

# Building R Packages

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# What is an R Package?

- ▶ A mechanism for extending the basic functionality of R
- ▶ A collection of R functions, or other (data) objects
- ▶ Organized in a systematic fashion to provide a minimal amount of consistency
- ▶ Written by users/developers everywhere

# Where are These R Packages?

- ▶ Primarily available from CRAN and Bioconductor
- ▶ Also available from GitHub, Bitbucket, Gitorious, etc. (and elsewhere)
- ▶ Packages from CRAN/Bioconductor can be installed with `install.packages()`
- ▶ Packages from GitHub can be installed using `install_github()` from the devtools package

You do not have to put a package on a central repository, but doing so makes it easier for others to install your package.

# What's the Point?

- ▶ “Why not just make some code available?”
- ▶ Documentation / vignettes
- ▶ Centralized resources like CRAN
- ▶ Minimal standards for reliability and robustness
- ▶ Maintainability / extension
- ▶ Interface definition / clear API
- ▶ Users know that it will at least load properly

# Package Development Process

- ▶ Write some code in an R script file (.R)
- ▶ Want to make code available to others
- ▶ Incorporate R script file into R package structure
- ▶ Write documentation for user functions
- ▶ Include some other material (examples, demos, datasets, tutorials)
- ▶ Package it up!

# Package Development Process

- ▶ Submit package to CRAN or Bioconductor
- ▶ Push source code repository to GitHub or other source code sharing web site
- ▶ People find all kinds of problems with your code
- ▶ Scenario #1: They tell you about those problems and expect you to fix it
- ▶ Scenario #2: They fix the problem for you and show you the changes
- ▶ You incorporate the changes and release a new version

# R Package Essentials

- ▶ An R package is started by creating a directory with the name of the R package
- ▶ A DESCRIPTION file which has info about the package
- ▶ R code! (in the R/ sub-directory)
- ▶ Documentation (in the man/ sub-directory)
- ▶ NAMESPACE (optional, but do it)
- ▶ Full requirements in Writing R Extensions

# The DESCRIPTION File

- ▶ Package: Name of package (e.g. library(name))
- ▶ Title: Full name of package
- ▶ Description: Longer description of package in one sentence (usually)
- ▶ Version: Version number (usually M.m-p format)
- ▶ Author, Authors@R: Name of the original author(s)
- ▶ Maintainer: Name + email of person who fixes problems
- ▶ License: License for the source code



# The DESCRIPTION File

These fields are optional but commonly used

- ▶ Depends: R packages that your package depends on
- ▶ Suggests: Optional R packages that users may want to have installed
- ▶ Date: Release date in YYYY-MM-DD format
- ▶ URL: Package home page
- ▶ Other fields can be added

## DESCRIPTION File: gpclib

Package: gpclib Title: General Polygon Clipping Library for R  
Description: General polygon clipping routines for R based on Alan Murta's C library Version: 1.5-5 Author: Roger D. Peng  
rpeng@jhsph.edu with contributions from Duncan Murdoch and Barry Rowlingson; GPC library by Alan Murta Maintainer: Roger D. Peng  
rpeng@jhsph.edu License: file LICENSE Depends: R ( $\geq$  2.14.0), methods Imports: graphics Date: 2013-04-01 URL:  
<http://www.cs.man.ac.uk/~toby/gpc/>,  
<http://github.com/rdpeng/gpclib>

# R Code

- ▶ Copy R code into the R/ sub-directory
- ▶ There can be any number of files in this directory
- ▶ Usually separate out files into logical groups
- ▶ Code for all functions should be included here and not anywhere else in the package

# The NAMESPACE File

- ▶ Used to indicate which functions are exported
- ▶ Exported functions can be called by the user and are considered the public API
- ▶ Non-exported functions cannot be called directly by the user (but the code can be viewed)
- ▶ Hides implementation details from users and makes a cleaner package interface

# The NAMESPACE File

- ▶ You can also indicate what functions you import from other packages
- ▶ This allows for your package to use other packages without making other packages visible to the user
- ▶ Importing a function loads the package but does not attach it to the search list

# The NAMESPACE File

Key directives - `export("<function>")` - `import("<package>")` -  
`importFrom("<package>", "<function>")`

Also important - `exportClasses("<class>")` -  
`exportMethods("<generic>")`

## NAMESPACE File: mvtsplot package

```
export("mvtsplot")  
importFrom(graphics, "Axis")  
import(splines)
```

## NAMESPACE File: gpc.lib package

```
export("read.polyfile", "write.polyfile")

importFrom(graphics, plot)

exportClasses("gpc.poly", "gpc.poly.nohole")

exportMethods("show", "get.bbox", "plot", "intersect", "unions",
              "[", "append.poly", "scale.poly", "area.poly",
              "coerce", "tristrip", "triangulate")
```



# Documentation

- ▶ Documentation files (.Rd) placed in man/ sub-directory
- ▶ Written in a specific markup language
- ▶ Required for every exported function
- ▶ Another reason to limit exported functions
- ▶ You can document other things like concepts, package overview

## Help File Example: line Function

```
\name{line}  
\alias{line}  
\alias{residuals.tukeyline}  
\title{Robust Line Fitting}  
\description{  
  Fit a line robustly as recommended in \emph{Exploratory D
```

## Help File Example: line Function

```
\usage{
line(x, y)
}
\arguments{
  \item{x, y}{the arguments can be any way of specifying x-
    \code{\link{xy.coords}}.}
}
```

## Help File Example: line Function

```
\details{
```

```
  Cases with missing values are omitted.
```

```
  Long vectors are not supported.
```

```
}
```

```
\value{
```

```
  An object of class "tukeyline".
```

```
  Methods are available for the generic functions coef,  
  residuals, fitted, and print.
```

```
}
```

## Help File Example: line Function

```
\references{  
  Tukey, J. W. (1977).  
  \emph{Exploratory Data Analysis},  
  Reading Massachusetts: Addison-Wesley.  
}
```

# Building and Checking

- ▶ R CMD build is a command-line program that creates a package archive file (.tar.gz)
- ▶ R CMD check runs a battery of tests on the package
- ▶ You can run R CMD build or R CMD check from the command-line using a terminal or command-shell application
- ▶ You can also run them from R using the system() function

```
system("R CMD build newpackage")  
system("R CMD check newpackage")
```

# Checking

- ▶ R CMD check runs a battery tests
- ▶ Documentation exists
- ▶ Code can be loaded, no major coding problems or errors
- ▶ Run examples in documentation
- ▶ Check docs match code
- ▶ All tests must pass to put package on CRAN

# Getting Started

- ▶ The `package.skeleton()` function in the `utils` package creates a “skeleton” R package
- ▶ Directory structure (`R/`, `man/`), `DESCRIPTION` file, `NAMESPACE` file, documentation files
- ▶ If there are functions visible in your workspace, it writes R code files to the `R/` directory
- ▶ Documentation stubs are created in `man/`
- ▶ You need to fill in the rest!



# Summary

- ▶ R packages provide a systematic way to make R code available to others
- ▶ Standards ensure that packages have a minimal amount of documentation and robustness
- ▶ Obtained from CRAN, Bioconductor, Github, etc.

# Summary

- ▶ Create a new directory with R/ and man/ sub-directories (or just use `package.skeleton()`)
- ▶ Write a DESCRIPTION file
- ▶ Copy R code into the R/ sub-directory
- ▶ Write documentation files in man/ sub-directory
- ▶ Write a NAMESPACE file with exports/imports
- ▶ Build and check