Running R jobs

R is installed on Prince. It is compiled with intel compiler. R can be run in interactive session or the batch mode. To check what versions are available:

```bash
$ module avail r/intel
```

```
+------------------------------------------ /share/apps/modulefiles
+---------------------------------------------------------------
gstreamer/intel/1.10.2   mothur/intel/1.35.1   r/intel/3.3.2
```

It is shown that R 3.3.2 exists presently as of Jan 12, 2017. You can check what packages are installed with this R installation. If a package you need does not show up in a check as below (please do run it as installation updating is a constantly ongoing process), please contact HPC support.
$ module purge
$ module list
No modules loaded
$ module load r/intel/3.3.2
$ module list
Currently Loaded Modules:
1) intel/17.0.1  2) jdk/1.8.0_111  3) r/intel/3.3.2

$ R
R version 3.3.2 (2016-10-31) -- "Sincere Pumpkin Patch"
Copyright (C) 2016 The R Foundation for Statistical Computing
Platform: x86_64-unknown-linux-gnu (64-bit)
[......]

> installed.packages()

Package         LibPath
AnnotationDbi  "AnnotationDbi"  "/share/apps/r/3.3.2/intel/lib64/R/library"
base           "base"          "/share/apps/r/3.3.2/intel/lib64/R/library"
Biobase        "Biobase"       "/share/apps/r/3.3.2/intel/lib64/R/library"
BiocGenerics   "BiocGenerics"  "/share/apps/r/3.3.2/intel/lib64/R/library"
BiocInstaller  "BiocInstaller" "/share/apps/r/3.3.2/intel/lib64/R/library"
boot           "boot"          "/share/apps/r/3.3.2/intel/lib64/R/library"
class          "class"         "/share/apps/r/3.3.2/intel/lib64/R/library"
codetools      "codetools"     "/share/apps/r/3.3.2/intel/lib64/R/library"
cluster        "cluster"      "/share/apps/r/3.3.2/intel/lib64/R/library"
compiler       "compiler"     "/share/apps/r/3.3.2/intel/lib64/R/library"
datasets       "datasets"     "/share/apps/r/3.3.2/intel/lib64/R/library"
DBI            "DBI"          "/share/apps/r/3.3.2/intel/lib64/R/library"
......

Long running and big data crunching jobs ought to be submitted as batch, so that they will run in the background and Slurm will drive their executions. Below are a R script "example.R", and a job script which can be used with sbatch command to send a job to Slurm:

```bash
$ 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)),]
$ 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/examples
## srun R CMD BATCH example.R example.out
R --no-save -q -f example.R > example.out 2>&1
exit
```

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