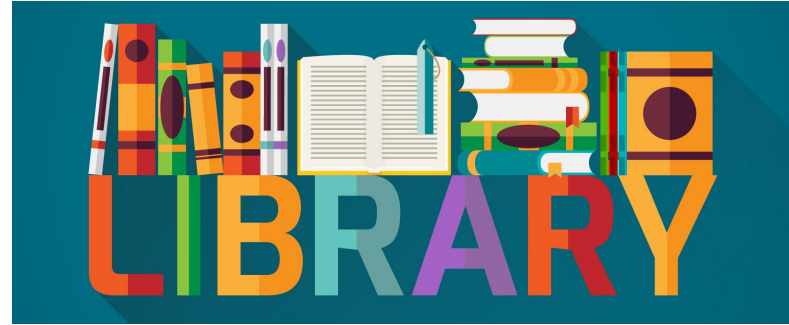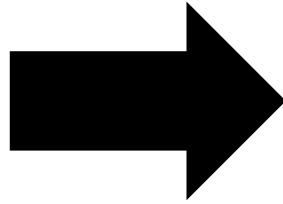# R packages

The Data Scientist's Toolbox

R Package = Library

CRAN

GitHub

Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

CRAN Task Views

[Bayesian](#)	Bayesian Inference
[ChemPhys](#)	Chemometrics and Computational Physics
[ClinicalTrials](#)	Clinical Trial Design, Monitoring, and Analysis
[Cluster](#)	Cluster Analysis & Finite Mixture Models
[DifferentialEquations](#)	Differential Equations
[Distributions](#)	Probability Distributions
[Econometrics](#)	Econometrics
[Environmetrics](#)	Analysis of Ecological and Environmental Data
[ExperimentalDesign](#)	Design of Experiments (DoE) & Analysis of Experimental Data
[ExtremeValue](#)	Extreme Value Analysis
[Finance](#)	Empirical Finance
[FunctionalData](#)	Functional Data Analysis
[Genetics](#)	Statistical Genetics
[Graphics](#)	Graphic Displays & Dynamic Graphics & Graphic Devices & Visualization
[HighPerformanceComputing](#)	High-Performance and Parallel Computing with R
[MachineLearning](#)	Machine Learning & Statistical Learning
[MedicalImaging](#)	Medical Image Analysis
[MetaAnalysis](#)	Meta-Analysis
[Multivariate](#)	Multivariate Statistics
[NaturalLanguageProcessing](#)	Natural Language Processing
[NumericalMathematics](#)	Numerical Mathematics

R RDocumentation

Task View

Bayesian

ChemPhys

ClinicalTrials

Cluster

DifferentialEquations

Distributions

Econometrics

Environmetrics

ExperimentalDesign

Finance

Genetics

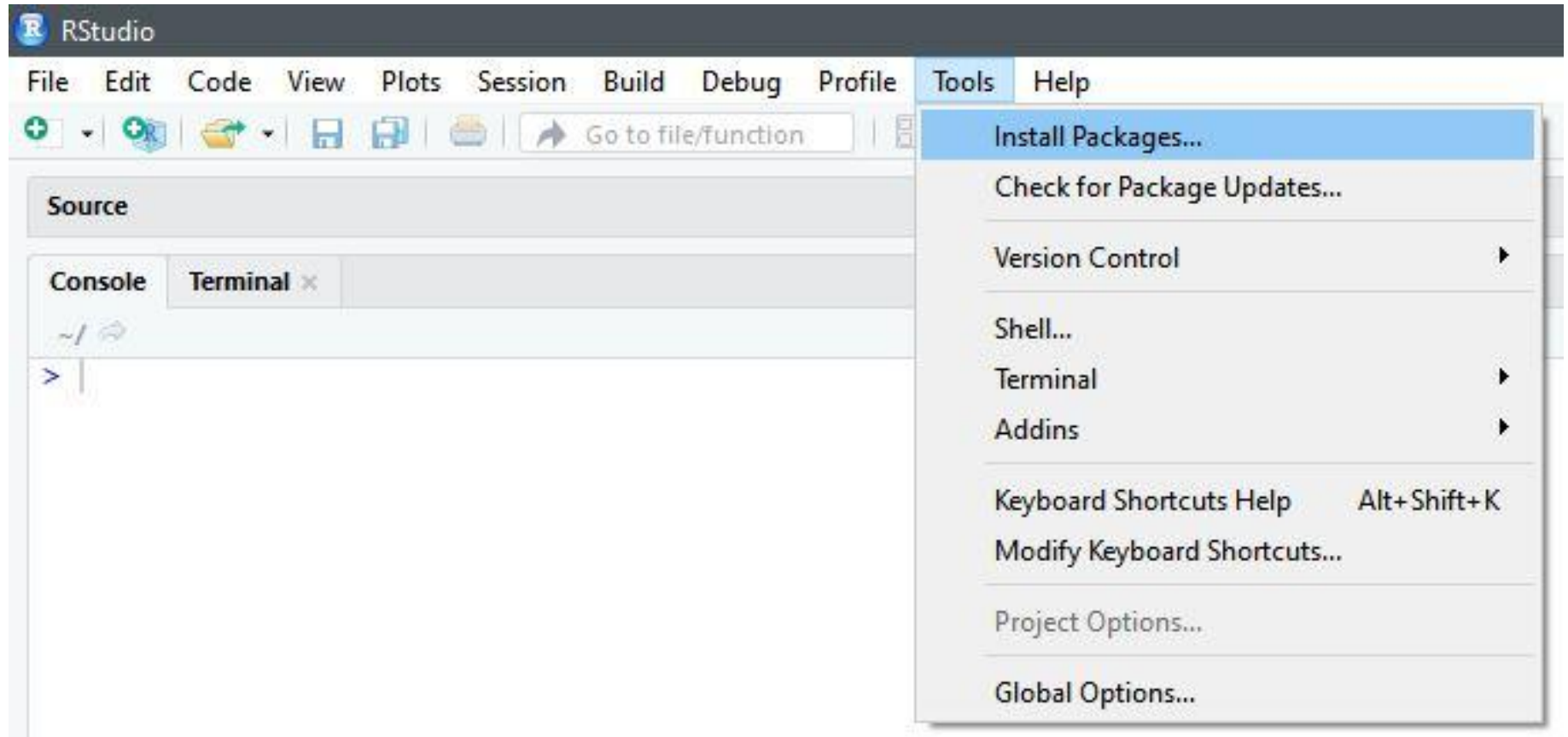**Search all 14,381 CRAN, BioConductor and Github packages.**

Search for packages, functions, etc   **Search**

Or explore packages in one of the Task Views.

```
install.packages("ggplot2")
```

```
install.packages(c("ggplot2", "devtools", "lme4"))
```

Install Packages

Install from: (?) Configuring Repositories

Repository (CRAN, CRANextra)   ▼

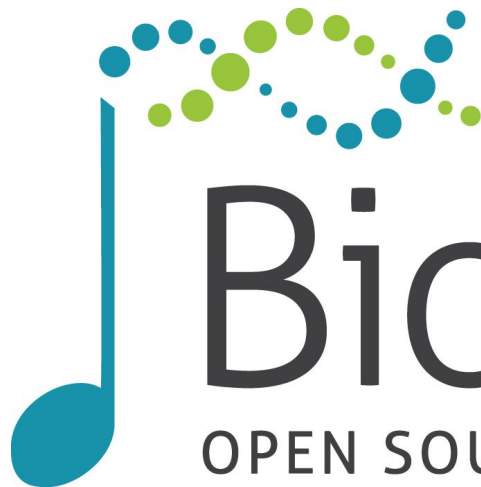Packages (separate multiple with space or comma):

[   ]

Install to Library:

C:/Users/Sarah_2/Documents/R/win-library/3.3 [Default]   ▼

☑ Install dependencies

[**Install**]   [Cancel]

Bioconductor

OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

```
source("https://bioconductor.org/biocLite.R")
```

```
biocLite()
```

```
biocLite("GenomicFeatures")
```
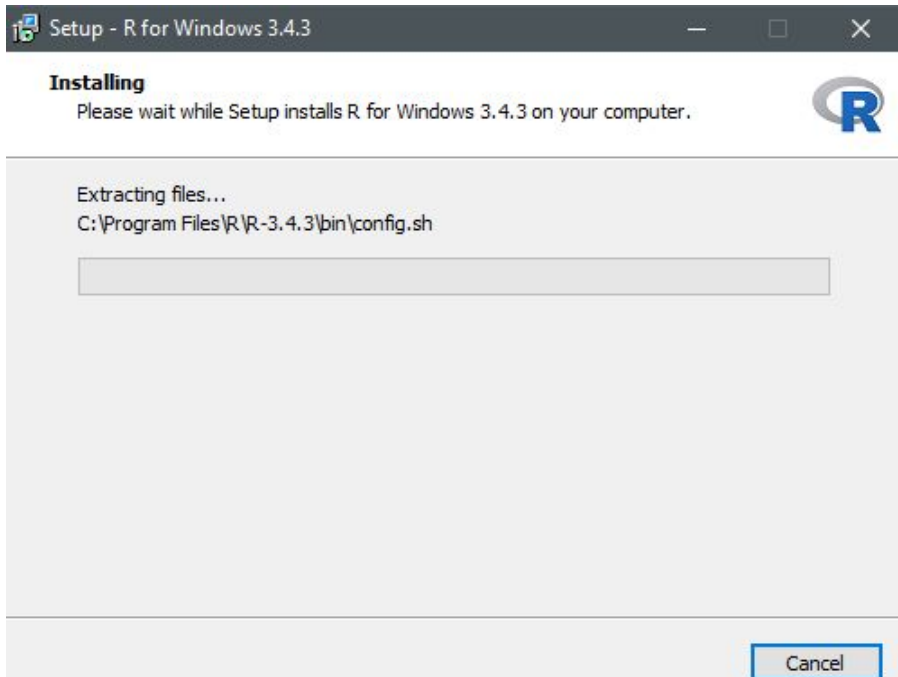
http://bioconductor.org

GitHub

```
install.packages("devtools")
```

```
library(devtools)
```

```
install_github("author/package")
```

Step 1: Install

```
install.packages("ggplot2")
```


Step 2: Load

```
library()
```

```
library(ggplot2)
```


R.exe

Files	Plots	**Packages**	Help	Viewer		

Install	Update	Packrat		

	Name	Description	Version	

User Library

☐	abind	Combine Multidimensional Arrays	1.4-5	⊗
☐	acepack	ACE and AVAS for Selecting Multiple Regression Transformations	1.4.1	⊗
☐	ade4	Analysis of Ecological Data : Exploratory and Euclidean Methods in Environmental Sciences	1.7-8	⊗
☐	AnnotationDbi	Annotation Database Interface	1.36.2	⊗
☐	ari	Automated R Instructor	0.1.0	⊗
☐	assertthat	Easy Pre and Post Assertions	0.2.0	⊗
☐	aws.iam	AWS IAM Client Package	0.1.7	⊗
☐	aws.polly	Client for AWS Polly	0.1.2	⊗
☐	aws.s3	AWS S3 Client Package	0.3.3	⊗
☐	aws.signature	Amazon Web Services Request Signatures	0.3.5	⊗
☐	backports	Reimplementations of Functions Introduced Since R-3.0.0	1.1.1	⊗
☐	base64enc	Tools for base64 encoding	0.1-3	⊗
☐	BB	Solving and Optimizing Large-Scale Nonlinear Systems	2014.10-1	⊗
☐	bedr	Genomic Region Processing using Tools Such as BEDtools, BEDOPS and Tabix	1.0.3	⊗
☐	BH	Boost C++ Header Files	1.65.0-1	⊗
☐	bindr	Parametrized Active Bindings	0.1	⊗
☐	bindrcpp	An 'Rcpp' Interface to Active Bindings	0.2	⊗
☐	Biobase	Biobase: Base functions for Bioconductor	2.34.0	⊗
☐	BiocGenerics	S4 generic functions for Bioconductor	0.20.0	⊗
☐	BiocInstaller	Install/Update Bioconductor, CRAN, and github Packages	1.24.0	⊗

What packages are installed?
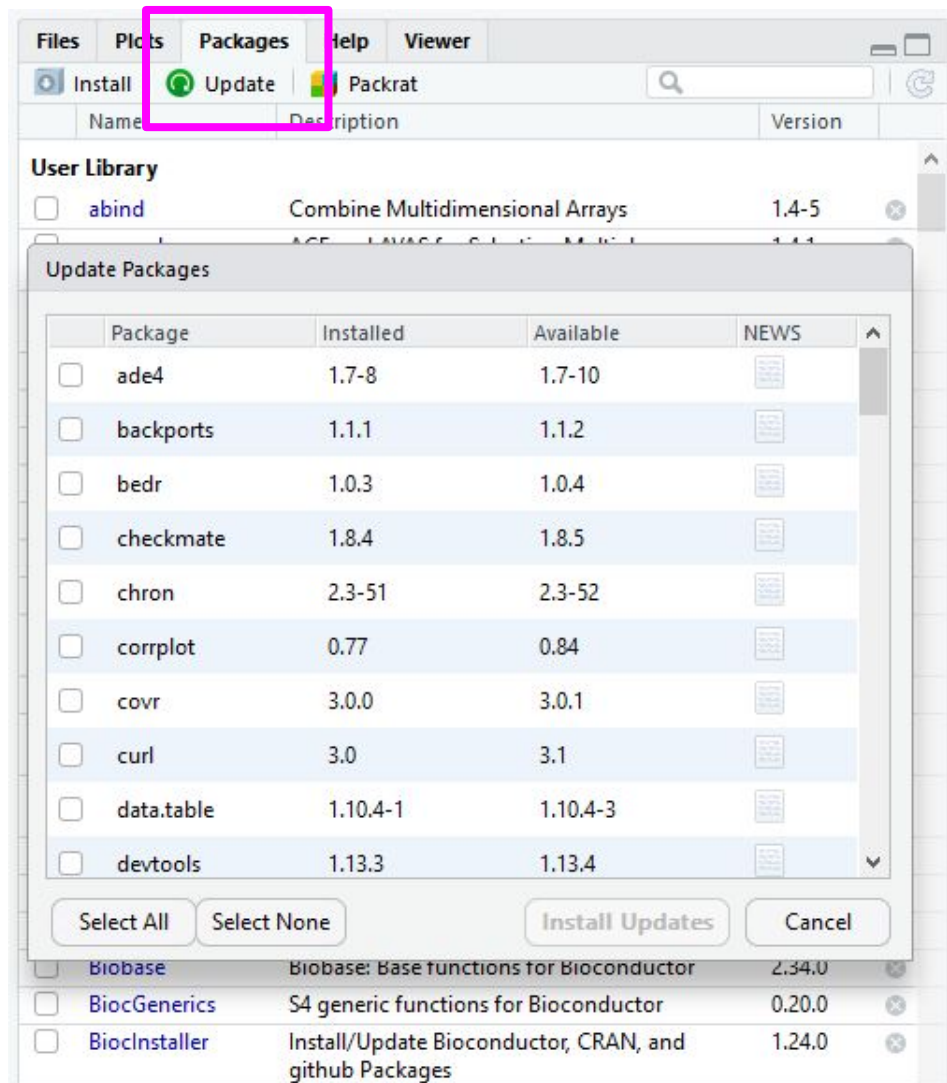
`installed.packages()` or `library()`
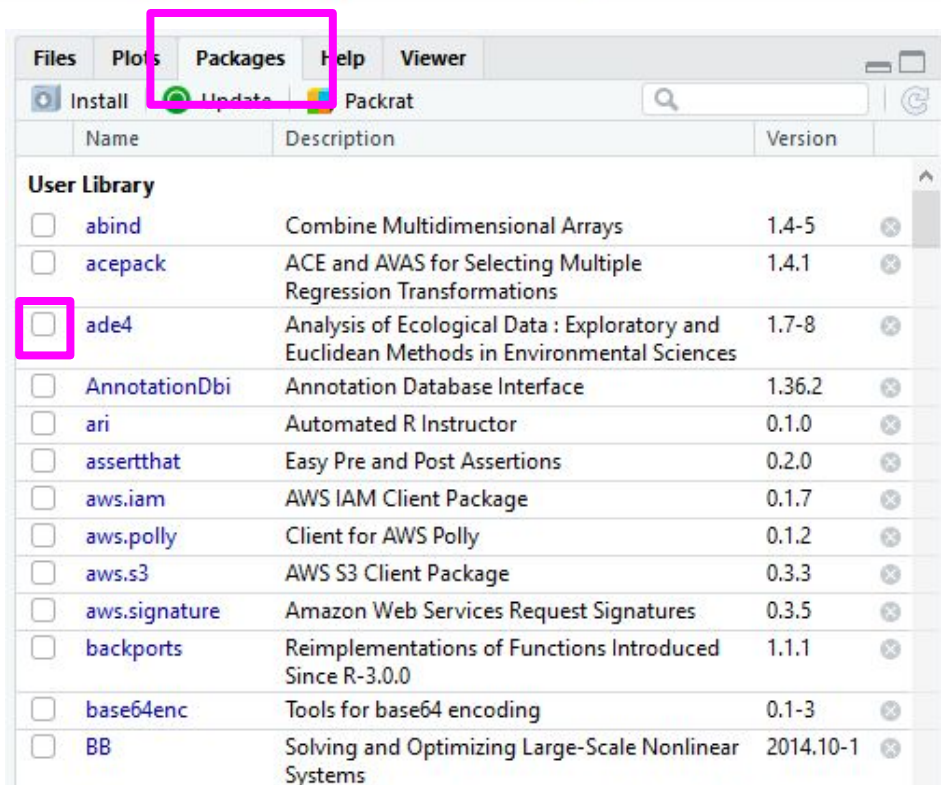
Updating packages

`old.packages()`

`update.packages()`

`install.packages("packagename")`

Files	Plots	**Packages**	Help	Viewer

Install	Update	Packrat		🔍

	Name	Description	Version

User Library

	abind	Combine Multidimensional Arrays	1.4-5

Update Packages

	Package	Installed	Available	NEWS
☐	ade4	1.7-8	1.7-10	📄
☐	backports	1.1.1	1.1.2	📄
☐	bedr	1.0.3	1.0.4	📄
☐	checkmate	1.8.4	1.8.5	📄
☐	chron	2.3-51	2.3-52	📄
☐	corrplot	0.77	0.84	📄
☐	covr	3.0.0	3.0.1	📄
☐	curl	3.0	3.1	📄
☐	data.table	1.10.4-1	1.10.4-3	📄
☐	devtools	1.13.3	1.13.4	📄

Select All	Select None		Install Updates	Cancel

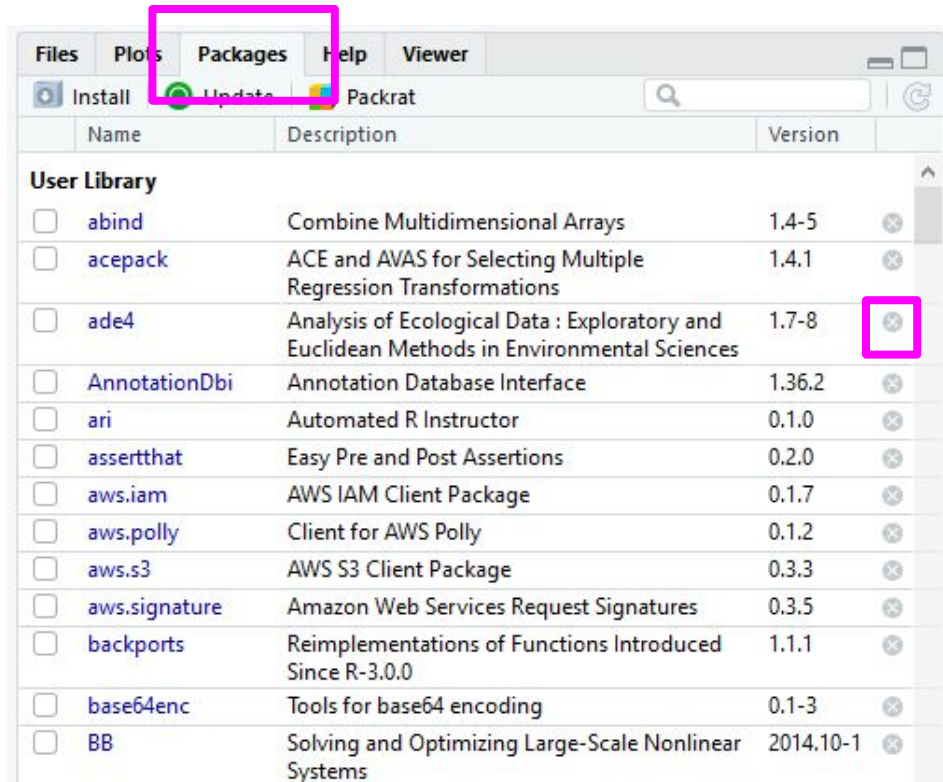|	Biobase	Biobase: Base functions for Bioconductor	2.34.0
☐	BiocGenerics	S4 generic functions for Bioconductor	0.20.0
☐	BiocInstaller	Install/Update Bioconductor, CRAN, and github Packages	1.24.0

```
detach()
```

```
detach("package:ggplot2", unload=TRUE)
```

```
remove.packages()
```

```
remove.packages("ggplot2")
```

```
R version 3.4.3 (2017-11-30) -- "Kite-Eating Tree"
Copyright (C) 2017 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
```
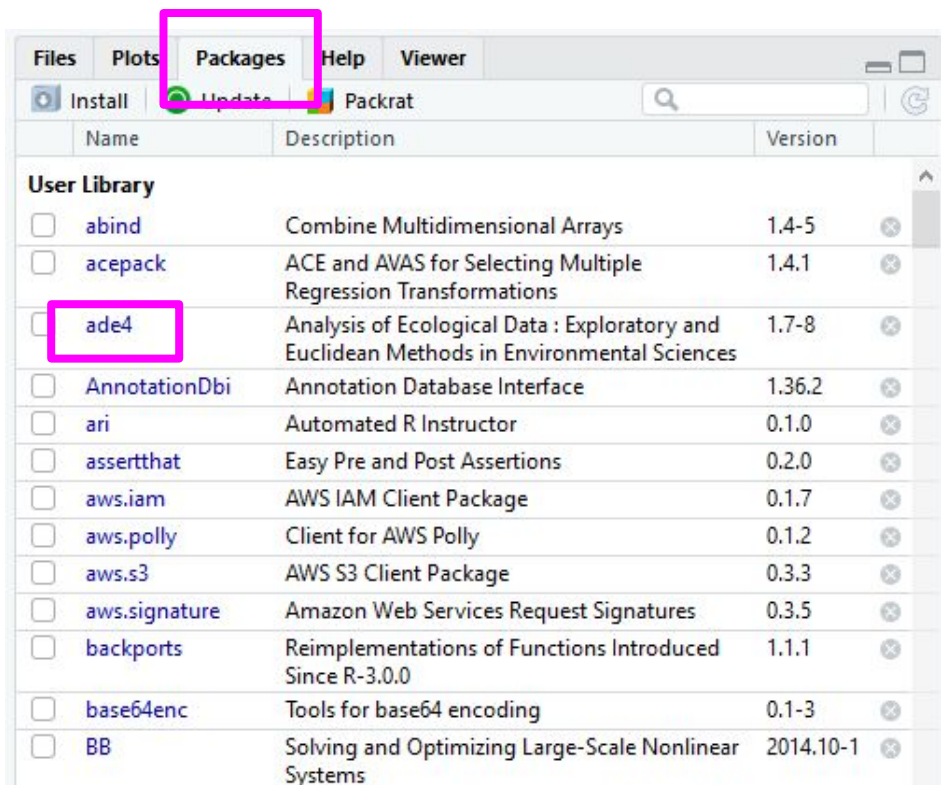
```
version
```

```
sessionInfo()
```

```
help()
```

```
help(package = "ggplot2")
```

```
browseVignettes()
```

```
browseVignettes("ggplot2")
```

Vignettes found by "browseVignettes("ggplot2")"

Vignettes in package ggplot2

- Aesthetic specifications - HTML source R code
- Extending ggplot2 - HTML source R code

Summarizing: R packages

The Data Scientist's Toolbox