

Package ‘RbcBook1’

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Title Support for Springer monograph on Bioconductor

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Description tools for building book

Depends R (>= 2.10), Biobase, graph, rpart

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bcr.cor

Illustrative datasets for distance measures

Description

Illustrative datasets for distance measures

Usage

```
data(ALL.dist) # all the components live in here
```

Details

These datasets are used in conjunction with the bioDist package for the distance chapter of the monograph

Value

these are `dist` objects

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
data(ALL.dist)
objects()
dim(as.matrix(bcr.cor))
```

bcStangle

A function to extract the code chunks from the book for the online supplement

Description

A function to extract the code chunks from the book for the online supplement.

Usage

```
bcStangle(files = .RbcBook1Files(), outfile= "bioCSpringer.R")
tangleToSingleFiles()
```

Arguments

`files` character vector with filenames of book chapters. Must have extension `.Rnw`
`outfile` character of length 1 with the name of the output file.

Details

It should suffice to change to the book's top level directory (e.g. .../Springer1/trunk/Book1) and run `bcStangle()`.

This function is specialized to its one purpose given in the title. It is not envisaged that it could be useful beyond, or even replace Stangle.

`tangleToSingleFiles` creates a directory named `Rfiles` and tangles each chapter separately into this directory. You must have the current working directory set to the top level directory of the book (Springer/Book1).

Value

Function is called for its side effects.

Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

See Also

`.RbcBook1Files`, `Stangle`

Examples

```
## bcStangle()
```

bcSweave

Wrapper for Sweave

Description

Wrapper for Sweave - allows to set options, or perform additional preprocessing or QC steps.

Usage

```
bcSweave(f)
```

Arguments

`f` character, filename. Must have extension `.Rnw`

Details

No details.

Value

Function is called for its side effects.

Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

Examples

```
## bcSweave("Intro.Rnw")
```

checkingBookSources *Formatting and standardization checks on book chapters*

Description

Formatting and standardization checks on book chapters

Usage

```
checkVerbatim(files = .RbcBook1Files(ext=".tex"),
              maxc = 70,
              which = "both",
              verbose = TRUE)
```

```
checkRnw(files = .RbcBook1Files(),
          verbose = TRUE, stopOnError=FALSE)
```

```
checkPackage(files = .RbcBook1Files(ext=".Rnw"),
             verbose = TRUE)
```

```
.RbcBook1Files(ext=".Rnw")
```

Arguments

| | |
|-------------|---|
| files | character vector with names (and path) of chapter source files |
| ext | character of length 1. File name extension. .Rnw (the default) and .tex should be the most important cases. |
| maxc | integer of length 1. Maximal number of characters in a verbatim line. All lines exceeding this limit will be reported in the return value of this function. |
| which | character of length 1. 'Sinput' will look at Sinput environments, 'Soutput' at Soutput environments, 'both' at both. |
| verbose | Logical. |
| stopOnError | Logical. If FALSE, first error found will lead to stop. If TRUE, try to continue checking. |

Details

checkVerbatimLines sees whether all verbatim lines have length at most maxc.

checkPackage finds all the occurrences of `\Rpackage{...}` in the text, checks whether the package is known, and returns a named list with all occurrences of the packages.

Value

For checkVerbatimLines and checkSetup, a data frame with one row for each offending line and various columns describing it.

For .RbcBook1Files, a character vector.

Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

Examples

```
f = tempfile()
zap = function(n) paste(formatC(1:n, width=2), collapse=" ")
writeLines(c("*begin{Sinput}", zap(20), zap(30), "*end{Sinput}"), con=f)
checkVerbatim(files=f)
```

imageSize

File info for all image files in the book

Description

File info for all image files in the book

Usage

```
imageSize(dirs= c("Preproc", "Analysis", "Metadata", "Graphs", "CaseStudies"), ext=c("pdf", "png"))
```

Arguments

dirs character vector with directories.
ext character vector with file name extensions.

Details

No details.

Value

Data frame.

Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

Examples

```
# a = imageSize()
# print(a[1:10,c(1,4)])
```

 perf

Results of tedious computations for computational inference

Description

Results of tedious computations for computational inference

Usage

```
data(Survperformance)
```

Details

These datasets are used in conjunction with the computational inference chapter of the monograph

Value

these are data.frame objects

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
data(Survperformance)
objects()
dim(performance)
```

 require.RbcBook1

Load a lengthy list of packages that are used in the Book

Description

Load a lengthy list of packages that are used in the Book

Usage

```
require.RbcBook1()
.RbcBook1.pkgs()
```

Details

require.RbcBook1 can be used to see at once whether all packages required for the book can be loaded.

To do for .RbcBook1.pkgs: version numbers?

Value

.RbcBook1.pkgs returns a character vector with the names of all packages used in the book.

Author(s)

Wolfgang Huber <huber@ebi.ac.uk>

Examples

```
## Not run:
library(reposTools)
install.packages2(.RbcBook1.pkgs(), develOK=TRUE)
require.RbcBook1()

## End(Not run)
```

rpart2gNEL

rpart to graphNEL Converter

Description

Creates an object of class graphNEL from one of class rpart.

Usage

```
rpart2gNEL(tr, remap=function(x) x, nsep="\n")
```

Arguments

| | |
|-------|---|
| tr | instance of rpart class from rpart package. |
| remap | function that maps node names in tree to node names in graph. |
| nsep | token that separates node name and vote tally in the rendering. |

Details

Not explicitly used in the book, but the basis for a certain graph illustrating application of rpart. The newer coin/party packages have more interesting rendering approaches based on graphviz.

grabSplitV is a utility function for acquiring the variable names, remapAff will remap affymetrix probe names to gene symbols for use in the remap parameter.

Value

a [graphNEL-class](#) instance with nodes constructed to convey information on the data tree fit

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

See Also

[rpart](#), [graphNEL-class](#)

Examples

```
library(rpart)
example(rpart)
ff = rpart2gNEL(fit2)
ff
nodes(ff)
```


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