

# Installing Monocle3 on bridges

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## First Try

We follow along this page. Note that all the prerequisite packages listed are already installed.

No module loaded. Just open **R** and do `devtools::install_github('cole-trapnell-lab/monocle3')`. This fails because some dependencies (`RhpcBLASctl`) couldn't be installed.

## Second try

We try with reinstalling everything from scratch.

```
R --vanilla
```

```
.libPaths("~/rpack_monocle/")
BiocManager::install(c('BiocGenerics', 'DelayedArray', 'DelayedMatrixStats',
                        'limma', 'S4Vectors', 'SingleCellExperiment',
                        'SummarizedExperiment'))
install.packages("reticulate")
reticulate::py_install("louvain")
devtools::install_github('cole-trapnell-lab/monocle3')
```

## Second try

Drawing on previous experiences, I start with a conda environment!! Let us see if conda is now compatible with newer versions of R...

```
module load anaconda3
conda create -n monocle3_env
source activate monocle3_env
R --version
```

This also fails We then revert to the old idea. Using the output from `zinbWave`, send that to the `scf` cluster and process it there...