Notebook

April 10, 2022

[ ]:
```
# This Python 3 environment comes with many helpful analytics libraries␣
 ↪installed
# It is defined by the kaggle/python Docker image: https://github.com/kaggle/
 ↪docker-python
# For example, here's several helpful packages to load

import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)

# Input data files are available in the read-only "../input/" directory
# For example, running this (by clicking run or pressing Shift+Enter) will list␣
 ↪all files under the input directory

import os
for dirname, _, filenames in os.walk('/kaggle/input'):
    for filename in filenames:
        print(os.path.join(dirname, filename))

# You can write up to 20GB to the current directory (/kaggle/working/) that␣
 ↪gets preserved as output when you create a version using "Save & Run All"
# You can also write temporary files to /kaggle/temp/, but they won't be saved␣
 ↪outside of the current session
```

```
/kaggle/input/dataset/cdbrfss1999.csv
```

Data Analysis in Astronomy and Physics

Exercise Set 1

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1.Sampling

[ ]:
```
import os
os.getcwd() # get current working dictory
```

[ ]:
```
'/kaggle/working'
```

[ ]:
```
os.chdir('/kaggle/') #change dirctory to kaggle
os.getcwd()
```

[ ]: '/kaggle'

[ ]:
```
os.listdir('/kaggle') # show the list of dictory 'kaggle'
```

[ ]: ['src', 'lib', 'input', 'working']

[ ]:
```
os.listdir('/kaggle/input/dataset')
```

[ ]: ['cdbrfss1999.csv']

Large data * > a. Take a sample of 30000 from this dataset and export it to an ASCII file. Make sure that your method allows to draw more than one sample from the population. * > b. Discuss your method to do so. Is your sampling a "good sample" in the sense that it is representative for the larger "population"?

solution: * a. 1. Get the total number of data in file by counting the number of rows and minus 1 2. Set the desired sample size(30000) 3. select (n-s) numbers randomly from range(1,n+1) 4. skip the corresponding rows when reading the csv * b. The method here is simple random sampling,each sample chosen by equal probability, so it's can be representative for larger "population"

5/10

discuss bias... what makes it a good sample

[ ]:
```
import pandas as pd
import random

filename = 'input/dataset/cdbrfss1999.csv'
n = sum(1 for line in open(filename)) - 1 #number of rows in file (excludes␣
↪header)
s = 30000 #desired sample size
skip = sorted(random.sample(range(1,n+1),n-s)) #select (n-s) numbers randomly␣
↪from range(1,n+1). In next step, skip the corresponding row when reading the␣
↪csv
cdbr = pd.read_csv(filename,skiprows = skip)
cdbr #display the 30000 samples by dataframe
```

indexes begin at 0

2/5

export & submit sample

```
/opt/conda/lib/python3.7/site-packages/IPython/core/interactiveshell.py:3457:
DtypeWarning: Columns (8) have mixed types.Specify dtype option on import or set
low_memory=False.
  exec(code_obj, self.user_global_ns, self.user_ns)
```

[ ]:

	STATE	GEOSTR	DENSTR	PSU	RECORD	IMONTH	IDAY	IYEAR	INTVID	\
0	1	1	1	10039	1	1	16	1999	0	
1	1	1	1	10105	1	1	11	1999	40	
2	1	1	1	10120	1	1	23	1999	33	
3	1	1	1	10142	1	1	12	1999	33	
4	1	1	1	10155	1	1	12	1999	0	
…	…	…	…	…	…	…	…	…	…	
29995	72	1	1	120976	1	12	20	1999	4	
29996	72	1	1	121012	1	12	22	1999	9	
29997	72	1	1	121021	1	12	19	1999	20	
29998	72	1	1	121040	1	12	2	1999	6	

```
29999     72       1       1  121057       1       12      9    1999      20

       Unnamed: 9  …  Unnamed: 272  Unnamed: 273  Unnamed: 274  \
0             NaN  …             1             9           1.0
1             NaN  …             1             9           1.0
2             NaN  …             1             9           1.0
3             NaN  …             1             9           3.0
4             NaN  …             1             9           1.0
…           …  …           …           …           …
29995         NaN  …             2             9           1.0
29996         NaN  …             1             9           1.0
29997         NaN  …             1             9           1.0
29998         NaN  …             1             9           3.0
29999         NaN  …             2             9           1.0

       Unnamed: 275  Unnamed: 276  Unnamed: 277  Unnamed: 278  Unnamed: 279  \
0                 1           2.0             6             1             1
1                 1           3.0             9             1             1
2                 1           1.0             3             1             1
3                 1           2.0             5             1             1
4                 1           2.0             7             1             1
…               …           …           …           …           …
29995             1           1.0             3             1             2
29996             1           3.0            10             2             2
29997             1           2.0             4             1             2
29998             1           1.0             1             1             2
29999             1           2.0             7             1             2

       Unnamed: 280  Unnamed: 281
0                 1             1
1                 1             1
2                 1             1
3                 1             1
4                 1             1
…               …           …
29995             3             1
29996             3             1
29997             3             1
29998             3             1
29999             3             1

[30000 rows x 282 columns]
```

> Large columns * > a. Locate the columns corresponding to the variables genhlth, exerany, htf, hti, smoke100, weight, wtdesire, age, and sex. * > b. Reduce your sample to include only these variables and export it to an ASCII file.

solution: export this Dataframe into an ASCII file that include only these variables

[ ]:
```
Large_Columns_b =␣
↪cdbr[['GENHLTH','EXERANY','HTF','HTI','SMOKE100','WEIGHT','WTDESIRE','AGE','SEX']]
filename_destination= 'working/Large_Columns_b.csv'
Large_Columns_b.to_csv(filename_destination)
Large_Columns_b  # display the Dataframe that question "Large Column b" required
```

5/5

[ ]:

	GENHLTH	EXERANY	HTF	HTI	SMOKE100	WEIGHT	WTDESIRE	AGE	SEX
0	1	NaN	5	8	1	175	NaN	49	2
1	4	NaN	5	10	1	180	NaN	60	1
2	1	NaN	5	3	2	147	NaN	34	2
3	3	NaN	5	5	1	110	NaN	42	2
4	2	NaN	5	3	2	126	NaN	52	2
…	…	…	…	…	…	…	…	…	…
29995	3	NaN	5	6	2	180	NaN	31	1
29996	3	NaN	5	4	2	120	NaN	69	2
29997	1	NaN	5	1	2	125	NaN	37	2
29998	1	NaN	5	1	2	120	NaN	24	2
29999	4	NaN	5	4	2	170	NaN	54	2

[30000 rows x 9 columns]

5/5

c. How many cases and how many variables are there in your sample?

(c) 30,000 cases; 9 variables

5/5

d. What type of variable is genhlth?

(d) categorical, ordinal

0/5

e. What type of variable is weight?

(b) numerical, discrete

5/5

f. What type of variable is smoke100?

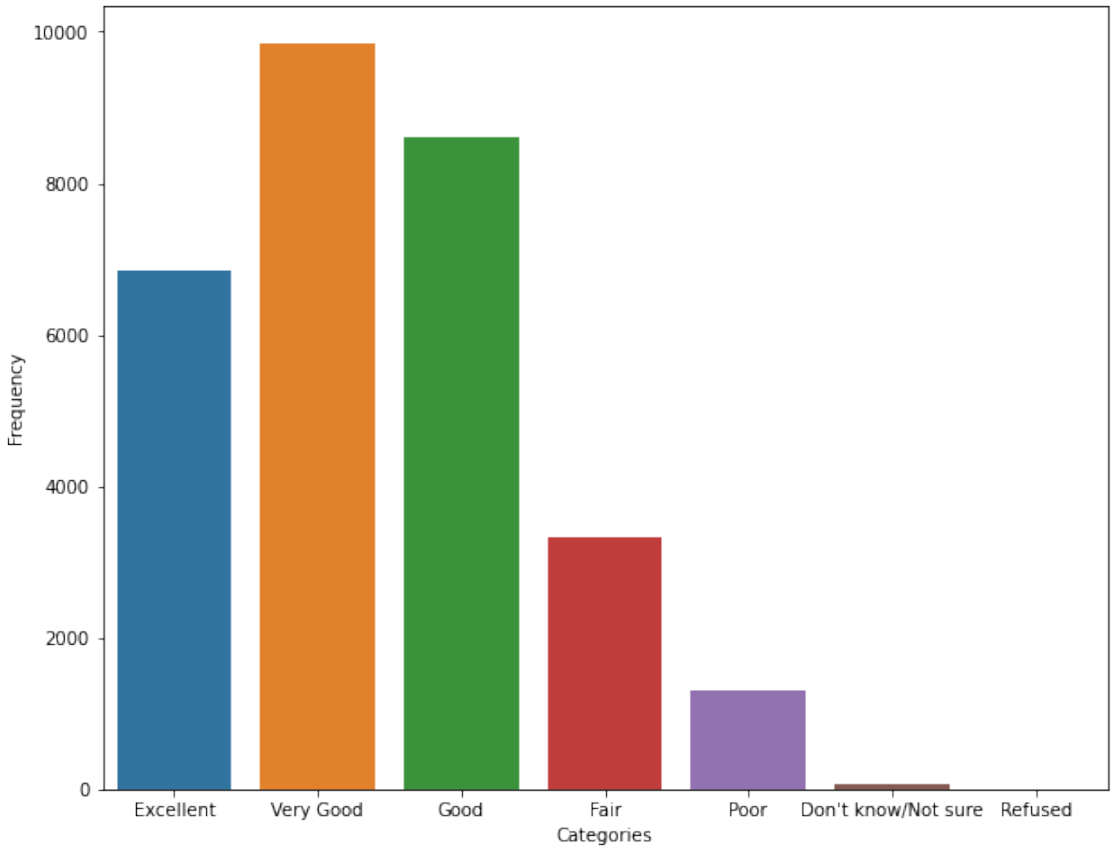
(c) categorical (not ordinal)

> **One Bar chart** * > Take all genhlth entries from your sample and draw a bar chart to visualize how the cases are distributed across the possible categories.

[ ]:
```
# x axis represents General Health. 1,2,3,4,5,7,9 means Excellent, Very good,␣
↪Good, Fair, Poor, Don't know, Refused respectively
# y axis represents freuquency
import numpy as np
import seaborn as sns
from matplotlib import rcParams
import matplotlib.pyplot as plt



genhlth = Large_Columns_b['GENHLTH']
```

```
genhlth_data_count = np.unique(genhlth,return_counts = True)
rcParams['figure.figsize'] = 10,8
ax = sns.barplot(x = genhlth_data_count[0],y = genhlth_data_count[1])
ax.set(xlabel = 'Categories',ylabel = 'Frequency',xticklabels =␣
↪["Excellent","Very Good","Good","Fair","Poor","Don't know/Not␣
↪sure","Refused"])
```

[ ]:
```
[Text(0.5, 0, 'Categories'),
 Text(0, 0.5, 'Frequency'),
 [Text(0, 0, 'Excellent'),
  Text(1, 0, 'Very Good'),
  Text(2, 0, 'Good'),
  Text(3, 0, 'Fair'),
  Text(4, 0, 'Poor'),
  Text(5, 0, "Don't know/Not sure"),
  Text(6, 0, 'Refused')]]
```



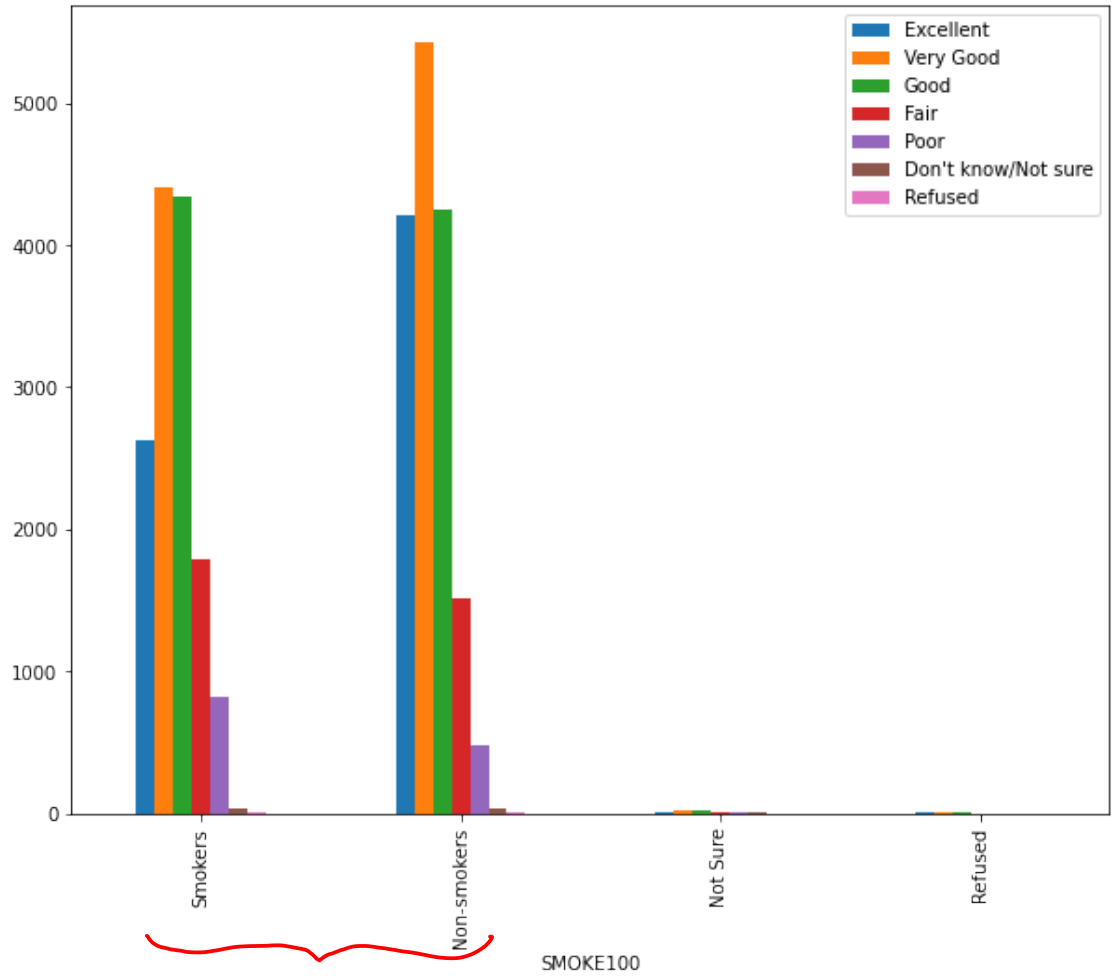
10/10

Two Bar Charts * > Combine the smoke100 with the genhlth entries from your sample and draw two bar charts, one showing the health of the smokers and a second one showing the health of the non-smokers.

[ ]:
```
genhlth_count_ifsmoke = Large_Columns_b.groupby(['SMOKE100','GENHLTH']).
 ↪SMOKE100.agg('count')
genhlth_count_ifsmoke.describe()
#genhlth_count_ifsmoke['SMOKE100'].describe()
#sns.barplot(x = 'SMOKE100', y = 'count', hue = 'GENHLTH',data =␣
 ↪genhlth_count_ifsmoke)
```

[ ]:
```
count      23.000000
mean     1304.347826
std      1877.661084
min         1.000000
25%         5.000000
50%        31.000000
75%      2206.500000
max      5424.000000
Name: SMOKE100, dtype: float64
```

[ ]:
```
#  x axis represents if smoke100, if so ,x=1; otherwise x=2. x=7,9 means 'not␣
 ↪sure'/'refused' respectively. y axis means frequency
fig, ax = plt.subplots()
genhlth_count_ifsmoke.unstack().plot.bar(ax=ax)
ax.legend(["Excellent","Very Good","Good","Fair","Poor","Don't know/Not␣
 ↪sure","Refused"])
ax.set_xticklabels(["Smokers","Non-smokers","Not Sure","Refused"])
plt.show()
```



20/20

you were only asked for these two

We can clearly see from the plot that the general wellness is higher in non-smokers than in smokers

> **BMI** * > Next let's consider a new variable bmi that doesn't show up directly in this data set: Body Mass Index (BMI). * > Compute the bmi for each case in your sample and add it to the sample (e.g. as additional column). * > Visualize the distribution of the BMI in your sample.

[ ]:
```
Large_Columns_b['BMI'] = Large_Columns_b['WEIGHT']/
 ↪((Large_Columns_b['HTF']*12+Large_Columns_b['HTI'])*(Large_Columns_b['HTF']*12+Large_Column
Large_Columns_b.drop(Large_Columns_b[Large_Columns_b.HTI > 11].index, inplace =␣
 ↪True) #drop the data whose height(iches) is 77 and 99(means Don't know and␣
 ↪refused respectively)
Large_Columns_b.drop(Large_Columns_b[Large_Columns_b.WEIGHT > 776].index,␣
 ↪inplace = True)#drop the data whose weight is 777 and 999(means Don't know␣
 ↪and refused respectively)
Large_Columns_b.drop(Large_Columns_b[Large_Columns_b.HTF > 7].index, inplace =␣
 ↪True)#drop the data whose height (feets) is 9(means refused)
```

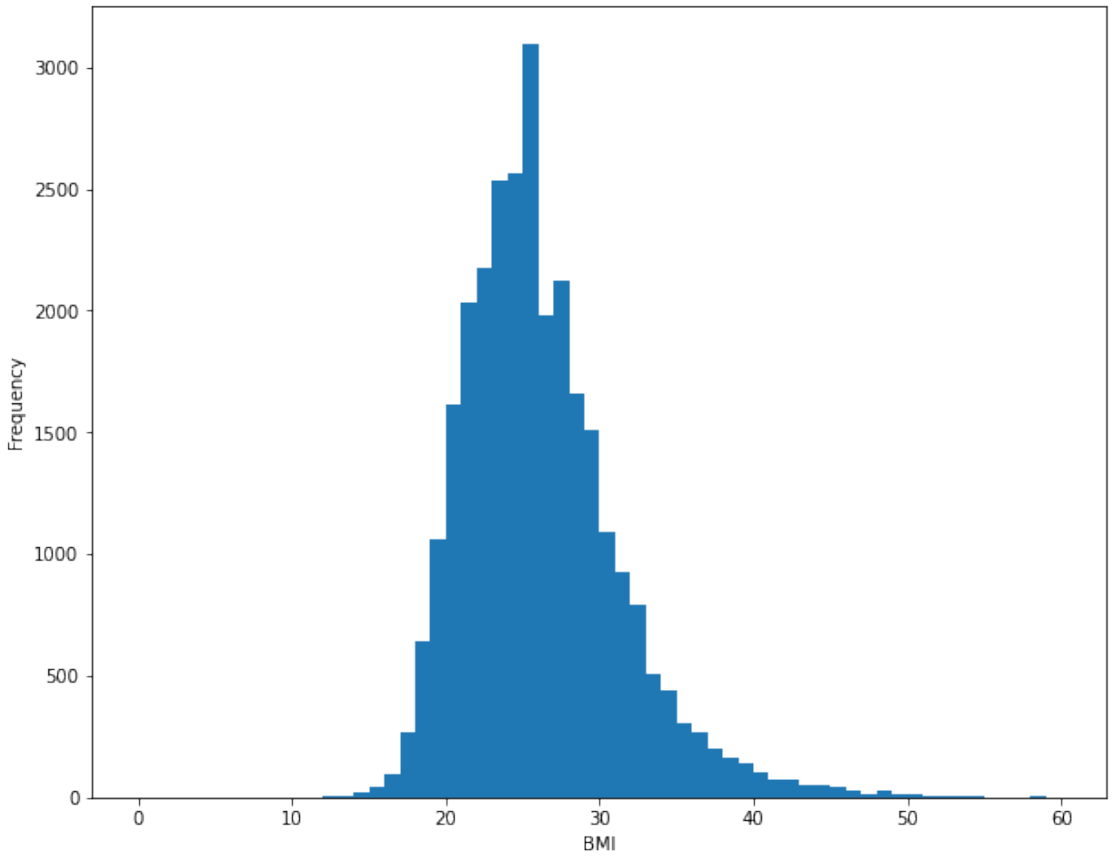
```
BMI_data = Large_Columns_b['BMI']
BMI_data.drop(BMI_data[BMI_data == np.inf].index, inplace=True)# drop the data␣
 ↪whose height is 0
BMI_data
```

```
/opt/conda/lib/python3.7/site-packages/ipykernel_launcher.py:1:
SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: https://pandas.pydata.org/pandas-
docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  """Entry point for launching an IPython kernel.
/opt/conda/lib/python3.7/site-packages/pandas/core/frame.py:4913:
SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-
docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  errors=errors,
/opt/conda/lib/python3.7/site-packages/pandas/core/generic.py:4153:
SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-
docs/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  self._update_inplace(obj)
```

[ ]:
```
0        26.605753
1        25.824490
2        26.037037
3        18.302959
4        22.317460
           …
29995    29.049587
29996    20.595703
29997    23.615963
29998    22.671325
29999    29.177246
Name: BMI, Length: 28810, dtype: float64
```

[ ]:
```
# It's a histogram, x axis represents BMI, y axis represents Frequency
ax = BMI_data.plot.hist('BMI', bins =60 , range=(0,60))
ax.set(xlabel = "BMI")
```

[ ]:
```
[Text(0.5, 0, 'BMI')]
```



30/30

The distribution of BMI peaks around 25. Most of the population lies in healthy-overweight categories but a heavy tailed distribution indicates that a significant fraction of population is obese.

Overall, we can see that different combinations and visualisations of data can provide with significant information about it.