Would recommend going through the demo found on this page first:

**https://docs.ycrc.yale.edu/clusters-at-yale/**

1. Go to cluster environment
2. Enter:

salloc               # allocate a compute node  
module load R/4.0.5-foss-2020b # initialize R used  
R                    # start R

* 1. It will likely prompt you to pick a location, I picked #77 in Ohio, since it’s the closest
  2. Need to create a personal R library using the interactive cluster (should pop-up when you load R)

1. Load all of the libraries needed to run both base\_model\_cluster.R and parallel\_processing.R

> install.packages('MCMCpack')

> install.packages('stats')

> install.packages('CARBayes')

> install.packages('rgdal')

> install.packages('RColorBrewer')

> install.packages('ggplot2')

> install.packages('rgeos')

> install.packages('maptools')

> install.packages('spdep')

> install.packages('ggmap')

> install.packages('sf')

> install.packages('dplyr')

> install.packages('tidyverse')

> install.packages('CARBayesST')

> install.packages('TSDT')

> install.packages('lubridate')

> install.packages('future')

> install.packages('parallel')

* 1. Don’t worry if warnings pop-up

1. Upload all necessary files to your project folder:
   1. parallel\_processing.R (needs to be a .R)
   2. base\_model\_cluster.R
   3. neighb.mat\_2.RDS
   4. base\_model\_final.RDS
2. Create a command file (+ New File button, I have also saved it)

#!/bin/bash

#SBATCH --time=20:00:00 # 20 hours, can change

#SBATCH --mail-type=ALL # get updates emailed

#SBATCH --mail-user=elisabeth.nelson@yale.edu

#SBATCH --cpus-per-task=20 # number of cores (max number is 200)

#SBATCH --mem=181G # max memory

module load R/4.0.5-foss-2020b

Rscript parallel\_processing.R

1. Run the command script:
   1. Go to the cluster environment

[en353@farnam2 ~]$ cd project

[en353@farnam2 project]$ sbatch base\_model.sh

[en353@farnam2 project]$ exit

* 1. To see project updates can use the command

[en353@farnam2 project]$ squeue --me