### **Get Started**

```
Summary
Set Environment
Install SSH Client on Your PC
Download NetLogo to HPC
Run Experiment
Set Model BahaviorSpace
Revise and Run create_xmls.sh
Revise and Run submit_jobarray.slurm
Merge CSV Results
Other Notes
Cheat Sheet
```

# **Get Started**

# Summary

The main idea is to run NetLogo's <u>BehavorSpace</u> in <u>"headless" mode</u>. Experiments in BehaviorSpace is split into a number of separate simulations, each of which is submitted to HPC as a separate job and run in parallel.

Four steps are required to run NetLogo models on HPC:

- 1. Install an <u>SSH</u> client to connect HPC (For Mac OS users, this is not required).
- 2. Download NetLogo software and unzip it to your project directory on HPC.
- 3. Add an experiment in the BahaviorSpace of your NetLogo model.
- 4. Make a copy of the templates in this repository, revise and run your model.

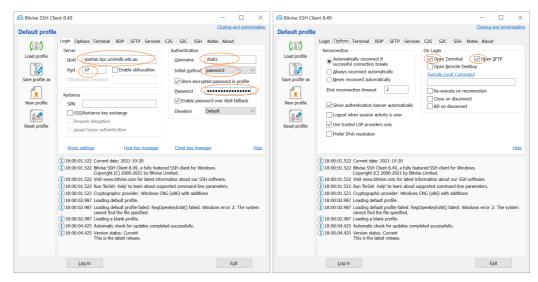
Steps 1 and 2 are to set up work environment, and are only need to be done once.

# **Set Environment**

# Install SSH Client on Your PC

This part is only required for Windows users. Mac (OS X) already has an SSH client built-in, so Mac users can skip this step.

- 1. Install an SSH client such as <u>PuTTY</u>, <u>Bitvise</u>, or <u>MobaXTerm</u>. Here we use <u>Bitvise SSH Client</u> as an example.
- 2. Set up Bitvise SSH client
  - Tab [Login]: Set Host as spartan.hpc.unimelb.edu.au (change here to use the host by your institute), Port as 22, Username as your username, Initial method as password, Password as your password.
  - Tab [Options]: Tick Open Terminal and Open SFTP.



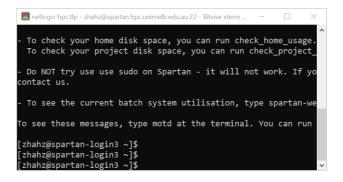
### 3. Save profile

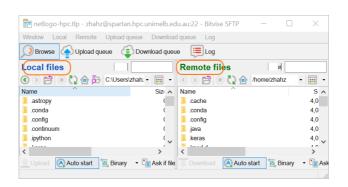
Click [Save profile] on the left panel, so that next time you do not need to type all these settings.

### 4. Log in Spartan

Click [**Log in**] button at the bottom, type your password and click [**OK**] to login. This should open a command prompt window and a SFTP window.

The command prompt is where you type and run your scripts. The SFTP window provides a graphical user interface where you can create/copy/delete files and folders, upload files to Spartan by dragging a file from left to right, and download files to your laptop by dragging files from right to left.





# **Download NetLogo to HPC**

In this example, we download NetLogo to this folder

/data/gpfs/projects/punim1439/workflow/netlogo\_hpc. In SFTP window, right click mouse and Create Folder netlogo\_hpc.

Then, in command line,

1. Run

```
cd /data/gpfs/projects/punim1439/workflow/netlogo_hpc
```

to change current directory to /data/gpfs/projects/punim1439/workflow/netlogo\_hpc.

2. Run

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

to download NetLogo installation file to current directory.

3. Run

```
tar -xzf NetLogo-6.2.0-64.tgz
```

to install (unzip) NetLogo to current directory.

Click **Refresh**, and you should be able to see the NetLogo 6.2.0 folder.



## Tips:

- Copy and paste in command prompt: **Right Click** mouse (§) in command prompt to paste content from clipboard.
- Press up arrow key 1 and down arrow key 1 in keyboard to recall command history.

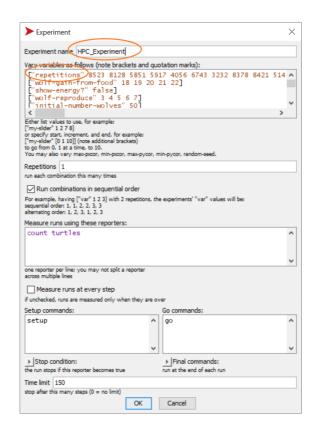
# **Run Experiment**

# **Set Model BahaviorSpace**

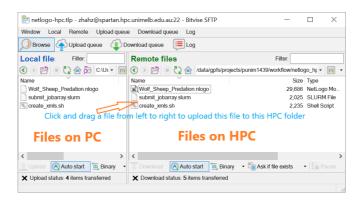
1. We used a wolf\_sheep\_predation.nlogo model as an example.

This model is adjusted on top of a NetLogo sample model NetLogo

6.2.0/app/models/Sample Models/Biology/Wolf Sheep Predation.nlogo. We created an HPC\_Experiment in the BahaviorSpace, added a global variable repetitions with 100 values, and removed user-message "The sheep have inherited the earth".



2. Upload wolf\_Sheep\_Predation.nlogo, create\_xmls.sh and submit\_jobarray.slurm to HPC folder.



### Tips:

If your model is on GitHub, clone the repo (for example https://github.com/JTHooker/COVIDModel) directly to HPC using:

git clone https://github.com/JTHooker/COVIDModel

# Revise and Run create\_xmls.sh

- 1. Edit create\_xmls.sh (using text editor notepad++, notepad, etc)
  - BEHAVIORSPACE\_NAME= 'HPC\_Experiment'
  - NETLOGO\_MODEL='/data/gpfs/projects/punim1439/workflow/netlogo\_hpc/wolf\_S heep\_Predation/wolf\_Sheep\_Predation.nlogo'
- 2. End of Line (EOL) Conversion

From Bitvise command line, change directory to Wolf\_Sheep\_Predation:

cd /data/gpfs/projects/punim1439/workflow/netlogo\_hpc/Wolf\_Sheep\_Predation

Then, run

```
sed -i.bak 's/\r$//g' create_xmls.sh
```

to convert Windows (CR LF) line ending to Unix (LF)

3. Run bash create\_xmls.sh

From Bitvise command line, run

```
bash create_xmls.sh
```

to create xmls folder and 100 xml files under this folder.

Tips:

MS-Windows to Unix like operation systems are using different End of Line (EOL).

If you want to see line ending in Notepad++, click menu **View > Show Symbol > Show All Characters**, then you will see Windows has line ending with invisible characters **CRLF**, while

Unix has **LF**. Click menu **Edit > EOL Conversion > Unix (LF)** to convert MS-Windows to Unix

EOL, as HPC is using Unix like operation systems.

Command sed -i.bak 's/\r\$//g' create\_xmls.sh did the same thing, using string editor to convert EOL of create\_xmls.sh to Unix removing all **CR**, and the original file is backed up as submit\_jobarray.slurm.bak.

# Revise and Run submit\_jobarray.slurm

- 1. Edit submit\_jobarray.slurm (using text editor notepad++, notepad, etc).
  - #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. In #SBATCH directive, --qos, -A, --job-name, --mail-user, --mail-type are optional, and can be deleted.
  - BASE\_FOLDER: current directory of submit\_jobarray.slurm, and the upper directory of xmls folder.
  - NETLOGO\_SH: file path of netlogo-headless.sh under NetLogo 6.2.0 directory.
  - NETLOGO\_MODEL: file path of wolf\_Sheep\_Predation.nlogo
  - OUTPUT\_FOLDER: name of output folder.
- 2. End of Line (EOL) Conversion

From Bitvise command line, run

```
sed -i.bak 's/\r$//g' submit_jobarray.slurm
```

3. Run sbatch submit\_jobarray.slurm

```
sbatch submit_jobarray.slurm
```

to submit 100 jobs to Spartan. You will receive an email when the computation ends.

### Tips:

- Run squeue -u yourusername to see current jobs, replacing yourusername with your username.
- Run scancel -n wolf\_sheep\_predation to cancel a job, replacing wolf\_sheep\_predation with the value after SBATCH --job-name= (file submit\_jobarray.slurm).
- Run spartan-weather to see usage of all partitions (optional).
- Run clear to clear screen.
- Run exit to quite command line.
- 4. Move all slurm\_\*.out files to slurm folder (optional)

When all jobs finished, run

```
cd /data/gpfs/projects/punim1439/workflow/netlogo_hpc/wolf_Sheep_Predation
mkdir -p slurms
mv ./slurm-*.out ./slurms/
```

to create a folder slurms, and move all slurm-\*.out files to slurms folder.

# **Merge CSV Results**

```
cd
/data/gpfs/projects/punim1439/workflow/netlogo_hpc/wolf_Sheep_Predation/outputs
awk '(NR < 8) || (FNR > 7)' *_table_*.csv > MergedResults.csv
```

This will create a file MergedResults.csv as the final output file.

# **Other Notes**

1. cd

Change directory command is to avoid always typing the absolute path when running script files.

```
cd /data/gpfs/projects/punim1439/workflow/netlogo_hpc/wolf_Sheep_Predation
bash create_xmls.sh
sbatch submit_jobarray.slurm
cd outputs
awk '(NR < 8) || (FNR > 7)' *_table_*.csv > MergedResults.csv
```

is the same as using

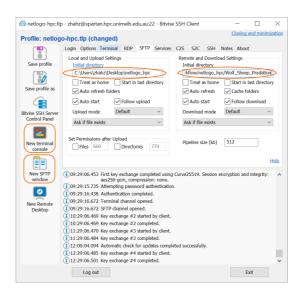
# bash /data/gpfs/projects/punim1439/workflow/netlogo\_hpc/Wolf\_Sheep\_Predation/crea te\_xmls.sh sbatch /data/gpfs/projects/punim1439/workflow/netlogo\_hpc/Wolf\_Sheep\_Predation/subm it\_jobarray.slurm awk '(NR < 8) || (FNR > 7)' /data/gpfs/projects/punim1439/workflow/netlogo\_hpc/Wolf\_Sheep\_Predation/outp uts/\*\_table\_\*.csv > /data/gpfs/projects/punim1439/workflow/netlogo\_hpc/Wolf\_Sheep\_Predation/outp uts/MergedResults.csv

2. In command prompt, put file path or directory path in "" if filename includes space, for example

```
cd "/data/gpfs/projects/punim1439/workflow/netlogo_hpc/NetLogo 6.2.0"
```

### 3. Bitvise

Click [New terminal console] to open a new command window. Click [New SFTP window] to open a new SFTP window. Set the **Initial directory** in Tab [SFTP] and Save profile, to specify initial directories for your new SFTP windows.



### 4. NetLogo RAM

To run models that require large memory, you need to change NetLogo's RAM of Java virtual machine (JVM).

• Make a copy of netlogo-headless.sh (e.g. netlogo-headless-10g.sh)

```
cd "/data/gpfs/projects/punim1439/workflow/netlogo_hpc/NetLogo 6.2.0"
cp netlogo-headless.sh netlogo-headless-10g.sh
```

 Edit netlogo-headless-10g.sh: Line 15, Change -Xmx10240m to -Xmx10g to increase 1GB RAM to 10GB RAM.

```
JVM_OPTS=(-Xmx10g -XX:+UseParallelGC -Dfile.encoding=UTF-8)
```

Notes: You can either edit netlogo-headless-10g.sh using any text editors, or edit in line on command prompt by running

```
nano netlogo-headless-10g.sh
```

After editing, press + to exit, type to save changes, then press to overwrite file.

### 5. NetLogo extensions

If your model requires an extension which is not a default extention of NetLogo software, the extension should be copied to the same folder of the NetLogo model or can be placed in the extension's folder in the NetLogo extensions directory. Refer <a href="here">here</a> for where to find extensions.

For example, we can copy rngs folder from C:\Program Files\NetLogo 6.2.0\app\extensions\.bundled\rngs on our laptop to /data/gpfs/projects/punim1439/workflow/netlogo\_hpc/NetLogo 6.2.0/app/extensions/.bundled/rngs on HPC.

### 6. Single run

If your experiment only has **one run** that cannot be split (Note the HPC\_Experiment of wolf\_sheep\_Predation.nlogo has 100 runs), or you just want to run your model by submitting one job to HPC, then you can simply save the following script as submit\_single\_job.slurm (i use Unix EOL), and run

```
sbatch submit_single_job.slurm
```

after you <u>Set Model BahaviorSpace</u> You do not need to run <u>Revise and Run</u> <u>create\_xmls.sh</u>, <u>Revise and Run <u>submit\_jobarray.slurm</u> and <u>Merge CSV Results</u>.</u>

```
# -- file submit_single_job.slurm --
#!/bin/bash
#SBATCH --nodes=1
#SBATCH --partition interactive
#SBATCH --time 1:00:00
#SBATCH --cpus-per-task=8

module load java
cd "/data/gpfs/projects/punim1439/workflow/netlogo_hpc/Wolf_Sheep_Predation"
"/data/gpfs/projects/punim1439/workflow/netlogo_hpc/NetLogo 6.2.0/netlogo-headless.sh" \
    --model "Wolf_Sheep_Predation.nlogo" \
    --experiment "HPC_Experiment" \
    --table "output_file.csv"
```

You can also run NetLogo headless mode on Windows PC (if JAVA\_HOME has been set or system PATH has included java.exe), using

```
cd "C:\Users\zhahz\Desktop\netlogo_hpc"
"C:\Program Files\NetLogo 6.2.0\netlogo-headless.bat" ^
    --model "Wolf_Sheep_Predation.nlogo" ^
    --experiment "HPC_Experiment" ^
    --table "output_file.csv"
```

# **Cheat Sheet**

```
# change work directory
cd /data/gpfs/projects/punim1439/workflow/netlogo_hpc/Wolf_Sheep_Predation
# create experiments
sed -i.bak 's/\r$//g' create_xmls.sh
bash create_xmls.sh
# check which partition has more available CPUs
spartan-weather
# submit jobs
sed -i.bak 's/\r$//g' submit_jobarray.slurm
sbatch submit_jobarray.slurm
# check job status
squeue -u yourusername
# clean log files
mkdir slurms
mv ./slurm-*.out ./slurms/
# merge results
cd outputs
awk '(NR < 8) || (FNR > 7)' *_table_*.csv > MergedResults.csv
# cancel job
scancel -n wolf_sheep_predation
```