

# Package ‘CyTOFpower’

October 9, 2022

**Type** Package

**Title** Power analysis for CyTOF experiments

**Version** 1.2.0

**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** RELEASE\_3\_15

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**R topics documented:**

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CyTOFpower	<i>CyTOFpower: R-package to predict the power of a CyTOF experiment</i>
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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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