

# Package ‘Rphylip’

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**Title** Rphylip: An R interface for PHYLIP

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**Depends** R (>= 2.10), ape (>= 3.0-10)

**ZipData** no

**Description** Rphylip provides an R interface for the PHYLIP package. All users of Rphylip will thus first have to install the PHYLIP phylogeny methods program package (Felsenstein 2013). See <http://evolution.genetics.washington.edu/phylip.html> for more information about installing PHYLIP.

**License** GPL (>= 2)

**URL** <http://www.phytools.org/Rphylip>

**Repository**

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## R topics documented:

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|                 |   |
|-----------------|---|
| Rphylip-package | <i>Rphylip: An R interface for PHYLIP</i> |
|-----------------|---|

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## Description

**Rphylip** provides an R interface for programs in the PHYLIP phylogeny methods package (Felsenstein 2013).

## Details

The complete list of functions can be displayed with `library(help = Rphylip)`.

Obviously, before any of the functions of this package can be used, users must first install PHYLIP (Felsenstein 2013). More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

More information on **Rphylip** can be found at <http://www.phytools.org/Rphylip/> or <http://blog.phytools.org>.

## Author(s)

Liam J. Revell

Maintainer: Liam J. Revell <liam.revell@umb.edu>

## References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

Revell, L. J. (2013) Rphylip: An R interface for PHYLIP. R package version x-y.z.

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|            |                                       |
|------------|---------------------------------------|
| opt.Rdnaml | <i>Parameter optimizer for Rdnaml</i> |
|------------|---------------------------------------|

---

## Description

This function is an wrapper for `Rdnaml` that attempts to optimize `gamma` (the alpha shape parameter of the gamma model of rate heterogeneity among sites), `kappa` (the transition:transversion ratio), and `bf` (the base frequencies).

## Usage

```
opt.Rdnaml(X, path=NULL, ...)
```

## Arguments

|                   |   |
|-------------------|---|
| <code>X</code>    | an object of class "DNAbin".  |
| <code>path</code> | path to the executable containing <code>dnaml</code> . If <code>path = NULL</code> , the R will search several commonly used directories for the correct executable file. |
| <code>...</code>  | optional arguments. See details for more information.   |

**Details**

Optional arguments include the following: `tree` fixed tree to use in optimization - if not provided, it will be estimated using `Rdnaml` under the default conditions; `bounds` a list with bounds for optimization - for `kappa` and `gamma` this should be a two-element vector, whereas for `bf` this should be a 4 x 2 matrix with lower bounds in column 1 and upper bounds in column 2.

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

**Value**

This function returns a list with the following components: `kappa`, `gamma`, `bf` (see Details), and `logLik` (the log-likelihood of the fitted model).

**Author(s)**

Liam Revell <[liam.revell@umb.edu](mailto:liam.revell@umb.edu)>

**References**

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

**See Also**

`opt.Rdnaml`

**Examples**

```
## Not run:
data(primates)
fit<-opt.Rdnaml(primates,bounds=list(kappa=c(0.1,40))
tree<-Rdnaml(primates,kappa=fit$kappa,gamma=fit$gamma,bf=fit$bf)

## End(Not run)
```

---

primates

*Example DNA dataset from primates*

---

**Description**

An object of class "DNAbin" containing nucleotide sequence data of mysterious origin for 12 species of primates.

**Usage**

```
data(primates)
```

**Format**

The data are stored as a modified object "DNAbin".

**Source**

Unknown.

---

Rcontml

*R interface for contml*


---

**Description**

This function is an R interface for contml in the PHYLIP package (Felsenstein 2013). contml can be used for ML phylogeny estimation from gene frequency data or continuous characters. The continuous characters should be rotated so as to be uncorrelated before analysis.

**Usage**

```
Rcontml(X, path=NULL, ...)
```

**Arguments**

|      |   |
|------|---|
| X    | either (a) a <i>matrix</i> of continuous valued traits (in columns) with rownames containing species names; or (b) a list of matrices in which each row contains the relative frequency of alleles at a locus for a species. In the latter case the rownames of each matrix in the list should contain the species names. |
| path | path to the executable containing contml. If path = NULL, the R will search several commonly used directories for the correct executable file.  |
| ...  | optional arguments to be passed to contml. See details for more information.  |

**Details**

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); tree object of class "phylo" - if supplied, then the model will be optimized on a fixed input topology; global perform global search (defaults to global = TRUE); random.order add taxa to tree in random order (defaults to random.order = TRUE); random.addition number of random addition replicates for random.order = TRUE (defaults to random.addition = 10); outgroup outgroup if outgroup rooting of the estimated tree is desired; and cleanup remove PHYLIP input/output files after the analysis is completed (defaults to cleanup = TRUE).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

**Value**

This function returns an object of class "phylo" that is the optimized tree.

**Author(s)**

Liam Revell <[liam.revell@umb.edu](mailto:liam.revell@umb.edu)>

**References**

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

**See Also**

Rdnaml

---

Rcontrast

*R interface for contrast*

---

**Description**

This function is an R interface for contrast in the PHYLIP package (Felsenstein 2013). contrast can be used to perform the among species phylogenetically independent contrasts method of Felsenstein (1985) and the within & among species method of Felsenstein (2008).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

**Usage**

```
Rcontrast(tree, X, path=NULL, ...)
```

**Arguments**

|      |   |
|------|---|
| tree | object of class "phylo".  |
| X    | a <i>matrix</i> of continuous valued traits (in columns) with rownames containing species names. For within-species contrasts analysis, the matrix should contain repeating (identical) row names for conspecifics. |
| path | path to the executable containing contrast. If path = NULL, the R will search several commonly used directories for the correct executable file.  |
| ...  | optional arguments to be passed to contrast. See details for more information.  |

**Details**

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); and cleanup remove PHYLIP input/output files after the analysis is completed (defaults to cleanup = TRUE).

**Value**

This function returns an object of class "phylo" that is the optimized tree.

**Author(s)**

Liam Revell <[liam.revell@umb.edu](mailto:liam.revell@umb.edu)>

**References**

Felsenstein, J. (1985) Phylogenies and the comparative method. *American Naturalist*, 125, 1-15.

Felsenstein, J. (2008) Comparative methods with sampling error and within-species variation: Contrasts revisited and revised. *American Naturalist*, 171, 713-725.

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

**See Also**

pic

Rdnadist

*R interfaces for dnadist***Description**

This function is an R interface for dnadist in the PHYLIP package (Felsenstein 2013). dnadist can be used to estimate the evolutionary distances between DNA sequences under various models.

**Usage**

```
Rdnadist(X, method=c("F84", "K80", "JC", "LogDet"), path=NULL, ...)
```

**Arguments**

|        |  |
|--------|--|
| X      | an object of class "DNABin".   |
| method | method for calculating the distances. Can be "F84" (Kishino & Hasegawa 1989; Felsenstein & Churchill 1996), "K80" (Kimura 1980), "JC" (Jukes & Cantor 1969), or "LogDet" (Barry & Hartigan 1987; Lake 1994; Steel 1994; Lockhart et. al. 1994). Also method="similarity" computes the sequence similarity among the rows of X. |
| path   | path to the executable containing dnadist. If path = NULL, the R will search several commonly used directories for the correct executable file.  |
| ...    | optional arguments to be passed to dnadist. See details for more information.  |

**Details**

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); gamma alpha shape parameter of a gamma model of rate heterogeneity among sites (defaults to no gamma rate heterogeneity); kappa transition:transversion ratio (defaults to kappa = 2.0); rates vector of rates (defaults to single rate); rate.categories vector of rate categories corresponding to the order of rates; weights vector of weights of length equal to the number of columns in X (defaults to unweighted); bf vector of base frequencies in alphabetical order (i.e., A, C, G, & T) - if not provided, then defaults to empirical frequencies; and cleanup remove PHYLIP input & output files after the analysis is completed (defaults to cleanup = TRUE).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

**Value**

This function returns an object of class "dist".

**Author(s)**

Liam Revell <[liam.revell@umb.edu](mailto:liam.revell@umb.edu)>

## References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

## See Also

Rneighbor

## Examples

```
## Not run:
data(primates)
D<-Rdnadist(primates,kappa=10)
tree<-Rneighbor(D)

## End(Not run)
```

---

Rdnaml

*R interfaces for dnaml and dnamlk*


---

## Description

This function is an R interface for dnaml in the PHYLIP package (Felsenstein 2013). dnaml can be used for ML phylogeny estimation from DNA sequences.

## Usage

```
Rdnaml(X, path=NULL, ...)
Rdnamlk(X, path=NULL, ...)
```

## Arguments

|      |   |
|------|---|
| X    | an object of class "DNABin".  |
| path | path to the executable containing dnaml. If path = NULL, the R will search several commonly used directories for the correct executable file. |
| ...  | optional arguments to be passed to dnaml or dnamlk. See details for more information.   |

## Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); tree object of class "phylo" - if supplied, then the model will be optimized on a fixed input topology; kappa transition:transversion ratio (defaults to kappa = 2.0); bf vector of base frequencies in alphabetical order (i.e., A, C, G, & T) - if not provided, then defaults to empirical frequencies; rates vector of rates (defaults to single rate); rate.categories vector of rate categories corresponding to the order of rates; gamma alpha shape parameter of a gamma model of rate heterogeneity among sites (defaults to no gamma rate heterogeneity); ncat number of rate categories for the gamma model; inv proportion of invariant sites for the invariant sites model (defaults to inv = 0); weights vector of weights of length equal to the number of columns in X (defaults to unweighted); speedier speedier but rougher analysis (defaults to speedier = FALSE); global perform global search (defaults to global = TRUE);

`random.order` add taxa to tree in random order (defaults to `random.order = TRUE`); `random.addition` number of random addition replicates for `random.order = TRUE` (defaults to `random.addition = 10`); `outgroup` outgroup if outgroup rooting of the estimated tree is desired; and `cleanup` remove PHYLIP input & output files after the analysis is completed (defaults to `cleanup = TRUE`).

Finally `clock=TRUE` enforces a molecular clock. The argument `clock` is only available for `Rdnaml`. If `clock=TRUE` then `dnamlk` is used internally. For `Rdnamlk` a molecular clock is assumed, thus `Rdnaml(..., clock=TRUE)` and `Rdnamlk(...)` are equivalent.

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

### Value

This function returns an object of class "phylo" that is the optimized tree.

### Author(s)

Liam Revell <[liam.revell@umb.edu](mailto:liam.revell@umb.edu)>

### References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

### See Also

`opt.Rdnaml`, `Rcontml`

### Examples

```
## Not run:
data(primates)
tree<-Rdnaml(primates,kappa=10)
clockTree<-Rdnamlk(primates,kappa=10)

## End(Not run)
```

---

Rdnapars

*R interface for dnapars*

---

### Description

This function is an R interface for `dnapars` in the PHYLIP package (Felsenstein 2013). `dnapars` can be used for MP phylogeny estimation from DNA sequences.

### Usage

```
Rdnapars(X, path=NULL, ...)
```



**Arguments**

|                   |   |
|-------------------|---|
| <code>X</code>    | an object of class "DNABin".  |
| <code>path</code> | path to the executable containing dnapars. If <code>path = NULL</code> , the R will search several commonly used directories for the correct executable file. |
| <code>...</code>  | optional arguments to be passed to dnapars. See details for more information.   |

**Details**

Optional arguments include the following: `quiet` suppress some output to R console (defaults to `quiet = FALSE`); `tree` object of class "phylo" - if supplied, then the parsimony score will be computed on a fixed input topology; `thorough` logical value indicating whether to conduct a more thorough search (defaults to `thorough=TRUE`); `nsave` number of trees to save if multiple equally parsimonious trees are found (defaults to `nsave=10000`); `random.order` add taxa to tree in random order (defaults to `random.order = TRUE`); `random.addition` number of random addition replicates for `random.order = TRUE` (defaults to `random.addition = 10`); `threshold` threshold value for threshold parsimony (defaults to ordinary parsimony); `transversion` logical value indicating whether to use transversion parsimony (defaults to `transversion=FALSE`); `weights` vector of weights of length equal to the number of columns in `X` (defaults to `unweighted`); `outgroup` outgroup if outgroup rooting of the estimated tree is desired; and `cleanup` remove PHYLIP input & output files after the analysis is completed (defaults to `cleanup = TRUE`).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

**Value**

This function returns an object of class "phylo" that is the optimized tree.

**Author(s)**

Liam Revell <[liam.revell@umb.edu](mailto:liam.revell@umb.edu)>

**References**

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

**See Also**

`Rdnaml`

**Examples**

```
## Not run:
data(primates)
tree<-Rdnapars(primates)

## End(Not run)
```

---

Rdnapenny

*R interface for dnapenny*


---

## Description

This function is an R interface for dnapenny in the PHYLIP package (Felsenstein 2013). dnapenny performs branch & bound parsimony searching following Hendy & Penny (1982).

## Usage

```
Rdnapenny(X, path=NULL, ...)
```

## Arguments

|      |  |
|------|--|
| X    | an object of class "DNABin".   |
| path | path to the executable containing dnapenny. If path = NULL, the R will search several commonly used directories for the correct executable file. |
| ...  | optional arguments to be passed to dnapenny. See details for more information.   |

## Details

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); groups number of groups of 1,000 trees (defaults to groups = 10000); report reporting frequency, in numbers of trees (defaults to report = 1000); simple simple branch & bound (defaults to simple = TRUE); threshold threshold value for threshold parsimony (defaults to ordinary parsimony); weights vector of weights of length equal to the number of columns in X (defaults to unweighted); outgroup outgroup if outgroup rooting of the estimated tree is desired; and cleanup remove PHYLIP input & output files after the analysis is completed (defaults to cleanup = TRUE).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

## Value

This function returns an object of class "phylo" or "multiPhylo" that is the tree or trees with the best parsimony score. tree\$score gives the parsimony score, for "phylo" object tree.

## Author(s)

Liam Revell <[liam.revell@umb.edu](mailto:liam.revell@umb.edu)>

## References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

## See Also

Rdnaml

**Examples**

```
## Not run:
data(primates)
tree<-Rdnapenny(primates)

## End (Not run)
```

Rneighbor

*R interface for neighbor***Description**

This function is an R interface for neighbor in the PHYLIP package (Felsenstein 2013). neighbor can be used for neighbor-joining and UPGMA phylogeny inference.

**Usage**

```
Rneighbor(D, path=NULL , ...)
```

**Arguments**

|      |  |
|------|--|
| D    | a distance matrix as an object of class "matrix" or "dist". If a matrix, then D should be symmetrical with a diagonal of zeros.                  |
| path | path to the executable containing neighbor. If path = NULL, the R will search several commonly used directories for the correct executable file. |
| ...  | optional arguments to be passed to neighbor. See details for more information.   |

**Details**

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); method - can be "NJ" or "nj" (for neighbor-joining), or "UPGMA" or "UPGMA" (for UPGMA); random.order add taxa to tree in random order (defaults to random.order = TRUE); outgroup outgroup if outgroup rooting of the estimated tree is desired (only works for method = "NJ", UPGMA trees are already rooted); and cleanup remove PHYLIP input & output files after the analysis is completed (defaults to cleanup = TRUE).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

**Value**

This function returns an object of class "phylo" that is the NJ or UPGMA tree.

**Author(s)**

Liam Revell <[liam.revell@umb.edu](mailto:liam.revell@umb.edu)>

**References**

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

**See Also**

Rdnaml

**Examples**

```
## Not run:
data(primates)
D<-dist.dna(data(primates),model="JC")
tree<-Rneighbor(D)

## End(Not run)
```

Rthreshml

*R interface for threshml***Description**

This function is an R interface for threshml in the PHYLIP package (Felsenstein 2013). threshml fits the threshold model of Felsenstein (2005; 2012).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

**Usage**

```
Rthreshml(tree, X, types=NULL, path=NULL, ...)
```

**Arguments**

|       |   |
|-------|---|
| tree  | object of class "phylo".  |
| X     | a <i>matrix</i> of continuous valued traits (in columns) with rownames containing species names. For within-species contrasts analysis, the matrix should contain repeating (identical) row names for conspecifics. |
| types | character vector containing the types (e.g., "discrete", "continuous"). If types are not supplied, Rthreshml will try to figure them out.   |
| path  | path to the executable containing contrast. If path = NULL, the R will search several commonly used directories for the correct executable file.  |
| ...   | optional arguments to be passed to threshml. See details for more information.  |

**Details**

Optional arguments include the following: `quiet` suppress some output to R console (defaults to `quiet = FALSE`); `burnin` burnin generations for the MCMC; `nchain` number of chains of the MCMC; `ngen` number of generations in each chain; `proposal` variance on the proposal distribution for the MCMC; `lrtest` logical value indicating whether to conduct a likelihood-ratio test of the hypothesis that some correlations are zero (does not appear to work in the present version); and `cleanup` remove PHYLIP input/output files after the analysis is completed (defaults to `cleanup = TRUE`).

**Value**

This function returns a list containing the results from threshml.

**Author(s)**

Liam Revell <liam.revell@umb.edu>

**References**

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

**See Also**

Rcontrast

---

Rtreedist

*R interface for treedist*


---

**Description**

This function is an R interface for treedist in the PHYLIP package (Felsenstein 2013). treedist can be used to compute the distance between trees by two different methods.

**Usage**

```
Rtreedist(trees, method=c("branch.score", "symmetric"), path=NULL, ...)
```

**Arguments**

|        |   |
|--------|---|
| trees  | an object of class "multiPhylo". (Or, under rare circumstances, an object of class "phylo". See below.)   |
| method | method to compute the distance between trees. method="branch.score" is the branch score method of Kuhner & Felsenstein (1994). method="symmetric" is the symmetric distance or Robinson-Foulds distance (Bourque 1978; Robinson & Foulds 1981). |
| path   | path to the directory containing the executable treedist. If path = NULL, the R will search several commonly used directories for the correct executable file.  |
| ...    | optional arguments to be passed to treedist. See details for more information.  |

**Details**

Optional arguments include the following: quiet suppress some output to R console (defaults to quiet = FALSE); trees2 object of class "multiPhylo" or "phylo" - if two sets of trees are to be compared; rooted logical value indicating whether trees should be treated as rooted (defaults to rooted = FALSE); distances argument telling treedist which distances to compute - could be "all" (all pairwise in trees), "all.1to2" (all in trees by all in trees2), "adjacent" (adjacent species in trees only), and "corresponding" (all corresponding trees in trees and trees2); and cleanup remove PHYLIP input & output files after the analysis is completed (defaults to cleanup = TRUE).

Obviously, use of any of the functions of this package requires that PHYLIP (Felsenstein 2013) should first be installed. More information about installing PHYLIP can be found on the PHYLIP webpage: <http://evolution.genetics.washington.edu/phylip.html>.

### Value

This function returns a matrix of pairwise distances for `distances = "all"` and `distances = "all.1to2"`, or a named vector for `distances = "adjacent"` and `distances = "corresponding"`.

### Author(s)

Liam Revell <[liam.revell@umb.edu](mailto:liam.revell@umb.edu)>

### References

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

### Examples

```
## Not run:
trees<-rmtree(n=10,N=10)
D<-Rtreedist(trees,method="symmetric")

## End(Not run)
```

---

setupOSX

*Help set up PHYLIP in Mac OS X*

---

### Description

This function attempts to help set up PHYLIP on a Mac OS X machine.

### Usage

```
setupOSX(path=NULL)
```

### Arguments

`path` path to the executable containing dnaml. If `path = NULL`, the R will search several commonly used directories for the correct executable file.

### Details

This function can be used to help set up PHYLIP (<http://evolution.genetics.washington.edu/phylip.html>) following the special instructions found here: <http://evolution.genetics.washington.edu/phylip/install.html>. `setupOSX` should only be run once - when PHYLIP is first installed.

### Author(s)

Liam Revell <[liam.revell@umb.edu](mailto:liam.revell@umb.edu)>

**References**

Felsenstein, J. (2013) PHYLIP (Phylogeny Inference Package) version 3.695. Distributed by the author. Department of Genome Sciences, University of Washington, Seattle.

**Examples**

```
## Not run:  
setupOSX()  
  
## End(Not run)
```