Package architecture

Physalia course 2023

Instructor: Jacques Serizay

What are packages

- R “core” is already a mix of several packages !
  - base
  - compiler
  - datasets
  - graphics
  - grDevices
  - grid
  - methods
  - parallel
  - splines
  - stats
  - stats4
  - tcltk
  - tools
  - translations
  - utils

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R preferred extension mechanism: new functionalities (through new functions, but not only!)

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    - tcltk
    - tools
    - translations
    - utils

22922 CRAN PACKAGES

2130 BIOCONDUCTOR PACKAGES

2206 R-FORGE PACKAGES

85749 GITHUB PACKAGES

https://rdrr.io/

R preferred extension mechanism: new <u>functionalities</u> (through new <u>functions</u>, but not only!)

Standard package source: the bare minimum

```
myPackage/
  R/
    functions.R
    utils.R
  DESCRIPTION
  NAMESPACE
```

Standard package source: more complete structure

```
myPackage/
  data/
  man/
  inst/
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  DESCRIPTION
  NAMESPACE
  README.md
  NEWS
  LICENSE
```

DESCRIPTION

- myPackage/
  - data/
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    - functions.R
    - utils.R
  - **DESCRIPTION**
  - NAMESPACE
  - README.md
  - NEWS
  - LICENSE

```
Package: HiContacts
Title: HiContacts: R interface to cool files
Version: 0.99.11
Date: 2022-08-16
Authors@R:
    c(person(given = "Jacques",
           family = "Serizay",
           role = c("aut", "cre"),
           email = "jacquesserizay@gmail.com",
           comment = c(ORCID = "0000-0002-4295-0624")))
Description: HiContacts: R interface to (m)cool files and other Hi-C
    processed file formats. HiContacts provides a collection of tools to
    analyse and visualize Hi-C datasets. It can import data from pairs
    or (m)cool files.
License: MIT + file LICENSE
URL: https://github.com/js2264/HiContacts
BugReports: https://github.com/js2264/HiContacts/issues
Depends:
    R (>= 4.2)
Imports:
    HiContactsData
Suggests:
    rmarkdown
biocViews:
    HiC
Encoding: UTF-8
VignetteBuilder: knitr
LazyData: false
Roxygen: list(markdown = TRUE)
RoxygenNote: 7.2.1
```

DESCRIPTION

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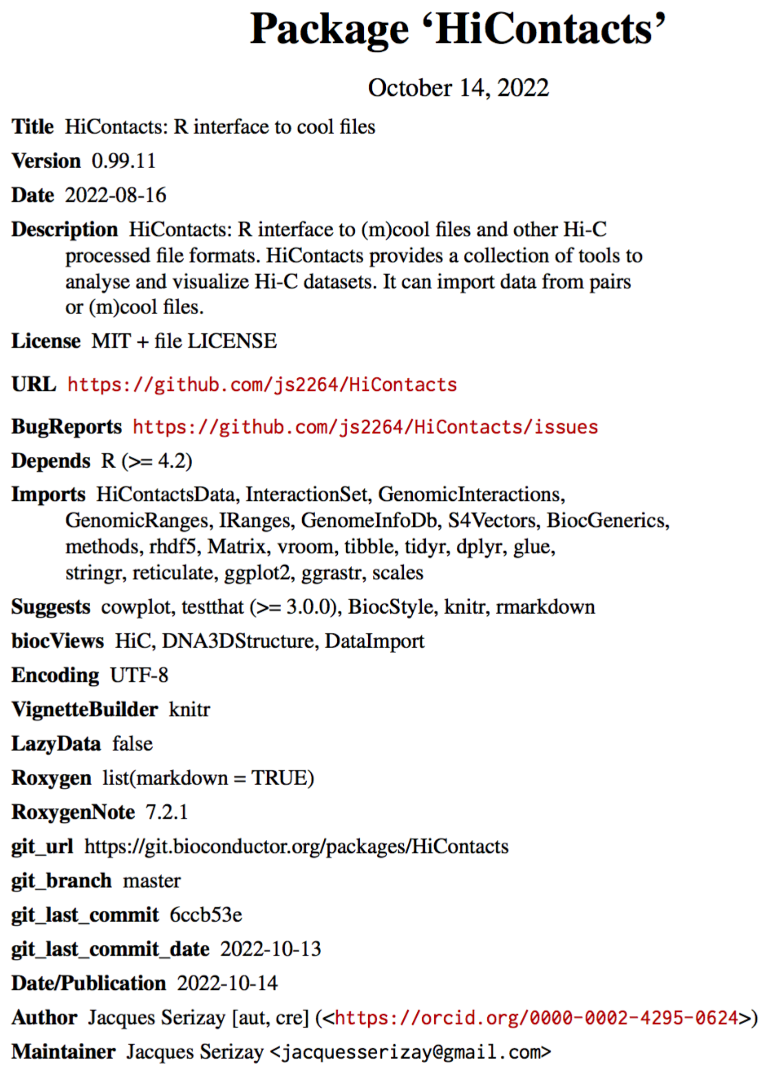

Package ‘HiContacts’

October 14, 2022

Title HiContacts: R interface to cool files

Version 0.99.11

Date 2022-08-16

Description HiContacts: R interface to (m)cool files and other Hi-C processed file formats. HiContacts provides a collection of tools to analyse and visualize Hi-C datasets. It can import data from pairs or (m)cool files.

License MIT + file LICENSE

URL https://github.com/js2264/HiContacts

BugReports https://github.com/js2264/HiContacts/issues

Depends R (>= 4.2)

Imports HiContactsData, InteractionSet, GenomicInteractions, GenomicRanges, IRanges, GenomeInfoDb, S4Vectors, BiocGenerics, methods, rhdf5, Matrix, vroom, tibble, tidyr, dplyr, glue, stringr, reticulate, ggplot2, ggrastr, scales

Suggests cowplot, testthat (>= 3.0.0), BiocStyle, knitr, rmarkdown

biocViews HiC, DNA3DStructure, DataImport

Encoding UTF-8

VignetteBuilder knitr

LazyData false

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.1

git_url https://git.bioconductor.org/packages/HiContacts

git_branch master

git_last_commit 6ccb53e

git_last_commit_date 2022-10-13

Date/Publication 2022-10-14

Author Jacques Serizay [aut, cre] (<https://orcid.org/0000-0002-4295-0624>)

Maintainer Jacques Serizay <jacquesserizay@gmail.com>

NAMESPACE

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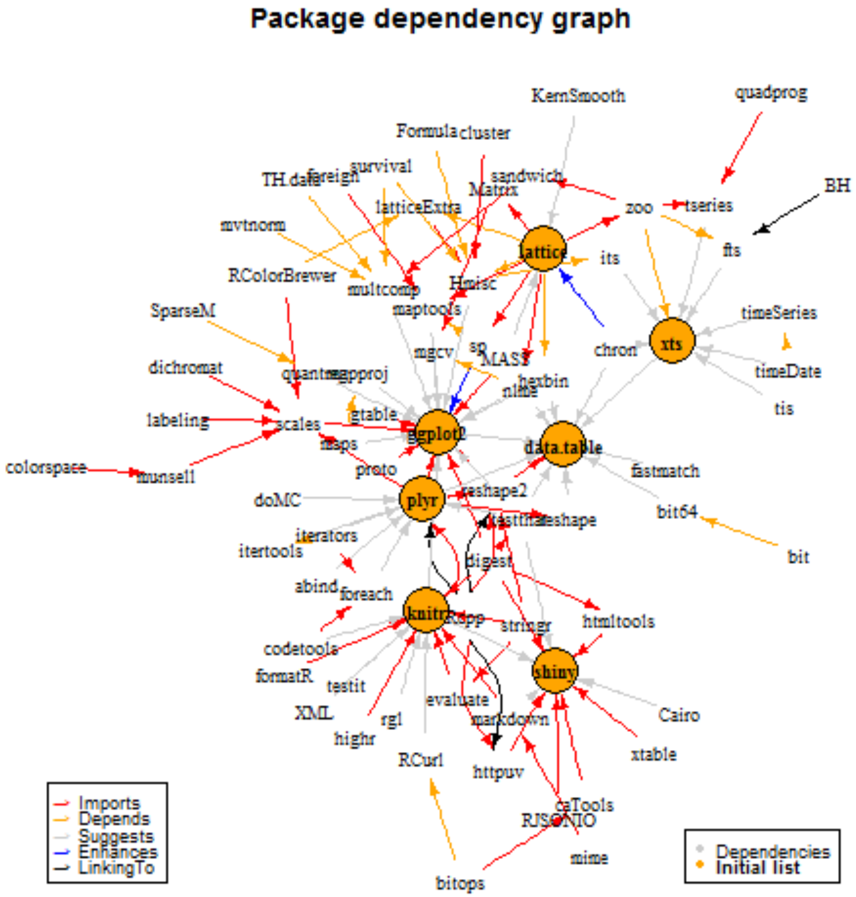
```

```
# Generated by roxygen2: do not edit by hand

export(APA)
export(cool2gi)
export(cool2seqinfo)
export(detrend)
export(fetchCool)
export(formatCoords)
export(getAnchors)
export(getCounts)
export(getHicStats)
export(getPs)
export(ggMatrix)
export(ggPs)
export(ggtheme_HiContacts)
export(ggtheme_HiContacts_tracks)
export(gi2cm)
export(lsCoolFiles)
export(lsCoolResolutions)
export(pairs2gi)
export(peekCool)
export(plotMatrix)
export(splitCoords)
import(BiocParallel)
import(InteractionSet)
import(dplyr)
import(ggplot2)
import(ggrastr)
import(rhdf5)
import(scales)
import(stringr)
import(tibble)
import(tidyr)
import(tools)
import(zeallot)
importFrom(GenomeInfoDb,Seqinfo)
importFrom(GenomeInfoDb,seqlengths)
importFrom(GenomicRanges,GRanges)
importFrom(GenomicRanges,end)
importFrom(GenomicRanges,findOverlaps)
importFrom(GenomicRanges,mcols)
importFrom(GenomicRanges,resize)
importFrom(GenomicRanges,seqnames)
importFrom(GenomicRanges,start)
```


Package dependency graph

README.md

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~~~
# HiContacts

HiContacts provides tools to import `(m)cool` matrices in R and work with them there.

It creates a new `Contacts` class of objects, built on pre-existing Bioconductor
objects, namely `InteractionSet`, `GenomicInterations` and `ContactMatrix` (`Lun,
Perry & Ing-Simmons, F1000Research 2016`), and provides **analytical** and
**visualization** tools to investigate contact maps.

## Installation

`HiContacts` will soon be available in Bioconductor.
To install the current release use:

```r
if (!requireNamespace("BiocManager", quietly = TRUE))
install.packages("BiocManager")
BiocManager::install("HiContacts")
```

For now, `HiContacts` can be installed from Github as follows:

```r
install.packages("devtools")
devtools::install_github("js2264/HiContacts")
library(HiContacts)
```

## Citation

If you are using `HiContacts` in your research, please cite:

> Serizay J (2022). _HiContacts: HiContacts: R interface to cool files_.
> R package version 0.99.0
> <https://github.com/js2264/HiContacts>.

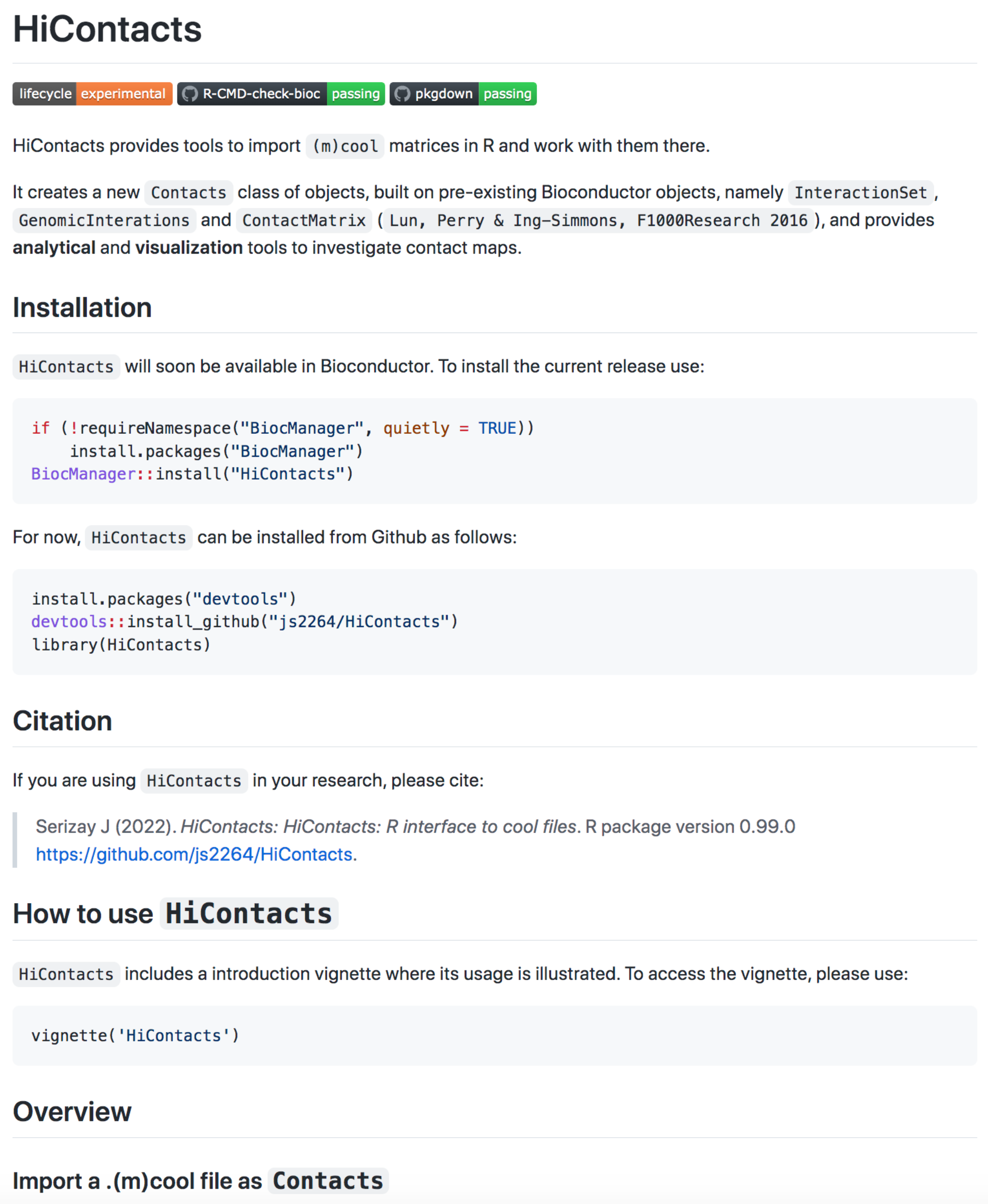
## How to use `HiContacts`

`HiContacts` includes a introduction vignette where its usage is
illustrated. To access the vignette, please use:

```r
vignette('HiContacts')
```

## Overview

### Import a .(m)cool file as `Contacts`
~~~



HiContacts

lifecycle experimental | R-CMD-check-bioc passing | pkgdown passing

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Overview

Import a .(m)cool file as `Contacts`

NEWS

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```
# periodicDNA 0.3.2 (dev)

* IMPORTANT:
  - Implemented data-raw for reproducibility

* MINOR:
  - Changed xlim of norm. distr. plot in plotPeriodicityResults()

# periodicDNA 0.3.1 (2020-05-05)

* IMPORTANT:
  - rollmean(k=3) is now applied *before* normalisation *as well*,
      on the raw distribution vector
  - plotPeriodicityResults() output returns one single plot (with cowplot)
  - getPeriodicityTrack() now returns the Rle
  - Improved plotting functions -now show shuffled for plotPeriodicityResults()
  - Added ggplot2 theming

* MINOR:
    * Changed many variable names (all to snake_case)
    * sampleGRanges is now full-fledged function
       (GRanges, DNAStringSet, character and BSgenome methods)
    * sampleGenome is an alias for sampleGRanges.character
    * Added sacCer3 to getPeriodicity BSgenomes
    * Added DNAString method for getPeriodicity
    * Added a vignette describing the internal steps
    * Clarified user-level functions in README
    * Added ce11_TSSs data
    * Renamed generateperiodicitytrack as getPeriodicityTrack
    * Renamed variables in getFPI and getPeriodicity
    * Created a utility char2BSgenome()

# periodicDNA 0.3.0 (2020-05-03)

* Added tests
* Added getFPI function
* cleaned-up functions
* cleaned-up function dependencies
* Added toy data
* Added vignette

# periodicDNA 0.2.1 (2020-03-04)

* Added Travis build check
* Simplified README.md
```

LICENSE

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  - **LICENSE**

```
GNU General Public License
==========================

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document, but changing it is not allowed.

    ## Preamble

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it in new free programs, and that you know you can do these things.

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    For example, if you distribute copies of such a program, whether gratis or for a fee,
you must pass on to the recipients the same freedoms that you received. You must make
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terms so they know their rights.

    Developers that use the GNU GPL protect your rights with two steps: **(1)** assert
copyright on the software, and **(2)** offer you this License giving you legal permission
to copy, distribute and/or modify it.

    For the developers' and authors' protection, the GPL clearly explains that there is
no warranty for this free software. For both users' and authors' sake, the GPL
requires that modified versions be marked as changed, so that their problems will not
be attributed erroneously to authors of previous versions.

    Some devices are designed to deny users access to install or run modified versions of
the software inside them, although the manufacturer can do so. This is fundamentally
```

Function files

- myPackage/
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  - vignettes/
  - R/
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  - LICENSE

```r
#' Parsing (m)cool files
#'
#' These functions are the workhorse internal functions used to import
#' a `.(m)cool` file as GenomicInteractions (wrapped into a `Contacts` object
#' by `Contacts()` function).
#'
#' @param file file
#' @param resolution resolution
#' @param balanced import balancing scores
#' @return anchors from (m)cool, stored as a GRanges
#'
#' @importFrom GenomicRanges GRanges
#' @importFrom GenomicRanges seqnames
#' @importFrom GenomicRanges start
#' @importFrom GenomicRanges end
#' @importFrom IRanges IRanges
#' @rdname parse

getAnchors <- function(file, resolution = NULL, balanced = "cooler") {
    bins <- fetchCool(file, "bins", resolution)
    anchors <- GenomicRanges::GRanges(
                bins$chr,
                IRanges::IRanges(bins$start + 1, bins$end),
                bin_id = seq_along(bins$chr),
                seqinfo = cool2seqinfo(file, resolution)
    )
    names(anchors) <- paste(GenomicRanges::seqnames(anchors), GenomicRanges::start(anchors), GenomicRanges::end(anchors), sep
    = "_")
    if ("weight" %in% names(bins) & {
                balanced == "cooler" | balanced == TRUE
    }) {
    anchors$weight <- as.numeric(bins$weight)
    } else {
                weight <- 1
    }
    return(anchors)
}
```

Doc files

- myPackage/
  - data/
  - man/
    - **functions.Rd**
  - inst/
  - tests/
  - vignettes/
  - R/
    - functions.R
    - utils.R
  - DESCRIPTION
  - NAMESPACE
  - README.md
  - NEWS
  - LICENSE

```
% Generated by roxygen2: do not edit by hand
% Please edit documentation in R/parse.R
\name{getAnchors}
\alias{getAnchors}
\alias{getCountsFromPair}
\alias{getCounts}
\alias{fetchCool}
\alias{lsCoolFiles}
\alias{lsCoolResolutions}
\alias{peekCool}
\alias{cool2seqinfo}
\alias{cool2gi}
\alias{gi2cm}
\alias{cm2matrix}
\alias{pairs2gi}
\title{Parsing (m)cool files}
\usage{
getAnchors(file, resolution = NULL, balanced = "cooler")

\arguments{
    \item{file}{pairs file: \verb{<readname>\\t<chr1>\\t<start1>\\t<chr2>\\t<start2>}}

    \item{resolution}{resolution}

    \item{balanced}{import balancing scores}
}

\value{
    anchors from (m)cool, stored as a GRanges
}

\description{
    These functions are the workhorse internal functions used to import
    a \verb{.(m)cool} file as GenomicInteractions (wrapped into a \code{Contacts} object
    by \code{Contacts()} function).
}
```

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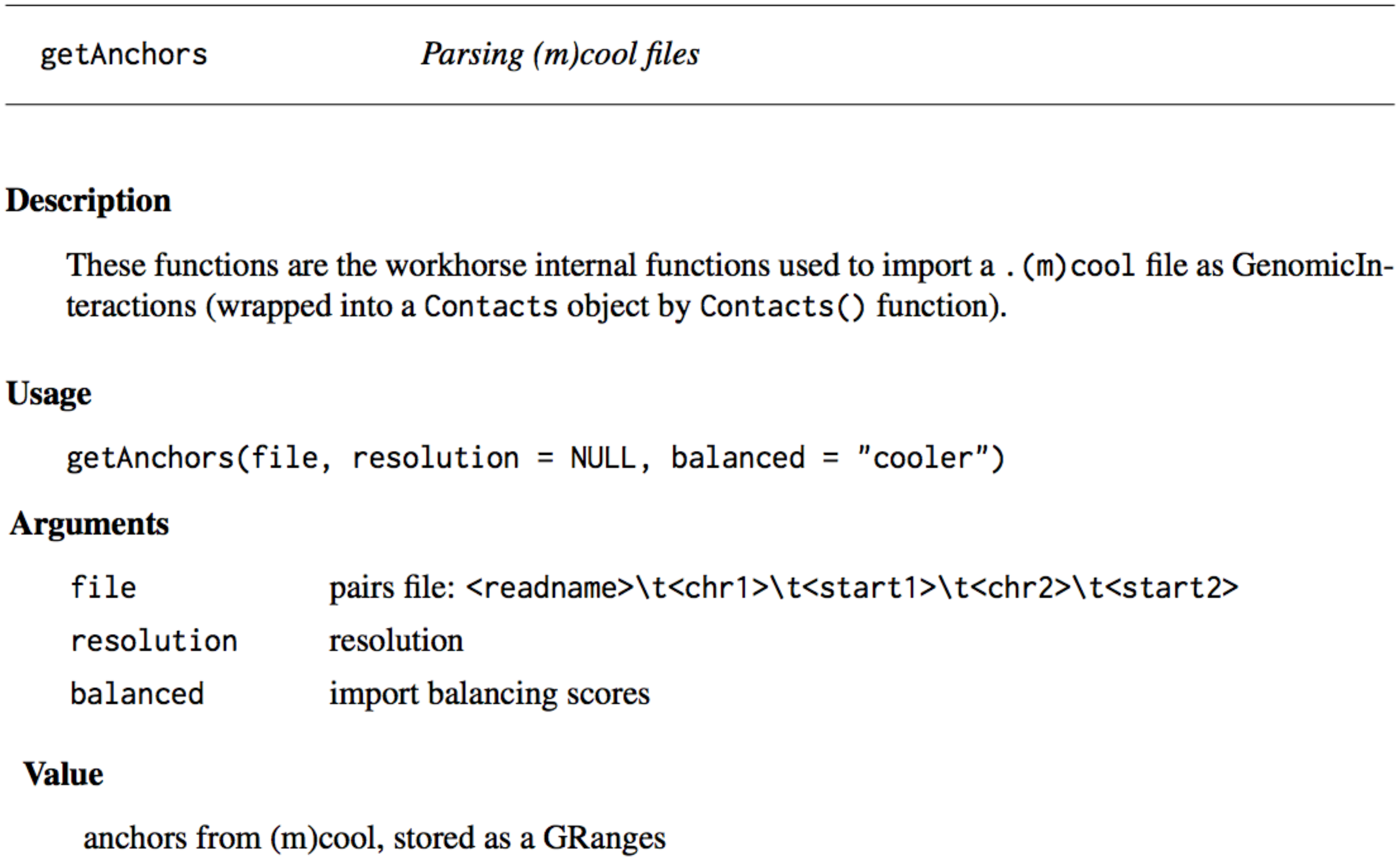
pdf documentation once package is published



`getAnchors` *Parsing (m)cool files*

Description

These functions are the workhorse internal functions used to import a `.(m)cool` file as GenomicInteractions (wrapped into a `Contacts` object by `Contacts()` function).

Usage

```
getAnchors(file, resolution = NULL, balanced = "cooler")
```

Arguments

`file`	pairs file: `<readname>\t<chr1>\t<start1>\t<chr2>\t<start2>`
`resolution`	resolution
`balanced`	import balancing scores

Value

anchors from (m)cool, stored as a GRanges

Doc files

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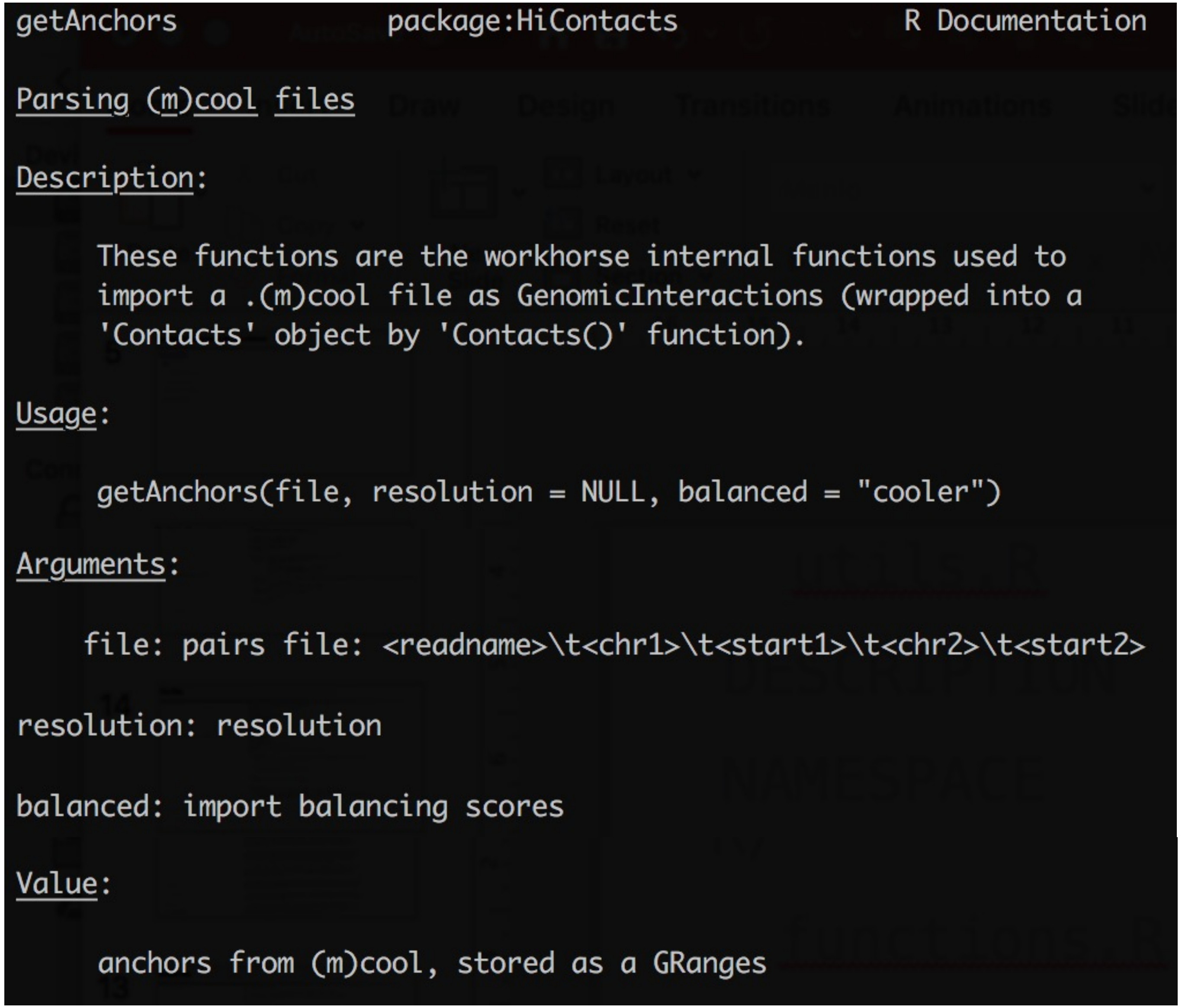
?getAnchors



```
getAnchors              package:HiContacts              R Documentation

Parsing (m)cool files

Description:

     These functions are the workhorse internal functions used to
     import a .(m)cool file as GenomicInteractions (wrapped into a
     'Contacts' object by 'Contacts()' function).

Usage:

     getAnchors(file, resolution = NULL, balanced = "cooler")

Arguments:

    file: pairs file: <readname>\t<chr1>\t<start1>\t<chr2>\t<start2>

resolution: resolution

balanced: import balancing scores

Value:

     anchors from (m)cool, stored as a GRanges
```

Source/Bundle/Binary/Installed/Loaded: késako?

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Source

Source/Bundle/ Binary /Installed/Loaded: késako?

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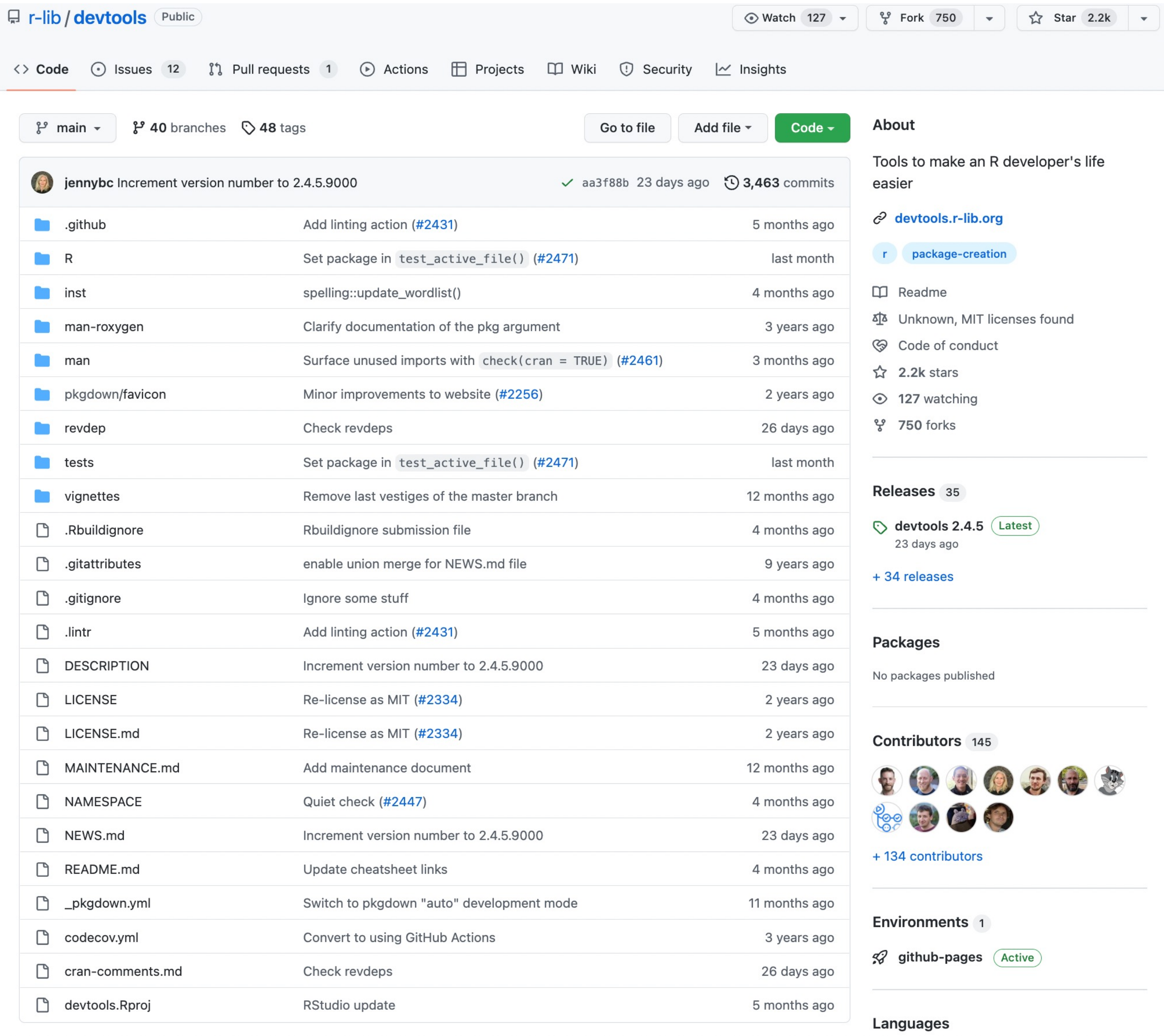

r-lib / devtools Public

jennybc Increment version number to 2.4.5.9000 ✓ aa3f88b 23 days ago 3,463 commits

.github	Add linting action (#2431)	5 months ago
R	Set package in `test_active_file()` (#2471)	last month
inst	spelling::update_wordlist()	4 months ago
man-roxygen	Clarify documentation of the pkg argument	3 years ago
man	Surface unused imports with `check(cran = TRUE)` (#2461)	3 months ago
pkgdown/favicon	Minor improvements to website (#2256)	2 years ago
revdep	Check revdeps	26 days ago
tests	Set package in `test_active_file()` (#2471)	last month
vignettes	Remove last vestiges of the master branch	12 months ago
.Rbuildignore	Rbuildignore submission file	4 months ago
.gitattributes	enable union merge for NEWS.md file	9 years ago
.gitignore	Ignore some stuff	4 months ago
.lintr	Add linting action (#2431)	5 months ago
DESCRIPTION	Increment version number to 2.4.5.9000	23 days ago
LICENSE	Re-license as MIT (#2334)	2 years ago
LICENSE.md	Re-license as MIT (#2334)	2 years ago
MAINTENANCE.md	Add maintenance document	12 months ago
NAMESPACE	Quiet check (#2447)	4 months ago
NEWS.md	Increment version number to 2.4.5.9000	23 days ago
README.md	Update cheatsheet links	4 months ago
_pkgdown.yml	Switch to pkgdown "auto" development mode	11 months ago
codecov.yml	Convert to using GitHub Actions	3 years ago
cran-comments.md	Check revdeps	26 days ago
devtools.Rproj	RStudio update	5 months ago

About

Tools to make an R developer's life easier

devtools.r-lib.org

r package-creation

Readme

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127 watching

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Releases 35

devtools 2.4.5 Latest
23 days ago

+ 34 releases

Packages

No packages published

Contributors 145

+ 134 contributors

Environments 1

github-pages Active

Languages

Source/Bundle/ Binary /Installed/Loaded: késako?

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→ `myPackage.tar.gz`

Bundle

Source/Bundle/ Binary /Installed/Loaded: késako?

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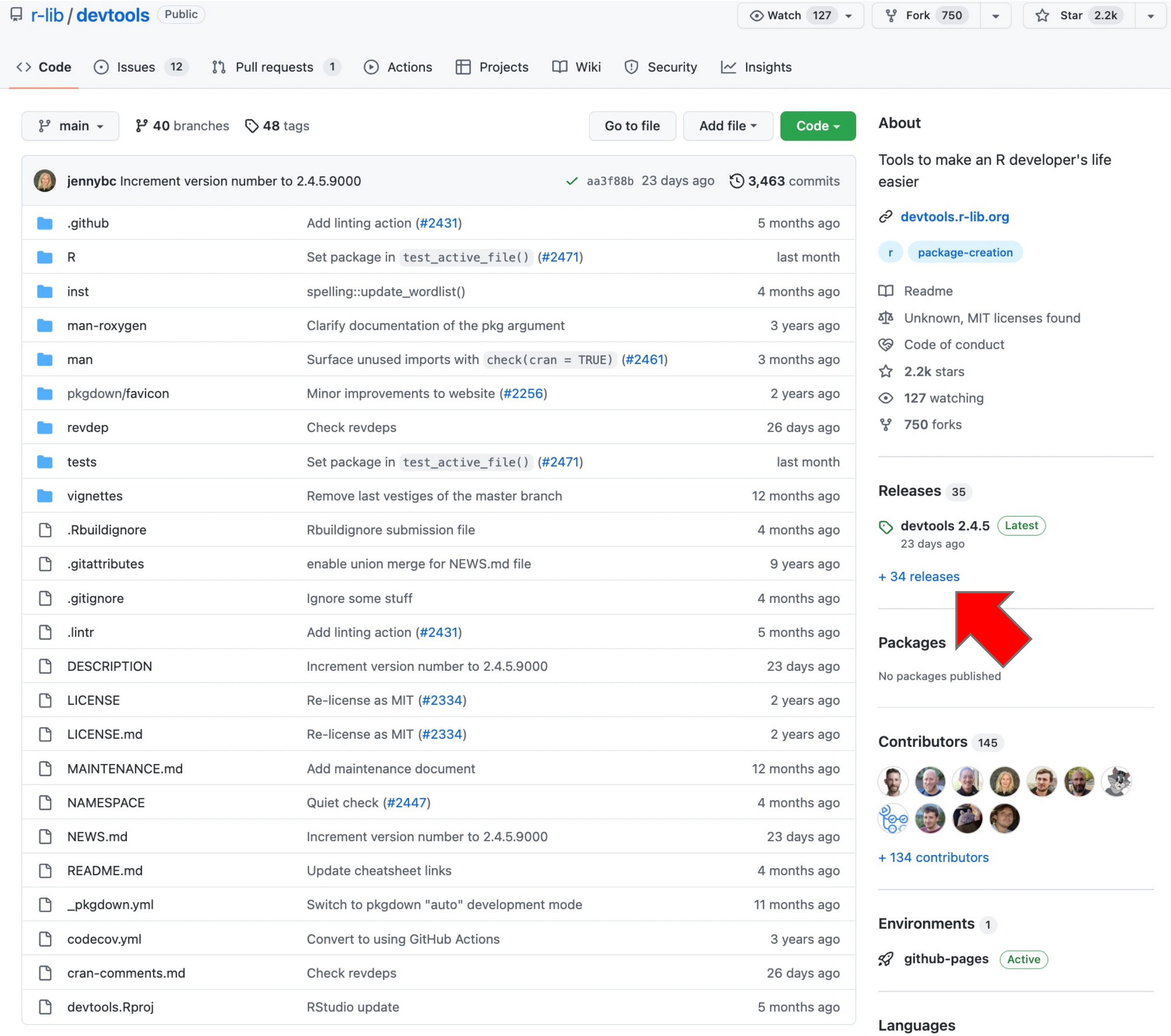

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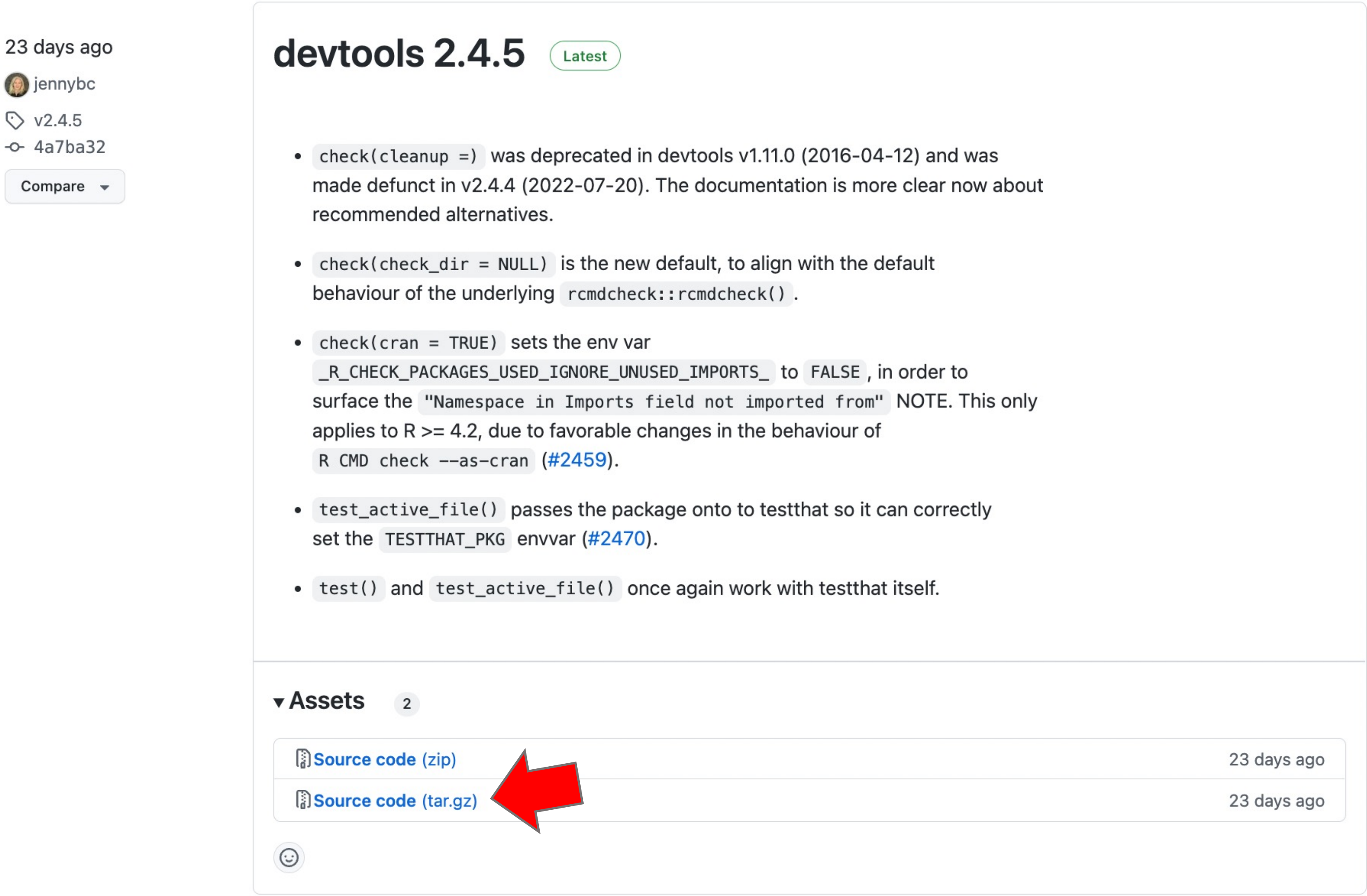
    functions.R
    utils.R
  DESCRIPTION
  NAMESPACE
  README.md
  NEWS
  LICENSE
```

myPacka



23 days ago

jennybc

v2.4.5

4a7ba32

devtools 2.4.5

- `check(cleanup =)` was deprecated in devtools v1.11.0 (2016-04-12) and was made defunct in v2.4.4 (2022-07-20). The documentation is more clear now about recommended alternatives.
- `check(check_dir = NULL)` is the new default, to align with the default behaviour of the underlying `rcmdcheck::rcmdcheck()`.
- `check(cran = TRUE)` sets the env var `_R_CHECK_PACKAGES_USED_IGNORE_UNUSED_IMPORTS_` to `FALSE`, in order to surface the `"Namespace in Imports field not imported from"` NOTE. This only applies to R >= 4.2, due to favorable changes in the behaviour of `R CMD check --as-cran` (#2459).
- `test_active_file()` passes the package onto to testthat so it can correctly set the `TESTTHAT_PKG` envvar (#2470).
- `test()` and `test_active_file()` once again work with testthat itself.

▾ **Assets** 2

Source code (zip)	23 days ago
Source code (tar.gz)	23 days ago

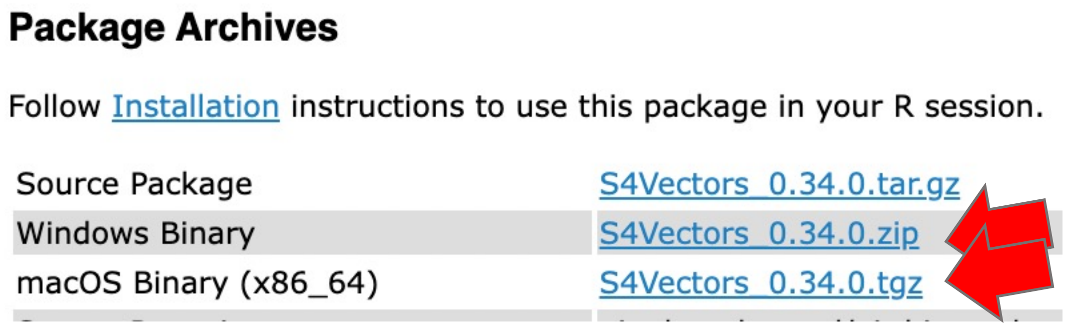
Source/Bundle/ Binary /Installed/Loaded: késako?

```
myPackage/
  data/
  man/
  inst/
  tests/
  vignettes/
  R/
    functions.R
    utils.R
  DESCRIPTION
  NAMESPACE
  README.md
  NEWS
  LICENSE
```

`myPackage.tar.gz`

Binary

CRAN,
Bioconductor

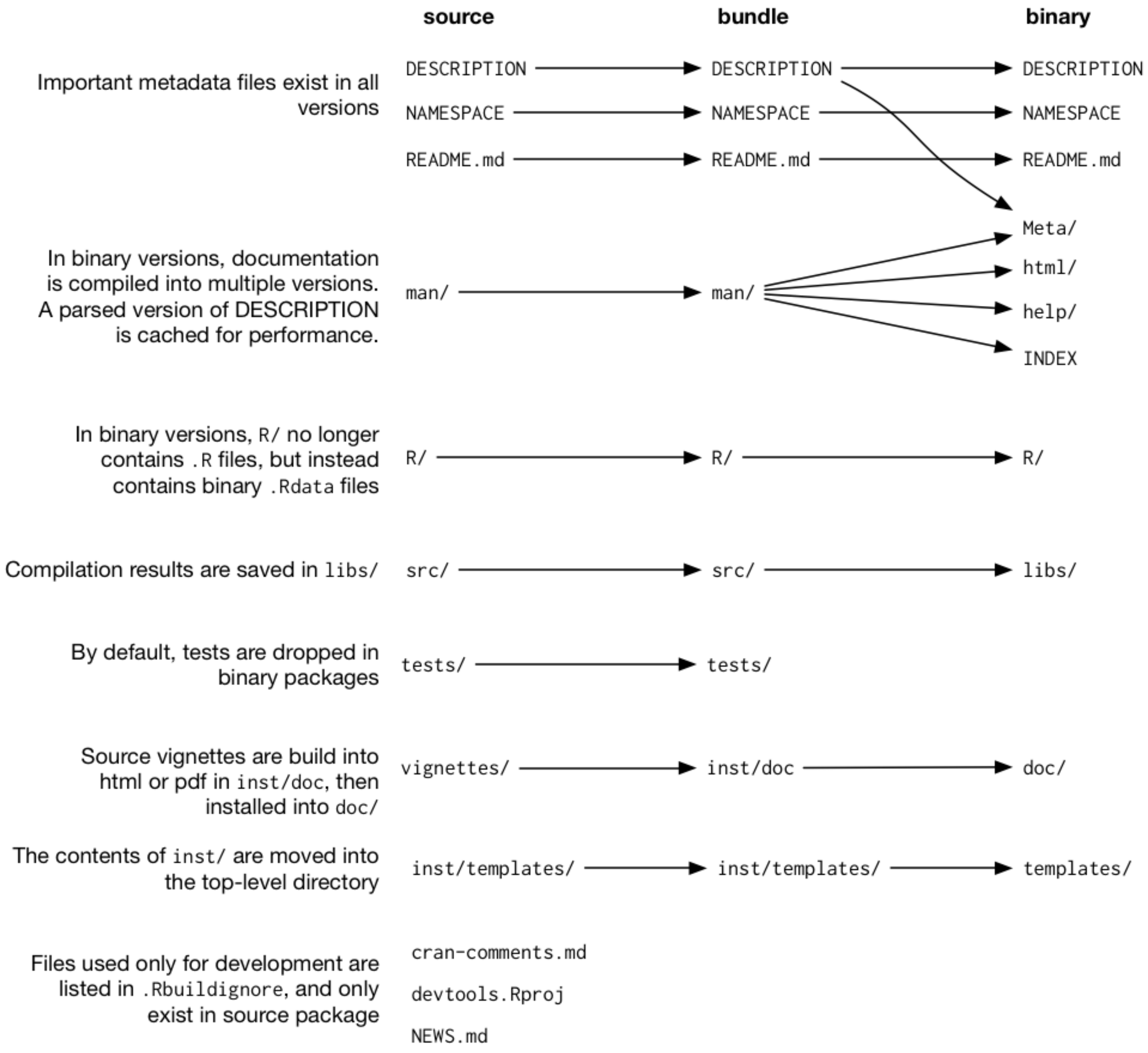


Package Archives

Follow Installation instructions to use this package in your R session.

Source Package	S4Vectors_0.34.0.tar.gz
Windows Binary	S4Vectors_0.34.0.zip
macOS Binary (x86_64)	S4Vectors_0.34.0.tgz

Source/Bundle/ Binary /Installed/Loaded: késako?



	source	**bundle**	**binary**

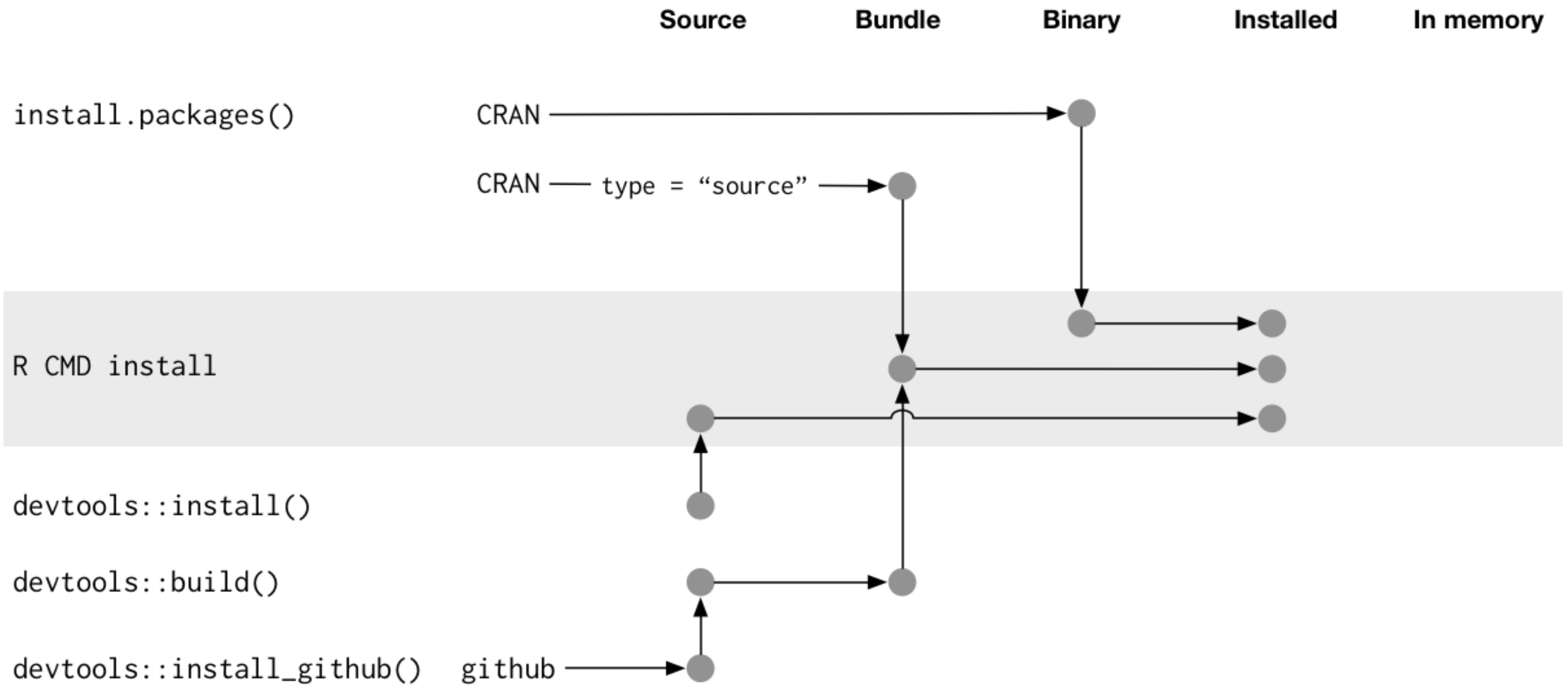
Important metadata files exist in all versions	`DESCRIPTION`
	`NAMESPACE`
	`README.md`
		`DESCRIPTION`
		`NAMESPACE`
		`README.md`
			`DESCRIPTION`
			`NAMESPACE`
			`README.md`

In binary versions, documentation is compiled into multiple versions. A parsed version of DESCRIPTION is cached for performance.	`man/`	`man/`	`Meta/`
			`html/`
			`help/`
			`INDEX`

In binary versions, `R/` no longer contains `.R` files, but instead contains binary `.Rdata` files	`R/`	`R/`	`R/`
Compilation results are saved in `libs/`	`src/`	`src/`	`libs/`
By default, tests are dropped in binary packages	`tests/`	`tests/`	
Source vignettes are build into html or pdf in `inst/doc`, then installed into `doc/`	`vignettes/`	`inst/doc`	`doc/`
The contents of `inst/` are moved into the top-level directory	`inst/templates/`	`inst/templates/`	`templates/`

Files used only for development are listed in `.Rbuildignore`, and only exist in source package	`cran-comments.md`
	`devtools.Rproj`
	`NEWS.md`		

Source/Bundle/ Binary /Installed/Loaded: késako?



Read more…

https://r-pkgs.org/Structure.html