Advance Genome Disorder Prediction Model Empowered With Deep Learning

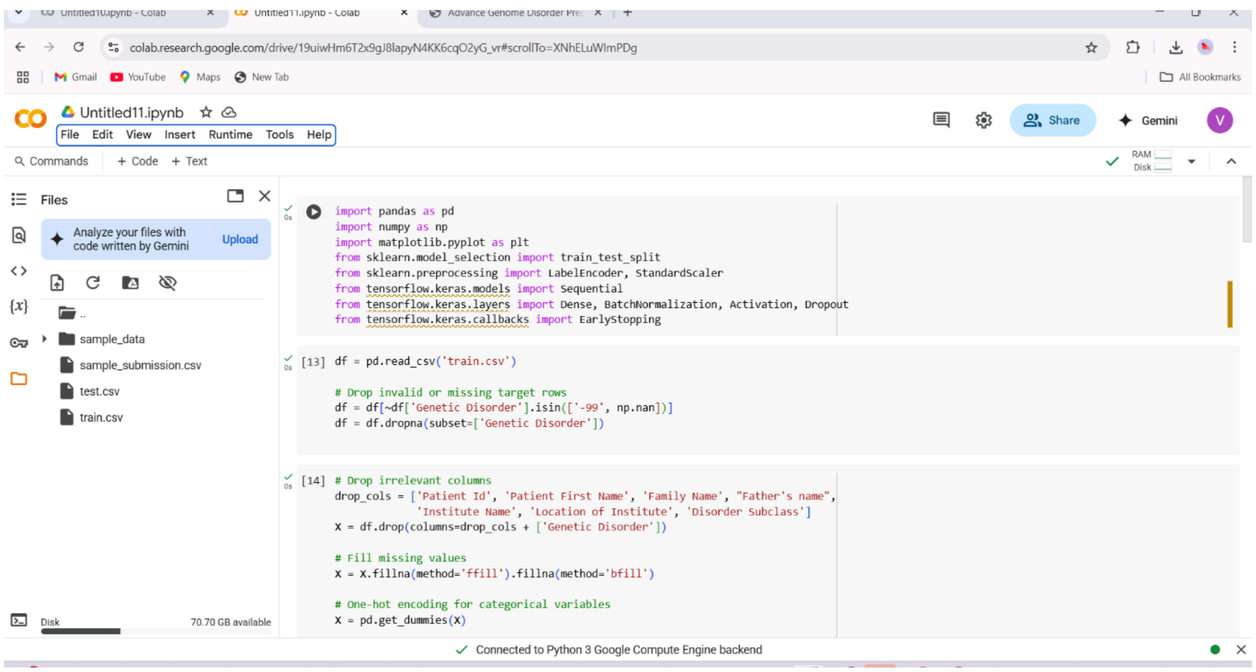
Spring 2025: Neural Networks & Deep Learning – Mini project

Name: Vanitha Chintalapudi

Student ID: 700756782

Git hub link:

https://github.com/VanithaChintalapudi10/Neural-network-deeplearning.git



```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder, StandardScaler
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense, BatchNormalization, Activation, Dropout
from tensorflow.keras.callbacks import EarlyStopping
```

```
[13] df = pd.read_csv('train.csv')

     # Drop invalid or missing target rows
     df = df[~df['Genetic Disorder'].isin(['-99', np.nan])]
     df = df.dropna(subset=['Genetic Disorder'])
```

```
[14] # Drop irrelevant columns
     drop_cols = ['Patient Id', 'Patient First Name', 'Family Name', "Father's name",
                  'Institute Name', 'Location of Institute', 'Disorder Subclass']
     X = df.drop(columns=drop_cols + ['Genetic Disorder'])

     # Fill missing values
     X = X.fillna(method='ffill').fillna(method='bfill')

     # One-hot encoding for categorical variables
     X = pd.get_dummies(X)
```

Connected to Python 3 Google Compute Engine backend

Untitled10.ipynb - Colab
Untitled11.ipynb - Colab
Advance Genome Disorder Pre
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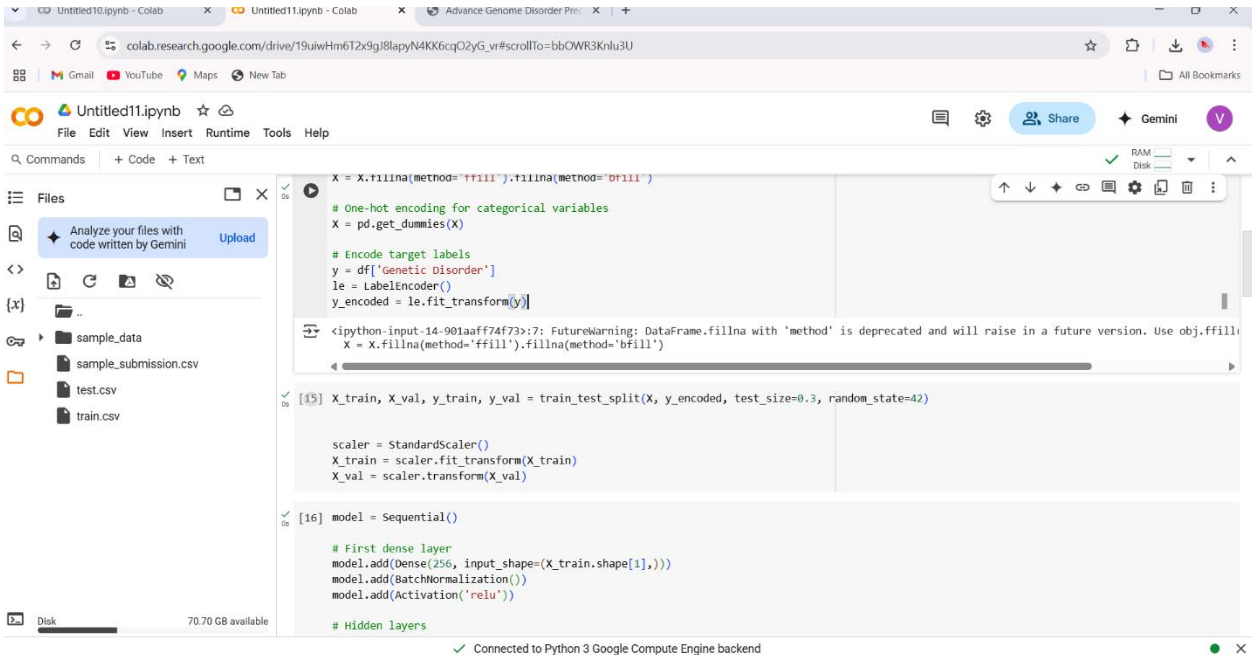
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Advance Genome Disorder Pre
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```
X = X.fillna(method='ffill').fillna(method='bfill')

# One-hot encoding for categorical variables
X = pd.get_dummies(X)

# Encode target labels
y = df['Genetic Disorder']
le = LabelEncoder()
y_encoded = le.fit_transform(y)
```

```
<ipython-input-14-901aaff74f73>:7: FutureWarning: DataFrame.fillna with 'method' is deprecated and will raise in a future version. Use obj.ffill
  X = X.fillna(method='ffill').fillna(method='bfill')
```

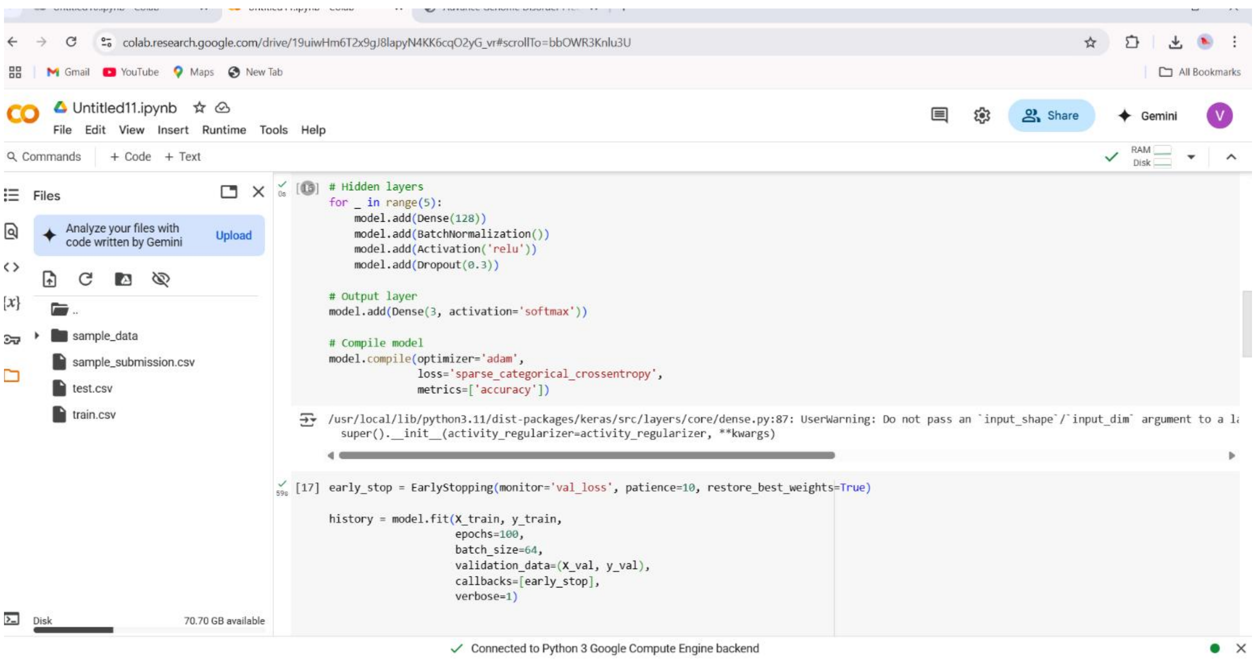
```
[15] X_train, X_val, y_train, y_val = train_test_split(X, y_encoded, test_size=0.3, random_state=42)


     scaler = StandardScaler()
     X_train = scaler.fit_transform(X_train)
     X_val = scaler.transform(X_val)
```

```
[16] model = Sequential()

     # First dense layer
     model.add(Dense(256, input_shape=(X_train.shape[1],)))
     model.add(BatchNormalization())
     model.add(Activation('relu'))

     # Hidden layers
```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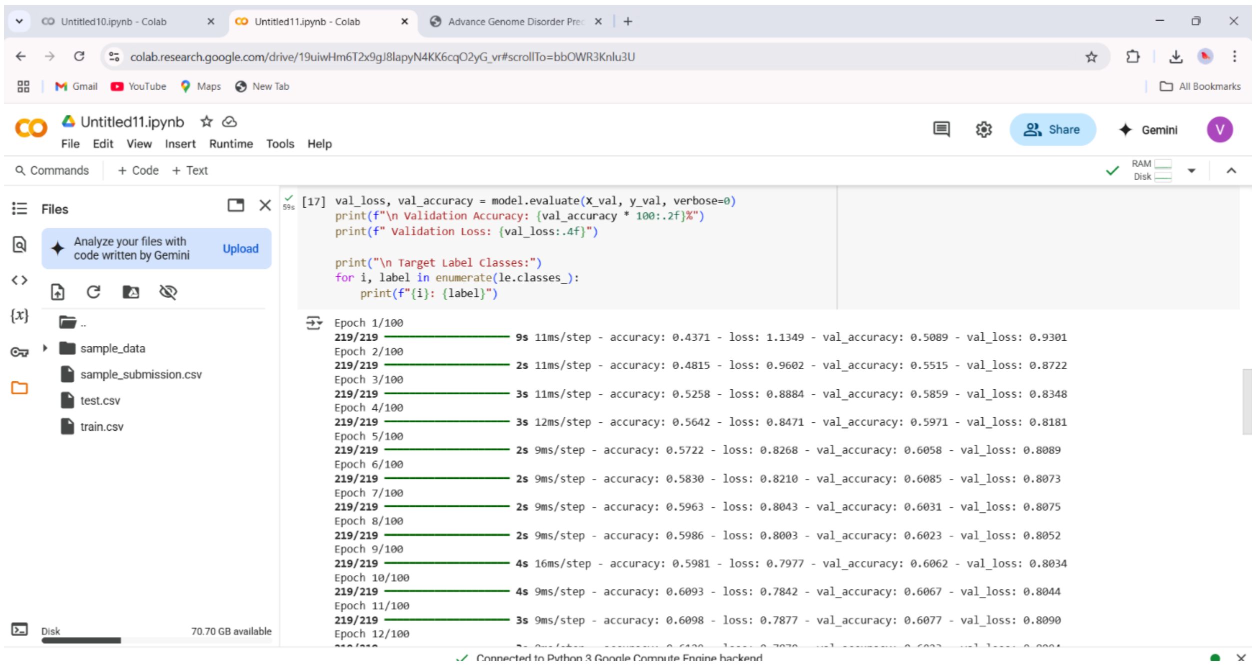
```
# Hidden layers
for _ in range(5):
    model.add(Dense(128))
    model.add(BatchNormalization())
    model.add(Activation('relu'))
    model.add(Dropout(0.3))

# Output layer
model.add(Dense(3, activation='softmax'))

# Compile model
model.compile(optimizer='adam',
              loss='sparse_categorical_crossentropy',
              metrics=['accuracy'])
```

```
/usr/local/lib/python3.11/dist-packages/keras/src/layers/core/dense.py:87: UserWarning: Do not pass an `input_shape`/`input_dim` argument to a la
  super().__init__(activity_regularizer=activity_regularizer, **kwargs)
```

```
[17] early_stop = EarlyStopping(monitor='val_loss', patience=10, restore_best_weights=True)

     history = model.fit(X_train, y_train,
                         epochs=100,
                         batch_size=64,
                         validation_data=(X_val, y_val),
                         callbacks=[early_stop],
                         verbose=1)
```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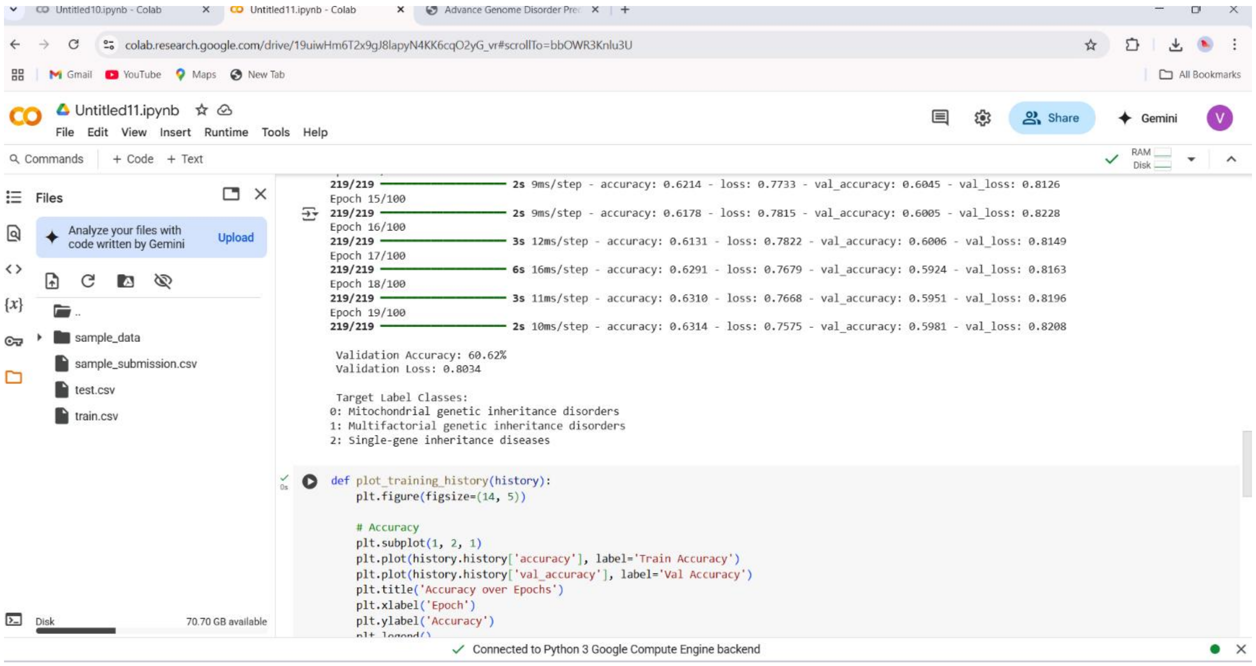
```
[17] val_loss, val_accuracy = model.evaluate(X_val, y_val, verbose=0)
     print(f"\n Validation Accuracy: {val_accuracy * 100:.2f}%")
     print(f" Validation Loss: {val_loss:.4f}")

     print("\n Target Label Classes:")
     for i, label in enumerate(le.classes_):
         print(f"{i}: {label}")
```

```
Epoch 1/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 9s 11ms/step - accuracy: 0.4371 - loss: 1.1349 - val_accuracy: 0.5089 - val_loss: 0.9301
Epoch 2/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 2s 11ms/step - accuracy: 0.4815 - loss: 0.9602 - val_accuracy: 0.5515 - val_loss: 0.8722
Epoch 3/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 3s 11ms/step - accuracy: 0.5258 - loss: 0.8884 - val_accuracy: 0.5859 - val_loss: 0.8348
Epoch 4/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 3s 12ms/step - accuracy: 0.5642 - loss: 0.8471 - val_accuracy: 0.5971 - val_loss: 0.8181
Epoch 5/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 2s 9ms/step - accuracy: 0.5722 - loss: 0.8268 - val_accuracy: 0.6058 - val_loss: 0.8089
Epoch 6/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 2s 9ms/step - accuracy: 0.5830 - loss: 0.8210 - val_accuracy: 0.6085 - val_loss: 0.8073
Epoch 7/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 2s 9ms/step - accuracy: 0.5963 - loss: 0.8043 - val_accuracy: 0.6031 - val_loss: 0.8075
Epoch 8/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 2s 9ms/step - accuracy: 0.5986 - loss: 0.8003 - val_accuracy: 0.6023 - val_loss: 0.8052
Epoch 9/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 4s 16ms/step - accuracy: 0.5981 - loss: 0.7977 - val_accuracy: 0.6062 - val_loss: 0.8034
Epoch 10/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 4s 9ms/step - accuracy: 0.6093 - loss: 0.7842 - val_accuracy: 0.6067 - val_loss: 0.8044
Epoch 11/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 3s 9ms/step - accuracy: 0.6098 - loss: 0.7877 - val_accuracy: 0.6077 - val_loss: 0.8090
Epoch 12/100
```



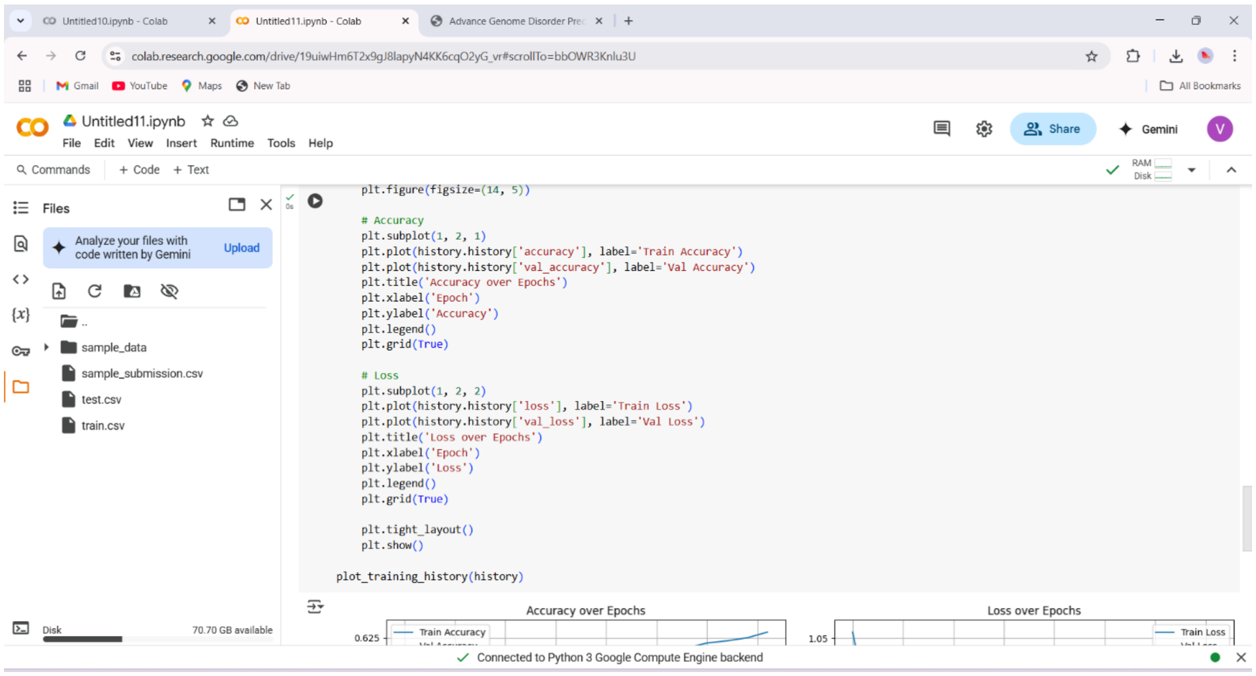
```
219/219 ━━━━━━━━━━━━━━━━━━━━ 2s 9ms/step - accuracy: 0.6214 - loss: 0.7733 - val_accuracy: 0.6045 - val_loss: 0.8126
Epoch 15/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 2s 9ms/step - accuracy: 0.6178 - loss: 0.7815 - val_accuracy: 0.6005 - val_loss: 0.8228
Epoch 16/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 3s 12ms/step - accuracy: 0.6131 - loss: 0.7822 - val_accuracy: 0.6006 - val_loss: 0.8149
Epoch 17/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 6s 16ms/step - accuracy: 0.6291 - loss: 0.7679 - val_accuracy: 0.5924 - val_loss: 0.8163
Epoch 18/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 3s 11ms/step - accuracy: 0.6310 - loss: 0.7668 - val_accuracy: 0.5951 - val_loss: 0.8196
Epoch 19/100
219/219 ━━━━━━━━━━━━━━━━━━━━ 2s 10ms/step - accuracy: 0.6314 - loss: 0.7575 - val_accuracy: 0.5981 - val_loss: 0.8208

 Validation Accuracy: 60.62%
 Validation Loss: 0.8034

 Target Label Classes:
0: Mitochondrial genetic inheritance disorders
1: Multifactorial genetic inheritance disorders
2: Single-gene inheritance diseases
```

```python
def plot_training_history(history):
    plt.figure(figsize=(14, 5))

    # Accuracy
    plt.subplot(1, 2, 1)
    plt.plot(history.history['accuracy'], label='Train Accuracy')
    plt.plot(history.history['val_accuracy'], label='Val Accuracy')
    plt.title('Accuracy over Epochs')
    plt.xlabel('Epoch')
    plt.ylabel('Accuracy')
```



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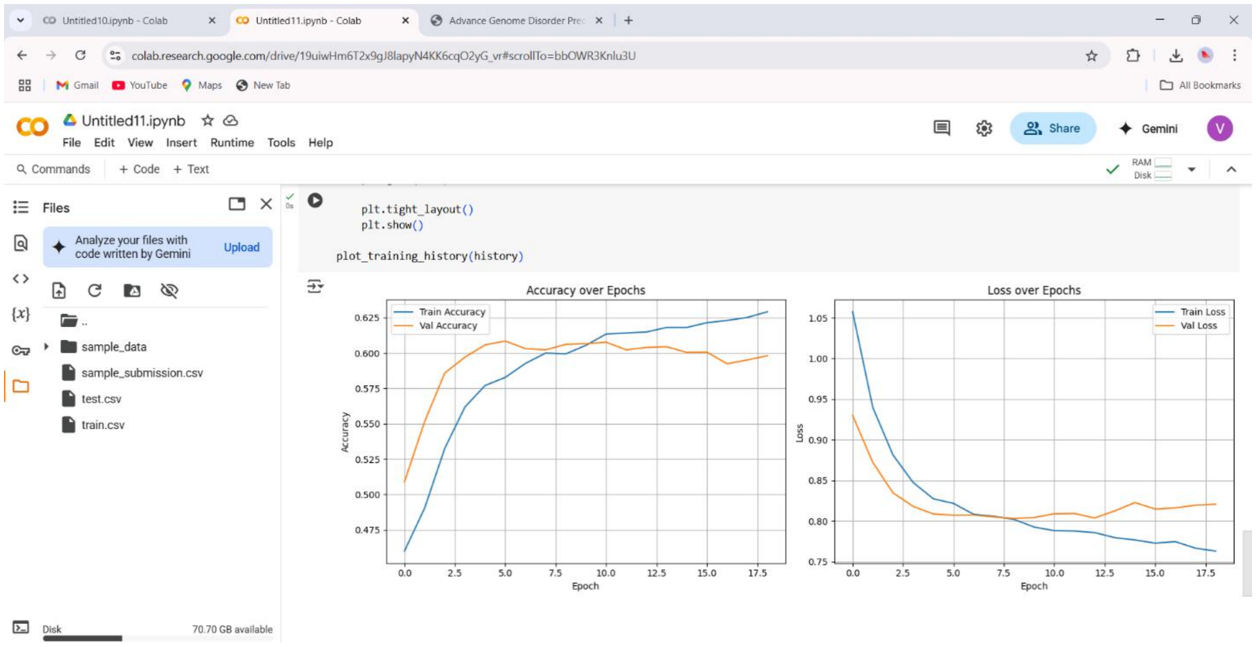
    plt.figure(figsize=(14, 5))

    # Accuracy
    plt.subplot(1, 2, 1)
    plt.plot(history.history['accuracy'], label='Train Accuracy')
    plt.plot(history.history['val_accuracy'], label='Val Accuracy')
    plt.title('Accuracy over Epochs')
    plt.xlabel('Epoch')
    plt.ylabel('Accuracy')
    plt.legend()
    plt.grid(True)

    # Loss
    plt.subplot(1, 2, 2)
    plt.plot(history.history['loss'], label='Train Loss')
    plt.plot(history.history['val_loss'], label='Val Loss')
    plt.title('Loss over Epochs')
    plt.xlabel('Epoch')
    plt.ylabel('Loss')
    plt.legend()
    plt.grid(True)

    plt.tight_layout()
    plt.show()

plot_training_history(history)
```



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

plot_training_history(history)
```