STA 250 HW2 Codes

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1 BLB_lin_reg_job.R

```
mini <- FALSE
args <- commandArgs(TRUE)
cat("Command-line arguments:\n")
print(args)
####
# sim_start ==> Lowest possible dataset number
##################
sim_start <- 1000
###################
if (length(args)==0){
 sim_num <- sim_start + 1</pre>
 set.seed(121231)
 # SLURM can use either 0- or 1-indexing...
 # Lets use 1-indexing here...
 sim_num <- sim_start + as.numeric(args[1])</pre>
 sim_seed <- (762*(sim_num-1) + 121231)
cat(paste("\nAnalyzing dataset number ",sim_num,"...\n\n",sep=""))
s = 5 ### s is no. of susets each of size b
r = 50 \text{ ### } r \text{ is no. of bootstrap samples from each subset}
# Find r and s indices:
s_{index} = floor((sim_num -1001)/r) + 1
#### For the 1st 50 jobs it takes 1, next 50 jobs it takes 2 and so on: 1 to 5
r_{index} = (sim_{num} -1001)\%r + 1
#### For the 1st 50 jobs it takes 1 to 50, next 50 jobs it again takes 1 to 50 and so on
#======= Run the simulation study =======#
# Load packages:
library(BH)
library(bigmemory.sri)
library(bigmemory)
library(biganalytics)
# I/O specifications:
```

```
datapath <- "/home/pdbaines/data"
outpath <- "output/"
# mini or full?
if (mini){
rootfilename <- "blb_lin_reg_mini"</pre>
} else {
rootfilename <- "blb_lin_reg_data"</pre>
# filenames:
infilename <- pasteO(rootfilename,".txt")</pre>
backingfilename <- paste0(rootfilename,".bin")</pre>
descriptorfilename <- paste0(rootfilename,".desc")</pre>
# Set up I/O stuff:
infile <- paste(datapath,infilename,sep="/")</pre>
backingfile <- paste(datapath,backingfilename,sep="/")</pre>
descriptorfile <- paste(datapath,descriptorfilename,sep="/")</pre>
### Attaching the data matrix using the description file already created by Prof. Baines ###
data <- attach.big.matrix(dget(descriptorfile),backingpath=datapath)</pre>
n = nrow(data)
p = ncol(data)
### We choose b = n^0.7 ####
gamma=0.7 ### used to choose b
b=n^gamma ### b is size of each subset
######### Setting same seed to have same subset when s_index is same######
set.seed(s_index*1000)
######## Sampling a subset of b rows from the whole data #########
index = sample(1:n, b, replace = FALSE)
subset = data[index,]
##### Nullifying set.seed and ensuring that for the same subset it produces different bootstrap samples #####
set.seed(s_index*1000 + r_index*10)
#### So basically want to draw a random sample sample from a multinomial distribution
#### Multinomial sample tells you how many times each unique datapoint of the subset is
repeated in the bootstrap sample
freq = rmultinom(1, n, rep(1/b, b))
### So basically fitting a linear model to the subset of data with weight equals to the multinomial sample
y = subset[ , p]
X = subset[, 1:(p-1)]
boot_mod = lm( y ~ X -1, weights = freq) # linear model without the intercept term
###### Output file ############
write(summary(boot_mod)$coefficients[,1], file =
paste0("output/","coef_",sprintf("%02d",s_index),"_",sprintf("%02d",r_index),".txt"))
```

2 MapReducer

Mapper:

```
#! /usr/bin/python
import sys
import math
# input comes from STDIN (standard input)
for line in sys.stdin:
   # remove leading and trailing whitespace
   line = line.strip()
   # split the line into two numbers
   numbers = line.split('\t')
   # Calculate the key
   \# For each pair of observation it produces x_lo and y_lo as the key
   # x_lo and y_lo of the bin in which the observation should be
   n = float((math.floor(10*float(numbers[0])))/10), float((math.floor(10*float(numbers[1])))/10)
   #convert keys into strings from floats
   num_st1 = str(n[0])
   num_st2 = str(n[1])
   print '%s,%s\t%s' % (num_st1, num_st2, 1)
```

Reducer:

```
#! /usr/bin/python
import sys
current_bin = None
current_freq = 0
bin = None
# Input comes from STDIN
for line in sys.stdin:
   #remove trailing '\n'
   line = line.strip()
   # extract key and value from the output of Mapper
   bin, freq = line.split('\t')
   # Convert freq (currently string)into int
   try:
       freq = int(freq)
   except ValueError:
       # count was not a number, so silently
       # ignore/discard this line
   # Assuming that Hadoop has sorted the output from Mapper before passing it to reducer
   if current_bin == bin:
       current_freq += freq
   else:
        if current_bin:
```

```
x_lo, y_lo = bin.split(',')
x_hi = str(float(x_lo) + 0.1)
y_hi = str(float(y_lo) + 0.1)
print '%s,%s,%s,%s,%s' % (x_lo,x_hi,y_lo,y_hi,current_freq)
current_freq = freq
current_bin = bin

# Printing the last one
if current_bin == bin:
x_lo, y_lo = bin.split(',')
x_hi = str(float(x_lo) + 0.1)
y_hi = str(float(y_lo) + 0.1)
print '%s,%s,%s,%s,%s' % (x_lo,x_hi,y_lo,y_hi,current_freq)
```

3 Hive:

```
[Creating an empty table with two columns similar as the data]
hive> CREATE TABLE bigdata(
    > groups INT,
    > obs DOUBLE)
    > ROW FORMAT DELIMITED
    > FIELDS TERMINATED BY '\t'
    > STORED AS TEXTFILE;
[Loading the data into the table bigdata]
hive > LOAD DATA INPATH 'data/groups.txt' INTO TABLE bigdata;
[Checking how many observations have been read in the table bigdata]
hive> SELECT COUNT(*) FROM bigdata;
[Creating an external table to store group means and within group variances at a specific location]
hive> CREATE EXTERNAL TABLE result(
   > mean DOUBLE,
   > variance DOUBLE)
   > ROW FORMAT DELIMITED
   > FIELDS TERMINATED BY ' '
    > LINES TERMINATED BY '\n'
    > STORED AS TEXTFILE LOCATION '/user/hadoop/results';
[Calculating group means and within group variances and storing them into the external table]
hive> INSERT INTO TABLE result
    > SELECT AVG(obs), VARIANCE(obs)
    > FROM bigdata
    > GROUP BY groups;
[Checking how many observations have been read in the table result]
hive> SELECT COUNT(*) FROM result;
```