# Alex Teboul - CSC 555 Assignment 1

## **CSC 555: Mining Big Data**

Assignment 1 (due Tuesday, January 21st)

Suggested reading: *Mining of Massive Datasets*: Chapter 1, Chapter 2 (sections 2.1, 2.1 only). *Hadoop: The Definitive Guide*: Appendix A (available on D2L)
Supplemental document **UsingAmazonAWS.doc**. My Code from this Homework @ Link: <a href="https://colab.research.google.com/drive/1uSBbqYDuBm1MD55nkJTW9tANDo63grc1">https://colab.research.google.com/drive/1uSBbqYDuBm1MD55nkJTW9tANDo63grc1</a>

## Part 1

a) Compute (you can use any tool to compute answers in this part – but if you do not know to perform this computation, please talk to me about prerequisites):

```
2^{10}
4<sup>5</sup>
85
837 MOD 100 (MOD is the modulo operator, a.k.a. the remainder)
842 MOD 20
16 MOD 37
37 MOD 16
    1. 2^10
    2.4^5
    3.8^5
    4. 837 MOD 100 (MOD is the modulo operator, a.k.a. the remainder)
    5. 842 MOD 20
     6. 16 MOD 37
    7. 37 MOD 16
 [ ] 1 #2^10
       2 print("1. 2^10 = ", 2**10)
       3 print("2. 4^5 = ", 4**5)
       4 print("3. 8^5 = ", 8**5)
       5 print("4. 837 MOD 100 = ", 837 % 100)
6 print("5. 842 MOD 20 = ", 842 % 20)
       7 print("6. 16 MOD 37 = ", 16 % 37)
       8 print("7. 37 MOD 16 = ", 37 % 16)
  T→ 1. 2^10 = 1024
      2. 4^5 = 1024
      3. 8^5 = 32768
      4. 837 MOD 100 = 37
      5. 842 MOD 20 = 2
      6. 16 MOD 37 = 16
```

b) Given vectors V1 = (1, 2, 3) and V2 = (2, 1, 2) and a 3x3 matrix M = [(2, 1, 3), (1, 2, 2), (1, 0, 2)], compute:

```
V2 - V1

V1 + V1

|V1| (vector length, not the number of dimensions)
```

```
|V2|
     M * V2 (matrix times vector, transpose it as necessary)
     M * M (or M^2)
    M^3
  1. V2 - V1
 2. V1 + V1
 3. |V1| (vector length, not the number of dimensions)
  5. M * V2 (matrix times vector, transpose it as necessary)
 6. M * M (or M^2)
] 1 import numpy as np
    2 \text{ V1} = (1, 2, 3)
    3 V1 = np.array(V1)
    5 \text{ V2} = (2, 1, 2)
    6 \text{ V2} = \text{np.array(V2)}
    8 M = [(2, 1, 3), (1, 2, 2), (1, 0, 2)]
    9 M = np.array(M)
   11 print("1. V2 - V1 = ", V2 - V1)
   12 print("2. V1 + V1 = ", V1 + V1)
13 print("3. |V1| = ", np.linalg.norm(V1))
14 print("4. |V2| = ", np.linalg.norm(V2))
   15 print("5. M * V2.T = \n", M*V2.T)
   16 print("6. M^2 = \n", np.linalg.matrix_power(M,2))
   17 print("7. M^3 = \n", np.linalg.matrix_power(M,3))
→ 1. V2 - V1 = [ 1 -1 -1]
   2. V1 + V1 = [2 4 6]
   3. |V1| = 3.7416573867739413
   4. |V2| = 3.0
   5. M * V2.T =
    [[4 1 6]
    [2 2 4]
    [2 0 4]]
   6. M^2 =
    [[8 4 14]
    [6 5 11]
    [4 1 7]]
   7. M^3 =
    [[34 16 60]
     [28 16 50]
    [16 6 28]]
```

- I assume that by vector length you mean the same as magnitude.
- c) Suppose we are flipping a coin with Head (H) and Tail (T) sides. The coin is <u>not</u> balanced with 0.6 probability of H coming up (and 0.4 of T). Compute the probabilities of getting:

## HTHT THTT

Exactly 1 Head out of a sequence of 4 coin flips.

Exactly 1 Tail out of sequence of 4 coin flips.

```
1. HTHT
2. THTT
3. Exactly 1 Head out of a sequence of 4 coin flips.
4. Exactly 1 Tail out of sequence of 4 coin flips.
4. Exactly 1 Tail out of sequence of 4 coin flips.

4. Exactly 1 Tail out of sequence of 4 coin flips.

4. I #just rounded for cleanliness sake and doesn't impact the numbers in this case
2 print("1. HTHT Probability is = (0.6 * 0.4 * 0.6 * 0.4) = ", round(0.6*0.4*0.6*0.4*0.6*0.4,4))
3 print("2. THTT Probability is = (0.4 * 0.6 * 0.4 * 0.4) = ", round(0.4*0.6*0.4*0.4,4))
4 print("3. Exactly 1 Head out of a sequence of 4 coin flips = 4 * (0.6 * 0.4 * 0.4 * 0.4) = ", round(4*(0.6*0.4*0.4*0.4),4))
5 print("4. Exactly 1 Tail out of a sequence of 4 coin flips = 4 * (0.4 * 0.6 * 0.6) = ", round(4*(0.4*0.6*0.6*0.6),4))

4 1. HTHT Probability is = (0.6 * 0.4 * 0.6 * 0.4) = 0.0576
2. THTT Probability is = (0.6 * 0.4 * 0.6 * 0.4) = 0.0384
3. Exactly 1 Head out of a sequence of 4 coin flips = 4 * (0.6 * 0.4 * 0.4 * 0.4) = 0.1536
4. Exactly 1 Tail out of a sequence of 4 coin flips = 4 * (0.4 * 0.6 * 0.6 * 0.6) = 0.3456
```

**Answers:** 0.0576, 0.0384, 0.1536, 0.3456

d) Consider a database schema consisting of two tables, Employee (<u>ID</u>, Name, Address), Project (<u>PID</u>, Name, Deadline), Assign(<u>EID</u>, <u>PID</u>, Date). Assign.EID is a foreign key referencing employee's ID and Assign.PID is a foreign key referencing the project.

Write SQL queries for:

i. Find projects that are not assigned to any employees (PID and Name of the project).

```
i. Find projects that are not assigned to any employees (PID and Name of the project).
```

```
SELECT PID as "PID", Name as "Project Name"
FROM Project
WHERE PID IN
(SELECT PID, EID
FROM Assign
WHERE EID IS NULL);
```

ii. For each date, found how many assignments were made that day.

ii. For each date, found how many assignments were made that day.

```
SELECT Date as "Date", COUNT(Date) as "# Assignments"
FROM Assign
WHERE Date IN
(SELECT Date, EID
FROM Assign
WHERE EID IS NOT NULL)
GROUP BY Date;
```

# iii. Find all projects that have fewer than 3 employees assigned to them (note that this should include 2, 1 and 0 in order to be correct)

iii. Find all projects that have fewer than 3 employees assigned to them (note that this should in SELECT

PID as "Project ID", COUNT(\*) as "# of Employees Assigned"

FROM Assign

WHERE PID IN

( SELECT DISTINCT PID, EID

FROM Assign
)

GROUP BY PID

HAVING COUNT(\*) < 3

\*Strange query because it seems like you can get multiple assignments to the same project if it's entered on different Assign.Dates. ^I think this should work despite that though.

# e) Mining of Massive Datasets, Exercise 1.3.3 Justify your answer.

ORDER BY COUNT(\*) DESC;

**Exercise 1.3.3**: Suppose hash-keys are drawn from the population of all nonnegative integers that are multiples of some constant c, and hash function h(x) is x mod 15. For what values of c will h be a suitable hash function, i.e., a large random choice of hash-keys will be divided roughly equally into buckets?

- In order for the hash function h to send approximately equal numbers of hashkeys to each of the buckets, they need to be chosen randomly from the population of possible hash-keys.
- Also, "The generalization of Example 1.4 is that when hash-keys are integers, chosing B so it has any common factor with all (or even most of) the possible hashkeys will result in nonrandom distribution into buckets."
- We know that h is x % 15 and that the population of possible hash keys must be
   the number of buckets.
- But B=15 seems like a bad choice because it is not a prime number...
- We know that the hash keys are positive integers.
- Following the logic presented in this chapter, for  $h(x) = x \mod B$ , where B is the number of buckets, B=15 in this exercise.
- Granted this is my first time learning about hashing, but it seems like c=1 would work to get 0 - 14 buckets filled, but c=2 would not get values into the even buckets.
- By this logic c could also be 1, 16, 31, 46, 61... (1, B+1, 2B+1, 3B+1, 4B+1...) for the same effect.
- From the textbook and other sources online, this doesn't seem like a good option do just do x mod 15 as the only hashing function used. At least use a prime B seems to be better practice.

f) Describe how you would implement a MapReduce job consisting of Map and Reduce description. You do not have to write code or even pseudo-code. Just describe, in your own words, what the Map and Reduce tasks are going to do. Map task reads the input file and produces (key, value) pairs. Reduce task takes a list of (key, value) pairs for each key and combines all values for each key. Please remember that Map operates on individual blocks and Reduce on individual keys with a set of values. Thus, for Mapper you need to state what your code does given a block of data (i.e., for each block, not for the whole file) and for Reduce you need to state what your reducer does for each key (without being able to see other keys).

For a data file that contains the following columns: (ID, First, Last, Grade)

- i. For each first name, find the GPA (grade point average) of each student, i.e., **SELECT First, AVG(Grade) FROM Student GROUP BY First**.
- **Map:** The mapper creates the pair of First and Grade, such that the key is the student's first name and their grades are the values.
- **Reduce:** The reducer looks at all the grades of that student, and gets the average = sum(grades)/count(grades).
  - ii. For each full student name, find the best grade, i.e.,SELECT First, Last, MAX(Grade) FROM Student GROUP BY First, Last.
- Map: The mapper creates joins First and Last, then creates the pair of FirstLast and Grade, such that the key is the student's First&Last name and their grades are the values.
- Reduce: The reducer looks at all the grades of that student, and gets the top or MAX grade from the list of grades for that student. Not sure if this task involves sorting to find the max.

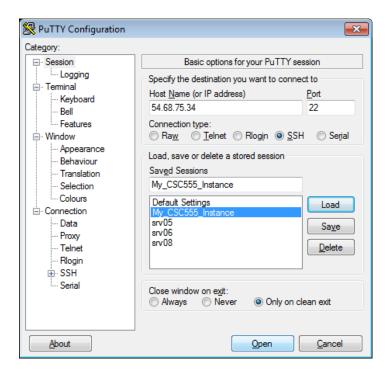
# Part 2: Linux Intro

This part of the assignment will serve as an introduction to Linux. Make sure you go through the steps below and submit screenshots where requested – submit the entire screenshot of a command terminal.

Use at least a t2.small instance or Hadoop may not run properly with insufficient memory. All Linux commands are in **Berlin Sans FB**. Do not type the "\$" symbol. The "\$" represents the prompt "[ec2-user@ip-xxx-xx-xxx-xx ~] \$" in your particular Linux instance.

**0. Login to your Amazon EC2 Instance** (NOTE: <u>instructions on how to create a new instance</u> and log in to it are provided in a separate file, UsingAmazonAWS.doc)

Connect to your instance through Putty.



Your instance should look like as the following image:

### 1. Create a text file.

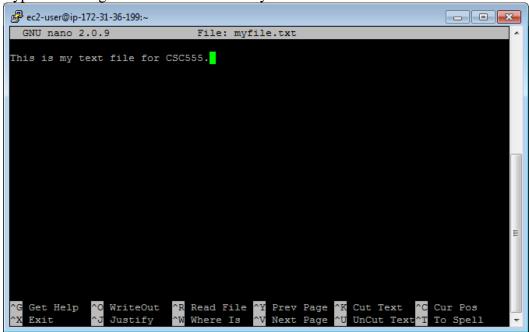
Instructions for 3 different text editors are provided below. You only need to choose <u>one</u> <u>editor</u> that you prefer. **nano** is a more basic text editor, and is much easier to start. **vim** and **emacs** are more advanced and rely on keyboard shortcuts quite a bit and thus have a steeper learning curve.

• **Tip**: To paste into Linux terminal you can use <u>right-click</u>. To copy from the Linux terminal, you only need to highlight the text that you want to copy with your mouse. Also please remember that Linux is <u>case-sensitive</u>, which means **Nano** and **nano** are not equivalent.

Nano Instructions(Option 1):

\$ nano myfile.txt

Type something into the file: "This is my text file for CSC555."



Save changes: Ctrl-o and hit Enter.

Exit: Ctrl-x

Emacs Instructions(Option 2):

You will need to install emacs.

### \$ sudo yum install emacs

Type "y" when asked if this is OK to install.

#### \$ emacs myfile.txt

Type something into the file: "This is my text file for CSC555."

Save changes: Ctrl-x, Ctrl-s

Exit: Ctrl-x Ctrl-z

Vim Instructions(Option 3):

• NOTE: When **vim** opens, you are in *command* mode. Any key you enter will be bound to a command instead of inserted into the file. To enter *insert* mode press the key "i". To save a file or exit you will need to hit Esc to get back into *command* mode.

## \$ vim myfile.txt

Type "i" to enter insert mode

Type something into the file: "This is my text file for CSC555."

Save changes: hit Esc to enter *command* mode then type ":w"

Exit: (still in *command* mode) type ":x"

Confirm your file has been saved by listing the files in the working directory.

#### \$ ls

You should see your file.

Display the contents of the file on the screen.

#### \$ cat myfile.txt

Your file contents should be printed to the terminal.

• **Tip**: Linux will fill in partially typed commands if you hit Tab.

#### \$cat myfi

Hit Tab and "myfi" should be completed to "myfile.txt". If there are multiple completion options, hit Tab twice and a list of all possible completions will be printed. This also

applies to commands themselves, i.e. you can type in  $c\alpha$  and see all possible commands that begin with ca.

# 2. Copy your file.

Make a copy.

## \$ cp myfile.txt mycopy.txt

Confirm this file has been created by listing the files in the working directory. Edit this file so it contains different text than the original file using the text editor instructions, and confirm your changes by displaying the contents of the file on the screen.

# **SUBMIT:** Take a screen shot of the <u>contents</u> of your copied file displayed on the terminal screen.

#### 3. Delete a file

Make a copy to delete.

\$ cp myfile.txt filetodelete.txt

\$ ls

Remove the file.

\$ rm filetodelete.txt

\$ ls

#### 4. Create a directory to put your files.

Make a directory.

#### \$mkdir CSC555

Change the current directory to your new directory.

#### \$cd CSC555

Print your current working directory **\$pwd** 

### 5. Move your files to your new directory.

Return to your home directory.

\$cd
OR

\$cd ..
OR
\$ cd /home/ec2-user/

• NOTE: **cd** will always take you to your home directory. **cd** .. will move you up one directory level (to the parent). Your home directory is "/home/[user name]", /home/ec2-user in our case

Move your files to your new directory.

\$ mv myfile.txt CSC555/ \$ mv mycopy.txt CSC555/

Change the current directory to CSC555 and list the files in this directory.

**SUBMIT:** Take a screen shot of the files listed in the CSC555 directory.

### 6. Zip and Unzip your files.

Zip the files.

\$ zip myzipfile mycopy.txt myfile.txt OR

\$ zip myzipfile \*

• NOTE: \* is the wildcard symbol that matches <u>everything</u> in current directory. If there should be any additional files in the current directory, they will also be placed into the zip archive. Wildcard can also be used to match files selectively. For example **zip myzipfile my\*** will zipup all files beginning with "my" in the current directory.

Move your zip file to your home directory.

\$ mv myzipfile.zip /home/ec2-user/

Return to your home directory.

Extract the files.

\$ unzip myzipfile.zip

#### 7. Remove your CSC555 directory.

• Warning: Executing "rm -rf" has the potential to delete ALL files in a given directory, including sub-directories ("r" stands for recursive). You should use this command very carefully.

Delete your CSC555 directory. \$ rm -rf CSC555/

#### 8. Download a file from the web.

Download the script for Monty Python and the Holy Grail. \$ wget http://www.textfiles.com/media/SCRIPTS/grail

The file should be saved as "grail" by default.

### 9. ls formats

List all contents of the current directory in long list format.

• Note: the option following "ls" is the character "l"; not "one".

\$ Is -I

The  $1^{st}$  column gives information regarding file permissions (which we will discuss in more detail later). For now, note that the first character of the 10 total will be "-" for normal files and "d" for directories. The  $2^{nd}$  Column is the number of links to the file. The  $3^{rd}$  and  $4^{th}$  columns are the owner and the group of the file. The  $5^{th}$  column displays the size of the file in bytes. The  $6^{th}$  column is the date and time the file was last modified. The  $7^{th}$  column is the file or directory name.

List all contents of the current directory in long list and human readable formats. "-h" will put large files in more readable units than bytes.

\$ Is -Ih

## **SUBMIT:** The size of the grail file.

#### 10. More on viewing files.

If you issue "cat grail", the contents of grail will be printed. However, this file is too large to fit on the screen.

Show the grail file one page at a time.

### \$ more grail

Hit the spacebar to go to the next page. Type "b" to go page up, hit "space" key to go page down. Type "q" to quit.

OR

#### \$ less arail

Less has more options than *more* ("less is more and *more* is less"). You can now use the keyboard Arrows and Page Up/Down to scroll. You can type "h" for help, which will display additional options.

View the line numbers in the grail file. The *cat* command has the -n option, which prints line numbers, but you may also want to use *more* to view the file one page at a time. A solution is to *pipe* the output from *cat* to *more*. A *pipe* redirects the output from one program to another program for further processing, and it is represented with "|".

#### \$ cat -n grail | more

Redirect the standard output (stdout) of a command.

\$ cat myfile.txt > redirect1.txt

\$ ls -lh > redirect2.txt

Append the stdout to a file.

### \$ cat mycopy.txt >> myfile.txt

mycopy.txt will be appended to myfile.txt.

• **Note**: "cat mycopy.txt > myfile.txt" will <u>overwrite</u> myfile.txt with the contents output by "cat mycopy.txt". Thus using >> is crucial if you want to preserve the existing file contents.

## 11. Change access permissions to objects with the *change mode* command.

```
The following represent roles:
```

```
u - user, g - group, o - others, a - all
```

The following represent permissions:

```
r – read, w – write, x – execute
```

Remove the read permission for your user on a file.

## \$ chmod u-r myfile.txt

Try to read this file. You should receive a "permission denied" message because you are the user who owns the file.

# **SUBMIT:** The screenshot of the permission denied error

```
[ec2-user@ip-172-31-41-200 ~]$ chmod u-r myfile.txt
[ec2-user@ip-172-31-41-200 ~]$ cat myfile.txt
cat: myfile.txt: Permission denied
[ec2-user@ip-172-31-41-200 ~]$
```

Give your user read permission on a file. Use the same file you removed the read permission from.

## \$ chmod u+r myfile.txt

You should now be able to read this file again.

## 12. Python examples

Install Python if it is not available on your machine.

## \$ sudo yum install python

Create a Python file. These instructions will use Emacs as a text editor, but you can still chose the text editor you want.

## \$ emacs lucky.py

```
(Write a simple Python program)
  print "*"*22
  print "My Lucky Numbers".rjust(20)
  print "*"*22

for i in range(10):
    lucky_nbr = (i + 1)*2
    print "My lucky number is %s!" % lucky_nbr
```

Run your Python program.

\$ python lucky.py

Redirect your output to a file

\$ python lucky.py > lucky.txt

Pipe the stdout from lucky.py to another Python program that will replace "is" with "was". \$ emacs was.py

```
import sys

for line in sys.stdin:
    print line.replace("is", "was")
```

#### \$ python lucky.py | python was.py

Write python code to read a text file (you can use myfile.txt) and output word count for each word with the number of times that word occurs in the entire file.

**SUBMIT:** The screen output from running your python code and a copy of your python code. Homework submissions without code will receive no credit

```
Homework submissions without code will receive no credit.
 [ec2-user@ip-172-31-41-200 ~]$ nano finalsubmit.txt
 ec2-user@ip-172-31-41-200 ~]$ nano wordcountp12.py
 ec2-user@ip-172-31-41-200 ~]$ python wordcountp12.py
    'am')
    'word')
    'red')
    'mean')
    'making')
    'counts')

♣ ec2-user@ip-172-31-41-200:~

                                             wordcountp12.py
  GNU nano 2.9.8
 doc = open('finalsubmit.txt', 'r')
 get the text and clean it
 textpre = doc.read()
 text = textpre.lower()
 for character in '`~!@#$%^&*() -+=[]{}|\;:"?/<>,.':
 for word in word list:
     d[word] = d.get(word, 0) + 1
 word freq list = []
     word freq list.append((value, key))
 word freq list.sort(reverse=True)
 print(textpre)
 for word in word freq list:
  print (word)
                                         [ Read 21 lines ]
                    Write Out
                                 ^W Where Is
```

# Part 3: Lab

For this part of the assignment, you will run wordcount on a single-node Hadoop instance. I am going to provide detailed instructions to help you get Hadoop running. The instructions are following Hadoop: The Definitive Guide instructions presented in Appendix A: Installing Apache Hadoop.

You can download 2.6.4 from here. You can copy-paste these commands (right-click in PuTTy to paste, but please watch out for error messages and run commands one by one)

Install ant to list java processes sudo yum install ant

(wget command stands for "web get" and lets you download files to your instance from a URL link)

wget http://rasinsrv07.cstcis.cti.depaul.edu/CSC555/hadoop-2.6.4.tar.gz

(unpack the archive)

tar xzf hadoop-2.6.4.tar.gz

Modify the conf/hadoop-env.sh to add to it the JAVA\_HOME configuration You can open it by running (using nano or your favorite editor instead of nano). nano hadoop-2.6.4/etc/hadoop/hadoop-env.sh

Note that the # comments out the line, so you would comment out the original JAVA\_HOME line replacing it by the new one as below.

**NOTE**: you would need to determine the correct Java configuration line by executing the following (underlined) command

[ec2-user@ip-172-31-16-63 ~]\$ <u>readlink -f \$(which java)</u> which will output:

/usr/lib/jvm/java-1.8.0-openjdk-1.8.0.191.b12-0.amzn2.x86 64/jre/bin/java

In my case, Java home is at (remove the bin/java from the output above): /usr/lib/jvm/java-1.8.0-openjdk-1.8.0.191.b12-0.amzn2.x86\_64/jre/

/usr/lib/jvm/java-1.8.0-openjdk-1.8.0.222.b10-0.amzn2.0.1.x86\_64/jre/bin/java - mine

```
# The only required environment variable is JAVA_HOME. All others are optional. When running a distributed configuration it is best to set JAVA_HOME in this file, so that it is correctly defined on remote nodes.

# The java implementation to use.
# export JAVA_HOME=${JAVA_HOME}
export JAVA_HOME=/usr/lib/jvm/jre-1.7.0-openjdk.x86_64

# The jsvc implementation to use. Jsvc is required to run secure datanodes that bind to privileged ports to provide authentication of data transfer
```

modify the .bashrc file to add these two lines: export HADOOP\_HOME=~/hadoop-2.6.4 export PATH=\$PATH:\$HADOOP\_HOME/bin:\$HADOOP\_HOME/sbin

.bashrc file contains environment settings to be configured automatically on each login. You can open the .bashrc file by running nano ~/.bashrc

```
# User specific aliases and functions

export HADOOP_HOME=~/hadoop-2.6.4

export PATH=$PATH:$HADOOP_HOME/bin:$HADOOP_HOME/sbin
```

To immediately refresh the settings (that will be <u>automatic on next login</u>), run **source** ~/.bashrc

Next, follow the instructions for Pseudodistributed Mode for all 4 files.

(to edit the first config file)
nano hadoop-2.6.4/etc/hadoop/core-site.xml

Make sure you paste the settings between the <configuration> and </configuration> tags, like in the screenshot below. NOTE: The screenshot below is only one of the 4 files, all files are different. The contents of each file are described in the **Appendix A** in the Hadoop book, the relevant appendix is also included with the homework assignment. I am also including a .txt file (HadoopConfigurationText) so that it is easier to copy-paste.

### nano hadoop-2.6.4/etc/hadoop/hdfs-site.xml

(mapred-site.xml file is not there, run the following single line command to create it by copying from template. Then you can edit it as other files.)

cp hadoop-2.6.4/etc/hadoop/mapred-site.xml.template hadoop-

#### 2.6.4/etc/hadoop/mapred-site.xml

nano hadoop-2.6.4/etc/hadoop/mapred-site.xml nano hadoop-2.6.4/etc/hadoop/yarn-site.xml

To enable passwordless ssh access (we will discuss SSH and public/private keys in class), run these commands:

```
ssh-keygen -t rsa -P " -f ~/.ssh/id_rsa
cat ~/.ssh/id_rsa.pub >> ~/.ssh/authorized_keys
```

test by running (and confirming yes to a one-time warning) ssh localhost exit

Format HDFS (i.e., first time initialize)

#### hdfs namenode -format

Start HDFS, Hadoop and history server (answer a 1-time yes if you asked about host authenticity)

start-dfs.sh start-yarn.sh mr-jobhistory-daemon.sh start historyserver

Verify if everything is running: **ips** 

(NameNode and DataNode are responsible for HDFS management; NodeManager and ResourceManager are serving the function similar to JobTracker and TaskTracker. We will discuss function of all of those on Thursday.)

Create a destination directory hadoop fs -mkdir /data

Download a large text file using

wget http://rasinsrv07.cstcis.cti.depaul.edu/CSC555/bioproject.xml

Copy the file to HDFS for processing

hadoop fs -put bioproject.xml /data/

(you can optimally verify that the file was uploaded to HDFS by hadoop fs -ls /data)

Submit a screenshot of this command

#### File is in.

```
[ec2-user@ip-172-31-41-200 ~]$ hadoop fs -ls /data
Found 1 items
-rw-r--r- 1 ec2-user supergroup 231149003 2020-01-22 21:46 /data/bioproject.xml
[ec2-user@ip-172-31-41-200 ~]$ □
```

Run word count on the downloaded text file, using the time command to determine the total runtime of the MapReduce job. You can use the following (single-line!) command. This invokes the wordcount example built into the example jar file, supplying /data/bioproject.xml as the input and /data/wordcount1 as the output directory. Please remember this is one command, if you do not paste it as a single line, it will not work.

time hadoop jar hadoop-2.6.4/share/hadoop/mapreduce/hadoop-mapreduce-examples-2.6.4.jar wordcount /data/bioproject.xml /data/wordcount1

Report the time that the job took to execute as screenshot

```
real 1m12.273s
user 0m4.018s
sys 0m0.179s
[ec2-user@ip-172-31-41-200 ~]$
```

(this reports the size of a particular file or directory in HDFS. The output file will be named part-r-00000)

hadoop fs -du /data/wordcount1/

```
[ec2-user@ip-172-31-41-200 ~]$ hadoop fs -du /data/wordcount1/
0 /data/wordcount1/_SUCCESS
20056175 /data/wordcount1/part-r-00000
[ec2-user@ip-172-31-41-200 ~]$ [
```

(Just like in Linux, the cat HDFS command will dump the output of the entire file and grep command will filter the output to all lines that matches this particular word). To determine the count of occurrences of "arctic", run the following command:

## hadoop fs -cat /data/wordcount1/part-r-00000 | grep arctic

It outputs the entire content of part-r-00000 file and then uses pipe | operator to filter it through grep (filter) command. If you remove the pipe and grep, you will get the entire word count content dumped to screen, similar to cat command.

```
ec2-user@ip-172-31-41-200:~

antarcticus</i&gt;&lt;/b&gt;.
antarcticus, 1
antarcticus, 1
antarcticus</name> 5
antarcticus</name> 5
arctica 27
arctica&lt;/i&gt; 3
arctica&lt;/i&gt; 3
arctica&lt;/i&gt; 3
arctica*(Name> 5
arctica*(Name> 5
arctica*(Name> 6
arcticus</name> 7
arcticus</name> 7
arcticus*(Name> 6
arcticus 31
arcticus&lt;/i&gt; 2
arcticus&lt;/i&gt; 2
arcticus*(Name> 4
arcticus*(Name> 4
arcticus*(OrganismName> 4
holarctica 77
humans.Antarctic 1
palearctica*(Name> 1
sub-Antarctic 4
sub-arctic 4
subantarcticus 7
subantarcticus</name> 1
subantarcticus</name> 1
subantarcticus
7
subantarcticus
7
subantarcticus
7
subantarcticus</name> 1
subantarcticus</name> 1
subantarcticus
7
subantarcticus
7
subantarcticus</name> 1
subantarcticus</name> 1
subantarcticus</name> 1
subantarcticus</name> 1
subantarcticus</name> 1
subantarcticus</name> 1
```

Congratulations, you just finished running wordcount using Hadoop.

Submit a single document containing your written answers. Be sure that this document contains your name and "CSC 555 Assignment 1" at the top.