

# 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

**License** GPL (>= 2)

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

**Repository**

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<code>opt.Rdnaml</code>	<i>Parameter optimizer for Rdnaml</i>
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## 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="." , ...)
```

**Arguments**

`X` an object of class "DNABin".

`path` path to the executable containing dnaml.

`...` 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.

**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>

**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`

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Rcontml

*R interface for contml*


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**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="." , ...)
```

**Arguments**

`X` either (a) a *matrix* 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.

`...` 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`); `root` 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`).

## Value

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

## 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

Rdnaml

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Rcontrast

*R interface for contrast*

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## 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).

## Usage

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

## Arguments

<code>tree</code>	object of class "phylo".
<code>X</code>	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.
<code>path</code>	path to the executable containing <code>contrast</code> .
<code>...</code>	optional arguments to be passed to <code>contrast</code> . 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>

## 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`

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Rdnaml

*R interface for dnaml*

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## 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="." , ...)
```

## Arguments

- |                   |   |
|-------------------|---|
| <code>X</code>    | an object of class <code>"DNAbin"</code> .                                  |
| <code>path</code> | path to the executable containing dnaml.                                    |
| <code>...</code>  | optional arguments to be passed to dnaml. 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`); `root` 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`).

## Value

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

## 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

`opt.Rdnaml`, `Rcontml`