

# R Package **CellPlot**

## User Manual

Sven E. Templer  
`sven.templer@gmail.com`

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# 1 Introduction

## CellPlot

A [GNU R](#) package for comparted bar plots.

Introduction text...

## 2 Installation & Development

You can install the package to use it in any R session. The stable versions are published on the comprehensive R archive network (CRAN) servers. The web description of this and previous versions can be found on the page [cran.r-project.org/web/packages/CellPlot](http://cran.r-project.org/web/packages/CellPlot). The installation takes place in an R session or script. Run the code:

```
> install.packages("CellPlot")
```

A more administrative way is to use the command line in a shell environment and install the package from a downloaded `.tar.gz` archive. Invoking R from the shell provides the syntax `R CMD INSTALL /path/to/package.tar.gz` therefore.

The most recent version can be found on [github.com/dieterich-lab/CellPlot](https://github.com/dieterich-lab/CellPlot). With the `devtools` package, it is easy to install it:

```
> install.packages("devtools")
> library(devtools)
> install_github(repo='dieterich-lab/CellPlot')
```

Once installed, you need to load the package into the current session to access the functions and help pages. With the functions `library` or `require` you perform this step:

```
> library(cellplot)
```

In the following sections the usage of the functions is shown with example data and the output. Each function is accompanied by a help page, which is typically invoked on the R shell with `?` in front of the function's name.

## 3 Example Dataset

### 3.1 Data golubstat

This data set contains microarray gene expression data from leukemia study of Golub et al. (1999). Processed as described in Dudoit et al. (2002). Adapted from package `multtest`. Differential gene expression was performed using a Student t-test to compare the two groups. GO annotation was done with the `annotate` and `hu6800.db` packages from Bioconductor. The `topGO` package was utilized to perform a GO enrichment test based on Fisher's exact test. Data of the DEG and GO enrichment was merged with the provided `go.enrich` function. The code to create the data object is shown in the examples section.

```
> data("golubstat")
```

See the help page of the data set on how it was created from the `golub` dataset using differential gene expression, GO annotation and GO enrichment.

```
> head(golubstat)
```

	id	term	annotated	significant
1	G0:0007068	negative regulation of transcription dur...	2	2
2	G0:0007070	negative regulation of transcription fro...	2	2
3	G0:0045896	regulation of transcription during mitos...	2	2
4	G0:0046021	regulation of transcription from RNA pol...	2	2
5	G0:0000710	meiotic mismatch repair	1	1
6	G0:0001675	acrosome assembly	1	1

	expected	p	padj	loge	genes	deg.log2fc
1	0.05	0.00065	1	3.688879	D26156_s_at, L41870_at	-2.617835, 1.575182
2	0.05	0.00065	1	3.688879	D26156_s_at, L41870_at	-2.617835, 1.575182
3	0.05	0.00065	1	3.688879	D26156_s_at, L41870_at	-2.617835, 1.575182
4	0.05	0.00065	1	3.688879	D26156_s_at, L41870_at	-2.617835, 1.575182
5	0.03	0.02571	1	3.506558	U73737_at	1.858002
6	0.03	0.02571	1	3.506558	U72342_at	5.306657

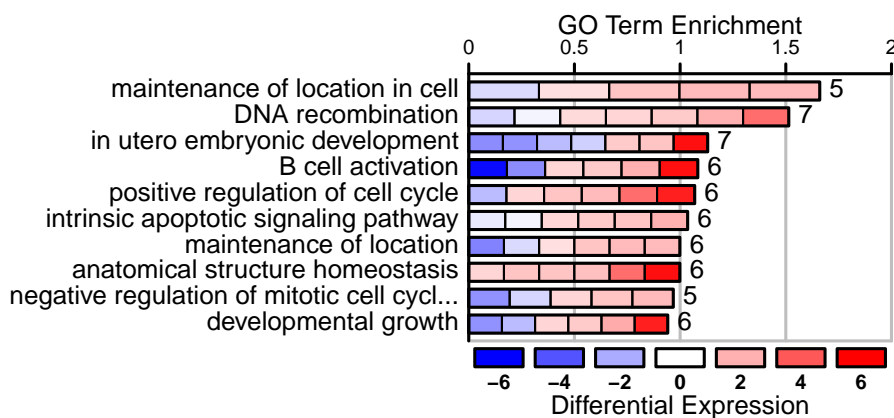
	deg.p.adj
1	0.0385442113, 0.0001725674
2	0.0385442113, 0.0001725674
3	0.0385442113, 0.0001725674
4	0.0385442113, 0.0001725674
5	0.001874989
6	0.008347597

## 4 Plots

### 4.1 cell.plot

Plots a horizontal barchart of strictly positive values in x. For each entry, a vector of additional values needs to be provided in a list. The additional values are plotted as cells subdividing the length of the corresponding bar. A typical usage scenario is plotting the enrichment of Gene Ontology terms, with individual cells reflecting the differential regulation of the constituent genes.

```
> x <- subset(golubstat, p<=.05 & significant>4 & !duplicated(genes))
> x <- head(x, 10)
> cell.plot( x = setNames(x$loge, x$term), cells =x$deg.log2fc, x.bound = 2,
+           cell.bounds = c(-6,6), space = 0.15, main="", y.mar =c(0.1,0),
+           x.mar =c(.47, 0), key.n=7, cex=1.6, grid.lwd=3, axis.cex=0.8, cell.outer=3 )
```



### 4.2 sym.plot

Plots a split barchart, showing the proportions of two mutually exclusive sets in relation to a set containing them both. E.g., Gene Ontology terms, showing the proportions of differentially down-regulated and up-

regulated annotated genes from a perturbation experiment. The color of the central column elements maps to the value provided in `x` (e.g. GO term enrichment). Associated genes may be provided as a list of vectors of expression values, same as for `cell.plot()`, or as separate vectors `x.up` and `x.down`, providing the numbers of up- and down-regulated genes in the same order as `x`.

```
> sym.plot( ticksize = 5, x = setNames(x$log2fc, x$term), cells = x$deg.log2fc,
+           x.annotated = x$annotated, y.mar = c(0.1,0), x.mar = c(.47, 0), key.n=7,
+           key.lab = "GO Term enrichment", cex = 1.6, axis.cex=0.8, group.cex=0.7,
+           grid.lwd=3 )
```

