

# Package ‘CyTOFpower’

June 29, 2022

**Type** Package

**Title** Power analysis for CyTOF experiments

**Version** 1.3.0

**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.

**biocViews** FlowCytometry, SingleCell, CellBiology, StatisticalMethod, Software

**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, tidyr

**RoxygenNote** 7.1.2

**VignetteBuilder** knitr

**Suggests** testthat (>= 3.0.0), BiocStyle, knitr

**Config/testthat/edition** 3

**git\_url** <https://git.bioconductor.org/packages/CyTOFpower>

**git\_branch** master

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

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### 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()
}
```

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