Installing Monocle

Hector Roux de Bézieux

21 May , 2019

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
```

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

This worked!!!

I can then run

```
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

```
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
```

```
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

We install from R, with no dependencies

```
install.packages("reticulate", dependencies=FALSE)
```

This fails with some compiler error.

We thus build a skeleton from scratch.

Installing github R packages

We try to install all dependencies first. Anything from conda-forge fails (it is based on a more advanced version of R).

We then try to do it with a skeleton.

```
conda skeleton cran lpSolveAPI --recursive
conda-build r-lpsolveapi
```

This fails as well with some compiler error (the infamous "unrecognized command line option '-qopenmp'; did you mean '-fopenmp'?").

Working with both clusters

A idea that could work is to use the clusters only to do the zinbwave reduction, and then to tranfer the data to the scf cluster and do there the UMAP reduction and the clustering. Since we only carry around a matrix of #n cells by 30, it will fit into memory on the scf. Moreover, UMAP and clustering should be coded well enough so as to not compute a full distance matrix.

So, we just need to install monocle 2 on bridges.

```
module unload intel
module load anaconda3
conda create -n monocle_env
source activate monocle_env
conda install -c bioconda bioconductor-monocle
conda install -c bioconda bioconductor-biobase
conda install -c bioconda bioconductor-s4vectors
conda install -c bioconda bioconductor-summarizedexperiment
# source deactivate
```