

# Package ‘ggtreeSpace’

November 23, 2024

**Title** Visualizing Phylomorphospaces using 'ggtree'

**Version** 1.3.0

**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)

**License** Artistic-2.0

**biocViews** Annotation, Visualization, Phylogenetics, Software

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

**URL** <https://github.com/YuLab-SMU/ggtreeSpace>

**RoxygenNote** 7.3.1

**Encoding** UTF-8

**VignetteBuilder** knitr

**Config/testthat/edition** 3

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geom_treespace	<i>A layer of phylomorphospace</i>
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### 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)
```

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geom_tsheatmap	<i>Add a layer of heat map with trait data</i>
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**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"
  )

```

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ggtreespace

*Plot phylomorphospace*


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## Description

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

## Usage

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

## Arguments

<code>tr</code>	a tree object. This should be an object of class that is compatible with ‘ <code>ggtree</code> ’, typically an object of class ‘ <code>phylo</code> ’ or ‘ <code>treedata</code> ’.
<code>data</code>	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.
<code>mapping</code>	aesthetic mapping
<code>...</code>	additional parameters for customization with ‘ <code>ggtree</code> ’. Please use ‘ <code>?ggtree::ggtree</code> ’ 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()
```

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make_ts_data	<i>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'.</i>
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**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)
```

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 phylospm

*Plot phylogenetic scatterplot matrix.*


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### 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 = "horizontal",
                    panel.grid = TRUE)
)
```

### Arguments

<code>tr</code>	A phylogenetic tree
<code>traits</code>	A data frame containing multiple column of trait data
<code>title</code>	Set the title for the phylogenetic scatterplot matrix
<code>xAxisLabels</code>	Set the label of the x axis
<code>yAxisLabels</code>	Set the label of the y axis
<code>tr.params</code>	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 grid.
<code>sptr.params</code>	List of parameters to customize the phylomorphospaces. Users can add tip point, add tip label, set tip label direction and set background grid.

### Value

phylospm object

### Examples

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

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

phylospm(tr, a)
```

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reexports	<i>Objects exported from other packages</i>
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### Description

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

**ggplot2** [ggplot\\_add](#)

### Value

ggplot object

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theme_treespace	<i>Phylomorphospace theme No.1, with arrow-end axis and grey panel grid.</i>
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### 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()
```

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theme_treespace2	<i>Phylomorphospace theme No.2, with blank background and panel border.</i>
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**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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