

# ProF\_Anderson\_Gonzalez\_Zuluaga

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UNIVERSIDAD TECNOLÓGICA DE PANAMÁ

FACULTAD DE INGENIERÍA DE SISTEMAS COMPUTACIONALES

DEPARTAMENTO DE COMPUTACIÓN Y SIMULACIÓN DE SISTEMAS

—PROYECTO FINAL: Aprendizaje Supervisado y No Supervisado—

Topicos Especiales II

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#

PARTE N.1 APRENDIZAJE SUPERVISADO

## 0.1 LIBRERIAS UTILIZADAS

```
[1]: # importar librerias a utilizar en el proyecto
import pandas as pd
from sklearn.preprocessing import LabelEncoder
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, label_binarize
import matplotlib.pyplot as plt
from sklearn.metrics import *
import warnings
warnings.filterwarnings("ignore")

# Importar modelos
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
from sklearn.neighbors import KNeighborsClassifier
from sklearn.tree import DecisionTreeClassifier
```

```

from sklearn.linear_model import LinearRegression
from sklearn.tree import DecisionTreeRegressor
from sklearn.svm import SVR
from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.linear_model import LinearRegression
from sklearn.tree import DecisionTreeRegressor
from sklearn.ensemble import RandomForestRegressor

```

## 0.2 PREPARACIÓN DE LOS DATOS

[2]: #Inicializar los DataSets

```

try:
    df_apple_quality = pd.read_csv('apple_quality.csv', encoding='ISO-8859-1')
    print(" Dataset 'Apple Quality' cargado exitosamente.")
    display(df_apple_quality.head())
except FileNotFoundError:
    print(" ERROR: No se encontró el archivo del dataset de terrorismo.")
    print("Por favor, asegúrate de que el archivo esté en la misma carpeta que tu notebook y que el nombre sea correcto.")

print("\n" + "="*80 + "\n") # Separador visual

# --- Cargar Dataset Obligatorio (Zenodo) ---
try:
    df_Pediatric= pd.read_excel('app_data.xlsx')
    print(" Dataset 'app_data.xlsx' (Pediatric Appendicitis Dataset) cargado exitosamente.")
    display(df_Pediatric.head())
except FileNotFoundError:
    print(" ERROR: No se encontró el archivo 'app_data.xlsx'.")
    print("Asegúrate de que el archivo esté en la misma carpeta que tu notebook.")

```

Dataset 'Apple Quality' cargado exitosamente.

	A_id	Size	Weight	Sweetness	Crunchiness	Juiciness	Ripeness	\
0	0.0	-3.970049	-2.512336	5.346330	-1.012009	1.844900	0.329840	
1	1.0	-1.195217	-2.839257	3.664059	1.588232	0.853286	0.867530	
2	2.0	-0.292024	-1.351282	-1.738429	-0.342616	2.838636	-0.038033	
3	3.0	-0.657196	-2.271627	1.324874	-0.097875	3.637970	-3.413761	
4	4.0	1.364217	-1.296612	-0.384658	-0.553006	3.030874	-1.303849	

	Acidity	Quality
0	-0.491590483	good
1	-0.722809367	good
2	2.621636473	bad

```
3 0.790723217    good
4 0.501984036    good
```

```
=====
Dataset 'app_data.xlsx' (Pediatric Appendicitis Dataset) cargado exitosamente.

      Age   BMI   Sex   Height   Weight   Length_of_Stay   Management \
0  12.68  16.9  female  148.0    37.0            3.0  conservative
1  14.10  31.9   male  147.0    69.5            2.0  conservative
2  14.14  23.3  female  163.0    62.0            4.0  conservative
3  16.37  20.6  female  165.0    56.0            3.0  conservative
4  11.08  16.9  female  163.0    45.0            3.0  conservative

      Severity Diagnosis_Presumptive   Diagnosis ... \
0 uncomplicated           appendicitis  appendicitis ...
1 uncomplicated           appendicitis  no appendicitis ...
2 uncomplicated           appendicitis  no appendicitis ...
3 uncomplicated           appendicitis  no appendicitis ...
4 uncomplicated           appendicitis  appendicitis ...

      Abscess_Location Pathological_Lymph_Nodes Lymph_Nodes_Location \
0             NaN          yes                  reUB
1             NaN          NaN                  NaN
2             NaN          NaN                  NaN
3             NaN          yes                  reUB
4             NaN          yes                  reUB

      Bowel_Wall_Thickening Conglomerate_of_Bowel_Loops Ileus Coprostasis \
0                 NaN                  NaN      NaN      NaN
1                 NaN                  NaN      NaN      NaN
2                 NaN                  NaN      NaN      NaN
3                 NaN                  NaN      NaN      NaN
4                 NaN                  NaN      NaN      NaN

      Meteorism Enteritis Gynecological_Findings
0       NaN     NaN          NaN
1      yes     NaN          NaN
2      yes     yes          NaN
3      NaN     yes          NaN
4      NaN     yes          NaN
```

[5 rows x 58 columns]

Visualizamos los datos del Dataset de Pediatric Apendicitis

```
[3]: #visualizar cantidad y tipo de datos originales
df_Pediatric.info()
```

```

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 782 entries, 0 to 781
Data columns (total 58 columns):
 #   Column           Non-Null Count Dtype  
 --- 
 0   Age              781 non-null    float64 
 1   BMI              755 non-null    float64 
 2   Sex              780 non-null    object  
 3   Height           756 non-null    float64 
 4   Weight            779 non-null    float64 
 5   Length_of_Stay    778 non-null    float64 
 6   Management        781 non-null    object  
 7   Severity          781 non-null    object  
 8   Diagnosis_Presumptive 780 non-null    object  
 9   Diagnosis         780 non-null    object  
 10  Alvarado_Score    730 non-null    float64 
 11  Paedriatic_Appendicitis_Score 730 non-null    float64 
 12  Appendix_on_US     777 non-null    object  
 13  Appendix_Diameter  498 non-null    float64 
 14  Migratory_Pain     773 non-null    object  
 15  Lower_Right_Abd_Pain 774 non-null    object  
 16  Contralateral_Rebound_Tenderness 767 non-null    object  
 17  Coughing_Pain      766 non-null    object  
 18  Nausea             774 non-null    object  
 19  Loss_of_Appetite   772 non-null    object  
 20  Body_Temperature   775 non-null    float64 
 21  WBC_Count          776 non-null    float64 
 22  Neutrophil_Percentage 679 non-null    float64 
 23  Segmented_Neutrophils 54 non-null    float64 
 24  Neutrophilia       732 non-null    object  
 25  RBC_Count          764 non-null    float64 
 26  Hemoglobin          764 non-null    float64 
 27  RDW                756 non-null    float64 
 28  Thrombocyte_Count  764 non-null    float64 
 29  Ketones_in_Urine    582 non-null    object  
 30  RBC_in_Urine        576 non-null    object  
 31  WBC_in_Urine        583 non-null    object  
 32  CRP                771 non-null    float64 
 33  Dysuria            753 non-null    object  
 34  Stool               765 non-null    object  
 35  Peritonitis         773 non-null    object  
 36  Psoas_Sign          745 non-null    object  
 37  Ipsilateral_Rebound_Tenderness 619 non-null    object  
 38  US_Performed        778 non-null    object  
 39  US_Number            760 non-null    float64 
 40  Free_Fluids          719 non-null    object  
 41  Appendix_Wall_Layers 218 non-null    object  
 42  Target_Sign          138 non-null    object 

```

```

43 Appendicolith          69 non-null   object
44 Perfusion              63 non-null   object
45 Perforation            81 non-null   object
46 Surrounding_Tissue_Reaction 252 non-null   object
47 Appendicular_Abscess    85 non-null   object
48 Abscess_Location        13 non-null   object
49 Pathological_Lymph_Nodes 203 non-null   object
50 Lymph_Nodes_Location    121 non-null   object
51 Bowel_Wall_Thickening   99 non-null   object
52 Conglomerate_of_Bowel_Loops 43 non-null   object
53 Ileus                  60 non-null   object
54 Coprostasis             71 non-null   object
55 Meteorism               140 non-null   object
56 Enteritis               66 non-null   object
57 Gynecological_Findings 26 non-null   object
dtypes: float64(18), object(40)
memory usage: 354.5+ KB

```

```

[4]: df_a_limpiar = df_Pediatric.copy()

print(f"--- Limpiando el DataFrame: Pediatric Apendicitis ---")
print(f"Dimensiones originales: {df_a_limpiar.shape[0]} filas, {df_a_limpiar.
      ↪shape[1]} columnas")
print("\n" + "="*50 + "\n")

# --- PASO 2: Calcular y mostrar el porcentaje de nulos ---
porcentaje_nulos = df_a_limpiar.isnull().mean() * 100
porcentaje_nulos = porcentaje_nulos.sort_values(ascending=False)
print("Porcentaje de nulos por columna (top 15):")
print(porcentaje_nulos.head(15))

# --- PASO 3: Eliminar columnas y filas con nulos ---
# Eliminar columnas con datos nulos por encima del 13%
columnas_a_eliminar = porcentaje_nulos[porcentaje_nulos > 13].index
df_limpio = df_a_limpiar.drop(columns=columnas_a_eliminar)

# Eliminar las filas restantes que todavía contengan algún dato nulo
df_limpio = df_limpio.dropna()

# --- PASO 4: Mostrar el resultado de la limpieza ---
print("\n" + "="*50 + "\n")
print("Resultado de la limpieza de la Data:")
print(f"Se eliminaron {len(columnas_a_eliminar)} columnas por exceso de nulos.")
print(f"Dimensiones finales: {df_limpio.shape[0]} filas, {df_limpio.shape[1]} u
      ↪columnas")

```

```
df_limpio.info()
```

```
--- Limpiando el DataFrame: Pediatric Apendicitis ---
Dimensiones originales: 782 filas, 58 columnas
```

```
=====
```

```
Porcentaje de nulos por columna (top 15):
```

```
Abscess_Location      98.337596
Gynecological_Findings 96.675192
Conglomerate_of_Bowel_Loops 94.501279
Segmented_Neutrophils    93.094629
Ileus                  92.327366
Perfusion               91.943734
Enteritis                91.560102
Appendicolith            91.176471
Coprostasis              90.920716
Perforation              89.641944
Appendicular_Abscess     89.130435
Bowel_Wall_Thickening    87.340153
Lymph_Nodes_Location      84.526854
Target_Sign                82.352941
Meteorism                 82.097187
dtype: float64
```

```
=====
```

```
Resultado de la limpieza de la Data:
```

```
Se eliminaron 24 columnas por exceso de nulos.
```

```
Dimensiones finales: 589 filas, 34 columnas
```

```
<class 'pandas.core.frame.DataFrame'>
```

```
Index: 589 entries, 0 to 781
```

```
Data columns (total 34 columns):
```

#	Column	Non-Null Count	Dtype
0	Age	589 non-null	float64
1	BMI	589 non-null	float64
2	Sex	589 non-null	object
3	Height	589 non-null	float64
4	Weight	589 non-null	float64
5	Length_of_Stay	589 non-null	float64
6	Management	589 non-null	object
7	Severity	589 non-null	object
8	Diagnosis_Presumptive	589 non-null	object
9	Diagnosis	589 non-null	object
10	Alvarado_Score	589 non-null	float64
11	Paedriatic_Appendicitis_Score	589 non-null	float64
12	Appendix_on_US	589 non-null	object

```

13 Migratory_Pain           589 non-null   object
14 Lower_Right_Abd_Pain    589 non-null   object
15 Contralateral_Rebound_Tenderness 589 non-null   object
16 Coughing_Pain           589 non-null   object
17 Nausea                  589 non-null   object
18 Loss_of_Appetite        589 non-null   object
19 Body_Temperature         589 non-null   float64
20 WBC_Count                589 non-null   float64
21 Neutrophilia            589 non-null   object
22 RBC_Count                589 non-null   float64
23 Hemoglobin               589 non-null   float64
24 RDW                      589 non-null   float64
25 Thrombocyte_Count       589 non-null   float64
26 CRP                      589 non-null   float64
27 Dysuria                 589 non-null   object
28 Stool                    589 non-null   object
29 Peritonitis              589 non-null   object
30 Psoas_Sign               589 non-null   object
31 US_Performed             589 non-null   object
32 US_Number                589 non-null   float64
33 Free_Fluids              589 non-null   object
dtypes: float64(15), object(19)
memory usage: 161.1+ KB

```

Visualizamos los datos del Dataset de Apple Quality

```
[5]: # 1. COPIA DEL DATAFRAME ORIGINAL
df_apple_limpio = df_apple_quality.copy()

# 2. ELIMINAR COLUMNAS CON MÁS DEL 20% DE NULOS
porcentaje_nulos = df_apple_limpio.isnull().mean() * 100
columnas_a_eliminar = porcentaje_nulos[porcentaje_nulos > 20].index
df_apple_limpio = df_apple_limpio.drop(columns=columnas_a_eliminar)

print(f"Se eliminaron {len(columnas_a_eliminar)} columnas por exceso de nulos.")
print(f"Dimensiones después de eliminar columnas: {df_apple_limpio.shape}")

# 3. ELIMINAR FILAS CON NULOS (sin imputar)
df_apple_limpio = df_apple_limpio.dropna()

# 4. Mostrar resultado final
print("\n--- Resultado de la Limpieza sin Imputación ---")
print("No deberían quedar valores nulos.")
print(f"Dimensiones finales: {df_apple_limpio.shape}")
df_apple_limpio.info()

print("\nPrimeras 5 filas del DataFrame limpio:")
display(df_apple_limpio.head())
```

```
Se eliminaron 0 columnas por exceso de nulos.  
Dimensiones después de eliminar columnas: (4001, 9)
```

```
--- Resultado de la Limpieza sin Imputación ---  
No deberían quedar valores nulos.  
Dimensiones finales: (4000, 9)  
<class 'pandas.core.frame.DataFrame'>  
Index: 4000 entries, 0 to 3999  
Data columns (total 9 columns):  
 #   Column      Non-Null Count  Dtype     
---  --          -----          -----  
 0   A_id        4000 non-null    float64  
 1   Size         4000 non-null    float64  
 2   Weight       4000 non-null    float64  
 3   Sweetness     4000 non-null    float64  
 4   Crunchiness   4000 non-null    float64  
 5   Juiciness     4000 non-null    float64  
 6   Ripeness      4000 non-null    float64  
 7   Acidity        4000 non-null    object    
 8   Quality        4000 non-null    object    
dtypes: float64(7), object(2)  
memory usage: 312.5+ KB
```

Primeras 5 filas del DataFrame limpio:

```
A_id      Size     Weight   Sweetness  Crunchiness  Juiciness  Ripeness  \\\n0  0.0 -3.970049 -2.512336  5.346330   -1.012009  1.844900  0.329840  
1  1.0 -1.195217 -2.839257  3.664059    1.588232  0.853286  0.867530  
2  2.0 -0.292024 -1.351282 -1.738429   -0.342616  2.838636 -0.038033  
3  3.0 -0.657196 -2.271627  1.324874   -0.097875  3.637970 -3.413761  
4  4.0  1.364217 -1.296612 -0.384658   -0.553006  3.030874 -1.303849  
  
Acidity  Quality  
0 -0.491590483   good  
1 -0.722809367   good  
2  2.621636473   bad  
3  0.790723217   good  
4  0.501984036   good
```

### 0.3 CREACIÓN DE LOS MODELOS DE APRENDIZAJE SUPERVISADO

```
[6]: modelo1 = LogisticRegression(random_state=42)  
modelo2 = RandomForestClassifier(random_state=42)  
modelo3 = DecisionTreeClassifier(random_state=42)  
  
clasificadores = [  
    ('Regresión Logistica', modelo1),  
    ('Random Forest', modelo2),
```

```
('Árbol de Decisión', modelo3)  
]
```

```
[7]: # Modelos de regresión  
modelo1 = LinearRegression()  
modelo2 = DecisionTreeRegressor(random_state=42)  
modelo3 = RandomForestRegressor(random_state=42)  
  
modelos_regresion = [  
    ('Regresión Lineal', modelo1),  
    ('Árbol de Decisión', modelo2),  
    ('Random Forest', modelo3)  
]
```

## 0.4 PROBLEMA N.1 (APRENDIZAJE AUTOMATICO)

Clasificación del Tratamiento para Apendicitis Pediátrica

```
[8]: # --- Separar el DataFrame en X y Y ---  
X = df_limpio.drop('Management', axis=1)  
Y = df_limpio['Management']  
  
# --- Codificar variables categóricas (como 'Sex') en X ---  
X = pd.get_dummies(X, drop_first=True)  
  
# --- Codificar la variable Y (target) a numérico ---  
from sklearn.preprocessing import LabelEncoder  
le = LabelEncoder()  
y = le.fit_transform(Y)  
  
# --- Verificación ---  
print("Columnas de X codificado:", X.columns.tolist())  
print("Dimensiones de X:", X.shape)  
print("Dimensiones de Y codificado:", y.shape)  
print("Primeros 5 valores codificados de y:", y[:5])  
print("Etiquetas originales de Y:", le.classes_)  
  
# --- Dividir datos en entrenamiento y prueba ---  
from sklearn.model_selection import train_test_split  
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3,  
                                                    random_state=42)  
  
# --- Verificar dimensiones ---  
print("Dimensiones de X_train:", X_train.shape)  
print("Dimensiones de X_test:", X_test.shape)  
print("Dimensiones de y_train:", y_train.shape)  
print("Dimensiones de y_test:", y_test.shape)
```

Columnas de X codificado: ['Age', 'BMI', 'Height', 'Weight', 'Length\_of\_Stay', 'Alvarado\_Score', 'Paedriatic\_Appendicitis\_Score', 'Body\_Temperature', 'WBC\_Count', 'RBC\_Count', 'Hemoglobin', 'RDW', 'Thrombocyte\_Count', 'CRP', 'US\_Number', 'Sex\_male', 'Severity\_uncomplicated', 'Diagnosis\_Presumptive\_Appendizitis/ Lymphadenitis mesenterialis', 'Diagnosis\_Presumptive\_Gastroenteritis', 'Diagnosis\_Presumptive\_appendicitis', 'Diagnosis\_Presumptive\_chronische Appendizitis', 'Diagnosis\_Presumptive\_diabetische Ketoazidose, Myokarditis', 'Diagnosis\_Presumptive\_no appendicitis', 'Diagnosis\_Presumptive\_prolongierte Gastroenteritis', 'Diagnosis\_no appendicitis', 'Appendix\_on\_US\_yes', 'Migratory\_Pain\_yes', 'Lower\_Right\_Abd\_Pain\_yes', 'Contralateral\_Rebound\_Tenderness\_yes', 'Coughing\_Pain\_yes', 'Nausea\_yes', 'Loss\_of\_Appetite\_yes', 'Neutrophilia\_yes', 'Dysuria\_yes', 'Stool\_constipation, diarrhea', 'Stool\_diarrhea', 'Stool\_normal', 'Peritonitis\_local', 'Peritonitis\_no', 'Psoas\_Sign\_yes', 'Free\_Fluids\_yes']

Dimensiones de X: (589, 41)

Dimensiones de Y codificado: (589,)

Primeros 5 valores codificados de y: [0 0 0 0 0]

Etiquetas originales de Y: ['conservative' 'primary surgical' 'secondary surgical']

Dimensiones de X\_train: (412, 41)

Dimensiones de X\_test: (177, 41)

Dimensiones de y\_train: (412,)

Dimensiones de y\_test: (177,)

```
[9]: from sklearn.metrics import (
    accuracy_score, precision_score, recall_score, f1_score,
    confusion_matrix
)

resultados = []
matrices_confusion_train = {}
matrices_confusion_test = {}

for nombre, modelo in clasificadores:
    modelo.fit(X_train, y_train)

    # Predicciones
    y_train_pred = modelo.predict(X_train)
    y_test_pred = modelo.predict(X_test)

    # Métricas
    acc_train = accuracy_score(y_train, y_train_pred)
    acc_test = accuracy_score(y_test, y_test_pred)
    prec = precision_score(y_test, y_test_pred, average='weighted', zero_division=0)
    rec = recall_score(y_test, y_test_pred, average='weighted')
```

```

f1 = f1_score(y_test, y_test_pred, average='weighted')

# Matrices de confusión
cm_train = confusion_matrix(y_train, y_train_pred)
cm_test = confusion_matrix(y_test, y_test_pred)
matrices_confusion_train[nombre] = cm_train
matrices_confusion_test[nombre] = cm_test

# Almacenar resultados
resultados.append({
    'Modelo': nombre,
    'Accuracy Train': acc_train,
    'Accuracy Test': acc_test,
    'Precision': prec,
    'Recall': rec,
    'F1 Score': f1
})

df_resultados = pd.DataFrame(resultados).sort_values(by='Accuracy Test',  

    ↴ ascending=False)

```

[10]: df\_resultados

```

[10]:          Modelo  Accuracy Train  Accuracy Test  Precision    Recall  \
1      Random Forest      1.000000     0.966102  0.960791  0.966102
2      Árbol de Decisión      1.000000     0.932203  0.947679  0.932203
0  Regresión Logistica      0.917476     0.898305  0.900608  0.898305

      F1 Score
1  0.963420
2  0.939697
0  0.899158

```

[11]: `for nombre, modelo in clasificadores:`  
 `y_pred = modelo.predict(X_test)`  
 `print("="*50)`  
 `print(f" Modelo: {nombre}")`  
 `print(classification_report(y_test, y_pred, target_names=le.classes_))`

```
=====
Modelo: Regresión Logistica
      precision    recall  f1-score   support
conservative       0.94      0.92      0.93      127
primary surgical     0.81      0.86      0.83       49
secondary surgical     0.00      0.00      0.00        1

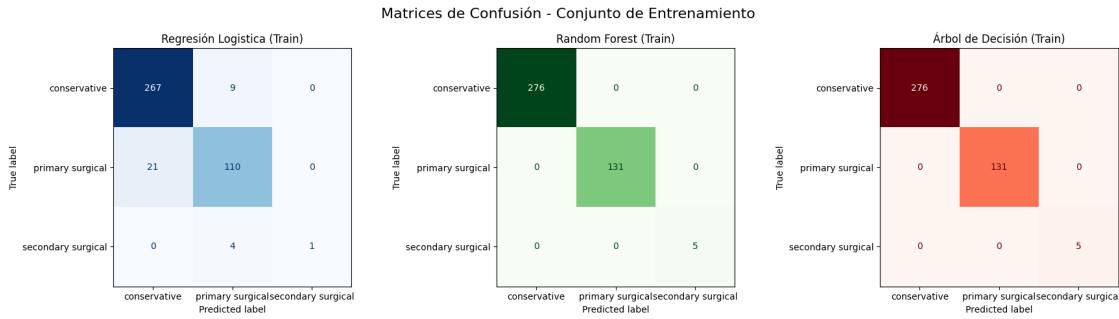
      accuracy                           0.90      177
```

macro avg	0.58	0.59	0.59	177
weighted avg	0.90	0.90	0.90	177
=====				
Modelo: Random Forest				
	precision	recall	f1-score	support
conservative	0.98	0.98	0.98	127
primary surgical	0.94	0.96	0.95	49
secondary surgical	0.00	0.00	0.00	1
accuracy			0.97	177
macro avg	0.64	0.65	0.64	177
weighted avg	0.96	0.97	0.96	177
=====				
Modelo: Árbol de Decisión				
	precision	recall	f1-score	support
conservative	0.97	0.97	0.97	127
primary surgical	0.91	0.86	0.88	49
secondary surgical	0.00	0.00	0.00	1
accuracy			0.93	177
macro avg	0.63	0.61	0.62	177
weighted avg	0.95	0.93	0.94	177

```
[12]: # Figura con matrices de entrenamiento
fig, axes = plt.subplots(1, 3, figsize=(18, 5))
etiquetas = le.classes_

for i, (nombre, _) in enumerate(clasificadores):
    ConfusionMatrixDisplay(
        confusion_matrix=matrices_confusion_train[nombre],
        display_labels=etiquetas
    ).plot(cmap=["Blues", "Greens", "Reds"][i], ax=axes[i], colorbar=False)
    axes[i].set_title(f"{nombre} (Train)")

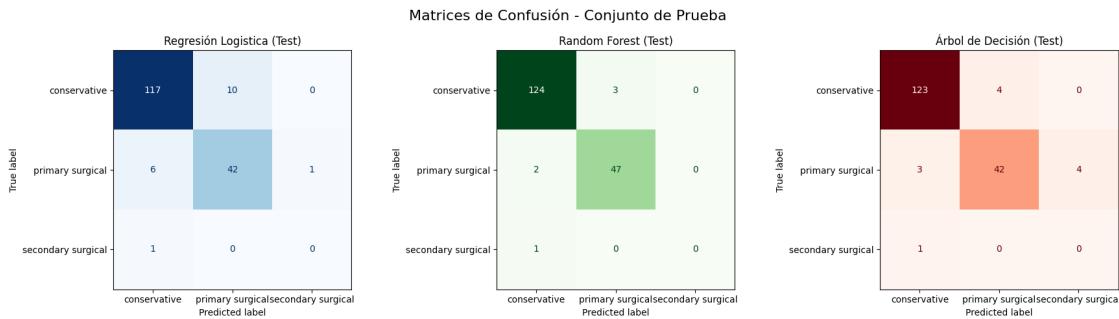
fig.suptitle("Matrices de Confusión - Conjunto de Entrenamiento", fontsize=16)
plt.tight_layout()
plt.show()
```



```
[13]: # Figura con matrices de prueba
fig, axes = plt.subplots(1, 3, figsize=(18, 5))
etiquetas = le.classes_

for i, (nombre, _) in enumerate(clasificadores):
    ConfusionMatrixDisplay(
        confusion_matrix=matrices_confusion_test[nombre],
        display_labels=etiquetas
    ).plot(cmap=["Blues", "Greens", "Reds"][i], ax=axes[i], colorbar=False)
    axes[i].set_title(f"{nombre} (Test)")

fig.suptitle("Matrices de Confusión - Conjunto de Prueba", fontsize=16)
plt.tight_layout()
plt.show()
```



```
[14]: # Binarizar y preparar clases
y_test_binarizado = label_binarize(y_test, classes=[0, 1, 2])
n_clases = y_test_binarizado.shape[1]
etiquetas = le.classes_

# Colores fijos para consistencia
colores = ['blue', 'orange', 'green'] # conservar orden: conservative, primary, secondary
```

```

# Crear figura
fig, axes = plt.subplots(1, 3, figsize=(18, 5))

# Tabla para resumen AUC promedio
auc_resumen = []

for i, (nombre, modelo) in enumerate(clasificadores):
    y_score = modelo.predict_proba(X_test)

    aucs_por_clase = []

    for clase in range(n_clases):
        fpr, tpr, _ = roc_curve(y_test_binarizado[:, clase], y_score[:, clase])
        roc_auc = auc(fpr, tpr)
        aucs_por_clase.append(roc_auc)

        axes[i].plot(fpr, tpr, lw=2, label=f'{etiquetas[clase]} (AUC = {roc_auc:.2f})', color=colores[clase])

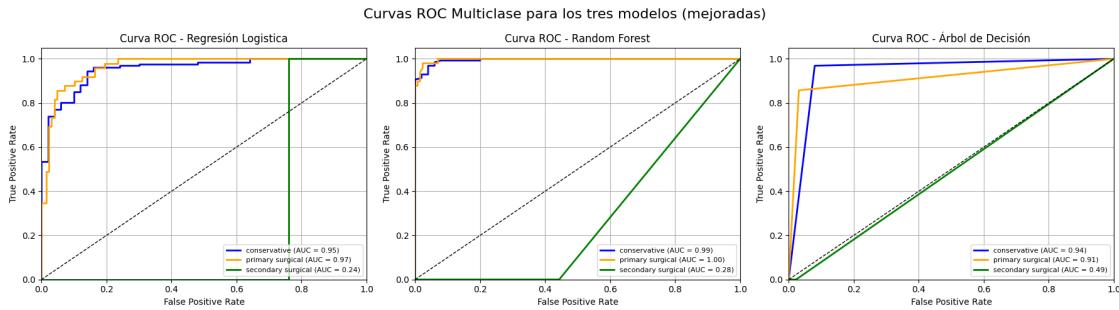
    # Gráfico de referencia
    axes[i].plot([0, 1], [0, 1], 'k--', lw=1)
    axes[i].set_xlim([0.0, 1.0])
    axes[i].set_ylim([0.0, 1.05])
    axes[i].set_xlabel('False Positive Rate')
    axes[i].set_ylabel('True Positive Rate')
    axes[i].set_title(f'Curva ROC - {nombre}')
    axes[i].legend(loc="lower right", fontsize=8)
    axes[i].grid(True)

# Guardar AUC promedio macro
auc_promedio = np.mean(aucs_por_clase)
auc_resumen.append({'Modelo': nombre, 'AUC Promedio (macro)': auc_promedio})

# Título general
fig.suptitle("Curvas ROC Multiclas para los tres modelos (mejoradas)", fontsize=16)
plt.tight_layout()
plt.show()

# Tabla resumen de AUC promedio
df_auc = pd.DataFrame(auc_resumen).sort_values(by='AUC Promedio (macro)', ascending=False)
display(df_auc)

```



	Modelo	AUC Promedio (macro)
2	Árbol de Decisión	0.781945
1	Random Forest	0.756754
0	Regresión Logistica	0.719507

```
[15]: import IPython.display as dsp

df_resumen_problema1 = pd.merge(df_resultados, df_auc, on='Modelo')
df_resumen_problema1.insert(0, 'Problema', 1)

columnas_ordenadas = [
    'Problema', 'Modelo', 'Accuracy Train', 'Accuracy Test',
    'Precision', 'Recall', 'F1 Score', 'AUC Promedio (macro)'
]
df_resumen_problema1 = df_resumen_problema1[columnas_ordenadas]

mejor_modelo = df_resumen_problema1.sort_values(by='Accuracy Test', ↴
    ascending=False).iloc[0]['Modelo']
df_resumen_problema1['Mejor Modelo'] = df_resumen_problema1['Modelo'].apply(
    lambda x: ' ' if x == mejor_modelo else ''
)

# Mostrar tabla
dsp.display(df_resumen_problema1.round(3))
```

Problema	Modelo	Accuracy Train	Accuracy Test	Precision	\
0 1 Random Forest		1.000	0.966	0.961	
1 1 Árbol de Decisión		1.000	0.932	0.948	
2 1 Regresión Logistica		0.917	0.898	0.901	
Recall	F1 Score	AUC Promedio (macro)	Mejor Modelo		
0 0.966	0.963		0.757		
1 0.932	0.940		0.782		
2 0.898	0.899		0.720		

## 0.5 PROBLEMA N.2 (APRENDIZAJE AUTOMATICO)

Clasificación de la calidad de una manzana a partir de sus propiedades físico-químicas

Dataset:<https://www.kaggle.com/datasets/nelgiriyewithana/apple-quality>

```
[16]: # --- Separar el DataFrame en X y ---
X = df_apple_limpio.drop('Quality', axis=1) # Quitamos la columna objetivo
y = df_apple_limpio['Quality'] # Variable objetivo binaria: good / bad

# --- Codificar variables categóricas (como 'Color', si existe) en X ---
X = pd.get_dummies(X, drop_first=True)

# --- Codificar la variable Y (target) a numérico ---
from sklearn.preprocessing import LabelEncoder

le = LabelEncoder()
y = le.fit_transform(y)

# --- Verificación ---
print("Columnas de X codificado:", X.columns.tolist())
print("Dimensiones de X:", X.shape)
print("Dimensiones de y codificado:", y.shape)
print("Primeros 5 valores codificados de y:", y[:5])
print("Etiquetas originales de y:", le.classes_)

# --- Dividir datos en entrenamiento y prueba ---
from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_state=42)

# --- Verificación de dimensiones ---
print("Dimensiones de X_train:", X_train.shape)
print("Dimensiones de X_test:", X_test.shape)
print("Dimensiones de y_train:", y_train.shape)
print("Dimensiones de y_test:", y_test.shape)
```

Columnas de X codificado: ['A\_id', 'Size', 'Weight', 'Sweetness', 'Crunchiness', 'Juiciness', 'Ripeness', 'Acidity\_-0.001593958', 'Acidity\_-0.003109107', 'Acidity\_-0.008136378', 'Acidity\_-0.009153027', 'Acidity\_-0.011438035', 'Acidity\_-0.011582814', 'Acidity\_-0.012061768', 'Acidity\_-0.012433307', 'Acidity\_-0.012611428', 'Acidity\_-0.014252196', 'Acidity\_-0.014548296', 'Acidity\_-0.01630256', 'Acidity\_-0.017094245', 'Acidity\_-0.021751811', 'Acidity\_-0.021881716', 'Acidity\_-0.022774534', 'Acidity\_-0.024607366', 'Acidity\_-0.024782906', 'Acidity\_-0.025322858', 'Acidity\_-0.026114955', 'Acidity\_-0.026177532', 'Acidity\_-0.0287965', 'Acidity\_-0.029111848', 'Acidity\_-0.030533085', 'Acidity\_-0.030536884', 'Acidity\_-0.031126053']

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'Acidity_7.404736238']

Dimensiones de X: (4000, 4006)
Dimensiones de y codificado: (4000,)
Primeros 5 valores codificados de y: [1 1 0 1 1]
Etiquetas originales de y: ['bad' 'good']
Dimensiones de X_train: (2800, 4006)
Dimensiones de X_test: (1200, 4006)
Dimensiones de y_train: (2800,)
Dimensiones de y_test: (1200,)

```

```

[17]: from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score, confusion_matrix

resultados2 = []
matrices_confusion_train2 = {}
matrices_confusion_test2 = {}

print("Iniciando entrenamiento de modelos (calidad de manzana)...")
```

```

for nombre, modelo in clasificadores:
    print(f"\nEntrenando {nombre}...")

    # Entrenamiento
    modelo.fit(X_train, y_train)

    # Predicciones
    y_train_pred = modelo.predict(X_train)
    y_test_pred = modelo.predict(X_test)

    # Métricas
    acc_train = accuracy_score(y_train, y_train_pred)
    acc_test = accuracy_score(y_test, y_test_pred)
    prec = precision_score(y_test, y_test_pred, average='weighted', zero_division=0)
    rec = recall_score(y_test, y_test_pred, average='weighted')
    f1 = f1_score(y_test, y_test_pred, average='weighted')

    # Matrices de confusión
    cm_train = confusion_matrix(y_train, y_train_pred)
    cm_test = confusion_matrix(y_test, y_test_pred)
    matrices_confusion_train2[nombre] = cm_train
    matrices_confusion_test2[nombre] = cm_test

    # Resultados
    resultados2.append({
        'Modelo': nombre,
        'Accuracy Train': acc_train,
        'Accuracy Test': acc_test,
        'Precision': prec,
        'Recall': rec,
        'F1 Score': f1
    })

    print(f" {nombre} completado. Accuracy Test: {acc_test:.4f}")

df_resultados2 = pd.DataFrame(resultados2).sort_values(by='Accuracy Test', ascending=False)

```

Iniciando entrenamiento de modelos (calidad de manzana)...

Entrenando Regresión Logistica...

Regresión Logistica completado. Accuracy Test: 0.7408

Entrenando Random Forest...

Random Forest completado. Accuracy Test: 0.8483

Entrenando Árbol de Decisión...

Árbol de Decisión completado. Accuracy Test: 0.7875

[18]: df\_resultados2

```
[18]:          Modelo  Accuracy Train  Accuracy Test  Precision  Recall  \
1      Random Forest      1.000000      0.848333  0.848401  0.848333
2      Árbol de Decisión      1.000000      0.787500  0.787520  0.787500
0  Regresión Logistica      0.727143      0.740833  0.741012  0.740833

   F1 Score
1  0.848308
2  0.787505
0  0.740836
```

[19]: print("Reporte de clasificación para cada modelo:\n")

```
for nombre, modelo in clasificadores:
    y_pred = modelo.predict(X_test)

    print("==" * 50)
    print(f"  Modelo: {nombre}")
    print(classification_report(y_test, y_pred, target_names=le.classes_))
```

Reporte de clasificación para cada modelo:

```
=====
Modelo: Regresión Logistica
      precision    recall  f1-score   support
      bad       0.73     0.75     0.74      593
      good      0.75     0.73     0.74      607

      accuracy                           0.74      1200
      macro avg       0.74     0.74     0.74      1200
weighted avg       0.74     0.74     0.74      1200
```

```
=====
Modelo: Random Forest
      precision    recall  f1-score   support
      bad       0.85     0.84     0.85      593
      good      0.84     0.86     0.85      607

      accuracy                           0.85      1200
      macro avg       0.85     0.85     0.85      1200
weighted avg       0.85     0.85     0.85      1200
```

Modelo: Árbol de Decisión

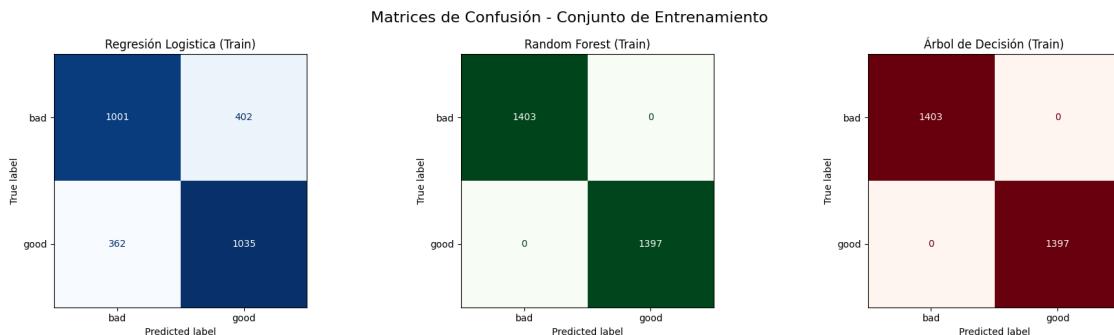
	precision	recall	f1-score	support
bad	0.78	0.79	0.79	593
good	0.79	0.79	0.79	607
accuracy			0.79	1200
macro avg	0.79	0.79	0.79	1200
weighted avg	0.79	0.79	0.79	1200

[20]: #Matrices de Confusión para conjunto de entrenamiento

```
fig, axes = plt.subplots(1, 3, figsize=(18, 5))
etiquetas = le.classes_ # Ya solo serán ['bad', 'good']

for i, (nombre, _) in enumerate(clasificadores):
    ConfusionMatrixDisplay(
        confusion_matrix=matrices_confusion_train2[nombre],
        display_labels=etiquetas
    ).plot(cmap=["Blues", "Greens", "Reds"][i], ax=axes[i], colorbar=False)
    axes[i].set_title(f"{nombre} (Train)")

fig.suptitle("Matrices de Confusión - Conjunto de Entrenamiento", fontsize=16)
plt.tight_layout()
plt.show()
```



[21]: #Matrices de Confusión para conjunto de prueba

```
fig, axes = plt.subplots(1, 3, figsize=(18, 5))
etiquetas = le.classes_

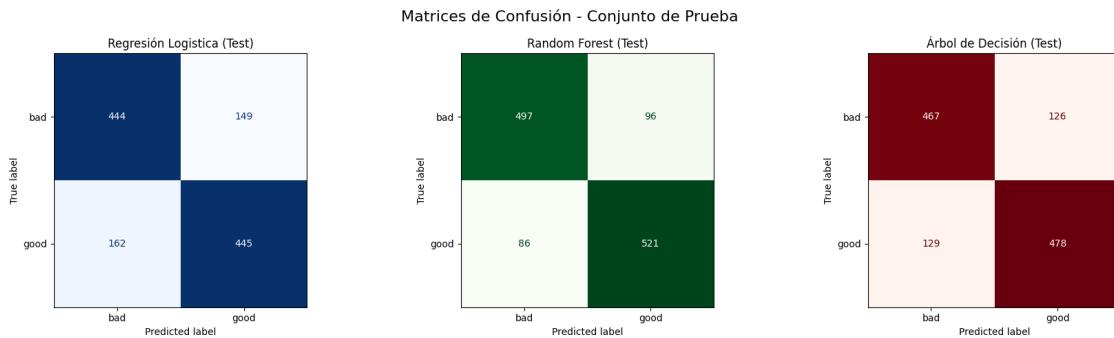
for i, (nombre, _) in enumerate(clasificadores):
    ConfusionMatrixDisplay(
        confusion_matrix=matrices_confusion_test2[nombre],
        display_labels=etiquetas
    ).plot(cmap=["Blues", "Greens", "Reds"][i], ax=axes[i], colorbar=False)
```

```

        axes[i].set_title(f"{{nombre}} (Test)")

fig.suptitle("Matrices de Confusión - Conjunto de Prueba", fontsize=16)
plt.tight_layout()
plt.show()

```



[22]: #Curvas Rog

```

y_test_bin = label_binarize(y_test, classes=[0, 1]).ravel() # ravel() para que sea vector plano
etiquetas = le.classes_

# Crear figura
fig, axes = plt.subplots(1, 3, figsize=(18, 5))

# Tabla para resumen AUC
auc_resumen = []

for i, (nombre, modelo) in enumerate(clasificadores):
    # Obtener probabilidades de clase positiva
    y_score = modelo.predict_proba(X_test)[:, 1]

    # Calcular curva ROC
    fpr, tpr, _ = roc_curve(y_test_bin, y_score)
    roc_auc = auc(fpr, tpr)

    # Graficar
    axes[i].plot(fpr, tpr, lw=2, label=f'AUC = {roc_auc:.2f}', color='darkorange')
    axes[i].plot([0, 1], [0, 1], 'k--', lw=1)
    axes[i].set_xlim([0.0, 1.0])
    axes[i].set_ylim([0.0, 1.05])
    axes[i].set_xlabel('False Positive Rate')
    axes[i].set_ylabel('True Positive Rate')

```

```

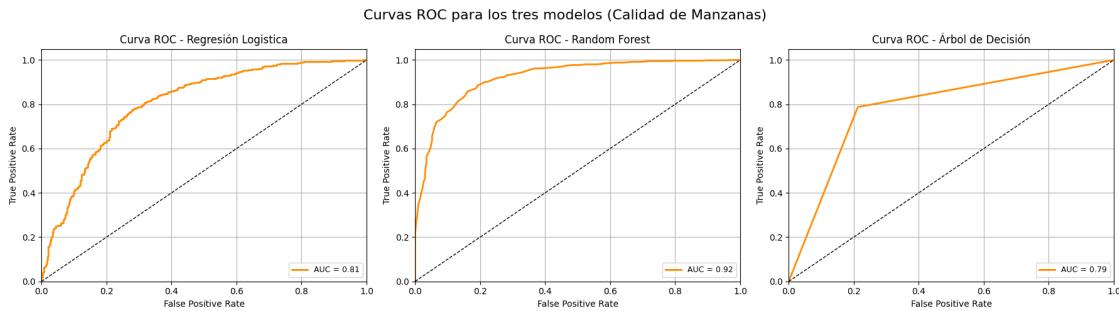
        axes[i].set_title(f'Curva ROC - {nombre}')
        axes[i].legend(loc="lower right", fontsize=9)
        axes[i].grid(True)

    # Guardar AUC para la tabla
    auc_resumen.append({'Modelo': nombre, 'AUC': roc_auc})

# Título general
fig.suptitle("Curvas ROC para los tres modelos (Calidad de Manzanas)", fontweight='bold', fontsize=16)
plt.tight_layout()
plt.show()

# Tabla resumen AUC
df_auc = pd.DataFrame(auc_resumen).sort_values(by='AUC', ascending=False)
display(df_auc)

```



	Modelo	AUC
1	Random Forest	0.921509
0	Regresión Logistica	0.806143
2	Árbol de Decisión	0.787500

```

[23]: # Unir las métricas con el AUC
df_resumen_problema2 = pd.merge(df_resultados2, df_auc, on='Modelo')

# Agregar número de problema
df_resumen_problema2.insert(0, 'Problema', 2)

# Reordenar columnas
columnas_ordenadas = [
    'Problema', 'Modelo', 'Accuracy Test', 'Precision', 'Recall',
    'F1 Score', 'AUC Promedio (macro)'
]
# Señalar el mejor modelo (según Accuracy Test)

```

```

mejor_modelo = df_resumen_problema2.sort_values(by='Accuracy Test',  

    ↪ascending=False).iloc[0]['Modelo']  

df_resumen_problema2['Mejor Modelo'] = df_resumen_problema2['Modelo'].  

    ↪apply(lambda x: '' if x == mejor_modelo else '')  
  

# Mostrar  

import pandas as pd  

import numpy as np  

import IPython.display as dsp  

dsp.display(df_resumen_problema2.round(3))

```

	Problema	Modelo	Accuracy Train	Accuracy Test	Precision \
0	2	Random Forest	1.000	0.848	0.848
1	2	Árbol de Decisión	1.000	0.788	0.788
2	2	Regresión Logistica	0.727	0.741	0.741
		Recall F1 Score AUC Mejor Modelo			
0	0.848	0.848	0.922		
1	0.788	0.788	0.788		
2	0.741	0.741	0.806		

## 0.6 PROBLEMA N.3 (APRENDIZAJE AUTOMATICO)

Predicción de la jugosidad de una manzana a partir de sus características

Dataset:<https://www.kaggle.com/datasets/nelgiriyewithana/apple-quality>

```

[24]: # --- Separar el DataFrame en X y Y ---  

X3 = df_apple_limpio.drop(columns=['Juiciness']) # Quitamos la columna objetivo  

y3 = df_apple_limpio['Juiciness'] # Variable objetivo continua  
  

# --- Codificar variables categóricas (como 'Color') ---  

X3 = pd.get_dummies(X3, drop_first=True)  
  

# --- Verificación ---  

print("Columnas de X codificado:", X3.columns.tolist())
print("Dimensiones de X:", X3.shape)
print("Dimensiones de y (objetivo):", y3.shape)
print("Primeros 5 valores de y:", y3.head())  
  

# --- Dividir datos en entrenamiento y prueba ---  

from sklearn.model_selection import train_test_split  

from sklearn.preprocessing import StandardScaler  
  

X3_train, X3_test, y3_train, y3_test = train_test_split(X3, y3, test_size=0.3,  

    ↪random_state=42)  
  

# --- Escalado ---

```

```

scaler = StandardScaler()
X3_train = scaler.fit_transform(X3_train)
X3_test = scaler.transform(X3_test)

# --- Verificación de dimensiones ---
print("Dimensiones de X_train:", X3_train.shape)
print("Dimensiones de X_test:", X3_test.shape)
print("Dimensiones de y_train:", y3_train.shape)
print("Dimensiones de y_test:", y3_test.shape)

```

Columnas de X codificado: ['A\_id', 'Size', 'Weight', 'Sweetness', 'Crunchiness', 'Ripeness', 'Acidity\_-0.001593958', 'Acidity\_-0.003109107', 'Acidity\_-0.008136378', 'Acidity\_-0.009153027', 'Acidity\_-0.011438035', 'Acidity\_-0.011582814', 'Acidity\_-0.012061768', 'Acidity\_-0.012433307', 'Acidity\_-0.012611428', 'Acidity\_-0.014252196', 'Acidity\_-0.014548296', 'Acidity\_-0.01630256', 'Acidity\_-0.017094245', 'Acidity\_-0.021751811', 'Acidity\_-0.021881716', 'Acidity\_-0.022774534', 'Acidity\_-0.024607366', 'Acidity\_-0.024782906', 'Acidity\_-0.025322858', 'Acidity\_-0.026114955', 'Acidity\_-0.026177532', 'Acidity\_-0.0287965', 'Acidity\_-0.029111848', 'Acidity\_-0.030533085', 'Acidity\_-0.030536884', 'Acidity\_-0.031126053', 'Acidity\_-0.032305611', 'Acidity\_-0.033737529', 'Acidity\_-0.035106956', 'Acidity\_-0.035775461', 'Acidity\_-0.037423169', 'Acidity\_-0.037817127', 'Acidity\_-0.03893581', 'Acidity\_-0.040585042', 'Acidity\_-0.041491395', 'Acidity\_-0.04287989', 'Acidity\_-0.043227512', 'Acidity\_-0.043436179', 'Acidity\_-0.045183862', 'Acidity\_-0.045203447', 'Acidity\_-0.045751867', 'Acidity\_-0.046495034', 'Acidity\_-0.049403327', 'Acidity\_-0.049725888', 'Acidity\_-0.050037559', 'Acidity\_-0.052342248', 'Acidity\_-0.052965085', 'Acidity\_-0.055333999', 'Acidity\_-0.058448189', 'Acidity\_-0.058599695', 'Acidity\_-0.059952688', 'Acidity\_-0.060036533', 'Acidity\_-0.060371554', 'Acidity\_-0.062892903', 'Acidity\_-0.064020014', 'Acidity\_-0.064257729', 'Acidity\_-0.064418364', 'Acidity\_-0.064779143', 'Acidity\_-0.067216749', 'Acidity\_-0.067312574', 'Acidity\_-0.06847672', 'Acidity\_-0.068995237', 'Acidity\_-0.069598119', 'Acidity\_-0.069879417', 'Acidity\_-0.07028261', 'Acidity\_-0.071538203', 'Acidity\_-0.072155984', 'Acidity\_-0.079761693', 'Acidity\_-0.083171176', 'Acidity\_-0.083337968', 'Acidity\_-0.08337454', 'Acidity\_-0.086582903', 'Acidity\_-0.087134055', 'Acidity\_-0.088663441', 'Acidity\_-0.08899782', 'Acidity\_-0.089084964', 'Acidity\_-0.089930972', 'Acidity\_-0.090021116', 'Acidity\_-0.092992357', 'Acidity\_-0.093251563', 'Acidity\_-0.095012373', 'Acidity\_-0.100716598', 'Acidity\_-0.101481348', 'Acidity\_-0.101619167', 'Acidity\_-0.101724645', 'Acidity\_-0.103006945', 'Acidity\_-0.104389292', 'Acidity\_-0.105291052', 'Acidity\_-0.105424932', 'Acidity\_-0.112472887', 'Acidity\_-0.113157751', 'Acidity\_-0.114319001', 'Acidity\_-0.114346995', 'Acidity\_-0.116073579', 'Acidity\_-0.116938612', 'Acidity\_-0.117891307', 'Acidity\_-0.12163975', 'Acidity\_-0.121784757', 'Acidity\_-0.122705371', 'Acidity\_-0.123379089', 'Acidity\_-0.125013797', 'Acidity\_-0.127366597', 'Acidity\_-0.127804206', 'Acidity\_-0.129357025', 'Acidity\_-0.129697828', 'Acidity\_-0.131763548', 'Acidity\_-0.13201002', 'Acidity\_-0.132407603', 'Acidity\_-0.135212578', 'Acidity\_-0.138584021'],

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'Acidity_7.404736238', 'Quality_good']
Dimensiones de X: (4000, 4006)
Dimensiones de y (objetivo): (4000,)
Primeros 5 valores de y: 0      1.844900
1    0.853286
2    2.838636
3    3.637970
4    3.030874
Name: Juiciness, dtype: float64
Dimensiones de X_train: (2800, 4006)
Dimensiones de X_test: (1200, 4006)
Dimensiones de y_train: (2800,)
Dimensiones de y_test: (1200,)

[25]: from sklearn.metrics import mean_absolute_error, mean_squared_error, r2_score
import numpy as np

resultados3 = []

print("Iniciando entrenamiento de modelos")

for nombre, modelo in modelos_regresion:
    print(f"\nEntrenando {nombre}...")

    modelo.fit(X3_train, y3_train)

    # Predicciones
    y3_train_pred = modelo.predict(X3_train)
    y3_test_pred = modelo.predict(X3_test)

    # Métricas
    r2_train = r2_score(y3_train, y3_train_pred)
    r2_test = r2_score(y3_test, y3_test_pred)

    # Guardar resultados
    resultados3.append({
        'Modelo': nombre,
        'R2 Train': r2_train,
        'R2 Test': r2_test,
    })

    print(f" {nombre} completado. R2 Test: {r2_test:.4f}")

df_resultados3 = pd.DataFrame(resultados3).sort_values(by='R2 Test', ↴
ascending=False)

```

Iniciando entrenamiento de modelos

```

Entrenando Regresión Lineal...
Regresión Lineal completado. R2 Test: 0.0028

Entrenando Árbol de Decisión...
Árbol de Decisión completado. R2 Test: 0.0278

Entrenando Random Forest...
Random Forest completado. R2 Test: 0.4210

```

[26]: df\_resultados3

	Modelo	R2 Train	R2 Test
2	Random Forest	0.920601	0.420977
1	Árbol de Decisión	1.000000	0.027840
0	Regresión Lineal	1.000000	0.002801

## 0.7 TABLA RESUMEN DE LOS 3 PROBLEMAS DE APRENDIZAJE SUPERVISADO

```

[27]: # Etiquetas para cada problema
df_resultados['Problema'] = "Problema 1"
df_resultados['Tema'] = "Clasificación del tratamiento médico"
df_resultados['Métrica'] = "Accuracy"

df_resultados2['Problema'] = "Problema 2"
df_resultados2['Tema'] = "Clasificación de calidad de manzanas"
df_resultados2['Métrica'] = "Accuracy"

df_resultados3['Problema'] = "Problema 3"
df_resultados3['Tema'] = "Predicción de jugosidad de la manzana"
df_resultados3['Métrica'] = "R2"

# Reorganizar columnas según tipo
df_clasif1 = df_resultados[['Problema', 'Tema', 'Modelo', 'Métrica', 'Accuracy',
                             'Train', 'Accuracy Test']].copy()
df_clasif2 = df_resultados2[['Problema', 'Tema', 'Modelo', 'Métrica', 'Accuracy',
                             'Train', 'Accuracy Test']].copy()
df_reg = df_resultados3[['Problema', 'Tema', 'Modelo', 'Métrica', 'R2 Train',
                           'R2 Test']].copy()

# Uniformar nombres de columnas
df_clasif1.rename(columns={'Accuracy Train': 'Train', 'Accuracy Test': 'Test'},
                  inplace=True)
df_clasif2.rename(columns={'Accuracy Train': 'Train', 'Accuracy Test': 'Test'},
                  inplace=True)
df_reg.rename(columns={'R2 Train': 'Train', 'R2 Test': 'Test'}, inplace=True)

```

```

# Unir todos los resultados
df_comparativo = pd.concat([df_clasif1, df_clasif2, df_reg], ignore_index=True)

# Marcar el mejor modelo (según mayor valor de Test)
df_comparativo['Mejor Modelo'] = ''
for problema in df_comparativo['Problema'].unique():
    idx_max = df_comparativo[df_comparativo['Problema'] == problema]['Test'].idxmax()
    df_comparativo.loc[idx_max, 'Mejor Modelo'] = ''

# Mostrar
import IPython.display as dsp
dsp.display(df_comparativo.round(3).sort_values(by=['Problema', 'Test'], ascending=[True, False]))

```

	Problema	Tema	Modelo \
0	Problema 1	Clasificación del tratamiento médico	Random Forest
1	Problema 1	Clasificación del tratamiento médico	Árbol de Decisión
2	Problema 1	Clasificación del tratamiento médico	Regresión Logistica
3	Problema 2	Clasificación de calidad de manzanas	Random Forest
4	Problema 2	Clasificación de calidad de manzanas	Árbol de Decisión
5	Problema 2	Clasificación de calidad de manzanas	Regresión Logistica
6	Problema 3	Predicción de jugosidad de la manzana	Random Forest
7	Problema 3	Predicción de jugosidad de la manzana	Árbol de Decisión
8	Problema 3	Predicción de jugosidad de la manzana	Regresión Lineal

	Métrica	Train	Test	Mejor Modelo
0	Accuracy	1.000	0.966	
1	Accuracy	1.000	0.932	
2	Accuracy	0.917	0.898	
3	Accuracy	1.000	0.848	
4	Accuracy	1.000	0.788	
5	Accuracy	0.727	0.741	
6	R <sup>2</sup>	0.921	0.421	
7	R <sup>2</sup>	1.000	0.028	
8	R <sup>2</sup>	1.000	0.003	

## 0.8 CONCLUSIÓN DE LA PARTE 1

En esta sección se abordaron tres problemas distintos de aprendizaje supervisado, empleando modelos de clasificación y regresión para evaluar su rendimiento en tareas específicas. A continuación, se destacan los principales hallazgos:

Problema 1 – Clasificación del tratamiento médico (multiclas): El modelo con mejor desempeño fue Random Forest, alcanzando un Accuracy Test de 0.966, superando tanto a los árboles de decisión como a la regresión logística. Este resultado refleja su capacidad para manejar relaciones no lineales y múltiples clases de forma eficiente.

Problema 2 – Clasificación de calidad de manzanas (binaria): Nuevamente, Random Forest obtuvo

el mejor resultado (Accuracy Test de 0.848), confirmando su robustez ante variables categóricas y numéricas en contextos de clasificación binaria. Aunque la regresión logística mostró un rendimiento aceptable, no fue competitiva frente a los modelos de árbol.

Problema 3 – Predicción de jugosidad de la manzana (regresión): En este escenario de regresión, Random Forest Regressor también demostró ser el modelo más eficaz, alcanzando un R<sup>2</sup> Test de 0.421, lo que indica que fue capaz de capturar mejor la variabilidad de la variable objetivo. Los modelos de regresión lineal y árbol de decisión tuvieron un ajuste pobre sobre los datos.

A través del análisis de métricas como Accuracy y R<sup>2</sup>, se evidenció que Random Forest fue el modelo más consistente y efectivo en todos los problemas planteados. Su versatilidad, capacidad de generalización y manejo de datos mixtos lo convierten en una excelente elección para tareas de clasificación y regresión dentro del aprendizaje supervisado.

#

## PARTE N.2 APRENDIZAJE NO SUPERVISADO

### 0.9 LIBRERIAS UTILIZADAS

```
[28]: #librerias a Utilizar
import scipy.stats
import seaborn as sns
from sklearn.decomposition import PCA
from scipy.cluster.hierarchy import dendrogram, linkage
from sklearn.metrics import silhouette_score, silhouette_samples
from sklearn.cluster import AgglomerativeClustering
from sklearn.cluster import KMeans
from yellowbrick.cluster import KElbowVisualizer
import matplotlib.cm as cm
import numpy as np
```

```
[29]: def graficaSilueta(X: np.array, cluster_labels, n_clusters):
    # Calcular coeficiente de silueta
    silhouette_avg = silhouette_score(X, cluster_labels)
    silhouette_vals = silhouette_samples(X, cluster_labels)
    print(f"Coeficiente de Silueta Promedio: {silhouette_avg:.3f}")

    # Subplots
    fig, (ax1, ax2) = plt.subplots(1, 2, figsize=(18, 7))
    ax1.set_xlim([-1, 1])

    # Gráfica de silueta
    y_lower = 10
    for i in range(n_clusters):
        cluster_silhouette_vals = silhouette_vals[cluster_labels == i]
        cluster_silhouette_vals.sort()
        y_upper = y_lower + len(cluster_silhouette_vals)
```

```

        ax1.fill_betweenx(np.arange(y_lower, y_upper), 0, y_upper + 10, cluster_silhouette_vals, alpha=0.7)
        ax1.text(-0.05, (y_lower + y_upper) / 2, str(i))
        y_lower = y_upper + 10

    ax1.axvline(x=silhouette_avg, color="red", linestyle="--", label="Silhouette Score")
    ax1.set_xlabel("Coeficiente de Silueta")
    ax1.set_ylabel("Muestras")
    ax1.set_title("Gráfico de Silueta")
    ax1.legend()

# Gráfico 2D de los clusters formados
colors = cm.nipy_spectral(cluster_labels.astype(float) / n_clusters)
ax2.scatter(X[:, 0], X[:, 1], marker=".", s=60, lw=0, alpha=0.7, c=colors, edgecolor="k")
ax2.set_title("Clusters visualizados en 2D")
ax2.set_xlabel("Componente 1")
ax2.set_ylabel("Componente 2")

plt.show()
return silhouette_avg

```

## 0.10 PROBLEMA N.1 (APRENDIZAJE NO SUPERVISADO)

Agrupar conjunto de datos en base a las características de los pacientes de los datos de Apendicitis pediátrica.

[30]: *# Cargar y preparar datos limpios del dataset de Apendicitis Pediátrica*

```

df_limpio = df_limpio.copy()      # Usamos el dataset ya limpio
df_limpio.dropna(inplace=True)    # Por si queda algún nulo
df_limpio.head(2)                # Verificamos las primeras filas

```

[30]:

	Age	BMI	Sex	Height	Weight	Length_of_Stay	Management	\
0	12.68	16.9	female	148.0	37.0	3.0	conservative	
1	14.10	31.9	male	147.0	69.5	2.0	conservative	

	Severity	Diagnosis_Presumptive	Diagnosis	...	RDW	\
0	uncomplicated	appendicitis	appendicitis	...	12.2	
1	uncomplicated	appendicitis	no appendicitis	...	12.7	

	Thrombocyte_Count	CRP	Dysuria	Stool	Peritonitis	Psoas_Sign	US_Performed	\
0	254.0	0.0	no	normal	no	yes	yes	
1	151.0	3.0	yes	normal	no	yes	yes	

US_Number	Free_Fluids
-----------	-------------

```
0      882.0          no
1      883.0          no
```

[2 rows x 34 columns]

```
[31]: # --- Convertir columnas categóricas a numéricas ---
df_encoded = df_limpio.copy()
le = LabelEncoder()

for column in df_encoded.columns:
    if df_encoded[column].dtype == 'object':
        df_encoded[column] = le.fit_transform(df_encoded[column])

# --- Aplicar PCA para reducción de dimensiones ---
random_state = 2018
pca = PCA(n_components=0.99, random_state=random_state) # Mantener 99% de lavarianza
X_pca = pca.fit_transform(df_encoded)

# Convertir a DataFrame para visualización/futuro uso
X_pca = pd.DataFrame(data=X_pca, index=df_encoded.index)

# Verificar resultado
X_pca.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 589 entries, 0 to 781
Data columns (total 3 columns):
 #   Column  Non-Null Count  Dtype  
---  --   -----  --   -- 
 0   0       589 non-null   float64
 1   1       589 non-null   float64
 2   2       589 non-null   float64
dtypes: float64(3)
memory usage: 18.4 KB
```

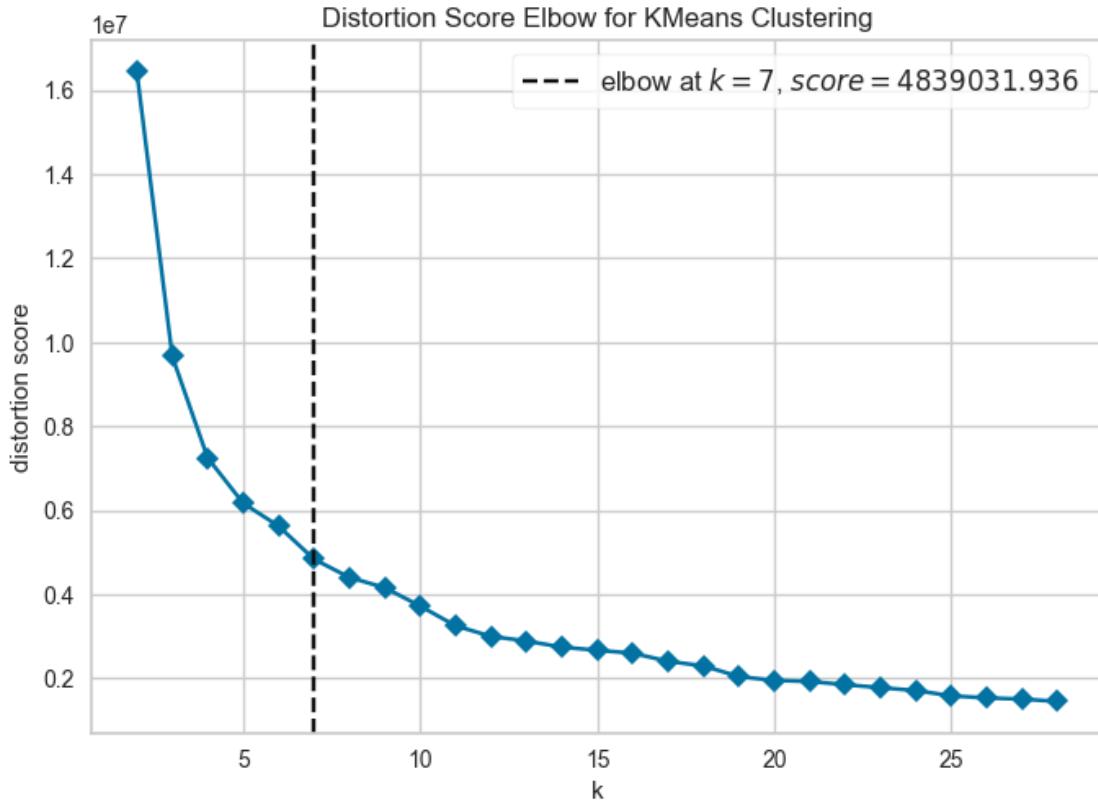
Metodo Aplicado: K-Means

```
[32]: # Modelo base
model = KMeans(random_state=20)

# Visualizador del método del codo
visualizer = KElbowVisualizer(model, k=(2, 29), timings=False)

# Usar X_pca como entrada (correcto en tu flujo)
visualizer.fit(X_pca)
visualizer.show()
```

```
# Obtener K óptimo
k_optimo = visualizer.elbow_value_
print(f"Número óptimo de clusters según el método del codo: {k_optimo}")
```



Número óptimo de clusters según el método del codo: 7

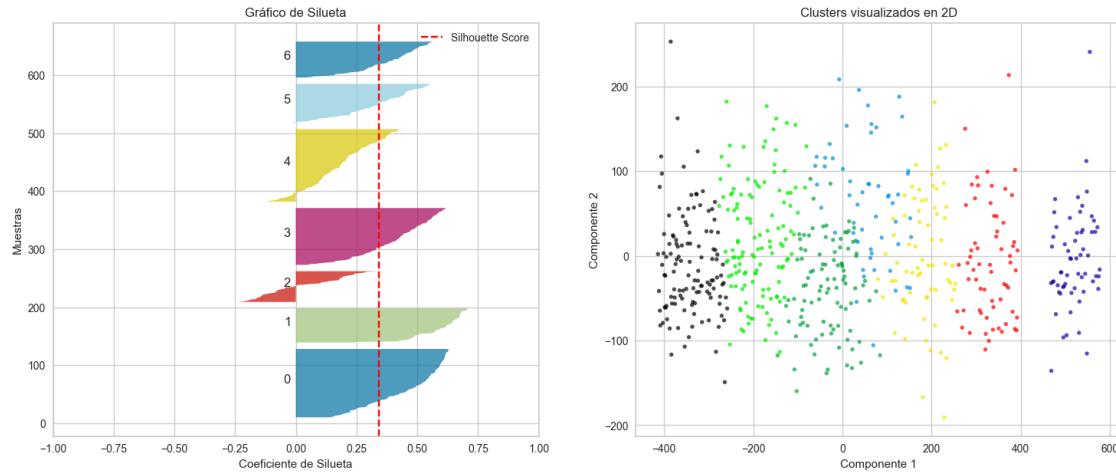
```
[33]: # Creación del modelo de K-Means Clustering
nombre2 = "K-Means Clustering"

kmeans = KMeans(n_clusters=k_optimo, random_state=35)
y_km = kmeans.fit_predict(X_pca)

# Guardar resultados en DataFrame
resultadokm = pd.DataFrame(X_pca)
resultadokm['cluster'] = y_km

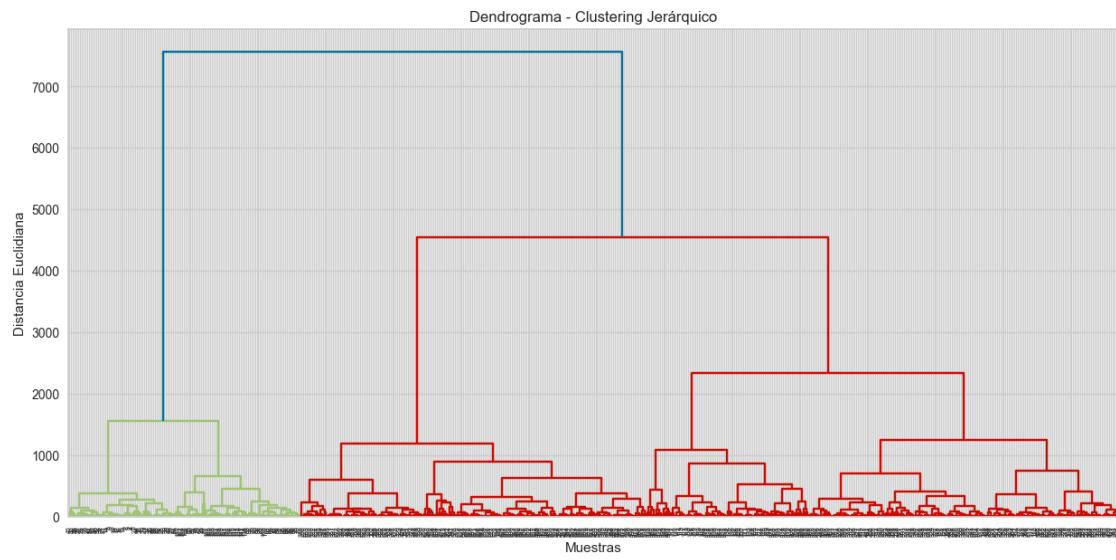
# Diccionario para almacenar el resultado del coeficiente de silueta
resultado_n = []
resultado_n[nombre2] = graficaSilueta(X_pca.values, y_km, kmeans.n_clusters)
```

Coeficiente de Silueta Promedio: 0.342



### Metodo Aplicado - Clustering jerárquico aglomerativo

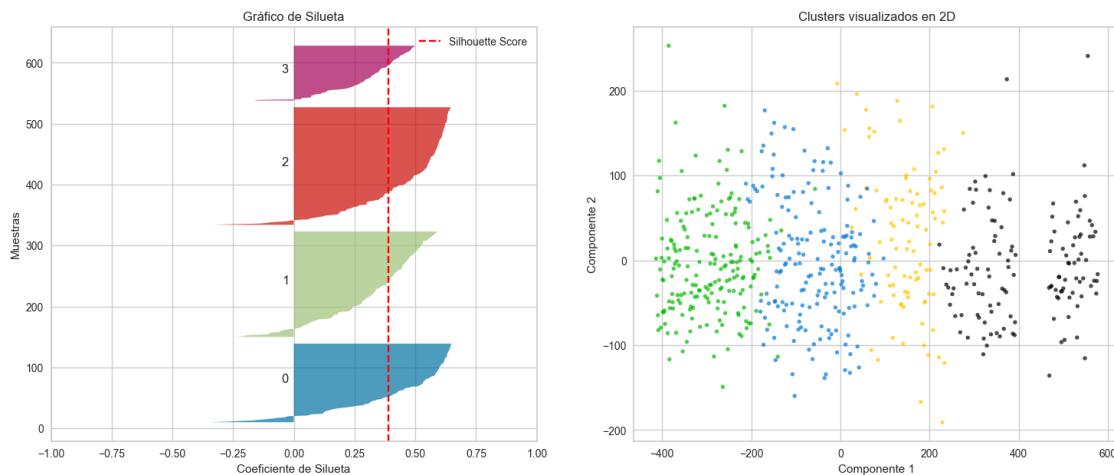
```
[34]: # Crear dendrograma para estimar el número de clusters
linked = linkage(X_pca, method='ward')
plt.figure(figsize=(15, 7))
dendrogram(linked, orientation='top')
plt.title("Dendrograma - Clustering Jerárquico")
plt.xlabel("Muestras")
plt.ylabel("Distancia Euclíadiana")
plt.show()
```



```
[35]: # Crear modelo y evaluar con gráfica de silueta
nombre3 = "Agglomerative Clustering"
cluster = AgglomerativeClustering(n_clusters=4, metric='euclidean', linkage='ward')
cluster_labels = cluster.fit_predict(X_pca)

# Guardar en el diccionario de resultados
resultado_n[nombre3] = graficaSilueta(X_pca.values, cluster_labels, cluster.n_clusters)
```

Coeficiente de Silueta Promedio: 0.390



```
[36]: # Crear DataFrame con los resultados del Problema 1
tabla_resultado_1 = pd.DataFrame(
    list(resultado_n.items()),
    columns=["Modelo/Algoritmo", "Coeficiente Silueta"]
)

# Agregar columna de identificación del problema
tabla_resultado_1["Problema"] = "Problema 1"

# Reordenar columnas
tabla_resultado_1 = tabla_resultado_1[["Problema", "Modelo/Algoritmo", "Coeficiente Silueta"]]

# Mostrar tabla
tabla_resultado_1
```

	Problema	Modelo/Algoritmo	Coeficiente Silueta
0	Problema 1	K-Means Clustering	0.342127
1	Problema 1	Agglomerative Clustering	0.390028

## 0.11 PROBLEMA N.2 (APRENDIZAJE NO SUPERVISADO)

Agrupar conjunto de datos en base a las características de la manzana.

```
[37]: # Cargar y preparar datos limpios del dataset de Características de la Manzana
df_apple = df_apple_limpio.copy()          # Usamos el dataset limpio
df_apple.dropna(inplace=True)               # Eliminamos posibles valores nulos
df_apple.head(2)                           # Mostramos las primeras filas
```

```
[37]:   A_id      Size    Weight  Sweetness  Crunchiness  Juiciness  Ripeness \
0    0.0 -3.970049 -2.512336     5.346330     -1.012009    1.844900    0.32984
1    1.0 -1.195217 -2.839257     3.664059      1.588232    0.853286    0.86753

          Acidity  Quality
0   -0.491590483    good
1   -0.722809367    good
```

```
[38]: # --- Convertir columnas categóricas a numéricas ---
df_encoded_apple = df_apple.copy()
le = LabelEncoder()

for column in df_encoded_apple.columns:
    if df_encoded_apple[column].dtype == 'object':
        df_encoded_apple[column] = le.fit_transform(df_encoded_apple[column])

# --- Aplicar PCA para reducción de dimensiones ---
random_state = 2018
pca = PCA(n_components=0.99, random_state=random_state)  # Mantener 99% de la varianza
X_pca_apple = pca.fit_transform(df_encoded_apple)

# Convertir a DataFrame para visualización/futuro uso
X_pca_apple = pd.DataFrame(data=X_pca_apple, index=df_encoded_apple.index)

# Verificar resultado
X_pca_apple.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 4000 entries, 0 to 3999
Data columns (total 2 columns):
 #   Column  Non-Null Count  Dtype  
---  --   ----   -----  -----
 0   0       4000 non-null   float64
 1   1       4000 non-null   float64
dtypes: float64(2)
memory usage: 93.8 KB
```

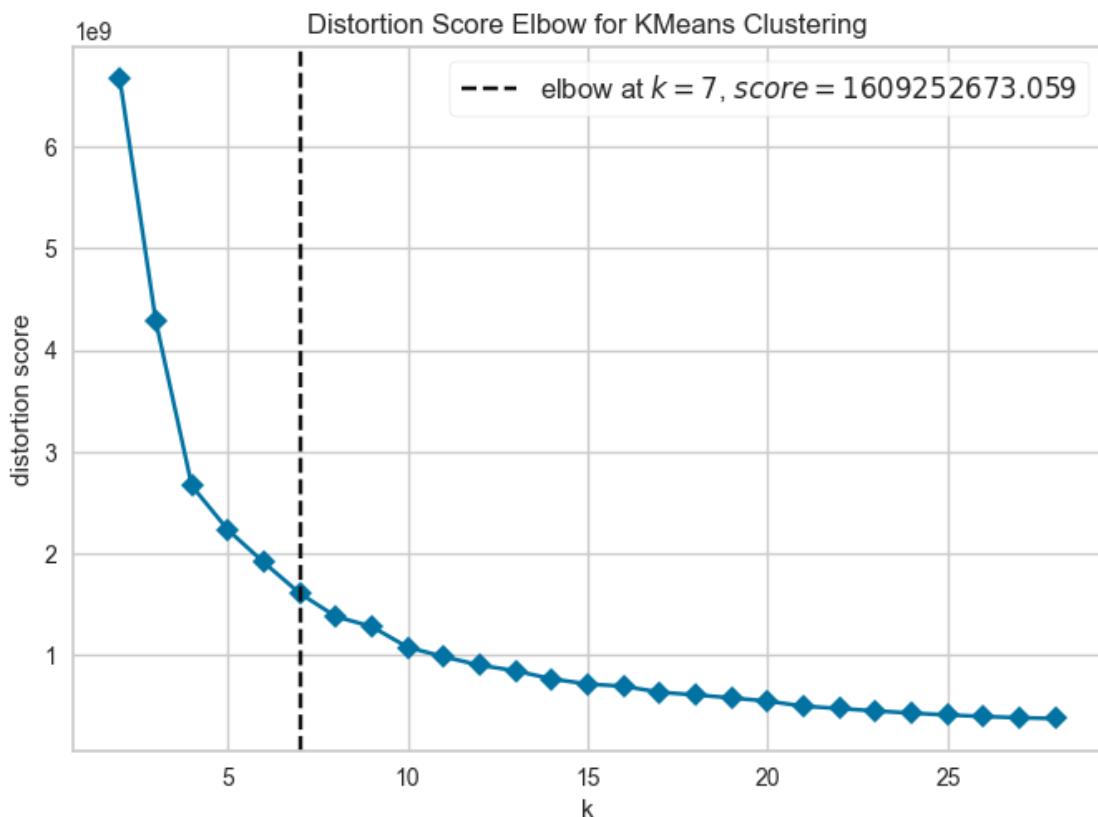
Metodo Aplicado - K-Means

```
[39]: # Modelo base
model_apple = KMeans(random_state=20)

# Visualizador del método del codo
visualizer_apple = KElbowVisualizer(model_apple, k=(2, 29), timings=False)

# Usar X_pca_apple como entrada
visualizer_apple.fit(X_pca_apple)
visualizer_apple.show()

# Obtener k óptimo
k_optimo_apple = visualizer_apple.elbow_value_
print(f"Número óptimo de clusters según el método del codo (manzanas): {k_optimo_apple}")
```



Número óptimo de clusters según el método del codo (manzanas): 7

```
[40]: # Creación del modelo de K-Means Clustering para manzanas
nombre_apple_kmeans = "K-Means Clustering"
kmeans_apple = KMeans(n_clusters=k_optimo_apple, random_state=35)
y_km_apple = kmeans_apple.fit_predict(X_pca_apple)
```

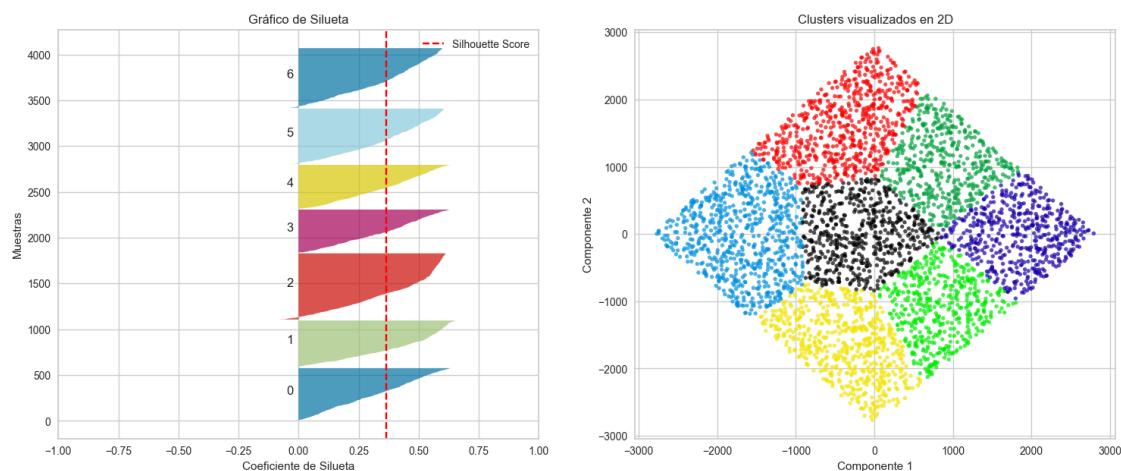
```

# Guardar resultados en DataFrame
resultado_km_apple = pd.DataFrame(X_pca_apple)
resultado_km_apple['cluster'] = y_km_apple

# Diccionario para almacenar el coeficiente de silueta
resultado_apple = {}
resultado_apple[nombre_apple_kmeans] = graficaSilueta(
    X_pca_apple.values, y_km_apple, kmeans_apple.n_clusters
)

```

Coeficiente de Silueta Promedio: 0.366

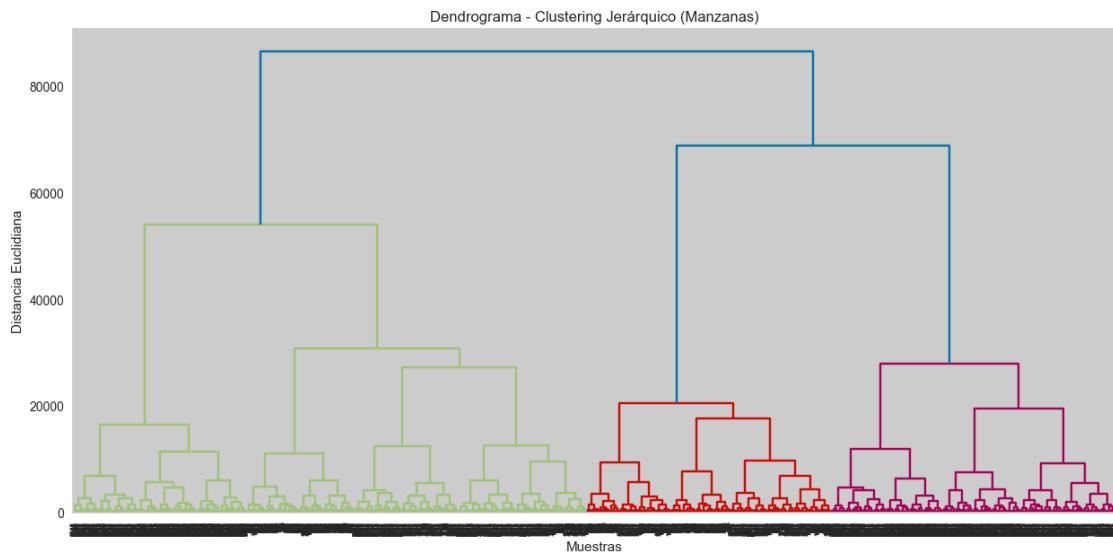


Metodo Aplicado - Clustering jerárquico aglomerativo

```

[41]: # Crear dendrograma para estimar el número de clusters
linked_apple = linkage(X_pca_apple, method='ward')
plt.figure(figsize=(15, 7))
dendrogram(linked_apple, orientation='top')
plt.title("Dendrograma - Clustering Jerárquico (Manzanas)")
plt.xlabel("Muestras")
plt.ylabel("Distancia Euclíadiana")
plt.show()

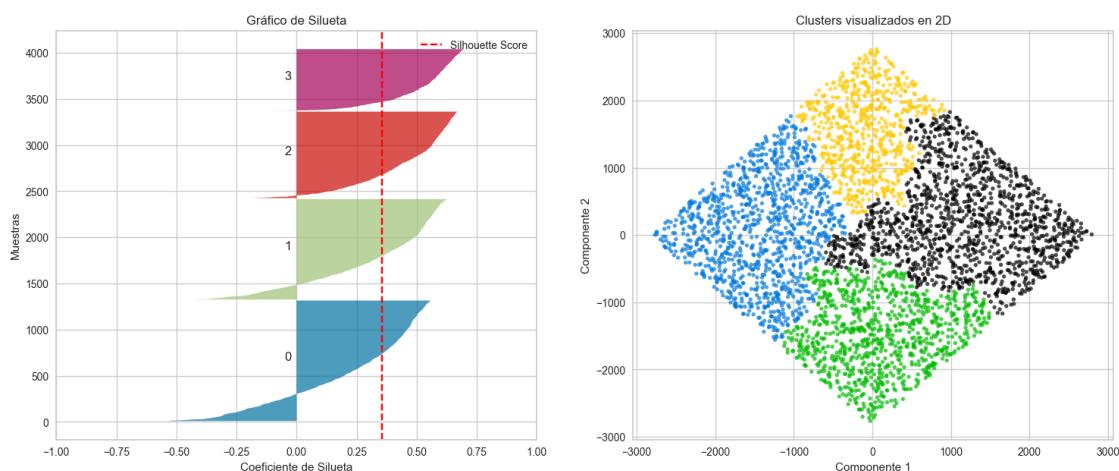
```



```
[42]: # Crear modelo y evaluar con gráfica de silueta
nombre_apple_agglom = "Agglomerative Clustering"
cluster_apple = AgglomerativeClustering(n_clusters=4, metric='euclidean', linkage='ward')
cluster_labels_apple = cluster_apple.fit_predict(X_pca_apple)

# Guardar en el diccionario de resultados
resultado_apple[nombre_apple_agglom] = graficaSilueta(
    X_pca_apple.values, cluster_labels_apple, cluster_apple.n_clusters
)
```

Coeficiente de Silueta Promedio: 0.356



```
[43]: # Crear DataFrame con los resultados del Problema 2
tabla_resultado_2 = pd.DataFrame(
    list(resultado_apple.items()),
    columns=["Modelo/Algoritmo", "Coeficiente Silueta"]
)

# Agregar columna de identificación del problema
tabla_resultado_2["Problema"] = "Problema 2"

# Reordenar columnas
tabla_resultado_2 = tabla_resultado_2[["Problema", "Modelo/Algoritmo", "Coeficiente Silueta"]]

# Mostrar tabla
tabla_resultado_2
```

```
[43]:      Problema      Modelo/Algoritmo  Coeficiente Silueta
0  Problema 2          K-Means Clustering       0.366423
1  Problema 2  Agglomerative Clustering       0.355615
```

## 0.12 TABLA RESUMEN DE LOS 2 PROBLEMAS DE APRENDIZAJE NO SUPERVISADO

```
[44]: tabla_final = pd.concat([tabla_resultado_1, tabla_resultado_2], ignore_index=True)
tabla_final
```

```
[44]:      Problema      Modelo/Algoritmo  Coeficiente Silueta
0  Problema 1          K-Means Clustering       0.342127
1  Problema 1  Agglomerative Clustering       0.390028
2  Problema 2          K-Means Clustering       0.366423
3  Problema 2  Agglomerative Clustering       0.355615
```

```
[45]: from matplotlib.colors import to_hex

# Apendicitis (Agglomerative Clustering)
n_clusters_ap = cluster.n_clusters
colors_ap = [to_hex(cm.nipy_spectral(i / n_clusters_ap)) for i in range(n_clusters_ap)]

# Manzanas (K-Means Clustering)
n_clusters_apple = kmeans_apple.n_clusters
colors_apple = [to_hex(cm.nipy_spectral(i / n_clusters_apple)) for i in range(n_clusters_apple)]

graficar_apendicitis = X_pca.copy()
```

```

graficar_apendicitis['cluster'] = cluster_labels # Etiquetas del modelo
    ↪Agglomerativo
graficar_apple = X_pca_apple.copy()
graficar_apple['cluster'] = y_km_apple # Etiquetas del modelo K-Means

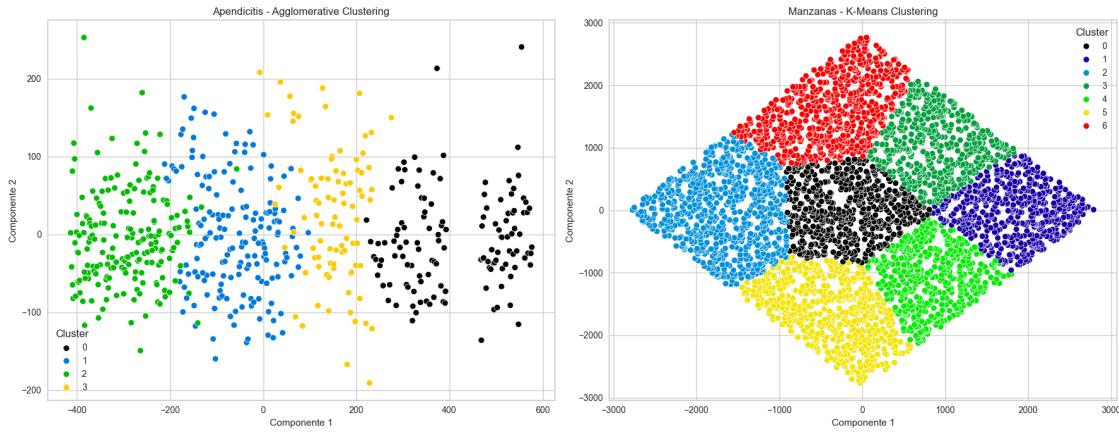
fig, axes = plt.subplots(1, 2, figsize=(18, 7))

# --- Subplot 1: Apendicitis ---
sns.scatterplot(
    data=graficar_apendicitis,
    x=0, y=1,
    hue='cluster',
    palette=colors_ap,
    legend='full',
    ax=axes[0]
)
axes[0].set_title("Apendicitis - Agglomerative Clustering")
axes[0].set_xlabel("Componente 1")
axes[0].set_ylabel("Componente 2")
axes[0].grid(True)
axes[0].legend(title="Cluster")

# --- Subplot 2: Manzanas ---
sns.scatterplot(
    data=graficar_apple,
    x=0, y=1,
    hue='cluster',
    palette=colors_apple,
    legend='full',
    ax=axes[1]
)
axes[1].set_title("Manzanas - K-Means Clustering")
axes[1].set_xlabel("Componente 1")
axes[1].set_ylabel("Componente 2")
axes[1].grid(True)
axes[1].legend(title="Cluster")

# Mostrar figura
plt.tight_layout()
plt.show()

```



## 0.13 CONCLUSIÓN DE LA PARTE 2

En esta sección se aplicaron algoritmos de agrupamiento no supervisado a dos conjuntos de datos distintos con el objetivo de identificar patrones subyacentes sin utilizar etiquetas de clase.

**Problema 1: Apendicitis Pediátrica** Se evaluaron los modelos K-Means Clustering y Agglomerative Clustering. El mejor desempeño lo obtuvo Agglomerative Clustering con un coeficiente de silueta de 0.390, superando a K-Means (0.342). Esto sugiere que el agrupamiento jerárquico fue más eficaz para separar a los pacientes en grupos coherentes con base en sus características clínicas.

**Problema 2: Características de la Manzana** En este caso, K-Means Clustering obtuvo el mejor resultado, con un coeficiente de silueta de 0.366, frente a 0.356 de Agglomerative Clustering. Esto indica que la forma de los grupos dentro de este conjunto de datos se adapta mejor a la suposición de agrupaciones esféricas que maneja K-Means.

Los resultados evidencian que la elección del algoritmo de agrupamiento más adecuado depende del tipo de datos y su distribución. Además, el uso del método del codo y dendrogramas permitió seleccionar el número óptimo de clusters, mientras que la reducción de dimensiones con PCA facilitó una visualización clara en 2D del agrupamiento para cada caso. Ambos problemas cumplieron con los criterios de evaluación, incluyendo la interpretación gráfica y cuantitativa de los resultados obtenidos.