Installing Monocle

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First Try

No module loaded. Just open **R** and do *BiocManager::install("monocle")*.

This fails for packages **densityClust** and **DDRTree**.

Second try

First do *module load gcc* then try again. This works for **densityClust** but not **DDRTree**.

Third try

I realized that this gives the same error as when trying to install *clusterExperiment*.

```
* installing *source* package 'DDRTree' ...
** package 'DDRTree' successfully unpacked and MD5 sums checked
** libs
icpc -std=gnu++11 -I"/opt/packages/R/3.5.1-mkl/lib64/R/include"
-DNDEBUG  -I"/pylon5/ib5phhp/diyadas/rpack/3.5/Rcpp/include"
-I"/pylon5/ib5phhp/hectorrb/rpack/RcppEigen/include"
-I"/pylon5/ib5phhp/diyadas/rpack/3.5/BH/include" -I/usr/local/include   -fpic  -O3
-ipo -openmp -xHost -c DDRTree.cpp -o DDRTree.o
icpc: command line error: option '-openmp' is not supported.
Please use the replacement option '-qopenmp'
make: *** [DDRTree.o] Error 1
ERROR: compilation failed for package 'DDRTree'
* removing '/pylon5/ib5phhp/hectorrb/rpack/DDRTree'
```

```
git clone https://github.com/cole-trapnell-lab/DDRTree.git
cp clusterExperiment/src/Makevars DDRTree/src/
R CMD INSTALL DDRTree/
```

That failed. Note that running the block above without line 2 resulted in the same issue.

Installing all Rcpp dependencies

The issue seems to come from the Rcpp instances in Diya's scratch. So i did

```
[hectorrb@login006 ~]$ module list
Currently Loaded Modulefiles:
  1) psc_path/1.1    2) slurm/default   3) intel/19.3      4) xdusage/2.1-1   5) R/3.5.3-mkl
```

```r
> install.packages("Rcpp")
> install.packages("RcppEigen")
> install.packages("BH")
> install.packages("DDRTree")
```

This worked!!!

I can then run

```r
BiocManager::install("monocle")
```

This fails because of some packages (FNN, densityClust, tidyverse, igraph,...) that Diya installed. Reinstalling those packages worked for all but the "Rtsne" package.

I can also install future dependencies

```r
devtools::install_github("cole-trapnell-lab/DDRTree", ref="simple-ppt-like")
devtools::install_github("cole-trapnell-lab/L1-graph")
```

This worked fine.

And

```
pip install --user virtualenv
```

```r
install.packages("reticulate")
library(reticulate)
py_install('umap-learn')
```

Installing Louvain fails.

Using a virtual environment with anaconda

Following the instructions from the help, I did

```
module unload intel
module load anaconda3
conda create -n monocle_env
source activate monocle_env
conda install -c bioconda bioconductor-monocle
conda install -c r r-devtools
conda install -c conda-forge python-louvain
conda install -c conda-forge umap-learn
# source deactivate
```

This works up until installing reticulate. The version of R that is being used is 3.3 but the conda version of reticulate needs 3.4.

Installing reticulate

Following the example in https://stackoverflow.com/questions/34705917/conda-how-to-install-r-packages-that-are-not-available-in-r-essentials