the title of the plot. Default is "", a blank title.
`xlab`	A character vector with the label for the x-axis on the plot. Default is `Chromosome`.
`ylab`	A character vector holding the label for the y-axis on the plot. Default is `-log10(Bonferroni PValue)` or `-log10(PValue)`, depending on whether Bonferroni correction was used.
`...`	Further arguments to be passed to the plotting methods, such as graphical parameters.

Details

Creates a plot of all p-values for each chromosome or chromosomal region.

Value

Creates a plot.

Author(s)

Caitlin McHugh `<mchughc@uw.edu>`

Examples

```
data(ancestries)
euroEsts <- ancestries[,c(seq(from=2,to=24))]
res <- CAnD(euroEsts)
#plotPvals(res,main="CAnD P-Values")
```

`pValues-methods` ~~ *Methods for Function* `pValues` ~~

Description

This function returns each p-value calculated from the CAnD test on all chromosomes/chromosomal segments.

Usage

```
pValues(object)
```

Arguments

`object`	An object of type `CAnDResult`

Value

A vector of p-values from the CAnD test.

Methods

Defined methods include:

Returns the p-values for each chromosome/chromosomal segment calculated using the CAnD test for a `CAnD` object

Author(s)

`signature(object = "CAnD")` Caitlin McHugh

See Also

CAnDResult-class

Examples

```
data(ancestries)
pValues( CAnD(ancestries[,c(5:12)]) )
```

`test-methods` *~~ Methods for Function* `test` *~~*

Description

This function returns the type of CAnD test applied to a set of ancestral proportions.

Usage

```
test(object)
```

Arguments

`object`	An object of type `CAnDResult`

Value

'Parametric.' Note the non-parametric CAnD test is defunct now.

Methods

Defined methods include:

Returns the type of CAnD test applied to calculate the p-values for a `CAnD` object

Author(s)

`signature(object = "CAnD")` Caitlin McHugh

See Also

CAnDResult-class

Examples

```
data(ancestries)
test( CAnD(ancestries[,c(2:5)]) )
```

Index