## R on HPC

**NUSHIPC** 

#### Module avail R

GNU C++

R-3.0.2

R-3.1.2

R-3.2.5

R-3.5.0

R-3.6.0

**Intel Optimized** 

R-3.2.3\_intel

R-3.4.3\_intel

### Install R packages

Load R module on the login node

\$ module load R -3.5.0

Launch R

\$ R

Install packages

\$ install.packages("dplyr")

Choose 0-Cloud [https] mirror for CRAN

# Custom r environment

Use miniconda to create your own R conda environment

- 1) Load miniconda environment in login node
- \$ module load miniconda
  - 1) Using conda create a conda environment
- \$ conda create -n myenv -c conda -forge r tidyverse
  - 1) Activate conda env and use R
- \$ source activate myenv
- \$ R

#### R serial job script

```
#!/bin/bash
#PBS-P Project Name of Job
#PBS-j oe
#PBS-N Job Name
#PBS -q serial
#PBS-I select=1:ncpus=1:mem=10GB
source /etc/profile.d/rec_modules.sh
module load R -3.2.5
Rscript mycode.R
```

```
#!/bin/bash
#PBS -P Project Name of Job
#PBS -j oe
#PBS -N Job Name
#PBS -q serial
\#PBS -1 select=1 :ncpus=1 :mem=10GB
source /etc/profile.d/rec modules.sh
module load miniconda
Source activate myenv
Rscript mycode.R
```

## Run R in parallel

Mostly can run multiprocessing in single node

Multi node parallelization require MPI

parallel

Rmpi

foreach

pdbMPI

doSNOW

https://bookdown.org/rdpeng/rprogdatascience/parallel

-computation.html

#### R-Parallel job script

```
#!/bin/bash
#PBS-P Project Name of Job
#PBS-j oe
#PBS-N Job Name
#PBS -q parallel24
#PBS-I select=1:ncpus=24:mem=50GB
source /etc/profile.d/rec modules.sh
module load R -3.2.5
Rscript myparallelcode.R
```

```
#!/bin/bash
#PBS -P Project Name of Job
#PBS -j oe
#PBS -N Job Name
#PBS -q parallel24
\#PBS - 1 \text{ select} = 1 : \text{ncpus} = 24 : \text{mem} = 50 \text{ GB}
source /etc/profile.d/rec modules.sh
module load miniconda
Source activate myenv
Rscript myparallelcode.R
```

#### Additional help

nTouch

https://ntouch.nus.edu.sg/

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