Putting all pieces together - an R example

<table>
<thead>
<tr>
<th>Quick Links</th>
</tr>
</thead>
<tbody>
<tr>
<td>HPC Home</td>
</tr>
<tr>
<td>Getting an account</td>
</tr>
<tr>
<td>Getting started on Prince</td>
</tr>
<tr>
<td>Prince How-to Articles</td>
</tr>
<tr>
<td>Logging in Windows</td>
</tr>
<tr>
<td>Mac / Linux</td>
</tr>
<tr>
<td>Clusters and Storage</td>
</tr>
<tr>
<td>Prince (HPC)</td>
</tr>
<tr>
<td>Dumbo (Hadoop)</td>
</tr>
<tr>
<td>Brooklyn (OpenStack)</td>
</tr>
<tr>
<td>Dalmata (NYU Abu Dhabi)</td>
</tr>
</tbody>
</table>
Transferri
ng data
to/from
the
clusters

Transferri
ng data
to/from
Prince
cluster
using
Globus

Submittin
g jobs
with
sbatch

Available
software

Licensed
Software
Available
on the
HPC
Cluster

Building
Software

Slurm
Tutorial

Tutorials

FAQs

Scratch
Area
Cleanup

Programming for
Biologist

Acknowle
dge
Statement

Research
Gallery

HPC
People
HPC Policies

(Tip: click "<<" at bottom left to close Confluence sidebar)

Running jobs on the Prince Cluster

Accessing the Prince Cluster

From Windows workstation
From Mac workstation

Software and Environment Module

Job script and resource request

Introduction to job scheduling

Submitting jobs with sbatch

Requesting resources

Using computing nodes interactively

Monitoring batch jobs

Monitoring batch jobs - squeue
Pulling it all together - Preparing, submitting and monitoring a job on Prince

In this section we will prepare, submit and monitor a small R job. Our test case comes from the NYU Data Services “Introduction to R” tutorial

Exercise
Start a terminal session on Prince and replicate this example in it.

Choose your own example
After - or instead of - following this example through, prepare and submit a run of something genuinely relevant to your research. This way, if you are doing this tutorial in a classroom, the presenter will be available should you have questions or strike difficulties

We're using R, so first we'll look for available modules. On Prince:

```
$ module avail r
------------------------------------------------- /share/apps/modulefiles
-------------------------------------------------
 gstreamer/intel/1.10.2  mothur/intel/1.35.1  r/intel/3.3.2
```

There's a few modules starting with r, and a couple of versions of R. We'll use the latest version, 3.1.2.

```
$ module purge
$ module list
No Modulefiles Currently Loaded.
$ module load r/intel/3.3.2
```

Take a look at what it did:
$ module list
Currently Loaded Modulefiles:
  1) jdk/1.8.0_111  2) intel/17.0.1  3) openmpi/intel/2.0.1  4) r/intel/3.3.2

... clearly, R uses a lot of other packages. The modulefile has looked after loading the correct ones.

$ module show r/intel/3.3.2
------------------------------------------------------------------------------------------------------------------------
-----
/share/apps/modulefiles/r/intel/3.3.2.lua:
------------------------------------------------------------------------------------------------------------------------
-----
whatis("R: a language and environment for statistical computing and graphics")
whatis("Name: r version: 3.3.2 compilers: intel")
load("intel/17.0.1")
load("jdk/1.8.0_111")
load("openmpi/intel/2.0.1")
prepend_path("MANPATH","/share/apps/r/3.3.2/intel/share/man")
prepend_path("PATH","/share/apps/r/3.3.2/intel/bin")
prepend_path("LD_LIBRARY_PATH","/share/apps/r/3.3.2/intel/lib64/R/lib")
prepend_path("PKG_CONFIG_PATH","/share/apps/r/3.3.2/intel/lib64/pkgconfig")
setenv("R_ROOT","/share/apps/r/3.3.2/intel")
setenv("R_INC","/share/apps/r/3.3.2/intel/lib64/R/include")
setenv("R_LIB","/share/apps/r/3.3.2/intel/lib64/R/lib")
family("R")

For our example, we'll get some code and data from /share/apps/examples:

    Hint: there are usage examples for a few common packages here

    $ mkdir /beegfs/$USER/R-example
    $ cd !$
    $ cp /share/apps/examples/r/basic/* .

Take a look at the job script:
There are a few steps we can try here:

1. Start an interactive batch session, and run the example.R script interactively
2. Close the interactive session, and submit the batch script as a job:

```
$ sbatch my_R_job.s
```

You'll get a job id returned.

Is it running yet?

```
$ squeue -u $USER
```

You could watch the output in the run directory:

```
$ ls -l ${SCRATCH}/R-example
```

Finally, when the job finishes, you should see a .out file in the directory you submitted from.

**Exercise**

Experiment with sbatch options for the job name, output and error file merging and location, resource limits.