BiocCaseStudies

April 19, 2010

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fixedWidthCat   *Control the output of show methods*

Description

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

`numName` converts an integer to it's 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.*

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 controling 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 simplewrapper around ref ignoring the second argument, for the labs this command is replaced in the useRlabs.sty file allowing for referencing bbetween 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 usful text markup that doesn't create indices:

- `\Robject`:an R object (in small typewriter font)
- `\Rfunarg`:the agument 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 consistantly 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

`mySessionInfo` *Wrapper around sessionInfo*

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   *Parse the library versions*

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   *check for missing and outdated packages*

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*

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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