

Package ‘hagis’

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Title Analysis of Plant Pathogen Pathotype Complexities, Distributions and Diversity

Version 3.1.12

Description Analysis of plant pathogen pathotype survey data. Functions provided calculate distribution of susceptibilities, distribution of complexities with statistics, pathotype frequency distribution, as well as diversity indices for pathotypes. This package is meant to be a direct replacement for Herrmann, Löwer and Schachtel's (1999) <doi:10.1046/j.1365-3059.1999.00325.x> Habgood-Gilmour Spreadsheet, 'HaGiS', previously used for pathotype analysis.

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URL <https://github.com/openplantpathology/hagis>,
<https://openplantpathology.github.io/hagis/>

BugReports <https://github.com/openplantpathology/hagis/issues>

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Contents

autoplot.hagis.complexities	2
autoplot.hagis.gene.summary	3
calculate_complexities	4
calculate_diversities	5
create_binary_matrix	7
diversities_table	8
individual_pathotypes	9
P_sojae_survey	10
sample_meta	11
summarize_gene	12
Index	13

autoplot.hagis.complexities
<i>Plot hagis Complexities Objects</i>

Description

Creates a **ggplot2** object of the frequency of complexity (percent per complexity) or a **ggplot2** object of the distribution (number per complexity) calculated by `calculate_complexities()`.

Usage

```
## S3 method for class 'hagis.complexities'
autoplot(object, type, color = NULL, order = NULL, ...)
```

Arguments

object	a hagis complexities object generated by <code>calculate_complexities()</code> . Character.
type	a vector of values for which the bar plot is desired. Specify whether to return a graph of the frequency of complexities as a percentage, "percentage", or as the count, "count". Character.
color	a named or hexadecimal color value to use for the bar color
order	sort the x-axis of the bar chart by ascending or descending order of frequency. Accepts ascending or descending input values. Defaults to complexity value. Character.
...	passed to the chosen geom(s)

Value

A **ggplot2** object

Examples

```
# Using the built-in data set, `P_sojae_survey`
data(P_sojae_survey)

# calculate susceptibilities with a 60 % cutoff value
complexities <- calculate_complexities(x = P_sojae_survey,
                                       cutoff = 60,
                                       control = "susceptible",
                                       sample = "Isolate",
                                       gene = "Rps",
                                       perc_susc = "perc.susc")

# Visualize the distribution (count or actual values)
autoplot(complexities, type = "count")

# Visualize the frequency (percentages)
autoplot(complexities, type = "percentage")
```

```
autoplot.hagis.gene.summary
```

Plot hagis Summary Objects

Description

Creates a **ggplot2** object of the gene summaries calculated by `summarize_gene()`

Usage

```
## S3 method for class 'hagis.gene.summary'
autoplot(object, type, color = NULL, order = NULL, ...)
```

Arguments

object	a hagis.gene.summary object generated by <code>summarize_gene()</code> . Character.
type	a vector of values for which the bar plot is desired. Specify whether to return a graph of the percent pathogenic isolates, percentage, or as the count, count. Character.
color	a named or hexadecimal color value to use for the bar color
order	sort the x-axis of the bar chart by ascending or descending order of N_virulent_isolates or percent_pathogenic. Accepts ascending or descending input values. Defaults to gene name. Character.
...	passed to the chosen geom(s)

Value

A **ggplot2** plot

Examples

```
# Using the built-in data set, `P-sojae_survey`
data(P-sojae_survey)

# calculate susceptibilities with a 60 % cutoff value
susc <- summarize_gene(x = P-sojae_survey,
                       cutoff = 60,
                       control = "susceptible",
                       sample = "Isolate",
                       gene = "Rps",
                       perc_susc = "perc.susc")

# Visualize the summary of genes
autoplot(susc, type = "percentage")
```

calculate_complexities

Calculate Distribution of Complexities by Sample

Description

Calculate the distribution of susceptibilities by sample id.

Usage

```
calculate_complexities(x, cutoff, control, sample, gene, perc_susc)
```

Arguments

x	a data.frame containing the data.
cutoff	value for percent susceptible cutoff. Numeric.
control	value used to denote the susceptible control in the gene column. Character.
sample	column providing the unique identification for each sample being tested. Character.
gene	column providing the gene(s) being tested. Character.
perc_susc	column providing the percent susceptible reactions. Character.

Value

An object of class `hagis.complexities`.

An object of class `hagis.complexities` is a list containing the following components

grouped_complexities a `data.table::data.table()` object of grouped complexities

individual_complexities a `data.table::data.table()` object of individual complexities

Examples

```
# Using the built-in data set, `P-sojae_survey`
data(P-sojae_survey)

P-sojae_survey

# calculate susceptibilities with a 60 % cutoff value
complexities <- calculate_complexities(x = P-sojae_survey,
                                       cutoff = 60,
                                       control = "susceptible",
                                       sample = "Isolate",
                                       gene = "Rps",
                                       perc_susc = "perc.susc")

complexities

summary(complexities)
```

calculate_diversities *Calculate Diversities Indices*

Description

Calculate five pathogen diversity indices.

Diversity indices include:

- Simple diversity index, which will show the proportion of unique pathotypes to total samples. As the values gets closer to 1, there is greater diversity in pathotypes within the population. Simple diversity is calculated as:

$$D = \frac{Np}{Ns}$$

where Np is the number of pathotypes and Ns is the number of samples.

- Gleason diversity index, an alternate version of Simple diversity index, is less sensitive to sample size than the Simple index.

$$D = \frac{(Np - 1)}{\log(Ns)}$$

Where Np is the number of pathotypes and Ns is the number of samples.

- Shannon diversity index is typically between 1.5 and 3.5, as richness and evenness of the population increase, so does the Shannon index value.

$$D = - \sum_{i=1}^R p_i \log p_i$$

Where p_i is the proportional abundance of species i .

- Simpson diversity index values range from 0 to 1, 1 represents high diversity and 0 represents no diversity. Where diversity is calculated as:

$$D = \sum_{i=1}^R p_i^2$$

- Evenness ranges from 0 to 1, as the Evenness value approaches 1, there is a more even distribution of each pathotype's frequency within the population. Where Evenness is calculated as:

$$D = \frac{H'}{\log(Np)}$$

where H' is the Shannon diversity index and Np is the number of pathotypes.

Usage

```
calculate_diversities(x, cutoff, control, sample, gene, perc_susc)
```

Arguments

<code>x</code>	a data.frame containing the data.
<code>cutoff</code>	value for percent susceptible cutoff. Numeric.
<code>control</code>	value used to denote the susceptible control in the gene column. Character.
<code>sample</code>	column providing the unique identification for each sample being tested. Character.
<code>gene</code>	column providing the gene(s) being tested. Character.
<code>perc_susc</code>	column providing the percent susceptible reactions. Character.

Value

a hgis.diversities object.

A hgis.diversities object is a list containing:

- Number of Samples
- Number of Pathotypes
- Simple Diversity Index
- Gleason Diversity Index
- Shannon Diversity Index
- Simpson Diversity Index
- Evenness Diversity Index

Examples

```
# Using the built-in data set, P_sojae_survey
data(P_sojae_survey)

P_sojae_survey

# calculate susceptibilities with a 60 % cutoff value
diversities <- calculate_diversities(x = P_sojae_survey,
                                   cutoff = 60,
                                   control = "susceptible",
                                   sample = "Isolate",
                                   gene = "Rps",
                                   perc_susc = "perc.susc")

diversities
```

create_binary_matrix *Create Binary Data Matrix From Pathotype Data*

Description

Creates a binary data matrix from pathotype data representing the pathotype of each isolate. This binary data matrix can be used to visualize beta-diversity of pathotypes using **vegan** and **ape**.

Usage

```
create_binary_matrix(x, cutoff, control, sample, gene, perc_susc)
```

Arguments

x	a data.frame containing the data.
cutoff	value for percent susceptible cutoff. Numeric.
control	value used to denote the susceptible control in the gene column. Character.
sample	column providing the unique identification for each sample being tested. Character.
gene	column providing the gene(s) being tested. Character.
perc_susc	column providing the percent susceptible reactions. Character.

Value

a binary matrix of pathotype data

Examples

```
# Using the built-in data set, `P_sojae_survey`
data(P_sojae_survey)

P_sojae_survey

# calculate susceptibilities with a 60 % cutoff value
final_matrix <- create_binary_matrix(x = P_sojae_survey,
                                     cutoff = 60,
                                     control = "susceptible",
                                     sample = "Isolate",
                                     gene = "Rps",
                                     perc_susc = "perc.susc")

final_matrix
```

diversities_table	<i>Custom Print for hagsis Diversities Tables</i>
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Description

Print the frequency table of diversities from a hagsis.diversities object The resulting object is a [pander](#) table (a text object for Markdown) for ease of use in reporting and viewing in the console.

Usage

```
diversities_table(x, ...)
```

Arguments

x	a hagsis.diversities object generated by calculate_diversities()
...	other arguments passed to pander::panderOptions()

Value

A [pander](#) object of diversities

See Also

[calculate_diversities\(\)](#), [individual_pathotypes\(\)](#)

Examples

```
# Using the built-in data set, P_sojae_survey
data(P_sojae_survey)

P_sojae_survey

# calculate susceptibilities with a 60 % cutoff value
diversities <- calculate_diversities(x = P_sojae_survey,
                                   cutoff = 60,
                                   control = "susceptible",
                                   sample = "Isolate",
                                   gene = "Rps",
                                   perc_susc = "perc.susc")

# print the diversities table
diversities_table(diversities)
```

`individual_pathotypes` *Prints Individual Pathotypes for Each Sample*

Description

Print an object from a `hagis.diversities` object with individual pathotypes, *i.e.* each sample's pathotype. The resulting object is a [pander](#) table (a text object for Markdown) for ease of use in reporting and viewing in the console.

Usage

```
individual_pathotypes(x, ...)
```

Arguments

`x` a `hagis.diversities` object generated by [calculate_diversities\(\)](#)
`...` other arguments passed to [pander::panderOptions\(\)](#)

Value

A [pander](#) object of individual pathotypes

See Also

`calculate_diversities(), diversities_table()`

Examples

```
# Using the built-in data set, P_sojae_survey
data(P_sojae_survey)

P_sojae_survey

# calculate susceptibilities with a 60 % cutoff value
diversities <- calculate_diversities(x = P_sojae_survey,
                                     cutoff = 60,
                                     control = "susceptible",
                                     sample = "Isolate",
                                     gene = "Rps",
                                     perc_susc = "perc.susc")

# print the diversities table
individual_pathotypes(diversities)
```

P_sojae_survey	Phytophthora sojae Survey Example Data
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Description

Data from a *Phytophthora sojae* survey

Usage

```
data(P_sojae_survey)
```

Format

An object of class `data.table` with 294 observations of 12 variables

Isolate *P. sojae* isolate identifier

Line Soybean cultivar

Rps *Rps* gene identifier

Total Total number of plants inoculated

HR (1) Number of plants that exhibit a hypersensitive response after inoculation

Lesion (2) Number of plants that develop a lesion at inoculation site

Lesion to cotyledon (3) Number of plants that develop a lesion, which advances to the hypocotyl of the seedling after infection

Dead (4) Number of dead plants that are observed after inoculation

total.susc The total number of susceptible plants (Lesion+Lesion to cotyledon+Dead)

total.resis The total number of resistant plants (equal to HR value)

Source

Data from an ongoing 2017 *Phytophthora sojae* survey in Michigan, conducted by A. G. McCoy *et al.*.

Examples

```
data(P_sojae_survey)
P_sojae_survey
```

sample_meta

Phytophthora sojae Survey Example Metadata

Description

Metadata to accompany internal data from a *Phytophthora sojae* survey used for an example in the "Beta-diversity Analyses" vignette.

Usage

```
data(sample_meta)
```

Format

An object of class `data.frame` with 21 observations of 2 variables

Sample *P. sojae* sample identifier

Locale US State where sample was collected, limited to Michigan

Source

Data from an ongoing 2017 *Phytophthora sojae* survey in Michigan, conducted by A. G. McCoy *et al.*.

Examples

```
data(sample_meta)
sample_meta
```

summarize_gene

Calculate and Summarize Distribution of Susceptibilities by Gene

Description

Calculate the distribution of susceptibilities by gene.

Usage

```
summarize_gene(x, cutoff, control, sample, gene, perc_susc)
```

Arguments

x	a data.frame containing the data.
cutoff	value for percent susceptible cutoff. Numeric.
control	value used to denote the susceptible control in the gene column. Character.
sample	column providing the unique identification for each sample being tested. Character.
gene	column providing the gene(s) being tested. Character.
perc_susc	column providing the percent susceptible reactions. Character.

Value

a hgis.gene.summary object.

An object of class hgis.gene.summary is a `data.table::data.table()` containing the following components columns

gene the gene

N_virulent_isolates the total number virulent isolates for a given gene in the gene column

percent_pathogenic the frequency with which a gene is pathogenic

Examples

```
# Using the built-in data set, `P_sojae_survey`
data(P_sojae_survey)

P_sojae_survey

# calculate susceptibilities with a 60 % cutoff value
susc <- summarize_gene(x = P_sojae_survey,
                       cutoff = 60,
                       control = "susceptible",
                       sample = "Isolate",
                       gene = "Rps",
                       perc_susc = "perc.susc")

susc
```

Index

* datasets

P_sojae_survey, [10](#)

sample_meta, [11](#)

autoplot.hagis.complexities, [2](#)

autoplot.hagis.gene.summary, [3](#)

calculate_complexities, [4](#)

calculate_complexities(), [2](#), [3](#)

calculate_diversities, [5](#)

calculate_diversities(), [8–10](#)

create_binary_matrix, [7](#)

data.table::data.table(), [5](#), [12](#)

diversities_table, [8](#)

diversities_table(), [10](#)

individual_pathotypes, [9](#)

individual_pathotypes(), [9](#)

P_sojae_survey, [10](#)

pander, [8](#), [9](#)

pander::panderOptions(), [8](#), [9](#)

sample_meta, [11](#)

summarize_gene, [12](#)

summarize_gene(), [3](#), [4](#)