Package ‘phylotate’

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Title Phylogenies with Annotations

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Description Functions to read and write APE-compatible phylogenetic trees in NEXUS and Newick formats, while preserving annotations.

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Suggests ape

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`phylotate-package` *Phylogenies with Annotations*

Description

phylotate provides functions that allow you to read and write NEXUS and Newick trees containing annotations, including those produced by MrBayes.

It does this by extending **ape**'s `phylo` object type with extra data members containing per-node annotation information. This information is stored in such a way that it can be manipulated easily and will survive most manipulations using standard **ape** functions (e.g. `reorder`, `chronopl`).

See the documentation for the `parse_annotated` function for more information on how annotations are stored internally.

The functions you probably want to use for most things are `read_annotated` and `write_annotated`.

Author(s)

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`finches` *NEXUS data example*

Description

A simple tree generated by MrBayes using the sequences for Darwin's finches from the example distributed with BEAST.

Usage

```
data(finches)
```

`mb_attrs` *Parse MrBayes-supplied attributes from a NEXUS file*

Description

This function takes a tree object and produces a dataframe containing attributes attached to each node by MrBayes.

Usage

```
mb_attrs(tree)
```

Arguments

`tree`	an object of type `"phylo"`

Details

The returned dataframe contains one row per node, and one column per attribute. The attributes parsed are `prob`, `prob_stddev`, `length_mean`, `length_median`, `length_95_HPD_low`, and `length_95_HPD_high`.

Attributes which are derivable from the others are not parsed (for example, the `prob_percent` attribute is not parsed, since it's `prob` times 100.

Value

A dataframe of attributes.

Author(s)

Anusha Beer <`anbeer29@gmail.com`>

See Also

`parse_annotated`, `read_annotated`

Examples

```
# Parse the example data included with this package
data(finches)
t <- parse_annotated(finches, format="nexus")

# Obtain a table of MrBayes attributes for each node
attrs <- mb_attrs(t)
```

`parse_annotated` *Parse an annotated phylogenetic tree*

Description

This function takes the given text string, containing data in either NEXUS or Newick format, and returns annotated phylogenetic trees.

Usage

```
parse_annotated(str, format="nexus")
```

Arguments

`str`	a text string, containing tree data
`format`	a format specifier; either `"nexus"` or `"newick"`

Details

The given file text is parsed and a tree object is constructed which can be used with the functions in the **ape** package. Annotations of the kind produced by, for example, MrBayes, are parsed and preserved in the returned object.

In addition to `edge`, `edge.length` and `tip.label`, two additional vectors are added. These are `node.comment` and `node.distance.comment`. These contain annotations associated with nodes and their distance values. These arrays are indexed by node number, not by edge. The reason for this is that this ensures that the object will remain in a valid state after a call to `reorder` which might change the ordering of the edge arrays without being aware of annotations. If you need to obtain annotations in edge-order, subset by the second column of the edge array.

Value

an object of type `"phylo"` or `"multiPhylo"`, augmented with node annotations.

Author(s)

Daniel Beer `<dlbeer@gmail.com>`

References

Paradis, E. Definition of Formats for Coding Phylogenetic Trees in R. `http://ape-package.ird.fr/misc/FormatTreeR_24Oct2012.pdf`

See Also

`print_annotated`, `read_annotated`, `write_annotated`, `finches`

Examples

```
# Parse the example data included with this package
data(finches)
t <- parse_annotated(finches, format="nexus")

# Obtain annotations in edge-order, rather than node-order
edge.comment <- t$node.comment[t$edge[,2]]
```

`print_annotated` *Serialize an annotated phylogenetic tree*

Description

This function takes the given tree object and returns a string representing the tree in the requested format. The difference between the `"newick"` and `"newick.named"` formats is that the former uses only node numbers in its output, whereas the latter uses the tip labels (sanitized and deduplicated if necessary).

Usage

```
print_annotated(tree, format="nexus")
```

Arguments

`tree`	a phylogentic tree, with optional annotations
`format`	a format specifier; either `"nexus"`, `"newick"`, or `"newick.named"`

Details

The tree object should be either a `"phylo"` or `"multiPhylo"` object. It may optionally be augmented with annotations, as described in the documentation for the `parse_annotated` function.

The output is a string suitable for writing to a file.

Value

a string containing a serialized tree.

Author(s)

Daniel Beer <`dlbeer@gmail.com`>

See Also

`parse_annotated`, `read_annotated`, `write_annotated`

`read_annotated` *Read an annotated phylogenetic tree*

Description

This function takes the given file, containing data in either NEXUS or Newick format, and returns annotated phylogenetic trees.

Usage

```
read_annotated(filename, format="nexus")
```

Arguments

`filename`	a file to read tree data from
`format`	a format specifier; either `"nexus"` or `"newick"`

Details

The given file text is parsed and a tree object is constructed which can be used with the functions in the **ape** package. Annotations of the kind produced by, for example, MrBayes, are parsed and preserved in the returned object.

See `parse_annotated` for more information about the structure of the returned value.

Value

an object of type `"phylo"` or `"multiPhylo"`, augmented with node annotations.

Author(s)

Daniel Beer `<dlbeer@gmail.com>`

See Also

`print_annotated`, `parse_annotated`, `write_annotated`

`write_annotated` *Write an annotated phylogenetic tree to a file*

Description

This function takes the given tree object and returns a string representing the tree in the requested format. The difference between the `"newick"` and `"newick.named"` formats is that the former uses only node numbers in its output, whereas the latter uses the tip labels (sanitized and deduplicated if necessary).

Usage

```
write_annotated(tree, filename, format="nexus")
```

Arguments

`tree`	a phylogentic tree, with optional annotations
`filename`	a file to write no
`format`	a format specifier; either `"nexus"`, `"newick"`, or `"newick.named"`

Details

The tree object should be either a `"phylo"` or `"multiPhylo"` object. It may optionally be augmented with annotations, as described in the documentation for the `parse_annotated` function.

Author(s)

Daniel Beer `<dlbeer@gmail.com>`

See Also

`parse_annotated`, `print_annotated`, `read_annotated`

Index