

# Hands on Workshop

-

## Your First Submission in R

Phuse US Connect

Bethesda, 2024



# Disclaimer

- This presentation/Workshop represents the views of the authors and not necessarily Novo Nordisk
- Any regulatory communication shown will not be applicable to all projects. Please communicate with the appropriate health authorities about your submission



# Who are we



**Kristian Trøjelsgaard**

Statistical Programming Specialist at Novo Nordisk

[ktqn@novonordisk.com](mailto:ktqn@novonordisk.com)



**Steffen Falgreen Larsen**

Principal Statistician at Novo Nordisk

[sffl@novonordisk.com](mailto:sffl@novonordisk.com)

# Aim



Collect insight and learnings when using R for regulatory submission



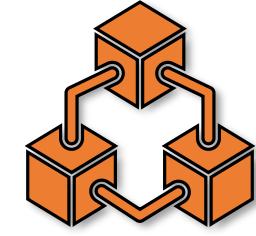
Get an understanding of the requirements and obstacles involved when using R



Motivate discussions between participants (and across companies)



# Structure of workshop

			
	Accuracy	Traceability	Reproducibility
• <b>Presentation</b>			
• <b>Exercise</b>			
• <b>Summary</b>			

**Let's get started**

# Welcome to Aristotle

A pharmaceutical company that recently did its first submission to FDA which included R programs



# Issue regarding submission



Realized that a lot of packages still need **risk-assessments (Accuracy)** and we have gotten questions from FDA on the **Traceability** and **Reproducibility** of our deliverables in R.

As a programmer in this company, we need you to help with this and write up our response to the FDA.

# The three essentials

**Accuracy**  
**Traceability**  
**Reproducibility**

# The three essentials

## Accuracy



### How do we ensure programs are accurate?

- There is a wealth of R packages available
- How do we ensure that the packages that we use are trustworthy?

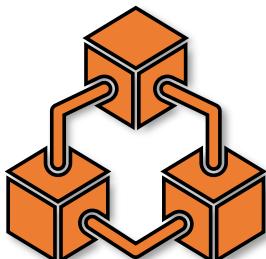
## Traceability



### How do we document what we have done?

- Many things in R can influence the final output
  - Packages, Options, Environmental Variables etc.
- What should a log include to provide traceability?

## Reproducibility



### How to ensure reproducibility when using R

- Package synchronization within a project
- Support authorities in environment replication



# Accuracy

How do we ensure accuracy?

# R vs SAS: Some fundamental differences



# R vs SAS: Some fundamental differences



2023: [R 4.3.2](#) (October, 2023)  
[R 4.3.1](#) (June, 2023)  
[R 4.3.0](#) (April, 2023)  
[R 4.2.3](#) (March, 2023)

2022: [R 4.2.2](#) (October, 2022)  
[R 4.2.1](#) (June, 2022)  
[R 4.2.0](#) (April, 2022)  
[R 4.1.3](#) (March, 2022)

2021: [R 4.1.2](#) (November, 2021)  
[R 4.1.1](#) (August, 2021)  
[R 4.1.0](#) (May, 2021)  
[R 4.0.5](#) (March, 2021)  
[R 4.0.4](#) (February, 2021)

2020: [R 4.0.3](#) (October, 2020)  
[R 4.0.2](#) (June, 2020)  
[R 4.0.1](#) (June, 2020)  
[R 4.0.0](#) (April, 2020)  
[R 3.6.3](#) (February, 2020)

2023: [SAS 9.4M8](#) (Jan, 2023)  
2020: [SAS 9.4M7](#) (August, 2020)  
2018: [SAS 9.4M6](#) (November, 2018)  
2017: [SAS 9.4M5](#) (September, 2017)  
2016: [SAS 9.4M4](#) (November, 2016)  
2015: [SAS 9.4M3](#) (July, 2015)  
2014: [SAS 9.4M2](#) (August, 2014)  
2013: [SAS 9.4M1](#) (December, 2013)  
[SAS 9.4](#) (July, 2013)

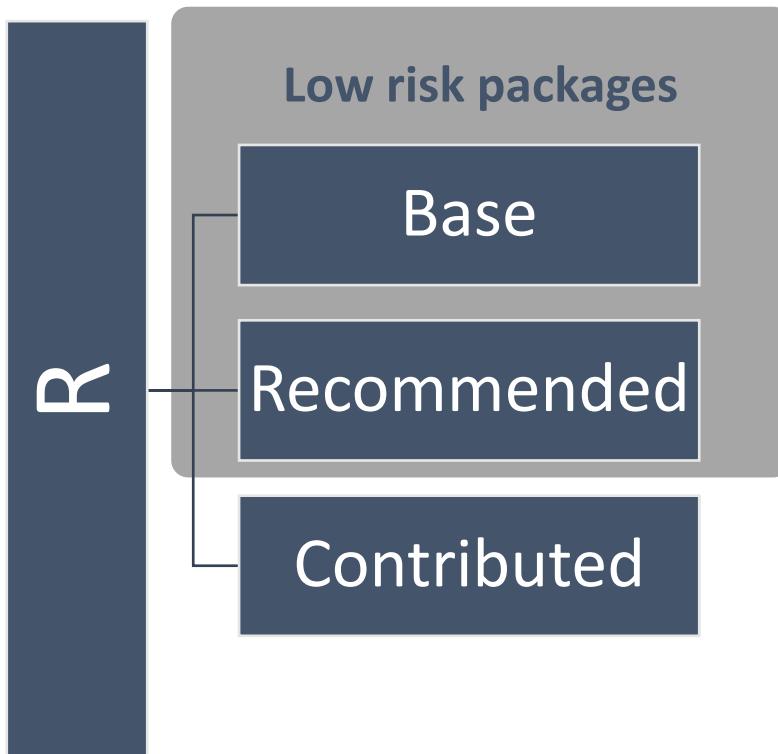
In Novo Nordisk



# R vs SAS: Some fundamental differences



# CRAN



- **Base/Recommended:** (Can be trusted)
  - The R Foundation develops both the base and recommended packages, and follows practices that ensures the accuracy of each
- **Contributed:** (Need internal testing)
  - 20.000+ **R** packages on CRAN, all tested to some extent, but not all can be considered validated

# Contributed

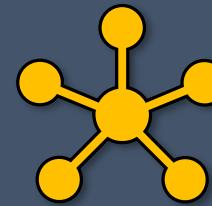
CRAN checks include (but is not limited to):



Execution  
of all test



Running all  
examples



Checking  
dependencies



Verifying  
documentation

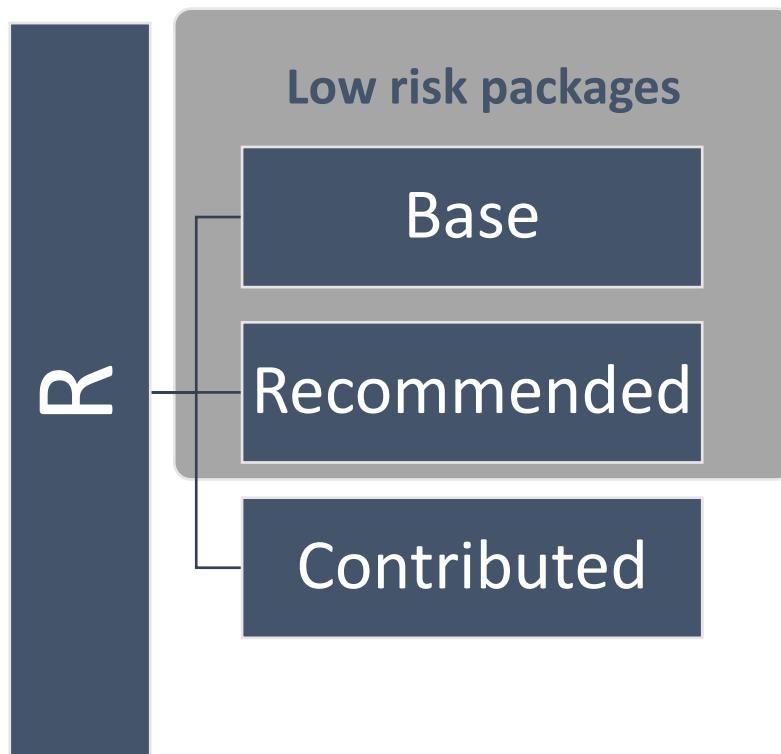


Looking for  
syntax errors



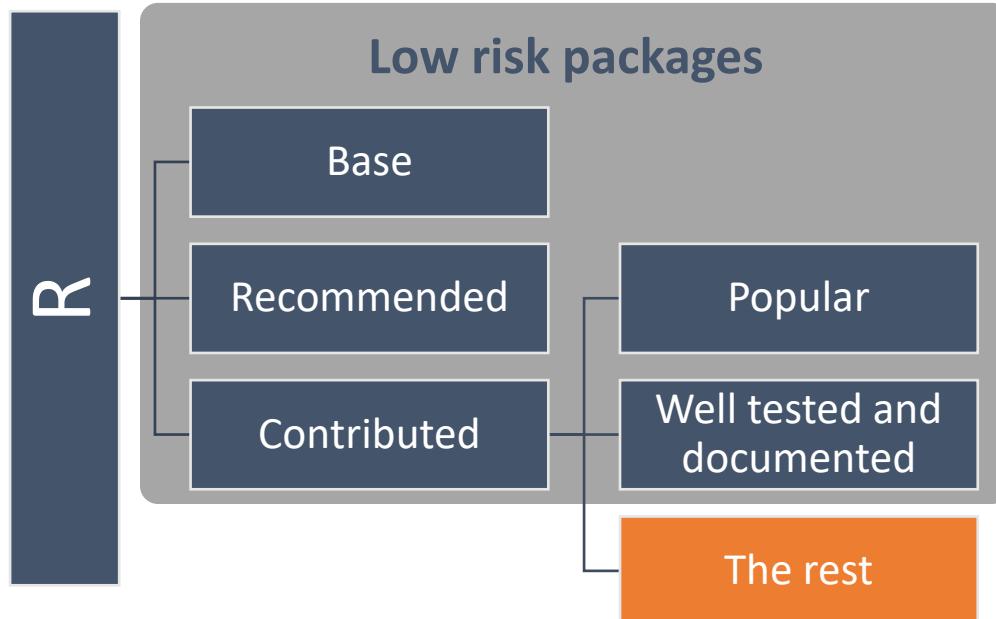
Re-building  
the vignettes

# CRAN



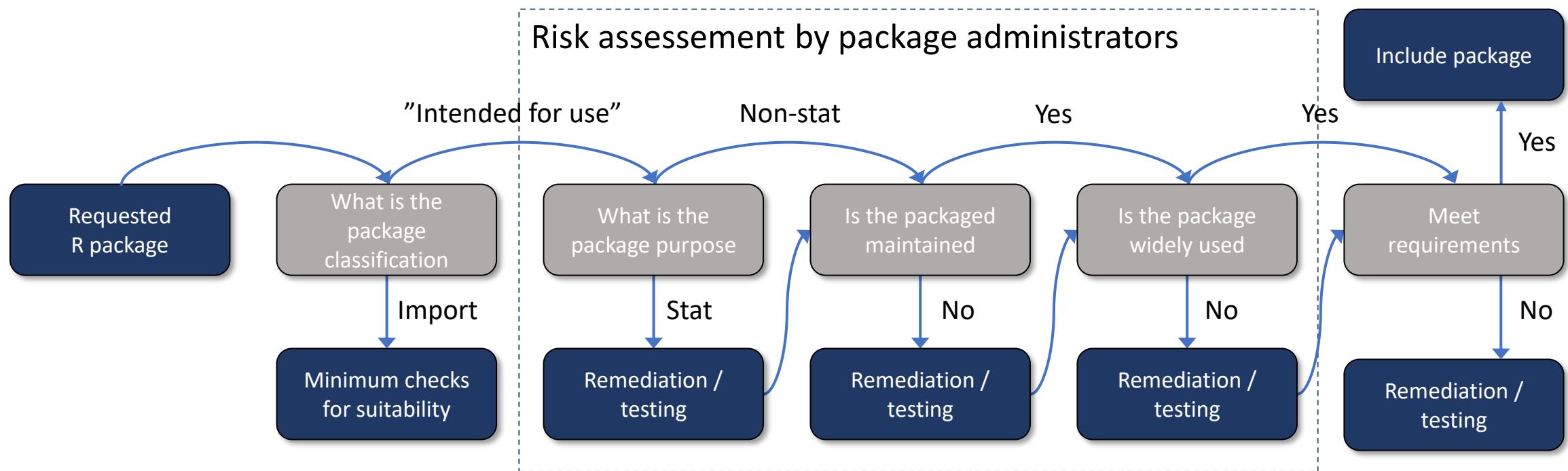
- **Base/Recommended:** (Can be trusted)
  - The R Foundation develops both the base and recommended packages, and follows practices that ensures the accuracy of each
- **Contributed:** (Need internal testing)
  - 20.000+ **R** packages on CRAN, all tested to some extent, but not all can be considered validated

# CRAN



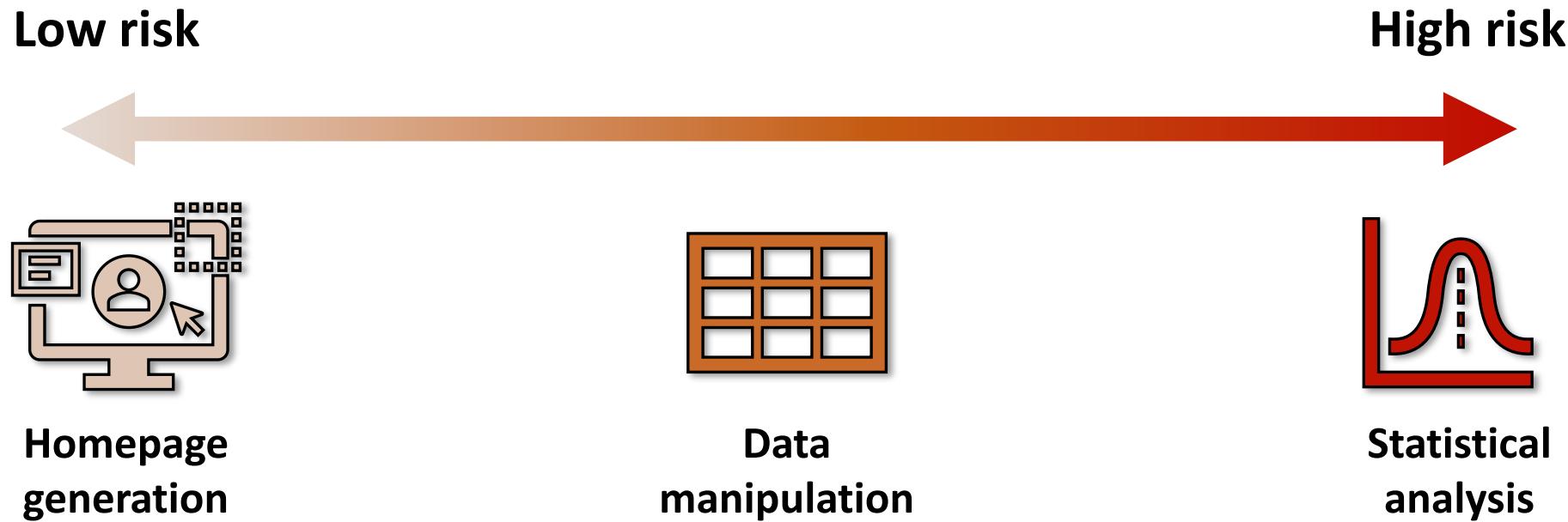
- **Base/Recommended:** (Can be trusted)
  - The R Foundation develops both the base and recommended packages, and follows practices that ensures the accuracy of each
- **Contributed:** (Need internal testing)
  - 20.000+ **R** packages on CRAN, all tested to some extent, but not all can be considered validated
- **Popular:** (Very low risk)
  - A subset of the contributed packages have an extremely large userbase and/or extensive test-suites
  - tidyverse, data.table, ...

# Risk assessment

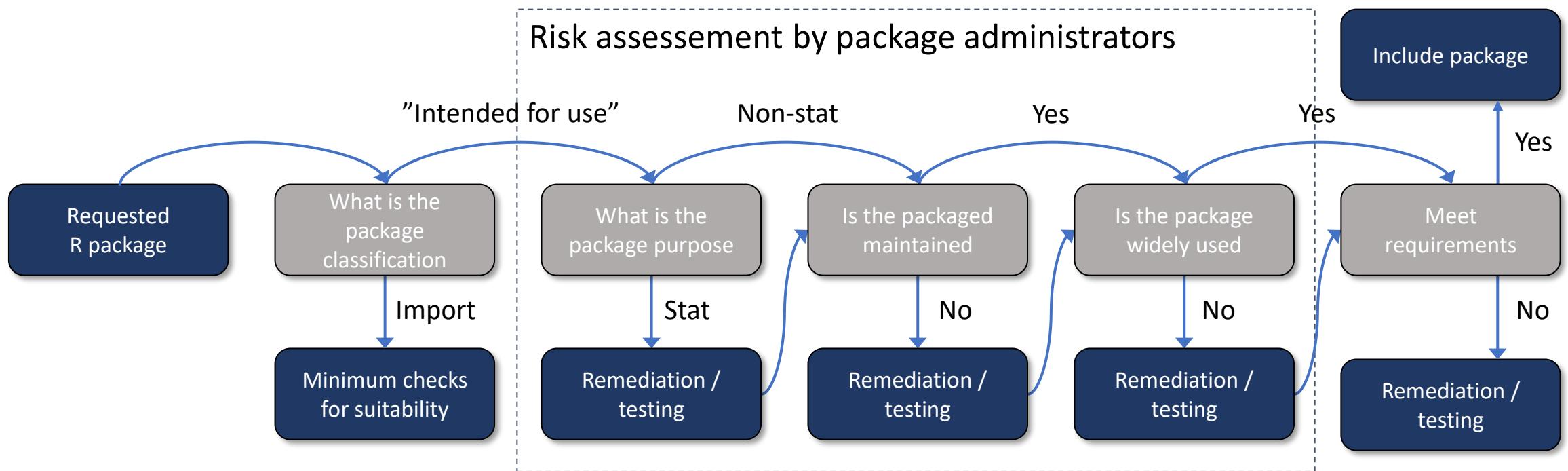


## What is the package purpose

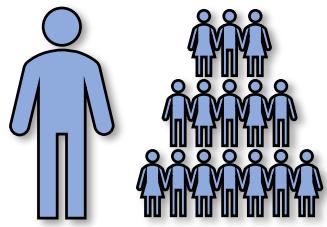
The **risk** of including a package is related to the **usage**



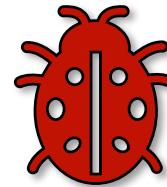
# Risk assessment



## Is the package maintained



- Number of contributors
- Reputation



Are issues solved at a reasonable pace



Pace of new releases



Last update



Testing  
(code coverage)



Vignettes

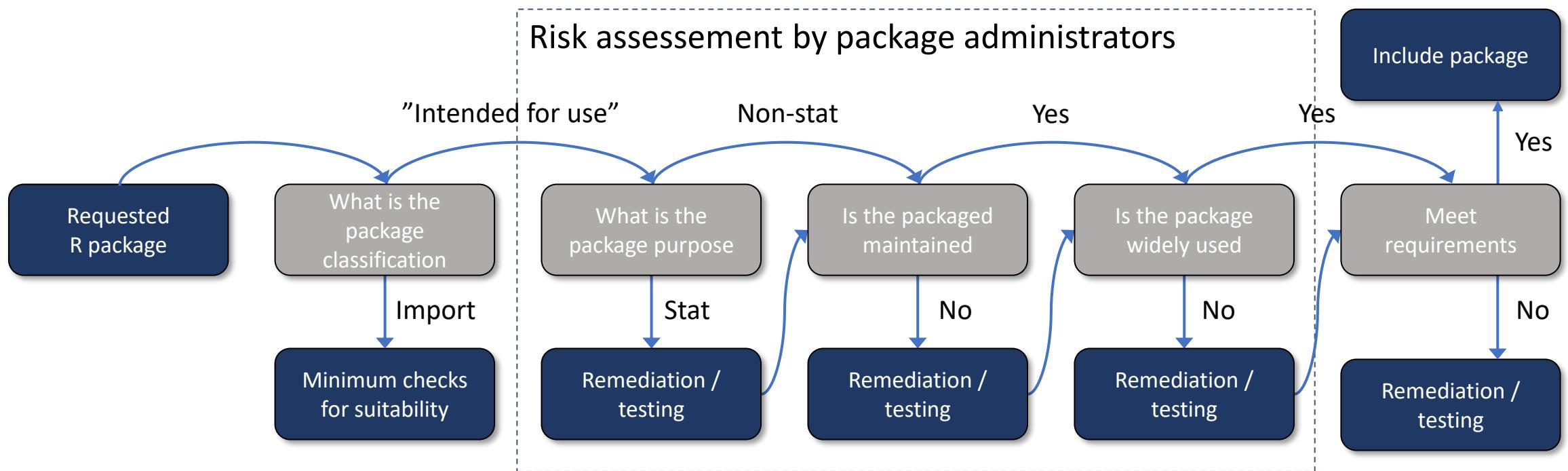


Does all functions have examples

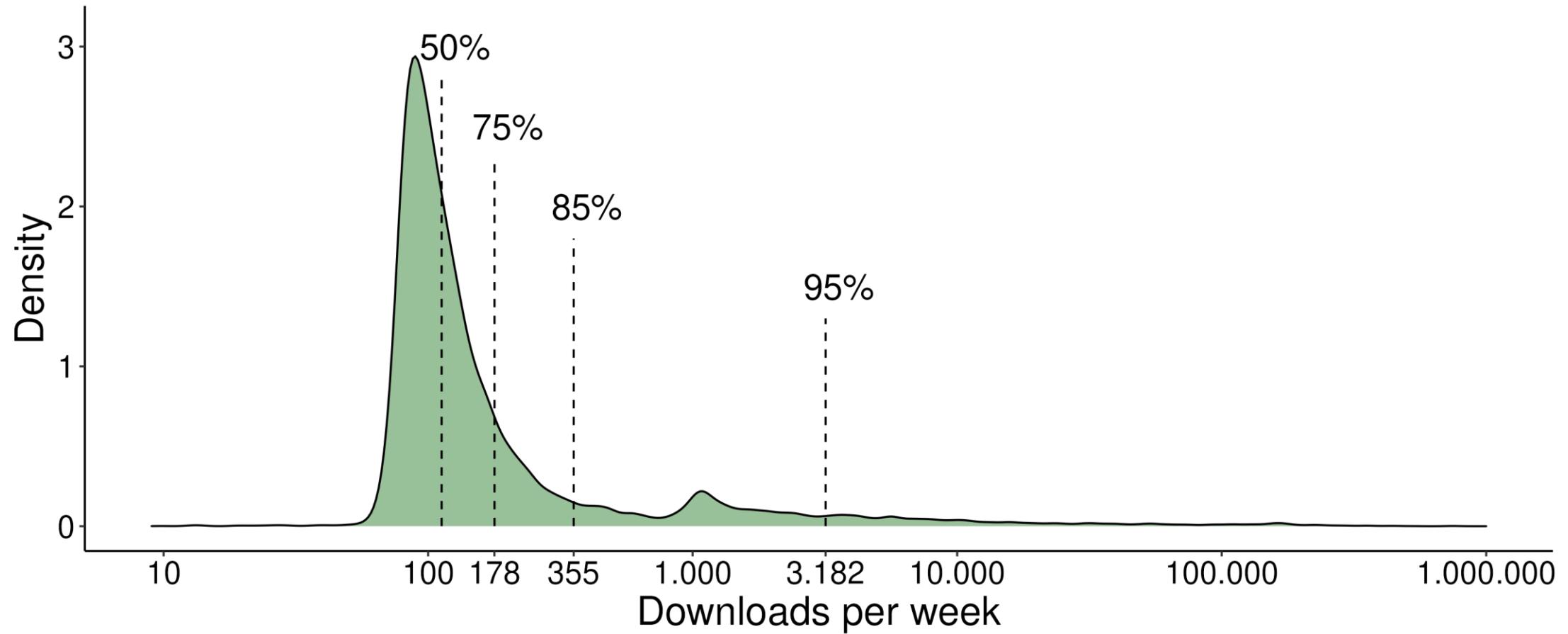


News for each release

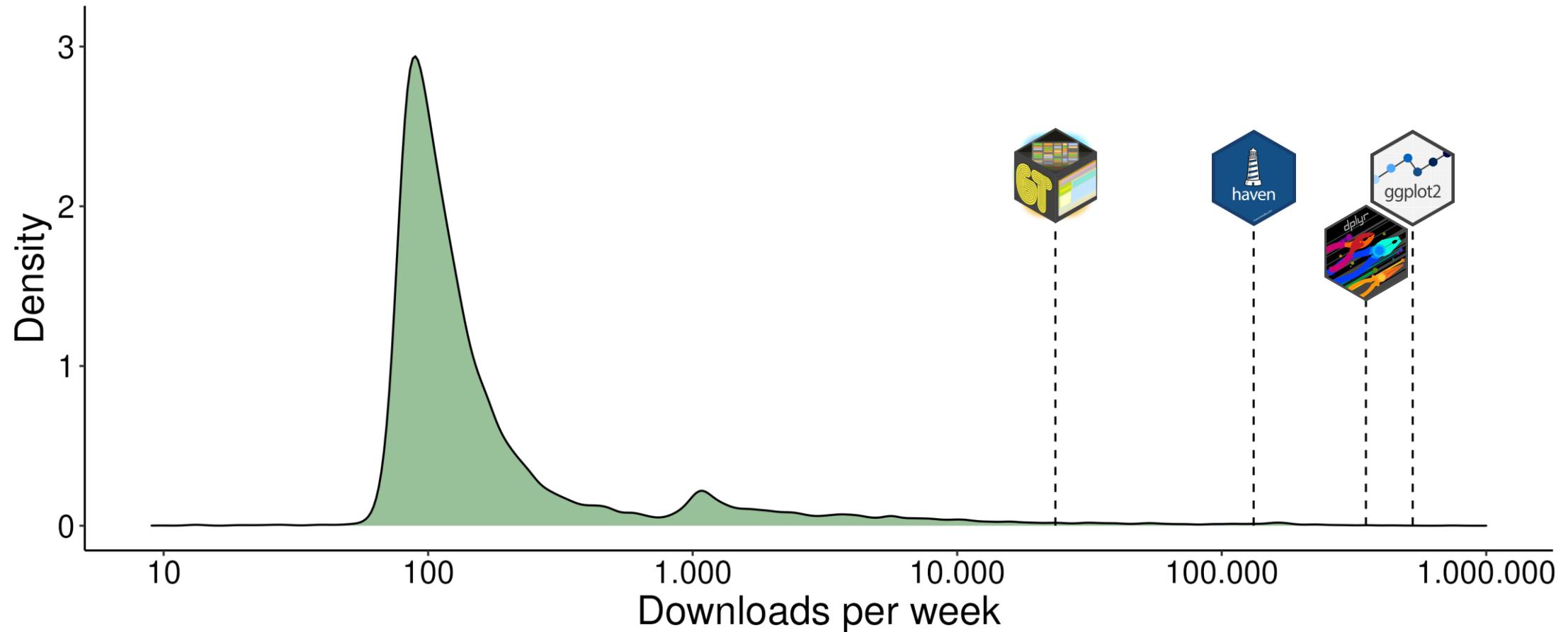
# Risk assessment



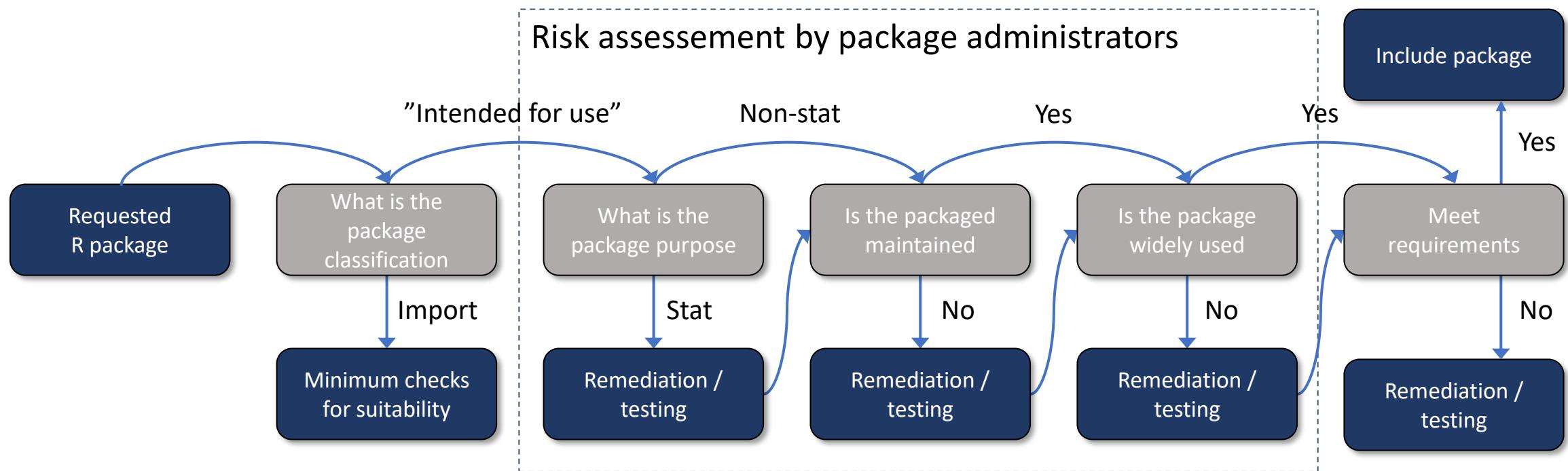
## Is the package widely used



# Is the package widely used



# Risk assessment



# Obtaining metrics



# Metrics



## dplyr

**First on CRAN:** 2014-01-29  
**Last update:** 2023-11-17  
**Contributors:** > 250  
**Code coverage:** 84 %  
**New releases:** 3-4 times a year  
**Downloads:** Approx. 350.000 per week  
**Examples:** 95% of the functions have examples



## stringr

**First on CRAN:** 2009-11-09  
**Last update:** 2023-11-14  
**Contributors:** > 50  
**Code coverage:** 99 %  
**New releases:** 1-2 times a year  
**Downloads:** Approx. 260.000 per week  
**Examples:** 100% of the functions have examples



# Accuracy

Exercise

# Exercise

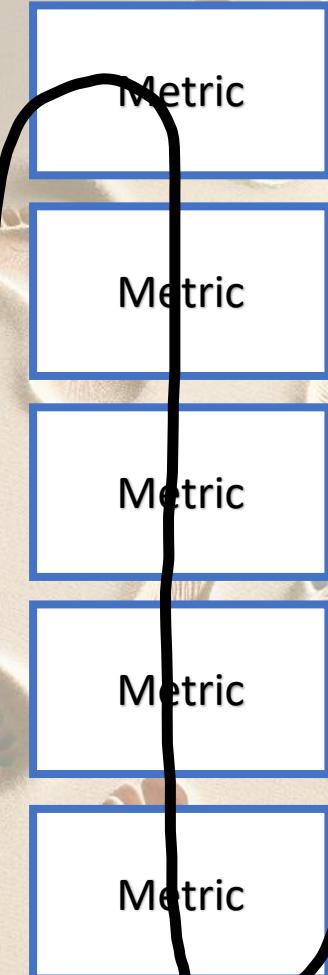
## Build workflow:

- Build your own assessment workflow based on the handouts
- Add additional steps if you believe anything is missing

## Assess packages:

- Assess the example packages

Rank according to importance

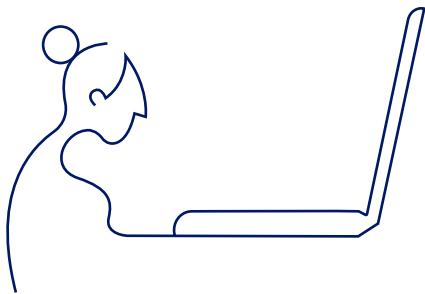




# Accuracy

Summary  
&  
Example from Novo Nordisk

# Package requests



## Package requester

Hi! This is where to submit a request for your desired package and your reason for request.

Please follow the reason template

Package name

mmrm

Reason

As a statistician, I want to fit mixed models to data with repeated measures so that I can correctly model observed data and follow planned work

Format: As a <type of user>, I want <some goal> so that <some reason>.

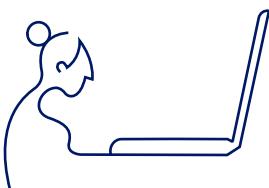
 Submit

Expected versions:

R version	mmrm version
4.0.1	N/A
4.0.2	N/A
4.0.4	N/A
4.1.1	N/A
4.2.0 (running)	N/A
latest	0.2.2

The 'latest' signifies the version (or newer) of mmrm that can be expected when the next R version is released.

# Package requests



## Package requester

Hi! This is where to submit a request for your desired package and your reason for request.

Please follow the reason template

Package name

Reason

As a statistician, I want to fit mixed models to data with repeated measures so that I can correctly model observed data and follow planned work

Format: As a <type of user>, I want <some goal> so that <some reason>.

Submit

Expected versions:

R version	mmrm version
4.0.1	N/A
4.0.2	N/A
4.0.4	N/A
4.1.1	N/A
4.2.0 (running)	N/A
latest	0.2.2

The 'latest' signifies the version (or newer) of mmrm that can be expected when the next R version is released.



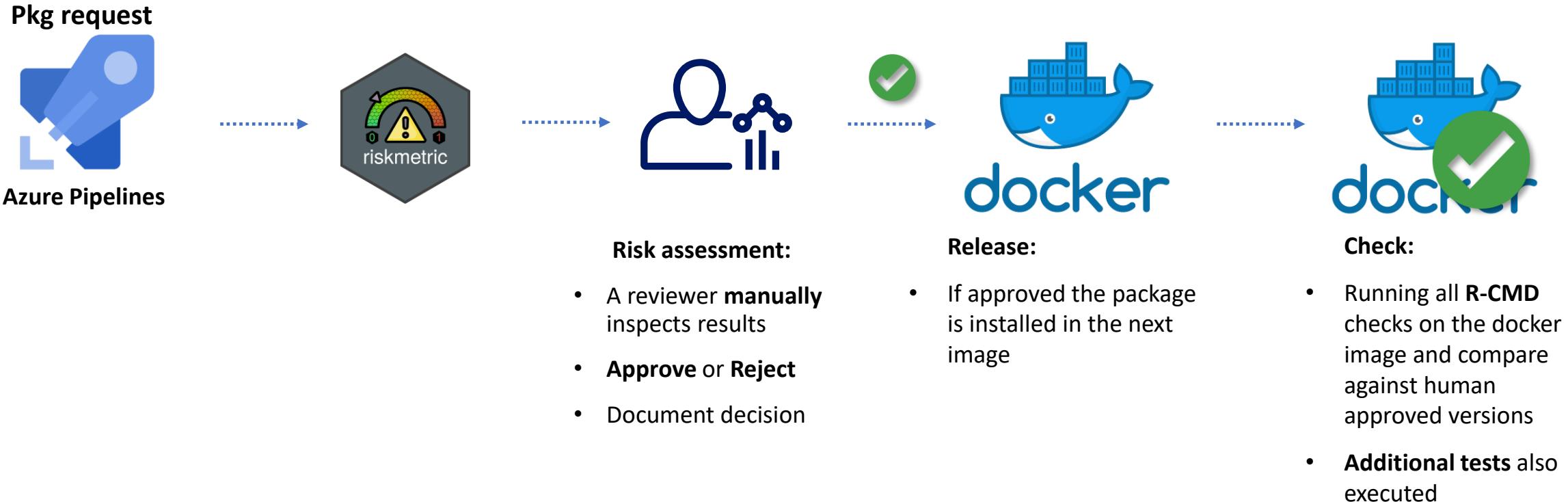
git



Azure Pipelines

# Package risk assessment

For every package requested by a user continuous integration is used to evaluate the package



# The three essentials

**Accuracy**



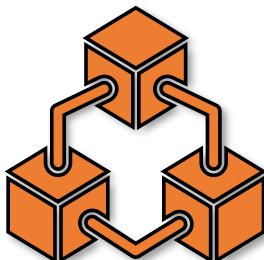
How do we ensure programs are accurate?

**Traceability**



How do we document what we have done?

**Reproducibility**



How to ensure reproducibility when using R

# The three essentials

## Accuracy



**How do we ensure programs are accurate?**

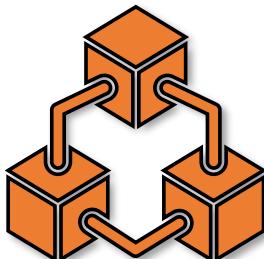
## Traceability



**How do we document what we have done?**

- Many things in R can influence the final output
  - Packages, Options, Environmental Variables etc.
- What should a log include to provide traceability?

## Reproducibility



**How to ensure reproducibility when using R**

# R and all the packages



# The essentials: Traceability

Each package usually exist in many different versions:



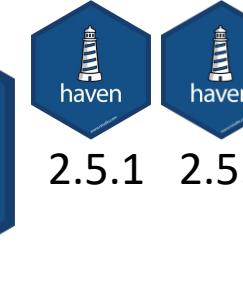
2.3.0  
(2020-05-24)



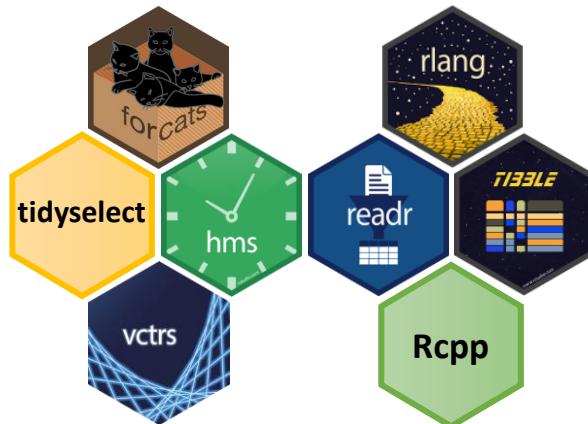
2.4.0  
(2021-04-15)



2.5.0  
(2022-04-15)



2.5.4  
(2023-11-30)



Multiple  
dependencies





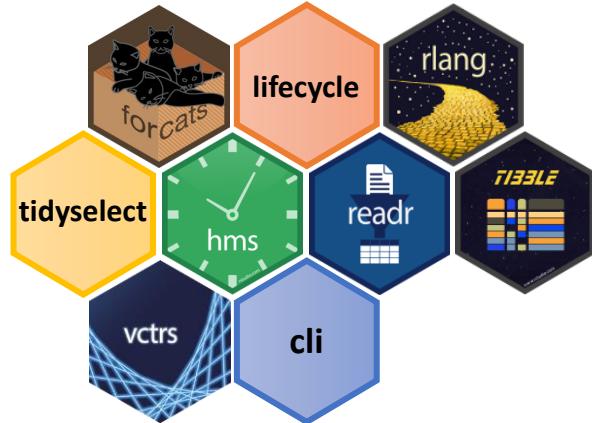
# Attached vs Imports.

## Attached

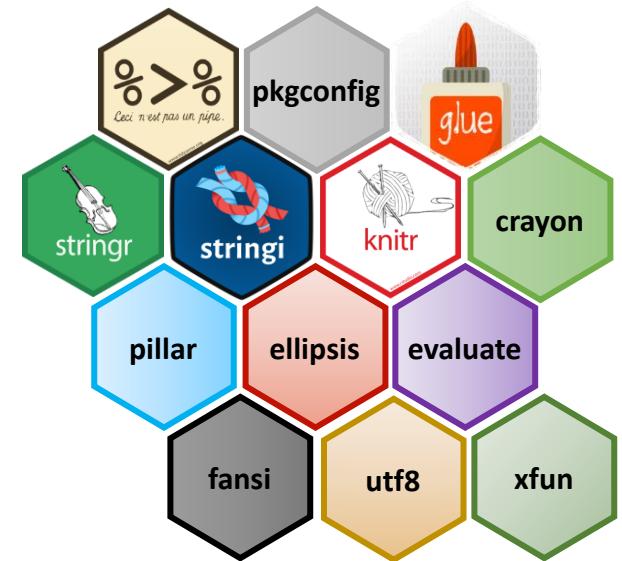


```
library("haven")
```

## Imports



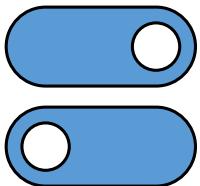
## Imports



# Options and Environment variables

- Options and environment variables can influence the behavior of the packages.

**Many packages rely heavily on R options. Examples could be:**



- Rules for rounding
- Contrasts: What is the default reference when comparing factors in statistical analysis
- Burn-in in Bayesian statistical modelling
- Some statistical packages use options to determine accuracy and/or number of runs



**Environment variables can also modify the outcome of R code:**

- Some R options might be modified through environment variables.
- Package can also rely directly on environment variables
- E.g. {renv} rely on environment variables when looking for R packages



# **Traceability**

**Exercise**

# Exercise

## Purpose:

- Create a log for R scripts
- Prioritize content according to criticality
- Create your own content if something vital and/or nice is missing

Rank according to importance

Most important

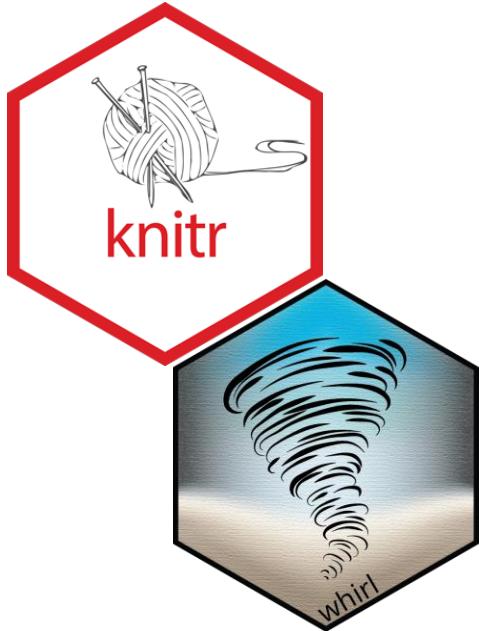


Least important



# **Traceability**

**Summary**  
**&**  
**Example from Novo Nordisk**



# General info

## f\_geo\_mean.log

Generated via [runScript](#) in **NNlog** (version 0.2.1).

File: R scripts/Phuse\_US/f\_geo\_mean.R

Executed with succes at: 2024-02-22 22:20:42; run time: 10 secs.

## Geometric Mean plots

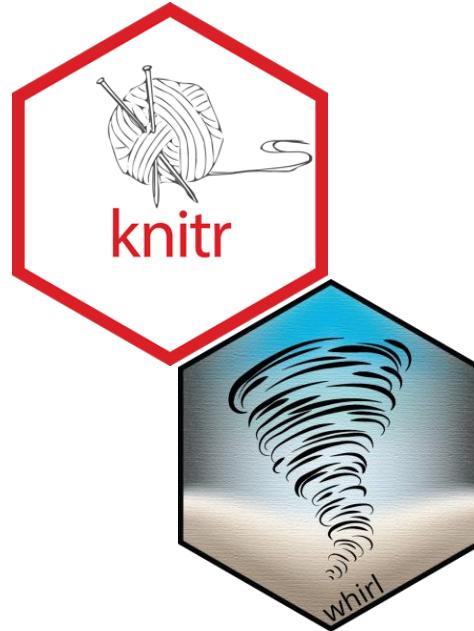
Programmer: ktqn

## Loading libraries and data —

```
# Access library etc.;  
library(NNBiostat)
```

```
## — Attaching packages —————— NNBiostat 4.2.0.4
```

```
## ✓ labelled    2.9.1      ✓ ggplot2    3.3.6  
## ✓ emmeans    1.7.4.1    ✓ patchwork  1.1.1  
## ✓ lme4       1.1.29     ✓ tibble     3.1.7  
## ✓ MASS        7.3.57     ✓ tidyverse  1.2.0  
## ✓ Matrix      1.4.1      ✓ readr      2.1.2  
## ✓ survival   3.3.1      ✓ purrr     0.3.4  
## ✓ mice        3.14.0     ✓ dplyr     1.0.9  
## ✓ glue        1.6.2      ✓ stringr   1.5.1  
## ✓ data.table  1.14.2     ✓ forcats   0.5.1
```

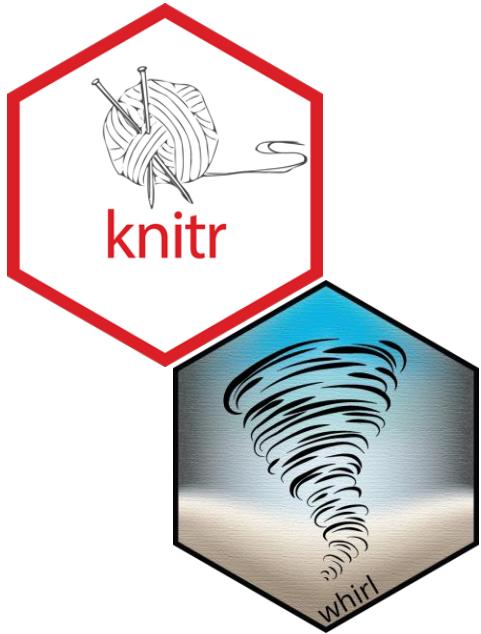


# Masked functions

```
## — Attaching packages —————— NNBiostat 4.2.0.4

## ✓ labelled  2.9.1      ✓ ggplot2  3.3.6
## ✓ emmeans   1.7.4.1    ✓ patchwork 1.1.1
## ✓ lme4      1.1.29     ✓ tibble    3.1.7
## ✓ MASS       7.3.57     ✓ tidyverse 1.2.0
## ✓ Matrix     1.4.1      ✓ readr     2.1.2
## ✓ survival  3.3.1      ✓ purrr     0.3.4
## ✓ mice       3.14.0     ✓ dplyr     1.0.9
## ✓ glue       1.6.2      ✓ stringr  1.5.1
## ✓ data.table 1.14.2    ✓forcats   0.5.1

## ✓ NNlog     0.2.1      ✓ NNexport 0.2.2
## ✓ NNremote  0.3.3      ✓ NNTfl    0.1.4.9004
## ✘ patchwork::area()  masks MASS::area()
## ✘ dplyr::between()  masks data.table::between()
## ✘ methods::body<-()  masks base::body<-()
## ✘ mice::cbind()    masks base::cbind()
## ✘ tidyverse::expand() masks Matrix::expand()
## ✘ dplyr::filter()   masks mice::filter(), stats::filter()
## ✘ dplyr::first()    masks data.table::first()
## ✘ methods::kronecker() masks base::kronecker()
## ✘ dplyr::lag()      masks stats::lag()
## ✘ dplyr::last()     masks data.table::last()
## ✘ tidyverse::pack()  masks Matrix::pack()
## ✘ mice::rbind()    masks base::rbind()
## ✘ NNaccess::saveSAS() masks NNremote::saveSAS()
## ✘ dplyr::select()   masks MASS::select()
## ✘ tidyverse::transpose() masks data.table::transpose()
## ✘ tidyverse::unpack() masks Matrix::unpack()
## ✘ Matrix::update()  masks stats::update()
```



# Code chunks

```
(db <- nnaccess("0002",root="~/training"))

## An object referencing
##   project      : nn1234
##   trial        : 0002
##   instance     : current
##
## Supplying access to data model functions via x$<data_model>()

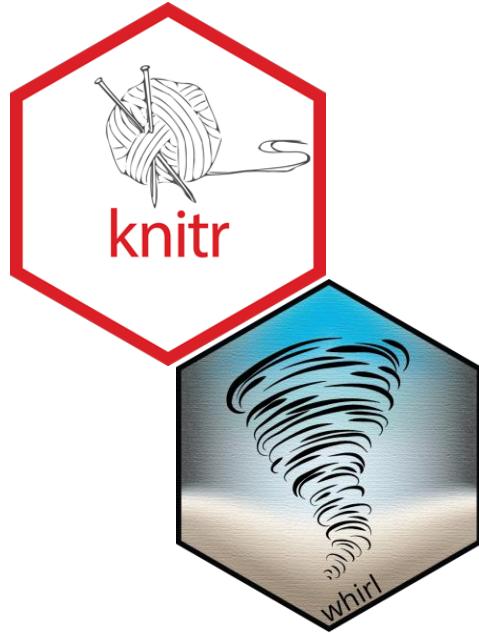
# Read in adam datasets to be used
ads1_f <- db$adam("ads1")

ad1b_f <- db$adam("ad1b") %>%
  filter(AVISITN <= 3000)

# Save metadata for figure symbols, colors etc.
mdsymbol <- mdsymbolTrans(db$metadata("mdsymbol")) %>%
  filter(VALUE %in% ads1_f$TRT01A) %>% mdSymbol()

# Re-level AVISIT variable : To maintain the order in meanplot
ad1b_f$AVISITF <- factor(ad1b_f$AVISITN, levels = unique(ad1b_f$AVISIT))
```

Create function for the mean plot —



# Creating a function

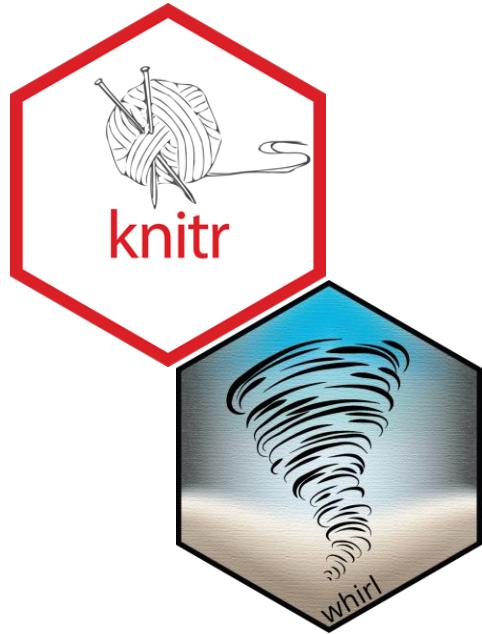
```
# Mean plot function
mean_plot = function(popfilter = TRUE, infilter = TRUE,
                      outputname) {

  # Create NNData
  NN_Data <- adlb_f %>%
    NNData({{popfilter}}, {{infilter}}, db = db)

  # Create meanPlot
  NN_fig <- do.call(
    meanPlot,
    list(
      NN_Data,
      xvar = "AVISITF",
      yvar = "AVAL",
      color_by = "TRTP",
      geometric = T,
      axis.label.x = "Visit",
      scale.y.continuous = scale_y_continuous(
        name = NN_Data$conv$labels$AVAL[1],
        sec.axis = sec_axis(
          name = NN_Data$conv$labels$AVAL[2],
          trans = NN_Data$conv$conv$AVAL[[1]]
        )
      ),
      dodge = position_dodge(width = 0.1),
      error.bar.width = 0.2
    )
  )

  NN_fig <- NN_fig &
    mdsymbol &
    theme(axis.text.x = element_text(angle = 60, vjust = 1, hjust = 1))

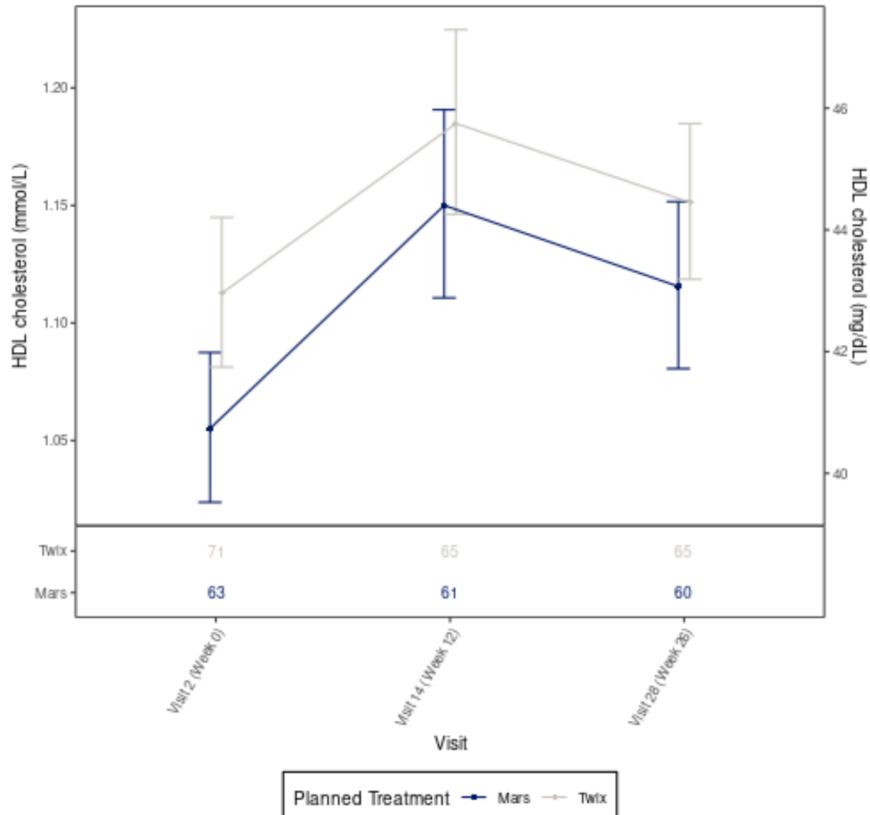
  print(NN_fig)
}
```



## Execute function

### Generating geometric mean plot of HDL —

```
# HDL plot -  
fgeomeanhdl <- mean_plot(popfilter = FASFL == "Y",  
                           infilter = ANELFL == "Y" &  
                           PARAMCD == "C105587S",  
                           outputname = "fgeomeanhdl")
```

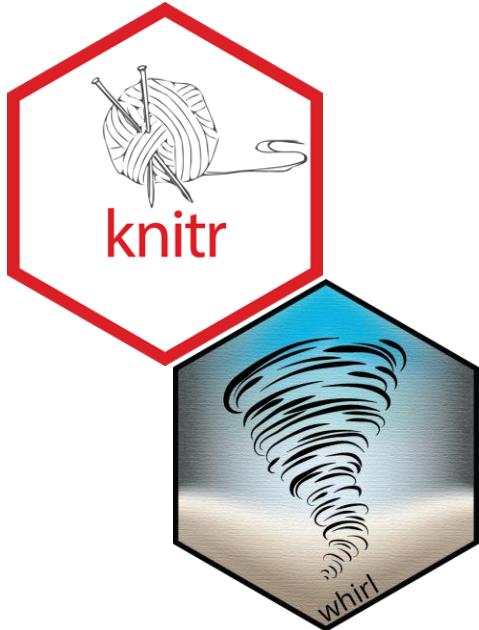


adlb.xpt; variable(s): AVAL; criteria: FASFL == "Y" & ANELFL == "Y" & PARAMCD == "C105587S"

### ▼ Session info

▼ The R version and operating system

# R version OS Packages



## ▼ Session info

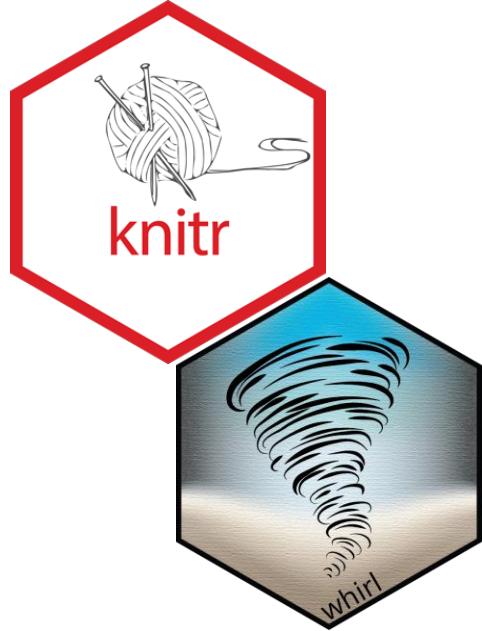
### ▼ The R version and operating system

```
##  setting  value
##  version  R version 4.2.0 (2022-04-22)
##  os        Red Hat Enterprise Linux 8.8 (ootpa)
##  system   x86_64, linux-gnu
##  ui        X11
##  language (EN)
##  collate  en_US.UTF-8
##  ctype    en_US.UTF-8
##  tz       Europe/Amsterdam
##  date     2024-02-22
##  pandoc  2.19.2 @ /usr/lib/rstudio-server/bin/quarto/bin/tools/ (via rmarkdown)
```

### ▼ The versions of packages attached

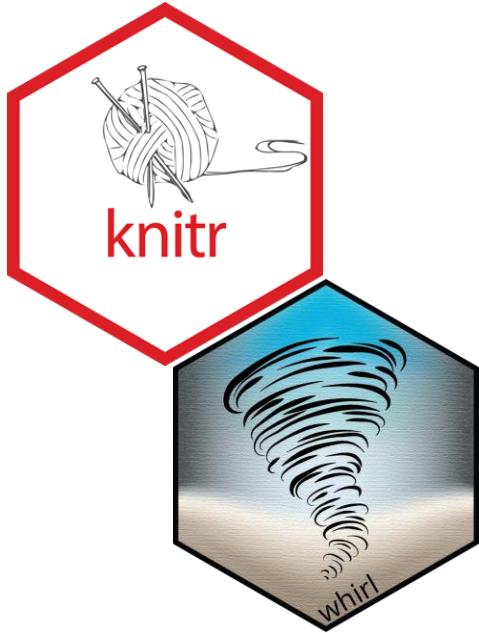
```
##  package    * version    date (UTC) lib source
##  data.table  * 1.14.2    2021-09-27 [2] RSPM (R 4.2.0)
##  dplyr      * 1.0.9     2022-04-28 [2] RSPM (R 4.2.0)
##  emmeans    * 1.7.4-1   2022-05-15 [2] RSPM (R 4.2.0)
## forcats    * 0.5.1     2021-01-27 [2] RSPM (R 4.2.0)
##  ggplot2    * 3.3.6     2022-05-03 [2] RSPM (R 4.2.0)
##  glue       * 1.6.2     2022-02-24 [2] RSPM (R 4.2.0)
##  labelled   * 2.9.1     2022-05-05 [2] RSPM (R 4.2.0)
##  lme4       * 1.1-29    2022-04-07 [2] RSPM (R 4.2.0)
##  MASS       * 7.3-57    2022-04-22 [2] RSPM (R 4.2.0)
##  Matrix     * 1.4-1     2022-03-23 [3] CRAN (R 4.2.0)
##  mice       * 3.14.0    2021-11-24 [2] RSPM (R 4.2.0)
##  NNaccess   * 0.2.1     2023-11-07 [1] RSPM (R 4.2.0)
##  NNAdam    * 0.0.8     2023-08-18 [1] RSPM (R 4.2.0)
##  NNBiostat * 4.2.0-40  2023-09-25 [2] RSPM (R 4.2.0)
##  NNcalc    * 1.0.5     2023-08-18 [1] RSPM (R 4.2.0)
##  NNexport   * 0.2.2     2023-08-18 [1] RSPM (R 4.2.0)
##  NNlog     * 0.2.1     2024-02-12 [1] RSPM (R 4.2.0)
##  NNplot    * 0.0.9     2023-08-18 [1] RSPM (R 4.2.0)
##  NNR       * 1.9.11    2023-09-25 [2] RSPM (R 4.2.0)
##  NNremote  * 0.3.3     2023-11-02 [1] RSPM (R 4.2.0)
```

# R version OS Packages



```
##  NNadam      * 0.0.8      2023-08-18 [1] RSPM (R 4.2.0)
##  NNBiostat   * 4.2.0-40   2023-09-25 [2] RSPM (R 4.2.0)
##  NNcalc       * 1.0.5      2023-08-18 [1] RSPM (R 4.2.0)
##  NNexport     * 0.2.2      2023-08-18 [1] RSPM (R 4.2.0)
##  NNlog        * 0.2.1      2024-02-12 [1] RSPM (R 4.2.0)
##  NNplot       * 0.0.9      2023-08-18 [1] RSPM (R 4.2.0)
##  NNR          * 1.9.11     2023-09-25 [2] RSPM (R 4.2.0)
##  NNremote     * 0.3.3      2023-11-02 [1] RSPM (R 4.2.0)
##  NNrender     * 0.2.10     2023-08-18 [1] RSPM (R 4.2.0)
##  NNsdtm       * 0.0.1      2023-09-25 [2] RSPM (R 4.2.0)
##  NNtable      * 0.1.5      2023-08-18 [1] RSPM (R 4.2.0)
##  NNTfL         * 0.1.4.9004 2023-11-10 [1] RSPM (R 4.2.0)
##  NNutility    * 0.1.1      2023-08-18 [1] RSPM (R 4.2.0)
##  patchwork    * 1.1.1      2020-12-17 [2] RSPM (R 4.2.0)
##  purrr        * 0.3.4      2020-04-17 [2] RSPM (R 4.2.0)
##  readr         * 2.1.2      2022-01-30 [2] RSPM (R 4.2.0)
##  stringr       * 1.5.1      2023-11-14 [1] RSPM (R 4.2.0)
##  survival     * 3.3-1      2022-03-03 [3] CRAN (R 4.2.0)
##  tibble        * 3.1.7      2022-05-03 [2] RSPM (R 4.2.0)
##  tidyverse     * 1.2.0      2022-02-01 [2] RSPM (R 4.2.0)
##
## [1] /scer/homedirs/ktqn/R/x86_64-pc-linux-gnu-library/4.2
## [2] /opt/R/4.2.0/lib/R/site-library
## [3] /opt/R/4.2.0/lib/R/library
```

- ▶ The versions of packages loaded via a namespace (and not attached):
- ▶ Information on all packages available in the libraries:
- ▶ Options set for the computing environment:



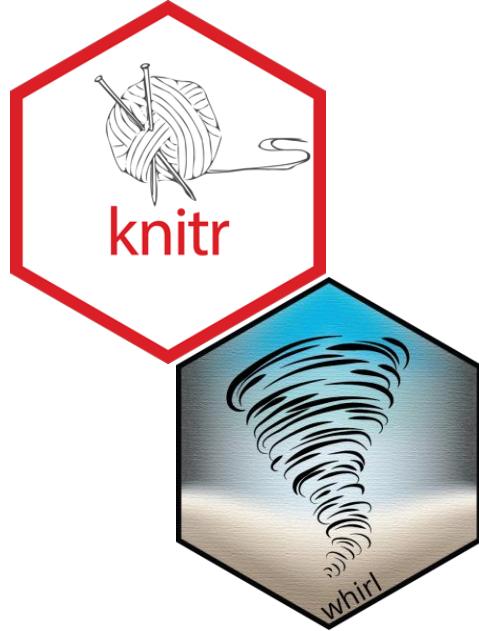
## Running multiple programs

All    Done    Warning    Error

Directory	Filename	Result	Link
/R scripts/Phuse_US	adae.R	Done	<a href="#">Go to detailed summary</a>
/R scripts/Phuse_US	adec.R	Done	<a href="#">Go to detailed summary</a>
/R scripts/Phuse_US	adlb.R	Warning	<a href="#">Go to detailed summary</a>
/R scripts/Phuse_US	admh.R	Done	<a href="#">Go to detailed summary</a>
/R scripts/Phuse_US	adpd.R	Done	<a href="#">Go to detailed summary</a>
/R scripts/Phuse_US	adsl.R	Error	<a href="#">Go to detailed summary</a>
/R scripts/Phuse_US	f_geo_mean.R	Done	<a href="#">Go to detailed summary</a>
/R scripts/Phuse_US	tae.R	Done	<a href="#">Go to detailed summary</a>

- 6: Done: The script executed without errors or warnings
- 1: Warning: The Script executed with at least one warning
- 1: Error: The Script executed with at least one error

# Running multiple programs



All    Done    Warning    Error

Directory	Filename	Result	Link
/R scripts/Phuse_US	adlb.R	Warning	<a href="#">Go to detailed summary</a>

• 6: Done: The script executed without errors or warnings  
• 1: Warning: The Script executed with at least one warning  
• 1: Error: The Script executed with at least one error

**adlb.log**  
Generated via [runScript](#) in **NNlog** (version 0.2.1).  
File: R scripts/Phuse\_US/adlb.R  
⚠ Executed with warnings at: 2024-02-22 22:20:14; run time: 0.6 secs.

**Description:**  
Purpose of the program  
Programmer: ktqn

**Name of the section —**  
Description

```
2+2  
## [1] 4  
warning("This is a test warning")  
## Warning: This is a test warning
```

► **Session info**

# The three essentials

**Accuracy**



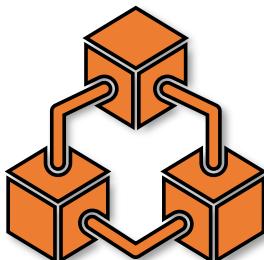
How do we ensure programs are accurate?

**Traceability**



How do we document what we have done?

**Reproducibility**



How to ensure reproducibility when using R

# The three essentials

**Accuracy**



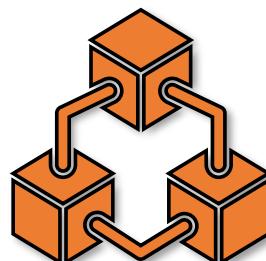
**How do we ensure programs are accurate?**

**Traceability**



**How do we document what we have done?**

**Reproducibility**

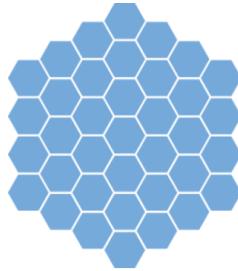


**How to ensure reproducibility when using R**

- Package synchronization within a project
- Support authorities in environment replication

# The essentials: Reproducibility

## Internal distribution



 **posit**™ Package Manager

- Manage R packages
- Sharing external packages
- Share internal packages
- Create subsets of approved packages

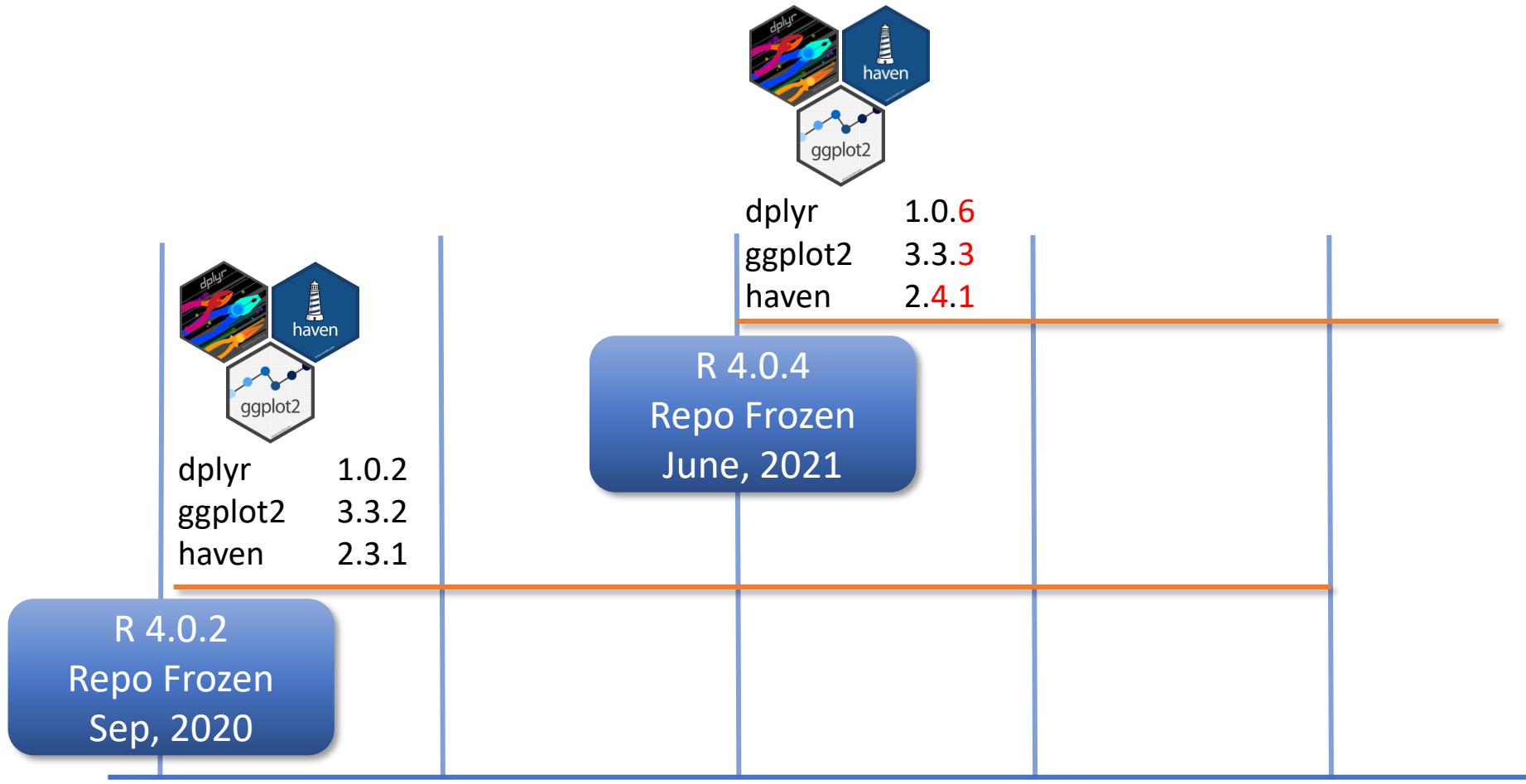
## Synchronization



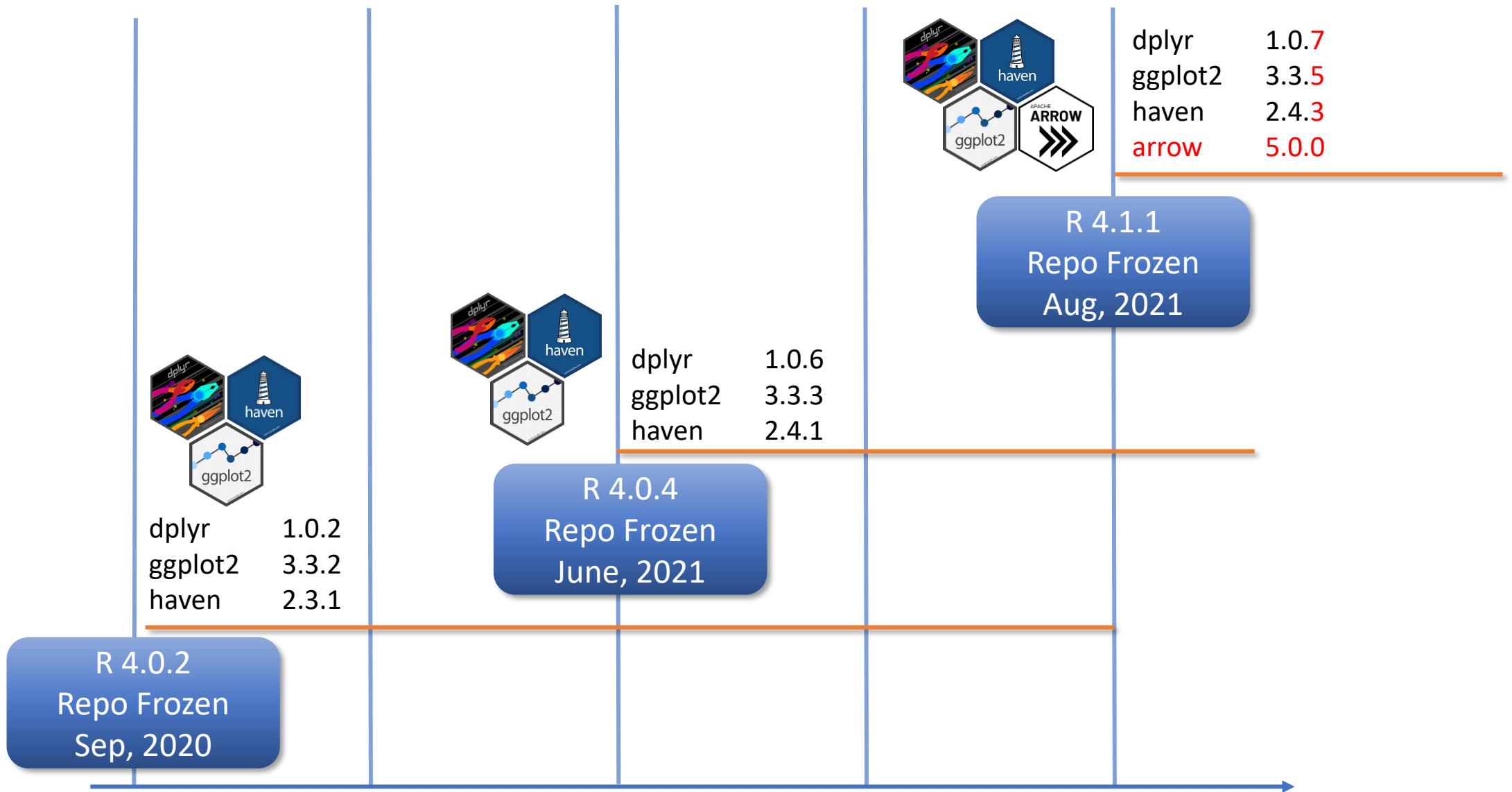
## External distribution



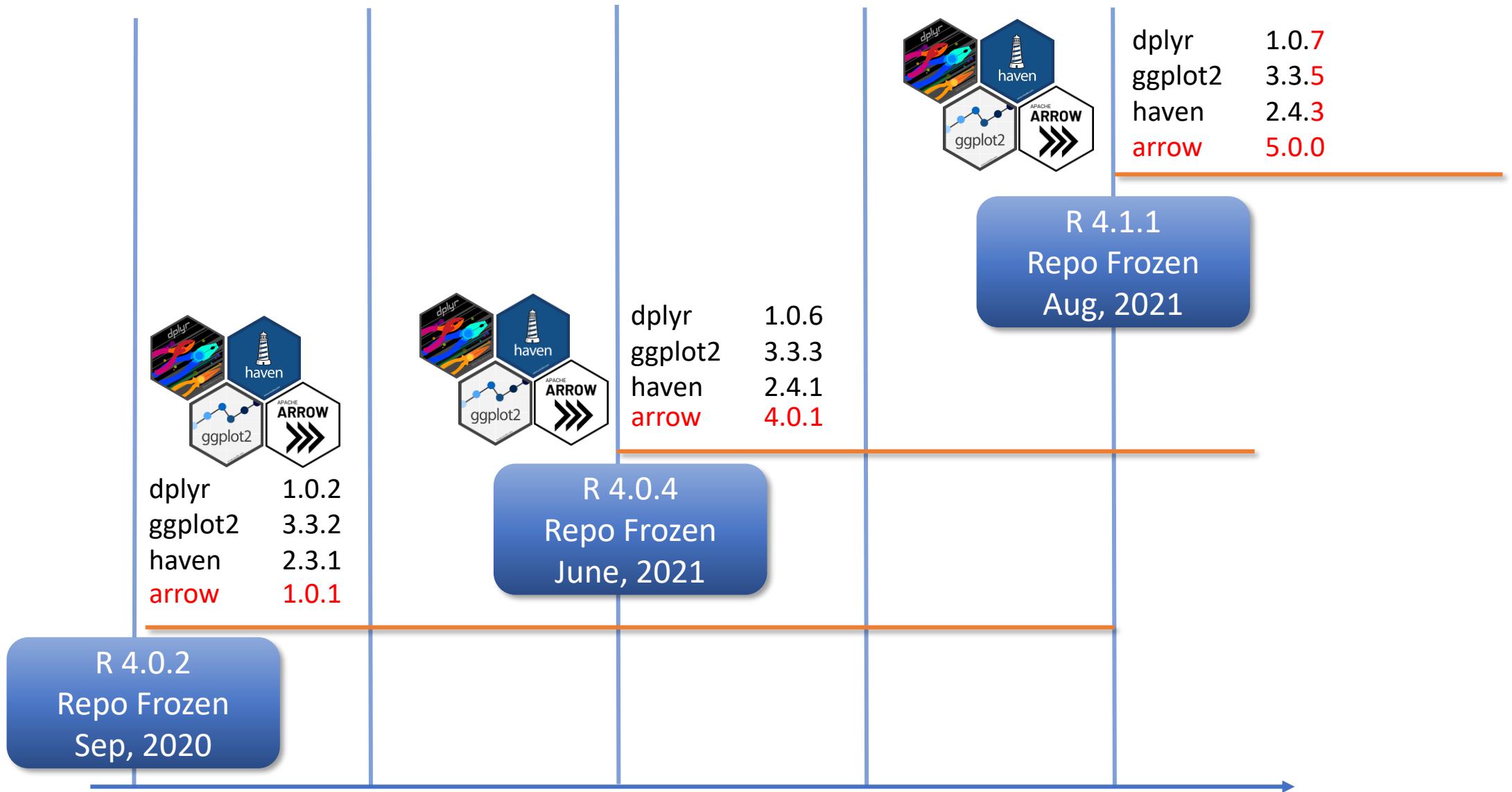
# The shared-baseline model



# The shared-baseline model



# The shared-baseline model



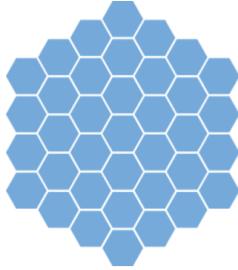
# Internal packages



- Several internal packages to streamline output generation
- Enable fast turn-around
  - Not locked to a specific R version
  - Shared-baseline + {renv} to keep track of these

# The essentials: Reproducibility

## Internal distribution



### posit™ Package Manager

- Manage R packages
- Sharing external packages
- Share internal packages
- Create subsets of approved packages

## Synchronization

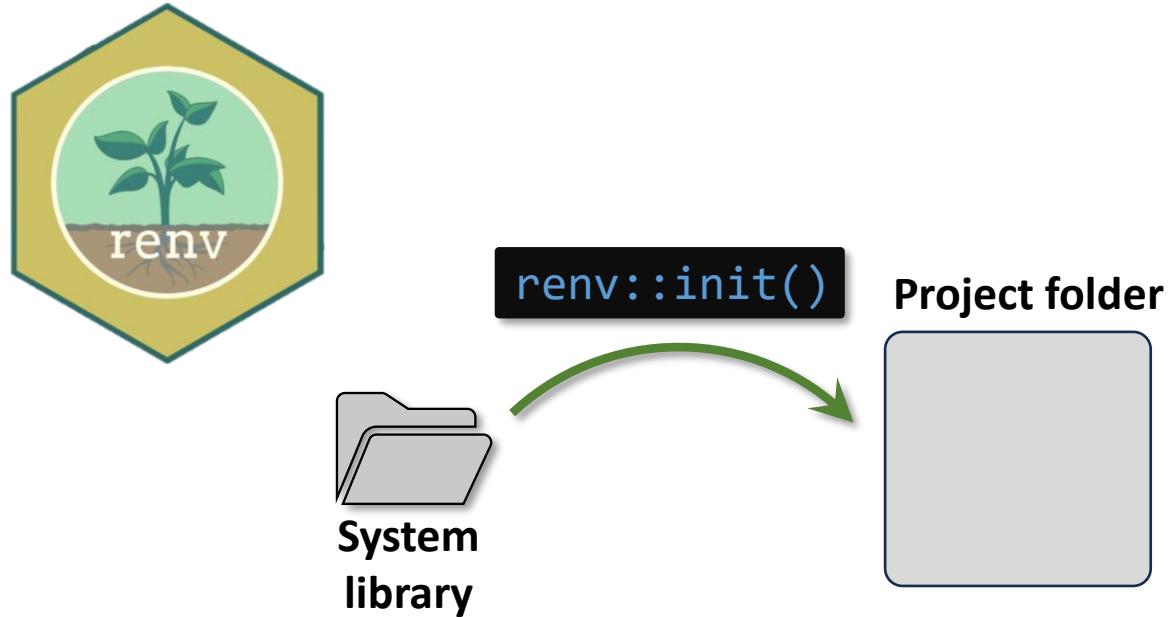


- Project-wise synchronization of internal & external packages
- Enable reproducing the same environment in another place

## External distribution



# The essentials: Reproducibility



```
renv::init()
```

- 1) Creates `renv/activate.R`
- 2) Update `.Rprofile` with:  
`source("renv/activate.R")`
- 3) Creates `renv/library` (project library)
- 4) Initiate the lockfile → `renv.lock`

```
└── project.Rproj
```



`renv/activate.R`



`.Rprofile`

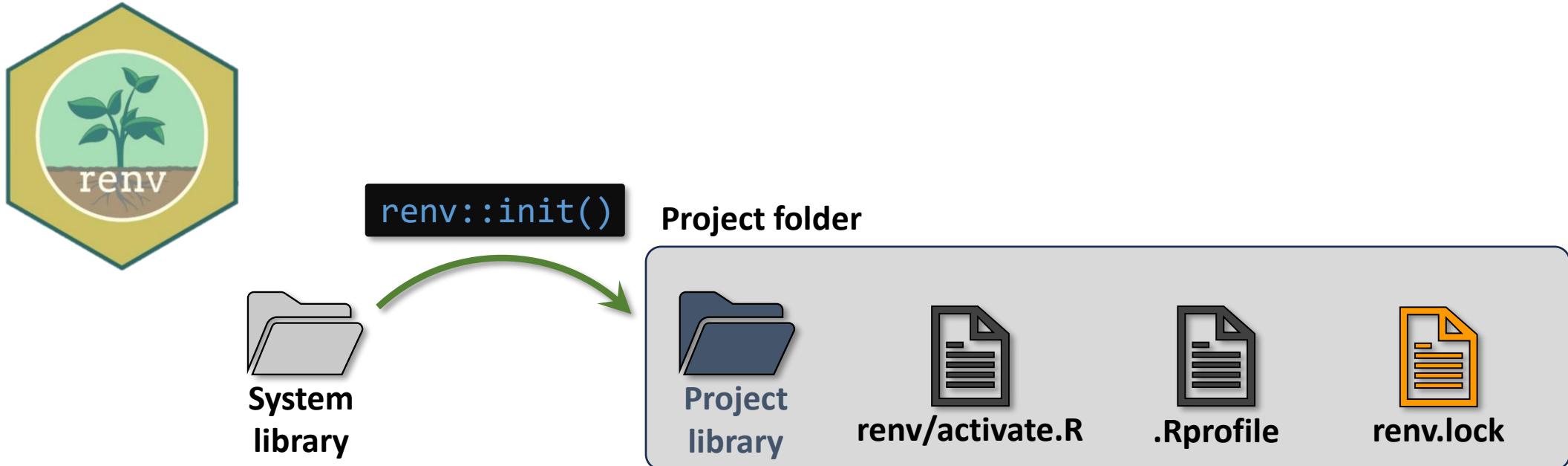


`Project  
library`



`renv.lock`

# The essentials: Reproducibility



```
{  
  "R": {  
    "Version": "4.3.1",  
    "Repositories": [  
      {  
        "Name": "CRAN",  
        "URL": "https://rspm.bifrost-dev.corp.aws.novonordisk.com/default-cran/2023-10-25"  
      },  
      {  
        "Name": "NN Prod",  
        "URL": "https://rspm.bifrost-dev.corp.aws.novonordisk.com/prod-internal-4.3.1/latest"  
      }  
    ],  
    "Packages": {  
      "renv": {  
        "Package": "renv",  
        "Version": "1.0.3",  
        "Source": "Repository",  
        "Repository": "RSPM",  
        "Requirements": [  
          "utils"  
        ],  
        "Hash": "41b847654f567341725473431dd0d5ab"  
      }  
    }  
  }  
}
```

Private package manager  
for CRAN packages

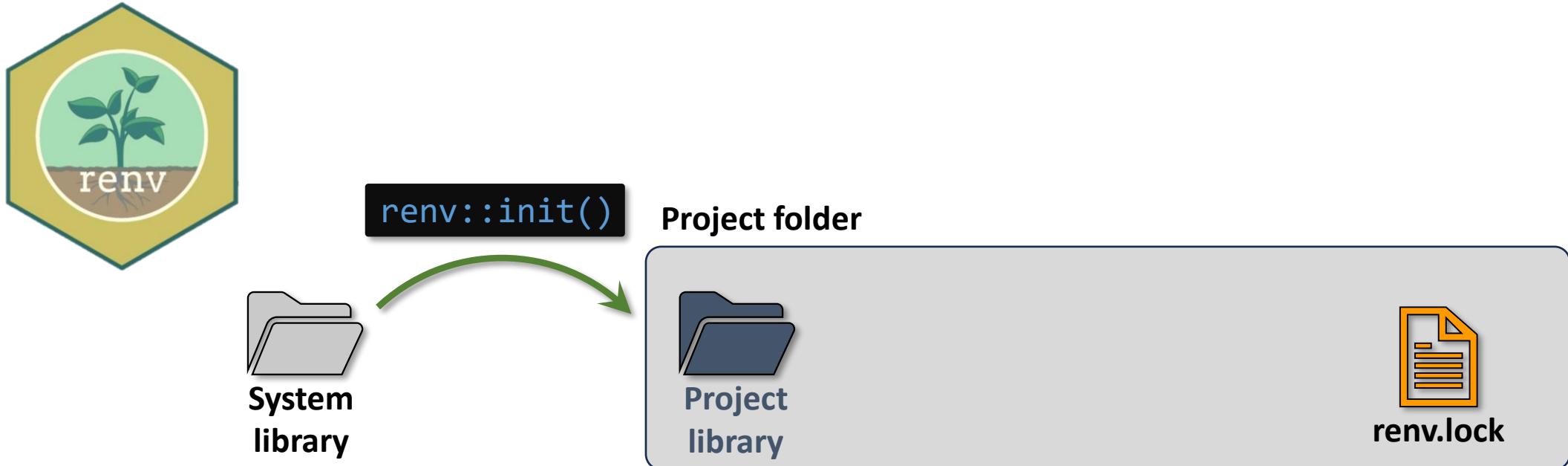


Private package manager  
for internal packages

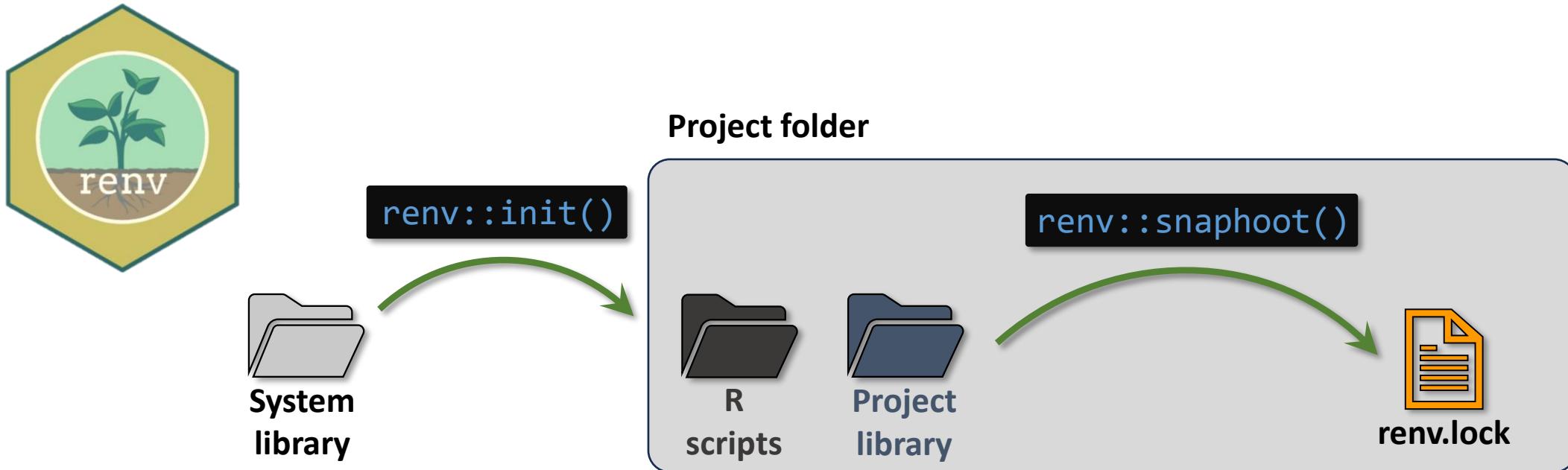


renv.lock

# The essentials: Reproducibility



# The essentials: Reproducibility



```
renv::snapshot()
```

```
└── project.Rproj
    └── ADaM
        ├── adsl.R
        ├── adae.R
        └── adlb.R
    └── Output
        ├── f_boxplot.R
        ├── f_meanplot.R
        └── t_adverse.R
    └── renv
        ├── activate.R
        └── library
    └── .Rprofile
    └── renv.lock
```

Attached + Imported  
packages



renv.lock

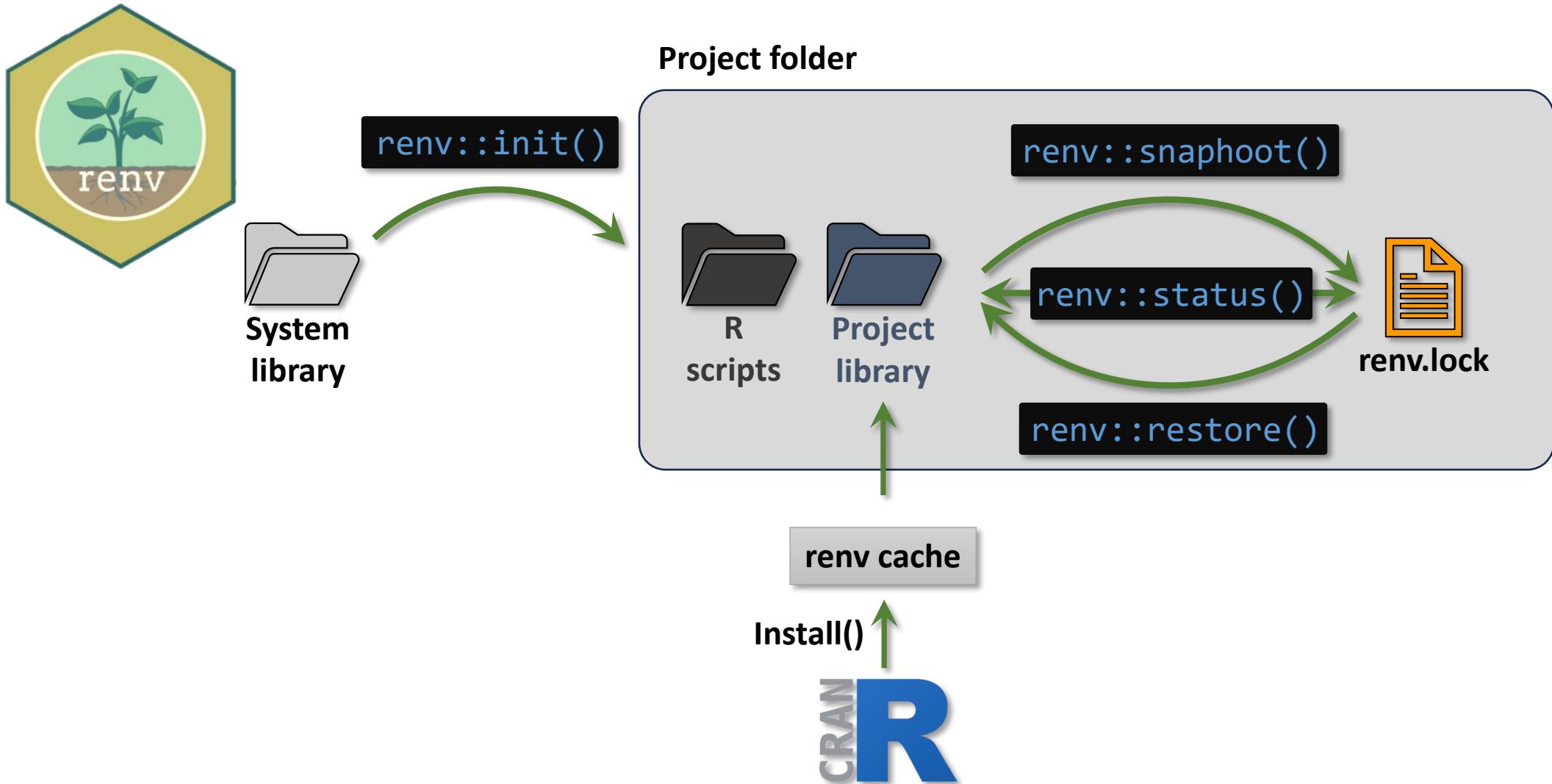


renv.lock

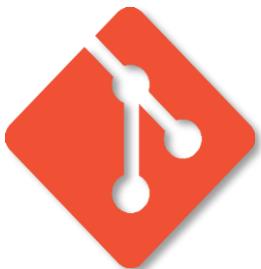


renv.lock

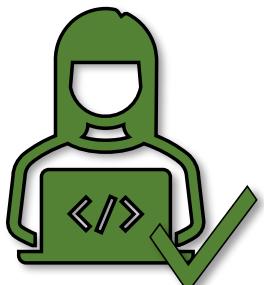
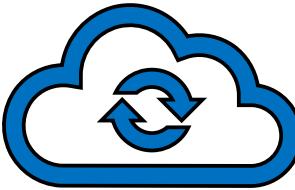
# The essentials: Reproducibility



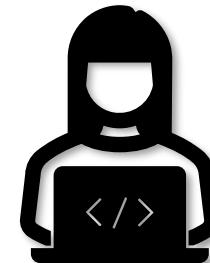
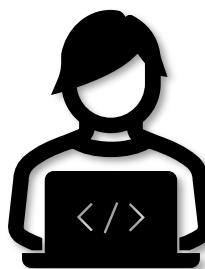
# The essentials: Reproducibility



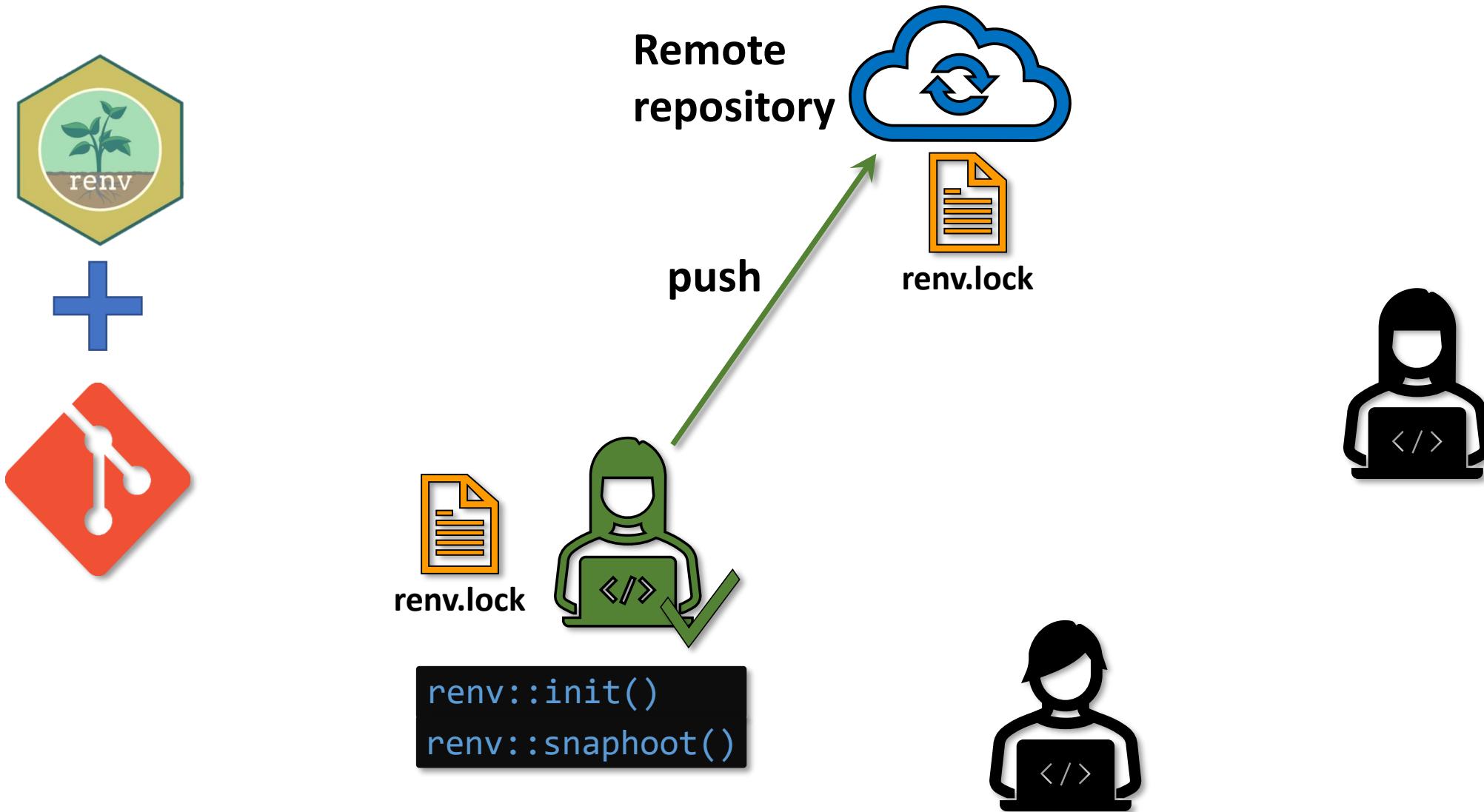
Remote  
repository



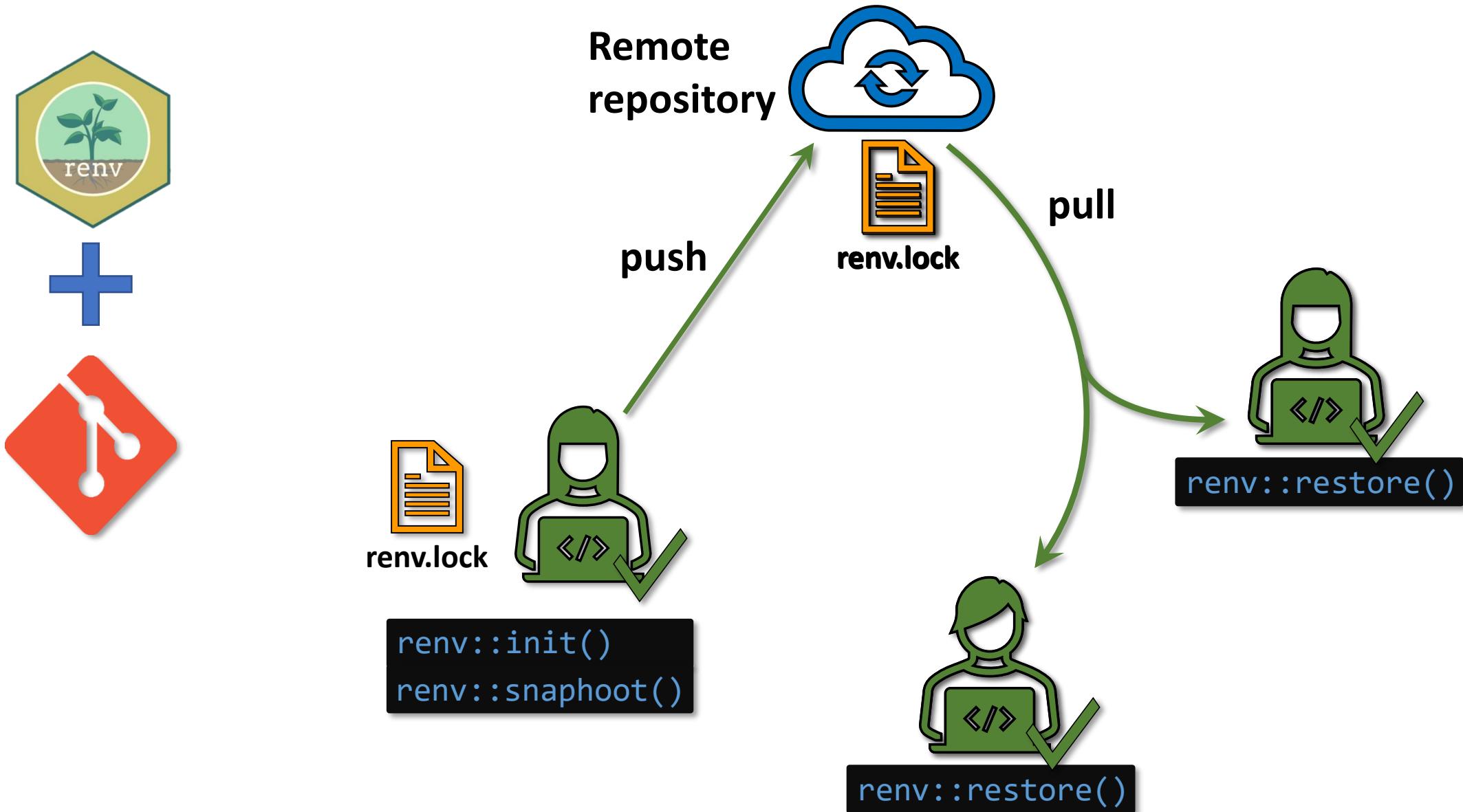
```
renv::init()  
renv::snapshot()
```



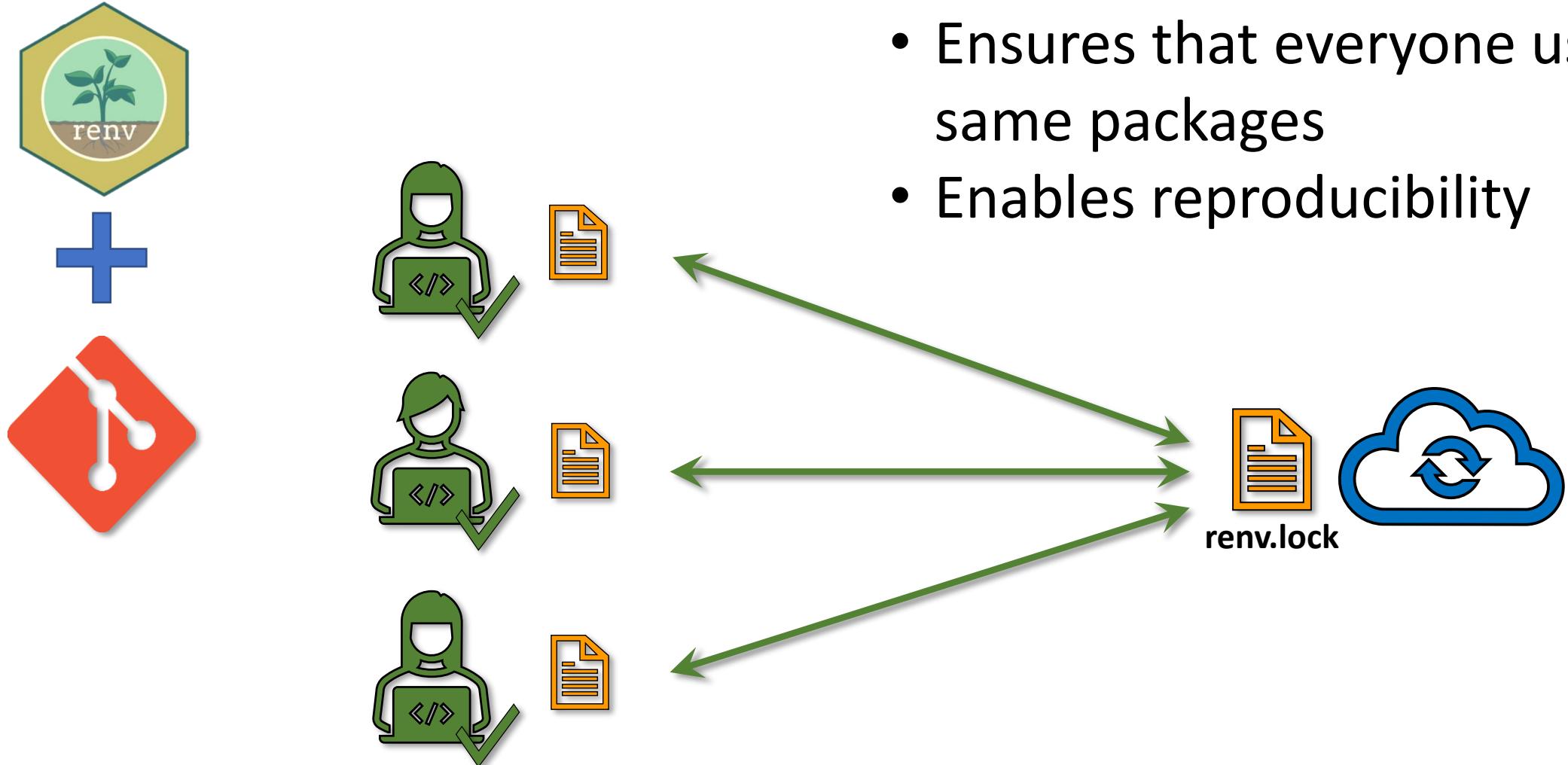
# The essentials: Reproducibility



# The essentials: Reproducibility

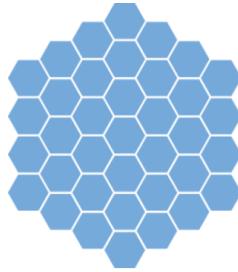


# The essentials: Reproducibility



# The essentials: Reproducibility

## Internal distribution



### **posit**™ Package Manager

- Manage R packages
- Sharing external packages
- Share internal packages
- Create subsets of approved packages

## Synchronization



- Project-wise synchronization of internal & external packages
- Enable reproducing the same environment in another place

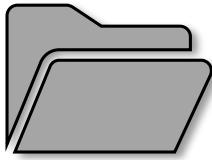
## External distribution



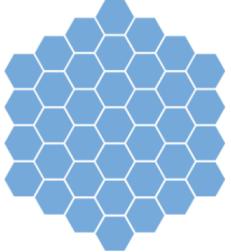
- Way to share internally developed packages as .txt files
- Enable distribution to authorities

# Sharing packages with authorities

## Non-public



Azure DevOps



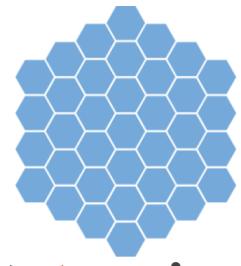
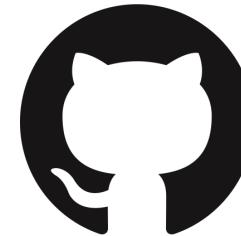
 **posit**  
Package Manager



Pkg1\_2.0.5.tar.gz

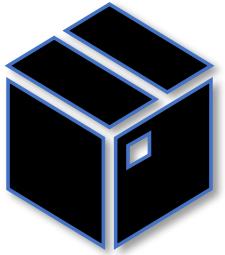


## Public



 **posit**  
Public Package  
Manager

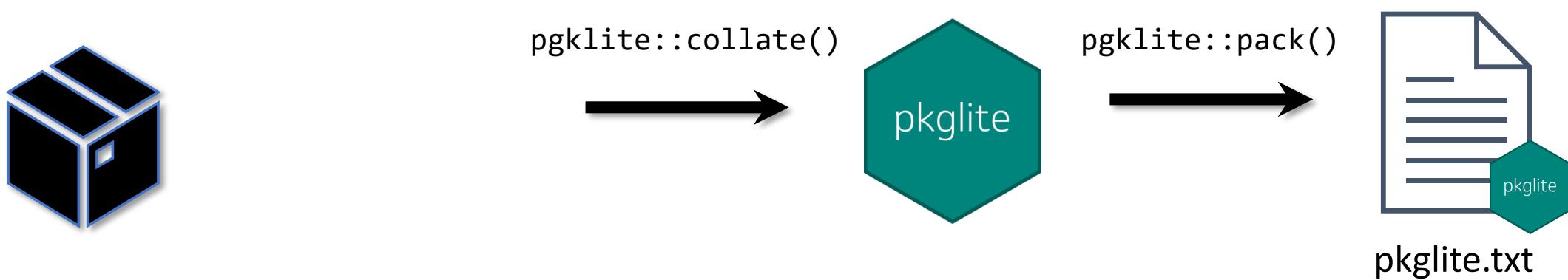
# Pack packages



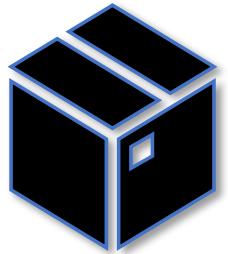
```
├── DESCRIPTION
├── inst
│   └── extdata
├── man
│   └── *.Rd
├── NAMESPACE
├── NEWS.md
├── R
│   └── *.R
├── README.md
├── tests
│   ├── testthat
│   │   └── *.R
│   └── testthat.R
└── vignettes
    └── *.Rmd
```



# Pack packages



# Pack packages

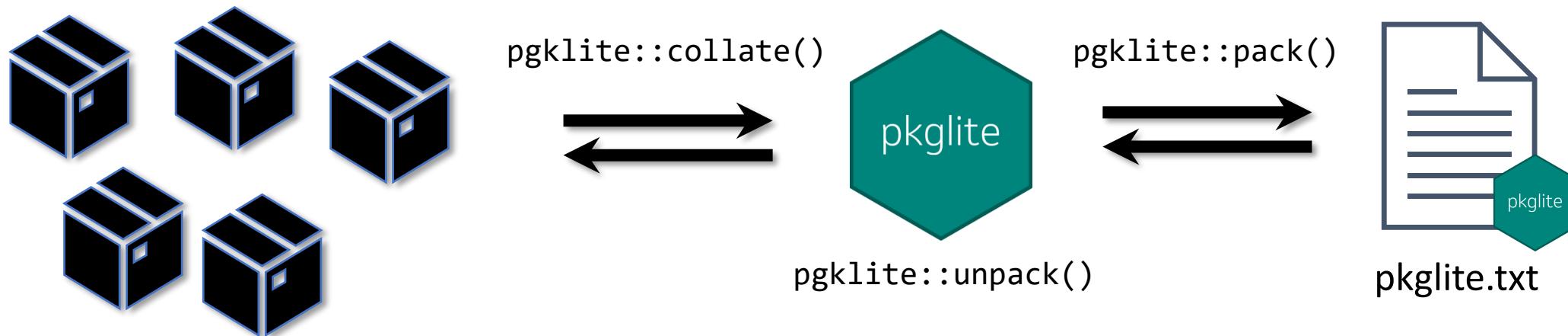


```
├── DESCRIPTION
├── inst
│   └── extdata
├── man
│   └── *.Rd
├── NAMESPACE
├── NEWS.md
├── R
│   └── *.R
├── README.md
├── tests
│   ├── testthat
│   │   └── *.R
│   └── testthat.R
└── vignettes
    └── *.Rmd
```

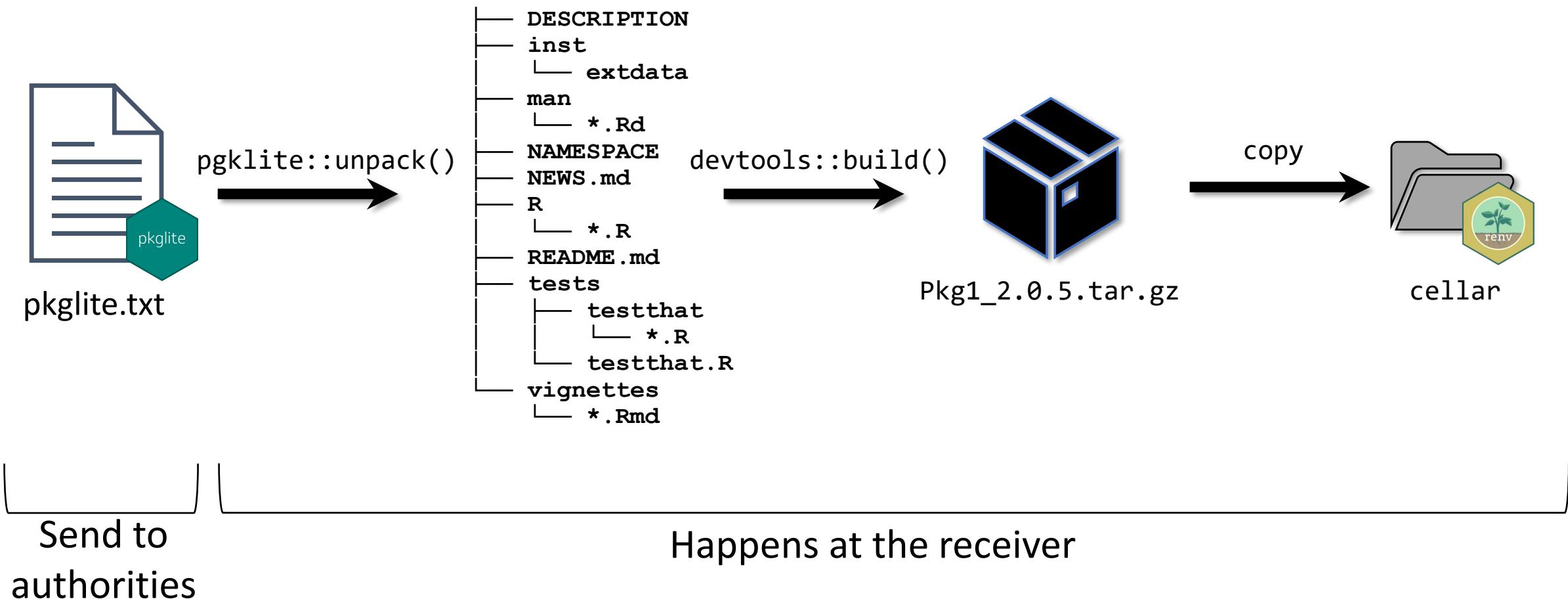


`pkglite::unpack()`

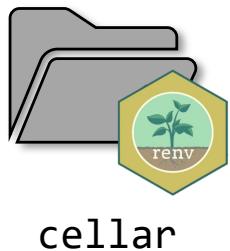
# Pack packages



# Combine pgklite with renv



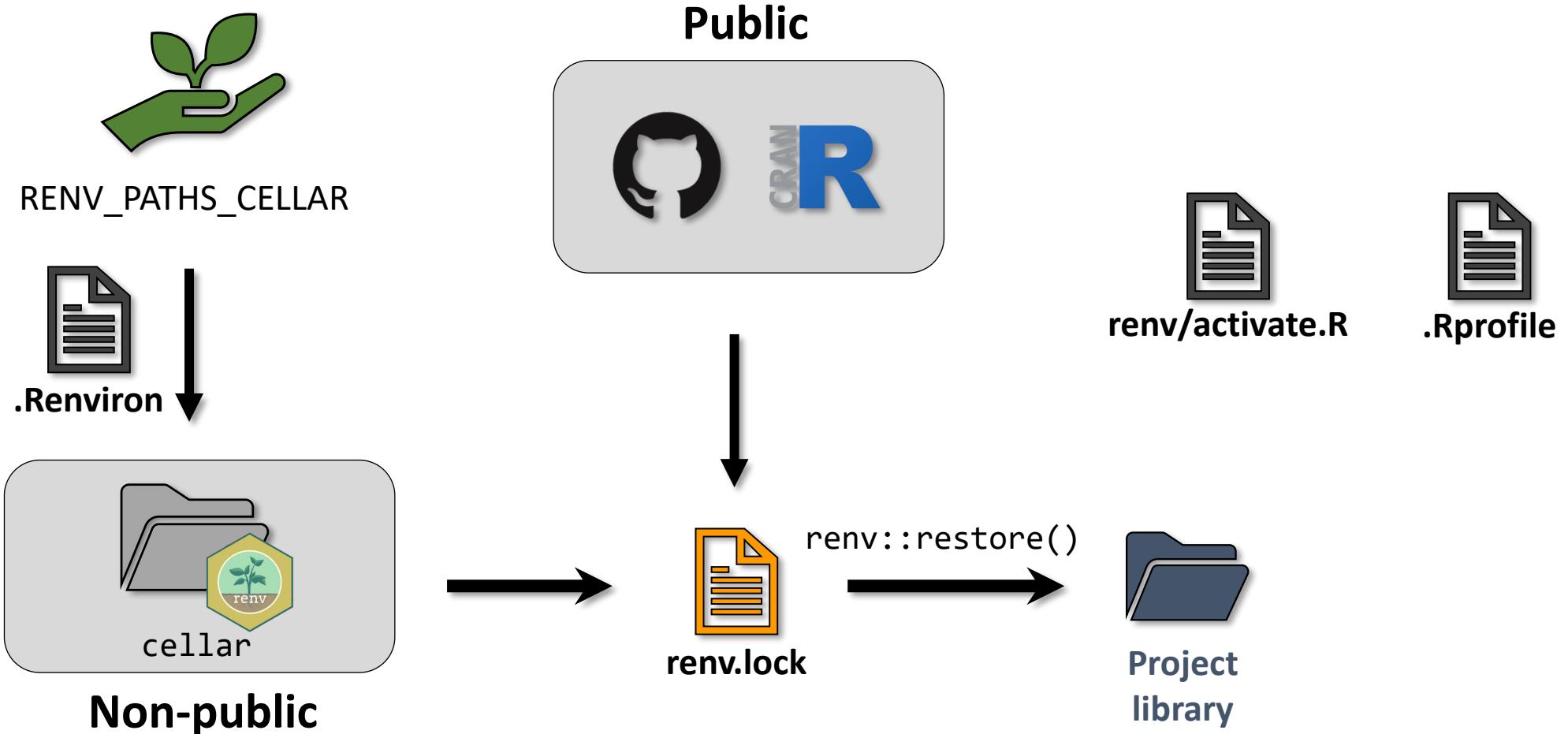
# Combine pgklite with renv

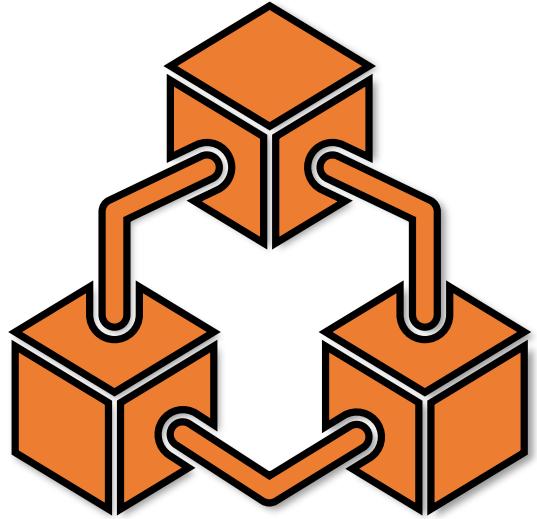


cellar

```
└── pkg1
    ├── pkg1_2.0.0.tar.gz
    └── pkg1_2.0.5.tar.gz
└── pkg2
    └── pkg2_1.1.1.tar.gz
└── pkg3
    ├── pkg3_4.1.0.tar.gz
    ├── pkg3_4.5.0.tar.gz
    ├── pkg3_5.1.0.tar.gz
    └── pkg3_5.2.1.tar.gz
└── pkg4
    └── pkg4_2.1.1.tar.gz
```

# Combine pgklite with renv





# Reproducibility

Exercise

# Exercise

## Background:

- We have submitted several trials to FDA
- Slightly different versions of our internal packages for each trial
- Same external packages on all trials
- We have used {renv} on all trials  
→ **renv.lock** exist on each trial

## Authorities asked for:

- Specific analysis using {Rstat} - a package not currently captured in `renv.lock`
- Reproducibility (they want to execute the programs)

## End product at recipient:

```
└── project.Rproj
└── SDTM data
    ├── ae.xpt
    └── lb.xpt
└── ADaM data
    ├── ads1.xpt
    ├── adae.xpt
    └── adlb.xpt
└── ADaM programs
    ├── ads1.R
    ├── adae.R
    └── adlb.R
└── Output programs
    ├── a_new_analysis.R
    ├── f_meanplot.R
    └── t_adverse.R
└── Output
└── renv
    ├── activate.R
    └── library
└── .Rprofile
└── renv.lock
```

# Exercise

## Background:

- We have submitted several trials to FDA
- Slightly different versions of our internal packages for each trial
- Same external packages on all trials
- We have used `{renv}` on all trials  
→ `renv.lock` exist on each trial

## Authorities asked for:

- Specific analysis using `{Rstat}` - a package not currently captured in `renv.lock`
- Reproducibility (they want to execute the programs)

Three groups of tasks

Each group should be arranged in sequence

New Analysis

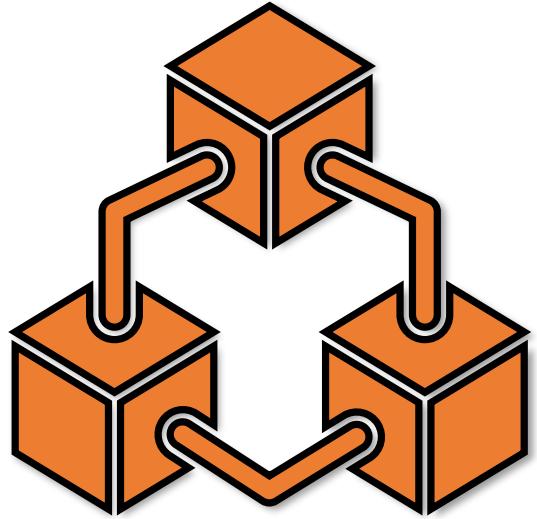
New Analysis

Preparation

Preparation

At recipient

At recipient



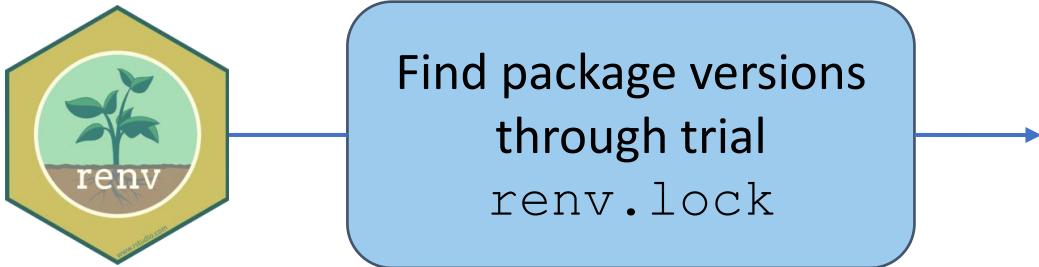
# **Reproducibility**

**Summary**

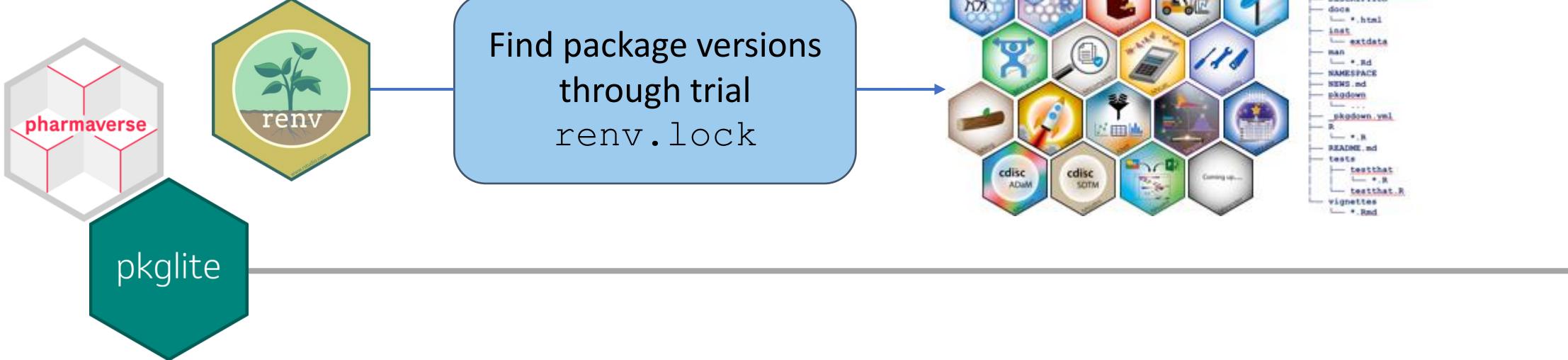
**&**

**Example from Novo Nordisk**

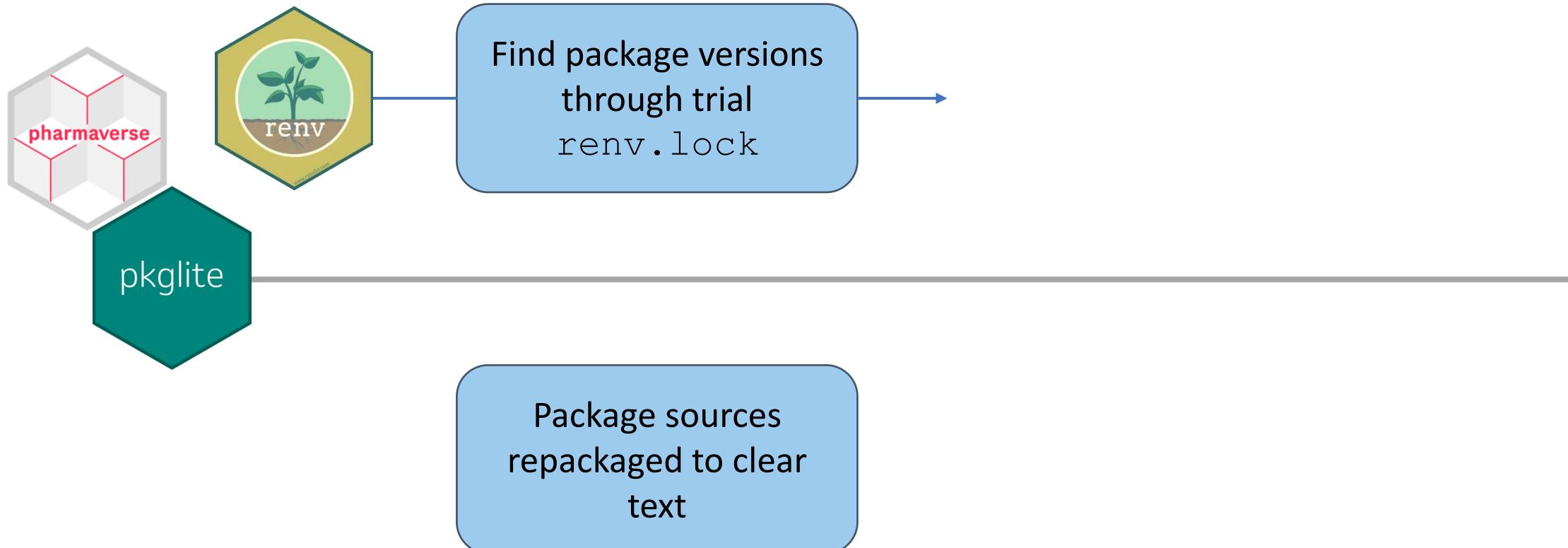
# Packing Packages



# Packing Packages



# Packing Packages



# Send to authorities



pkglite-{trial}.txt

Re-packaged NN  
packages



renvlock-{trial}.txt

renv.lock with  
reference to MRAN



activate.txt

renv bootstrapping  
script



buildrenviron.r

Unpack, setup, rebuild  
and initialise  
environment

```
{  
  "R": {  
    "Version": "4.3.1",  
    "Repositories": [  
      {  
        "Name": "CRAN",  
        "URL": "https://rspm.bifrost-dev.corp.aws.novonordisk.com/default-cran/2023-10-25"  
      },  
      {  
        "Name": "NN Prod",  
        "URL": "https://rspm.bifrost-dev.corp.aws.novonordisk.com/prod-internal-4.3.1/latest"  
      }  
    ]  
  },  
}
```

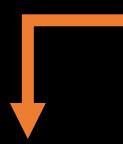


Delete



renvlock-{trial}.txt

```
{  
  "R": {  
    "Version": "4.3.1",  
    "Repositories": [  
      {  
        "Name": "CRAN",  
        "URL": "https://rspm.bifrost-dev.corp.aws.novonordisk.com/default-cran/2023-10-25"  
      }  
    ]  
  },  
}
```



Point to Private  
Package Manager



renvlock-{trial}.txt

```
{
```

```
  "R": {
```

```
    "Version": "4.3.1",
```

```
    "Repositories": [
```

```
    {
```

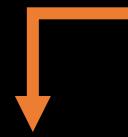
```
      "Name": "CRAN",
```

```
      "URL": "https://packagemanager.posit.co/cran/2023-10-25"
```

```
    }
```

```
  ]
```

```
},
```



Point to Posit Public  
Package Manager



renvlock-{trial}.txt

# Send to authorities



pkglite-{trial}.txt

Re-packaged NN  
packages



renvlock-{trial}.txt

renv.lock with  
reference to MRAN



activate.txt

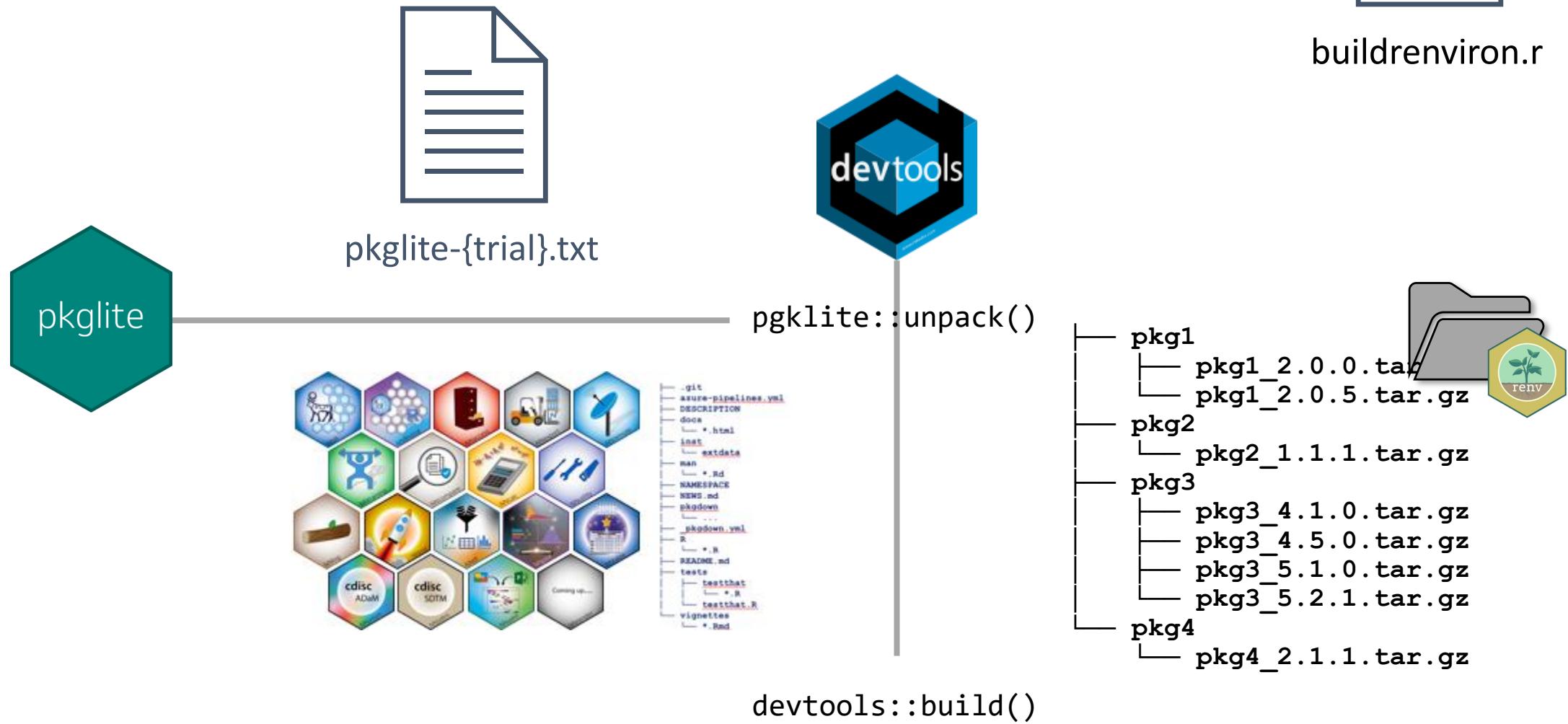
renv bootstrapping  
script



buildrenviron.r

Unpack, setup, rebuild  
and initialise  
environment

# Rebuilding environment



# Rebuild environment



buildr environ.r

`renv::restore()`



## For each trial

```
└── project.Rproj
└── SDTM data
    └── ae.xpt
    └── lb.xpt
└── ADaM data
    └── adsl.xpt
    └── adae.xpt
    └── adlb.xpt
└── ADaM programs
    └── adsl.R
    └── adae.R
    └── adlb.R
└── Output programs
    └── f_meanplot.R
    └── t_adverse.R
└── Output
└── renv
    └── activate.R
└── .Renvironment
└── .Rprofile
└── renv.lock
```

# Rebuild environment

Instructions to programs in R

## Contents

0.1	Submission files . . . . .	1
0.2	Software needed . . . . .	1
0.3	Recreation of the R environment . . . . .	2
0.4	Populating folders . . . . .	15
0.5	Program modification . . . . .	16
0.6	Program execution . . . . .	18



buildr environ.r

renv::restore()



## For each trial

```
└── project.Rproj
└── SDTM data
    └── ae.xpt
    └── lb.xpt
└── ADaM data
    └── adsl.xpt
    └── adae.xpt
    └── adlb.xpt
└── ADaM programs
    └── adsl.R
    └── adae.R
    └── adlb.R
└── Output programs
    └── f_meanplot.R
    └── t_adverse.R
└── Output
└── renv
    └── activate.R
    └── library
└── .Renvironment
└── .Rprofile
└── renv.lock
```

A close-up photograph of a lit incandescent lightbulb. The bulb is clear glass with a visible filament and a warm, yellow-orange glow. The background is dark and out of focus, with several blurred, glowing circular lights of the same color, creating a bokeh effect.

Thanks for joining