1. How many distinct genes are represented in the data set?
   * There are 5001 distinct genes represented in the data set.
2. Which two time points are the most highly correlated for each cell type?
   * In HL60 0 hrs and 4 hrs are most highly correlated
   * In U937 0.5 hrs and 4 hrs are most highly correlated
   * In NB4 24 hrs and 48 hrs are most highly correlated
   * In Jurkat 0.5 hrs and 4 hrs are most highly correlated
3. Which two cell types are the most similar?
   * Jurkat at 0 hrs and U937 at 0 hrs are most highly correlated.
4. It is often useful to know which genes change very little across samples for the sake of normalization or calibration. Based on this data set, what are ten good candidates for genes to use to calibrate machinery or analyses across all these samples?
   * H85478, H88261, M95586\_r\_i, X73424\_i, X73424\_i, R94219, U39231, H82137, L20814, R39006, X86401 have the lowest variances.
5. Do any genes show two-fold higher expression at 24 hours versus 0 hours for all four cell types? If so, which ones?
   * D16227, H24635, J04076, M15395, M26383, M87503, R32804, R56881, R85690, R94861, T77537, T79846, U00115\_f, U00672, U27467, U27467, U30498, X04500, X79066
6. Which genes are differentially regulated (at least two-fold higher or lower) in HL60 cells as compared to U937 cells at 0 hours?
   * BioB, BioC, D00003\_i, D00137, D00173, D00306, D00596, D00726, D10202, D10216, D10522\_i, D10522\_r, D10570, D10656, D10704, D10872, D11086, D11327\_r, D11428\_r, D12686\_r, D12765\_i, D12765\_r, D13138, D13243, D13292\_i, D13305, D13626, D13627\_f, D13628, D13630, D13634, D13635\_i, D13635\_r, D13636, D13640, D13641\_f, D13641\_i, D13641\_r\_i, D13642\_f, D13642\_i, D13643, D13644, D13645, D13789, D13902, D14134, D14520, D14658, D14661, D14662, D14664, D14665, D14689, D14694, D14695, D14812, D14823, D14838, D14874, D15049, D15056, D16431, D16469, D16593, D16626, D17390, D17400, D17530, D17570\_r, D21090\_r, D21094, D21163, D21205, D21235, D21260, D21261, D21262, D21337, D21851, D21852, D21853\_f, D23672, D25218\_f, D25218\_i, D25235, D25278, D25303, D25304, D25538, D26018, D26067, D26068\_f, D26125\_f, D26129\_f, D26135, D26309, D26528, D28124, D28475, D28588, D29642\_f, D29642\_r\_i, D29767, D29805, D29808, D29954, D29992, D30036, D30742, D31716, D31766, D31883\_f, D31889\_i, 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7. Take the list of Gene Accession codes from (F), and run them through the DAVID ontology analyzer. (at http://david.abcc.ncifcrf.gov/summary.jsp . These are GenBank Accession codes.) Are there any enriched ontology terms?
   * No, there were no positive Gene Accession Conversion Statistics. 1673 were given a definitive “No.” 1283 were assigned “Ambiguous.”

Ack! Code! In a Word doc? Please, no, never! Presentation matters. This looks totally newb, and makes the job of your TA harder.

**Script: Should be an object ☺**

from pandas import \*

from pandas.io import parsers

## Importing the data file and converting to a DataFrame

data = parsers.read\_csv('data\_set\_HL60\_U937\_NB4\_Jurkat.csv',index\_col = 1)

df = DataFrame(data)

## Determining Distinct Genes

unique\_genes = set(df['Gene Description'])

print('There are '+ str(len(unique\_genes))+' distinct genes represented in the data set.')

# Nicely done with the set.

## Correlating Cell Types

corr\_matrix = df.corr(method ='pearson') #DataFrame correlation function .corr

corr\_matrix.to\_csv('output.csv') # Outputs correlation array to a csv

# What exactly are you correlating here? Cell types as a whole, or just one timepoint of a cell? The answer you give is for a single timepoint, presumably manually selected from the output array? Ideally, you would have some way of analyzing over all cell types.

## Determining Gene Variance

var\_matrix = df.var(axis=1) #DataFrame variance function .var

var\_matrix.sort() #DataFrame sort function .sort

print(var\_matrix) #Displays variance matrix sorted by lowest variance

## Two-Fold Gene Expression

#Boolean array checking for gene expression across all 4 cell types

division\_matrix = (abs(df['HL60\_24\_hrs']/df['HL60\_0\_hrs']) > 2) & (abs(df['U937\_24\_hrs']/df['U937\_0\_hrs']) > 2) & (abs(df['NB4\_24\_hrs']/df['NB4\_0\_hrs']) > 2) & (abs(df['Jurkat\_24\_hrs']/df['Jurkat\_0\_hrs']) > 2)

division\_matrix.sort() #DataFrame sort function .sort

division\_matrix.to\_csv('twoFold.csv') # Outputs boolean gene expression array to a csv

# See note in email about division by zero.

## Differential regulation

#Similar method to Two-Fold Gene Expression

division\_HU\_matrix = (abs(df['HL60\_0\_hrs']/df['U937\_0\_hrs']) > 2) | (abs(df['U937\_0\_hrs']/df['HL60\_0\_hrs']) > 2)

division\_HU\_matrix.sort()

division\_HU\_matrix.to\_csv('twoFold\_HU.csv')

# Well commented code, which is appreciated!