Package 'specificity.shiny'

July 29, 2021

Title Interactive Visualization for package `specificity`

Version 0.1.0.9000

Description This package is a companion for `specificity`, providing interactive visualization for analyses conducted in that package.

License GPL

Depends R (>= 3.5.0)

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

Suggests specificity, rsconnect

Imports shiny, DT, ggplot2, colourpicker

NeedsCompilation no

Author John L Darcy [aut, cre]

Maintainer John L Darcy <darcyj@colorado.edu>

R topics documented:

`aggregate_specs_list`   *aggregate_specs_list*

Description

Aggregates a list of outputs from specificity::phy_or_env_spec() into a single data.frame object. Can also include feature data (e.g. species taxonomy) into that output. Output can also be byFeature, with one row per feature, and multiple columns for different variables.

Usage

```
aggregate_specs_list(sl, byFeature = FALSE, fd = NULL, fd_id = 1)
```

Arguments

sl	specs_list. A named list of outputs from phy_or_env_spec. See examples.
byFeature	bool. If true, each feature will occupy only one row, with multiple columns to represent the different variables in specs_list (default: FALSE)
fd	data.frame. Optional feature data - a data.frame object with one row per feature, including some column with feature IDs that includes feature IDs in sl as rownames (default:NULL)
fd_id	integer or string. If integer, specifies the column index of fd that contains feature ids. If character, specifies the column name (default: 1).

Value

a data.frame object.

Author(s)

John L. Darcy

Examples

```
# attach(antarctica)
# # to see details of the antarctica data set, see ?antarctica
# # aggregate data long format:
# ant_long <- aggregate_specs_list(antarctica_specs_list, byFeature=FALSE,
#   fd=antarctica_taxonomy, fd_id=1)
# head(ant_long)
# ant_wide <- aggregate_specs_list(antarctica_specs_list, byFeature=TRUE,
#   fd=antarctica_taxonomy, fd_id=1)
# head(ant_wide)
# # aggregation can also be done without feature data (fd):
# ant_long <- aggregate_specs_list(antarctica_specs_list, byFeature=FALSE)
# head(ant_long)
# ant_wide <- aggregate_specs_list(antarctica_specs_list, byFeature=TRUE)
# head(ant_wide)
```

| antarctica | *Specificity results from Antarctic cryoconite holes* |

Description

A dataset containing a specs list (a named list of outputs from specificity::phy_or_env_spec), and taxonomic information for each feature (bacterial OTU) within the specs list.

Usage

```
antarctica
```

Format

A list containing 2 objects:

antarctica_specs_list: A list of outputs from specificity::phy_or_env_spec(), with entries for Nitrogen ("N"), Phosphorus ("P"), geographic distance ("Geo"), fungal beta-diversity ("Fungi"), and algal beta-diversity ("Algae").

antarctica_taxonomy: data.frame object containing taxonomic information for the species in antarctica_specs_list. Columns are as follows:

Columns in antarctica_taxonomy:

id: species identity. corresponds to rownames in antarctica_specs_list.

eval: e-value from BLAST, which was used to assign taxonomy from the greengenes database.

hit: identity of the closest match within the greengenes database.

k: kingdom-level taxonomy

p: phylum-level taxonomy

c: class-level taxonomy

o: order-level taxonomy

f: family-level taxonomy

g: genus-level taxonomy

s: species-level taxonomy

Source

Sommers et al. (2019) Comparison of microbial communities in the sediments and water columns of frozen cryoconite holes in the McMurdo Dry Valleys, Antarctica. Front Microbiol 10(65) https://doi.org/10.3389/fmicb.2019.

make_specs_app	*make_specs_app*

Description

Makes a portable version of the interactive visualization from plot_specs_shiny() that can be up-loaded to shinyapps.io (or similar?). Note that this function takes the same arguments as plot_specs_shiny(). It is advised to make sure your visualization works properly using that function, before making it portable with this function. An additional argument for the name of your output app directory is also required; this name will become the last part of your URL if you upload to shinyapps.io, so use care when choosing. Note that this function automatically includes a portable version of the specificity.shiny R package inside your app, so you don't need to deal with installing it on the server; although the server will need specificity.shiny's dependencies installed (shinyapps.io already does, you don't need to do anything).

Usage

```
make_specs_app(sl, fd, fd_id_col = 1, app_fp = "mySpecApp")
```

Arguments

sl	specs_list. A named list of outputs from phy_or_env_spec. See examples.
fd	data.frame. Optional feature data - a data.frame object with one row per feature, including some column with feature IDs that includes feature IDs in sl as rownames. If NULL, no feature data will be used (default:NULL).
fd_id_col	integer or string. Either the column number of fd containing feature IDs (see above), or the column name of that column (default: 1).
app_fp	filepath to a folder where the app should be stored. Only forward slashes ("/") are supported! The folder should *not* exist yet, and this function will throw an error if it does exist. This is to avoid overwriting. As mentioned above, the name of this folder will become the last part of your URL if you upload to shinyapps.io. For example, if you set app_fp="~/Desktop/mySpecApp", this function will first check if directory "mySpecApp" exists on your desktop. Then, if it doesn't, it will create that directory and put all the necessary files inside of it (default:"mySpecApp").

Value

Returns nothing, but creates a folder containing a shiny app.

Author(s)

John L. Darcy

Examples

```
# attach(antarctica)
# # test that it works:
# plot_specs_shiny(antarctica_specs_list, antarctica_taxonomy, 1)
# # make the app:
# make_specs_app(antarctica_specs_list, antarctica_taxonomy, 1, "antarctica_specs_shiny_app")
# # upload to shinyapps.io (will automatically open in browser when done)
# # package "rsconnect" is required for this next step, and requires an account with
# # shinyapps.io and configuration of the rsconnect package; see their VERY easy guide
# # here: https://docs.rstudio.com/shinyapps.io/getting-started.html
# # Just make an account and configure rsconnect, no need to do anything after that.
# rsconnect::deployApp("antarctica_specs_shiny_app")
```

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plot_specs_shiny *plot_specs_shiny*

Description

Runs an interactive shiny visualization. Data can be re-downloaded from that visualization, in either "wide" or "long" format. See ?aggregate_specs_list for explanation of those formats.

Usage

```
plot_specs_shiny(sl, fd = NULL, fd_id_col = 1)
```

Arguments

sl   specs_list. A named list of outputs from phy_or_env_spec. See examples.

fd   data.frame. Optional feature data - a data.frame object with one row per fea-
              ture, including some column with feature IDs that includes feature IDs in sl as
              rownames. If NULL, no feature data will be used (default:NULL).

fd_id_col   integer or string. Either the column number of fd containing feature IDs (see
              above), or the column name of that column (default: 1).

Value

Returns output of shiny::shinyApp(). If run locally, this will manifest as a browser window opening with an interactive visualization.

Author(s)

John L. Darcy

Examples

```
# attach(antarctica)
# plot_specs_shiny(antarctica_specs_list, antarctica_taxonomy, 1)
```

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specShinyFuns   *Portable source code for specificity.shiny functions*

Description

This source code is included so that functions can be written out as .r files, so that a server running
the shiny visualization does not need to have the specificity.shiny R package installed.

Usage

```
specShinyFuns
```

Format

A list containing 2 objects:

plot_specs_shiny: Source code for plot_specs_shiny(). Can be written to file using writeLines().

aggregate_specs_list: Source code for aggregate_specs_list(). Can be written to file using write-
Lines().

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