

# 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

**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. <code>.Rnw</code> (the default) and <code>.tex</code> 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**

<code>tr</code>	instance of <code>rpart</code> class from <a href="#">rpart</a> package.
<code>remap</code>	function that maps node names in tree to node names in graph.
<code>nsep</code>	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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