

# Package ‘RbcBook1’

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**Version** 1.30.0

**Title** Support for Springer monograph on Bioconductor

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**Description** tools for building book

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

**License** Artistic-2.0

**URL** <http://www.biostat.harvard.edu/~carey>

**biocViews** Software

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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. 'Sinuput' will look at Sinuput 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 <a href="#">rpart</a> 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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