

# Creating R Packages: A Tutorial

Friedrich Leisch

Department of Statistics, Ludwig-Maximilians-Universität München, and  
R Development Core Team, *Friedrich.Leisch@R-project.org*

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## Abstract

This tutorial gives a practical introduction to creating R packages. We discuss how object oriented programming and S formulas can be used to give R code the usual look and feel, how to start a package from a collection of R functions, and how to test the code once the package has been created. As running example we use functions for standard linear regression analysis which are developed from scratch.

**Keywords:** R packages, statistical computing, software, open source

## 1 Introduction

The R packaging system has been one of the key factors of the overall success of the R project (R Development Core Team 2008). Packages allow for easy, transparent and cross-platform extension of the R base system. An R package can be thought of as the software equivalent of a scientific article: Articles are the de facto standard to communicate scientific results, and readers expect them to be in a certain format. In Statistics, there will typically be an introduction including a literature review, a section with the main results, and finally some application or simulations.

But articles need not necessarily be the usual 10–40 pages communicating a novel scientific idea to the peer group, they may also serve other purposes. They may be a tutorial on a certain topic (like this paper), a survey, a review etc.. The overall format is always the same: text, formulas and figures on pages in a journal or book, or a PDF file on a web server. Contents and quality will vary immensely, as will the target audience. Some articles are intended for a world-wide audience, some only internally for a working group or institution, and some may only be for private use of a single person.

R packages are (after a short learning phase) a comfortable way to maintain collections of R functions and data sets. As an article distributes scientific ideas to others, a package distributes statistical methodology to others. Most users first see the packages of functions distributed with R or from CRAN. The package system allows many more people to contribute to R while still enforcing some standards. But packages are also a convenient way to maintain private functions and share them with your colleagues. I have a private package of utility function, my working group has several “experimental” packages where we try out new things. This provides a transparent way of sharing code with co-workers, and the final transition from “playground” to production code is much easier.

But packages are not only an easy way of sharing computational methods among peers, they also offer many advantages from a system administration point of view. Packages can be dynamically loaded and unloaded on runtime and hence only occupy memory when actually used. Installations and updates are fully automated and can be executed from inside or outside R. And

last but not least the packaging system has tools for software validation which check that documentation exists and is technically in sync with the code, spot common errors, and check that examples actually run.

Before we start creating R packages we have to clarify some terms which sometimes get confused:

**Package:** An extension of the R base system with code, data and documentation in standardized format.

**Library:** A directory containing installed packages.

**Repository:** A website providing packages for installation.

**Source:** The original version of a package with human-readable text and code.

**Binary:** A compiled version of a package with computer-readable text and code, may work only on a specific platform.

**Base packages:** Part of the R source tree, maintained by R Core.

**Recommended packages:** Part of every R installation, but not necessarily maintained by R Core.

**Contributed packages:** All the rest. This does not mean that these packages are necessarily of lesser quality than the above, e.g., many contributed packages on CRAN are written and maintained by R Core members. We simply try to keep the base distribution as lean as possible.

See R Development Core Team (2008a) for the full manual on R installation issues, and Ligges (2003) for a short introduction.

The remainder of this tutorial is organized as follows: As example we implement a function for linear regression models. We first define classes and methods for the statistical model, including a formula interface for model specification. We then structure the pieces into the form of an R package, show how to document the code properly and finally discuss the tools for package validation and distribution. This tutorial is meant as a starting point on how to create an R package, see R Development Core Team (2008b) for the full reference manual. Note that R implements a dialect of the S programming language (Becker et al 1988), in the following we will primarily use the name “S” when we speak of the language, and “R” when the complete R software environment is meant or extensions of the S language which can only be found in R.

## 2 R code for linear regression

As running example in this tutorial we will develop R code for the standard linear regression model

$$y = x'\beta + \epsilon, \quad \epsilon \sim N(0, \sigma^2)$$

Our goal is not to implement all the bells and whistles of the standard R function `lm()` for the problem, but to write a simple function which computes the OLS estimate and has a “professional look and feel” in the sense that the interface is similar to the interface of `lm()`.

If we are given a design matrix  $X$  and response vector  $y$  then the OLS estimate is of course

$$\hat{\beta} = (X'X)^{-1}X'y$$

with covariance matrix

$$\text{var}(\hat{\beta}) = \sigma^2(X'X)^{-1}$$

For numerical reasons it is not advisable to compute  $\hat{\beta}$  using the above formula, it is better to use, e.g., a QR decomposition or any other numerically good way to solve a linear system of equations (e.g., Gentle 1998). Hence, a minimal R function for linear regression is

```

linmodEst <- function(x, y)
{
  ## compute QR-decomposition of x
  qx <- qr(x)

  ## compute  $(x'x)^{-1} x'y$ 
  coef <- solve.qr(qx, y)

  ## degrees of freedom and standard deviation of residuals
  df <- nrow(x)-ncol(x)
  sigma2 <- sum((y - x%*%coef)^2)/df

  ## compute  $\sigma^2 * (x'x)^{-1}$ 
  vcov <- sigma2 * chol2inv(qx$qr)
  colnames(vcov) <- rownames(vcov) <- colnames(x)

  list(coefficients = coef,
        vcov = vcov,
        sigma = sqrt(sigma2),
        df = df)
}

```

If we use this function to predict heart weight from body weight in the classic Fisher cats data from package MASS (Venables & Ripley 2002), we get

```

R> data(cats, package="MASS")
R> linmodEst(cbind(1, cats$Bwt), cats$Hwt)
$coefficients
[1] -0.3566624  4.0340627

$vcov
      [,1]      [,2]
[1,]  0.4792475 -0.17058197
[2,] -0.1705820  0.06263081

$sigma
[1] 1.452373

$df
[1] 142

```

The standard R function for linear models:

```

R> lm1 <- lm(Hwt~Bwt, data=cats)
R> lm1

Call:
lm(formula = Hwt ~ Bwt, data = cats)

Coefficients:
(Intercept)      Bwt
   -0.3567      4.0341
R> vcov(lm1)
      (Intercept)      Bwt
(Intercept)  0.4792475 -0.17058197
Bwt         -0.1705820  0.06263081

```

The numerical estimates are exactly the same, but our code lacks a convenient user interface:

1. Prettier formatting of results.
2. Add utilities for fitted model like a `summary()` function to test for significance of parameters.
3. Handle categorical predictors.
4. Use formulas for model specification.

Object oriented programming helps us with issues 1 and 2, formulas with 3 and 4.

## 3 Object oriented programming in R

### 3.1 S3 and S4

Our function `linmodEst` returns a list with four named elements, the parameter estimates and their covariance matrix, and the standard deviation and degrees of freedom of the residuals. From the context it is clear to us that this is a linear model fit, however, nobody told the computer so far. For the computer this is simply a list containing a vector, a matrix and two scalar values. Many programming languages, including S, use so-called

1. *classes* to define how *objects* of a certain type look like, and
2. *methods* to define special functions operating on objects of a certain class

A class defines how an object is represented in the program, while an object is an instance of the class that exists at run time. In our case we will shortly define a class for linear model fits. The class is the abstract definition, while every time we actually use it to store the results for a given data set, we create an object of the class.

Once the classes are defined we probably want to perform some computations on objects. In most cases we do not care how the object is stored internally, the computer should decide how to perform the tasks. The S way of reaching this goal is to use *generic functions* and *method dispatch*: the same function performs different computations depending on the *classes* of its arguments.

S is rare because it is both interactive *and* has a system for object-orientation. Designing classes clearly is programming, yet to make S useful as an interactive data analysis environment, it makes sense that it is a functional language. In “real” object-oriented programming (OOP) languages like C++ or Java class and method definitions are tightly bound together, methods are part of classes (and hence objects). We want incremental and interactive additions like user-defined methods for pre-defined classes. These additions can be made at any point in time, even on the fly at the command line prompt while we analyze a data set. S tries to make a compromise between object orientation and interactive use, and although compromises are never optimal with respect to all goals they try to reach, they often work surprisingly well in practice.

The S language has two object systems, known informally as S3 and S4.

**S3** objects, classes and methods have been available in R from the beginning, they are informal, yet “very interactive”. S3 was first described in the “White Book” (Chambers & Hastie 1992).

**S4** objects, classes and methods are much more formal and rigorous, hence “less interactive”. S4 was first described in the “Green Book” (Chambers 1998). In R it is available through the `methods` package, attached by default since version 1.7.0.

S4 provides formal object oriented programming within an interactive environment. It can help a lot to write clean and consistent code, checks automatically if objects conform to class definitions, and has much more features than S3, which in turn is more a set of naming conventions than a true OOP system, but it is sufficient for most purposes (take almost all of R as proof). Because S3 is much easier to learn than S4 and sufficient for our purposes, we will use it throughout this tutorial.

## 3.2 The S3 system

If we look at the following R session we already see the S3 system of classes and methods at work:

```
R> x <- rep(0:1, c(10, 20))
R> x
[1] 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 ...
R> class(x)
[1] "integer"
R> summary(x)
      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
0.0000  0.0000  1.0000  0.6667  1.0000  1.0000
R> y <- as.factor(x)
R> class(y)
[1] "factor"
R> summary(y)
 0  1
10 20
```

Function `summary()` is a generic function which performs different operations on objects of different classes. In S3 only the class of the first argument to a generic function counts. For objects of class `"integer"` (or more generally `"numeric"`) like `x` the five number summary plus the mean is calculated, for objects of class `"factor"` like `y` a table of counts.

Classes are attached to objects as an attribute:

```
R> attributes(y)
$levels
[1] "0" "1"

$class
[1] "factor"
```

In S3 there is no formal definition of a class. To create an object from a new class, one simply sets the class attribute of an object to the name of the desired class:

```
R> myx <- x
R> class(myx) <- "myvector"
R> class(myx)
[1] "myvector"
```

Of course in most cases it is useless to define a class without defining any methods for the class, i.e., functions which do special things for objects from the class. In the simplest case one defines new methods for already existing generic functions like `print()`, `summary()` or `plot()`. These are available for objects of many different classes and should do the following:

`print(x, ...)`: this method is called, when the name of an object is typed at the prompt. For data objects it usually shows the complete data, for fitted models a short description of the model (only a few lines).

`summary(x, ...)`: for data objects summary statistics, for fitted models statistics on parameters, residuals and model fit (approx. one screen). The summary method should not directly create screen output, but return an object which is then `print()`ed.

`plot(x, y, ...)`: create a plot of the object in a graphics device.

Generic functions in S3 take a look at the class of their first argument and do method dispatch based on a naming convention: `foo()` methods for objects of class `"bar"` are called `foo.bar()`,

e.g., `summary.factor()` or `print.myvector()`. If no `bar` method is found, S3 searches for `foo.default()`. Inheritance can be emulated by using a class vector.

Let us return to our new class called "myvector". To define a new `print()` method for our class, all we have to do is define a function called `print.myvector()`:

```
print.myvector <- function(x, ...){
  cat("This is my vector:\n")
  cat(paste(x[1:5]), "... \n")
}
```

If we now have a look at `x` and `myx` they are printed differently:

```
R> x
[1] 0 0 0 0 0 0 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
R> myx
This is my vector:
0 0 0 0 0 0 0 0 0 0 ...
```

So we see that S3 is highly interactive, one can create new classes and change methods definitions on the fly, and it is easy to learn. Because everything is just solved by naming conventions (which are not checked by R at runtime<sup>1</sup>), it is easy to break the rules. A simple example: Function `lm()` returns objects of class "lm". Methods for that class of course expect a certain format for the objects, e.g., that they contain regression coefficients etc as the following simple example shows:

```
R> nolm <- "This is not a linear model!"
R> class(nolm) <- "lm"
R> nolm
Call:
NULL

No coefficients

Warning messages:
1: In x$call : $ operator is invalid for
  atomic vectors, returning NULL
2: In object$coefficients :
  $ operator is invalid for atomic vectors,
  returning NULL
```

The computer should detect the real problem: a character string is not an "lm" object. S4 provides facilities for solving this problem, however at the expense of a steeper learning curve.

In addition to the simple naming convention on how to find objects, there are several more conventions which make it easier to use methods in practice:

- A method must have all the arguments of the generic, including ... if the generic does.
- A method must have arguments in exactly the same order as the generic.
- If the generic specifies defaults, all methods should use the same defaults.

The reason for the above rules is that they make it less necessary to read the documentation for all methods corresponding to the same generic. The user can rely on common rules, all methods operate "as similar" as possible. Unfortunately there are no rules without exceptions, as we will see in one of the next sections ...

---

<sup>1</sup>There is checking done as part of package quality control, see the section on R CMD check later in this tutorial.

### 3.3 Classes and methods for linear regression

We will now define classes and methods for our linear regression example. Because we want to write a formula interface we make our main function `linmod()` generic, and write a default method where the first argument is a design matrix (or something which can be converted to a matrix). Later-on we will add a second method where the first argument is a formula.

A generic function is a standard R function with a special body, usually containing only a call to `UseMethod()`:

```
linmod <- function(x, ...) UseMethod("linmod")
```

To add a default method, we define a function called `linmod.default()`:

```
linmod.default <- function(x, y, ...)  
{  
  x <- as.matrix(x)  
  y <- as.numeric(y)  
  
  est <- linmodEst(x, y)  
  
  est$fitted.values <- as.vector(x %*% est$coefficients)  
  est$residuals <- y - est$fitted.values  
  est$call <- match.call()  
  
  class(est) <- "linmod"  
  est  
}
```

This function tries to convert its first argument `x` to a matrix, `as.matrix()` will throw an error if the conversion is not successful<sup>2</sup>, similarly for the conversion of `y` to a numeric vector. We then call our function for parameter estimation, and add fitted values, residuals and the function call to the results. Finally we set the class of the return object to `"linmod"`.

Defining the `print()` method for our class as

```
print.linmod <- function(x, ...)  
{  
  cat("Call:\n")  
  print(x$call)  
  cat("\nCoefficients:\n")  
  print(x$coefficients)  
}
```

makes it almost look like the real thing:

```
R> x = cbind(Const=1, Bwt=cats$Bwt)  
R> y = cats$Hw  
R> mod1 <- linmod(x, y)  
R> mod1  
Call:  
linmod.default(x = x, y = y)
```

```
Coefficients:  
      Const      Bwt  
-0.3566624  4.0340627
```

---

<sup>2</sup>What we do not catch here is conversion to a non-numeric matrix like character strings.

Note that we have used the standard names "coefficients", "fitted.values" and "residuals" for the elements of our class "linmod". As a bonus on the side we get methods for several standard generic functions for free, because their default methods work for our class:

```
R> coef(mod1)
      Const      Bwt
-0.3566624  4.0340627
R> fitted(mod1)
[1] 7.711463 7.711463 7.711463 8.114869 8.114869 8.114869 ...
R> resid(mod1)
[1] -0.7114630 -0.3114630  1.7885370 -0.9148692 -0.8148692 ...
```

The notion of functions returning an object of a certain class is used extensively by the modelling functions of S. In many statistical packages you have to specify a lot of options controlling what type of output you want/need. In S you first fit the model and then have a set of methods to investigate the results (summary tables, plots, ...). The parameter estimates of a statistical model are typically summarized using a matrix with 4 columns: estimate, standard deviation,  $z$  (or  $t$  or ...) score and  $p$ -value. The summary method computes this matrix:

```
summary.linmod <- function(object, ...)
{
  se <- sqrt(diag(object$vcov))
  tval <- coef(object) / se

  TAB <- cbind(Estimate = coef(object),
               StdErr = se,
               t.value = tval,
               p.value = 2*pt(-abs(tval), df=object$df))

  res <- list(call=object$call,
              coefficients=TAB)

  class(res) <- "summary.linmod"
  res
}
```

The utility function `printCoefmat()` can be used to print the matrix with appropriate rounding and some decoration:

```
print.summary.linmod <- function(x, ...)
{
  cat("Call:\n")
  print(x$call)
  cat("\n")

  printCoefmat(x$coefficients, P.value=TRUE, has.Pvalue=TRUE)
}
```

The results is

```
R> summary(mod1)
Call:
linmod.default(x = x, y = y)

      Estimate StdErr t.value p.value
Const -0.35666  0.69228 -0.5152  0.6072
```



```
Bwt      4.03406  0.25026 16.1194 <2e-16 ***
```

```
---
```

```
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1  1
```

Separating computation and screen output has the advantage, that we can use all values if needed for later computations. E.g., to obtain the  $p$ -values we can use

```
R> coef(summary(mod1))[,4]
      Const      Bwt
6.072131e-01 6.969045e-34
```

## 4 S Formulas

The unifying interface for selecting variables from a data frame for a plot, test or model are S formulas. The most common formula is of type

```
y ~ x1+x2+x3
```

The central object that is usually created first from a formula is the

`model.frame`, a data frame containing only the variables appearing in the formula, together with an interpretation of the formula in the

`terms` attribute. It tells us whether there is a response variable (always the first column of the `model.frame`), an intercept, ...

The `model.frame` is then used to build the design matrix for the model and get the response. Our code shows the simplest handling of formulas, which however is already sufficient for many applications (and much better than no formula interface at all):

```
linmod.formula <- function(formula, data=list(), ...)
{
  mf <- model.frame(formula=formula, data=data)
  x <- model.matrix(attr(mf, "terms"), data=mf)
  y <- model.response(mf)

  est <- linmod.default(x, y, ...)
  est$call <- match.call()
  est$formula <- formula
  est
}
```

The above function is an example for the most common exception to the rule that all methods should have the same arguments as the generic and in the same order. By convention formula methods have arguments `formula` and `data` (rather than `x` and `y`), hence there is at least a difference in names of the first argument: `x` in the generic, `formula` in the formula method. This exception is hard-coded in the quality control tools of R CMD `check` described below.

The few lines of R code above give our model access to the wide variety of design matrices S formulas allow us to specify. E.g., to fit a model with main effects and an interaction term for body weight and sex we can use

```
R> summary(linmod(Hwt~Bwt*Sex, data=cats))
Call:
linmod.formula(formula = Hwt ~ Bwt * Sex, data = cats)
```

	Estimate	StdErr	t.value	p.value
(Intercept)	2.98131	1.84284	1.6178	0.1079605

```

Bwt          2.63641  0.77590  3.3979 0.0008846 ***
SexM         -4.16540  2.06176 -2.0203 0.0452578 *
Bwt:SexM      1.67626  0.83733  2.0019 0.0472246 *

```

```
---
```

```
Signif. codes:  0 *** 0.001 ** 0.01 * 0.05 . 0.1 1
```

The last missing methods most statistical models in S have are a `plot()` and `predict()` method. For the latter a simple solution could be

```

predict.linmod <- function(object, newdata=NULL, ...)
{
  if(is.null(newdata))
    y <- fitted(object)
  else{
    if(!is.null(object$formula)){
      ## model has been fitted using formula interface
      x <- model.matrix(object$formula, newdata)
    }
    else{
      x <- newdata
    }
    y <- as.vector(x %*% coef(object))
  }
  y
}

```

which works for models fitted with either the default method (in which case `newdata` is assumed to be a matrix with the same columns as the original `x` matrix), or for models fitted using the formula method (in which case `newdata` will be a data frame). Note that `model.matrix()` can also be used directly on a formula and a data frame rather than first creating a `model.frame`.

The formula handling in our small example is rather minimalistic, production code usually handles much more cases. We did not bother to think about treatment of missing values, weights, offsets, subsetting etc. To get an idea of more elaborate code for handling formulas, one can look at the beginning of function `lm()` in R.

## 5 R packages

Now that we have code that does useful things and has a nice user interface, we may want to share our code with other people, or simply make it easier to use ourselves. There are two popular ways of starting a new package:

1. Load all functions and data sets you want in the package into a clean R session, and run `package.skeleton()`. The objects are sorted into data and functions, skeleton help files are created for them using `prompt()` and a `DESCRIPTION` file is created. The function then prints out a list of things for you to do next.
2. Create it manually, which is usually faster for experienced developers.

### 5.1 Structure of a package

The extracted sources of an R package are simply a directory<sup>3</sup> somewhere on your hard drive. The directory has the same name as the package and the following contents (all of which are described in more detail below):

---

<sup>3</sup>Directories are sometimes also called *folders*, especially on Windows.

- A file named `DESCRIPTION` with descriptions of the package, author, and license conditions in a structured text format that is readable by computers and by people.
- A `man/` subdirectory of documentation files.
- An `R/` subdirectory of R code.
- A `data/` subdirectory of datasets.

Less commonly it contains

- A `src/` subdirectory of C, Fortran or C++ source.
- `tests/` for validation tests.
- `exec/` for other executables (eg Perl or Java).
- `inst/` for miscellaneous other stuff. The contents of this directory are completely copied to the installed version of a package.
- A `configure` script to check for other required software or handle differences between systems.

All but the `DESCRIPTION` file are optional, though any useful package will have `man/` and at least one of `R/` and `data/`. Note that capitalization of the names of files and directories is important, R is case-sensitive as are most operating systems (except Windows).

## 5.2 Starting a package for linear regression

To start a package for our R code all we have to do is run function `package.skeleton()` and pass it the name of the package we want to create plus a list of all source code files. If no source files are given, the function will use all objects available in the user workspace. Assuming that all functions defined above are collected in a file called `linmod.R`, the corresponding call is

```
R> package.skeleton(name="linmod", code_files="linmod.R")
Creating directories ...
Creating DESCRIPTION ...
Creating Read-and-delete-me ...
Copying code files ...
Making help files ...
Done.
Further steps are described in './linmod/Read-and-delete-me'.
```

which already tells us what to do next. It created a directory called `"linmod"` in the current working directory, a listing can be seen in Figure 1. R also created subdirectories `man` and `R`, copied the R code into subdirectory `R` and created stumps for help file for all functions in the code.

File `Read-and-delete-me` contains further instructions:

- \* Edit the help file skeletons in `'man'`, possibly combining help files for multiple functions.
- \* Put any C/C++/Fortran code in `'src'`.
- \* If you have compiled code, add a `.First.lib()` function in `'R'` to load the shared library.
- \* Run `R CMD build` to build the package tarball.
- \* Run `R CMD check` to check the package tarball.

Read `"Writing R Extensions"` for more information.

We do not have any C or Fortran code, so we can forget about items 2 and 3. The code is already in place, so all we need to do is edit the `DESCRIPTION` file and write some help pages.

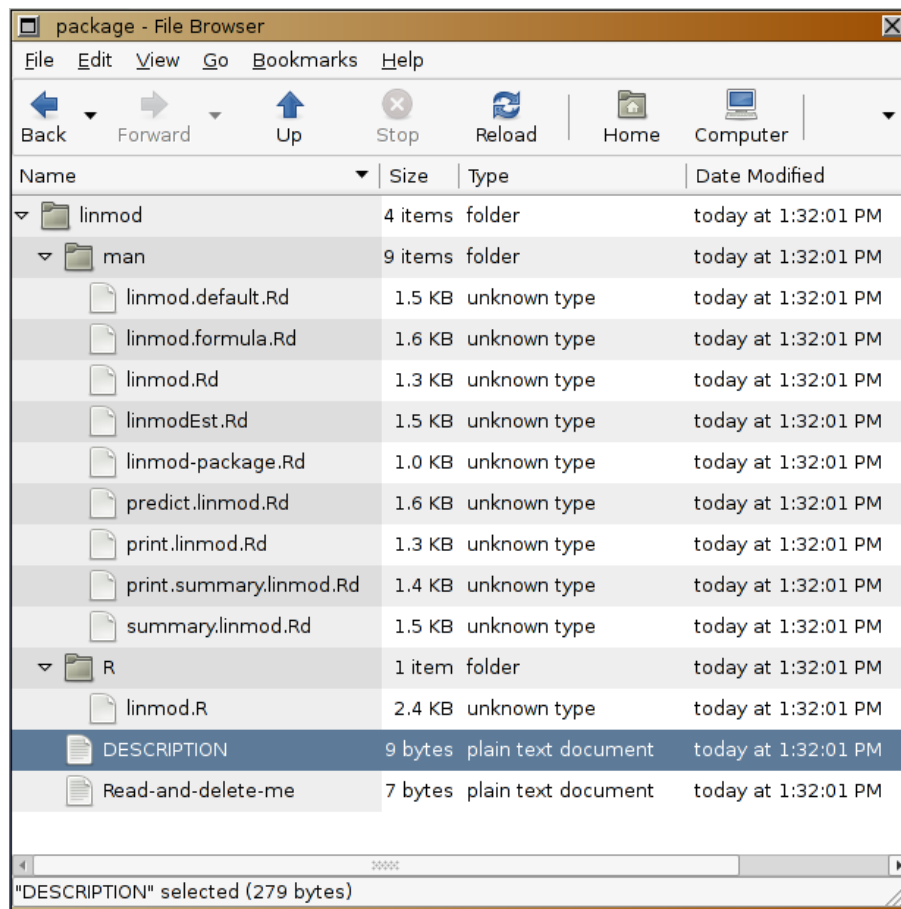


Figure 1: Directory listing of package `linmod` after running function `package.skeleton()`.

### 5.3 The package DESCRIPTION file

An appropriate DESCRIPTION for our package is

```
Package: linmod
Title: Linear Regression
Version: 1.0
Date: 2008-05-13
Author: Friedrich Leisch
Maintainer: Friedrich Leisch <Friedrich.Leisch@R-project.org>
Description: This is a demo package for the tutorial "Creating R
  Packages" to Compstat 2008 in Porto.
Suggests: MASS
License: GPL-2
```

The file is in so called Debian-control-file format, which was invented by the Debian Linux distribution (<http://www.debian.org>) to describe their package. Entries are of form

**Keyword:** Value

with the keyword always starting in the first column, continuation lines start with one or more space characters. The **Package**, **Version**, **License**, **Description**, **Title**, **Author**, and **Maintainer** fields are mandatory, the remaining fields (**Date**, **Suggests**, ...) are optional.

The **Package** and **Version** fields give the name and the version of the package, respectively. The name should consist of letters, numbers, and the dot character and start with a letter. The version is a sequence of at least two (and usually three) non-negative integers separated by single dots or dashes.

The **Title** should be no more than 65 characters, because it will be used in various package listings with one line per package. The **Author** field can contain any number of authors in free text format, the **Maintainer** field should contain only one name plus a valid email address (similar to the “corresponding author” of a paper). The **Description** field can be of arbitrary length. The **Suggests** field in our example means that some code in our package uses functionality from package MASS, in our case we will use the cats data in the example section of help pages. A stronger form of dependency can be specified in the optional **Depends** field listing packages which are necessary to run our code.

The **License** can be free text, if you submit the package to CRAN or Bioconductor and use a standard license, we strongly prefer that you use a standardized abbreviation like **GPL-2** which stands for “GNU General Public License Version 2”. A list of license abbreviations R understands is given in the manual “Writing R Extensions” (R Development Core Team 2008b). The manual also contains the full documentation for all possible fields in package DESCRIPTION files. The above is only a minimal example, much more meta-information about a package as well as technical details for package installation can be stated.

### 5.4 R documentation files

The sources of R help files are in R documentation format and have extension **.Rd**. The format is similar to  $\text{\LaTeX}$ , however processed by R and hence not all  $\text{\LaTeX}$  commands are available, in fact there is only a very small subset. The documentation files can be converted into HTML, plain text, GNU info format, and  $\text{\LaTeX}$ . They can also be converted into the old nroff-based S help format.

A joint help page for all our functions is shown in Figure 2. First the name of the help page, then aliases for all topics the page documents. The title should again be only one line because it is used for the window title in HTML browsers. The descriptions should be only 1–2 paragraphs, if more text is needed it should go into the optional details section not shown in the example. Regular R users will immediately recognize most sections of **Rd** files from reading other help pages.

The usage section should be plain R code with additional markup for methods:

```

\name{linmod}
\alias{linmod}
\alias{linmod.default}
\alias{linmod.formula}
\alias{print.linmod}
\alias{predict.linmod}
\alias{summary.linmod}
\alias{print.summary.linmod}
\title{Linear Regression}
\description{Fit a linear regression model.}
\usage{
linmod(x, ...)

\method{linmod}{default}(x, y, ...)
\method{linmod}{formula}(formula, data = list(), ...)
\method{print}{linmod}(x, ...)
\method{summary}{linmod}(object, ...)
\method{predict}{linmod}(object, newdata=NULL, ...)
}
\arguments{
  \item{x}{ a numeric design matrix for the model. }
  \item{y}{ a numeric vector of responses. }
  \item{formula}{ a symbolic description of the model to be fit. }
  \item{data}{ an optional data frame containing the variables in the model. }
  \item{object}{ an object of class \code{"linmod"}, i.e., a fitted model. }
  \item{\dots}{ not used. }
}
\value{
  An object of class \code{logreg}, basically a list including elements
  \item{coefficients}{ a named vector of coefficients }
  \item{vcov}{ covariance matrix of coefficients }
  \item{fitted.values}{ fitted values }
  \item{residuals}{ residuals }
}
\author{Friedrich Leisch}
\examples{
data(cats, package="MASS")
mod1 <- linmod(Hwt~Bwt*Sex, data=cats)
mod1
summary(mod1)
}
\keyword{regression}

```

Figure 2: Help page source in Rd format.

- For regular functions it is the full header with all arguments and their default values: Copy & paste from the code and remove `<- function`.
- For S3 methods, use the special markup

```
\method{generic}{class}(arguments)
```

which will print as `generic(arguments)` but makes the true name and purpose available for checking.

- For data sets it is typically simply `data(name)`.

The examples section should contain *executable* R code, and automatically running the code is part of checking a package. There are two special markup commands for the examples:

**dontrun:** Everything inside `\dontrun{}` is not executed by the tests or `example()`. This is useful, e.g., for interactive functions, functions accessing the Internet etc.. Do not misuse it to make life easier for you by giving examples which cannot be executed.

**dontshow:** Everything inside `\dontshow{}` is executed by the tests, but not shown to the user in the help page. This is meant for additional tests of the functions documented.

There are other possible sections, and ways of specifying equations, URLs, links to other R documentation, and more. The manual “Writing R Extensions” has the full list of all Rd commands. The packaging system can check that all objects are documented, that the **usage** corresponds to the actual definition of the function, and that the **examples** will run. This enforces a minimal level of accuracy on the documentation. There is an Emacs mode for editing R documentation (Rossini et al 2004), and a function `prompt()` to help produce it.

There are two “special” help files:

**pkgname-package:** it should be a short overview, to give a reader unfamiliar with the package enough information to get started. More extensive documentation is better placed into a package vignette (and referenced from this page), or into individual man pages for the functions, datasets, or classes. This file can be used to override the default contents of `help(package="pkgname")`.

**pkgname-internal:** Popular name for a help file collecting functions which are not part of the package application programming interface (API), should not directly be used by the user and hence are not documented. Only there to make R CMD check happy, you really should use a name space instead.

For our simple package it makes no sense to create `linmod-package.Rd`, because there is only one major function anyway. With `linmodEst` we do have one internal function in our code, which is not intended to be used at the prompt. One way to document this fact is to create a file `linmod-internal.Rd`, include an alias for `linmodEst` and say that this function is for internal usage only.

## 5.5 Data in packages

Using example data from recommended packages like **MASS** is no problem, because recommended packages are part of any R installation anyway. In case you want to use your own data, simply create a subdirectory **data** in your package, write the data to disk using function `save()` and copy the resulting files (with extension `.rda` or `.RData`) to the **data** subdirectory. Typing `data("foo")` in R will look for files with name `foo.rda` or `foo.RData` in all attached packages and `load()` the first it finds. To get a help file skeleton for a data set, simply type `prompt("foo")` when `foo` is a data object present in your current R session. Data in packages can be in other formats (text, csv, S code, ...), see again “Writing R Extensions” for details.

## 5.6 Other package contents

The aim of this tutorial is to give an introduction to creating R packages, hence we have deliberately left out several possibilities of things that can also go into a package. Many packages contain code in compilable languages like C or Fortran for number crunching. In addition to Rd files, package authors can write and include additional user guides, preferably as PDF files. If user guides are written using Sweave (Leisch 2002), they are called package vignettes (e.g., Leisch 2003), see also `help("vignette")`. Name spaces (Tierney 2003) allow fine control over which functions a user shall be able to see and which are only internal. A CITATION file can be used to include references to literature connected to the package, the contents of the file can be accessed from within R using `citation("pkgname")`. See also Hornik (2004) for more details on R packages we have no space to cover in this tutorial.

## 6 Installation and Checking

In order to install a source package, several additional tools (on top of a working R installation) are necessary, e.g., perl to process the Rd files.

A Unix machine should have everything needed, but a regular Windows machine will not: Read the section on packages in the “R Windows FAQ” on what to install. Currently, the easiest way is to download and install RtoolsXX.exe from <http://www.murdoch-sutherland.com/Rtools/>.

Once all tools are in place, there are three commands of form

R CMD command pkgname

available to process the package:

**INSTALL:** installs the package into a library and makes it available for usage in R.

**check:** runs a battery of tests on the package.

**build:** removes temporary files from the source tree of the package and packs everything into an archive file.

All should be executed in the directory containing the source tree of the package. To install the package open a shell and go to the directory containing the package tree (i.e., the directory containing `linmod`, not into `linmod` itself). The package can be installed using a command of form

```
shell$ R CMD INSTALL -l /path/to/library linmod
* Installing *source* package 'linmod' ...
** R
** help
*** Building/Updating help pages for package 'linmod'
    Formats: text html latex example
    linmod          text      html      latex      example
** building package indices ...
* DONE (linmod)
```

R installs the source code, converts the help pages from Rd to text, HTML and latex, and extracts the examples.

R CMD check helps you do quality assurance on packages:

- The directory structure and the format of DESCRIPTION are checked.
- The documentation is converted into text, HTML, and L<sup>A</sup>T<sub>E</sub>X, and run through latex if available.
- The examples are run.



```

shell$ R CMD check linmod
* checking for working pdflatex ... OK
* using log directory 'compstat-2008-tutorial/package/linmod.Rcheck'
* using R version 2.7.0 (2008-04-22)
* using session charset: UTF-8
* checking for file 'linmod/DESCRIPTION' ... OK
* checking extension type ... Package
* this is package 'linmod' version '1.0'
* checking package name space information ... OK
* checking package dependencies ... OK
* checking if this is a source package ... OK
* checking whether package 'linmod' can be installed ... OK
* checking package directory ... OK
* checking for portable file names ... OK
* checking for sufficient/correct file permissions ... OK
* checking DESCRIPTION meta-information ... OK
* checking top-level files ... OK
* checking index information ... OK
* checking package subdirectories ... OK
* checking R files for non-ASCII characters ... OK
* checking R files for syntax errors ... OK
* checking whether the package can be loaded ... OK
* checking whether the package can be loaded with stated dependencies ... OK
* checking whether the name space can be loaded with stated dependencies ... OK
* checking for unstated dependencies in R code ... OK
* checking S3 generic/method consistency ... OK
* checking replacement functions ... OK
* checking foreign function calls ... OK
* checking R code for possible problems ... OK
* checking Rd files ... OK
* checking Rd cross-references ... OK
* checking for missing documentation entries ... WARNING
Undocumented code objects:
  linmodEst
All user-level objects in a package should have documentation entries.
See the chapter 'Writing R documentation files' in manual 'Writing R
Extensions'.
** checking for code/documentation mismatches ... OK
* checking Rd \usage sections ... OK
* creating linmod-Ex.R ... OK
* checking examples ... OK
* creating linmod-manual.tex ... OK
* checking linmod-manual.tex using pdflatex ... OK

```

Figure 3: Running R CMD check on package linmod.

- Any tests in the `tests/` subdirectory are run.
- Undocumented objects, and those whose `usage` and definition disagree are reported.

Figure 3 shows the output of R command `check` when run on package `linmod`. There is one warning, because we have not documented function `linmodEst`.

R CMD `build` will create a compressed package file from your package directory. It does this in a reasonably intelligent way, omitting object code, emacs backup files, and other junk. The resulting file is easy to transport across systems and can be `INSTALLED` without decompressing. R CMD `build` makes source packages by default. If you want to distribute a package that contains C or Fortran for Windows users, they may well need a binary package, as compiling under Windows requires downloading exactly the right versions of quite a number of tools. Binary packages are created by

- `INSTALLing` the source package and then making a zip file of the installed version, or
- running R CMD `build --binary`.

For our package building a source package looks like

```
shell$ R CMD build linmod
* checking for file 'linmod/DESCRIPTION' ... OK
* preparing 'linmod':
* checking DESCRIPTION meta-information ... OK
* removing junk files
* checking for LF line-endings in source and make files
* checking for empty or unneeded directories
* building 'linmod_1.0.tar.gz'
```

and results in a file `linmod_1.0.tar.gz` which we can pass to other people.

If you have a package that does something useful and is well-tested and documented, you might want other people to use it, too. Contributed packages have been very important to the success of R (and before that of S). Packages can be submitted to CRAN by ftp. Make sure to run R CMD `check` with the latest version of R before submission. The CRAN maintainers will make sure that the package passes CMD `check` (and will keep improving CMD `check` to find more things for you to fix in future versions). Submit only the package sources, binaries are built automatically by designated platform maintainers.

## 7 Summary

In this paper we have given step-by-step instructions on how to write code in R which conforms to standards for statistical models and hence is intuitive to use. Object oriented programming allows the usage of common generic functions like `summary()` or `predict()` for a wide range of different model classes. Using S formulas we can create design matrices with possibly complex interaction and nesting structures. We then have turned a loose collection of functions into a regular R package, which can easily be documented, checked and distributed to other users. The tutorial is meant as a starting point only. The R packaging system has much more features than we have covered, most of which are not necessary when first creating an R package.

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