

# Package ‘CascadeData’

August 22, 2025

**Type** Package

**Title** Experimental Data of Cascade Experiments in Genomics

**Version** 1.5

**Date** 2025-08-21

**Depends** R (>= 2.10)

**Suggests** testthat (>= 3.0.0)

**Author** Frederic Bertrand [cre, aut] (ORCID:

<<https://orcid.org/0000-0002-0837-8281>>),

Myriam Maumy-Bertrand [aut] (ORCID:

<<https://orcid.org/0000-0002-4615-1512>>),

Laurent Vallat [ctb],

Nicolas Jung [ctb]

**Maintainer** Frederic Bertrand <[frederic.bertrand@utt.fr](mailto:frederic.bertrand@utt.fr)>

**Description** These experimental expression data (5 leukemic 'CLL' B-lymphocyte of aggressive form from 'GSE39411', <[doi:10.1073/pnas.1211130110](https://doi.org/10.1073/pnas.1211130110)>), after B-cell receptor stimulation, are used as examples by packages such as the 'Cascade' one, a modeling tool allowing gene selection, reverse engineering, and prediction in cascade networks. Jung, N., Bertrand, F., Bahram, S., Vallat, L., and Maumy-Bertrand, M. (2014) <[doi:10.1093/bioinformatics/btt705](https://doi.org/10.1093/bioinformatics/btt705)>.

**License** GPL (>= 2)

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**URL** <https://fbertran.github.io/CascadeData/>,

<https://github.com/fbertran/CascadeData/>

**BugReports** <https://github.com/fbertran/CascadeData/issues/>

**Config/testthat/edition** 3

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2025-08-22 00:10:01 UTC

Contents

|                    |   |
|--------------------|---|
| micro_S . . . . .  | 2 |
| micro_US . . . . . | 3 |
| Index              | 4 |

---

|         |                           |
|---------|---------------------------|
| micro_S | <i>Stimulated dataset</i> |
|---------|---------------------------|

---

Description

This is the stimulated data part of the GSE39411 dataset, <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE39411>. Data were normalized and are ready to use.

Format

A data frame with 54613 probesets measured 6 times through 4 time points. It features 54613 rows and 24 numeric columns. Columns are named **\*\*exactly\*\*** as: N1\_S\_T60, N1\_S\_T90, N1\_S\_T210, N1\_S\_T390, N2\_S\_T60, N2\_S\_T90, N2\_S\_T210, N2\_S\_T390, N3\_S\_T60, N3\_S\_T90, N3\_S\_T210, N3\_S\_T390, N4\_S\_T60, N4\_S\_T90, N4\_S\_T210, N4\_S\_T390, N5\_S\_T60, N5\_S\_T90, N5\_S\_T210, N5\_S\_T390, N6\_S\_T60, N6\_S\_T90, N6\_S\_T210, N6\_S\_T390.

The ordering is strict: for each replicate N1, N2, N3, N4 , N5, N6 the time points are ordered T60, T90, T210, T390.

Details

5 leukemic CLL B-lymphocyte of aggressive form were stimulated in vitro with an anti-IgM antibody, activating the B-cell receptor (BCR). We analyzed the gene expression at 4 time points (60, 90, 210 and 390 minutes). Each gene expression measurement is performed both in stimulated cells and in control unstimulated cells. This is the stimulated cells dataset.

Data were collected on HG-U133\_Plus\_2, Affymetrix Human Genome U133 Plus 2.0 Array.

References

Vallat, L., Kemper, C. A., Jung, N., Maumy-Bertrand, M., Bertrand, F., . . . , Bahram, S. (2013). Reverse-engineering the genetic circuitry of a cancer cell with predicted intervention in chronic lymphocytic leukemia. Proceedings of the National Academy of Sciences, 110(2), 459-464, [doi:10.1073/pnas.1211130110](https://doi.org/10.1073/pnas.1211130110).

Examples

```
data(micro_S)
```

---

micro\_US*Unstimulated control dataset*

---

**Description**

This is the unstimulated data part of the GSE39411 dataset, <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE39411>. Data were normalized and are ready to use.

**Format**

A data frame with 54613 probesets measured 6 times through 4 time points. It features 54613 rows and 24 numeric columns. Columns are named **exactly** as: N1\_US\_T60, N1\_US\_T90, N1\_US\_T210, N1\_US\_T390, N2\_US\_T60, N2\_US\_T90, N2\_US\_T210, N2\_US\_T390, N3\_US\_T60, N3\_US\_T90, N3\_US\_T210, N3\_US\_T390, N4\_US\_T60, N4\_US\_T90, N4\_US\_T210, N4\_US\_T390, N5\_US\_T60, N5\_US\_T90, N5\_US\_T210, N5\_US\_T390, N6\_US\_T60, N6\_US\_T90, N6\_US\_T210, N6\_US\_T390.

The ordering is strict: for each replicate N1, N2, N3, N4, N5, N6 the time points are ordered T60, T90, T210, T390.

A data frame with 54613 probesets measured 6 times through 4 time points.

**Details**

5 leukemic CLL B-lymphocyte of aggressive form were stimulated in vitro with an anti-IgM antibody, activating the B-cell receptor (BCR). We analyzed the gene expression at 4 time points (60, 90, 210 and 390 minutes). Each gene expression measurement is performed both in stimulated cells and in control unstimulated cells. This is the unstimulated cells dataset.

Data were collected on HG-U133\_Plus\_2, Affymetrix Human Genome U133 Plus 2.0 Array.

**References**

Vallat, L., Kemper, C. A., Jung, N., Maumy-Bertrand, M., Bertrand, F., ..., Bahram, S. (2013). Reverse-engineering the genetic circuitry of a cancer cell with predicted intervention in chronic lymphocytic leukemia. *Proceedings of the National Academy of Sciences*, 110(2), 459-464, [doi:10.1073/pnas.1211130110](https://doi.org/10.1073/pnas.1211130110).

**Examples**

```
data(micro_US)
```

# Index

## \* datasets

micro\_S, [2](#)

micro\_US, [3](#)

micro\_S, [2](#)

micro\_US, [3](#)