Package 'PanVizGenerator'

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Type Package

Title Generate PanViz visualisations from your pangenome

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Description PanViz is a JavaScript based visualisation tool for functionaly
annotated pangenomes. PanVizGenerator is a companion for PanViz that
facilitates the necessary data preprocessing step necessary to create a
working PanViz visualization. The output is fully self-contained so the
recipient of the visualization does not need R or PanVizGenerator installed.

License GPL (>= 2)

URL https://github.com/thomasp85/PanVizGenerator

BugReports https://github.com/thomasp85/PanVizGenerator/issues

biocViews ComparativeGenomics, GUI, Visualization

Depends methods

Imports shiny, tools, jsonlite, pcaMethods, FindMyFriends, igraph,
stats, utils

VignetteBuilder knitr

Suggests BiocStyle, knitr, rmarkdown, testthat, digest

Collate 'GO.R' 'aaa.R' 'IO.R' 'panviz.R' 'shinyStuff.R' 'zzz.R'

RoxygenNote 5.0.1

NeedsCompilation no

R topics documented:

1

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getGO *Download and store the Gene Ontology*

Description

This function downloads a copy of the gene ontology and formats it for quick access. It can optionally check the current version and only download a new if it supersede the current one.

Usage

```
getGO(mode = "force")
```

Arguments

mode   Either 'force' (default) or 'auto'. If 'force' the gene ontology will get fetched no matter what. If 'auto' it will only get fetched if the current local version is older than the one available on the net.

Value

This function is called for its side effects

References

<http://geneontology.org>

Examples

```
if (interactive()) {
    getGO('auto')
}
```

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panviz *Convert pangenome into PanViz*

Description

This method contains the main functionality of PanVizGenerator. It takes the pangenome data and properly formats it, combines it with the PanViz code and creates the PanViz files needed for the visualization. Per default everything is consolidated into the PanViz.html file but data and code can also be destributed into separate files. Currently pangenome data from FindMyFriends is supported natively (And FindMyFriends support grouping based on other algorithms), while more general use is supported by supplying a pangenome matrix along with functional annotation of each row. A last option is to provide the file path to a csv file containing the pangenome matrix along with the functional annotation.

Usage

```
panviz(object, ...)

## S4 method for signature 'character'
panviz(object, name = "name", go = "go", ec = "ec",
  ignore, location, consolidate = TRUE, showcase = FALSE, ...)

## S4 method for signature 'pgVirtual'
panviz(object, location, useDescription = TRUE,
  consolidate = TRUE, showcase = FALSE, ...)

## S4 method for signature 'matrix'
panviz(object, name, go, ec, location, consolidate = TRUE,
  showcase = FALSE, ...)

## S4 method for signature 'data.frame'
panviz(object, ...)
```

Arguments

`object`	The object containing the pangenome data. If supplied as pangenome matrix it is expected that rows are gene groups and columns are genomes.
`...`	Parameters passed along to the clustering and dimensionality reduction functions. See details.
`name`	Depending on object either the name of the column with the gene group names or a vector of gene group names. See details.
`go`	Depending on object either the name of the column with the gene group gene ontology annotation or a vector/list of gene group ontologies. See details.
`ec`	Depending on object either the name of the column with the gene group E.C. annotation or a vector/list of gene group enzyme numbers. See details.
`ignore`	Columns in the csv file to ignore, either given as column names or indexes
`location`	The path to write the resulting PanViz files to.
`consolidate`	Logical. Should all data and code be consolidated into the PanViz.html file or spread out to multiple files.
`showcase`	Logical. Should the resulting PanViz.html be opened in the default browser upon completion.
`useDescription`	Logical. Should the description column in orgInfo be used in favor of group names (if description is NA it falls back to group name)

Details

The calculation of mds/pca as well as the hierarchical clustering can be controlled with the use of dist (default: 'canberra') for setting the method used in the [dist](#) calls, clust (default: 'ward.D2') for setting the method used in the [hclust](#) calls, center (default: TRUE) to control whether variables should be centered prior to doing PCA and scale (default: TRUE) to control whether scaling should be performed prior to PCA.

When using `panviz` with a csv file the `name`, `go` and `ec` parameters should point to the columns in the csv file containing the respective information, either by name or index. If E.C. annotation is not given in the csv file it can be set to NA. For column with multiple possible values (go and ec) any

delimiter can be used but ',', '.', and numbers (don't know why you would use numbers as delimiter anyway).

For panviz with a matrix or data.frame the name, go and ec parameters should contain the actual annotation as character vectors or lists of strings. For character vectors the same delimiting restrictions exists as for csv files described above. ec and name can be omitted. If name is missing the rownames of the matrix or data.frame will be used instead - if these are not present an error will be thrown. name, go and ec must match the number of rows in the pangenome matrix if given.

Value

NULL. This function is called for its side effects. If showcase=TRUE the resulting PanViz.html file will be opened in the default browser.

Methods (by class)

- character: Method for file paths
- pgVirtual: Method for pgVirtual subclasses from FindMyFriends
- matrix: Method for pangenome matrix as numeric/integer matrix
- data.frame: Method for pangenome matrix as data.frame (will be coerced to matrix)

See Also

PanVizGenerator for a shiny interface to converting csv files.

Examples

```
if(interactive()) {
    exampleFile <- system.file('extdata', 'exampleData.csv')
    panviz(exampleFile, location = tempdir(), showcase = TRUE)
}
```

PanVizGenerator   *Launch the PanVizGenerator shiny app*

Description

This function launches a shiny based GUI that lets the user create panviz visualizations from csv files. The same formatting restriction as in panviz applies to the csv file. Furthermore the GUI also contains descriptions of the ideas behind the visualization as well as a demonstration video.

Usage

```
PanVizGenerator(...)
```

Arguments

...   Parameters passed on to runApp

Value

This function is called for its side effects.

See Also

[panviz](#) for an R API for the same functionality.

Examples

```
if (interactive()) {
    PanVizGenerator()
}
```

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