Contents

Quick Start

1. Download and install "**Bitvise SSH Client**" from here.

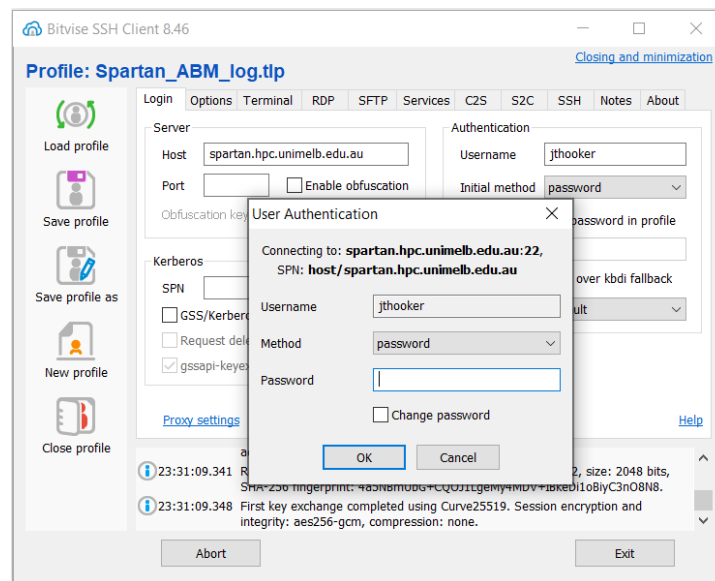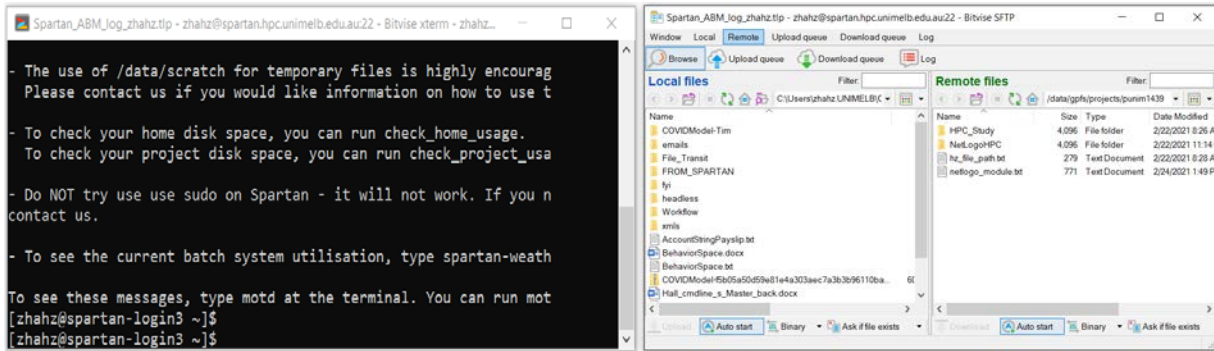2. Launch "**Bitvise SSH Client**", click [**Load profile**] on the left, and select "Spartan_ABM_log.tlp" (see attachment).
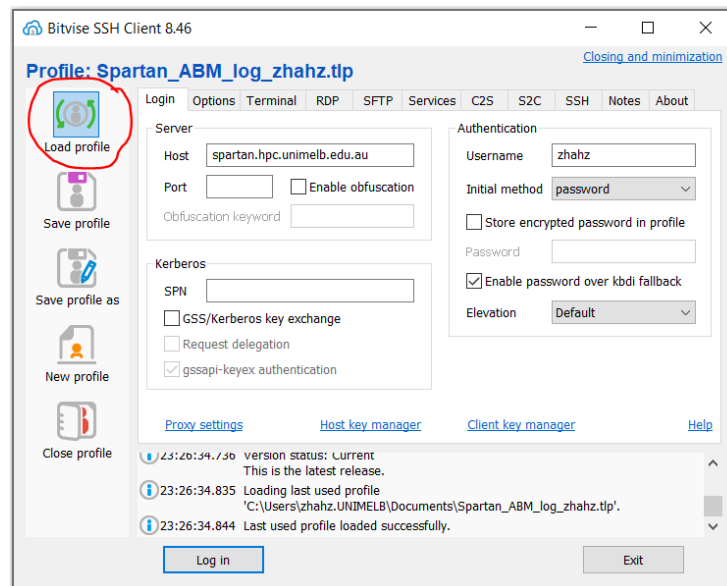
3. Click [**Log in**] button at the bottom, type your password for spartan, click [**OK**] to login.

This should open a command line window and a SFTP window

4. On command line, run
   cd /data/gpfs/projects/punim1439/workflow/Test
   Then run
   bash create_parallel_xmls.sh
   Then run
   sbatch jobarray_8core_8thread_snowy_test.slurm

   You will receive an email when the computation ends. Output csv files will be in folder /data/gpfs/projects/punim1439/workflow/Test/jobarray_8core_8thread_snowy.

Note: To paste cd /data/gpfs/projects/punim1439/workflow/Test to command line, copy the text and **Right Click** your mouse in command line to paste this text.

Slow Start

1. Install SSH Client on laptop

a. Install an SSH client such as PuTTY or Bitvise.
In this example, we installed "Bitvise SSH Client".

b. Set "Bitvise SSH Client"

Tab **[Login]**: Set Host as spartan.hpc.unimelb.edu.au, Port as 22 or leave empty, Username as your username, Initial method as password, Store encrypted password in profile as ticked.

Tab **[Options]**: tick Open Terminal, tick Open SFTP.
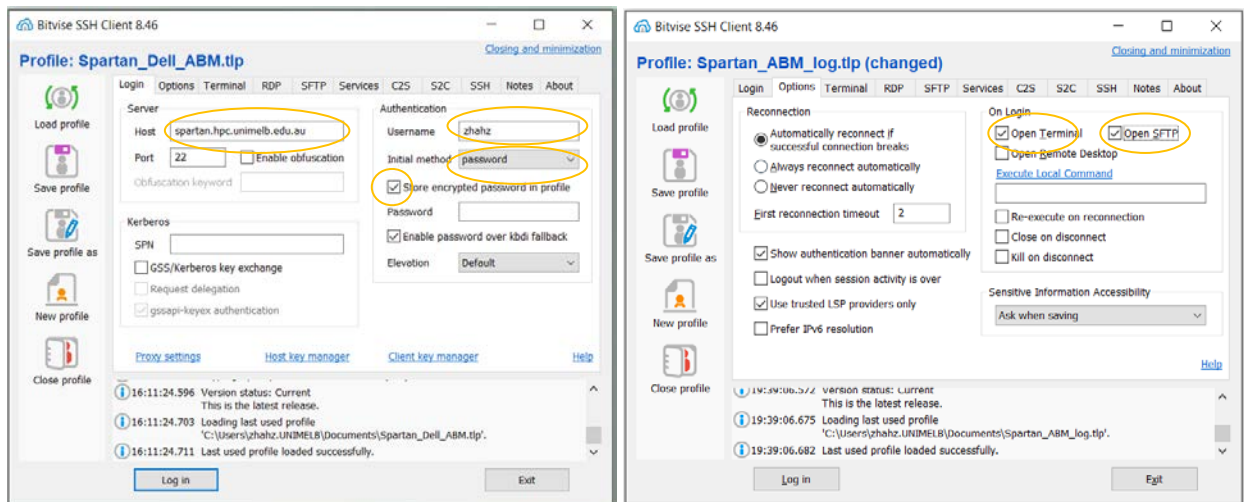
Tab **[SFTP]**: Set Remote and Download Settings - Initial directory as /data/gpfs/projects/punim1439, leave Initial directory for Local and Upload Settings as empty or your preferred folder on your local computer.
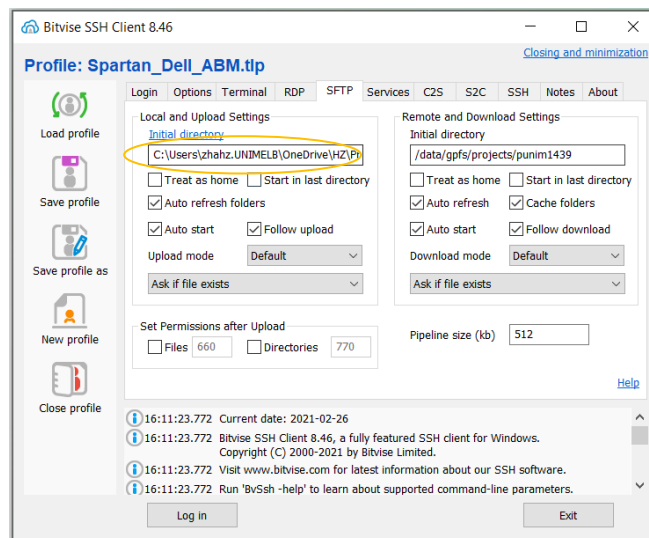
c. Save profile

Click [**Save profile**] on the left, so next time you can [**Load profile**] and select the saved profile to load all these settings.

d. Log in Spartan

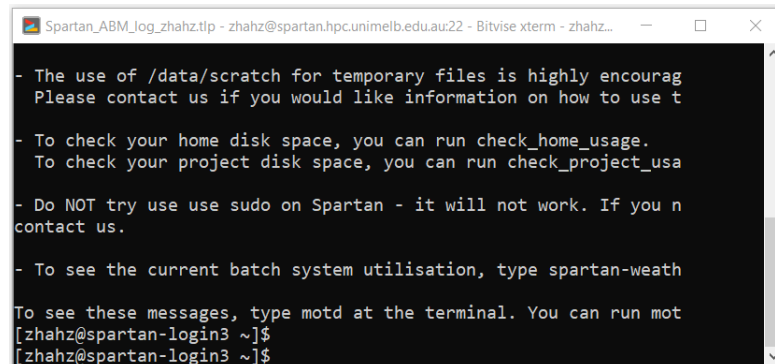Click [**Log in**] button at the bottom, type your password for spartan, which can be different from your staff account password, click [**OK**] to login. This should open a command line window and a SFTP window.

The command line is where you type and run your scripts.
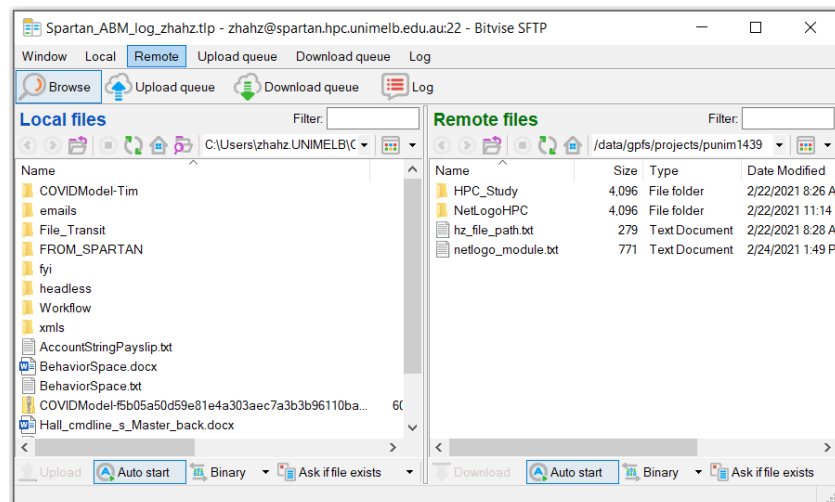
The SFTP is like the explorer in Windows, where you can create/copy/delete files and folders. You can upload a file to Spartan by dragging a file from left to right, and download a file to your laptop by dragging a file from right to left.

2. Install Netlogo on Spartan

In this example, we install NetLogo in this folder /data/gpfs/projects/punim1439/workflow. In SFTP window, right click and Create Folder workflow.

Then, in command line,

a. Run
   cd /data/gpfs/projects/punim1439/workflow

to change current directory to workflow.

b. Run
   wget https://ccl.northwestern.edu/netlogo/6.2.0/NetLogo-6.2.0-64.tgz

to download NetLogo installation file to current directory.

c. Run
   tar -xzf NetLogo-6.2.0-64.tgz

to install NetLogo to current directory. Done.

Note: To paste cd /data/gpfs/projects/punim1439/workflow/Test to command line, copy this text and **Right Click** your mouse in command line to paste this text.

When the NetLogo installation file is downloaded, it may not show in the SFTP window immediately. Click **Refresh**, and the new file will show.
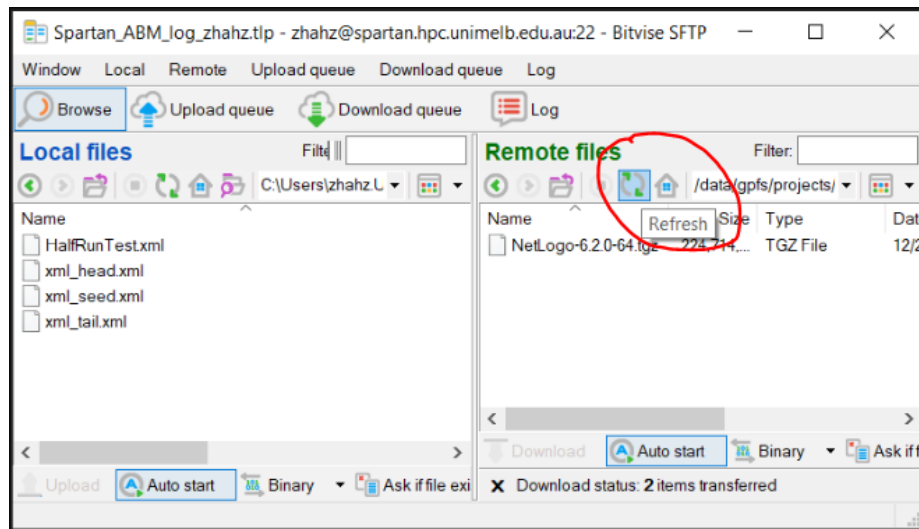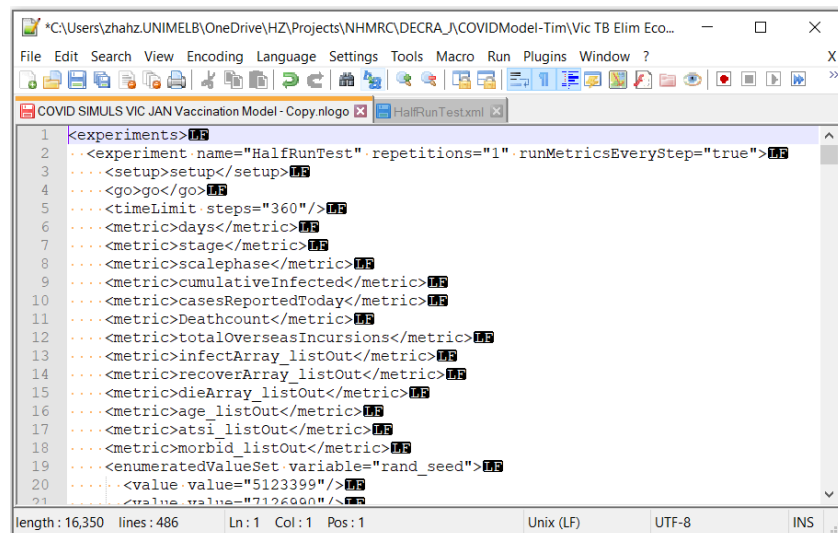
3. Prepare Netlogo model and XML files

a. NetLogo model file

- Download the desired NetLogo model "FILENAME.nlogo" to your local computer.
- Open the file and add a new Global variable called "repetitions".
- In the setup procedure of the Netlogo file, set repetitions to 1 i.e., <set repetitions 1>
- Save and close the file
- Copy this NetLogo model from your computer to the workflow folder on Spartan (using SFTP window).
- Copy rngs folder or any other Netlogo dependencies to the same directory as where "FILENAME.nlogo" is, because this model requires rng extension which is not a default extension of NetLogo software.

b. XML file

- Make a copy of "FILENAME.nlogo" file.
- Open it using notepad or notepad++.
- Delete text and leave only text between <experiments> and </experiments>.
- You can see more than one experiment settings starting with "<experiment name=…" and ending with "</experiment>". Delete all other experiment settings and leave only HalfRunTest.

- Add the following two lines to the front, and save this file as HalfRunTest.xml

<?xml version="1.0" encoding="UTF-8"?>

<!DOCTYPE experiments SYSTEM "behaviorspace.dtd">

- HalfRunTest.xml is the experiment setting of 38400 runs, which can be split to 100 files by the first variable "repetitions", which share the same head and tail, but with a different value of "repetitions".
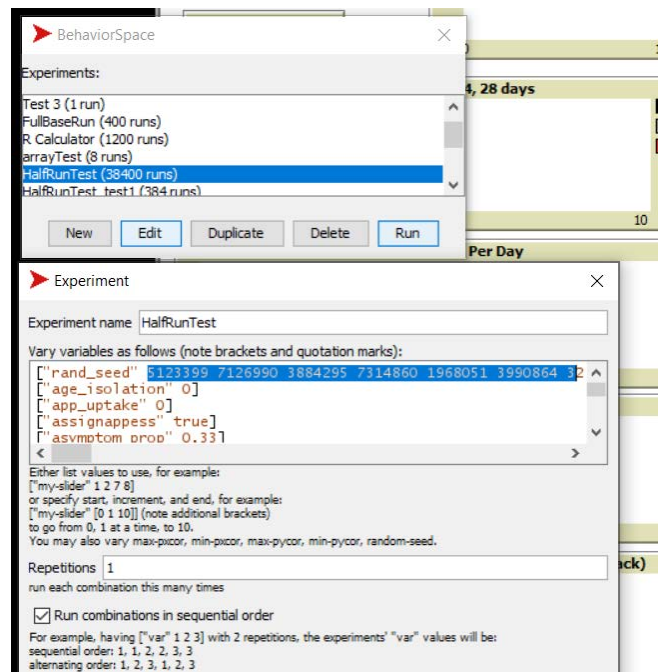
- Split HalfRunTest.xml to three files: xml_head.xml, xml_tail.xml, xml_seed.xml, where xml_seed.xml has 100 lines, each line with a different value of "repetitions" like this
  <value value="3884295"/>

4. Prepare Spartan scripts

a. Create folder Test, and copy the following files to this folder.

xml_head.xml

xml_tail.xml

xml_seed.xml
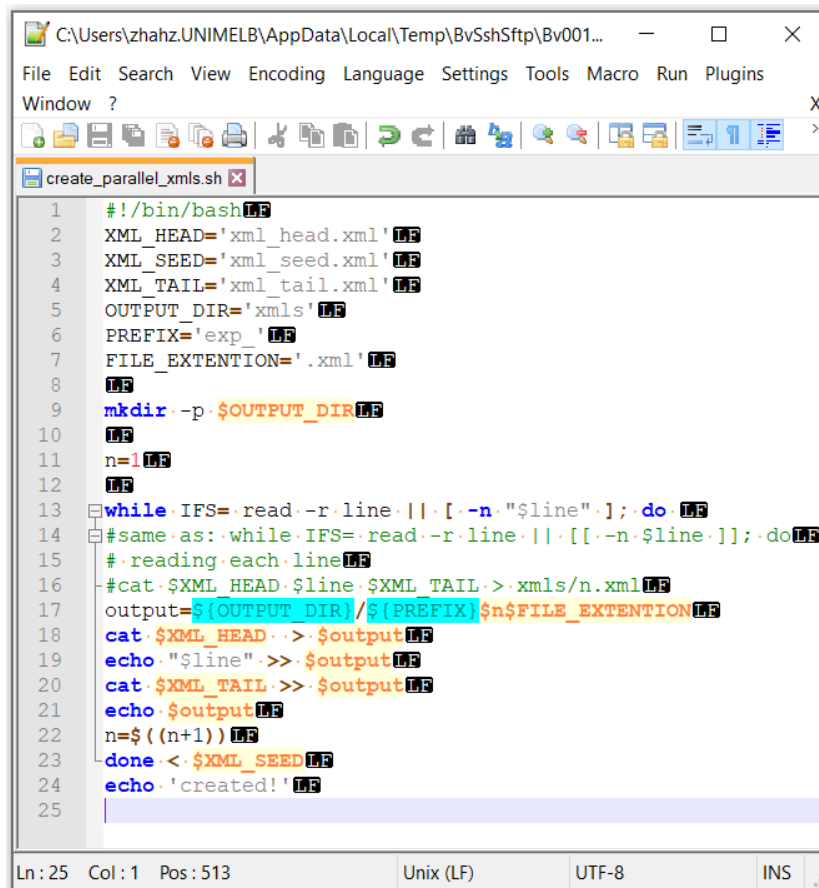
create_parallel_xmls.sh

jobarray_8core_8thread_snowy_test.slurm

b. Open "create_parallel_xmls.sh" with notepad or notepad++.

Change name of files or output directory name if required.

This script will read the three xml files, and create 100 xml files in folder xmls, with output file names exp_1.xml, exp_2.xml, …, exp_100.xml.

c. Open "jobarray_8core_8thread_snowy_test.slurm" with notepad or notepad++.

Change Spartan settings, input and/or output file and/or directory names if required.

```
jobarray_8core_8thread_snowy_test.slurm

1   #!/bin/bash
2   #SBATCH --nodes=1
3   #SBATCH --partition snowy
4   #SBATCH --qos=normal
5   #SBATCH --time 2:00:00
6   #SBATCH --cpus-per-task=8
7   #SBATCH --job-name="netlogo-test-snowy"
8   #SBATCH --mail-user=haifeng.zhao@unimelb.edu.au
9   #SBATCH --mail-type=END
10  #SBATCH --array=1-100
11
12  module load java
13  #module load netlogo/6.2.0-64
14
15  NETLOGO_SH='/data/gpfs/projects/punim1439/workflow/NetLogo·
    6.2.0/netlogo-headless-10g.sh'
16  NETLOGO_MODEL='/data/gpfs/projects/punim1439/workflow/COVIDModel-Tim/Vic·TB·
    Elim·Economic·Models/VIC·JAN/COVID·SIMULS·VIC·JAN·Vaccination·Model.nlogo'
17  BASE_FOLDER='/data/gpfs/projects/punim1439/workflow/Test'
18  OUTPUT_FOLDER="jobarray_8core_8thread_snowy"
19  EXPERIMENT="xmls/exp_${SLURM_ARRAY_TASK_ID}.xml"
20  TABLE_SUFFIX="_table"
21  SPREADSHEET_SUFFIX="_spreadsheet"
22  OUTPUT_SUFFIX="_test"
23
24  OUTPUT_TABLE=${OUTPUT_FOLDER}/
    "${SLURM_ARRAY_TASK_ID}${TABLE_SUFFIX}${OUTPUT_SUFFIX}_${SLURM_ARRAY_TASK_ID}.
    csv"
25  OUTPUT_SPREADSHEET=${OUTPUT_FOLDER}/
    "${SLURM_ARRAY_TASK_ID}${SPREADSHEET_SUFFIX}${OUTPUT_SUFFIX}_${SLURM_ARRAY_TAS
    K_ID}.csv"
26  mkdir -p ${BASE_FOLDER}/$OUTPUT_FOLDER
27  cd $BASE_FOLDER
28  echo $OUTPUT_FOLDER
29  date '+%A·%W·%Y·%X'
30
31  "$NETLOGO_SH" \
32    --model "$NETLOGO_MODEL" \
33    --setup-file "$EXPERIMENT" \
34    --table "$OUTPUT_TABLE" \
35    --spreadsheet "$OUTPUT_SPREADSHEET" \
36    --threads 8
37
38  date '+%A·%W·%Y·%X'

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```

- This script will read the three xml files, and create 100 xml files in folder xmls, with file names exp_1.xml, exp_2.xml, …, exp_100.xml.
- #SBATCH are script directive for Spartan. This script creates a job array of 100 jobs. Each job requires 1 computer node and 8 cpu cores on snowy cluster for a maximum wall time of 2 hours. When all jobs are ended, an email notification will be sent to –mail-user.
- NETLOGO_SH is about file path of NetLogo software.
- NETLOGO_MODEL is file path of "FILENAME.nlogo"
- BASE_FOLDER is current directory of "jobarray_8core_8thread_snowy_test.slurm", and is the upper directory of xmls.
- OUTPUT_FOLDER, TABLE_SUFFIX, SPREADSHEET_SUFFIX, OUTPUT_SUFFIX specify how you want to name output folder and filenames.

5. Submit jobs on Spartan

On command line,

    a. Run
`cd /data/gpfs/projects/punim1439/workflow/Test`

to change current directory to Test folder.

    b. Run
`bash create_parallel_xmls.sh`

to create xmls folder and 100 xml files.

    c. Run
`sbatch jobarray_8core_8thread_snowy_test.slurm`

to submit 100 jobs to Spartan.

You will receive an email when the computation ends. Output csv files will be in folder "/data/gpfs/projects/punim1439/workflow/Test/jobarray_8core_8thread_snowy".

6. Check job status

On command line,

    Run
`showq -u`

to show current jobs.

7. Other Notes

- On command line, press Up Arrow key in keyboard to load previous command.

- Put file or directory path in '' or "" if filename includes space, for example
`cd "/data/gpfs/projects/punim1439/workflow/NetLogo 6.2.0"`

- In this example, slurm-*.out should be less than 1000 byte, otherwise it may have error, open this file and check.
To cancel a job, run
`scancel 24311976`
replace 24311976 with your job id, which can be found from "showq -u", or from the filename of "slurm-*.out"

Remote files

/data/gpfs/projects/punim1439/work

Name
- jobarray_8core_8thread_qos_phy
- jobarray_8core_8thread_snowy
- xmls
- slurm-24311976_1.out
- slurm-24311976_10.out
- slurm-24311976_11.out
- slurm-24311976_12.out
- slurm-24311976_13.out
- slurm-24311976_14.out
- slurm-24311976_15.out
- slurm-24311976_16.out
- slurm-24311976_17.out
- slurm-24311976_18.out
- slurm-24311976_19.out
- slurm-24311976_2.out
- slurm-24311976_20.out
- slurm-24311976_21.out
- slurm-24311976_22.out
- slurm-24311976_3.out
- slurm-24311976_4.out
- slurm-24311976_5.out
- slurm-24311976_6.out
- slurm-24311976_7.out
- slurm-24311976_8.out
- slurm-24311976_9.out

- Run
  squeue -p snowy
  to see all jobs on snowy partition

- Run
  spartan-weather
  to see usage of all partitions

- Ctrl+C to clear this command line.

- Run
  Clear
  to clear screen.

- Run
  Exit
  to quite command line.