

```

import pandas as pd

# Read data from a specific sheet within the Excel file
df = pd.read_excel('/content/Datos Modelos Lineales.xlsx',
sheet_name='Regresión Lineal Múltiple Ej')

df.head()

{"summary":{"\n  \"name\": \"df\",\n  \"rows\": 108,\n  \"fields\": [\n    {\n      \"column\": \"Factor Coagulaci\u00f3n\",\n      \"properties\": {\n        \"dtype\": \"number\",\n        \"std\": 1.4251714658823018,\n        \"min\": 2.6,\n        \"max\": 11.2,\n        \"num_unique_values\": 48,\n        \"samples\": [\n          3.9,\n          6.9,\n          4.5\n        ],\n        \"semantic_type\": \"\",\n        \"description\": \"\"\n      },\n      \"column\": \"\n    cdndice pron\u00f3stico\",\n      \"properties\": {\n        \"dtype\": \"number\",\n        \"std\": 16,\n        \"min\": 8,\n        \"max\": 99,\n        \"num_unique_values\": 54,\n        \"samples\": [\n          54,\n          88,\n          50\n        ],\n        \"semantic_type\": \"\",\n        \"description\": \"\"\n      },\n      \"column\": \"\n    Funci\u00f3n de enzima\",\n      \"properties\": {\n        \"dtype\": \"number\",\n        \"std\": 20,\n        \"min\": 23,\n        \"max\": 119,\n        \"num_unique_values\": 63,\n        \"samples\": [\n          33,\n          48,\n          81\n        ],\n        \"semantic_type\": \"\",\n        \"description\": \"\"\n      },\n      \"column\": \"\n    Funci\u00f3n de h\u00e9dado\",\n      \"properties\": {\n        \"dtype\": \"number\",\n        \"std\": 1.0056046943582424,\n        \"min\": 0.74,\n        \"max\": 6.4,\n        \"num_unique_values\": 90,\n        \"samples\": [\n          4.1,\n          3.5,\n          2.91\n        ],\n        \"semantic_type\": \"\",\n        \"description\": \"\"\n      },\n      \"column\": \"\n    Edad\",\n      \"properties\": {\n        \"dtype\": \"number\",\n        \"std\": 11,\n        \"min\": 30,\n        \"max\": 70,\n        \"num_unique_values\": 40,\n        \"samples\": [\n          70,\n          67,\n          59\n        ],\n        \"semantic_type\": \"\",\n        \"description\": \"\"\n      },\n      \"column\": \"\n    G\u00e9nero\",\n      \"properties\": {\n        \"dtype\": \"number\",\n        \"std\": 0,\n        \"min\": 0,\n        \"max\": 1,\n        \"num_unique_values\": 2,\n        \"samples\": [\n          1,\n          0\n        ],\n        \"semantic_type\": \"\",\n        \"description\": \"\"\n      },\n      \"column\": \"\n    Alcohol(moderado)\",\n      \"properties\": {\n        \"dtype\": \"number\",\n        \"std\": 0,\n        \"min\": 0,\n        \"max\": 1,\n        \"num_unique_values\": 2,\n        \"samples\": [\n          0,\n          1\n        ],\n        \"semantic_type\": \"\",\n        \"description\": \"\"\n      },\n      \"column\": \"\n    Alcohol(severo)\",\n      \"properties\": {\n        \"dtype\": \"number\",\n        \"std\": 0,\n        \"min\": 0,\n        \"max\": 1,\n        \"num_unique_values\": 2,\n        \"samples\":

```

```
[{"column": 1, "description": "Sobrevivencia\\n(d\\u00edas)", "dtype": "number", "std": 347, "min": 181, "max": 2343, "num_unique_values": 101, "samples": [569, 716], "semantic_type": "number"}, {"column": 9, "description": "Unnamed: 9", "dtype": "number", "std": null, "min": null, "max": null, "num_unique_values": 0, "samples": [], "semantic_type": "number"}, {"column": 10, "description": "Unnamed: 10", "dtype": "number", "std": null, "min": null, "max": null, "num_unique_values": 0, "samples": [], "semantic_type": "number"}, {"column": 11, "description": "Unnamed: 11", "dtype": "category", "num_unique_values": 3, "samples": [], "semantic_type": "category", "description": "Alcohol\\n(moderado)", "description": "Alcohol\\n(severo)"}], "type": "dataframe", "variable_name": "df"}
```

```
from sklearn.preprocessing import MinMaxScaler
```

```
# Crear el scaler
```

```
scaler = MinMaxScaler()
```

```
# Normalizar las columnas especificadas
```

```
df[['Factor Coagulación', 'Índice pronóstico', 'Función de enzima',  
'Función de hígado']] = scaler.fit_transform(df[['Factor Coagulación',  
'Índice pronóstico', 'Función de enzima', 'Función de hígado']])
```

```
import statsmodels.api as sm
```

```
X = df[['Factor Coagulación', 'Índice pronóstico', 'Función de  
enzima', 'Función de hígado', 'Edad', 'Género', 'Alcohol\\n(moderado)',  
'Alcohol\\n(severo)']]  
y = df['Sobrevivencia\\n(días)']
```

```
# Agregar constante (intercepto) al modelo
```

```
X = sm.add_constant(X)
```

```
# Ajustar el modelo
```

```
model = sm.OLS(y, X).fit()
```

```
print(model.summary())
```

OLS Regression Results

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=====
Dep. Variable:      Sobrevivencia
(días)   R-squared:      0.775
Model:      OLS   Adj. R-squared:
0.757
Method:      Least Squares   F-statistic:
42.69
Date:      Wed, 04 Sep 2024   Prob (F-statistic):
8.70e-29
Time:      01:17:03   Log-Likelihood:
-704.12
No. Observations:      108   AIC:
1426.
Df Residuals:      99   BIC:
1450.
Df Model:      8

Covariance Type:      nonrobust

=====
=====
                                coef      std err          t      P>|t|
[0.025      0.975]
-----
-----
const      -595.0929      119.740      -4.970      0.000      -
832.683      -357.503
Factor Coagulación      453.2609      125.622      3.608      0.000
204.000      702.522
Índice pronóstico      738.2324      103.242      7.151      0.000
533.379      943.086
Función de enzima      854.1430      97.046      8.801      0.000
661.582      1046.704
Función de hígado      429.4316      144.560      2.971      0.004
142.593      716.271
Edad      0.6410      1.447      0.443      0.659      -
2.229      3.511
Género      13.0926      34.118      0.384      0.702      -
54.606      80.791
Alcohol
(moderado)      -41.2676      38.529      -1.071      0.287      -117.718
35.183
Alcohol
(severo)      195.7070      50.095      3.907      0.000      96.308
295.106
=====
=====
Omnibus:      45.879   Durbin-Watson:
1.770

```

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Prob(Omnibus):                0.000   Jarque-Bera (JB):
214.951
Skew:                        1.304   Prob(JB):
2.11e-47
Kurtosis:                    9.401   Cond. No.
629.
=====
=====

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

```

Observamos que todas las variables a excepción de edad y género son variables significativas.

```

# Variables predictoras significativas
X_significativas = df[['Factor Coagulación', 'Índice pronóstico',
'Función de enzima', 'Función de hígado']]
X_significativas = sm.add_constant(X_significativas)

# Ajustar el modelo con variables significativas
model_significativas = sm.OLS(y, X_significativas).fit()

# Ver el resumen del modelo
print(model_significativas.summary())

```

OLS Regression Results

```

=====
=====
Dep. Variable:      Sobrevivencia
(días)   R-squared:                0.711
Model:                                OLS   Adj. R-squared:
0.700
Method:                Least Squares   F-statistic:
63.40
Date:                  Wed, 04 Sep 2024   Prob (F-statistic):
6.30e-27
Time:                  01:17:19   Log-Likelihood:
-717.67
No. Observations:      108   AIC:
1445.
Df Residuals:          103   BIC:
1459.
Df Model:              4

Covariance Type:      nonrobust

=====
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```

		coef	std err	t	P> t	
[0.025	0.975]					

const		-580.0033	99.363	-5.837	0.000	-
777.067	-382.939					
Factor Coagulación		564.8957	134.644	4.195	0.000	
297.862	831.930					
Índice pronóstico		768.7555	113.355	6.782	0.000	
543.943	993.568					
Función de enzima		888.3017	107.234	8.284	0.000	
675.628	1100.975					
Función de hígado		317.3125	155.538	2.040	0.044	
8.840	625.785					

Notes:

```
from statsmodels.tools import add_constant
from sklearn.preprocessing import PolynomialFeatures

poly = PolynomialFeatures(degree=2, include_bias=False)
X_poly = poly.fit_transform(X_significativas.drop('const', axis=1))
X_poly = pd.DataFrame(X_poly,
                      columns=poly.get_feature_names_out(X_significativas.columns[1:]))
X_poly = add_constant(X_poly)
```

OLS Regression Results

Dep. Variable: Sobrevivencia
 (días) R-squared: 0.790
 Model: OLS Adj. R-squared:
 0.759
 Method: Least Squares F-statistic:
 25.06
 Date: Wed, 04 Sep 2024 Prob (F-statistic):
 1.49e-25
 Time: 01:17:27 Log-Likelihood:
 -700.33
 No. Observations: 108 AIC:
 1431.
 Df Residuals: 93 BIC:
 1471.
 Df Model: 14

Covariance Type: nonrobust

			coef	std err	t
P> t	[0.025	0.975]			

const			336.4146	381.004	0.883
0.380	-420.183	1093.013			
Factor Coagulación			-765.7353	808.553	-0.947
0.346	-2371.361	839.891			
Índice pronóstico			817.5406	819.336	0.998
0.321	-809.498	2444.579			
Función de enzima			-1239.9252	638.485	-1.942
0.055	-2507.830	27.980			
Función de hígado			-574.8781	906.262	-0.634
0.527	-2374.535	1224.778			
Factor Coagulación^2			589.1580	717.533	0.821
0.414	-835.721	2014.037			
Factor Coagulación Índice pronóstico			-375.0895	803.616	-0.467
0.642	-1970.913	1220.734			
Factor Coagulación Función de enzima			1992.7951	822.977	2.421
0.017	358.527	3627.064			
Factor Coagulación Función de hígado			62.1117	1319.603	0.047
0.963	-2558.359	2682.582			
Índice pronóstico^2			-451.2967	522.440	-0.864
0.390	-1488.759	586.166			
Índice pronóstico Función de enzima			17.2073	649.056	0.027
0.979	-1271.689	1306.103			
Índice pronóstico Función de hígado			1724.8054	1044.696	1.651
0.102	-349.754	3799.365			
Función de enzima^2			1403.8805	459.054	3.058

0.003	492.291	2315.470			
Función de enzima	Función de hígado		-96.8656	1099.007	-0.088
0.930	-2279.275	2085.544			
Función de hígado^2			-465.8850	905.897	-0.514
0.608	-2264.817	1333.047			

```

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=====
Omnibus:                23.564    Durbin-Watson:
2.121
Prob(Omnibus):          0.000    Jarque-Bera (JB):
43.790
Skew:                   0.900    Prob(JB):
3.10e-10
Kurtosis:               5.548    Cond. No.
231.
=====
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```

Notes:

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

```

from statsmodels.stats.outliers_influence import
variance_inflation_factor

```

Calcular FIV para el modelo con variables significativas

```

fiv = pd.DataFrame()
fiv['variable'] = X_significativas.columns
fiv['VIF'] = [variance_inflation_factor(X_significativas.values, i)
for i in range(X_significativas.shape[1])]
print(fiv)

```

	variable	VIF
0	const	29.370301
1	Factor Coagulación	1.467321
2	Índice pronóstico	1.291654
3	Función de enzima	1.610220
4	Función de hígado	2.250657

```

import seaborn as sns
import matplotlib.pyplot as plt

```

Gráfico de residuos vs. valores ajustados

```

plt.figure(figsize=(10, 6))
plt.subplot(1, 2, 1)
sns.scatterplot(x=fitted, y=residuals)
plt.axhline(y=0, color='r', linestyle='--')
plt.xlabel('Fitted values')
plt.ylabel('Residuals')
plt.title('Residuals vs Fitted')

```

```
# Histograma de residuos
plt.subplot(1, 2, 2)
sns.histplot(residuals, kde=True)
plt.xlabel('Residuals')
plt.title('Histogram of Residuals')

plt.tight_layout()
plt.show()
```

