1) Read in table 1 from the following website: https://www.cdc.gov/coronavirus/2019-ncov/hcp/planning-scenarios.html
    a. Use the data from Scenario 5 to create a dataframe of IFR by age, where one column is age from 0 to 100 years old and the other column is the IFR for that age
    b. Read in the World Demographics csv file as a dataframe.
    c. Create a list of all of the countries within the World Demographics file and the total population of each country using a groupby.
    d. Create a function that takes in the World Demographics dataframe, the name of a country, and the IFR dataframe and returns the IFR for that country. Do this by filtering the population dataframe to the data for the country, adding the IFR data by age to that table, creating a new column that is the expected number of people that will die from covid for that age, and then using a summary method to calculate the total number of deaths.

2) Read in the data from the 021821_medium_threshold2.csv example file.
    a. Identify the 10 genes with the highest average expression (axis and sort_values will be useful here)
    b. Identify the cell types with that has the gene with highest expression
    c. Identify genes that are expressed in ASEL but not ASER.
    d. Identify genes that are not expressed in ASH or ASI.
    e. Convert the data in the table to Booleans, True if there is expression in a cell type and False if the expression is 0.
    f. Use this table to identify the 3 cell types with the most genes with expression within them and the 3 cell types with the least number of genes expressed in them
    g. Use this table to identify the number of genes that expressed in both ASH and ASI, ASH but not ASI, not ASH but ASI, and not in either
    h. Use this table to identify the cell types that share the most genes with ASH. The least number of genes with ASH