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# 🌈 SVM Cancer Prediction (Linear, Poly, RBF, Sigmoid) with Metrics + ROC Graphs
import io, pandas as pd, numpy as np, matplotlib.pyplot as plt, seaborn as sns
from google.colab import files
from sklearn.preprocessing import LabelEncoder, StandardScaler
from sklearn.model_selection import train_test_split
from sklearn.svm import SVC
from sklearn.metrics import (accuracy_score, recall_score, precision_score, f1_score,
                             jaccard_score, confusion_matrix, roc_curve, auc)

# ----- Load CSV -----
print("📁 Upload your CSV file (e.g. samples_cancer (1).csv)")
uploaded = files.upload()
fname = list(uploaded.keys())[0]
df = pd.read_csv(io.BytesIO(uploaded[fname]))

# ----- Data Prep -----
# Detect target column (diagnosis/label/class/target or last)
for cand in ("diagnosis", "target", "class", "label"):
    if cand in df.columns:
        target_col = cand
        break
    else:
        target_col = df.columns[-1]

X = df.drop(columns=[target_col])
y_raw = df[target_col]

# Encode target and features
le = LabelEncoder()
y = le.fit_transform(y_raw.astype(str))
for c in X.select_dtypes(include=['object', 'category']).columns:
    X[c] = LabelEncoder().fit_transform(X[c].astype(str))
X = X.fillna(0)
X = StandardScaler().fit_transform(X)

# Split data
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.25, random_state=42, stratify=y)

# ----- Train SVM Models -----
kernels = ['linear', 'poly', 'rbf', 'sigmoid']
results, models = [], {}

for k in kernels:
    clf = SVC(kernel=k, probability=True, random_state=42)
    clf.fit(X_train, y_train)
    y_pred = clf.predict(X_test)
    try:
        y_score = clf.predict_proba(X_test)[:, 1]
    except Exception:
        y_score = clf.decision_function(X_test)
        y_score = (y_score - y_score.min()) / (y_score.max() - y_score.min() + 1e-12)

    acc = accuracy_score(y_test, y_pred)
    rec = recall_score(y_test, y_pred)
    prec = precision_score(y_test, y_pred, zero_division=0)
    f1 = f1_score(y_test, y_pred)
    jacc = jaccard_score(y_test, y_pred)
    err = 1 - acc
    cm = confusion_matrix(y_test, y_pred)
    fpr, tpr, _ = roc_curve(y_test, y_score)
    roc_auc = auc(fpr, tpr)

    models[k] = {'fpr': fpr, 'tpr': tpr, 'auc': roc_auc}
    results.append({'Kernel': k, 'Accuracy': acc, 'Recall': rec, 'Precision': prec,
                   'F1-Score': f1, 'Jaccard': jacc, 'Error Rate': err, 'ConfusionMatrix': cm})

# ----- Results Table -----
res_df = pd.DataFrame(results).set_index('Kernel')
print("\n==== Metrics Table ===")
display(res_df[['Accuracy', 'Recall', 'Precision', 'F1-Score', 'Jaccard', 'Error Rate']])

# ----- Confusion Matrices -----
fig, axes = plt.subplots(1, 4, figsize=(16, 4))
for ax, k in zip(axes, kernels):
    sns.heatmap(results[kernels.index(k)][['ConfusionMatrix']], annot=True, fmt='d', cmap='Blues', ax=ax)
    ax.set_title(k)
    ax.set_xlabel("Predicted")
    ax.set_ylabel("Actual")
plt.suptitle("Confusion Matrices")
plt.tight_layout(rect=[0, 0, 1, 0.95])
plt.show()
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# ----- ROC Curve -----
plt.figure(figsize=(8,6))
for k in kernels:
    plt.plot(models[k]['fpr'], models[k]['tpr'], label=f'{k} (AUC={models[k]["auc"]:.3f})')
plt.plot([0,1],[0,1], '--', color='gray')
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('ROC Curve Comparison - SVM Kernels')
plt.legend()
plt.grid(alpha=0.3)
plt.show()
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█ Upload your CSV file (e.g. samples_cancer (1).csv)

Choose Files samples_cancer (1).csv

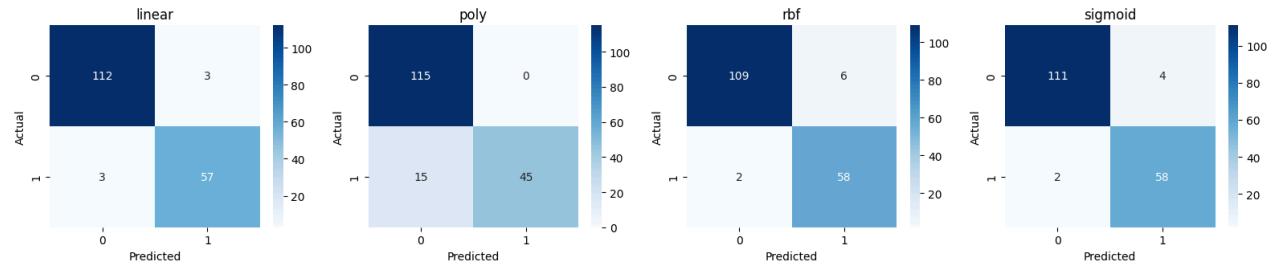
samples_cancer (1).csv(text/csv) - 20675 bytes, last modified: 11/8/2025 - 100% done

Saving samples_cancer (1).csv to samples_cancer (1).csv

==== Metrics Table ===

	Accuracy	Recall	Precision	F1-Score	Jaccard	Error Rate
Kernel						
linear	0.965714	0.950000	0.950000	0.950000	0.904762	0.034286
poly	0.914286	0.750000	1.000000	0.857143	0.750000	0.085714
rbf	0.954286	0.966667	0.906250	0.935484	0.878788	0.045714
sigmoid	0.965714	0.966667	0.935484	0.950820	0.906250	0.034286

Confusion Matrices



ROC Curve Comparison - SVM Kernels

