Part 2: Basic Inferential Data Analysis Instructions

Data Dictionary (The Effect of Vitamin C on Tooth Growth in Guinea Pigs)

Field	Description
len	Tooth length
supp	Supplement type (VC or OJ)
dose	Dose in milligrams.

Dependant Variable (DV) is tooth length, Independant variables (IV) are supplement type and dose.

Assumptions made

1. Sampled guinea pigs are repesentative for the population of guinea pigs
2. Dosage and supplement were randomly assigned
3. The population must be close to a normal distribution

Import Libraries

In [1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import statsmodels.api as sm
from statsmodels.formula.api import ols
import datetime
from datetime import datetime, timedelta
import scipy.stats
import pandas_profiling
from pandas_profiling import ProfileReport


%matplotlib inline
#sets the default autosave frequency in seconds
%autosave 60
sns.set_style('dark')
sns.set(font_scale=1.2)

plt.rc('axes', titlesize=9)
plt.rc('axes', labelsize=14)
plt.rc('xtick', labelsize=12)
plt.rc('ytick', labelsize=12)

import warnings
warnings.filterwarnings('ignore')


pd.set_option('display.max_columns',None)
#pd.set_option('display.max_rows',None)
pd.set_option('display.width', 1000)
pd.option_context('float_format','{:.2f}'.format)

np.random.seed(0)
np.set_printoptions(suppress=True)
```

```
Autosaving every 60 seconds
```

In [2]:
```
df = pd.read_csv("ToothGrowth.csv")
```

In [3]:
```
df.head()
```

Out[3]:

	len	supp	dose
0	4.2	VC	0.5
1	11.5	VC	0.5
2	7.3	VC	0.5
3	5.8	VC	0.5
4	6.4	VC	0.5

Exploratory Data Analysis

In [4]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 60 entries, 0 to 59
Data columns (total 3 columns):
 #   Column  Non-Null Count  Dtype
---  ------  --------------  -----
 0   len     60 non-null     float64
 1   supp    60 non-null     object
 2   dose    60 non-null     float64
dtypes: float64(2), object(1)
memory usage: 1.5+ KB
```

In [5]:
```
df.describe(include='all')
```

Out[5]:

	len	supp	dose
count	60.000000	60	60.000000
unique	NaN	2	NaN
top	NaN	VC	NaN
freq	NaN	30	NaN
mean	18.813333	NaN	1.166667
std	7.649315	NaN	0.628872
min	4.200000	NaN	0.500000
25%	13.075000	NaN	0.500000
50%	19.250000	NaN	1.000000
75%	25.275000	NaN	2.000000
max	33.900000	NaN	2.000000

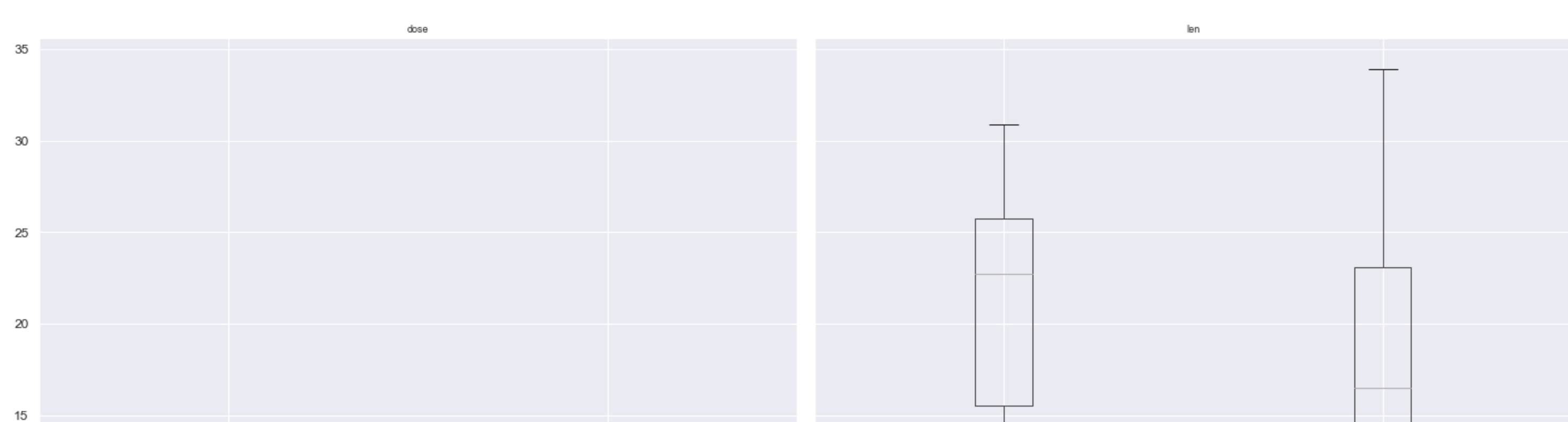
In [6]:
```
df.columns
```

Out[6]:
```
Index(['len', 'supp', 'dose'], dtype='object')
```

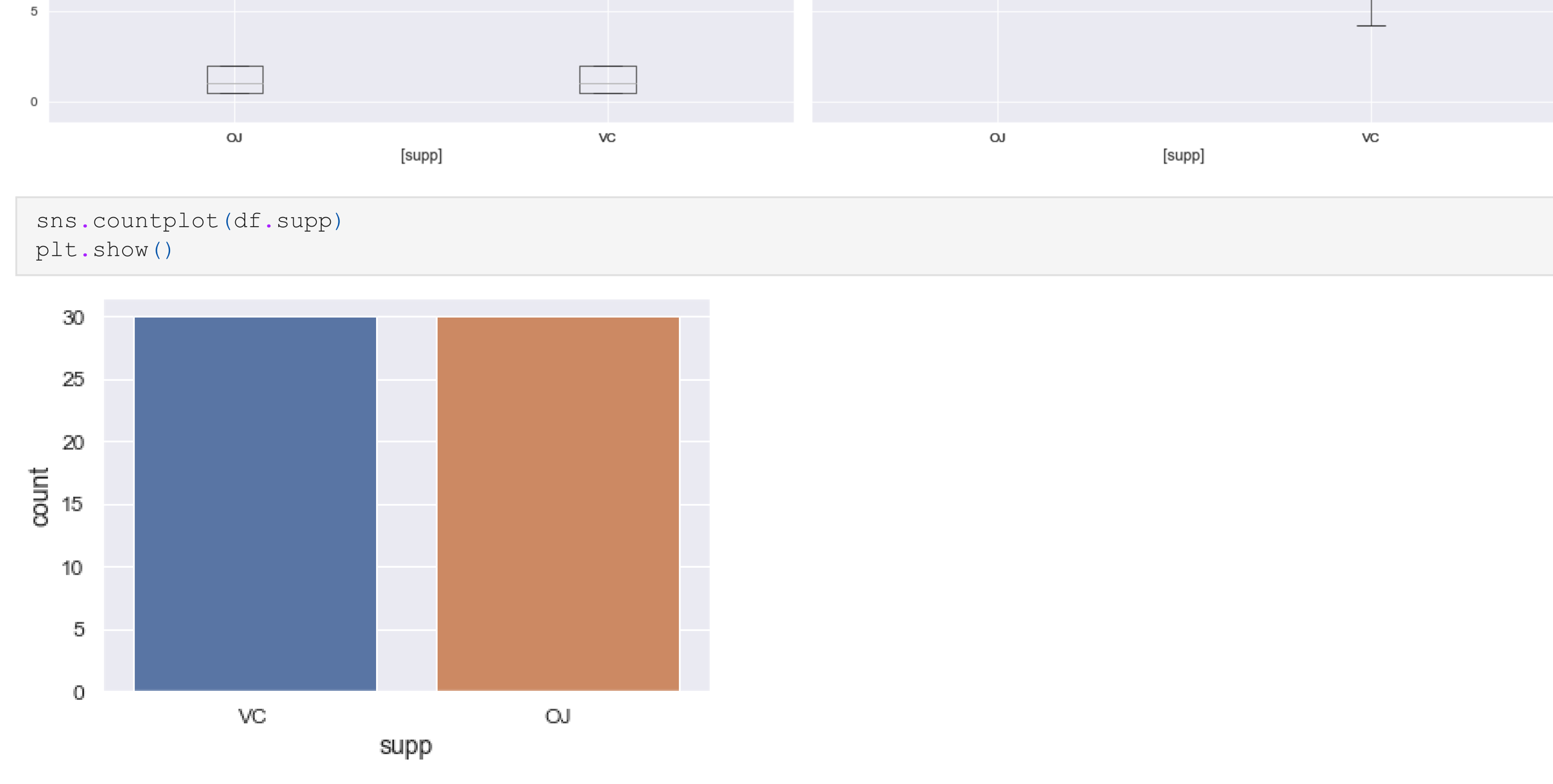
Data Visualization

Univariate Data Exploration

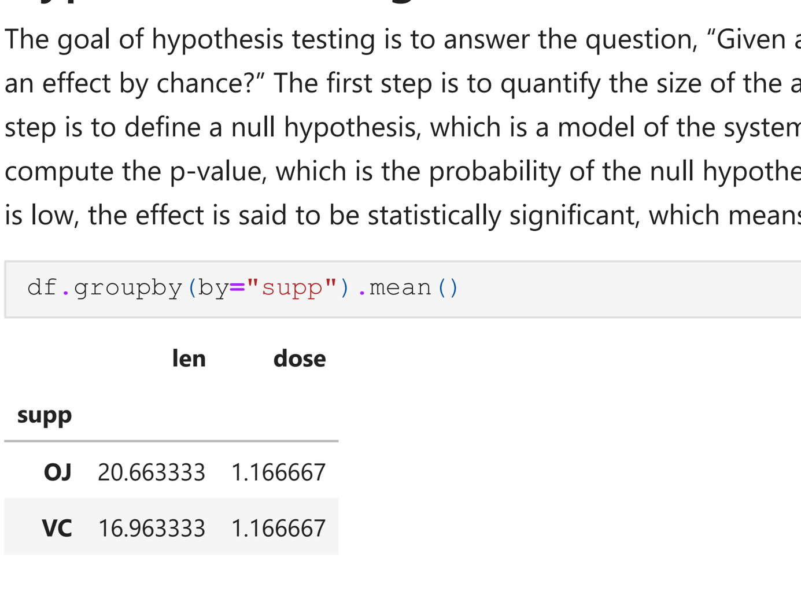
In [7]:
```
df.hist(bins=50, figsize=(20,5))
plt.suptitle('Feature Distribution', x=0.5, y=1.02, ha='center', fontsize=20)
plt.tight_layout()
plt.show()
```



In [32]:
```
df.boxplot(figsize=(20,10), by='supp')
plt.suptitle('BoxPlot', x=0.5, y=1.02, ha='center', fontsize='large')
plt.tight_layout()
plt.show()
```



In [9]:
```
sns.countplot(df.supp)
plt.show()
```



Hypothesis Testing

The goal of hypothesis testing is to answer the question, "Given a sample and an apparent effect, what is the probability of seeing such an effect by chance?" The first step is to quantify the size of the apparent effect by choosing a test statistic (t-test, ANOVA, etc). The next step is to define a null hypothesis, which is a model of the system based on the assumption that the apparent effect is not real. Then compute the p-value, which is the probability of the null hypothesis being true, and finally interpret the result of the p-value, if the value is low, the effect is said to be statistically significant, which means that the null hypothesis may not be accurate.

In [10]:
```
df.groupby(by="supp").mean()
```

Out[10]:

supp	len	dose
OJ	20.663333	1.166667
VC	16.963333	1.166667

In [11]:
```
df.groupby(by="supp").var()
```

Out[11]:

supp	len	dose
OJ	43.633437	0.402299
VC	68.327230	0.402299

T-Test

We will be using the t-test for independent samples. For the independent t-test, the following assumptions must be met.

- One independent, categorical variable with two levels or group
- One dependent continuous variable
- Independence of the observations. Each subject should belong to only one group. There is no relationship between the observations in each group.
- The dependent variable must follow a normal distribution
- Assumption of homogeneity of variance

State the hypothesis

- $H_0: μ\_1 = μ\_2$ ("there is no difference in dose between OJ and VC")
- $H_1: μ\_1 \neq μ\_2$ ("there is a difference in dose between OJ and VC")

T-Test

One Sample T-Test

In [13]:
```
t, p = scipy.stats.ttest_1samp(a=df.dose, popmean=1.166667)
```

In [14]:
```
print("T-test value is: ",t)
print("p-value value is: ",p)
```

```
T-test value is:  -4.1057451016103215e-06
p-value value is:  0.9999967379403212
```

Two Samples T-Test

In [15]:
```
t, p = scipy.stats.ttest_ind(a=df.len,b=df.dose, equal_var = False)
```

In [16]:
```
print("T-test value is: ",t)
print("p-value value is: ",p)
```

```
T-test value is:  17.80955225252292
p-value value is:  1.3802361569449393e-25
```

ANOVA

First, we group the data into categories as the one-way ANOVA can't work with continuous variable - using the example from the video, we will create a new column for this newly assigned group our categories will be teachers that are:

- 40 years and younger
- between 40 and 57 years
- 57 years and older

State the hypothesis

- $H_0: \mu_1 = \mu_2$ (the two population means are equal)
- $H_1:$ At least one of the means differ

One Way ANOVA

In [17]:
```
mod = ols('len~supp', data=df).fit()
```

In [18]:
```
aov_table = sm.stats.anova_lm(mod,typ=2)
```

In [19]:
```
aov_table
```

Out[19]:

	sum_sq	df	F	PR(>F)
supp	205.350000	1.0	3.668253	0.060393
Residual	3246.859333	58.0	NaN	NaN

p-value is more than 0.05, hence failed to reject Null Hypothesis

In [20]:
```
df["dose"].value_counts()
```

Out[20]:
```
2.0    20
1.0    20
0.5    20
Name: dose, dtype: int64
```

In [21]:
```
f_statistic, p_value = scipy.stats.f_oneway(df.dose, df.len)
print("F_Statistic: {0}, P-Value: {1}".format(f_statistic,p_value))
```

```
F_Statistic: 317.18015143534444, P-Value: 3.104466162339778e-35
```

Two-way ANOVA

In [22]:
```
mod1 = ols('len~supp+dose', data=df).fit()
```

In [23]:
```
aov1 = sm.stats.anova_lm(mod1,typ=2)
```

In [24]:
```
aov1
```

Out[24]:

	sum_sq	df	F	PR(>F)
supp	205.350000	1.0	11.446768	1.300662e-03
dose	2224.304298	1.0	123.988774	6.313519e-16
Residual	1022.555036	57.0	NaN	NaN

Both p-values is more than 0.05, hence failed to reject Null Hypothesis. Both supp and dose have association with tooth length.

Correlation

State the hypothesis:

- H_0: Teaching evaluation score is not correlated with beauty score
- H_1: Teaching evaluation score is correlated with beauty score

In [25]:
```
scipy.stats.pearsonr(df['len'], df['dose'])
```

Out[25]:
```
(0.8026912693324918, 1.2326982210946766e-14)
```

In [26]:
```
df.corr()
```

Out[26]:

	len	dose
len	1.000000	0.802691
dose	0.802691	1.000000

Regression Analysis

In [27]:
```
df.columns
```

Out[27]:
```
Index(['len', 'supp', 'dose'], dtype='object')
```

In [28]:
```
y = df['len']
X = df['dose']
```

In [29]:
```
X = sm.add_constant(X)
```

In [30]:
```
model = sm.OLS(y,X).fit()
```

In [31]:
```
model.summary()
```

Out[31]:

OLS Regression Results

Dep. Variable:	len	R-squared:	0.644
Model:	OLS	Adj. R-squared:	0.638
Method:	Least Squares	F-statistic:	105.1
Date:	Wed, 10 Mar 2021	Prob (F-statistic):	1.23e-14
Time:	18:41:25	Log-Likelihood:	-175.70
No. Observations:	60	AIC:	355.4
Df Residuals:	58	BIC:	359.6
Df Model:	1		
Covariance Type:	nonrobust		

	coef	std err	t	P>|t|	[0.025	0.975]
const	7.4225	1.260	5.890	0.000	4.900	9.945
dose	9.7636	0.953	10.250	0.000	7.857	11.670

Omnibus:	2.684	Durbin-Watson:	1.299
Prob(Omnibus):	0.261	Jarque-Bera (JB):	2.537
Skew:	0.435	Prob(JB):	0.281
Kurtosis:	2.491	Cond. No.	4.17

Notes:
[1] Standard Errors assume that the covariance matrix of the errors is correctly specified.

In [ ]: