# Package: RbcBook1 (via r-universe)

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**Version** 1.73.0

**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

**Repository** https://bioc.r-universe.dev

**RemoteUrl** https://github.com/bioc/RbcBook1

**RemoteRef** HEAD

**RemoteSha** 882d9bb788b2a0a8685565966c9895ec0fa28dce

## Contents

## 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()
```

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## `bcSweave` *Wrapper for Sweave*

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### 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")
```

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## checkingBookSources *Formatting and standardization checks on book chapters*

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### 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 occurences of \Rpackage{...} in the text, checks whether the package is known, and returns a named list will all occurences 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)
```

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## imageSize — *File info for all image files in the book*

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### 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)
```

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## rpart2gNEL *rpart to graphNEL Converter*

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### 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)
```

# Index