

# R on the clusters

R is provided via the [new software environment](#)

## Interactive mode

To load R:

```
module load gcc r
R
# Then you can use R interactively
> ...
```

## Batch mode

While using R in batch mode, you have to use `Rscript` to launch your script. Here is an example of sbatch script, `run_r.sh`:

```
#!/bin/bash

#SBATCH --time 00-00:20:00
#SBATCH --nodes 1
#SBATCH --ntasks 1
#SBATCH --cpus-per-task 1
#SBATCH --mem 4G

module load gcc r

Rscript my_r_script.R
```

Then, just submit the job to Slurm:

```
sbatch run_r.sh
```

## Package installation

A number of core packages are installed centrally - you can see what is available by using the `library()` function. Given the number of packages and multiple versions available other packages should be installed by the user.

Installing R packages is pretty straightforward thanks to [install.packages\(\)](#) function. However, be careful since it might fill your home directory very quickly. For big packages with large amount of dependencies, like `adegenet` for instance, you will probably reach the quota before the end of the installation. Here is a solution to mitigate that problem:

- Remove your current R library (or set up an alternate one as explained in the section [Setting up an alternate personal library](#) below):

```
rm -rf $HOME/R
```

- Create a new library in your scratch directory (obviously modify the path according to your situation):

```
mkdir -p /scratch/wally/FAC/FBM/DEE/my_py/default/jdoe/R
```

- Create a symlink to locate the R library on the scratch dir:

```
cd $HOME  
ln -s /scratch/wally/FAC/FBM/DEE/my_py/default/jdoe/R
```

- Install your R packages

## Warning for Axiom and Wally!!!

When working on Axiom and Wally clusters please be aware that the frontend nodes might have a more recent CPU architecture than that of the compute nodes. This leads to problems when installing R packages that involve compiling code as anything compiled on a newer machine will not work on an older one.

You **should install your R packages on a node in the debug partition** since these nodes have the oldest CPU architecture of the whole infrastructure (which is a way to ensure that it will work everywhere).

You can reserve a node interactively for up to one hour to perform your installation as follows:

```
Sinteractive -p debug -c 4 -m 16G -t 1:00:00
```

Once connected you can launch R as usual and perform the installation.

## Warning for Jura!!!

Please refer to [the page dedicated to offline installation on Jura](#).

# Setting up an alternate personal library

If you want to set up an alternate location where to install R packages, you can proceed as follows:

```
mkdir -p ~/R/my_personal_lib2

# If you already have a ~/.Renvirom file, make a backup
cp -iv ~/.Renvirom ~/.Renvirom_backup

echo 'R_LIBS_USER=~R/my_personal_lib2' > ~/.Renvirom
```

Then relaunch R. Packages will then be installed under `~/R/my_personal_lib2`.

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