

Amarel tutorial, data club 3/2/2020

Cluster computing resources:

- Register to use Amarel here: <https://oarc.rutgers.edu/access/>
- OARC cluster guide: <https://rutgers-oarc.github.io/training/>
- Notepad++ download for job files: <https://notepad-plus-plus.org/downloads/v7.8.4/>
 - To make sure you are using the appropriate line endings, go to Edit menu, select EOL Conversion" submenu, and then select the "UNIX" option.
- Installing miniconda3: <http://deeplearning.lipingyang.org/2018/12/24/install-miniconda-on-centos-7-redhat-7/>
- Managing environments in Conda: <https://docs.conda.io/projects/conda/en/latest/user-guide/tasks/manage-environments.html#creating-an-environment-with-commands>
- Installing R in conda: <https://anaconda.org/r/r>

Installing miniconda3, R, and R packages

1. Log on to OnDemand: <https://ondemand.hpc.rutgers.edu/pun/sys/dashboard>
2. Click Clusters-> Amarel Cluster Shell Access
3. Log on with your netID password. No text will appear; this is normal.
4. To install miniconda3, copy and paste this into your command line. (to paste, use ctrl+shift+v)

```
wget https://repo.continuum.io/miniconda/Miniconda3-latest-Linux-x86_64.sh
```

Then paste:

```
sh Miniconda3-latest-Linux-x86_64.sh
```

To test that miniconda3 has installed, paste:

```
conda -V
```

This should return the version installed.

5. Next we will create an environment where we will install R and the packages we need. Later, we will need to activate this environment in our job file. I am naming this environment `renv`.

```
conda create --name env
```

6. Activate this environment. For future reference, if you want to leave this environment, and go back to your home directory, type 'conda deactivate'

```
conda activate env
```

7. Next we're going to install R. Whenever you want to install something in an environment with miniconda, it's useful to google "conda install 'name of thing to install' ". Often, an early result will give you the command you need.

To install R, paste:

```
conda install -c r r
```

Stick around and enter ‘Y’ when prompted.

8. At this point we are done using the shell access. Go back to the OnDemand GUI.

Writing a job file

I have provided a simple R script (“test.script.R”), input data (“input.data.csv”), and a job file (“test.script.sh”). See the job file for details of what each of the commands means. In short, the job file tells Amarel where to find the script, what language it’s in, how many resources the job needs, and which partition you want to use.

Make sure to provide a file path to your script that matches where you have placed (or will place) the job in your home directory.

Submitting a job

1. Using the File Explorer, upload the input data, R script, and job file to a subdirectory of your home directory. for example, home/netid/data.club Make sure this matches the file path you’ve listed on your job file.
2. Click ‘Jobs,’ then ‘Job composer’
3. Click “New Job,” and “From specified path”
4. Under Source path, type the file path to the subdirectory where you have placed the job. (e.g. home/netid/data.club)
5. Under Name, give a short name for the job. This should probably match the name you gave in the job file.
6. Under script name, give the name of the job file. In our example, this is test.script.sh
7. Under Cluster, select Amarel
8. Click Save
9. Click the green submit button.