

# Package ‘CyTOFpower’

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**Type** Package

**Title** Power analysis for CyTOF experiments

**Version** 1.8.0

**Description** This package is a tool to predict the power of CyTOF experiments in the context of differential state analyses. The package provides a shiny app with two options to predict the power of an experiment:  
i. generation of in-silico CyTOF data, using users input  
ii. browsing in a grid of parameters for which the power was already precomputed.

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**License** LGPL-3

**Encoding** UTF-8

**Depends** R (>= 4.1)

**Imports** CytoGLMM, diffcyt, DT, dplyr, ggplot2, magrittr, methods, rlang, stats, shiny, shinyFeedback, shinyjs, shinyMatrix, SummarizedExperiment, tibble, tidy

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**VignetteBuilder** knitr

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**Config/testthat/edition** 3

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compute_effectsize	<i>Compute effect size</i>
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---

### Description

Compute effect size

### Usage

```
compute_effectsize(raw_data_lg)
```

### Arguments

raw\_data\_lg      data.frame, cells values in long format.

### Details

Compute observed Cohen's effect size and observed fold change.

**Value**

data.frame, Cohen's effect size and fold change that were observed in the data for each marker.

---

compute_pwr	<i>Compute power</i>
-------------	----------------------

---

**Description**

Compute power

**Usage**

```
compute_pwr(model_values, alpha = 0.05)
```

**Arguments**

model_values	data.frame, output of run_models().
alpha	numeric, significance level.

**Details**

Compute the power based on the model values.

**Value**

numeric, power.

---

compute_variance	<i>Compute variance</i>
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---

**Description**

Compute variance

**Usage**

```
compute_variance(raw_data_lg)
```

**Arguments**

raw_data_lg	data.frame, cells values in long format.
-------------	--

**Details**

Compute the observed variance in the data.

**Value**

numeric, observed variance mean.

---

CyTOFpower

*CyTOFpower: R-package to predict the power of a CyTOF experiment*

---

### Description

This package provides functions and a shiny app to predict the power of a CyTOF experiment.  
Interactive shiny app to predict the power of a CyTOF experiment.

### Usage

```
CyTOFpower()
```

### Value

Interactive shiny app.

### Examples

```
# Launch the shiny app
if (interactive()) {
  CyTOFpower()
}
```

---

function\_apply\_modelcomputations\_modelchoice

*Run DS tests for one simulation.*

---

### Description

Run DS tests for one simulation.

### Usage

```
function_apply_modelcomputations_modelchoice(
  list_combined_output,
  model = c("cytoglm", "cytoglm", "testDS_limma_random", "testDS_limma_fixed",
            "testDS_lmm")
)
```

### Arguments

`list_combined_output` list, of simulated data (output of the function\_apply\_onesimulation\_withmarkerinfo function).

`model` vector, name(s) of models to test.

**Details**

Wrapper to run the models through the different simulations.

**Value**

data.frame of results for each simulation.

---

function\_apply\_onesimulation\_withmarkerinfo

*One simulation with markers NB information.*

---

**Description**

One simulation with markers NB information.

**Usage**

```
function_apply_onesimulation_withmarkerinfo(variation)
```

**Arguments**

variation      list, list of list containing the different input parameter variations @describeIn  
function\_create\_mock\_dataset\_withmarkerinfo.

**Details**

Apply one simulation for a given parameter combination number times (iterations), when we have prior information about the markers distribution parameters (mean and dispersion of the negative binomial).

**Value**

list of simulated data. Each list member contains 5 slots: - variation: the variation of input parameters which has been used in input; - df\_info: experimental information (donor IDs, group IDs, samples IDs); - DE\_markers\_names: name of the differentially expressed markers; - ls\_mock\_data: list of data.frames, each data.frame being one simulation of the cell values using the input parameters provided (list is length nb\_sim).

function\_check\_nbDEmarkers

*Number of DE markers greater than 1.*

---

**Description**

Number of DE markers greater than 1.

**Usage**

```
function_check_nbDEmarkers(nb_DEmarker)
```

**Arguments**

nb\_DEmarker      numeric, number of differentially expressed markers.

**Details**

Function to check that the number of DE markers is greater than 1.

**Value**

error message

---

function\_check\_nbmarkers

*Number of markers greater than 2.*

---

**Description**

Number of markers greater than 2.

**Usage**

```
function_check_nbmarkers(nb_marker)
```

**Arguments**

nb\_marker      numeric, total number of markers.

**Details**

Function to check that the number of markers is greater than 2.

**Value**

error message if the total number of markers is lower than 3.

---

```
function_compute_diffcyt_features
```

*Compute cells counts and medians.*

---

**Description**

Compute cells counts and medians.

**Usage**

```
function_compute_diffcyt_features(mock_flowset)
```

**Arguments**

mock\_flowset     data.frame, cell values for each marker.

**Details**

Function to calculate features for diffcyt package models.

**Value**

list with cell counts and medians for each markers.

---

```
function_create_mock_dataset_withmarkerinfo
```

*Compute simulated cell values for one simulation with markers NB information.*

---

**Description**

Compute simulated cell values for one simulation with markers NB information.

**Usage**

```
function_create_mock_dataset_withmarkerinfo(variation)
```

**Arguments**

variation     list, list of data.frames containing the different variable input parameters to generate the data: - marker\_name: name of the marker (character); - nb\_donor: number of donors; - rho: fold change; - subject\_effect: standard deviation for the normal distribution from which the donor's means will be drawn; - mu0: mean of the negative binomial for the gamma distribution from which the means of the different donor will be drawn; - dispersion: dispersion of the negative binomial from which the DE marker's cell values will be drawn; - nb\_cell\_per\_sample: number of cells per sample.

**Details**

Function to compute the simulated cell values using a combination of variable parameters, when we have prior information about the markers distribution parameters (mean and dispersion of the negative binomial).

**Value**

list with 4 slots: - df\_info: data.frame of experimental information; - DEmarkers\_names: vector of DE marker names; - raw\_data: data.frame of raw cell values; - data: data.frame of transformed cell values.

---

function\_DEmarkers\_sup\_nbmarkers

*Check on the number of DE markers.*

---

**Description**

Check on the number of DE markers.

**Usage**

```
function_DEmarkers_sup_nbmarkers(nb_markers, nb_DEmarker)
```

**Arguments**

nb\_markers      numeric, total number of markers.

nb\_DEmarker    numeric, number of differentially expressed markers.

**Details**

Function to check that number of DE markers greater than number of markers.

**Value**

error message if the number of DE markers is greater than the total number of markers.



---

function\_desigmat\_contrast\_diffcytDSLimma\_fixedeffect

*Design and contrast matrices for diffcyt-DS-limma with fixed effect.*

---

### **Description**

Design and contrast matrices for diffcyt-DS-limma with fixed effect.

### **Usage**

```
function_desigmat_contrast_diffcytDSLimma_fixedeffect(df_experiment_info)
```

### **Arguments**

df\_experiment\_info

data.frame, information about the experiment (donor IDs, group IDs and sample IDs).

### **Details**

Function to create the design matrix and contrast for the diffcyt-DS-limma model with fixed effect.

### **Value**

list with 3 slots: - design\_matrix: the design matrix; - contrast: the contrast matrix; - effect: the specification of the "fixed" effect.

---

function\_desigmat\_contrast\_diffcytDSLimma\_randomeffect

*Design and contrast matrices for diffcyt-DS-limma with random effect.*

---

### **Description**

Design and contrast matrices for diffcyt-DS-limma with random effect.

### **Usage**

```
function_desigmat_contrast_diffcytDSLimma_randomeffect(df_experiment_info)
```

### **Arguments**

df\_experiment\_info

data.frame, information about the experiment (donor IDs, group IDs and sample IDs).

**Details**

Function to create the design matrix and contrast for the diffcyt-DS-limma model with random effect from the diffcyt package.

**Value**

list with 3 slots: - design\_matrix: the design matrix; - contrast: the contrast matrix; - effect: the specification of the "random" effect.

---

function\_extract\_marker\_names

*Extract marker names.*

---

**Description**

Extract marker names.

**Usage**

```
function_extract_marker_names(mock_dataset)
```

**Arguments**

mock\_dataset    data.frame, containing the cell values for each marker.

**Details**

Function to extract the marker names.

**Value**

vector of marker names.

---

function\_formula\_contrast\_diffcytDSLMM\_randomeffect

*Formula and contrast matrix for diffcyt-DS-LMM with random effect.*

---

**Description**

Formula and contrast matrix for diffcyt-DS-LMM with random effect.

**Usage**

```
function_formula_contrast_diffcytDSLMM_randomeffect(df_experiment_info)
```

**Arguments**

df\_experiment\_info  
data.frame, information about the experiment (donor IDs, group IDs and sample IDs).

**Details**

Function to create formula and contrast for diffcyt-DS-LMM with random effect.

**Value**

list with 3 slots: - formula: the formula for the model; - contrast: the contrast matrix.

---

function\_is\_data\_paired  
*Data paired.*

---

**Description**

Data paired.

**Usage**

```
function_is_data_paired(data)
```

**Arguments**

data data.frame, experimental information containing (sample IDS, donor IDS).

**Details**

Function to check if the data is paired.

**Value**

logical, TRUE is the data are paired - FALSE if the data are not paired

---

function\_names\_DE\_markers

*Generate name of the DE markers.*

---

### Description

Generate name of the DE markers.

### Usage

```
function_names_DE_markers(total_nb_marker, nb_DE_marker)
```

### Arguments

total\_nb\_marker      numeric, total number of markers.  
nb\_DE\_marker        numeric, number of DE markers.

### Details

Function to generate the name of the DE markers.

### Value

vector of marker names.

---

function\_run\_bootstrapcytoGLMM

*Run cytoglm.*

---

### Description

Run cytoglm.

### Usage

```
function_run_bootstrapcytoGLMM(mock_dataset, nb_bootstrap = 500)
```

### Arguments

mock\_dataset      data.frame, cell values for each marker.  
nb\_bootstrap      numeric, number of bootstrap (by defaults nb\_bootstrap = 1000).

### Details

Function to run the Generalized Linear Model with Bootstrap, from the CytoGLMM package.

**Value**

list of 3 slots: - model\_fit: fit of the model; - plot: plot of the effects; - results\_summary: data.frame containing the results of the models for each marker.

---

function\_run\_cytoGLMM *Run cytoglmm*

---

**Description**

Run cytoglmm

**Usage**

```
function_run_cytoGLMM(mock_dataset)
```

**Arguments**

mock\_dataset    data.frame, cell values for each marker.

**Details**

Function to run GLMM model from CytoGLMM package.

**Value**

list of 3 slots: - model\_fit: fit of the model; - plot: plot of the effects; - results\_summary: data.frame containing the results of the models for each marker.

---

function\_run\_diffcytDSLimma  
*Run diffcyt-DS-limma model.*

---

**Description**

Run diffcyt-DS-limma model.

**Usage**

```
function_run_diffcytDSLimma(  
  ls_desigmat_contrast,  
  df_experiment_info,  
  ls_features  
)
```

**Arguments**

- ls\_designmat\_contrast      list, with design and contrast matrices.
- df\_experiment\_info        data.frame, information about the experiment (donor IDs, group IDs and sample IDs).
- ls\_features                list, with cell counts and medians for each markers.

**Details**

Function to run diffcyt-DS-limma model from the diffcyt package.

**Value**

list with 2 slots: - model\_fit: the model fit; - result\_summary: results of the model for each marker.

---

function\_run\_diffcytDSLMM  
*Run diffcyt-DS-LMM model.*

---

**Description**

Run diffcyt-DS-LMM model.

**Usage**

```
function_run_diffcytDSLMM(ls_form_contrast, df_experiment_info, ls_features)
```

**Arguments**

- ls\_form\_contrast        list, with formula and constrat matrix.
- df\_experiment\_info     data.frame, information about the experiment (donor IDs, group IDs and sample IDs).
- ls\_features             list, with cell counts and medians for each markers.

**Details**

Function to run diffcyt-DS-LMM model from the diffcyt package.

**Value**

list with 2 slots: - model\_fit: the model fit; - result\_summary: results of the model for each marker.

---

function\_run\_diffcyt\_full\_pipeline  
*Run diffcyt pipeline*

---

**Description**

Run diffcyt pipeline

**Usage**

```
function_run_diffcyt_full_pipeline(  
  onevariation,  
  model = c("limma", "LMM"),  
  effect = c("random", "fixed")  
)
```

**Arguments**

onevariation	list, of simulated data (output of the function_wrapper_apply_simulation_nbtimes function).
model	character, model to run: "limma" or "LMM".
effect	character, effect: "random" or "fixed".

**Details**

Function to run diffcyt pipeline. We do not used the diffcyt function directly because of the limma model run differently with the effects.

**Value**

list with 2 slots: - model\_fit: the model fit; - result\_summary: results of the model for each marker.

---

function\_summary\_results\_models  
*Summarize data and results.*

---

**Description**

Summarize data and results.

**Usage**

```
function_summary_results_models(summary_from_model, package)
```

**Arguments**

summary\_from\_model      list, output from the functions running the models.

package                  character, package used to run the test: "CytoGLMM" or "diffcyt".

**Details**

Function to do a summary of the tested data and model's results for the CytoGLMM and diffcyt packages.

**Value**

data.frame of results for each simulation.

---

*function\_to\_compute\_model\_computation\_onesimulation\_modelchoice*  
*Run DS tests for one simulation.*

---

**Description**

Run DS tests for one simulation.

**Usage**

```
function_to_compute_model_computation_onesimulation_modelchoice(
  onevariation,
  model
)
```

**Arguments**

onevariation      list, of simulated data (output of the function\_wrapper\_apply\_simulation\_nbtimes function).

model              vector, name(s) of models to test.

**Details**

Function to run the DS tests through the different models.

**Value**

data.frame of results for each simulation all models combined.



---

function\_to\_transform\_data  
*arcsinh transformation.*

---

**Description**

arcsinh transformation.

**Usage**

```
function_to_transform_data(data, cofactor = 5)
```

**Arguments**

data                data.frame, cell values to transform.  
cofactor            numeric, co-factor used in the arcsinh (by default cofactor = 5).

**Details**

Function to transform the data with the recommended transformation for cyTOF data: arcsinh with cofactor equals to 5.

**Value**

data.frame of transformed data.

---

function\_value\_onemarker  
*Compute simulated cell values for one marker with markers NB informations*

---

**Description**

Compute simulated cell values for one marker with markers NB informations

**Usage**

```
function_value_onemarker(  
  marker_name,  
  mu0,  
  dispersion,  
  subject_effect,  
  nb_donor,  
  nb_cell_per_sample,  
  rho = 1  
)
```

**Arguments**

<code>marker_name</code>	character, name of the marker.
<code>mu0</code>	numeric, general donor mean from which the individual $\mu_{0i}$ will be drawn.
<code>dispersion</code>	numeric, dispersion of the markers.
<code>subject_effect</code>	numeric, standard deviation for the normal distribution from which the donor's means will be drawn (by default <code>subject_effect = 0.01</code> ).
<code>nb_donor</code>	numeric, number of donors.
<code>nb_cell_per_sample</code>	numeric, number of cells per sample (by default <code>nb_cell_per_sample = 500</code> ).
<code>rho</code>	numeric, fold change.

**Details**

Function to generate value for one marker with a mean and dispersion specified for the negative binomiale.

**Value**

data.frame of cell values.

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