Package 'ggtreeSpace'

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Title Visualizing Phylomorphospaces using 'ggtree'

Version 1.8.0

Description This package is a comprehensive visualization tool specifically designed for exploring phylomorphospace. It not only simplifies the process of generating phylomorphospace, but also enhances it with the capability to add graphic layers to the plot with grammar of graphics to create fully annotated phylomorphospaces. It also provide some utilities to help interpret evolutionary patterns.

Imports interp, ape, dplyr, GGally, ggplot2, grid, ggtree, phytools, rlang, tibble, tidyr, tidyselect, stats

Suggests knitr, prettydoc, rmarkdown, BiocStyle, testthat (>= 3.0.0)

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biocViews Annotation, Visualization, Phylogenetics, Software

BugReports https://github.com/YuLab-SMU/ggtreeSpace/issues

URL https://github.com/YuLab-SMU/ggtreeSpace

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`geom_treespace` *A layer of phylomorphospace*

Description

A layer of phylomorphospace

Usage

```
geom_treespace(tr, data, mapping = NULL, ...)
```

Arguments

`tr`	a tree object. This should be an object of class that is compatible with 'ggtree', typically an object of class 'phylo' or 'treedata'.
`data`	Trait data as a data frame or matrix, where each row represents a tree tip or node. For data matching the number of tips, ancestral traits are reconstructed for internal nodes. For data equal to the total number of nodes, values are directly used as node coordinates.
`mapping`	aesthetic mapping
`...`	additional parameters for customization with 'geom_tree'. Please use '?ggtree::geom_tree' for more information.

Value

ggplot object

Examples

```
library(ggplot2)
library(ggtree)
library(phytools)

tr <- rtree(10)
a <- fastBM(tr, nsim = 2)

p <- ggplot() +
    geom_treespace(tr, a)
```

`geom_tsheatmap` *Add a layer of heat map with trait data*

Description

Add a layer of heat map with trait data

Usage

```
geom_tsheatmap(trait, resolution = 0.001, bins = 24, ...)
```

Arguments

`trait`	trait data. It can be either a data frame with node numbers and trait, or a trait name present in the plot data.
`resolution`	resolution of the heat map
`bins`	number of contour bins
`...`	additional parameters for ‘geom_contour_filled‘. Please use ‘?ggplot2::geom_contour_filled‘ for more information.

Value

ggplot object

Examples

```
library(ggtree)
library(phytools)
library(ggplot2)
library(ggtreeSpace)

tr <- rtree(15)
td <- fastBM(tr, nsim = 2, bounds = c(0, Inf))
col <- colorRampPalette(c(
    "#FFFFCC", "#FFEDA0", "#FED976", "#FEB24C",
    "#FD8D3C", "#FC4E2A", "#E31A1C", "#B10026"
))(24)
```

```
tdex <- data.frame(
    z = fastBM(tr, nsim = 1, bounds = c(0, Inf)),
    node = 1:15
)
p <- ggtreespace(tr, td)
p %<+% tdex +
    geom_tippoint() +
    geom_tsheatmap(trait = "z", alpha = 0.7, resolution = 0.01, bin = 24) +
    scale_fill_manual(
        values = col,
        guide = guide_colorsteps(show.limits = TRUE)
    ) +
    theme_treespace2() +
    theme(
        legend.key.height = unit(1, "null"),
        legend.justification.top = "right"
    )
```

`ggtreespace` *Plot phylomorphospace*

Description

This function plots a phylomorphospace by mapping a tree object onto a vector space like morphospace.

Usage

```
ggtreespace(tr, data, mapping = NULL, ...)
```

Arguments

`tr`	a tree object. This should be an object of class that is compatible with 'ggtree', typically an object of class 'phylo' or 'treedata'.
`data`	Trait data as a data frame or matrix, where each row represents a tree tip or node. For data matching the number of tips, ancestral traits are reconstructed for internal nodes. For data equal to the total number of nodes, values are directly used as node coordinates.
`mapping`	aesthetic mapping
`...`	additional parameters for customization with 'ggtree'. Please use '?ggtree::ggtree' for more information.

Value

ggtreeSpace object

Examples

```
library(ggtree)
library(phytools)
library(ggtreeSpace)

tr <- rtree(15)
td <- fastBM(tr, nsim = 2)
ggtreespace(tr, td) +
    geom_tippoint()
```

`make_ts_data` *Make plot data for ggtreespace. This function processes a phylogenetic tree and associated trait data to create a data frame suitable for plotting with 'ggtreespace'.*

Description

Make plot data for ggtreespace. This function processes a phylogenetic tree and associated trait data to create a data frame suitable for plotting with 'ggtreespace'.

Usage

```
make_ts_data(tr, data)
```

Arguments

`tr`	a tree object. This should be an object of class that is compatible with 'ggtree', typically an object of class 'phylo' or 'treedata'.
`data`	Trait data as a data frame or matrix, where each row represents a tree tip or node. For data matching the number of tips, ancestral traits are reconstructed for internal nodes. For data equal to the total number of nodes, values are directly used as node coordinates.

Value

ggplot object

Examples

```
library(ggplot2)
library(ggtree)
library(phytools)

tr <- rtree(10)
a <- fastBM(tr, nsim = 2)

trd <- make_ts_data(tr, a)
```

phylospm *Plot phylogenetic scatterplot matrix.*

Description

This function creates a scatterplot matrix for comparing multiple continuous traits mapped onto the same phylogenetic tree, providing a visual representation of trait correlations and evolutionary patterns.

Usage

```
phylospm(
tr,
traits = NULL,
title = NULL,
xAxisLabels = NULL,
yAxisLabels = NULL,
tr.params = list(size = 1, colors = NULL, panel.grid = TRUE),
sptr.params = list(tippoint = TRUE, tiplab = FALSE, labdir = "horizonal",
                   panel.grid = TRUE)
)
```

Arguments

tr	A phylogenetic tree
traits	A data frame containing multiple column of trait data
title	Set the title for the phylogenetic scatterplot matrix
xAxisLabels	Set the label of the x axis
yAxisLabels	Set the label of the y axis
tr.params	List of parameters to customize the phylogenetic tree with continuous trait mapping as continuous colors on the branch. Users can add tip point, add tip label, set tip label direction and set background gird.
sptr.params	List of parameters to customize the phylomorphospaces. Users can add tip point, add tip label, set tip label direction and set background gird.

Value

phylospm object

Examples

```
library(ggtree)
library(phytools)
library(ggtreeSpace)
```

```
tr <- rtree(10)
a <- fastBM(tr, nsim = 4)

phylospm(tr, a)
```

`reexports` *Objects exported from other packages*

Description

These objects are imported from other packages. Follow the links below to see their documentation.

ggplot2 `ggplot_add`

Value

ggplot object

`theme_treespace` *Phylomorphospace theme No.1, with arrow-end axis and grey panel grid.*

Description

Phylomorphospace theme No.1, with arrow-end axis and grey panel grid.

Usage

```
theme_treespace(...)
```

Arguments

`...`	additional parameters for 'ggplot2::theme'. Please use '?ggplot2::theme()' to learn more information.

Value

a theme object with arrow-end axis

Examples

```
library(ggtree)
library(phytools)
library(ggtreeSpace)

tr <- rtree(15)
td <- fastBM(tr, nsim = 2)
ggtreespace(tr, td) +
    geom_tippoint() +
    theme_treespace()
```

theme_treespace2 *Phylomorphospace theme No.2, with blank background and panel border.*

Description

Phylomorphospace theme No.2, with blank background and panel border.

Usage

```
theme_treespace2(...)
```

Arguments

...	additional parameters for ‘ggplot2::theme‘. Please use ‘?ggplot2::theme()‘ to learn more information.

Value

a theme object with blank background and panel border

Examples

```
library(ggtree)
library(phytools)
library(ggtreeSpace)

tr <- rtree(15)
td <- fastBM(tr, nsim = 2)
ggtreespace(tr, td) +
    geom_tippoint() +
    theme_treespace2()
```

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