

# Offline installation on Jura

Installing new software on Jura is complicated because the cluster does not have Internet access. This page covers the installation of R, BioConductor, and Python packages.

## R packages

### For packages in CRAN

Since Jura cluster is not connected to the Internet, it won't be possible to install R packages directly. A local CRAN mirror has been deployed to ease the installation, it can be used as follows:

```
source /dcsrsoft/spack/bin/setup_dcsrsoft
module load gcc r
R
>install.packages(c('dplyr','ggplot2','cluster'), repos='http://mirror.dcsr.unil.ch/cran/')
```

### For packages **not** in CRAN

For packages not available in the local CRAN mirror, you will have to go through the following procedure:

**STEP 1:** download the package on a machine connected to the internet, e.g.:

```
wget http://cnsgenomics.com/software/gsmr/static/gsmr_1.0.9.tar.gz
```

**STEP 2:** transfer the package to Jura using the standard procedure detailed [here](#)

**STEP 3:** log into Jura

**STEP 4:** launch R

```
$ source /dcsrsoft/spack/bin/setup_dcsrsoft
$ module load gcc r
$ R
```

**STEP 5:** install the package with:

```
> install.packages("/path/to/gsmr_1.0.9.tar.gz", repos = NULL, type="source")
```

## For packages with the source on a Git server

For packages provided on a Git server, you will have to first build a package to transfer to Jura before you can proceed with the installation of the package per se. From a machine connected to the internet:

**STEP 1:** clone the Git repository in directory hereinafter referred to as "/path/to"

```
$ git clone https://github.com/jean997/causeSims.git
```

**STEP 2:** launch R

```
$ source /dcsrsoft/spack/bin/setup_dcsrsoft
$ module load gcc r
$ R
```

**STEP 3:** build the R package

```
> require("devtools")
> build("causeSims")
```

which should output something along these lines:

```
> build("causeSims")
✓ checking for file '/path/to/causeSims/DESCRIPTION' ...
- preparing 'causeSims':
✓ checking DESCRIPTION meta-information ...
- checking for LF line-endings in source and make files and shell scripts
- checking for empty or unneeded directories
- building 'causeSims_0.1.0.tar.gz'
  Warning: invalid uid value replaced by that for user 'nobody'

[1] "/path/to/causeSims_0.1.0.tar.gz"
```

Then continue with STEPS 2, 3, 4 & 5 of paragraph "For packages **not** in CRAN" above.

# BioConductor packages

BioConductor is a package manager that enhances R with bio-informatic packages. A local BioConductor mirror has been deployed to ease the installation.

First, you have to define a `~/.Rprofile` file with, at least, the following content:

```
options(  
  BioC_mirror = "http://mirror.dcsr.unil.ch/bioconductor",  
  repos = "http://mirror.dcsr.unil.ch/cran"  
)  
options(  
  BIOCONDUCTOR_ONLINE_VERSION_DIAGNOSIS = FALSE  
)
```

It is very important to have an empty new line at the end of the file!

Then you can launch R:

```
source /dcsrsoft/spack/bin/setup_dcsrsoft  
module load gcc r  
R
```

And install the BioConductor package manager:

```
>  
install.packages("http://mirror.dcsr.unil.ch/cran/src/contrib/Archive/BiocManager/BiocManager_  
1.30.10.tar.gz", repos=NULL, type="source")  
> install.packages("http://mirror.dcsr.unil.ch/bioconductor/BiocVersion_3.12.0.tar.gz",  
repos=NULL, type="source")  
> library(BiocManager)
```

The first step might ask if you want to use a personal library, you can answer yes to both questions.

Finally, you can install the BioConductor packages, for instance `edgeR`:



