Act1

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Importamos las librerias necesarias

[ ]:
```
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
import pandas as pd
import statsmodels.api as sm
from statsmodels.formula.api import ols
from scipy.stats import f_oneway
```

Leemos la base de datos

[ ]:
```
df = pd.read_csv("aldrin.csv")
df.head()
```

[ ]:

	aldrin	depth
0	3.8	bottom
1	4.8	bottom
2	4.9	bottom
3	5.3	bottom
4	5.4	bottom

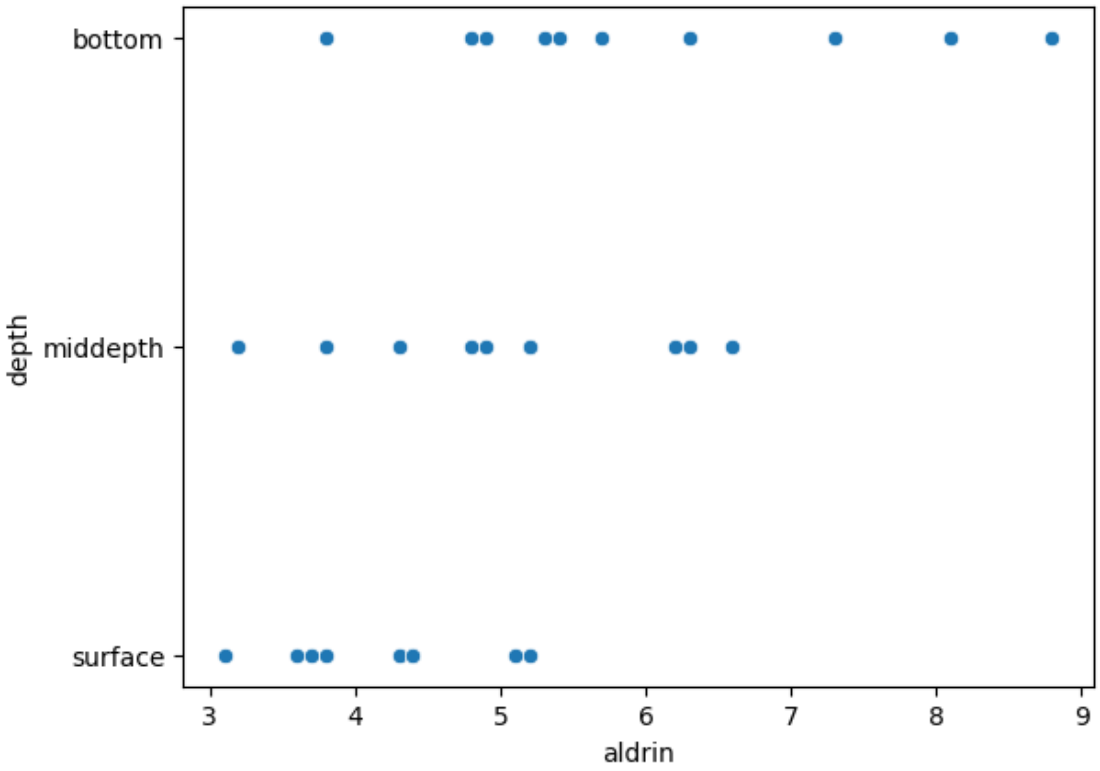
[ ]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 30 entries, 0 to 29
Data columns (total 2 columns):
 #   Column  Non-Null Count  Dtype
---  ------  --------------  -----
 0   aldrin  30 non-null     float64
 1   depth   30 non-null     object
dtypes: float64(1), object(1)
memory usage: 608.0+ bytes
```

Graficamos las distintas categorias

[ ]:
```
sns.scatterplot(x='aldrin', y='depth', data=df)
```

[ ]: <Axes: xlabel='aldrin', ylabel='depth'>



[ ]:
```
df.groupby('depth').describe()
```

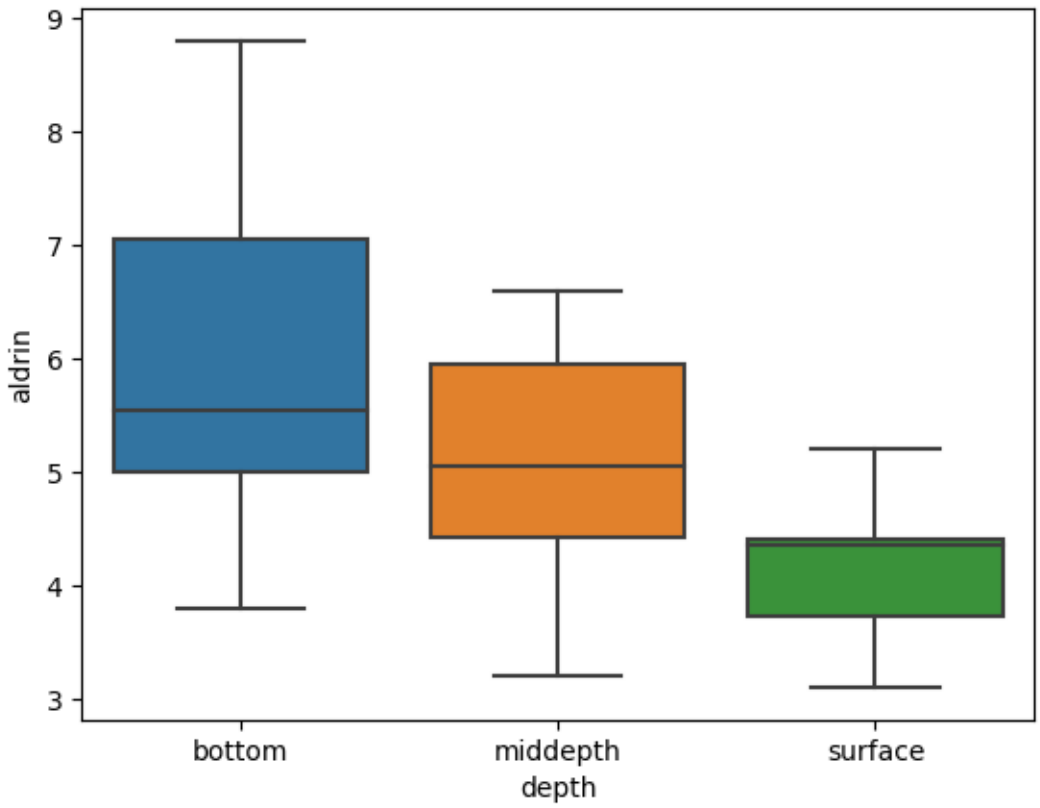
[ ]:

	aldrin							
	count	mean	std	min	25%	50%	75%	max
depth								
bottom	10.0	6.04	1.579170	3.8	5.000	5.55	7.05	8.8
middepth	10.0	5.05	1.103781	3.2	4.425	5.05	5.95	6.6
surface	10.0	4.20	0.659966	3.1	3.725	4.35	4.40	5.2

Parece que la base de datos muestra una diferencia entre los promedios de concentración, pero es necesario comprobarlo mediante una prueba

[ ]:
```
sns.boxplot(x='depth', y='aldrin', data=df)
```

[ ]: <Axes: xlabel='depth', ylabel='aldrin'>



[ ]:
```
bottom,middle,top=df.groupby('depth')
```

[ ]:
```
x = pd.DataFrame(bottom[1])
x.drop(columns='depth', inplace=True)
y = pd.DataFrame(middle[1])
y.drop(columns='depth', inplace=True)
z = pd.DataFrame(top[1])
z.drop(columns='depth', inplace=True)
```

1 ¿Existe una diferencia entre la concentración promedio de aldrin en el fondo y a media profundidad?

[ ]:
```
# Perform one-way ANOVA
f_statistic, p_value = f_oneway(x,y)

# Set the significance level (alpha)
alpha = 0.05

# Compare p-value to alpha
if p_value < alpha:
```

```
    print("Reject the null hypothesis. There is a significant difference in the␣
 ↪mean test scores.")
else:
    print("Fail to reject the null hypothesis. There is no significant␣
 ↪difference in the mean test scores.")

# Display the results
print("F-statistic:", f_statistic)
print("P-value:", p_value)

# Create a DataFrame
data = df

# Fit the ANOVA model
model = ols('aldrin ~ depth', data=data).fit()

# Create the ANOVA table
anova_table = sm.stats.anova_lm(model, typ=2)

# Display the ANOVA table
print("ANOVA Table:")
print(anova_table)
```

```
Fail to reject the null hypothesis. There is no significant difference in the
mean test scores.
F-statistic: [2.64027657]
P-value: [0.12156624]
ANOVA Table:
             sum_sq    df         F    PR(>F)
depth     16.960667   2.0  6.13381  0.006367
Residual  37.329000  27.0       NaN       NaN
```

[ ]:
```
anova_table["MSE"] = anova_table["sum_sq"]/anova_table["df"]
```

[ ]:
```
def tstadistic(anova,x,y):
    x_mean=x.mean()[0]
    y_mean=y.mean()[0]
    return (x_mean-y_mean)/np.sqrt((anova["MSE"][1]/len(x))+(anova["MSE"][1]/
 ↪len(y)))
```

[ ]:
```
import scipy.stats as stats

# Define the t-value and degrees of freedom
t_value = tstadistic(anova_table,x,y)
degrees_of_freedom = anova_table["df"][1] #Residuals

# Calculate the p-value for a two-tailed test
```

```
p_value = 2 * (1 - stats.t.cdf(abs(t_value), df=degrees_of_freedom))

# Round the p-value to three decimal places
rounded_p_value = round(p_value, 3)

print("The p-value is approximately", rounded_p_value)
```

```
The p-value is approximately 0.071
```

1.1 Sin el metodo de Benferroni

[ ]:
```
if rounded_p_value < alpha:
    print("Reject the null hypothesis. There is a significant difference in the␣
 ↪mean test scores.")
else:
    print("Fail to reject the null hypothesis. There is no significant␣
 ↪difference in the mean test scores.")
```

```
Fail to reject the null hypothesis. There is no significant difference in the
mean test scores.
```

1.2 Con el metodo de Benferroni

[ ]:
```
if rounded_p_value < alpha/3:
    print("Reject the null hypothesis. There is a significant difference in the␣
 ↪mean test scores.")
else:
    print("Fail to reject the null hypothesis. There is no significant␣
 ↪difference in the mean test scores.")
```

```
Fail to reject the null hypothesis. There is no significant difference in the
mean test scores.
```

No hay suficiente evidencia para demostrar que existe diferencia en los promedios, incluso con el metodo de Benferroni no se puede mostrar que existe una diferencia en los promedios de concentración de aldrin en el fondo y a media profundidad

2 ¿Existe una diferencia entre la concentración promedio de aldrin en el fondo y la superficie?

[ ]:
```
# Perform one-way ANOVA
f_statistic, p_value = f_oneway(x,z)

# Set the significance level (alpha)
alpha = 0.05

# Compare p-value to alpha
if p_value < alpha:
```

```
    print("Reject the null hypothesis. There is a significant difference in the␣
 ↪mean test scores.")
else:
    print("Fail to reject the null hypothesis. There is no significant␣
 ↪difference in the mean test scores.")

# Display the results
print("F-statistic:", f_statistic)
print("P-value:", p_value)

# Create a DataFrame
data = df

# Fit the ANOVA model
model = ols('aldrin ~ depth', data=data).fit()

# Create the ANOVA table
anova_table = sm.stats.anova_lm(model, typ=2)

# Display the ANOVA table
print("ANOVA Table:")
print(anova_table)
```

```
Reject the null hypothesis. There is a significant difference in the mean test
scores.
F-statistic: [11.55757852]
P-value: [0.00319403]
ANOVA Table:
              sum_sq    df         F    PR(>F)
depth      16.960667   2.0  6.13381  0.006367
Residual   37.329000  27.0       NaN       NaN
ANOVA Table:
              sum_sq    df         F    PR(>F)
depth      16.960667   2.0  6.13381  0.006367
Residual   37.329000  27.0       NaN       NaN
```

[ ]:
```
anova_table["MSE"] = anova_table["sum_sq"]/anova_table["df"]
```

[ ]:
```
import scipy.stats as stats

# Define the t-value and degrees of freedom
t_value = tstadistic(anova_table,x,z)
degrees_of_freedom = anova_table["df"][1] #Residuals

# Calculate the p-value for a two-tailed test
p_value = 2 * (1 - stats.t.cdf(abs(t_value), df=degrees_of_freedom))
```

```
# Round the p-value to three decimal places
rounded_p_value = round(p_value, 3)

print("The p-value is approximately", rounded_p_value)
```

```
The p-value is approximately 0.002
```

2.1 Sin el metodo de Benferroni

[ ]:
```
if rounded_p_value < alpha:
    print("Reject the null hypothesis. There is a significant difference in the␣
 ↪mean test scores.")
else:
    print("Fail to reject the null hypothesis. There is no significant␣
 ↪difference in the mean test scores.")
```

```
Reject the null hypothesis. There is a significant difference in the mean test
scores.
```

2.2 Con el metodo de Benferroni

[ ]:
```
if rounded_p_value < alpha/3:
    print("Reject the null hypothesis. There is a significant difference in the␣
 ↪mean test scores.")
else:
    print("Fail to reject the null hypothesis. There is no significant␣
 ↪difference in the mean test scores.")
```

```
Reject the null hypothesis. There is a significant difference in the mean test
scores.
```

Si existe una diferencia significativa en la prueba, por lo que se rechaza la hipotesis nula, lo que demuestra que los promedios son distintos. Esto sucede incluso con el metodo de Benferroni

De esta manera podemos concluir que dada la información que tenemos no hay manera de comprobar que la concentración promedio de aldrin en el fondo y media profundidad sea distinta. Sin embargo la concentración promedio de aldrin en el fondo y la superficie sí es distinta.