

# Installing R Packages at CHPC

Brett Milash and Anita Orendt

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## **solaR: Radiation and Photovoltaic Systems**

Calculation methods of solar radiation and performance of photovoltaic systems from daily and intradaily irradiation data sources.

<https://cran.r-project.org/web/packages/solaR/index.html>

```
$ module load R/4.2.2
```

```
$ R
```

```
R version 4.2.2 (2022-10-31) -- "Innocent and Trusting"  
Copyright (C) 2022 The R Foundation for Statistical Computing  
Platform: x86_64-pc-linux-gnu (64-bit)
```

```
...
```

```
> library(solaR)
```

```
Error in library(solaR) : there is no package called 'solaR'
```

# Strategies for handling missing R libraries

1. Tell R where to find the already-installed package
2. Find a version of R that has the package installed
3. Install the package yourself

## Strategy 1: Tell R where to find the already-installed package

- When loading a library R searches the path returned by `.libPaths()`

```
> .libPaths()  
[1] "/uufs/chpc.utah.edu/sys/installldir/r8/R/4.2.2/lib64/R/library"  
[2] "/uufs/chpc.utah.edu/sys/installldir/r8/Rlibs/4.2.2"
```

- One can append additional *existing* directories to this path:

```
> .libPaths( c( .libPaths(), "~u0253283/R/x86_64-pc-linux-gnu-library/4.2" ) )  
> .libPaths()  
[1] "/uufs/chpc.utah.edu/sys/installldir/r8/R/4.2.2/lib64/R/library"  
[2] "/uufs/chpc.utah.edu/sys/installldir/r8/Rlibs/4.2.2"  
[3] "/uufs/chpc.utah.edu/common/home/u0253283/R/x86_64-pc-linux-gnu-library/4.2"
```

## Strategy 1 (continued)

- Or use the `R_LIBS_USER` environment variable:

```
# In bash:
$ export R_LIBS_USER=~u0253283/R/x86_64-pc-linux-gnu-library/4.2
# Or in tcsh:
$ setenv R_LIBS_USER ~u0253283/R/x86_64-pc-linux-gnu-library/4.2
$ R

R version 4.2.2 (2022-10-31) -- "Innocent and Trusting"
Copyright (C) 2022 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

> .libPaths()
[1] "/uufs/chpc.utah.edu/sys/installdir/r8/R/4.2.2/lib64/R/library"
[2] "/uufs/chpc.utah.edu/sys/installdir/r8/Rlibs/4.2.2"
[3] "/uufs/chpc.utah.edu/common/home/u0253283/R/x86_64-pc-linux-gnu-library/4.2"
```

- This strategy isn't used very often - typically by research labs with group space (i.e. a shared file system)

## Strategy 2: Find a version of R that has the package installed

“The best R package installation is the one you don’t have to do.”

-- Brett Milash

### R modules at CHPC:

- R/4.1.2-basic
- R/4.1.2-bioconductor
- R/4.1.2-geospatial
- R/4.1.3
- R/4.2.1-Bioconductor
- R/4.2.2

# CHPC's R modules

- Every CHPC R module has useful libraries in addition to the base package:

car	ggvis	maptools	reshape2	testthat
caret	glmnet	mgcv	rgl	threeJS
data.table	googleVis	microbenchmark	rmarkdown	tidyr
devtools	htmlwidgets	multcomp	RMySQL	vcd
DiagrammeR	httr	network3D	RODBC	XLConnect
dplyr	jsonlite	nlme	roxygen2	xlsx
DT	knitr	parallel	RPostgresSQL	XML
dygraphs	leaflet	pryr	RSQLite	xtable
foreign	lme4	qcc	shiny	xts
gcbd	locfit	quantmod	sp	zoo
ggmap	lubridate	randomForest	stringr	
ggplot2	maps	Rcpp	survival	

- Certain CHPC R modules have additional library collections:
  - Bioconductor
  - Geospatial packages (e.g. proj4, rgdal, RNetCDF, hdf5r)

## Strategy 3: Install the package yourself

Main repositories of R code:

- CRAN: Comprehensive R Archive Network
  - <https://cran.r-project.org>
  - [https://cran.r-project.org/web/packages/available\\_packages\\_by\\_name.html](https://cran.r-project.org/web/packages/available_packages_by_name.html)
- Bioconductor: Open-source software for bioinformatics
  - <https://www.bioconductor.org>
  - <https://bioconductor.org/packages/release/bioc/>
- Github
  - <https://github.com>
  - <https://github.com/qinwf/awesome-R>

Installation method varies depending on repository



# Installing packages from CRAN

Use the `install.packages()` function, with package name in quotes:

```
$ module load R/4.2.2
$ R

R version 4.2.2 (2022-10-31) -- "Innocent and Trusting"
""
> .libPaths()
[1] "/uufs/chpc.utah.edu/sys/installdir/r8/R/4.2.2/lib64/R/library"
[2] "/uufs/chpc.utah.edu/sys/installdir/r8/RLibs/4.2.2"
> install.packages("solaR")
Installing package into
'/uufs/chpc.utah.edu/sys/installdir/r8/R/4.2.2/lib64/R/library'
(as 'lib' is unspecified)
Warning in install.packages("solaR") :
  'lib = "/uufs/chpc.utah.edu/sys/installdir/r8/R/4.2.2/lib64/R/library"' is not
writable
Would you like to use a personal library instead? (yes/No/cancel) yes
```

# Installing packages from CRAN (continued)

```
Would you like to create a personal library
'/uufs/chpc.utah.edu/common/home/u0424091/R/x86_64-pc-linux-gnu-library/4.2'
to install packages into? (yes/No/cancel) yes
--- Please select a CRAN mirror for use in this session ---
(A list of CRAN mirror sites pops up - I selected "USA (IA)(https)")
also installing the dependencies 'interp', 'latticeExtra'

trying URL 'https://mirror.las.iastate.edu/CRAN/src/contrib/interp_1.1-4.tar.gz'
**
* DONE (solar)

The downloaded source packages are in
'/tmp/RtmpdZF0ge/downloaded_packages'
>
```

# Installing packages from CRAN (continued)

```
> library(solaR)
Loading required package: zoo

Attaching package: 'zoo'

The following objects are masked from 'package:base':

    as.Date, as.Date.numeric

Loading required package: lattice
Loading required package: latticeExtra
Time Zone set to UTC.
> find.package("solaR")
[1] "/uufs/chpc.utah.edu/common/home/u0424091/R/x86_64-pc-linux-gnu-
library/4.2/solaR"
> .libPaths()
[1] "/uufs/chpc.utah.edu/common/home/u0424091/R/x86_64-pc-linux-gnu-library/4.2"
[2] "/uufs/chpc.utah.edu/sys/installdir/r8/R/4.2.2/lib64/R/library"
[3] "/uufs/chpc.utah.edu/sys/installdir/r8/R/Libs/4.2.2"
```

# Installing packages from Github

Use the `devtools::install_github()` function, with package name in quotes.

Note that “`lib=`” is specified! Without that the installation of dependencies will fail.

```
$ module load R/4.2.2
$ R

R version 4.2.2 (2022-10-31) -- "Innocent and Trusting"
**
> devtools::install_github("boxuancui/DataExplorer",
lib=c("/uufs/chpc.utah.edu/common/home/u0424091/R/x86_64-pc-linux-gnu-
library/4.2"))
Downloading GitHub repo boxuancui/DataExplorer@HEAD
**
** testing if installed package keeps a record of temporary installation path
* DONE (DataExplorer)
> library(DataExplorer)
```

# Installing packages from Bioconductor

```
> install.packages("BiocManager")
Installing package into
‘/uufs/chpc.utah.edu/sys/installdir/r8/R/4.2.2/lib64/R/library’
(as ‘lib’ is unspecified)
Warning in install.packages("BiocManager") :
  'lib = "/uufs/chpc.utah.edu/sys/installdir/r8/R/4.2.2/lib64/R/library"' is not
writable
Would you like to use a personal library instead? (yes/No/cancel) yes

...

** testing if installed package can be loaded from final location
** testing if installed package keeps a record of temporary installation path
* DONE (BiocManager)

The downloaded source packages are in
‘/tmp/RtmpzCb3wb/downloaded_packages’
>
```

# Installing packages from Bioconductor (continued)

Like `devtools::install_github()`, it is safest to specify the `"lib="` argument.

```
> BiocManager::install("PFAM.db",  
lib=c("/uufs/chpc.utah.edu/common/home/u0424091/R/x86_64-pc-linux-gnu-  
library/4.2"))  
  
**  
** testing if installed package can be loaded from final location  
** testing if installed package keeps a record of temporary installation path  
* DONE (PFAM.db)
```

The downloaded source packages are in  
'/tmp/RtmpzCb3wb/downloaded\_packages'  
>

# Installing packages from source code

- `install.packages`, `BiocManager::install`, and `devtools::install_github` download the package source code, then compile and install it
- If you have the source code URL you can compile and install it like this:

```
$ wget https://bioconductor.org/packages/3.16/bioc/src/contrib/limma_3.54.2.tar.gz  
$ R CMD INSTALL --library=$HOME/R/x86_64-pc-linux-gnu-library/4.2 limma_3.54.2.tar.gz
```

- This method doesn't handle dependencies however

# CHPC's R documentation

- <https://www.chpc.utah.edu/documentation/software/r-language.php>
  - A few things are out of date:
    - We no longer use Intel's compiler icc for R, we use gcc exclusively
    - \$HOME/.R/Makevars file is largely obsolete
    - Setting up a personal library: R version 4.X handles (most) of this automatically
- <https://git.io/CHPC-Intro-to-Parallel-Computing-R>
  - Excellent examples of parallel R code, both single- and multi-node



# anyLib: Install and Load Any Package from CRAN, Bioconductor or Github

- “Made to make your life simpler with packages, by installing and loading a list of packages, whether they are on CRAN, Bioconductor or github. For github, if you do not have the full path, with the maintainer name in it (e.g. "achateigner/topReviGO"), it will be able to load it but not to install it.”
- <https://cran.r-project.org/web/packages/anyLib/index.html>