

Package ‘titeR’

November 21, 2016

Title Tools for analyzing and visualizing antibody titer data.

Version 0.0.1.0010

Description This package contains methods to calculate endpoints from antibody titer data and visualize titers.

Depends R (>= 3.0.2)

License CCO

LazyData true

RoxygenNote 5.0.1

R topics documented:

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| | |
|----------|--|
| +.uneval | <i>Addition for aes() and aes_string()</i> |
|----------|--|

Description

+.uneval is a helper function to allow adding aes and aes_string in ggplot2

Usage

```
## S3 method for class 'uneval'
a + b
```

References

<http://stackoverflow.com/questions/28777626/how-do-i-combine-aes-and-aes-string-options>

Examples

```
v1 <- "mpg"
v2 <- "qsec"
ggplot(mtcars, aes(x=wt)) + ylab("") +
  geom_line(aes_string(y=v1) + aes(color="one")) +
  geom_line(aes_string(y=v2) + aes(color="two")) +
  scale_color_manual(name="Val", values=c(one="#105B63",two="#BD4932"))
```

Barplot

Titer bar plots.

Description

Barplot plots the baseline and day 28 titers

Usage

```
Barplot(dat_list, subjectCol = "SubjectID", cols = 1, groupVar = NULL,
  colors = c("#A6CEE3", "#1F78B4", "#B2DF8A", "#33A02C", "#FB9A99", "#E31A1C",
    "#FDBF6F", "#FF7F00"))
```

Arguments

| | |
|-------------------------|---|
| <code>dat_list</code> | a named list like the one returned by FormatTitters . |
| <code>subjectCol</code> | |
| <code>cols</code> | numeric specifying how many columns to layout plot |
| <code>colors</code> | a vector of colors specifying bar colors. If <code>dat_list</code> contains more than 4 elements, you must specify your own colors. |

Value

(invisibly) a list of ggplot2 object(s).

Author(s)

Stefan Avey

Examples

```
## First Example
```

BubbleChart*Bubble Chart*

Description

BubbleChart visualizes baseline vs fold change in titers

Usage

```
BubbleChart(dat_list, fit = NULL, subjectCol = "SubjectID",
  colorBy = NULL, xlimits = c(1.5, 10.5), xbreaks = 2:10, plot = TRUE,
  cols = 2, ...)
```

Arguments

| | |
|------------|--|
| dat_list | a named list like the one returned by FormatTiters |
| fit | what type of fit to add. Current options are "lm" for linear model, "exp" for exponential, or NULL for no smoothing. |
| subjectCol | the name of the column specifying a subject ID. Default is "SubjectID". |
| colorBy | a character string specifying an endpoint to colorBy or NULL (default) for no coloring. |
| xlimits | the x-axis limits (passed to <code>scale_x_continuous</code>) |
| xbreaks | the x-axis breaks (passed to <code>scale_x_continuous</code>) |
| plot | logical indicating whether to plot or not. Default is TRUE |
| cols | numeric specifying how many columns to layout plot |
| ... | other arguments besides method and subjectCol passed to CalculateSAdjMFC . |
| scale_y | a character string specifying whether the y axis should be "fixed" for all strains or "free". |

Details

This plot was designed for HAI titer data with baseline columns and fold change columns for multiple strains.

Value

(invisibly) a list of ggplot2 objects.

Author(s)

Stefan Avey

See Also

[FormatTiters](#)

Examples

```
## Prepare the data
library(dplyr)
library(ggplot2)
strains <- c("A_California_7_2009", "A_Perth_16_2009", "B_Brisbane_60_2008")
titer_list <- FormatTiters(Year2_Titers, strains, subjectCol = "YaleID")

## Basic plot without any fitted model
BubbleChart(titer_list)

## Change layout to plot 3 strains in a single column
BubbleChart(titer_list, cols = 1)

## Add a linear fit
BubbleChart(titer_list, method = "lm", subjectCol = "YaleID")

## Add an exponential fit
BubbleChart(titer_list, method = "exp", subjectCol = "YaleID")

## Add coloring by age
```

CalculateD0NormPaired *CalculateD0NormPaired*

Description

CalculateD0NormPaired calculates the normalized day 0 titer paired with the titer with maximum normalized fold change

Usage

```
CalculateD0NormPaired(dat, fcStdCols = grep("fc_std_norm", colnames(dat),
  value = TRUE))
```

Arguments

| | |
|-----------|---|
| dat | data frame containing fcStdCols |
| fcStdCols | column names containing the titer fold changes for each strain standardized across subjects |

Details

If there are multiple strains that have the maximal fold change, choose the day 0 titer that is higher since this will allow for a greater adjustment and better chance of being a high responder.

Column names containing the day 0 titers for each strain standardized across subjects are assumed to follow the same pattern as fcStdCols with "d0" replacing "fc" in the name.

Value

a numeric vector containing the values from d0StdCols that correspond to the maximum over the strains of fcStdCols

Author(s)

Stefan Avey

Examples

First Example

 CalculatePadjMFC

CalculatePadjMFC

Description

CalculatePadjMFC calculates the paired, adjusted maximum fold change (padjMFC)

Usage

```
CalculatePadjMFC(dat, fcCol = "fc_norm_max_ivt", d0Col = "d0_norm_paired",
  discretize = c(0.2, 0.3), scaleResiduals = FALSE,
  responseLabels = paste0(c("low", "moderate", "high"), "Responder"), ...)
```

Arguments

| | |
|-----------------------------|---|
| <code>dat</code> | the data containing the columns <code>fcCol</code> and <code>d0Col</code> |
| <code>fcCol</code> | character string specifying the name of the fold change column from <code>dat</code> |
| <code>d0Col</code> | character string specifying the name of the day 0 column from <code>dat</code> |
| <code>discretize</code> | a vector of quantiles in (0, 0.5] specifying where to make the cutoff for low, moderate and high responses. Default is 20% and 30%. |
| <code>scaleResiduals</code> | Logical. Should residuals be scaled inversely by the square of the confidence intervals from the linear model. |
| <code>responseLabels</code> | names for low, moderate and high responses |
| <code>...</code> | Additional arguments passed to <code>lm</code> |

Details

Calculate the paired, adjusted maximum fold change (padjMFC) from `fc_norm_max_ivt` and `d0_norm_paired` using linear regression to remove the effect of baseline titers. Missing (NA) values are handled and any missing values in `fcCol` and `d0Col` will also be missing in the output.

Value

A list with the first element named "linearModel" for the linear model and then "padjMFC" containing the continuous padjMFC metric and one additional element for each value of `discretize` giving the discrete labels.

Author(s)

Stefan Avey

See Also

lm

Examples

First Example

CalculateSAdjMFC

*Calculate SAdjMFC***Description**

CalculateSAdjMFC calculates the baseline-adjusted maximum fold change (MFC) for each viral strain

Usage

```
CalculateSAdjMFC(datList, subjectCol = "SubjectID", method = c("lm", "exp"),
  scoreFun = max, fcCol = "fc", d0Col = "d0", normalize = TRUE,
  discretize = c(0.2, 0.3), scaleResiduals = FALSE,
  responseLabels = paste0(c("low", "moderate", "high"), "Responder"),
  na_action = "na.fail", ...)
```

Arguments

| | |
|----------------|---|
| datList | a list with one data frame for each strain and each data frame containing the columns fcCol and d0Col. The order of each data frame must be the same and they must be the same dimensions. In addition, each data frame must be sorted by d0Col from low to high. |
| subjectCol | the name of the column specifying a subject ID. Default is "SubjectID". |
| method | a character string specifying the method used to model the relationship between day 0 and fold change values. One of either "lm" for a linear model or "exp" for an exponential model. |
| scoreFun | a function applied to all (potentially scaled) residuals for each subject to determine the endpoint. Default is max but sum may also be useful to quantify the total response. |
| fcCol | character string specifying the name of the fold change column in each element of datList |
| d0Col | character string specifying the name of the day 0 column in each element of datList |
| normalize | Logical specifying whether residuals should be normalized with the inverse normal transform. Default is TRUE. |
| discretize | a vector of quantiles in (0, 0.5] specifying where to make the cutoff for low, moderate and high responses. Default is 20% and 30%. |
| scaleResiduals | Logical. Should residuals be scaled inversely by the square of the confidence intervals from the linear model. |
| responseLabels | names for low, moderate and high responses |
| na_action | how should missing NA values be treated. Default is "na.fail" |
| ... | Additional arguments passed to lm if method == "lm" or nls if method == "exp" |

Details

Calculates the baseline-adjusted fold change for each strain of virus using (unnormalized) fold change and baseline titers. Linear regression or an exponential curve is used to remove the effect of baseline titers on fold changes. The score function (scoreFun) is used to combine the adjusted fold change across multiple strains. Missing (NA) values are handled by being returned as missing in the endpoints in the output

Value

A list with the following elements: "models": the models calculated on each strain separately (with names the same as on datList) "residualMatrix": the matrix of residuals "SAdjMFC": a list containing the continuous and discrete SAdjMFC metrics

Author(s)

Stefan Avey

See Also

lm, nls

Examples

```
## First Example
```

CalculateStdNorm

Calculate Normalized Titers

Description

CalculateStdNorm calculates the standardized d0 or fc titers

Usage

```
CalculateStdNorm(dat, type, fcToOne = FALSE, idCol = "SubjectID",
  cols = grep(paste0(type, "_[AB]"), colnames(dat), value = TRUE))
```

Arguments

| | |
|---------|---|
| dat | Data frame containing fcStdCols |
| type | What should be standarized. Either "d0", or "fc". |
| fcToOne | Logical. Are titer fold changes allowed to be less than 1 or should these be changed to 1 before standardization? Default is FALSE and no changes will be made. Only relevant when type == "fc" |
| idCol | Name of column containing subject IDs |
| cols | column names containing the titer measurements for each strain |

Details

This must be run on only 1 cohort at a time because titers will be normalized across all subjects. The median is used but unlike the original reference, the standard deviation is calculated rather than the maximum absolute deviation.

Value

A data frame like `dat` but with standardized columns added

Author(s)

Stefan Avey

References

Tsang JS, et al. (2014) Global analyses of human immune variation reveal baseline predictors of postvaccination responses. *Cell* 157(2):499–513.

Examples

```
## First Example
```

| | |
|--------------|--------------------------------|
| FormatTiters | <i>Format antibody titers.</i> |
|--------------|--------------------------------|

Description

FormatTiters formats titers into a list with one tidy data frame per viral strain

Usage

```
FormatTiters(titers, strains, subjectCol = "SubjectID",
  otherCols = vector(mode = "character"), d0Cols = paste0("d0_", strains),
  fcCols = paste0("fc_", strains), fcMinZero = TRUE, log2Transform = TRUE)
```

Arguments

| | |
|----------------------------|--|
| <code>titers</code> | a data frame containing the titer information |
| <code>strains</code> | the names of the virus strains |
| <code>subjectCol</code> | the name of the column specifying a subject ID. Default is "SubjectID". |
| <code>otherCols</code> | a character vector specifying which additional columns of titers to retain. (Defaults to an empty character vector). |
| <code>d0Cols</code> | the column names of day 0 (baseline) columns |
| <code>fcCols</code> | the column names of fold change columns |
| <code>fcMinZero</code> | should negative fold changes be set to 0? Default is TRUE |
| <code>log2Transform</code> | logical specifying whether titer values should be log2 transformed |

Value

a list of data frames with one data frame per viral strain containing the baseline ("d0"), fold change ("fc") and any other columns specified by the otherColumns argument.

Author(s)

Stefan Avey

Examples

```
strains <- c("A_California_7_2009", "A_Perth_16_2009", "B_Brisbane_60_2008")
titer_list <- FormatTiters(Year1_Titers, strains, subjectCol = "YaleID")
```

GetEqn

Get Formatted Model Equation

Description

GetEqn gets the equation for various models in a human readable format

Usage

```
GetEqn(m)
```

Arguments

m a model object

Author(s)

Stefan Avey

References

original lm_eqn and inspiration from this SO post <http://stackoverflow.com/questions/7549694/ggplot2-adding-regression-line-equation-and-r2-on-graph>.

Examples

```
## First Example
```

Multiplot

Multiple ggplot2 plots on the same page

Description

Multiple Plot Function for ggplot

Usage

```
Multiplot(..., plotlist = NULL, file, cols = 1, layout = NULL)
```

Arguments

| | |
|----------|---|
| ... | ggplot objects |
| plotlist | a list of ggplot objects |
| cols | Number of columns in layout |
| layout | A matrix specifying the layout. If present, 'cols' is ignored |

Details

If the layout is something like `matrix(c(1,2,3,3), nrow=2, byrow=TRUE)`, then plot 1 will go in the upper left, 2 will go in the upper right, and 3 will go all the way across the bottom.

Author(s)

R Cookbook

References

http://www.cookbook-r.com/Graphs/Multiple_graphs_on_one_page_%28ggplot2%29/

Examples

```
library(ggplot2)

## This example uses the ChickWeight dataset, which comes with ggplot2
## First plot
p1 <- ggplot(ChickWeight, aes(x=Time, y=weight, colour=Diet, group=Chick)) +
  geom_line() +
  ggtitle("Growth curve for individual chicks")

                                # Second plot
p2 <- ggplot(ChickWeight, aes(x=Time, y=weight, colour=Diet)) +
  geom_point(alpha=.3) +
  geom_smooth(alpha=.2, size=1) +
  ggtitle("Fitted growth curve per diet")

                                # Third plot
p3 <- ggplot(subset(ChickWeight, Time==21), aes(x=weight, colour=Diet)) +
  geom_density() +
  ggtitle("Final weight, by diet")
```

```

# Fourth plot
p4 <- ggplot(subset(ChickWeight, Time==21), aes(x=weight, fill=Diet)) +
  geom_histogram(colour="black", binwidth=50) +
  facet_grid(Diet ~ .) +
  ggtitle("Final weight, by diet") +
  theme(legend.position="none")      # No legend (redundant in this graph)

Multiplot(p1, p2, p3, p4, cols=2)

```

titeR

titeR - An R package for antibody titer data

Description

titeR - An R package for antibody titer data

Year1_Titers

Year 1 titers.

Description

Antibody titers to 3 strains of influenza in a cohort of young and older adults from Yale during the 2010-2011 flu season.

Usage

Year1_Titers

Format

A data frame with 42 rows and 11 variables:

YaleID subject identifier, unique

AgeGroup age of subject. 20-35 (Young), >= 65 (Older)

... Other columns follow the format <type>_<strain> where <type> is either Day 0 ("d0"), Day 28 ("d28"), or fold change ("fc").

References

Thakar J, et al. (2015) Aging-dependent alterations in gene expression and a mitochondrial signature of responsiveness to human influenza vaccination. *Aging (Albany NY)* 7(1):38-52.
<https://www.ncbi.nlm.nih.gov/pubmed/25596819>

| | |
|--------------|-----------------------|
| Year2_Titers | <i>Year 2 titers.</i> |
|--------------|-----------------------|

Description

Antibody titers to 3 strains of influenza in a cohort of young and older adults from Yale during the 2011-2012 flu season.

Usage

Year2_Titers

Format

A data frame with 69 rows and 11 variables:

YaleID subject identifier, unique

AgeGroup age of subject. 20-35 (Young), >= 65 (Older)

... Other columns follow the format <type>_<strain> where <type> is either Day 0 ("d0"), Day 28 ("d28"), or fold change ("fc").

References

Thakar J, et al. (2015) Aging-dependent alterations in gene expression and a mitochondrial signature of responsiveness to human influenza vaccination. *Aging (Albany NY)* 7(1):38-52.
<https://www.ncbi.nlm.nih.gov/pubmed/25596819>

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