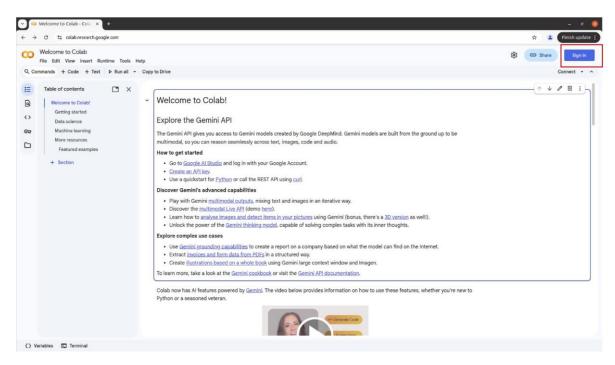
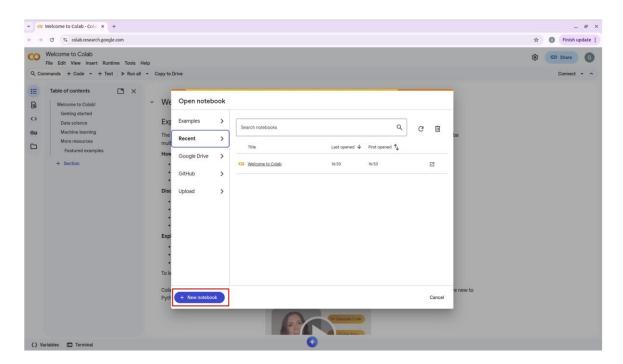
Open google colab using following link

https://colab.research.google.com/

-sign in via email id (on top right corner)



-click on New Notebook



```
# Create data
data = {
  'CellLine': ['CL1', 'CL2', 'CL3', 'CL4', 'CL5', 'CL6'],
  'GeneA Expression': [8.1, 6.5, 9.0, 7.2, None, 5.8],
  'GeneB Expression': [4.3, 3.0, 5.1, 2.8, 4.5, None],
  'Drug Response': ['Sensitive', 'Resistant', 'Sensitive', 'Resistant', 'Sensitive', 'Resistant']
}
df = pd.DataFrame(data)
# Fill missing values with mean
df = df.fillna(df.mean(numeric only=True))
print(df)
# Convert sensitive and resistant to binary digits
df['Drug Response'] = df['Drug Response'].map({'Sensitive': 1, 'Resistant': 0})
X = df[['GeneA Expression', 'GeneB Expression']]
y = df['Drug Response']
# Separate Data into test and training
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)
from sklearn.linear model import LogisticRegression
```

model = LogisticRegression()

model.fit(X_train, y_train)

```
y_pred = model.predict(X_test)
from sklearn.metrics import accuracy_score, confusion_matrix, ConfusionMatrixDisplay
import matplotlib.pyplot as plt
print("Accuracy:", accuracy_score(y_test, y_pred))
# Create confusion matrix
cm = confusion_matrix(y_test, y_pred)
disp = ConfusionMatrixDisplay(confusion matrix=cm, display labels=["Resistant",
"Sensitive"])
disp.plot(cmap="Blues")
plt.title("Confusion Matrix - Drug Sensitivity Prediction")
plt.show()
# Plot Drug Sensitivity Based on Gene Expression
import seaborn as sns
sns.scatterplot(data=df, x='GeneA_Expression', y='GeneB_Expression',
         hue='Drug Response', palette='coolwarm', s=100)
plt.title("Drug Sensitivity Based on Gene Expression")
plt.xlabel("GeneA Expression")
plt.ylabel("GeneB Expression")
plt.show()
```