

# Package ‘CAnD’

October 17, 2017

**Type** Package

**Title** Perform Chromosomal Ancestry Differences (CAnD) Analyses

**Version** 1.8.0

**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.

**License** Artistic-2.0

**biocViews** Genetics, StatisticalMethod, GeneticVariability, SNP

**NeedsCompilation** no

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ancestries	<i>Sample Chromosomal Proportions of Ancestral Subpopulations to Use for CAnD Testing</i>
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### 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.

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barPlotAncest	<i>Create a Barplot of Ancestry Proportion Estimates for Every Sample and a Given Chromosome or Chromosomal Region</i>
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### 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 its 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

*Perform the CAnD Test*

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### 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	<i>Class "CAnDResult"</i>
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### 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")
```

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getDiffMatrices	<i>Calculate the Mean Ancestry Proportion Excluding Each Chromosome/Chromosomal Segment in Turn</i>
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### 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 argument 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
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**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)]) )
```



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plotPvals	<i>Create a Plot of P-Values for Each Chromosome or Chromosomal Region</i>
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---

**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 $-\log_{10}(\text{Bonferroni PValue})$ or $-\log_{10}(\text{PValue})$ , 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)]) )
```

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