Cervical Cancer Classification

Loading Python Libraries

In [1]:
```
import numpy as np
import pandas as pd
from typing import List
import missingno as msno
from sklearn.svm import SVC
import plotly.express as px
import matplotlib.pyplot as plt
import plotly.graph_objects as go
from sklearn.pipeline import Pipeline
from sklearn.decomposition import PCA
from sklearn.impute import SimpleImputer
from plotly.subplots import make_subplots
from sklearn.model_selection import GridSearchCV
from sklearn.neighbors import KNeighborsClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.model_selection import StratifiedShuffleSplit
from sklearn.metrics import accuracy_score,confusion_matrix
from sklearn.metrics import precision_recall_fscore_support
from sklearn.preprocessing import RobustScaler,StandardScaler
from sklearn.ensemble import RandomForestClassifier, VotingClassifier

from imblearn.over_sampling import SMOTE, ADASYN
from imblearn.over_sampling import RandomOverSampler
```

Importing the Data

In [2]:
```
# Let's fetch the youtube spam comments dataset into a data_frame
cancer_dataframe = pd.read_csv('risk_factors_cervical_cancer.csv')



# Let's take a quick look at the shape of the dataframe
print("Cancer Risk factors data shape -->", cancer_dataframe.shape)
print()

# Let's take a brief look at the contents of the dataframe
cancer_dataframe.head().style.background_gradient()
```

```
Cancer Risk factors data shape --> (858, 36)
```

Out[2]:

	Age	Number of sexual partners	First sexual intercourse	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	Hormonal Contraceptives	Con
0	18	4.0	15.0	1.0	0.0	0.0	0.0	0.0	
1	15	1.0	14.0	1.0	0.0	0.0	0.0	0.0	
2	34	1.0	?	1.0	0.0	0.0	0.0	0.0	
3	52	5.0	16.0	4.0	1.0	37.0	37.0	1.0	
4	46	3.0	21.0	4.0	0.0	0.0	0.0	1.0	

Gaining Insights from Data

In [3]:
```
# Let's obtain a brief overview of the dataframe
cancer_dataframe.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 858 entries, 0 to 857
Data columns (total 36 columns):
 #   Column                              Non-Null Count  Dtype 
---  ------                              --------------  ----- 
 0   Age                                 858 non-null    int64 
 1   Number of sexual partners           858 non-null    object
 2   First sexual intercourse            858 non-null    object
 3   Num of pregnancies                  858 non-null    object
 4   Smokes                              858 non-null    object
 5   Smokes (years)                      858 non-null    object
 6   Smokes (packs/year)                 858 non-null    object
 7   Hormonal Contraceptives             858 non-null    object
 8   Hormonal Contraceptives (years)     858 non-null    object
 9   IUD                                 858 non-null    object
 10  IUD (years)                         858 non-null    object
 11  STDs                                858 non-null    object
 12  STDs (number)                       858 non-null    object
 13  STDs:condylomatosis                 858 non-null    object
 14  STDs:cervical condylomatosis        858 non-null    object
 15  STDs:vaginal condylomatosis         858 non-null    object
 16  STDs:vulvo-perineal condylomatosis  858 non-null    object
 17  STDs:syphilis                       858 non-null    object
 18  STDs:pelvic inflammatory disease    858 non-null    object
 19  STDs:genital herpes                 858 non-null    object
 20  STDs:molluscum contagiosum          858 non-null    object
 21  STDs:AIDS                           858 non-null    object
 22  STDs:HIV                            858 non-null    object
 23  STDs:Hepatitis B                    858 non-null    object
 24  STDs:HPV                            858 non-null    object
 25  STDs: Number of diagnosis           858 non-null    int64 
 26  STDs: Time since first diagnosis    858 non-null    object
 27  STDs: Time since last diagnosis     858 non-null    object
 28  Dx:Cancer                           858 non-null    int64 
 29  Dx:CIN                              858 non-null    int64 
 30  Dx:HPV                              858 non-null    int64 
 31  Dx                                  858 non-null    int64 
 32  Hinselmann                          858 non-null    int64 
 33  Schiller                            858 non-null    int64 
 34  Citology                            858 non-null    int64 
 35  Biopsy                              858 non-null    int64 
dtypes: int64(10), object(26)
memory usage: 241.4+ KB
```

In [4]:

```python
# Let's see descriptive statistics for all numeric columns
cancer_dataframe.describe()
```

Out [4]:

	Age	STDs: Number of diagnosis	Dx:Cancer	Dx:CIN	Dx:HPV	Dx	Hinselm
count	858.000000	858.000000	858.000000	858.000000	858.000000	858.000000	858.000
mean	26.820513	0.087413	0.020979	0.010490	0.020979	0.027972	0.040
std	8.497948	0.302545	0.143398	0.101939	0.143398	0.164989	0.197
min	13.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000
25%	20.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000
50%	25.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000
75%	32.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000
max	84.000000	3.000000	1.000000	1.000000	1.000000	1.000000	1.000

Observations

1. **The dataset mainly covers young pepople with an average age of approximately 26.82 years, yet with a broad age spectrum (13 to 84 years).**
2. **Diagnosed conditions and positive test outcomes for STDs, cancer, HPV, and related health screenings are remarkably low, with most participants having zero diagnoses, reflecting either a generally healthy population or limited diagnostic testing among the subjects.**

Data Cleaning and Processing

In [5]:

```
# Let's identify columns of type object
object_cols = cancer_dataframe.select_dtypes(include=["object"]).columns
cancer_dataframe[object_cols] = cancer_dataframe[object_cols].apply(pd.to_nu

# Let's fill NaN values with np.nan
cancer_dataframe[object_cols].fillna(np.nan, inplace=True)

# Initialize the SimpleImputer to replace missing values with the median of
imp = SimpleImputer(strategy="median")

# Let's fit the imputer and transform the data, imputing missing values
X = imp.fit_transform(cancer_dataframe)
cancer_dataframe = pd.DataFrame(X, columns=cancer_dataframe.columns)
```

```
<ipython-input-5-85b3a7dd27b4>:6: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-doc
s/stable/user_guide/indexing.html#returning-a-view-versus-a-copy
  cancer_dataframe[object_cols].fillna(np.nan, inplace=True)
```

In [6]:
```
def categorize_age(age):
    """
    Categorize age into predefined age groups.
    """
    if age < 12:
        category = "Child"
    elif age < 20:
        category = "Teen"
    elif age < 30:
        category = "20s"
    elif age < 40:
        category = "30s"
    elif age < 50:
        category = "40s"
    elif age < 60:
        category = "50s"
    elif age < 70:
        category = "60s"
    else:
        category = "70+"
    return category

cancer_dataframe["Age"] = cancer_dataframe["Age"].apply(int)
# Let's apply the age categorization function to each age in the dataframe
cancer_dataframe["Age_Group"] = cancer_dataframe["Age"].apply(categorize_age
```

In [7]:
```
std_columns = {
    'STDs:condylomatosis',
    'STDs:cervical condylomatosis',
    'STDs:vaginal condylomatosis',
    'STDs:vulvo-perineal condylomatosis',
    'STDs:syphilis',
    'STDs:pelvic inflammatory disease',
    'STDs:genital herpes',
    'STDs:molluscum contagiosum',
    'STDs:AIDS',
    'STDs:HIV',
    'STDs:Hepatitis B',
    'STDs:HPV'
}

# Let's calculate the total number of STDs for each row and add it as a new
cancer_dataframe["Total_STD_Count"] = cancer_dataframe[list(std_columns)].su
std_summary_by_age = cancer_dataframe.groupby("Age_Group")[list(std_columns)
```

In [8]:
```
test_cols = ["Hinselmann", "Schiller", "Citology", "Biopsy"]
cancer_dataframe["total_tests"] = cancer_dataframe[test_cols].sum(axis = 1)
```

In [9]:
```
# Combine general columns with STD-specific columns into a single set for co
columns_to_convert_to_int = {
    "total_tests",
    "Total_STD_Count",
    "Smokes",
    "Biopsy",
    "Dx:Cancer",
    "Num of pregnancies",
    "Number of sexual partners",
    "First sexual intercourse",
    "Hormonal Contraceptives",
    "IUD",
    "STDs",
    "STDs (number)",
    "STDs: Number of diagnosis",
    "Dx:CIN",
    "Dx:HPV",
    "Dx",
    "Hinselmann",
    "Schiller",
    "Citology"
}

columns_to_convert_to_int.update(std_columns)

for column_name in columns_to_convert_to_int:
    # Use .apply(pd.to_numeric, errors='coerce') to handle non-numeric value
    cancer_dataframe[column_name] = pd.to_numeric(cancer_dataframe[column_na
```

Check Duplicate Values

In [10]:
```
# Let's check for the duplicate values
cancer_dataframe[cancer_dataframe.duplicated(keep=False)][:5]
```

Out[10]:

	Age	Number of sexual partners	First sexual intercourse	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	Hormonal Contraceptives	C
1	15	1	14	1	0	0.0	0.0	0	
60	34	3	19	3	0	0.0	0.0	1	
66	34	3	19	3	0	0.0	0.0	1	
143	28	1	19	2	0	0.0	0.0	1	
206	28	2	20	2	0	0.0	0.0	1	

5 rows × 39 columns

In [11]:
```
# Let's take a quick look at the shape of the dataframe
print("Cervical cancer data shape -->", cancer_dataframe.shape)
print()

# Let's take a brief look at the contents of the dataframe
cancer_dataframe.head().style.background_gradient()
```

```
Cervical cancer data shape --> (858, 39)
```

Out[11]:

	Age	Number of sexual partners	First sexual intercourse	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	Hormonal Contraceptives
0	18	4	15	1	0	0.000000	0.000000	0
1	15	1	14	1	0	0.000000	0.000000	0
2	34	1	17	1	0	0.000000	0.000000	0
3	52	5	16	4	1	37.000000	37.000000	1
4	46	3	21	4	0	0.000000	0.000000	1

In [12]:

```python
# Function to get unique_counts based on specific column
def value_counts(column_name):
    return cancer_dataframe.loc[
        :, column_name
    ].value_counts()  # Returns the unique value counts
```

In [13]:

```python
# Iterates over all the columns of the dataframe and calls value_counts func
required_columns = [
    "total_tests",
    "Total_STD_Count",
    "Smokes",
    "Biopsy",
    "Dx:Cancer",
    "Hormonal Contraceptives",
    "IUD",
    "STDs",
    "STDs (number)",
    "STDs: Number of diagnosis",
    "Dx:CIN",
    "Dx:HPV",
    "Dx",
    "Hinselmann",
    "Schiller",
    "Citology",
]
for column_name in required_columns:
    print(f"Value Counts of {column_name}")
    value_counts_data = value_counts(column_name=column_name)
    for index, value in value_counts_data.items():
        print(f"{column_name} {index}: {value}")
    print()
```

```
Value Counts of total_tests
total_tests 0: 756
total_tests 1: 41
total_tests 3: 33
total_tests 2: 22
total_tests 4: 6

Value Counts of Total_STD_Count
Total_STD_Count 0: 779
Total_STD_Count 2: 37
Total_STD_Count 1: 34
Total_STD_Count 3: 7
Total_STD_Count 4: 1

Value Counts of Smokes
Smokes 0: 735
Smokes 1: 123

Value Counts of Biopsy
Biopsy 0: 803
Biopsy 1: 55

Value Counts of Dx:Cancer
Dx:Cancer 0: 840
Dx:Cancer 1: 18

Value Counts of Hormonal Contraceptives
Hormonal Contraceptives 1: 589
Hormonal Contraceptives 0: 269

Value Counts of IUD
IUD 0: 775
IUD 1: 83

Value Counts of STDs
STDs 0: 779
STDs 1: 79

Value Counts of STDs (number)
STDs (number) 0: 779
STDs (number) 2: 37
STDs (number) 1: 34
STDs (number) 3: 7
STDs (number) 4: 1

Value Counts of STDs: Number of diagnosis
STDs: Number of diagnosis 0: 787
STDs: Number of diagnosis 1: 68
STDs: Number of diagnosis 2: 2
STDs: Number of diagnosis 3: 1

Value Counts of Dx:CIN
Dx:CIN 0: 849
Dx:CIN 1: 9

Value Counts of Dx:HPV
Dx:HPV 0: 840
Dx:HPV 1: 18
```

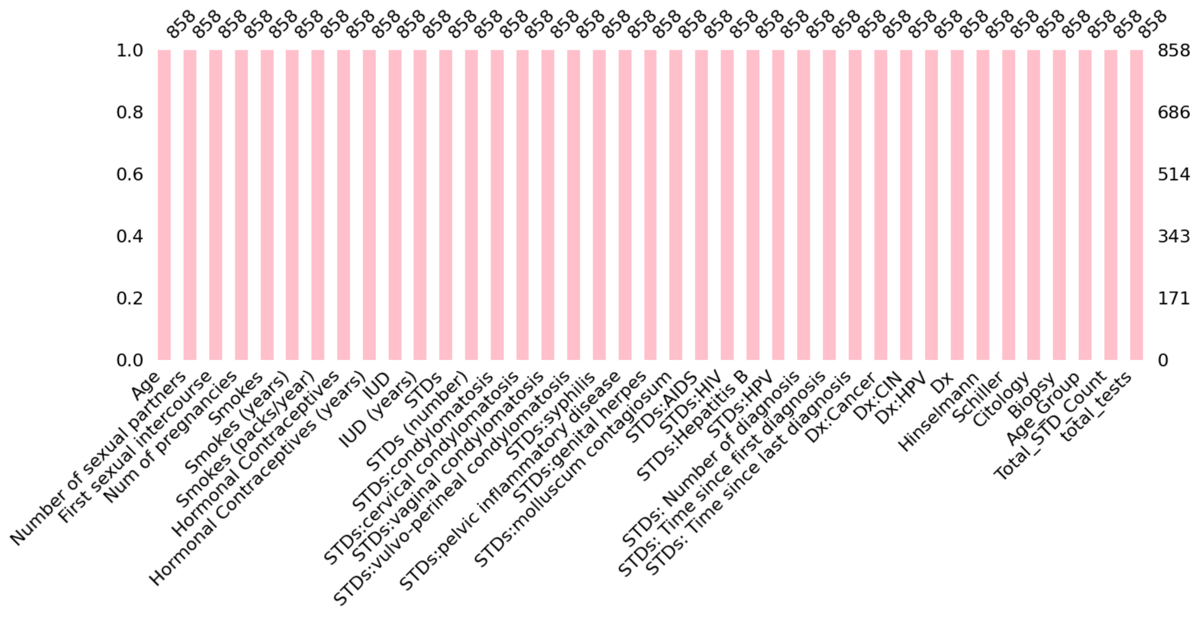
```
Value Counts of Dx
Dx 0: 834
Dx 1: 24

Value Counts of Hinselmann
Hinselmann 0: 823
Hinselmann 1: 35

Value Counts of Schiller
Schiller 0: 784
Schiller 1: 74

Value Counts of Citology
Citology 0: 814
Citology 1: 44
```

See how many missing data points we have

In [14]:
```
cancer_dataframe.isnull().sum()
```

Out[14]:
```
Age                                   0
Number of sexual partners             0
First sexual intercourse              0
Num of pregnancies                    0
Smokes                                0
Smokes (years)                        0
Smokes (packs/year)                   0
Hormonal Contraceptives               0
Hormonal Contraceptives (years)       0
IUD                                   0
IUD (years)                           0
STDs                                  0
STDs (number)                         0
STDs:condylomatosis                   0
STDs:cervical condylomatosis          0
STDs:vaginal condylomatosis           0
STDs:vulvo-perineal condylomatosis    0
STDs:syphilis                         0
STDs:pelvic inflammatory disease      0
STDs:genital herpes                   0
STDs:molluscum contagiosum            0
STDs:AIDS                             0
STDs:HIV                              0
STDs:Hepatitis B                      0
STDs:HPV                              0
STDs: Number of diagnosis             0
STDs: Time since first diagnosis      0
STDs: Time since last diagnosis       0
Dx:Cancer                             0
Dx:CIN                                0
Dx:HPV                                0
Dx                                    0
Hinselmann                            0
Schiller                              0
Citology                              0
Biopsy                                0
Age_Group                             0
Total_STD_Count                       0
total_tests                           0
dtype: int64
```

In [15]:
```
msno.bar(cancer_dataframe, figsize = (16,5),color = "pink")
plt.show()
```



Data Visualization

In [16]:
```
# Let's visulaize the distribution of age
age_dist = px.histogram(cancer_dataframe, x="Age", marginal="box", color_dis
age_dist.update_layout(title="Age distribution")
age_dist.show()
```

In [17]:
```
diagnoses_num_partner_compare_cols = ['Dx:Cancer',
                                      'Dx:HPV',
                                      "Number of sexual partners",]
corr_matrix = cancer_dataframe[diagnoses_num_partner_compare_cols].corr()
diagnoses_num_partner_heatmap = px.imshow(corr_matrix,
                              aspect="auto",
                              color_continuous_scale="gnbu",
                              text_auto=True)
diagnoses_num_partner_heatmap.show()
```

Imbalance Data

```
In [18]: dx_cancer = px.histogram(cancer_dataframe, y="Dx:Cancer")
dx_cancer.update_layout(bargap=0.2)
dx_cancer.update_layout(title = "Imbalanced Classes")
dx_cancer.show()
```

In [19]:
```python
X = cancer_dataframe.drop(["Dx:Cancer", "Age_Group"], axis=1)
y = cancer_dataframe["Dx:Cancer"].copy()
```

In [20]:
```python
# Let's initialize ADASYN sample
adaptive_sampling = ADASYN(random_state=42)

# Let's apply ADASYN to resample the features (X) and target (y)
features_resampled, target_resampled = adaptive_sampling.fit_resample(X, y)

cancer_dataframe = features_resampled.join(target_resampled, how='outer')
```

In [21]:
```python
# Let's apply the age categorization function to each age in the dataframe
cancer_dataframe["Age_Group"] = cancer_dataframe["Age"].apply(categorize_age
```

In [22]:
```python
# Let's create a histogram to visualize the distribution of Dx:Cancer in the
cancer_diagnosis_distribution = px.histogram(cancer_dataframe, y="Dx:Cancer"
cancer_diagnosis_distribution.update_layout(
    bargap=0.2,  # Adjust the gap between bars
    title_text="Distribution of Cancer Diagnosis - Balanced Classes"  # Upda
)

# Let's display the histogram
cancer_diagnosis_distribution.show()
```

In [23]:
```
def prepare_data(df, target, stratify_col, test_ratio=0.2, random_seed=62, c
    split = StratifiedShuffleSplit(n_splits=1, test_size=test_ratio, random_
    for train_idx, test_idx in split.split(df, df[stratify_col]):
        train_set = df.loc[train_idx]
        test_set = df.loc[test_idx]

    if cols_to_remove:
        for set_ in (train_set, test_set):
            set_.drop(cols_to_remove, axis=1, inplace=True)

    X_train = train_set.drop(target, axis=1)
    y_train = train_set[target].copy()

    X_test = test_set.drop(target, axis=1)
    y_test = test_set[target].copy()

    return X_train, y_train, X_test, y_test


cols_to_drop = ["Age_Group", "Total_STD_Count", "total_tests"]
X_train, y_train, X_test, y_test = prepare_data(cancer_dataframe, "Dx:Cancer
```

PCA and Model

In [24]:
```
def preprocess_features(feature_data, n_pca_components=13, pipeline=None):
    if pipeline is None:
        # Define and fit a new preprocessing pipeline if none is provided
        pipeline = Pipeline([
            ("data_scaler", RobustScaler()),
            ("dimensionality_reducer", PCA(n_components=n_pca_components))
        ])
        transformed_features = pipeline.fit_transform(feature_data)
    else:
        # Use the provided pipeline to transform the data
        transformed_features = pipeline.transform(feature_data)

    return transformed_features, pipeline

X_train_preprocessed, training_pipeline = preprocess_features(X_train, n_pca
X_test_preprocessed, _ = preprocess_features(X_test, pipeline=training_pipel
```

In [25]:
```
from sklearn.pipeline import make_pipeline

# Let's define a parameter grid for hyperparameter tuning
parameter_grid = {'logisticregression__C': np.logspace(-5, 8, 15)}

# Let's create a pipeline that first scales the data
pipeline = make_pipeline(StandardScaler(), LogisticRegression(max_iter=1000)

# Set up GridSearchCV with the pipeline
grid_search = GridSearchCV(pipeline, parameter_grid, cv=10, refit=True)

# Let's fit the grid search to the training data
logistic_regression_cv = grid_search.fit(X_train_preprocessed, y_train)
```

Random Forest Classifier

In [26]:
```
random_forest_classifier = RandomForestClassifier(n_estimators=2500, max_lea
                                  max_features="sqrt")
```

KNN Classifier

In [27]:
```
# Let's define KNNClassifier

knn_classifier = KNeighborsClassifier()
knn_param_grid = {"n_neighbors": list(np.arange(1, 100, 2))}
knn_classifier_cv = GridSearchCV(knn_classifier, knn_param_grid, cv=10,refit
knn_classifier_cv = KNeighborsClassifier(**knn_classifier_cv.best_params_)
```

SVM Classifier

In [28]:
```
# Let's define SVM Classifier
svm_classifier = SVC()
svc_param_grid = {"C": np.logspace(-3, 2, 6), "gamma": np.logspace(-3, 2, 6)
svm_classifier_cv = GridSearchCV(svm_classifier, svc_param_grid, cv=5)
```

In [29]:
```
col_names = ["Classifier Name", "Accuracy Score", "Precision Score",
             "Recall Score", "F1 Score"]
summary_df = pd.DataFrame(columns=col_names)

est_name = []
est_acc = []
precision_score = []
recall_score = []
f1score = []
est_conf_matrix = []

estimators = [
    ("LogisticRegression", logistic_regression_cv),
     ("RandomForestClassifier ", random_forest_classifier),
    ("KNeighborsClassifier", knn_classifier_cv),
    ("SupportVectorClassifier", svm_classifier_cv)]

for i in range(0, len(estimators)):
    clf_name = estimators[i][0]
    clf = estimators[i][1]
    clf.fit(X_train, y_train)
    y_pred = clf.predict(X_test)
    # print(pd.crosstab(y_test,y_pred,rownames=["Actual"],colnames=["predict
    est_name.append(estimators[i][0])
    est_acc.append(accuracy_score(y_test, y_pred))
    scores = precision_recall_fscore_support(y_test, y_pred, average="weight
    precision_score.append(scores[0])
    recall_score.append(scores[1])
    f1score.append(scores[2])
    est_conf_matrix.append(confusion_matrix(y_test,y_pred))


summary_df[col_names[0]] = est_name
summary_df[col_names[1]] = est_acc
summary_df[col_names[2]] = precision_score
summary_df[col_names[3]] = recall_score
summary_df[col_names[4]] = f1score
```

Results

In [30]:
```
# Let's print the resuts of LogisticRegression, Random Forest, KNN and SVC
summary_df
```

Out[30]:

	Classifier Name	Accuracy Score	Precision Score	Recall Score	F1 Score
0	LogisticRegression	1.000000	1.000000	1.000000	1.000000
1	RandomForestClassifier	0.991071	0.991226	0.991071	0.991070
2	KNeighborsClassifier	0.955357	0.959057	0.955357	0.955292
3	SupportVectorClassifier	1.000000	1.000000	1.000000	1.000000

In [31]:
```
# Define a list of color scales for visual variety
unique_color_scales = ["agsunset", "teal", "purples", "viridis"]

# Iterate over the confusion matrices and their corresponding names
for index, conf_matrix in enumerate(est_conf_matrix):
    # Generate a heatmap for each confusion matrix
    heatmap_visual = px.imshow(conf_matrix, aspect="auto", text_auto=True,
                               color_continuous_scale=unique_color_scales[ir

    # Customize the layout with dynamic titles and axis labels
    heatmap_visual.update_layout(title=est_name[index])
    heatmap_visual.update_xaxes(title="Predicted Labels")
    heatmap_visual.update_yaxes(title="Actual Labels")

    # Display the heatmap
    heatmap_visual.show()
```