

# Package ‘BiocCaseStudies’

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**Title** BiocCaseStudies: Support for the Case Studies Monograph

**Version** 1.22.0

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**Description** Software and data to support the case studies.

**Maintainer** Bioconductor Package Maintainer <maintainer@bioconductor.org>

**License** Artistic-2.0

**LazyLoad** true

**biocViews** Infrastructure, Bioinformatics

**Collate** init.R requiredLibs.R resample.R mySessionInfo.R colors.R fixedWidthCat.R

**Depends** tools, methods, utils, Biobase

**Suggests** affy (>= 1.17.3), affyPLM (>= 1.15.1), affyQCReport (>= 1.17.0), ALL (>= 1.4.3), annaffy (>= 1.11.1), annotate (>= 1.17.3), AnnotationDbi (>= 1.1.6), apComplex (>= 2.5.0), Biobase (>= 1.17.5), bioDist (>= 1.11.3), biocGraph (>= 1.1.1), biomaRt (>= 1.13.5), CCI4 (>= 1.0.6), CLL (>= 1.2.4), Category (>= 2.5.0), class (>= 7.2-38), cluster (>= 1.11.9), convert (>= 1.15.0), gcrma (>= 2.11.1), genefilter (>= 1.17.6), geneplotter (>= 1.17.2), GO.db (>= 2.0.2), GOstats (>= 2.5.0), graph (>= 1.17.4), GSEABase (>= 1.1.13), hgu133a.db (>= 2.0.2), hgu95av2.db, hgu95av2cdf (>= 2.0.0), hgu95av2probe (>= 2.0.0), honen (>= 2.0.2), lattice (>= 0.17.2), latticeExtra (>= 0.3-1), limma (>= 2.13.1), MASS (>= 7.2-38), MLInterfaces (>= 1.13.17), multtest (>= 1.19.0), org.Hs.eg.db (>= 2.0.2), ppiStats (>= 1.5.4), randomForest (>= 4.5-20), RBGL (>= 1.15.6), RColorBrewer (>= 1.0-2), Rgraphviz (>= 1.17.11), vsn (>= 3.4.0), weaver (>= 1.5.0), xtable (>= 1.5-2), yeastExpData (>= 0.9.11)

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fixedWidthCat	<i>Control the output of show methods</i>
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**Description**

fixedWidthCat makes sure that the output of a show method fits on the page by inserting line breaks into long strings.

numName converts an integer to its literal name.

sepInt prints integers with a comma as separator between 1000s

**Usage**

```
fixedWidthCat(x, width=getOption("width"))
```

**Arguments**

x	An R object which is to be shown.
width	The number of characters after which lines are to be broken.

**Value**

A character vector of the output with long lines broken

**Author(s)**

Florian Hahne

**Examples**

```
long <- paste(rep(letters[1:24], 5), sep="", collapse="")
fixedWidthCat(long)
```

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markup

*Markup commands.*

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## Description

Usage of predefined markup commands for layout of Bioc Case Studies book.

## Details

The following markup commands, LaTeX makros and environments are available for controlling the layout and structure of the book:

- `Ex:`environment for exercise chunks.
- `solution:`environment for solutions to the exercises.
- `\myincfig:`macro for figure environments with three parameters: (1) figure filename (2) figure width (3) figure caption
- `\solfig:`macro for figure environments within solution chunks. This is necessary because LaTeX doesn't allow for floats within minipage environments.
- `\myref:`reference to other labs/chapters. For the book this is a simple wrapper around `ref` ignoring the second argument, for the labs this command is replaced in the `useRlabs.sty` file allowing for referencing between the individual documents.
- `\booklab:`macro for conditional text input with two parameters. The first parameter will be used for the book while the second will be used for the labs.

The following makros will automatically create index entries as side effect. Apart from that they do text highlighting as well.

- `\R:`the R language glyph (in sans serif font)
- `\Rpackage:`an R package (in bold font)
- `\Rclass:`an R class (in italics)
- `\Rmethod:`an R method (in small typewriter font)
- `\Rfunction:`an R function (in small typewriter font)

Implicit index terms can be generated using

- `\indexTerm:`with the optional first argument giving the actual term and the second argument giving a string that appears in the text. E.g. `indexTerm[tree]{trees}` would give you "trees" in the text but create an index for "tree". Omitting the optional first argument will create an index for the same string that appears in the text.

Some more useful text markup that doesn't create indices:

- `\Robject:`an R object (in small typewriter font)
- `\Rfunarg:`the argument to an R function (in italics)
- `\code:`typewriter font

- `\term:whatever \{emph}` is set to
- `\file:italics`
- `\reg:`The registered trademark glyph

The following environments are used to structure the document and for parsing . They do not impose any layout.

- `chapterheader:`this contains title, authors and abstract of the chapter/lab
- `chapterbody:`this contains the actual chapter body
- `chaptertrailer:`this contains session info and references for a chapter
- `\yaa:`This is a wrapper for `input` also setting the graphics include path. Its first parameter is filename, second parameter is graphics path

#### Color and options

- `colors:`There are some predefined colors that should be used consistently throughout the whole book for things like histograms, barplots, etc. They are defined by `BiocCaseStudies` as objects `lcol1`, `lcol2` and `lcol3` for light colors, and `dcol1`, `dcol2` and `dcol3` for dark colors.
- `Sweave options:`The boolean option `hideme` can be used in Sweave code chunks that should not be part of the Stangle output. This only effects Stangle, so a "regular" Sweave will evaluate these chunks. The intention is to have the possibility for sanity checks or conditional code evaluation which should not confuse the users when they work with the extracted code.

#### Author(s)

Florian Hahne

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mySessionInfo

*Wrapper around sessionInfo*

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#### Description

This will produce the LaTeX output for the `sessionInfo` and the references at the end of each lab.

#### Usage

```
mySessionInfo(ref=TRUE)
```

#### Arguments

`ref`                      logical controlling whether to include references

#### Value

This function is called for its side effects

#### Author(s)

Florian Hahne

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parseLibVers	<i>Parse the library versions</i>
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**Description**

This is a helper function to check for valid package versions

**Usage**

```
parseLibVers()
```

**Value**

Called for its side effects

**Author(s)**

Florian Hahne

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requiredPackages	<i>check for missing and outdated packages</i>
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**Description**

Both functions compare the Depends field of the DESCRIPTION of the BiocCaseStudies package. requiredPackages is run before a build of the book. It throws an error if there are any missing or outdated packages. packages2install returns a character vector of packages that need (re)installing.

**Usage**

```
requiredPackages(load=FALSE)  
packages2install()
```

**Arguments**

load                    Logical. Should all packages be loaded?

**Value**

requiredPackages returns invisible(NULL). The function is called for its side effects. packages2install returns a character vector that can be passed to the biocLite function from the biocLite.R script.

**Author(s)**

Florian Hahne

**Examples**

```
## Not run:  
  biocLite(packages2install())  
  
## End(Not run)
```

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resample

*Resample from ALL ExpressionSet and plot*

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**Description**

A function to resample samples from each class of an ExpressionSet and plot the results calculated by a function that returns the number of differentially expressed genes between the classes.

**Usage**

```
resample(x, selfun, groupsize = 6 * (1:6), nrep = 25)
```

**Arguments**

x	An ExpressionSet object derived from the ALL data package.
selfun	A function that takes the resampling subset of the ExpressionSet and computes the number of differentially expressed genes between the two classes
groupsize	The number of samples for each class
nrep	number of iterations of resampling procedure

**Value**

The function is called for the side effect of producing a plot.

**Author(s)**

Florian Hahne

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