#### Lecture 10: Supercomputing at CRC

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

## Objectives

#### Supercomputing at CRC

- Server access through SSH
- Running jobs
- HW3/ML wrap-up
- Let's share your HW3
  - Copy your HW3 jupyter notebook into <u>https://github.com/Data-Science-for-Linguists-</u> 2021/Class-Exercise-Repo/tree/main/hw3 shared
  - Rename your JNB file to have your name in it "\_narae"
  - Push to your repo, create a pull request

#### 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!	
Center for Research Computing	Mar 12
To You	
This is an automatically generated email. F	lease do
not reply	
Dear user,	
Welcome to CRC!	
An account has been created for you on Center	for
Research Computing (CRC) resources. Your us	ername is
apb63 and the password is your Pitt password.	To get
started, please browse to our website at crc.pit	t.edu,
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

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## Accessing CRC's cluster

#### > 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.

Connections	+ /
Pitt Disconnected	5 Connec

## Shared data space for the group

You are all assigned to our class group: ling2340\_2021s

#### Our shared datasets are stored in: /bgfs/ling2340\_2021s/shared\_data/



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

- PATH configuration
- Prompt in pink!! Add this line: export PS1="\[\e[0;35m\][\u@\h \w]\\$ \[\e[m\]"

Some aliases

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

For immediate effect, run:
 source .bash\_profile

```
[naraehan@login1 ~]$ cat .bash_profile
  .bash_profile
 Get the aliases and functions
if [ -f ~/.bashrc ]; then
        . ~/.bashrc
fi
 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'
```

### Using the right python module

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- ▶ We have to "load" the correct python module via module load python/3.7.0
- Popular data science libraries are already installed (pandas, sklearn, nltk...):

🚸 naraehan@login0:~	_		$\times$
[naraehan@login0 ~]\$ python			$\sim$
Python 3.7.0 (default, Jun 28 2018, 13:15:42)			
[GCC 7.2.0] :: Anaconda, Inc. on linux			
Type "help", "copyright", "credits" or "license" for more inf	formation.		
>>> import pandas			
>>> import nltk			
/ihome/crc/install/python/miniconda3-3.7/lib/python3.7/site-p	packages/sk	learn/	fea
ture_extraction/text.py:17: DeprecationWarning: Using or impo	orting the A	ABCs f	rom
'collections' instead of from 'collections.abc' is deprecate			
11 stop working			

## 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 #11 redux on CRC: setting up

(1) New location of yelp review data file:

/bgfs/ling2340\_2021s/shared\_data/yelp\_dataset\_2021/yelp\_academic\_dataset\_review.json

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

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

- (3) Copy 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/3.7.0
- (5) Now we can toss all this into a bash script. Let's call it todo11.sh
- (6) Start with hello.sh (make a copy, then edit)

(7) Change the bash commands at the bottom to run our script for To-do 11, and change the job name and output file to something like todo11 and todo11.out



### To-do #11 redux on CRC

- Submit your job:
  - \* sbatch todo11.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 todo11.out

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

```
🚸 naraehan@login0:~
naraehan@login0 ~]$ Is
                                                shared_data try
hello.sh old2
                              pyling
                                                                    w2v
         process_reviews.py review_1mil.json todo11.sh
                                                             vault
o]d
[naraehan@login0 ~]$ sbatch todo11.sh
Submitted batch job 2824655 on cluster smp
naraehan@login0 ~]$ squeue -u naraehan
                                                              NODES NODELIST(REASON)
             JOBID PARTITION
                                 NAME
                                          USER ST
                                                        TIME
           2824655
                               todo11 naraehan R
                                                        0:05
                                                                  1 smp-n111
                         smp
[naraehan@login0 ~]$ squeue -u naraehan
             JOBID PARTITION
                                 NAME
                                          USER ST
                                                        TIME
                                                              NODES NODELIST(REASON)
                                                        0:15
                                                                  1 smp-n111
           2824655
                               todo11 naraehan R
                         smp
[naraehan@login0 ~]$ squeue -u naraehan -i 10
Tue Mar 23 23:05:16 2021
             JOBID PARTITION
                                 NAME
                                          USER ST
                                                              NODES NODELIST(REASON)
                                                        TIME
                                                        0:23
           2824655
                         smp
                               todo11 naraehan R
                                                                  1 smp-n111
Тие Mar 23 23:05:26 2021
             JOBID PARTITION
                                 NAME
                                          USER ST
                                                             NODES NODELIST(REASON)
                                                        TIME
                                                        0:33
           2824655
                               todo11 naraehan R
                                                                  1 smp-n111
                         smp
Tue Mar 23 23:05:36 2021
                                          USER ST
                                                              NODES NODELIST(REASON)
             JOBID PARTITION
                                 NAME
                                                        TIME
           2824655
                         smp
                               todo11 naraehan R
                                                        0:43
                                                                  1 smp-n111
Tue Mar 23 23:05:46 2021
                                 NAME
                                          USER ST
                                                              NODES NODELIST(REASON)
             JOBID PARTITION
                                                        TIME
                               todo11 naraehan R
                                                        0:53
           2824655
                         smp
                                                                  1 smp-n111
Tue Mar 23 23:05:56 2021
             JOBID PARTITION
                                 NAME
                                          USER ST
                                                        TIME NODES NODELIST(REASON)
[naraehan@login0 ~]$ ls
                              pyling
 ello.sh old2
                                                shared_data todo11.sh vault
         process_reviews.py review_1mil.json todo11.out
                                                                        w2v
                                                            try
naraehan@login0 ~]$ cat todo11.out
                review_id ...
                                              date
  BiRkTZrn8x_zspT8sRt-Qw ... 2018-10-10 23:43:25
  24pRZcBLDM_kbTvF1bC1-w
                          ... 2014-04-12 16:42:59
  x0xa2icr6U4E7G93trPwfw
                          ... 2017-12-18 22:13:04
  <u>JOFOhMZF9DWi</u>B9_SRWgKCA ... 2018-12-31 23:45:56
  Fk2LP1ft8TrQcrUS19w80A ... 2019-06-20 21:04:28
[5 rows x 9 columns]
 ('the', 4516590), ('and', 3799781), ('I', 2887729), ('a', 2788950), ('to', 2697926)
 1878049), ('of', 1603693), ('is', 1313227), ('for', 1258119), ('in', 1170009), ('The
  , ('it', 940556), ('with', 896436), ('my', 896209), ('that', 883825), ('but', 76059
 , 725910), ('have', 677351), ('you', 666733), ('this', 635577)]
```

# 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:
  - 9.4GB of memory (RAM)
  - 55 seconds of CPU time

[naraehan@login0 ~]\$ seff 2824655
Job ID: 2824655
Cluster: smp
User/Group: naraehan/nhan
State: COMPLETED (exit code 0)
Cores: 1
CPU Utilized: 00:00:55
CPU Efficiency: 90.16% of 00:01:01 core-walltime
Job Wall-clock time: 00:01:01
Memory Utilized: 9.43 GB
Memory Efficiency: 240.38% of 3.92 GB
[naraehan@login0~]\$

## Quick aside

Memory here refers to Random Access Memory (RAM)

- You probably have 4, 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 will probably 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 #12: bigger data + better code

- 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 8.6 million reviews, with the new (better!) python script



# Wrapping up

- ▶ To-do #12
- PyLing! Next Wed 6pm.

- Next class
  - Joey presents: computational efficiency
  - More CRC exploration: Jupyter Hub, clustering