

# Package ‘windex’

January 27, 2015

**Type** Package

**Title** windex: Analysing convergent evolution using the Wheatsheaf index

**Version** 1.0

**Date** 2014-09-05

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**Description** Analysing convergent evolution using the Wheatsheaf index.

**License** GPL-2

**Depends** geiger (>= 2.0), ape, scatterplot3d, utils, R (>= 3.0.0)

**NeedsCompilation** no

**Repository** CRAN

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windex-package

*windex: Analysing convergent evolution using the Wheatsheaf index*

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## Description

Functions to calculating the Wheatsheaf index of the strength of convergent evolution and testing whether this represents stronger convergence than expected.

## Details

Package: windex  
Type: Package  
Version: 1.0  
Date: 2014-07-02  
License: GPL2.0

There are three main functions in the package. The first, `plot.trait`, gives a visual representation of the data although the plot does not account for phylogeny and so is only intended for (very rough-scale) visual data exploration. The second, `windex`, is the core function of the package. This takes a phylogenetic tree of class `'phylo'` and a dataset and calculates the Wheatsheaf index of convergent evolution along with jackknived 95% confidence intervals. The third function, `test.windex`, runs the `windex` function but also performs bootstrapped randomisations of the tips in the tree to generate a null distribution. This distribution is then used to test whether the calculated value of the Wheatsheaf index represents stronger convergence than is expected given the topological constraints of the tree. The datasets required for these functions must have the first column called `'species'` and containing a list of species names that match those in the phylogenetic tree. One other column must be a vector denoting which species are part of the focal group (1) and which are in the non-focal group (0). Remaining columns contain values of traits that can be quantified (often continuous traits but see Arbuckle et al., 2014 for other examples).

## Author(s)

Kevin Arbuckle and Amanda Minter

Maintainer: Kevin Arbuckle <k.arbuckle@liverpool.ac.uk>

## References

Arbuckle, K., Bennett, C.M. and Speed, M.P. 2014. A simple measure of the strength of convergent evolution. *Methods in Ecology and Evolution* 5:685 - 693. This citation is for the method, there is currently a manuscript being prepared to describe this package.

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plotTrait	<i>Provides a visualisation of up to three-dimensional trait space (not accounting for phylogeny) for data exploration</i>
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**Description**

Plots the trait space occupied by up to 3 traits with focals highlighted in red.

**Usage**

```
plotTrait(dat, traits, focal = dat[, 2])
```

**Arguments**

dat	A dataframe containing a column of 0s and 1s to denote non-focal and focal taxa respectively, and columns of trait data which you which to plot.
traits	Column numbers (or names) for 1-3 traits which you want to plot.
focal	Column in the dataframe containing the focal designations.

**Author(s)**

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**References**

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**Examples**

```
data(sample.data)  
plotTrait(sample.data, c("ou1", "ou2"), focal=sample.data[, 2])
```

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sample.data	<i>Sample data for windex</i>
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**Description**

Simulated data in a format suitable for use with the functions in the windex package.

**Usage**

```
data(sample.data)
```

**Format**

A data frame with 100 observations on the following 9 variables.

species a factor  
focals a numeric vector  
bm1 a numeric vector  
bm2 a numeric vector  
bm3 a numeric vector  
ou1 a numeric vector  
ou2 a numeric vector  
ou3 a numeric vector  
bin a numeric vector

**Details**

The three 'bm' columns are values for three trait that have not evolved convergently. The three 'ou' columns are values for three traits that have evolved convergently with respect to the focal designation. bin is a column that was only for utility when creating the dataset.

**Examples**

```
dat<-data(sample.data)
summary(dat)
```

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sample.tree

*Phylogenetic tree to accompany sample.data*

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**Description**

A simulated phylogeny from which the sample.data dataset was simulated, for use with the functions in the windex package.

**Usage**

```
data(sample.tree)
```

**Format**

Phylogenetic tree of the class 'phylo' with 100 tips and (ultrametric) branch lengths.

**Examples**

```
data(sample.tree)
summary(sample.tree)
plot(sample.tree)
```

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test.windex	<i>Calculates P-value for the strength of convergent evolution</i>
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### Description

The P-value returned is for the null hypothesis that the calculated Wheatsheaf index is no higher than expected by chance given the topology of the phylogenetic tree. Note that this is not a test for convergence per se, but of whether the convergence is unusually strong.

### Usage

```
test.windex(dat, tree, traits, focal = dat[, 2], SE = TRUE, reps,
plot = TRUE, ...)
```

### Arguments

dat	A dataframe containing a column of 0s and 1s to denote non-focal and focal taxa respectively, and columns of trait data which you which to plot. The first column must be named 'species' and contain species names that correspond to those in the phylogenetic tree.
tree	Phylogenetic tree of class 'phylo' containing branch lengths. The tree should also be ultrametric.
traits	Column numbers (or names) for the traits for which you want to calculate a Wheatsheaf index.
focal	Column in the dataframe containing the focal designations.
SE	A logical specifying whether to standardise the traits by their standard error across species, default is SE=FALSE.
reps	Number of bootstrap replicates on which to base the P-value.
plot	A logical indicating whether to plot the bootstrap distribution. If TRUE, a histogram is plotted with the calculated Wheatsheaf index and it's 95% confident interval overlaid on the histogram as a solid and dashed lines (respectively).
...	Additional arguments passed to hist() to customise the histogram (when plot=TRUE).

### Value

P-value	P-value from bootstrapping the tips of the phylogenetic tree
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### Author(s)

Kevin Arbuckle and Amanda Minter

### References

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**See Also**[windex](#)**Examples**

```
## Not run: data(sample.data)
data(sample.tree)
test.windex(sample.data,sample.tree,traits=c("bm1","bm2"),focal=sample.data[,2],
reps=1000,plot=TRUE,col="light grey")
## End(Not run)
```

windex

*Calculates Wheatsheaf index with 95% confidence intervals***Description**

Takes a phylo object and trait data and returns the Wheatsheaf index for the traits on the tree along with 95% confidence intervals obtained from jackkniving.

**Usage**

```
windex(dat, tree, traits, focal = dat[, 2], SE = FALSE)
```

**Arguments**

dat	A dataframe containing a column of 0s and 1s to denote non-focal and focal taxa respectively, and columns of trait data which you which to plot. The first column must be named 'species' and contain species names that correspond to those in the phylogenetic tree.
tree	Phylogenetic tree of class 'phylo' containing branch lengths. The tree should also be ultrametric.
traits	Column numbers (or names) for the traits for which you want to calculate a Wheatsheaf index.
focal	Column in the dataframe containing the focal designations.
SE	A logical specifying whether to standardise the traits by their standard error across species, default is SE=FALSE.

**Value**

Wheatsheaf Index	Calculated Wheatsheaf index
Lower 95% CI	lower bound of 95% confidence interval for the Wheatsheaf index obtained by jackkiving
Upper 95% CI	Upper bound of 95% confidence interval for the Wheatsheaf index obtained by jackkiving

**Author(s)**

Kevin Arbuckle and Amanda Minter

**References**

Arbuckle, K., Bennett, C.M. and Speed, M.P. 2014. A simple measure of the strength of convergent evolution. *Methods in Ecology and Evolution* 5:685 - 693. This citation is for the method, there is currently a manuscript being prepared to describe this package.

**See Also**

[test.windex](#)

**Examples**

```
data(sample.data)
data(sample.tree)
windex(sample.data,sample.tree,traits=c("ou1","ou2"),focal=sample.data[,2],
SE=FALSE)
```

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