### Lecture 16: Supercomputing @CRC

LING 1340/2340: Data Science for Linguists Na-Rae Han

### Objectives

- Supercomputing at CRC
  - Server access through SSH
  - Running a job on CRC

### Let us now supercompute.



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### You got a supercomputing account.

> You received this mysterious email:

I got you all an account at Pitt's Center for Research Computing (CRC)

- CRC: Center for Research Computing
  - https://crc.pitt.edu
  - Handy links in "Resource" page!

Welcome!	
CF Center for Research Computing	Mar 12 
This is an automatically generated email. F	Please do
Dear user,	
Welcome to CRC!	
An account has been created for you on Center	for
Research Computing (CRC) resources. Your use apb63 and the password is your Pitt password. started, please browse to our website at crc.pit	To get
where you can find getting started guides and o	detailed
documentation. For any future problems, quest	ions, help
requests, suggestions, or even for helping othe	rs, please
feel free to post at crc.pitt.edu/contact. The fas	test way
to get help is to submit a support ticket at	
crc.pitt.edu/tickets	

H2P and HTC are the primary CRC cluster, and your account is created there (HTC is specifically for biomedical users). You can access H2P and HTC using your Pitt credentials. More information about access, file

# Accessing CRC's cluster

#### If you're OFF CAMPUS, your laptop should be running a Secure Remote Access client.

- Install and run PulseSecure  $\rightarrow$
- Details in the h2p cluster user guide: <u>https://crc.pitt.edu/resources/h2p-user-guide</u>
- Remote-access your account via SSH:
  - \* ssh yourpittid@h2p.crc.pitt.edu
- Getting your bearings:
  - Where are you? pwd
  - What is your user 'group'? groups
  - Is python installed on this machine? which python
  - What are your configuration files? 1s -a
    - .bash\_profile
      - ← Customize with your own aliases, etc.
    - .bash\_history
      - ← Bash commands you typed in are logged here.



### Na-Rae's .bash\_profile on CRC

- PATH configuration
- Prompt in pink!! Add this line: export PS1="\[\e[0;35m\][\u@\h \w]\\$ \[\e[m\]"
- Some aliases
  - grep: perl style, colored output
  - Is: colored output, folders marked with "/"

If you edit this file, changes take effect after logging back in.

For immediate effect, run: source .bash\_profile

🚸 naraehan@login0:~

naraehan@login0 ~]\$ cat .bash\_profile .bash\_profile

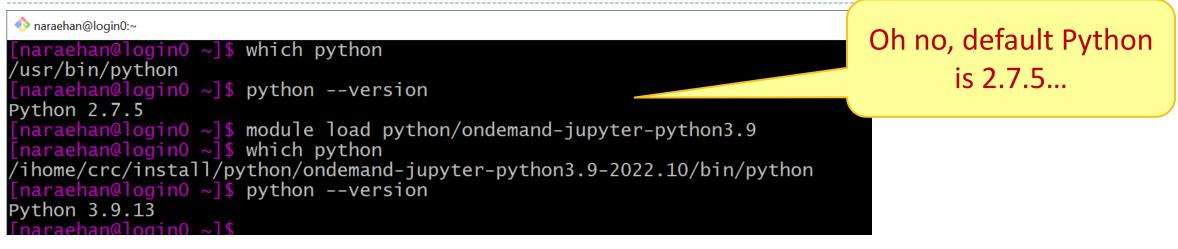
# User specific environment and startup programs

PATH=\$PATH:\$HOME/.local/bin:\$HOME/bin export PATH

# Prompt in pink color
export PS1="\[\e[0;35m\][\u@\h \W]\\$ \[\e[m\]"

# perl-style regex, color alias grep='grep -P --color' alias ls='ls -F --color=auto'

# Using the right python module



We have to "load" the correct python module via module load python/ondemand-jupyter-python3.9

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> Popular data science libraries are already installed (pandas, sklearn, nltk...):

```
    Naraehan@login0:~
    [naraehan@login0 ~]$ python
    Python 3.9.13 (main, Aug 25 2022, 23:26:10)
    [GCC 11.2.0] :: Anaconda, Inc. on linux
    Type "help", "copyright", "credits" or "license" for more information.
    >>> import pandas
    >>> import nltk
    >>>
```

### Using CRC clusters

### Job submissions

- On a computing cluster, many people are using the same resources so we have a "job queue" that accepts job submissions
- CRC and many other clusters use <u>Slurm</u> for managing and scheduling these jobs.
- What this means:
  - You don't directly execute your Python script. (A big NO-NO)
  - You create a BASH SCRIPT to run a PYTHON SCRIPT (job).



# Before you get carried away

- Do NOT yet run any commands/jobs that may be resource-intensive.
- This is a powerful super-computer, shared by many research groups at Pitt.
  - Our class as a group has a limited, shared allocation. We have a reserve of 10000 Service Units (SUs), which is 10k hours of computing time.
  - You do not want to accidentally initiate a run-away process and hog resources.
- There are PROPER ways to run jobs.
  - We will show you now.

### Slurm Jobs

- To make a slurm job script, you basically need to write a **bash script** of what you would do to run your program on the command line. This is just a text file, usually with a **.sh** ending.
- Also need some slurm configs
- Example (let's call this hello.sh)

```
#SBATCH --job-name=hello
#SBATCH --output=hello.out
#SBATCH --nodes=1
#SBATCH --ntasks=1
#SBATCH --partition=smp
#SBATCH --cluster=smp
```

echo "hello world"

#!/usr/bin/env bash

<-- Copy this into a file and name it something like **hello.sh**  Below are some other Slurm config options (prefix with #SBATCH) as in hello.sh. EVEN MORE at <u>https://slurm.schedmd.com/sbatch.html</u>

Option	Environment Variables
output	-
time	(Format: DAYS-HOURS:MINUTES:SECONDS)
job-name	SLURM_JOB_NAME
nodes	SLURM_NNODES
ntasks	SLURM_NTASKS
cpus-per-task	SLURM_CPUS_PER_TASK
ntasks-per-node	SLURM_NTASKS_PER_NODE
partition	SLURM_JOB_PARTITION
mem	SLURM_MEM_PER_NODE
account	SLURM_JOB_ACCOUNT

So from the directory with our hello.sh script, we can submit it with sbatch hello.sh

This should run pretty much instantly and we can check our hello.out output file.

Command	Description
sinfo	Quick view of partitions
sbatch <job></job>	Submit your job <sup>a</sup>
squeue	View all jobs
squeue -u <user></user>	Look at <b>your</b> jobs
scancel <jobid></jobid>	Cancel your job
crc-sinfo.py	sinfo <b>wrapper</b>
crc-squeue.py	squeue <b>wrapper</b>
crc-scancel.py <jobid></jobid>	scancel <b>wrapper</b>
crc-usage.pl	<b>View your group's usage</b>

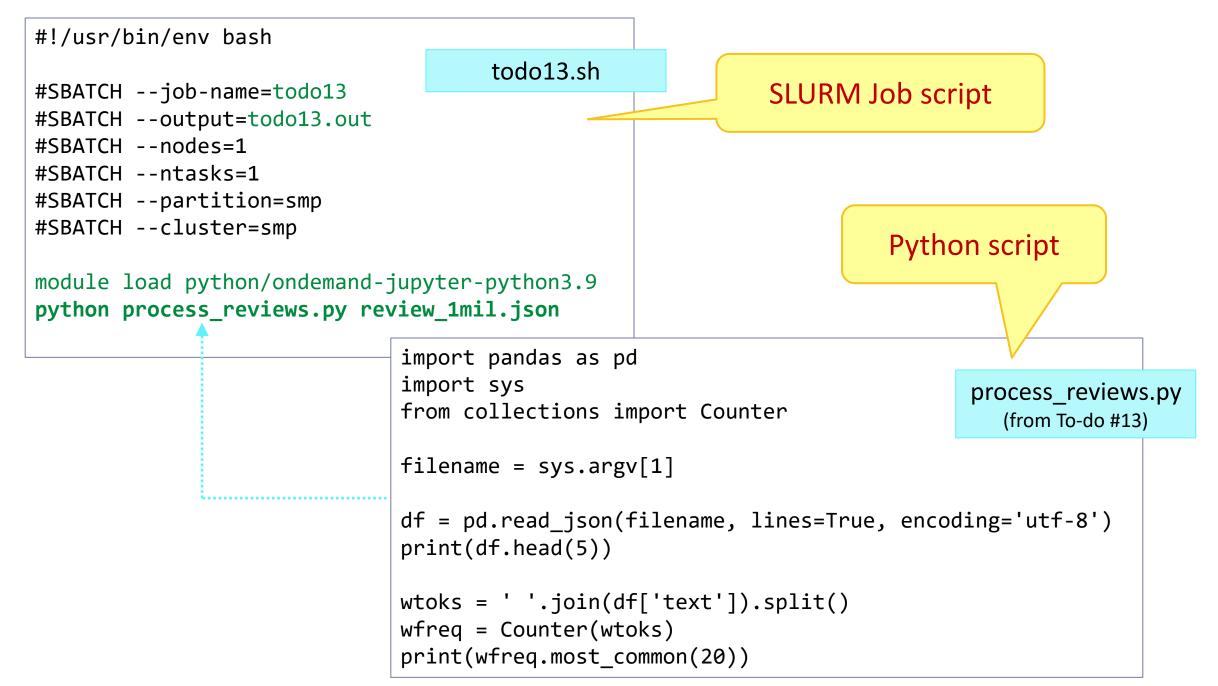
### To-do #13 redux on CRC: setting up

(1) New location of yelp review data file (you all have access):
 /bgfs/shared\_data/yelp\_dataset/yelp\_academic\_dataset\_review.json

(2) We'll sample 1 million lines (shuffled):

shuf yelp\_academic\_dataset\_review.json -n 1000000 > ~/review\_1mil.json

- (3) Copy over our python script. Running it on this data will look like: (but don't run this!!) python process\_reviews.py review\_1mil.json
- (4) But before that, we should load the appropriate python environment: module load python/ondemand-jupyter-python3.9
- (5) Now we can toss all this into a bash script. Let's call it todo13.sh:
  - Start with hello.sh (make a copy using cp file1 file2, then edit)
  - Change the bash commands at the bottom to run our script for To-do 13, and change the job name and output file to something like todo13 and todo13.out



### To-do #13 redux on CRC

- Submit your job:
  - \* sbatch todo13.sh
- and check status with:
  - \* squeue -u <user-id>
  - Done when squeue no longer shows job (keep re-running with up arrow)
  - Or: add -i 10 to auto-run every 10 seconds (Ctrl+c to get out)
- Check the output with:
  - \* cat todo13.out

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Success! 1 million reviews weren't much of a challenge

	🚸 naraehan@logi	in0:~							
	hello.out hello.sh multicore/	ogin0 ~]\$ 1 notes.txt old/ ondemand/ ogin0 ~]\$ s patch job 82	process_ pyling@ review 1	1mil.isor	tidy n tidy	red_data/ y/ y_2022/	todo: vaul w2v/		work yelp
	[naraehan@] [naraehan@]	ogin0 ~]\$ s JOBID PAR 8265190 ogin0 ~]\$ s JOBID PAR 8265190	queue -u TITION smp queue -u TITION smp	naraehar NAME todo13 r naraehar NAME todo13 r	n USER naraehan n USER naraehan	R ST	TIME 0:06 TIME 0:16	NODES	smp-I
	[naraehan@] Mon Mar 27	ogin0 ~]\$ s 11:06:09 20 JOBID PAR 8265190	queue -u 23 TITION smp	naraehar NAME	USER USER	ST	TIME 0:34	NODES	
)		11:06:19 20 JOBID PAR 8265190		NAME todo13 r	USER naraehan		TIME 0:44	NODES 1	NODEI smp-i
	Mon Mar 27	11:06:29 20 JOBID PAR		NAME	USER	ST	TIME	NODES	NODEI
	hello.out hello.sh multicore/ [naraehan@l 0 KM0l4Oax 1 5QlYUCBP 2 pF9SJ8hj 3 8Hecs6zT	ogin0 ~]\$ 1 notes.txt old/ ondemand/ ogin0 ~]\$ c review ZZOOhtZ3gbr PuA_uCnIgQEg xwsjhB7tdPt lgk5a_OgKQ1 1YrvXL4K_zu	process_ pyling@ review_1 at todo13 _id EIw MDw YnQ 9DA	1mil.jsor	tidy 1 tidy -10 13:48 -12 04:53 -06 16:49 -17 03:39	3:35 5:21 5:34	todo	13.sh	w2v, worl yel
	50), ('of', 77394), ('w	279303), ('a 1469647), vith', 84133 ('this', 6	('is', 12 7), ('my'	212863), ', 809005	('for', 5), ('tha	1172767)	, ('in	', 109	5658)

# How did the job go?

- ▶ Job ID was shown earlier →
- Check finished job's stats by:
  - \* seff <job-id>
- Our Python script on 1million reviews used:
  - 8.65GB of memory (RAM)
  - 49 seconds of CPU time

[naraehan@login0 ~]\$ seff 8265190 Job ID: 8265190 Cluster: smp User/Group: naraehan/nhan State: COMPLETED (exit code 0) Cores: 1 CPU Utilized: 00:00:46 CPU Efficiency: 93.88% of 00:00:49 core-walltime Job Wall-clock time: 00:00:49 Memory Utilized: 8.65 GB Memory Efficiency: 220.53% of 3.92 GB [naraehan@login0 ~]\$

## Quick aside

Memory here refers to Random Access Memory (RAM)

- You probably have 8 or 16 GB on your laptop
- Running programs uses RAM to store temporary data (in our case opened file content, variables, lists, DataFrame, etc) that they use or produce
- Stuff stored in RAM is removed when a program terminates, or if your computer shuts off.
- Running out of RAM on your laptop could cause your computer to freeze/crash
- Expensive per GB
- NOT disk drive -->
  - Disk space stores files long-term
  - Cheap per GB, 256+GB is pretty standard.



### To-do #14: bigger data + better code @ CRC!

- Take 1: use 4 million reviews
- Take 2: use 4 million reviews, with a new (better!) python script

← Compare Take 1 vs. Take 2

Take 3 (optional): all 7 million reviews, with the new (better!) python script

