

# Package ‘titer’

November 23, 2016

**Title** Tools for analyzing and visualizing antibody titer data

**Version** 0.0.2.0003

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

**Depends** R (>= 3.0.2)

**Imports** dplyr,  
ggplot2,  
grid,  
tidyr

**BugReports** <https://github.com/stefanavey/titer/issues>

**License** MIT + file LICENSE

**LazyData** true

**RoxygenNote** 5.0.1

**Suggests** knitr,  
rmarkdown

**VignetteBuilder** knitr

## R topics documented:

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<code>+.uneval</code>	<i>Addition for aes() and aes_string()</i>
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### 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>

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Barplot	<i>Titer bar plots.</i>
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### 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 <a href="#">FormatTiters</a> .
<code>subjectCol</code>	the name of the column specifying a subject ID. Default is "SubjectID".
<code>cols</code>	numeric specifying how many columns to layout plot
<code>groupVar</code>	an optional character string specifying a grouping variable. May be either a variable in <code>dat_list</code> or an endpoint. Default is NULL
<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

```
## Prepare the data
titer_list <- FormatTiters(Year1_Titers)

## Bar plot of a single strain
Barplot(titer_list["A California 7 2009"])

## Bar plot of all 3 strains
Barplot(titer_list)

## Can improve readability of previous plot by separating into groups
## For example, group by AgeGroup
Barplot(titer_list, groupVar = "AgeGroup")
```

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BubbleChart	<i>Bubble Chart</i>
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## Description

BubbleChart visualizes baseline vs fold change in titers

## Usage

```
BubbleChart(dat_list, subjectCol = "SubjectID", fit = NULL,
  yMinZero = FALSE, eqSize = 6/log2(length(dat_list) + 1), colorBy = NULL,
  xlimits = c(1.5, 10.5), xbreaks = 2:10, ylimits = c(-0.5, 10),
  ybreaks = seq(0, 10, 2), plot = TRUE, cols = 2, ...)
```

## Arguments

dat_list	a named list like the one returned by <a href="#">FormatTiters</a> . Values are assumed to be log2-transformed.
subjectCol	the name of the column specifying a subject ID. Default is "SubjectID".
fit	what type of fit to add. Current options are "lm" for linear model, "exp" for exponential, or NULL for no smoothing.
yMinZero	a logical specifying whether fitted y values below 0 should be set to 0.
eqSize	Text size of the equation. Only relevant if fit is not NULL
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> )
ylimits	the y-axis limits (passed to <code>scale_y_continuous</code> )
ybreaks	the y-axis breaks (passed to <code>scale_y_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 <a href="#">CalculateSadjMFC</a> .

**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
titer_list <- FormatTiters(Year2_Titers)

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

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

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

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

## Add coloring by age
BubbleChart(titer_list, fit = "exp", colorBy = "AgeGroup")
```

---

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**

dat	the data containing the columns fcCol and d0Col
fcCol	character string specifying the name of the fold change column from dat
d0Col	character string specifying the name of the day 0 column from dat
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
...	Additional arguments passed to lm

**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(dat_list, subjectCol = "SubjectID", method = c("exp",
  "lm"), yMinZero = FALSE, scoreFun = max, discretize = c(0.2, 0.3),
  normalize = TRUE, scaleResiduals = FALSE,
  responseLabels = paste0(c("low", "moderate", "high"), "Responder"),
  na_action = "na.fail", ...)
```

**Arguments**

dat_list	a named list like the one returned by <a href="#">FormatTiters</a> .
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.
yMinZero	a logical specifying whether fitted y values below 0 should be set to 0.
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.
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%.
normalize	Logical specifying whether residuals should be normalized with the inverse normal transform. Default is TRUE.

**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 `dat_list`)

**residualMatrix** the matrix of residuals

**SAdjMFC** a list containing the continuous and discrete SAdjMFC metrics

## Author(s)

Stefan Avey

## See Also

`lm`, `nls`

## Examples

```
## Prepare the data
titer_list <- FormatTiters(Year2_Titers)

## Using a linear fit
endpoints <- CalculateSAdjMFC(titer_list, method = "lm")
summary(endpoints)
## Get discrete endpoints using upper/lower 30%
endpoints$SAdjMFC_d30

## Get endpoints with a 50% split into high and low
endpoints <- CalculateSAdjMFC(titer_list, method = "exp", discretize = 0.5)
endpoints$SAdjMFC_d50
```

---

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 standardized. 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
```



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FormatTiters	<i>Format antibody titers.</i>
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### Description

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

### Usage

```
FormatTiters(titers, log2Transform = TRUE, fcMinZero = TRUE)
```

### Arguments

titers	a data frame containing one row per subject per strain. The following columns are required: <b>SubjectID</b> Subject IDs (column name can vary) <b>Strain</b> The name of the viral strain for the observation <b>Pre</b> The pre-vaccination (or pre-infection) titer <b>Post</b> The post-vaccination (or post-infection) titer ... Other columns which will be preserved
log2Transform	logical specifying whether titer values should be log2 transformed
fcMinZero	should negative fold changes be set to 0? Default is TRUE

### Value

a list of data frames with one data frame per viral strain containing the "Pre" and "Post" titer measurements (row names are removed).

### Author(s)

Stefan Avey

### Examples

```
titer_list <- FormatTiters(Year1_Titers, log2Transform = TRUE, fcMinZero = TRUE)
```

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FormatTiters_OLD	<i>Format antibody titers.</i>
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---

### Description

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

### Usage

```
FormatTiters_OLD(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**

<code>m</code>	a model object
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**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>.

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Multiplot	<i>Multiple ggplot2 plots on the same page</i>
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---

## Description

Multiple Plot Function for ggplot

## Usage

```
Multiplot(..., plotlist = NULL, 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/](http://www.cookbook-r.com/Graphs/Multiple_graphs_on_one_page_%28ggplot2%29/)

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titeR	<i>titeR - An R package for antibody titer data</i>
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## Description

titeR - An R package for antibody titer data

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Year1_Titers	<i>Year 1 titers.</i>
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### 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:

**SubjectID** a unique subject identifier

**AgeGroup** age of subject. 20-35 (Young), 65+ (Older)

**Strain** The name of the viral strain for the observation

**Pre** The pre-vaccination titer

**Post** The post-vaccination titer

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

### 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:

**SubjectID** a unique subject identifier

**AgeGroup** age of subject. 20-35 (Young), 65+ (Older)

**Strain** The name of the viral strain for the observation

**Pre** The pre-vaccination titer

**Post** The post-vaccination titer

## 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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