## BIS 634 HW1

## Exercise 1:

```
In [1]: def temp_tester(temp):
             def case_temp(case_temp):
                if (abs(case_temp - temp) <= 1):</pre>
                     print('true')
                 else:
                     print('false')
                 return
             return case_temp
         human_tester = temp_tester(37)
         chicken_tester = temp_tester(41.1)
         chicken_tester(42) # True - i.e. not a fever for a chicken
         human_tester(42) # False — this would be a severe fever for a human
         chicken_tester(43) # False
         human_tester(35) # False - too low
         human_tester(98.6) # False — normal in degrees F but our reference temp was in degrees C
         false
         false
         false
         false
```

A simple function to identify whether the temperature is normal or not.

## Exercise 2:

- 1. Has columns name, age, weight, and eye color
- 2. 152361 cases in the total population

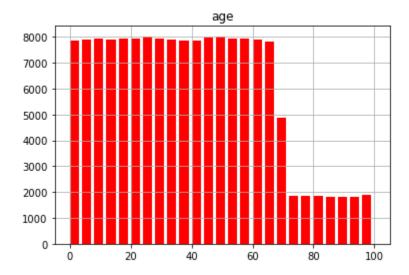
```
In [21]: print(list(data.columns))
    print(data['name'].count())

['name', 'age', 'weight', 'eyecolor']
    152361
```

3. The distribution of age is:

```
[22]:
      print(data['age'].describe())
                152361.000000
       count
                    39.510528
       mean
                    24.152760
       std
                     0.000748
       \min
       25%
                    19.296458
       50%
                    38.468955
       75%
                    57.623245
                    99.991547
       max
       Name: age, dtype: float64
```

4. The number of bins is 25 as the range is 0-100. Each bin represents 4 years. The presentation of chart is clear and detailed. The outlier is around age 70, the population size drops sharply

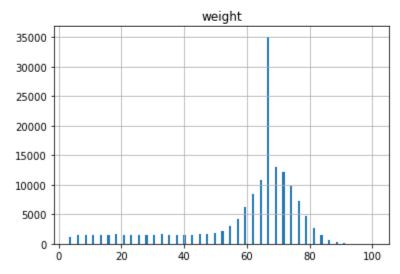


5. The number of bins is 40 for weight as it is a continuous value. More bins can demonstrate more details. The population of 68 kg is extraordinarily large

```
print(data['weight'].describe())
weight_dist=data.hist(column=['weight'],bins=40,width=0.7);
```

```
152361.000000
count
             60.884134
mean
std
             18.411824
              3.382084
min
25%
             58.300135
50%
             68.000000
75%
             71.529860
            100.435793
max
```

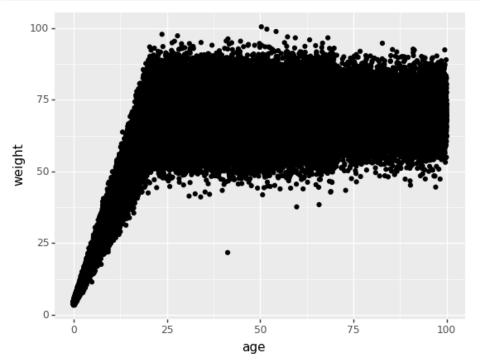
Name: weight, dtype: float64



6. When age is less than 20, age and weight are strongly correlated. Body weight increases with age. After the age of about 20, weight stabilizes around 60-85 kg. In addition, people between the ages of 20 and 100 seem to have a greater standard deviation in body weight.

7. There is an outlier in the graph, his name is Anthony Freeman. His weight is unusually low. He can be found by the constraints.

```
In [85]: from plotnine import *
ggplot(df, aes(x='age', y='weight')) + geom_point()
```



```
Out[85]: <ggplot: (154721296366)>
```

```
In [88]: outlier=data.loc[data['age']>35].loc[data['weight']<25]
print(outlier)</pre>
```

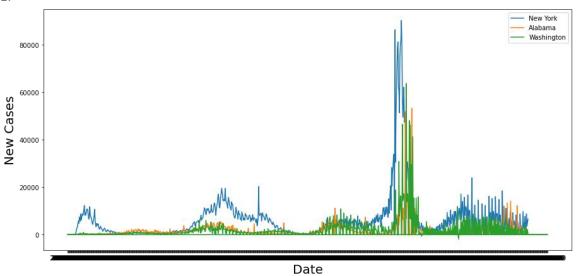
```
name age weight eyecolor
537 Anthony Freeman 41.3 21.7 green
```

## Exercise 3:

Data download on 9/22/2022

Data source is The New York Times

1.



Function plot\_state\_cases() is used to plot state new cases. Too many selected states will overlap and be difficult to read. Intensive areas can also be difficult to read. The time range is too close that the X-axis is too dense.

### 2. Function for identify the date of new cases peak

```
def peak(state):
    case=data[data.state=state].cases
    new_case=[case.iloc[i+1]-case.iloc[i] for i in range(case.shape[0]-1)]
   new_case=np.insert(new_case, 0, case.iloc[0])
    state_case=data[data.state=state]
    new=state_case.loc[:,'new cases']=new_case
    new_case_number=state_case['new cases']
    peak_number=new_case_number.max()
    date = state_case[state_case['new cases'] == peak_number]['date']
    return date.iloc[0]
print(peak('Connecticut'))
print(peak('Washington'))
print(peak('New York'))
print(peak('New Jersey'))
print(peak('Illinois'))
2022-01-10
2022-01-18
2022-01-08
2021-01-04
2022-01-18
```

## 3. Peak comparision between the states

```
from dateutil.parser import parse as parse
def state_comp(state1, state2):
    peak1 = peak(state1)
    peak2 = peak(state2)

date1 = parse(peak1)
    date2 = parse(peak2)

if (date1 == date2):
    print(state1, 'and', state2, 'had same peak on', peak1)
    elif (date1 < date2):
        print(state1, "had its peak", (date2-date1).days, "days earlier than", state2)
    else:
        print(state2, "had its peak", (date1-date2).days, "days earlier than", state1)

state_comp('Washington', 'New York')
state_comp('Connecticut', 'Ohio')</pre>
```

New York had its peak 10 days earlier than Washington Connecticut had its peak 5 days earlier than Ohio

#### Exercise 4:

- 1. The DescriptorName of DescriptorUI D007154 is Immune System Diseases.
- 2. The DescriptorUI of DescriptorName Nervous System Diseases is "D009422".
- 3. The DescriptorNames of items in the MeSH hierarchy that are subtypes of both Nervous System Diseases and D007154 is:

```
['Autoimmune Hypophysitis',
'Ataxia Telangiectasia',
'Diffuse Cerebral Sclerosis of Schilder',
'Encephalomyelitis, Acute Disseminated',
'Encephalomyelitis, Autoimmune, Experimental',
'Leukoencephalitis, Acute Hemorrhagic',
'Kernicterus',
'Multiple Sclerosis',
'Myasthenia Gravis',
'Myelitis, Transverse',
'Neuritis, Autoimmune, Experimental',
'Neuromyelitis Optica',
'Polyradiculoneuropathy',
'Giant Cell Arteritis',
'Uveomeningoencephalitic Syndrome',
'AIDS Dementia Complex',
'Lambert-Eaton Myasthenic Syndrome',
'Stiff-Person Syndrome',
'POEMS Syndrome',
'Miller Fisher Syndrome',
'Autoimmune Diseases of the Nervous System',
'Guillain-Barre Syndrome',
'Polyradiculoneuropathy, Chronic Inflammatory Demyelinating',
'Demyelinating Autoimmune Diseases, CNS',
'Vasculitis, Central Nervous System',
'Multiple Sclerosis, Chronic Progressive',
'Multiple Sclerosis, Relapsing-Remitting',
'Myasthenia Gravis, Autoimmune, Experimental',
'Nervous System Autoimmune Disease, Experimental',
'Myasthenia Gravis, Neonatal',
'AIDS Arteritis, Central Nervous System',
'Lupus Vasculitis, Central Nervous System',
'Mevalonate Kinase Deficiency',
'Microscopic Polyangiitis',
'Anti-N-Methyl-D-Aspartate Receptor Encephalitis']
```

4. These diseases are a subtype of both immune system disorders and neurological disorders. Because their tree numbers include both C20 and C10.

## Code

## Exercise 1:

```
In [1]: def temp_tester(temp):
              def case_temp(case_temp):
                   if(abs(case_temp - temp) <= 1):</pre>
                       print('true')
                   else:
                       print('false')
                   return
              return case_temp
          human_tester = temp_tester(37)
          chicken_tester = temp_tester(41.1)
          chicken_tester(42) # True — i.e. not a fever for a chicken human_tester(42) # False — this would be a severe fever for a human
          chicken_tester(43) # False
          human_tester(35) # False — too low
          human_tester(98.6) # False — normal in degrees F but our reference temp was in degrees C
          true
          false
          false
          false
          false
```

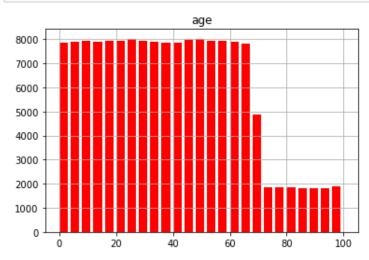
# Exercise 2:

```
In [24]: import pandas as pd
           import sqlite3
           with sqlite3.connect("hwl-population.db") as db:
               data = pd.read_sql_query("SELECT * FROM population", db)
           df = pd.DataFrame(data)
           df.head(5)
Out[24]:
                      name
                                  age
                                         weight eyecolor
            0
                Edna Phelps
                            88.895690 67.122450
                                                   brown
            1
                 Cara Yasso
                             9.274597
                                      29.251244
                                                   brown
                   Gail Rave
                            18.345613 55.347903
                                                   brown
              Richard Adams
                            16.367545 70.352184
                                                   brown
                 Krista Slater 49.971604 70.563859
                                                   brown
In [21]: print(list(data.columns))
           print(data['name'].count())
           ['name', 'age', 'weight', 'eyecolor']
           152361
```

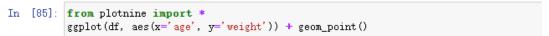
```
In [22]: print(data['age'].describe())
```

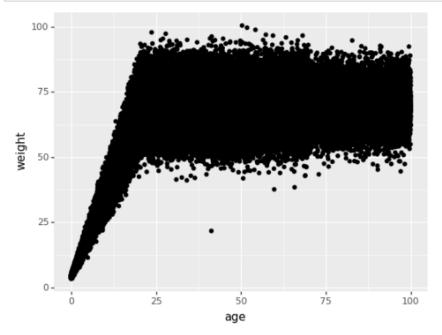
```
152361.000000
count
             39.510528
mean
             24.152760
std
min
              0.000748
25%
             19.296458
50%
             38.468955
75%
             57.623245
             99.991547
Name: age, dtype: float64
```

# In [75]: age\_dist=data.hist(column=['age'],bins=25,color='red',width=3)



```
In [83]: print(data['weight'].describe())
           weight_dist=data.hist(column=['weight'], bins=40, width=0.7);
                     152361.000000
           count
                          60.884134
           mean
           \operatorname{std}
                         18.411824
                          3.382084
           min
                          58.300135
           25%
           50%
                          68.000000
           75%
                          71.529860
                         100.435793
           max
           Name: weight, dtype: float64
                                       weight
            35000
            30000
            25000
            20000
            15000
            10000
             5000
                                                              100
                          20
                                                      80
```





```
Out[85]: <ggplot: (154721296366)>
```

```
In [88]: outlier=data.loc[data['age']>35].loc[data['weight']<25]
print(outlier)</pre>
```

```
name age weight eyecolor
537 Anthony Freeman 41.3 21.7 green
```

## Exercise 3:

```
In [200]: import pandas as pd
   import numpy as np
   import matplotlib.pyplot as plt
   import seaborn as sns

original_data = pd.read_csv("us-states.csv")

# simplify dataset
data = original_data.drop(['fips','deaths'], axis=1)
df.head(1000)
```

#### Out [200]:

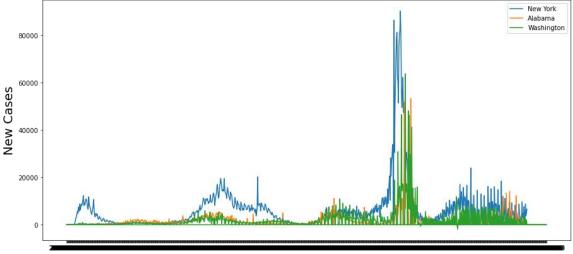
	date	state	cases
0	2020-01-21	Washington	1
1	2020-01-22	Washington	1
2	2020-01-23	Washington	1
3	2020-01-24	Illinois	1
4	2020-01-24	Washington	1
995	2020-03-20	Oregon	114
996	2020-03-20	Pennsylvania	269
997	2020-03-20	Puerto Rico	14
998	2020-03-20	Rhode Island	44
999	2020-03-20	South Carolina	126

## 1000 rows × 3 columns

```
In [231]: def plot_state_cases(state):
    for i in range(len(state)):
        case=data[data.state==state[i]].cases
        new_case=[case.iloc[i+1]-case.iloc[i] for i in range(case.shape[0]-1)]
        new_case=np.insert(new_case,0,case.iloc[0])
        state_case=data[data.state==state[i]]
        new=state_case.loc[:,'new_cases']=new_case
        state_case = state_case.reset_index(drop=True)

        plt.plot(state_case['date'], state_case['new_cases'], label = state[i])
        plt.legend()
        plt.xlabel('Date',fontsize=20)|
        plt.ylabel('New_Cases',fontsize=20))

    plot_state_cases(['New_York','Alabama','Washington'])
```



## Date

2022-01-10

2022-01-18

2022-01-08

2021-01-04

2022-01-18

```
In [237]: from dateutil.parser import parse as parse
            def state_comp(state1, state2):
                peak1 = peak(state1)
                peak2 = peak(state2)
                date1 = parse(peak1)
                date2 = parse(peak2)
                if (date1 == date2):
                    print(state1, 'and', state2, 'had same peak on', peak1)
                elif (date1 < date2):</pre>
                    print(state1, "had its peak", (date2-date1).days, "days earlier than", state2)
                else:
                    print(state2, "had its peak", (date1-date2).days, "days earlier than", state1)
           state_comp('Washington', 'New York')
state_comp('Connecticut', 'Ohio')
```

New York had its peak 10 days earlier than Washington Connecticut had its peak 5 days earlier than Ohio

```
Exercise 4:
 In [9]: import xml.etree.ElementTree as ET
            from pprint import pprint as pp
tree = ET.parse('desc2022.xml')
root = tree.getroot()
In [11]: def find_des_name(UI):
                for DescRe in root:
    if (DescRe.find('DescriptorUI').text == UI):
                           print(DescRe.find('DescriptorName').find('String').text)
            find_des_name('D007154')
             Immune System Diseases
In [21]: def find_des_ui(Name):
                for DescRe in root:
    if (DescRe.find('DescriptorName').find('String').text == Name);
                           print(DescRe.find('DescriptorUI').text)
            find_des_ui('Nervous System Diseases')
            D009422
In [21]: def shared_child(parent1, parent2):
                 shared_child = []
#get treenumbers
                  for child in root:
                      if (child.find('DescriptorUI').text == parent1):
                      treel = child.find('TreeNumberList').findall('TreeNumber')
if (child.find('DescriptorUI').text == parent2):
    tree2 = child.find('TreeNumberList').findall('TreeNumber')
                  def child_identifier(parent, child):
                       for i in range(len(parent))
                           if (parent[i].text in child):
                                 return True
                       return False
                  for child in root:
                       if (child.attrib['DescriptorClass']!= '3'):
                            tree = child.find('TreeNumberList').findall('TreeNumber')
                            tree text =
                           for i in range(len(tree)):
                           tree_text = tree_text + tree[i].text
#check if child of both parents
                           if (child_identifier(tree1, tree_text) and child_identifier(tree2, tree_text)):
    shared_child.append(child.find('DescriptorName')[0].text)
                  return shared_child
             shared_child('D007154', 'D009422')
```