Lab 10

November 18, 2021

1 Lab 10

In this lab we discuss sampling distribution and central limit theorem.

1.1 Sampling Distribution

[1]:
```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
```

np.random.normal: https://numpy.org/doc/stable/reference/random/generated/numpy.random.normal.html

np.concatenate: https://numpy.org/doc/stable/reference/generated/numpy.concatenate.html

[2]:
```
# First we generate two normal distributions of mass values for males and␣
 ↪females.
# Then we concatenate these two arrays and create the dataframe "df_mass".
np.random.seed(0)
male_mass = np.random.normal(loc = 180, scale = 30, size = 2000)
female_mass = np.random.normal(loc = 140, scale = 20, size = 2000)
all_values = np.concatenate((male_mass, female_mass), axis = 0)
df_mass = pd.DataFrame({'people_mass': all_values})
```

[3]:
```
# Let's see the first 5 rows of the dataframe!
df_mass.head()
```

[3]:

	people_mass
0	232.921570
1	192.004716
2	209.362140
3	247.226796
4	236.026740

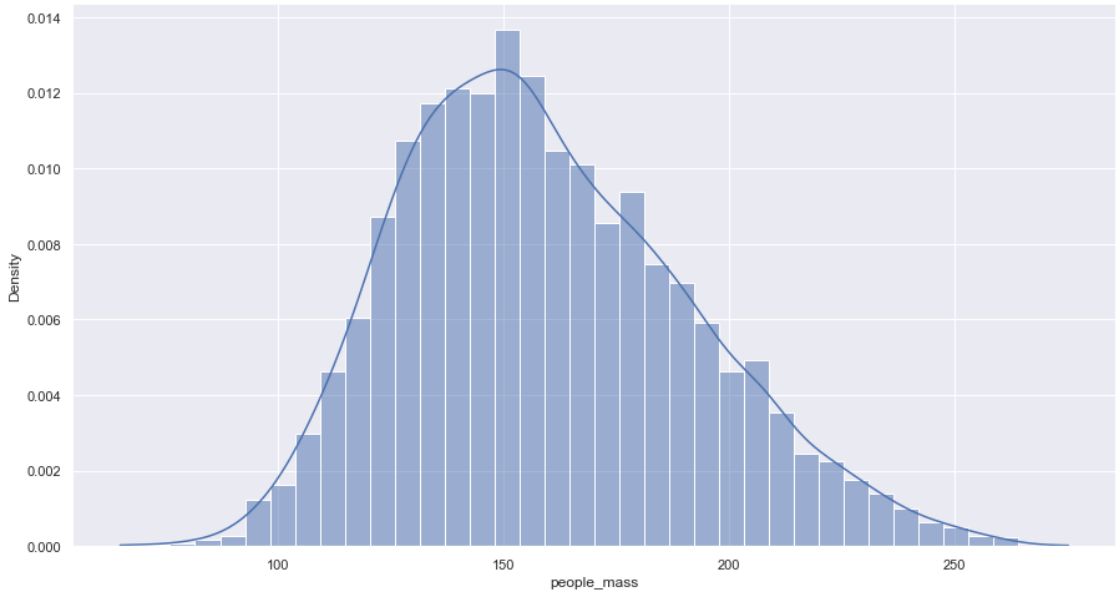
[4]:
```
# Calculating summary statistics for the variable "people_mass"
df_mass.describe()
```

[4]:
```
        people_mass
count   4000.000000
mean     159.411846
std       32.087054
min       65.197987
25%      135.918187
50%      155.533992
75%      180.564731
max      275.129243
```

sns.set_theme: https://seaborn.pydata.org/generated/seaborn.set_theme.html#seaborn.set_theme

sns.histplot: https://seaborn.pydata.org/generated/seaborn.histplot.html

[5]:
```
# We can see the distribution of the values in the column "people_mass".
# This is not a normal distribution!
sns.set_theme(rc = {'figure.figsize':(15, 8)})
sns.histplot(df_mass['people_mass'], stat = 'density', kde = True)
plt.show()
```



np.random.choice: https://numpy.org/doc/stable/reference/random/generated/numpy.random.choice.html

[6]:
```
# Function for creating the list of sample means
# The number of samples is "n_samples" and size of each sample is "sample_size".
# We calculate the mean of each sample and store all those sample mean values␣
 ↪in the list "sample_means".
def sample_mean_calculator(population_array, sample_size, n_samples):
    sample_means = []
```

```
    for i in range(n_samples):
        sample = np.random.choice(population_array, size = sample_size)
        sample_mean = np.mean(sample)
        sample_means.append(sample_mean)
    return sample_means
```

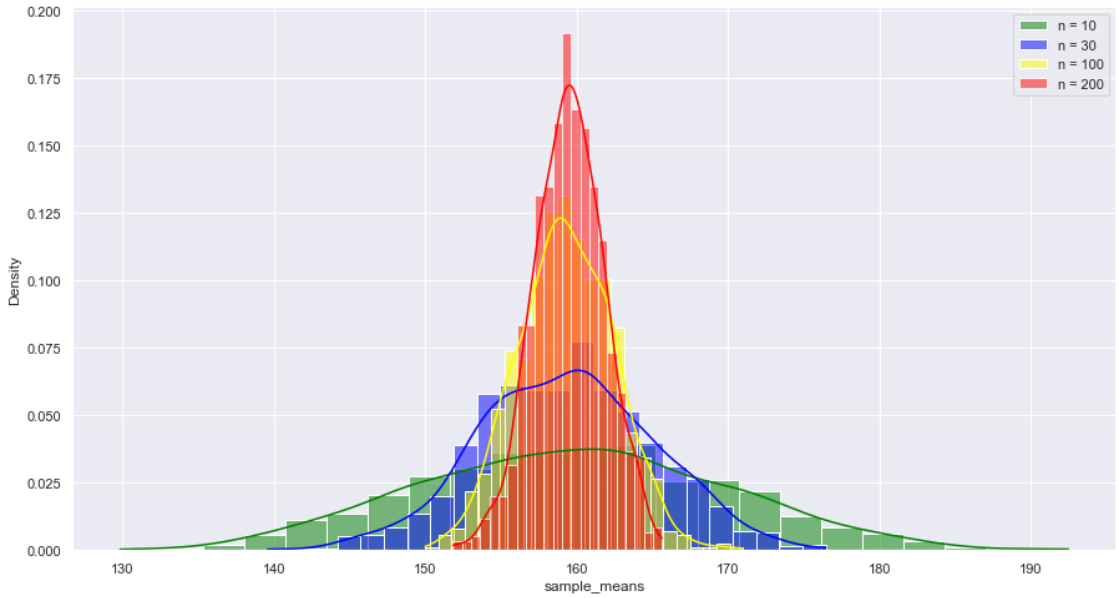
[7]:
```
# Taking 1000 samples each of 10 random values with replacement!
sample_means_10 = sample_mean_calculator(df_mass['people_mass'], 10, 1000)
```

[8]:
```
# Taking 1000 samples each of 30 random values with replacement!
sample_means_30 = sample_mean_calculator(df_mass['people_mass'], 30, 1000)
```

[9]:
```
# Taking 1000 samples each of 100 random values with replacement!
sample_means_100 = sample_mean_calculator(df_mass['people_mass'], 100, 1000)
```

[10]:
```
# Taking 1000 samples each of 200 random values with replacement!
sample_means_200 = sample_mean_calculator(df_mass['people_mass'], 200, 1000)
```

[11]:
```
# Let's view the distribution of the sample_means values!
# The distribution of sample means for n = 200 looks normal!
# The red curve is fairly symmetrical around the central value and the median␣
 ↪is roughly equivalent to the mean.
# Sampling a sufficient number of times with a sufficient size will result in a␣
 ↪normal distribution of sample means.
sns.histplot(sample_means_10, stat = 'density', color = "green", label = "n =␣
 ↪10", kde = True)
sns.histplot(sample_means_30, stat = 'density', color = "blue", label = "n =␣
 ↪30", kde = True)
sns.histplot(sample_means_100, stat = 'density', color = "yellow", label = "n =␣
 ↪100", kde = True)
sns.histplot(sample_means_200, stat = 'density', color = "red", label = "n =␣
 ↪200", kde = True)
plt.xlabel("sample_means")
plt.legend()
plt.show()
```



[12]:
```
# Let's check the mean of sample_means_200!
# This value is close to the meean of "people_mass".
np.mean(sample_means_200)
```

[12]: 159.50252788067945

[13]:
```
# Let's check the standard deviation of sample_means_200!
np.std(sample_means_200, ddof = 1)
```

[13]: 2.2796728551263783

[14]:
```
# The standard deviation of sample means is called the standard error (SE).
# We can calculate the standard error by just using the standard deviation of␣
 ↪"people_mass" and sample size.
# We see that SE is roughly equal to the standard deviation of sample_means_200.
SE = np.std(df_mass['people_mass'], ddof = 1) / np.sqrt(200)
SE
```

[14]: 2.2688973280058047