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Basic R jobs

Multiple R versions exist in HPC environment. To check what are available, on Prince:

```
$ module avail r

--------------------------------------------- /share/apps/modules/modulefiles
---------------------------------------------
r/intel/3.0.3                       ray/openmpi/intel/20160114
reprozip/intel/1.0.3                    rpy2/intel/2.5.6
r/intel/3.1.2                       rdkit/intel/201409.2                   requests/2.7.0
rsem/intel/1.2.15                        rdp_classifier/2.11
ribopicker/0.4.3                      rseqc/intel/2.3.9
r/intel/3.2.2                       recon/intel/1.08                   rmblast/2.2.28
rstudio/0.98.1028                        rendertoolbox3/2.1-18
randfold/intel/2.0                   requests/2.7.0
rtdax/0.984                                rose/20151118
raxml/intel/7.3.0                    repeat_masker/4.0.5
rosetta/intel/54167                      ruby/gnu/2.1.1
raxml/intel/8.0.23                   repeatmodeler/1.0.8
rosetta/openmpi/intel/2014.35.57232         repeatscout/intel/1.0.5
raxml/intel/8.2.5          repeatscout/intel/1.0.5
rosetta/openmpi/intel/54167
```

Suppose we want to use 3.3.2, run these commands:
We first clean up the environment by doing `module purge`. Then we load the R version selected, check what are available in current environment. We can see that R 3.3.2 is indeed loaded along with its dependency modules. Let's try this basic R example. We name it "example.R":

```r
df <- data.frame(x=c(1,2,3,1), y=c(7,19,2,2))
df
indices <- order(df$x)
order(df$x)
df[indices,]
df[rev(order(df$y)),]
```

Below is the screen scene while running it on Prince:
What is shown above is a simple demo case on login nodes. For real interactive analysis scenario, users are encouraged to run on compute nodes using the 'srun' command to request dedicated resources, e.g.:

```bash
$ srun --x11 --nodes=1 --ntasks-per-node=4 --mem=4000 -t2:00:00 --pty /bin/bash
$ xterm
$ module load r/intel/3.3.2
$ R
```

Besides running our analysis interactively, long running and big data crunching jobs ought to be submitted to the batch system slurm. The "example.R" can be submitted to slurm to run in batch mode.

Copy example files to your newly created directory.
Below is how the example looks like:

```r
$ cat example.R
df <- data.frame(x=c(1,2,3,1), y=c(7,19,2,2))
df
indices <- order(df$x)
order(df$x)
df[indices,]
df[rev(order(df$y)),]
```

Then create a sbatch job script as:

```bash
$ cat run-R.sbatch
#!/bin/bash
#
#SBATCH --job-name=RTest
#SBATCH --nodes=1
#SBATCH --tasks-per-node=1
#SBATCH --mem=2GB
#SBATCH --time=01:00:00
module purge
module load r/intel/3.3.2

cd /scratch/$USER/example
R --no-save -q -f example.R > example.out 2>&1
```

Once the sbatch script file is ready, it can be submitted to the job scheduler using sbatch. After successful completion of job, verify output log file for detail output information.