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## cellHTS2 - Analysis of cell-based RNAi screens

cellHTS2 is a software package implemented in Bioconductor/R to analyze cell-based high-throughput RNAi screens.

The cellHTS2 package is the new version of the cellHTS package, offering improved functionality for the analysis and integration of multi-channel screens and multiple screens. We advise users starting new projects to use cellHTS2. For your existing projects, you may keep using cellHTS, which is still supported.

Please cite the following paper when using cellHTS2:

Boutros, M., L. Bras, and W. Huber. (2006). Analysis of cell-based RNAi screens. *Genome Biology* 7:R66.

[\[Pubmed\]](#) [\[Fulltext PDF\]](#)

### Online documentation

- End-to-end analysis of cell-based screens: from raw intensity readings to the annotated hit list [\[pdf\]](#)
- Analysis of multi-channel cell-based screens [\[pdf\]](#)
- Analysis of suppressor/enhancer screens [\[pdf\]](#)

### Demo data sets and results

- Experiment report for a viability screen in Drosophila Kc cells [\[link\]](#)
- Experiment report for a dual-channel screen, logRatio [\[link\]](#)
- Experiment report for a dual-channel screen, raw [\[link\]](#)

### Sample session

```
## load cellHTS2 and set directory for sample session
library('cellHTS2')
datadir <- system.file("KcViab", package = "cellHTS2")

## read screen description and the result file index
x = readPlateList("Platelist.txt", name="KcViab", path=datadir)

## add plate configuration and screen log
x <- configure(x, "Description.txt", "Plateconf.txt", "Screenlog.txt", path=datadir)

## normalize results
xn = normalizePlates(x, scale="multiplicative", log=FALSE, method="median", varianceAdjust="none")

## score and summarize replicates
xsc = scoreReplicates(xn, sign="-", method="zscore")
xsc = summarizeReplicates(xsc, summary="mean")

## add reagent and target annotation
xsc = annotate(xsc, geneIDFile="GeneIDs_Dm_HFA_1.1.txt", path=datadir)

## save the data object for further use
save(xsc, file=paste("KcViab", ".rda", sep=""))

## create the HTML linked (web) report
out = writeReport(raw=x, normalized=xn, outdir=tempdir(), scored=xsc, force=TRUE, map=TRUE, plotPlateArgs = TRUE,
imageScreenArgs=list(zrange=c(-4,8)))

## open HTML report
browseURL(out)
```

### Installation

Install the most recent release of R which can be obtained for Windows, Mac OS X and Unix from [www.r-project.org](http://www.r-project.org). Start the R interpreter and run the following commands (an internet connection is required):

### Install

```
>source('http://www.bioconductor.org/biocLite.R')  
>biocLite('cellHTS2')
```

This command will install the latest version of cellHTS2 including its dependencies. The current development version can be found at: <http://bioconductor.org/packages/devel/bioc/html/cellHTS2.html>

### Links

[Boutros group homepage](#)  
[Huber group homepage](#)

[Bioconductor Project](#)  
[R Project](#)

[E-RNAi](#) - Webservice to design of RNAi constructs  
[GenomeRNAi](#) - Database of RNAi phenotypes in Drosophila

Visits:

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