

Package: CytoGLMM (via r-universe)

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Type Package

Title Conditional Differential Analysis for Flow and Mass Cytometry Experiments

Version 1.13.0

Description The CytoGLMM R package implements two multiple regression strategies: A bootstrapped generalized linear model (GLM) and a generalized linear mixed model (GLMM). Most current data analysis tools compare expressions across many computationally discovered cell types. CytoGLMM focuses on just one cell type. Our narrower field of application allows us to define a more specific statistical model with easier to control statistical guarantees. As a result, CytoGLMM finds differential proteins in flow and mass cytometry data while reducing biases arising from marker correlations and safeguarding against false discoveries induced by patient heterogeneity.

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URL <https://christofseiler.github.io/CytoGLMM>,
<https://github.com/ChristofSeiler/CytoGLMM>

BugReports <https://github.com/ChristofSeiler/CytoGLMM/issues>

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LazyData true

Imports stats, methods, BiocParallel, RColorBrewer, cowplot, doParallel, dplyr, factoextra, flexmix, ggplot2, magrittr, mbest, pheatmap, stringr, strucchange, tibble, ggrepel, MASS, logging, Matrix, tidyr, caret, rlang, grDevices

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biocViews FlowCytometry, Proteomics, SingleCell, CellBasedAssays, CellBiology, ImmunoOncology, Regression, StatisticalMethod, Software

Repository <https://bioc.r-universe.dev>

RemoteUrl <https://github.com/bioc/CytoGLMM>

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cytoflexmix

Logistic mixture regression

Description

Logistic mixture regression

Usage

```
cytoflexmix(
  df_samples_subset,
  protein_names,
  condition,
  group = "donor",
  cell_n_min = Inf,
  cell_n_subsample = 0,
  ks = seq_len(10),
  num_cores = 1
)
```

Arguments

<code>df_samples_subset</code>	Data frame or tibble with proteins counts, cell condition, and group information
<code>protein_names</code>	A vector of column names of protein to use in the analysis
<code>condition</code>	The column name of the condition variable
<code>group</code>	The column name of the group variable
<code>cell_n_min</code>	Remove samples that are below this cell counts threshold
<code>cell_n_subsample</code>	Subsample samples to have this maximum cell count
<code>ks</code>	A vector of cluster sizes
<code>num_cores</code>	Number of computing cores

Value

A list of class `cytoglm` containing

<code>flexmixfits</code>	list of <code>flexmix</code> objects
<code>df_samples_subset</code>	possibly subsampled <code>df_samples_subset</code> table
<code>protein_names</code>	input protein names
<code>condition</code>	input condition variable
<code>group</code>	input group names
<code>cell_n_min</code>	input <code>cell_n_min</code>
<code>cell_n_subsample</code>	input <code>cell_n_subsample</code>
<code>ks</code>	input <code>ks</code>
<code>num_cores</code>	input <code>num_cores</code>

Examples

```

set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
mix_fit <- CytoGLMM::cytoflexmix(df,
                                protein_names = protein_names,
                                condition = "condition",
                                group = "donor",
                                ks = 2)

mix_fit

```

cytoglm

*Fit GLM with bootstrap resampling***Description**

Fit GLM with bootstrap resampling

Usage

```

cytoglm(
  df_samples_subset,
  protein_names,
  condition,
  group = "donor",
  covariate_names = NULL,
  cell_n_min = Inf,
  cell_n_subsample = 0,
  num_boot = 100,
  num_cores = 1
)

```

Arguments

<code>df_samples_subset</code>	Data frame or tibble with proteins counts, cell condition, and group information
<code>protein_names</code>	A vector of column names of protein to use in the analysis
<code>condition</code>	The column name of the condition variable
<code>group</code>	The column name of the group variable
<code>covariate_names</code>	The column names of covariates
<code>cell_n_min</code>	Remove samples that are below this cell counts threshold
<code>cell_n_subsample</code>	Subsample samples to have this maximum cell count
<code>num_boot</code>	Number of bootstrap samples
<code>num_cores</code>	Number of computing cores

Value

A list of class `cytoGLM` containing

<code>tb_coef</code>	coefficient table
<code>df_samples_subset</code>	possibly subsampled <code>df_samples_subset</code> table
<code>protein_names</code>	input protein names
<code>condition</code>	input condition variable
<code>group</code>	input group names
<code>covariate_names</code>	input covariates
<code>cell_n_min</code>	input <code>cell_n_min</code>
<code>cell_n_subsample</code>	input <code>cell_n_subsample</code>
<code>unpaired</code>	true if unpaired samples were provided as input
<code>num_boot</code>	input <code>num_boot</code>
<code>num_cores</code>	input <code>num_cores</code>
<code>formula_str</code>	formula use in the regression model

Examples

```
set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
glm_fit <- CytoGLMM::cytoGLM(df,
                             protein_names = protein_names,
                             condition = "condition",
                             group = "donor",
                             num_boot = 10) # in practice >=1000
glm_fit
```

 cytoGLMM

Fit GLMM with method of moments

Description

Fit GLMM with method of moments

Usage

```
cytoglmm(
  df_samples_subset,
  protein_names,
  condition,
  group = "donor",
  covariate_names = NULL,
  cell_n_min = Inf,
  cell_n_subsample = 0,
  num_cores = 1
)
```

Arguments

<code>df_samples_subset</code>	Data frame or tibble with proteins counts, cell condition, and group information
<code>protein_names</code>	A vector of column names of protein to use in the analysis
<code>condition</code>	The column name of the condition variable
<code>group</code>	The column name of the group variable
<code>covariate_names</code>	The column names of covariates
<code>cell_n_min</code>	Remove samples that are below this cell counts threshold
<code>cell_n_subsample</code>	Subsample samples to have this maximum cell count
<code>num_cores</code>	Number of computing cores

Value

A list of class `cytoglm` containing

<code>glmfit</code>	<code>mbest</code> object
<code>df_samples_subset</code>	possibly subsampled <code>df_samples_subset</code> table
<code>protein_names</code>	input protein names
<code>condition</code>	input condition variable
<code>group</code>	input group names
<code>covariate_names</code>	input covariates
<code>cell_n_min</code>	input <code>cell_n_min</code>
<code>cell_n_subsample</code>	input <code>cell_n_subsample</code>
<code>num_cores</code>	input <code>num_cores</code>

Examples

```

set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
glmm_fit <- CytoGLMM::cytoglmm(df,
                               protein_names = protein_names,
                               condition = "condition",
                               group = "donor")

glmm_fit

```

cytgroup

Group-specific fixed effects model

Description

Group-specific fixed effects model

Usage

```

cytgroup(
  df_samples_subset,
  protein_names,
  condition,
  group = "donor",
  cell_n_min = Inf,
  cell_n_subsample = 0
)

```

Arguments

df_samples_subset	Data frame or tibble with proteins counts, cell condition, and group information
protein_names	A vector of column names of protein to use in the analysis
condition	The column name of the condition variable
group	The column name of the group variable
cell_n_min	Remove samples that are below this cell counts threshold
cell_n_subsample	Subsample samples to have this maximum cell count

Value

A list of class `cytoglm` containing

groupfit	<code>glm</code> object
df_samples_subset	possibly subsampled df_samples_subset table

```

protein_names  input protein names
condition      input condition variable
group         input group names
cell_n_min    input cell_n_min
cell_n_subsample
              input cell_n_subsample

```

Examples

```

set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
group_fit <- CytoGLMM::cytogroup(df,
                                protein_names = protein_names,
                                condition = "condition",
                                group = "donor")

group_fit

```

cytostab

Evaluate parameter stability with respect to gating scheme

Description

Evaluate parameter stability with respect to gating scheme

Usage

```

cytostab(
  df_samples_subset,
  protein_names,
  condition,
  group = "donor",
  cell_n_min = Inf,
  cell_n_subsample = 0
)

```

Arguments

```

df_samples_subset      Data frame or tibble with proteins counts, cell condition, and group information
protein_names         A vector of column names of protein to use in the analysis
condition             The column name of the condition variable
group                 The column name of the group variable
cell_n_min           Remove samples that are below this cell counts threshold
cell_n_subsample     Subsample samples to have this maximum cell count

```


Value

A data frame

Examples

```
set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
stab <- CytoGLMM::cytostab(df,
                           protein_names = protein_names,
                           condition = "condition",
                           group = "donor")

stab
```

cyto_check

Check if input to cytoxxx function have errors

Description

Check if input to cytoxxx function have errors

Usage

```
cyto_check(cell_n_subsample, cell_n_min, protein_names)
```

Arguments

cell_n_subsample Subsample samples to have this maximum cell count

cell_n_min A vector of column names of protein to use in the analysis

protein_names A vector of column names of protein to use in the analysis

Value

NULL.

generate_data *Generate dataset for vignettes and simulation studies*

Description

Generate dataset for vignettes and simulation studies

Usage

```
generate_data()
```

Value

[tibble](#) data frame

Examples

```
set.seed(23)
df <- generate_data()
str(df)
df
```

glmm_moment *Generalized linear mixed model with maximum likelihood*

Description

Generalized linear mixed model with maximum likelihood

Usage

```
glmm_moment(
  df_samples,
  protein_names,
  response,
  group = "donor",
  covariate_names = NULL,
  num_cores = 1
)
```

Arguments

df_samples	Data frame or tibble with proteins counts, cell condition, and group information
protein_names	A vector of column names of protein to use in the analysis
response	The column name of the condition variable
group	The column name of the group variable
covariate_names	The column names of covariates
num_cores	Number of computing cores

Value

`mbest` object

is_unpaired	<i>Check if samples match or paired on condition</i>
-------------	--

Description

Check if samples match or paired on condition

Usage

```
is_unpaired(df_samples_subset, condition, group)
```

Arguments

df_samples_subset	Data frame or tibble with proteins counts, cell condition, and group information
condition	The column name of the condition variable
group	The column name of the group variable

Value

A boolean

plot.cytoflexmix *Plot all components of mixture regression*

Description

Plot all components of mixture regression

Usage

```
## S3 method for class 'cytoflexmix'
plot(x, k = NULL, separate = FALSE, ...)
```

Arguments

x	A cytoflexmix class
k	Number of clusters
separate	create two separate ggplot2 objects
...	Other parameters

Value

[ggplot2](#) object

Examples

```
set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
mix_fit <- CytoGLMM::cytoflexmix(df,
                                protein_names = protein_names,
                                condition = "condition",
                                group = "donor",
                                ks = 2)

plot(mix_fit)
```

plot.cytoglm *Plot bootstrapped coefficients*

Description

Plot bootstrapped coefficients

Usage

```
## S3 method for class 'cytoglm'
plot(x, order = FALSE, separate = FALSE, ...)
```

Arguments

x	A cytoglm class
order	Order the markers according to the mangintute of the coefficients
separate	create two separate <code>ggplot2</code> objects
...	Other parameters

Value

`ggplot2` object

Examples

```
set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
glm_fit <- CytoGLMM::cytoglm(df,
                             protein_names = protein_names,
                             condition = "condition",
                             group = "donor",
                             num_boot = 10) # in practice >=1000
plot(glm_fit)
```

plot.cytoglm	<i>Plot fixed coefficients of random effects model</i>
--------------	--

Description

Plot fixed coefficients of random effects model

Usage

```
## S3 method for class 'cytoglm'
plot(x, order = FALSE, separate = FALSE, ...)
```

Arguments

x	A cytoglm class
order	Order the markers according to the mangintute of the coefficients
separate	create two separate <code>ggplot2</code> objects
...	Other parameters

Value

`ggplot2` object

plot_coeff	<i>Helper function to plot regression coefficient</i>
------------	---

Description

Helper function to plot regression coefficient

Usage

```
plot_coeff(
  tb,
  title_str,
  title_str_right,
  xlab_str,
  redline = 0,
  order = FALSE,
  separate = FALSE
)
```

Arguments

tb	A data frame
title_str	Title string for summary plot
title_str_right	Title for bootstrap sample plot
xlab_str	Label on x-axis
redline	Point on x-axis to draw the red line
order	Order the markers according to the magnitude of the coefficients
separate	Plot both summary and bootstrap samples

Value

[ggplot2](#) object or list of two objects if separate is true

plot_heatmap	<i>Heatmap of median marker expression</i>
--------------	--

Description

Heatmap of median marker expression

Usage

```
plot_heatmap(
  df_samples,
  sample_info_names,
  protein_names,
  arrange_by_1,
  arrange_by_2 = "",
  cluster_cols = FALSE,
  fun = median
)
```

Arguments

<code>df_samples</code>	Data frame or tibble with proteins counts, cell condition, and group information
<code>sample_info_names</code>	Column names that contain information about the cell, e.g. donor, condition, file name, or cell type
<code>protein_names</code>	A vector of column names of protein to use in the analysis
<code>arrange_by_1</code>	Column name
<code>arrange_by_2</code>	Column name
<code>cluster_cols</code>	Apply hierarchical cluster to columns
<code>fun</code>	Summary statistics of marker expression

Value

`pheatmap` object

Examples

```
set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
CytoGLMM::plot_heatmap(df,
  protein_names = protein_names,
  sample_info_names = c("donor", "condition"),
  arrange_by_1 = "condition")
```

plot_lda

LDA on marker expression

Description

LDA on marker expression

Usage

```
plot_lda(
  df_samples,
  protein_names,
  group,
  cor_scaling_factor = 1,
  arrow_color = "black",
  marker_color = "black",
  marker_size = 5
)
```

Arguments

df_samples	Data frame or tibble with proteins counts, cell condition, and group information
protein_names	A vector of column names of protein to use in the analysis
group	The column name of the group variable
cor_scaling_factor	Scaling factor of circle of correlations
arrow_color	Color of correlation circle
marker_color	Colors of marker names
marker_size	Size of markerr names

Value

`ggplot2` object

Examples

```
set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
df$condition <- rep(c("A", "B", "C", "D"), each = length(df$condition)/4)
CytoGLMM::plot_lda(df,
  protein_names = protein_names,
  group = "condition",
  cor_scaling_factor = 2)
```

plot_mds

MDS on median marker expression

Description

MDS on median marker expression

Usage

```
plot_mds(
  df_samples,
  protein_names,
  sample_info_names,
  color,
  sample_label = ""
)
```

Arguments

df_samples	Data frame or tibble with proteins counts, cell condition, and group information
protein_names	A vector of column names of protein to use in the analysis
sample_info_names	Column names that contain information about the cell, e.g. donor, condition, file name, or cell type
color	Column name
sample_label	Column name

Value

cowplot object

Examples

```
set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
CytoGLMM::plot_mds(df,
  protein_names = protein_names,
  sample_info_names = c("donor", "condition"),
  color = "condition")
```

plot_model_selection *Plot model selection to choose number optimal number of clusters*

Description

Plot model selection to choose number optimal number of clusters

Usage

```
plot_model_selection(fit, k = NULL)
```

Arguments

fit A cytoflexmix class
 k Number of clusters

Value

cowplot object

Examples

```
set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
mix_fit <- CytoGLMM::cytoflexmix(df,
                                protein_names = protein_names,
                                condition = "condition",
                                group = "donor",
                                ks = 1:2)
plot_model_selection(mix_fit)
```

 plot_prcomp

Plot PCA of subsampled data using ggplot

Description

Plot PCA of subsampled data using ggplot

Usage

```
plot_prcomp(
  df_samples,
  protein_names,
  color_var = "treatment",
  subsample_size = 10000,
  repel = TRUE
)
```

Arguments

df_samples Data frame or tibble with proteins counts, cell condition, and group information
 protein_names A vector of column names of protein to use in the analysis
 color_var A column name
 subsample_size Subsample per color_var variable
 repel Repel labels

Value

cowplot object

Examples

```
set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
CytoGLMM::plot_prcomp(df,
                      protein_names = protein_names,
                      color_var = "condition")
```

```
print.cytoglm
```

```
Extract and print bootstrap GLM fit
```

Description

Extract and print bootstrap GLM fit

Usage

```
## S3 method for class 'cytoglm'
print(x, ...)
```

Arguments

x	A cytoglm class
...	Other parameters

Value

NULL.

Examples

```
set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
glm_fit <- CytoGLMM::cytoglm(df,
                             protein_names = protein_names,
                             condition = "condition",
                             group = "donor",
                             num_boot = 10) # in practice >=1000

print(glm_fit)
```

print.cytoglmm	<i>Extact and print GLMM fit</i>
----------------	----------------------------------

Description

Extact and print GLMM fit

Usage

```
## S3 method for class 'cytoglmm'  
print(x, ...)
```

Arguments

x	A cytoglmm class
...	Other parameters

Value

NULL.

Examples

```
set.seed(23)  
df <- generate_data()  
protein_names <- names(df)[3:12]  
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))  
glmm_fit <- CytoGLMM::cytoglmm(df,  
                               protein_names = protein_names,  
                               condition = "condition",  
                               group = "donor")  
  
print(glmm_fit)
```

remove_samples	<i>Remove samples based on low cell counts</i>
----------------	--

Description

Remove samples based on low cell counts

Usage

```
remove_samples(df_samples_subset, condition, group, unpaired, cell_n_min)
```

Arguments

df_samples_subset	Data frame or tibble with proteins counts, cell condition, and group information
condition	The column name of the condition variable
group	The column name of the group variable
unpaired	true if unpaired samples were provided as input
cell_n_min	Remove samples that are below this cell counts threshold

Value

NULL.

summary.cytoglm	<i>Extract and calculate p-values of bootstrap GLM fit</i>
-----------------	--

Description

Extract and calculate p-values of bootstrap GLM fit

Usage

```
## S3 method for class 'cytoglm'
summary(object, method = "BH", ...)
```

Arguments

object	A cytoglm class
method	Multiple comparison adjustment method
...	Other parameters

Value

[tibble](#) data frame

Examples

```
set.seed(23)
df <- generate_data()
protein_names <- names(df)[3:12]
df <- dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))
glm_fit <- CytoGLMM::cytoglm(df,
                             protein_names = protein_names,
                             condition = "condition",
                             group = "donor",
                             num_boot = 10) # in practice >=1000

summary(glm_fit)
```

summary.cytoglmm	<i>Extract and calculate p-values of GLMM fit</i>
------------------	---

Description

Extract and calculate p-values of GLMM fit

Usage

```
## S3 method for class 'cytoglmm'  
summary(object, method = "BH", ...)
```

Arguments

object	A cytoglmm class
method	Multiple comparison adjustment method
...	Other parameters

Value

[tibble](#) data frame

Examples

```
set.seed(23)  
df = generate_data()  
protein_names = names(df)[3:12]  
df = dplyr::mutate_at(df, protein_names, function(x) asinh(x/5))  
glmm_fit = CytoGLMM::cytoglmm(df,  
                               protein_names = protein_names,  
                               condition = "condition",  
                               group = "donor")  
  
summary(glmm_fit)
```

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