

Microbiome Workshop: Software requirements and installation

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Minimum software requirements

- Operating system
 - Windows 7 (64-bit)
 - OS X 10.12 (64-bit)
- Memory
 - 10 GB hard-drive space
 - 8 GB RAM

Install R from this website



The screenshot shows the homepage of the Comprehensive R Archive Network (CRAN) at cran.case.edu. The page features the R logo and navigation links for CRAN mirrors, what's new, task views, and search. The main content area is titled "The Comprehensive R Archive Network" and includes sections for "Download and Install R", "Source Code for all Platforms", and "Questions About R". Each section contains a list of links or instructions.

Download and Install R

Precompiled binary distributions of the base system and contributed packages, **Windows and Mac** users most likely want one of these versions of R:

- [Download R for Linux](#)
- [Download R for \(Mac\) OS X](#)
- [Download R for Windows](#)

R is part of many Linux distributions, you should check with your Linux package management system in addition to the link above.

Source Code for all Platforms

Windows and Mac users most likely want to download the precompiled binaries listed in the upper box, not the source code. The sources have to be compiled before you can use them. If you do not know what this means, you probably do not want to do it!

- The latest release (2019-07-05, Action of the Toes) [R-3.6.1.tar.gz](#), read [what's new](#) in the latest version.
- Sources of [R alpha and beta releases](#) (daily snapshots, created only in time periods before a planned release).
- Daily snapshots of current patched and development versions are [available here](#). Please read about [new features and bug fixes](#) before filing corresponding feature requests or bug reports.
- Source code of older versions of R is [available here](#).
- Contributed extension [packages](#)

Questions About R

- If you have questions about R like how to download and install the software, or what the license terms are, please read our [answers to frequently asked questions](#) before you send an email.

What are R and CRAN?

R is ‘GNU S’, a freely available language and environment for statistical computing and graphics which provides a wide variety of statistical and graphical techniques: linear and nonlinear modelling, statistical tests, time series analysis, classification, clustering, etc. Please consult the [R project homepage](#) for further information.

CRAN is a network of ftp and web servers around the world that store identical, up-to-date, versions of code and documentation for R. Please use the CRAN [mirror](#) nearest to you to minimize network load.

Submitting to CRAN

To “submit” a package to CRAN, check that your submission meets the [CRAN Repository Policy](#) and then use the [web form](#).

For Mac Choose



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[Manuals](#)
[FAQs](#)
[Contributed](#)

This directory contains binaries for a base distribution and packages to run on Mac OS X (release 10.6 and above). Mac OS 8.6 to 9.2 (and Mac OS X 10.1) are no longer supported but you can find the last supported release of R for these systems (which is R 1.7.1) [here](#). Releases for old Mac OS X systems (through Mac OS X 10.5) and PowerPC Macs can be found in the [old](#) directory.

Note: CRAN does not have Mac OS X systems and cannot check these binaries for viruses. Although we take precautions when assembling binaries, please use the normal precautions with downloaded executables.

Package binaries for R versions older than 3.2.0 are only available from the [CRAN archive](#) so users of such versions should adjust the CRAN mirror setting (<https://cran-archive.r-project.org>) accordingly.

R 4.0.4 "Lost Library Book" released on 2021/02/15

Please check the SHA1 checksum of the downloaded image to ensure that it has not been tampered with or corrupted during the mirroring process. For example type `openssl sha1 R-4.0.4.pkg` in the *Terminal* application to print the SHA1 checksum for the R-4.0.4.pkg image. On Mac OS X 10.7 and later you can also validate the signature using `pkgutil --check-signature R-4.0.4.pkg`

[R-4.0.4.pkg](#) (notarized and signed)
SHA1-hash: 0b2b3bc846f6ebc72a8bc0b53e6e85d600d95deb
(ca. 85MB)

Latest release:

R 4.0.4 binary for macOS 10.13 (High Sierra) and higher, signed and notarized package. Contains R 4.0.4 framework, R.app GUI 1.74 in 64-bit for Intel Macs, Tcl/Tk 8.6.6 X11 libraries and Texinfo 6.7. The latter two components are optional and can be omitted when choosing "custom install", they are only needed if you want to use the `tcltk` R package or build package documentation from sources.

Note: the use of X11 (including `tcltk`) requires [XQuartz](#) to be installed since it is no longer part of OS X. Always re-install XQuartz when upgrading your macOS to a new major version. Also please do not install beta versions of XQuartz (even if offered).

This release supports Intel Macs, but it is also known to work using Rosetta2 on M1-based Macs. Native Apple silicon binary is expected for R 4.1.0 if support for Fortran stabilizes, for experimental builds and updates see [mac.R-project.org](#).

Important: this release uses Xcode 12.4 and GNU Fortran 8.2. If you wish to compile R packages from sources, you will need to download GNU Fortran 8.2 - see the [tools](#) directory.

[NEWS](#) (for Mac GUI)

[Mac-GUI-1.74.tar.gz](#)
SHA1-hash: 2c791fd1fd2d8f90b0887cf19541882200a6eab8

News features and changes in the R.app Mac GUI

Sources for the R.app GUI 1.74 for Mac OS X. This file is only needed if you want to join the development of the GUI, it is not intended for regular users. Read the INSTALL file for further instructions.

For Windows



[CRAN
Mirrors](#)
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[About R](#)
[R Homepage](#)
[The R Journal](#)

Subdirectories:

[base](#)

[contrib](#)

[old contrib](#)

[Rtools](#)

Binaries for base distribution. This is what you want to [install R for the first time](#).

Binaries of contributed CRAN packages (for R >= 2.13.x; managed by Uwe Ligges). There is also information on [third party software](#) available for CRAN Windows services and corresponding environment and make variables.

Binaries of contributed CRAN packages for outdated versions of R (for R < 2.13.x; managed by Uwe Ligges).

Tools to build R and R packages. This is what you want to build your own packages on Windows, or to build R itself.

Please do not submit binaries to CRAN. Package developers might want to contact Uwe Ligges directly in case of questions / suggestions related to Windows binaries.

You may also want to read the [R FAQ](#) and [R for Windows FAQ](#).

Note: CRAN does some checks on these binaries for viruses, but cannot give guarantees. Use the normal precautions with downloaded executables.



R-4.0.4 for Windows (32/64 bit)

[Download R 4.0.4 for Windows](#) (85 megabytes, 32/64 bit)

[Installation and other instructions](#)

[New features in this version](#)

If you want to double-check that the package you have downloaded matches the package distributed by CRAN, you can compare the [md5sum](#) of the .exe to the [fingerprint](#) on the master server. You will need a version of md5sum for windows: both [graphical](#) and [command line versions](#) are available.

[Frequently asked questions](#)



[CRAN
Mirrors](#)
[What's new?](#)
[Task Views](#)
[Search](#)

Install RStudio

The screenshot shows the official RStudio website at rstudio.com. The page features a background pattern of hexagonal icons representing various R packages like tidyverse, dplyr, and ggplot2. In the top right corner, there's a navigation bar with links for DOWNLOAD, SUPPORT, COMMUNITY, and a search icon. The DOWNLOAD link is highlighted with a red box. Below the navigation, there are menu items for Products, Resources, Pricing, About, and Blogs. A large central image displays a computer monitor showing a Shiny application interface titled "Access to Care App". The app includes a dashboard with metrics: 58 hospitals, 345 facilities, 39M population, and 4 underinsured counties. It also features a map of California with county-level hospital data overlays.

Open source and enterprise-ready professional software for data science.

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DOWNLOAD SUPPORT COMMUNITY

DOWNLOAD

Access to Care App

Access to Hospital Care Dashboard

58 hospitals

345 facilities

39M Population

4 Underinsured Counties

County Map

Legend

Less hospitals than expected

More hospitals than expected

Wilton Range

Hospital Location (Zipsode)

Choose the free version of RStudio

Choose Your Version

RStudio is a set of integrated tools designed to help you be more productive with R. It includes a console, syntax-highlighting editor that supports direct code execution, and a variety of robust tools for plotting, viewing history, debugging and managing your workspace.

[LEARN MORE ABOUT RSTUDIO FEATURES](#)



RStudio's new solution for every professional data science team. RStudio Team includes RStudio Server Pro, RStudio Connect and RStudio Package Manager.

[LEARN MORE](#)

RStudio Desktop	RStudio Desktop	RStudio Server	RStudio Server Pro
Open Source License	Commercial License	Open Source License	Commercial License
Free	\$995 /year	Free	\$4,975 /year
DOWNLOAD	BUY	DOWNLOAD	BUY
Learn more	Learn more	Learn more	Evaluation Learn more

Integrated Tools for R



Priority Support



Access via Web Browser



Choose the Rstudio Installer for your operating system

OS	Download	Size	SHA-256
Windows 10	 RStudio-1.4.1106.exe	155.97 MB	d2ff8453
macOS 10.13+	 RStudio-1.4.1106.dmg	153.35 MB	c64d2cda
Ubuntu 16	 rstudio-1.4.1106-amd64.deb	118.45 MB	1fc82387
Ubuntu 18/Debian 10	 rstudio-1.4.1106-amd64.deb	121.07 MB	3b5d3835
Fedora 19/Red Hat 7	 rstudio-1.4.1106-x86_64.rpm	138.18 MB	a9e6ddc4
Fedora 28/Red Hat 8	 rstudio-1.4.1106-x86_64.rpm	138.16 MB	35e57c1c
Debian 9	 rstudio-1.4.1106-amd64.deb	121.33 MB	c7c9dd68
OpenSUSE 15	 rstudio-1.4.1106-x86_64.rpm	123.57 MB	3539d9c3

Installing DAD2

← → ⌂ bioconductor.org/packages/release/bioc/html/dada2.html ☆ ⚙



Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

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Search:

Home » Bioconductor 3.9 » Software Packages » dada2

dada2

platforms all rank 105 / 1741 posts 0 in Bioc 3.5 years
build warnings updated since release dependencies 76

DOI: [10.18129/B9.bioc.dada2](https://doi.org/10.18129/B9.bioc.dada2) [f](#) [t](#)

Accurate, high-resolution sample inference from amplicon sequencing data

Bioconductor version: Release (3.9)

The dada2 package infers exact amplicon sequence variants (ASVs) from high-throughput amplicon sequencing data, replacing the coarser and less accurate OTU clustering approach. The dada2 pipeline takes as input demultiplexed fastq files, and outputs the sequence variants and their sample-wise abundances after removing substitution and chimera errors. Taxonomic classification is available via a native implementation of the RDP naïve Bayesian classifier, and species-level assignment to 16S rRNA gene fragments by exact matching.

Author: Benjamin Callahan <benjamin.j.callahan@gmail.com>, Paul McMurdie, Susan Holmes

Maintainer: Benjamin Callahan <benjamin.j.callahan@gmail.com>

Citation (from within R, enter `citation("dada2")`):

Callahan BJ, McMurdie PJ, Rosen MJ, Han AW, Johnson AJA, Holmes SP (2016). "DADA2: High-resolution sample inference from Illumina amplicon data." *Nature Methods*, **13**, 581–583. doi: [10.1038/nmeth.3869](https://doi.org/10.1038/nmeth.3869).

Installation

To install this package, start R (version "3.6") and enter:

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

BiocManager::install("dada2")
```

For older versions of R, please refer to the appropriate [Bioconductor release](#).

Documentation »

Bioconductor

- Package [vignettes](#) and [manuals](#).
- [Workflows](#) for learning and use.
- [Course and conference](#) material.
- [Videos](#).
- Community [resources](#) and [tutorials](#).

R / CRAN packages and [documentation](#)

Support »

Please read the [posting guide](#). Post questions about Bioconductor to one of the following locations:

- [Support site](#) - for questions about Bioconductor packages
- [BioC-devel](#) mailing list - for package developers

Copy this text

Install Dada2

Console ~/ ↗

```
R version 3.6.1 (2019-07-05) -- "Action of the Toes"  
Copyright (C) 2019 The R Foundation for Statistical Computing  
Platform: x86_64-apple-darwin15.6.0 (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.
```

```
Natural language support but running in an English locale
```

```
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.
```

```
.Rprofile: Setting repository[Workspace loaded from ~/.RData]
```

```
> if (!requireNamespace("BiocManager", quietly = TRUE))  
  install.packages("BiocManager")
```

```
BiocManager::install("dada2")|
```

Open Rstudio
paste the text
into the consul
and press enter

Install Dada2

If this appears type “a” and press enter

```
The downloaded binary packages are in  
    /var/folders/bc/ldp2tt3n79gd7hvk_q_nf5xc0000gq/T//Rtmp3bsoVr/downloaded_packages  
Old packages: 'digest'  
Update all/some/none? [a/s/n]:  
|
```

If this appears type “no” and press enter

```
Do you want to install from sources the package which needs compilation? (Yes/no/cancel)
```

Installing the R Microbiome Package

Type at the console and press enter

```
> BiocManager::install("microbiome")
```

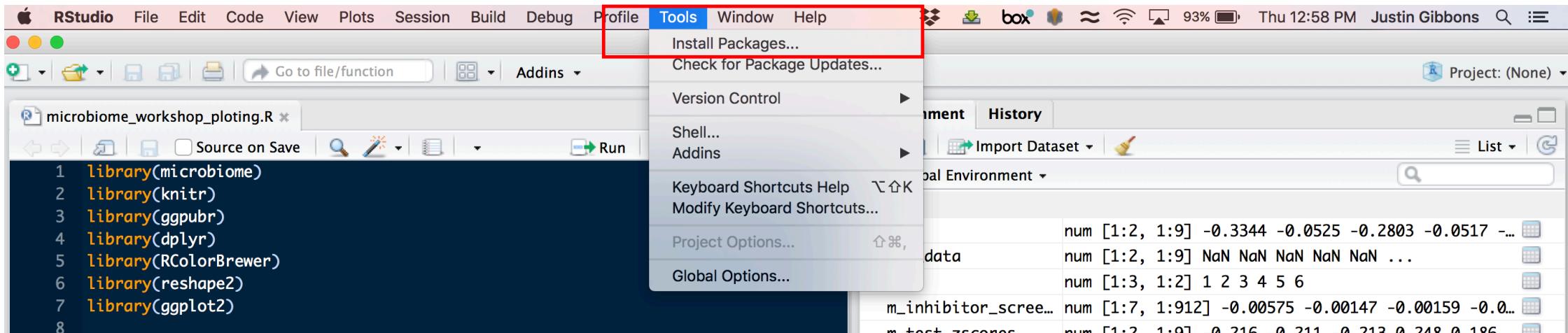
When this appears type “a” and press enter

```
Update all/some/none? [a/s/n]: —
```

When this appears type “no” and press enter

```
Do you want to install from sources the package which needs compilation? (Yes/no/cancel)
```

Some packages can be installed directly using Rstudio



The screenshot shows the RStudio interface. The top menu bar has 'Tools' selected, and a red box highlights the 'Install Packages...' option in the dropdown menu. The main workspace shows an R script named 'microbiome_workshop_plotting.R' with code for loading various R packages and preparing data. Below the script is a 'Console' window displaying the R startup message and license information. To the right, the 'Environment' tab of the 'Global Environment' viewer is open, showing variables like 'data', 'm_inhibitor_scree...', 'm_test_zscores', 'test_m', and 'v_test_z_scores'. A 'Help' tab for the 'dada2' package is also visible.

```
library(microbiome)
library(knitr)
library(ggpubr)
library(dplyr)
library(RColorBrewer)
library(reshape2)
library(ggplot2)

####Create a phyloseq object out of the dada2 output#####
infile_asv_counts<-"/Users/justingibbons/Box/Microbiome_Package_Tutorial/microbiome/asvcounts.txt"
infile_asv_tax<-"/Users/justingibbons/Box/Microbiome_Package_Tutorial/microbiome/taxonomy.txt"
infile_sample_data<-"/Users/justingibbons/Box/Microbiome_Package_Tutorial/microbiome/sample_data.txt"

df_asv_counts<-read.delim(infile_asv_counts)
df_asv_tax<-read.delim(infile_asv_tax)
df_sample_data<-read.delim(infile_sample_data)
rownames(df_sample_data)<-df_sample_data[,1]
#Convert the data to matrix format
m_asv_counts<-as.matrix(df_asv_counts[2:length(df_asv_counts)])
rownames(m_asv_counts)<-df_asv_counts[,1]
```

R version 3.6.1 (2019-07-05) -- "Action of the Toes"
Copyright (C) 2019 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin15.6.0 (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.

Natural language support but running in an English locale

R is a collaborative project with many contributors

DADA2 package

Description

The `dada2` package is centered around the DADA2 algorithm for accurate high-resolution of sample composition from amplicon sequencing data. The DADA2 algorithm is both more sensitive and more specific than commonly used OTU methods, and resolves amplicon sequence variants (ASVs) that differ by as little as one nucleotide.

Details

The `dada2` package also provides a full set of tools for taking raw amplicon sequencing data and producing a phyloseq object ready for downstream analysis.

Install additional packages using the Rstudio Package installer

- Install the following packages using the Rstudio installer:
 - knitr
 - ggpubr
 - dplyr
 - RColorBrewer
 - reshape2
 - ggplot2

