# Generating commands and jobs in Python

**HORT 530** 

Lecture/Lab 13

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## When to use supercomputers

- Need to run hundreds to thousands of similar jobs.
- Need to run a few large jobs quickly.
- Tasks can be divided into smaller portions and run in parallel.

### Parallelization

- Refers to the ability of dividing a large task into smaller parts that can all be run in parallel.
- E.g., Correlation matrix of 10,000 genes.
- Can be divided into 10,000 jobs where each job works on one gene.

# Script creates its own Shell

 A script is always executed in its own shell, i.e., when you execute a shell script it starts a new child shell within the shell you executed the program from.



# Task: Download all sequencing runs from GSE18110

- https://www.ncbi.nlm.nih.gov/Traces/study/?acc=SRP002313
- Download the "Accession List"
- Use scp to copy file over to scholar.rcac.purdue.edu
- This file contains the list of SRR IDs.
- The command to download the results from a sequencing result is:
  - fastq-dump SRR039929
- This command needs the bioinfo and sra-toolkit modules.

#### Generating UNIX commands from Python

|           | Option 1                 | Option 2                            | Option 3                               |  |  |
|-----------|--------------------------|-------------------------------------|--|--|--|
| SRR039920 | Run each download        | Generate commands                   | Use Python to                          |  |  |
| SRR039921 | command<br>individually. | in Python.                          | generate multiple<br>SLURM scripts.    |  |  |
| SRR039922 |                          | <b>A</b>                            |  |  |  |
| SRR039923 | created manually.        | 1 script can run jobs sequentially. | Each SLURIM Job<br>runs in background. |  |  |
| SRR039924 | No record of             | Script keeps track of               | Script keeps track of                  |  |  |
| SRR039925 | parameters give to       | parameters given to                 | parameters given to                    |  |  |
| SRR039926 | command.                 | command.                            | command.                               |  |  |
| SRR039927 | Run time for             | Run time for commands is            | Run time for                           |  |  |
| SRR039928 | cumulative and           | cumulative and                      | <= cumulative and                      |  |  |
| SRR039929 | needs user<br>attention. | DOESN'T need user attention.        | DOESN'T need user attention.           |  |  |

#### Controlling processes from command line

- Foreground: Default mode for running commands. The shell waits on the process to finish.
  - Process retains control of the command line.
  - Key input is directed to the active process.
- Background: Process is initiated and pushed to the background.
  - Control of command-line is returned to the user.
  - Key input and other interactions are no longer passed to the process.
  - Processes can be pushed to background at initiation using &

#### Controlling processes from Python

- Wait: Default mode for running commands. The python interpreter waits on the process to finish.
  - Process retains control of the shell.
  - Both os.system() and subprocess.call() do this by default
- Submit and forget: Command is initiated in a separate process.
  - Processes can be pushed to background at initiation using &
  - subprocess.Popen(), by default, does not wait for child process to finish

#### Creating command strings vs. scripts

- Command strings: Use python to generate the command string with a combination of fixed strings and variables.
  - Submit command using os.system() or subprocess.call()
  - Submit command using subprocess.Popen() if you need to capture output.
- Scripts: Use file handle object to create a new script file with commands and parameters embedded.
  - subprocess.Popen() to submit the script as a job
  - Remember to make shell scripts executable (chmod 755)
  - SLURM scripts need not be executable
- When submitting multiple jobs, creating scripts helps keep track of the exact command and parameters used.

#### Generating UNIX commands from Python

- Python can be used to generate repetitive UNIX commands that operate over multiples of a set
  - For example, find a given sequence in all fastq files
- Key: A UNIX command is a string with fixed words, such as command name, and variable words, such as name of input file(s)



#### Making system calls from python

- We can use python to make calls to the system i.e., call commands and scripts available on the system command line.
- The 'os' and 'subprocess' module are the two main ways to interact with the system command line.
- The 'os' module is "deprecated", which means it's the old way of doing things and will not be supported in the future.

#### Running UNIX commands from Python

```
>>> import os
>>> import subprocess
>>> cmd = "grep -f AraLip.ids -A 1 AraPep.fasta > AraLip.fasta"
>>> os.system(cmd)
0
>>> subprocess.call(cmd,shell=True)
0
```

- os.system & subprocess.call() sent the 'cmd' command to the operating system.
- 'cmd' was run on the operating system and its output was dumped to the screen.
- Result: A new file called AraLip.fasta was created on the file system in the same directory

#### Capturing output of UNIX commands from Python

>>> import subprocess as sp

- >>> cmd = 'ls /scratch/scholar/kvarala/ICB'
- >>> p=sp.Popen(cmd,shell=True)

| >>> OutDir                            |        | Week1  | Week11 | Week13 | Week3 | Week5 |
|---------------------------------------|--------|--------|--------|--------|-------|-------|
| <pre>rcac_cluster_reference.pdf</pre> | Week10 | Week12 | Week2  | Week4  | Week6 | Week8 |

Output is not captured in 'p'

#### Capturing output of UNIX commands from Python

>>> import subprocess as sp >>> cmd = 'ls /scratch/scholar/kvarala/ICB' >>> p=sp.Popen(cmd,shell=True) >>> OutDir Week1 Week11 Week13 Week3 Week5 rcac\_cluster\_reference.pdf Week10 Week12 Week2 Week4 Week6 Week8 >>> p=sp.Popen(cmd,shell=True,stdout=sp.PIPE) Output is >>> for line in p.stdout: captured in 'p' line=line.rstrip() ... print(line) . . . . . . b'OutDir' Extra characters b'rcac\_cluster\_reference.pdf' b'Week1' from new line b'Week10' b'Week11' character b'Week12' b'Week13' b'Week2' b'Week3' b'Week4' b'Week5' b'Week6' b'Week7' b'Week8' b'Week9'

#### Capturing output of UNIX commands from Python

```
>>> import subprocess as sp
>>> cmd = 'ls /scratch/scholar/kvarala/ICB'
>>> p=sp.Popen(cmd,shell=True)
>>> OutDir
                                     Week1
                                             Week11 Week13 Week3
                                                                     Week5
rcac_cluster_reference.pdf Week10
                                     Week12 Week2
                                                      Week4 Week6 Week8
>>> p=sp.Popen(cmd,shell=True,stdout=sp.PIPE)
>>> for line in p.stdout:
        line=line.rstrip()
...
        print(line)
...
. . .
b'OutDir'
b'rcac_cluster_reference.pdf'
b'Week1'
b'Week10'
b'Week11'
b'Week12'
b'Week13'
b'Week2'
b'Week3'
b'Week4'
b'Week5'
b'Week6'
b'Week7'
b'Week8'
b'Week9'
>>> p=sp.Popen(cmd,shell=True,stdout=sp.PIPE,universal_newlines=True)
                                                                                 Output is
>>> for line in p.stdout:
                                                                              captured in 'p'
        line=line.rstrip()
. . .
        print(line)
. . .
. . .
OutDir
rcac_cluster_reference.pdf
Week1
Week10
Week11
```

Newline

processed

#### Generating shell scripts from Python

- Python can be used to generate shell scripts that differ in few parameters
  - For example, SLURM scripts with different job parameters
- Key: A job script is made of fixed lines, such as job parameters, module loads etc. and variable lines, such as the lines specifying the input line.



#### Generating shell scripts from Python

• Example 1: Write a python script that creates one SLURM job to fastq-dump the series of SRR IDs

• Example 2: Write a python script that creates one SLURM job for each SRR ID to fastq-dump the data