

Package ‘hagis’

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Title Analysis of Plant Pathogen Pathotype Complexities, Distributions and Diversity

Version 2.0.0

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, 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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Imports data.table, ggplot2, graphics, pander, stats, utils, vegan

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<https://openplantpathology.github.io/hagis/>

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

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calculate_complexities

Calculate Distribution of Complexities by Sample

Description

This function will calculate the distribution of susceptibilities by sample

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 field. Character.
sample	field providing the unique identification for each sample being tested. Character.
gene	field providing the gene(s) being tested. Character.
perc_susc	field providing the percent susceptible reactions. Character.

Value

calculate_complexities returns 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

```
# locate system file for import
Ps <- system.file("extdata", "practice_data_set.csv", package = "hagis")

# import 'practice_data_set.csv'
Ps <- read.csv(Ps)
head(Ps)

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

complexities

summary(complexities)

# plot complexities frequency or by percentage
plot(complexities, type = "percentage")
```

calculate_diversities *Calculate Diversities Indices*

Description

Calculates pathogen diversity index

Usage

```
calculate_diversities(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 field. Character.
sample	field providing the unique identification for each sample being tested. Character.
gene	field providing the gene(s) being tested. Character.
perc_susc	field providing the percent susceptible reactions. Character.

Examples

```
# locate system file for import
Ps <- system.file("extdata", "practice_data_set.csv", package = "hagis")

# import 'practice_data_set.csv'
Ps <- read.csv(Ps)
head(Ps)

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

diversities
```

diversities_table *Prints Table of Diversities*

Description

Print the frequency table of diversities from a `hagis.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 `hagis.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

```
# locate system file for import
Ps <- system.file("extdata", "practice_data_set.csv", package = "hagis")

# import 'practice_data_set.csv'
Ps <- read.csv(Ps)
head(Ps)

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

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

hagis

Tools for Analysis of Plant Pathogen Pathotype Complexities, Distributions and Diversity

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, 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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See Also

Useful links:

- <https://github.com/openplantpathology/hagis>
- <https://openplantpathology.github.io/hagis/>
- Report bugs at <https://github.com/openplantpathology/hagis/issues>

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

```
# locate system file for import
Ps <- system.file("extdata", "practice_data_set.csv", package = "hagis")

# import 'practice_data_set.csv'
Ps <- read.csv(Ps)
head(Ps)

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

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

summarize_gene	<i>Calculate and Summarize Distribution of Susceptibilities by Gene</i>
----------------	---

Description

This function will 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 field. Character.
sample	field providing the unique identification for each sample being tested. Character.
gene	field providing the gene(s) being tested. Character.
perc_susc	field providing the percent susceptible reactions. Character.

Value

returns an object of `class()` `hagis.gene.summary` An object of class `hagis.summaries` is a `data.table::data.table()` containing the following components fields

gene the gene

N_susc the total number susceptible for a given gene in the gene field

percent_pathogenic the frequency with which a gene is pathogenic

Examples

```
# locate system file for import
Ps <- system.file("extdata", "practice_data_set.csv", package = "hagis")

# import 'practice_data_set.csv'
Ps <- read.csv(Ps)
head(Ps)

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

susc
```

```
# plot susceptibilities  
plot(susc, type = "percentage")
```


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