

```
# -*- coding: utf-8 -*-  
"""Lung_Cancer.ipynb
```

Automatically generated by Colab.

Original file is located at
https://colab.research.google.com/drive/17G23eTAyD9OXJ_qFdmGuyLECjPt51Fr9
"""

```
from google.colab import files  
uploaded = files.upload()  
print(f"dataset {uploaded} has been uploaded to this notebook")  
  
from google.colab import drive  
drive.mount('/content/drive')  
  
import os  
for filename in uploaded.keys():  
    with open('/content/drive/My Drive/' + filename, 'wb') as f:  
        f.write(uploaded[filename])  
    print(f"dataset {filename} saved to Google Drive")  
  
import pandas as pd  
import matplotlib.pyplot as plt  
import os  
  
try:  
  
    file_path = '/content/Lung Cancer/dataset_med.csv'  
    df = pd.read_csv(file_path)  
    print("DataFrame loaded successfully.")  
    print(df.head())  
  
    print("\nDataFrame Information:")  
    print(f"Shape: {df.shape}")  
    print(f"Columns: {df.columns.tolist()}")  
    print(f>Data Types:\n{df.dtypes}")  
  
    if df.select_dtypes(include=['number']).empty:  
        print("No numerical columns found for plotting.")  
    else:  
  
        numerical_column = df.select_dtypes(include=['number']).columns[0]  
        plt.figure(figsize=(10, 6))  
        df[numerical_column].hist(bins=20)  
        plt.title(f'Distribution of {numerical_column}')  
        plt.xlabel(numerical_column)  
        plt.ylabel('Frequency')  
        plt.show()  
  
except FileNotFoundError:  
    print(f"Error: The file '{file_path}' was not found. Please ensure the zip file was extracted correctly and the path is correct.")  
except Exception as e:  
    print(f"An error occurred: {e}")  
  
import zipfile  
import os  
  
zip_file_path = '/content/drive/My Drive/lung_cancer.zip'  
  
extract_dir = '/content/'  
  
os.makedirs(extract_dir, exist_ok=True)  
  
with zipfile.ZipFile(zip_file_path, 'r') as zip_ref:  
    zip_ref.extractall(extract_dir)  
  
print(f"Files extracted to {extract_dir}")  
  
extracted_files = os.listdir(extract_dir)  
print("Files in extraction directory:", extracted_files)  
  
df.info()  
df.describe(include='all')  
  
df.info()  
df.head()  
  
print(f"Rows: {df.shape[0]}, Columns: {df.shape[1]}")  
  
"""visualizing distributions"""  
  
import seaborn as sns  
import matplotlib.pyplot as plt  
  
sns.histplot(df['age'], kde=True)  
plt.title('Age Distribution')  
plt.show()  
  
sns.countplot(data=df, x='cancer_stage', hue='survived')  
plt.title('Cancer Stage vs Survival')  
plt.show()  
  
sns.countplot(data=df, x='cancer_stage', hue='survived')  
plt.title('Cancer Stage vs Survival')  
plt.show()  
  
sns.countplot(data=df, x='smoking_status', hue='survived')  
plt.title('Smoking Status vs Survival')  
plt.show()  
  
import pandas as pd  
import seaborn as sns  
import matplotlib.pyplot as plt  
  
# Inspect  
print(df.shape)  
print(df.info())  
print(df.isnull().sum())  
  
# Stats  
print(df.describe(include='all'))  
  
# Visual  
sns.countplot(data=df, x='cancer_stage', hue='survived')  
plt.show()
```

```
!pip install torch torchvision scikit-learn
```

```
"""importing libraries"""
```

```
import torch
import torch.nn as nn
import torch.optim as optim
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, LabelEncoder
import pandas as pd
import numpy as np
```

```
device = torch.device('cuda' if torch.cuda.is_available() else 'cpu')
print(f"Using device: {device}")
```

```
data = df.drop(['id', 'diagnosis_date', 'end_treatment_date'], axis=1)
```

```
cat_cols = data.select_dtypes(include='object').columns
for col in cat_cols:
    le = LabelEncoder()
    data[col] = le.fit_transform(data[col].astype(str))
```

```
X = data.drop("survived", axis=1).values
y = data["survived"].values
```

```
scaler = StandardScaler()
X = scaler.fit_transform(X)
```

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
```

```
X_train = torch.tensor(X_train, dtype=torch.float32)
X_test = torch.tensor(X_test, dtype=torch.float32)
y_train = torch.tensor(y_train, dtype=torch.float32).unsqueeze(1)
y_test = torch.tensor(y_test, dtype=torch.float32).unsqueeze(1)
```

```
class LungCancerNN(nn.Module):
    def __init__(self, input_dim):
        super(LungCancerNN, self).__init__()
        self.net = nn.Sequential(
            nn.Linear(input_dim, 64),
            nn.ReLU(),
            nn.Dropout(0.3),
            nn.Linear(64, 32),
            nn.ReLU(),
            nn.Linear(32, 1),
            nn.Sigmoid()
        )

    def forward(self, x):
        return self.net(x)
```

```
model = LungCancerNN(X_train.shape[1]).to(device)
```

```
"""defining loss and optimizer"""
```

```
criterion = nn.BCELoss()
optimizer = optim.Adam(model.parameters(), lr=0.001)
```

```
"""model training"""
```

```
epochs = 50
for epoch in range(epochs):
    model.train()

    # Move data to the same device as the model
    X_train_device = X_train.to(device)
    y_train_device = y_train.to(device)

    optimizer.zero_grad()
    outputs = model(X_train_device)
    loss = criterion(outputs, y_train_device)
    loss.backward()
    optimizer.step()

    if (epoch+1) % 10 == 0:
        print(f"Epoch [{epoch+1}/{epochs}], Loss: {loss.item():.4f}")
```

```
"""model evaluating"""
```

```
model.eval()
with torch.no_grad():
    # Move test data to the same device as the model
    X_test_device = X_test.to(device)
    y_test_device = y_test.to(device)

    y_pred = model(X_test_device)
    y_pred_class = (y_pred >= 0.5).float()
    accuracy = (y_pred_class == y_test_device).float().mean()
    print(f"Test Accuracy: {accuracy:.4f}")
```

```
learning_rates = [0.01, 0.001, 0.0001]
epochs_list = [50, 100, 150]
```

```
dropout_rates = [0.3, 0.4, 0.5]
```

```
best_accuracy = 0
best_hyperparameters = {}
```

```
for lr in learning_rates:
    for epochs in epochs_list:
        for dropout_rate in dropout_rates:
            print(f"Training with LR: {lr}, Epochs: {epochs}, Dropout: {dropout_rate}")

            model = LungCancerNN(X_train.shape[1]).to(device)
            criterion = nn.BCELoss()
            optimizer = optim.Adam(model.parameters(), lr=lr)

            for epoch in range(epochs):
                model.train()
                X_train_device = X_train.to(device)
                y_train_device = y_train.to(device)

                optimizer.zero_grad()
                outputs = model(X_train_device)
                loss = criterion(outputs, y_train_device)
                loss.backward()
                optimizer.step()

            model.eval()
            with torch.no_grad():
```

```

X_test_device = X_test.to(device)
y_test_device = y_test.to(device)
y_pred = model(X_test_device)
y_pred_class = (y_pred >= 0.5).float()
accuracy = (y_pred_class == y_test_device).float().mean()

print(f"Test Accuracy: {accuracy:.4f}")

if accuracy > best_accuracy:
    best_accuracy = accuracy
    best_hyperparameters = {
        'learning_rate': lr,
        'epochs': epochs,
        'dropout_rate': dropout_rate
    }

```

```

print("\nBest Hyperparameters:")
print(best_hyperparameters)
print(f"Best Test Accuracy: {best_accuracy:.4f}")

```

```

learning_rates = [0.01, 0.001, 0.0001]
epochs_list = [50, 100, 150]
dropout_rates = [0.3, 0.4, 0.5]

```

```

best_accuracy = 0
best_hyperparameters = {}

```

```

for lr in learning_rates:
    for epochs in epochs_list:
        for dropout_rate in dropout_rates:
            print(f"Training with LR: {lr}, Epochs: {epochs}, Dropout: {dropout_rate}")

```

```

model = LungCancerNN(X_train.shape[1]).to(device)
criterion = nn.BCELoss()
optimizer = optim.Adam(model.parameters(), lr=lr)

```

```

for epoch in range(epochs):
    model.train()
    X_train_device = X_train.to(device)
    y_train_device = y_train.to(device)

    optimizer.zero_grad()
    outputs = model(X_train_device)
    loss = criterion(outputs, y_train_device)
    loss.backward()
    optimizer.step()

```

```

model.eval()
with torch.no_grad():
    X_test_device = X_test.to(device)
    y_test_device = y_test.to(device)
    y_pred = model(X_test_device)
    y_pred_class = (y_pred >= 0.5).float()
    accuracy = (y_pred_class == y_test_device).float().mean()

```

```

print(f"Test Accuracy: {accuracy:.4f}")

if accuracy > best_accuracy:
    best_accuracy = accuracy
    best_hyperparameters = {
        'learning_rate': lr,
        'epochs': epochs,
        'dropout_rate': dropout_rate
    }

```

```

print("\nBest Hyperparameters:")
print(best_hyperparameters)
print(f"Best Test Accuracy: {best_accuracy:.4f}")

```

```

class EnhancedLungCancerNN(nn.Module):
    def __init__(self, input_dim):
        super(EnhancedLungCancerNN, self).__init__()
        self.net = nn.Sequential(
            nn.Linear(input_dim, 128),
            nn.ReLU(),
            nn.Dropout(0.4),
            nn.Linear(128, 64),
            nn.ReLU(),
            nn.Linear(64, 32),
            nn.ReLU(),
            nn.Dropout(0.4),
            nn.Linear(32, 1),
            nn.Sigmoid()
        )

    def forward(self, x):
        return self.net(x)

```

```

model_enhanced = EnhancedLungCancerNN(X_train.shape[1]).to(device)
criterion_enhanced = nn.BCELoss()
optimizer_enhanced = optim.Adam(model_enhanced.parameters(), lr=0.001)

```

```

epochs_enhanced = 50
for epoch in range(epochs_enhanced):
    model_enhanced.train()
    X_train_device = X_train.to(device)
    y_train_device = y_train.to(device)

    optimizer_enhanced.zero_grad()
    outputs = model_enhanced(X_train_device)
    loss = criterion_enhanced(outputs, y_train_device)
    loss.backward()
    optimizer_enhanced.step()

    if (epoch+1) % 10 == 0:
        print(f"Epoch [{epoch+1}/{epochs_enhanced}], Loss: {loss.item():.4f}")

```

```

model_enhanced.eval()
with torch.no_grad():
    X_test_device = X_test.to(device)
    y_test_device = y_test.to(device)
    y_pred_enhanced = model_enhanced(X_test_device)
    y_pred_class_enhanced = (y_pred_enhanced >= 0.5).float()
    accuracy_enhanced = (y_pred_class_enhanced == y_test_device).float().mean()
    print(f"Enhanced Model Test Accuracy: {accuracy_enhanced:.4f}")

```

```

optimizer_configs = [
    {'name': 'Adam', 'optimizer': optim.Adam, 'params': {'lr': best_hyperparameters['learning_rate']}},
    {'name': 'SGD', 'optimizer': optim.SGD, 'params': {'lr': best_hyperparameters['learning_rate'], 'momentum': 0.9}},
    {'name': 'RMSprop', 'optimizer': optim.RMSprop, 'params': {'lr': best_hyperparameters['learning_rate']}}
]

```

```

best_accuracy_optimizer = 0

```

```

best_optimizer_name = None
best_optimizer_params = None

for config in optimizer_configs:
    print(f"Training with Optimizer: {config['name']} and parameters: {config['params']}")

    model = LungCancerNN(X_train.shape[1]).to(device)

    optimizer = config['optimizer'](model.parameters(), **config['params'])

    epochs = best_hyperparameters['epochs']

    # Training loop
    for epoch in range(epochs):
        model.train()
        X_train_device = X_train.to(device)
        y_train_device = y_train.to(device)

        optimizer.zero_grad()
        outputs = model(X_train_device)
        loss = criterion(outputs, y_train_device)
        loss.backward()
        optimizer.step()

    # Evaluation
    model.eval()
    with torch.no_grad():
        X_test_device = X_test.to(device)
        y_test_device = y_test.to(device)
        y_pred = model(X_test_device)
        y_pred_class = (y_pred >= 0.5).float()
        accuracy = (y_pred_class == y_test_device).float().mean()

    print(f"Test Accuracy with {config['name']}: {accuracy:.4f}")

    if accuracy > best_accuracy_optimizer:
        best_accuracy_optimizer = accuracy
        best_optimizer_name = config['name']
        best_optimizer_params = config['params']

print("\nBest Optimizer:")
print(f"Name: {best_optimizer_name}")
print(f"Parameters: {best_optimizer_params}")
print(f"Best Test Accuracy: {best_accuracy_optimizer:.4f}")

class LungCancerNN_L2(nn.Module):
    def __init__(self, input_dim):
        super(LungCancerNN_L2, self).__init__()
        self.net = nn.Sequential(
            nn.Linear(input_dim, 64),
            nn.ReLU(),
            nn.Dropout(best_hyperparameters['dropout_rate']),
            nn.Linear(64, 32),
            nn.ReLU(),
            nn.Linear(32, 1),
            nn.Sigmoid()
        )

    def forward(self, x):
        return self.net(x)

model_l2 = LungCancerNN_L2(X_train.shape[1]).to(device)
criterion_l2 = nn.BCELoss()
optimizer_l2 = optim.RMSprop(model_l2.parameters(), lr=best_hyperparameters['learning_rate']) # Use the best optimizer and learning rate
lambda_l2 = 0.001

epochs_l2 = best_hyperparameters['epochs']

for epoch in range(epochs_l2):
    model_l2.train()
    X_train_device = X_train.to(device)
    y_train_device = y_train.to(device)

    optimizer_l2.zero_grad()
    outputs = model_l2(X_train_device)
    loss = criterion_l2(outputs, y_train_device)

    l2_reg = torch.tensor(0.).to(device)
    for param in model_l2.parameters():
        l2_reg += torch.norm(param, 2)
    loss += lambda_l2 * l2_reg

    loss.backward()
    optimizer_l2.step()

    if (epoch+1) % 10 == 0:
        print(f"Epoch [{epoch+1}/{epochs_l2}], Loss with L2: {loss.item():.4f}")

model_l2.eval()
with torch.no_grad():
    X_test_device = X_test.to(device)
    y_test_device = y_test.to(device)
    y_pred_l2 = model_l2(X_test_device)
    y_pred_class_l2 = (y_pred_l2 >= 0.5).float()
    accuracy_l2 = (y_pred_class_l2 == y_test_device).float().mean()
    print(f"Test Accuracy with L2 regularization: {accuracy_l2:.4f}")

from sklearn.model_selection import KFold

n_splits = 5
kf = KFold(n_splits=n_splits, shuffle=True, random_state=42)
fold_accuracies = []

# Combine X and y back for KFold splitting
X_np = X_train.cpu().numpy() if X_train.is_cuda else X_train.numpy()
y_np = y_train.cpu().numpy().squeeze() if y_train.is_cuda else y_train.numpy().squeeze()

for fold, (train_index, val_index) in enumerate(kf.split(X_np)):
    print(f"Fold {fold+1}/{n_splits}")

    X_train_fold, X_val_fold = X_np[train_index], X_np[val_index]
    y_train_fold, y_val_fold = y_np[train_index], y_np[val_index]

    X_train_fold = torch.tensor(X_train_fold, dtype=torch.float32).to(device)
    X_val_fold = torch.tensor(X_val_fold, dtype=torch.float32).to(device)
    y_train_fold = torch.tensor(y_train_fold, dtype=torch.float32).unsqueeze(1).to(device)
    y_val_fold = torch.tensor(y_val_fold, dtype=torch.float32).unsqueeze(1).to(device)

    # Instantiate a new model for each fold with best hyperparameters

```

```

model_cv = LungCancerNN(X_train_fold.shape[1]).to(device)

criterion_cv = nn.BCELoss()
optimizer_cv = optim.RMSprop(model_cv.parameters(), lr=best_hyperparameters['learning_rate'])

# Train the model
epochs_cv = best_hyperparameters['epochs']
for epoch in range(epochs_cv):
    model_cv.train()
    optimizer_cv.zero_grad()
    outputs_cv = model_cv(X_train_fold)
    loss_cv = criterion_cv(outputs_cv, y_train_fold)
    loss_cv.backward()
    optimizer_cv.step()

# Evaluate the model
model_cv.eval()
with torch.no_grad():
    y_pred_cv = model_cv(X_val_fold)
    y_pred_class_cv = (y_pred_cv >= 0.5).float()
    accuracy_cv = (y_pred_class_cv == y_val_fold).float().mean()
    fold accuracies.append(accuracy_cv.item())
    print(f"Fold {fold+1} Accuracy: {accuracy_cv:.4f}")

average_accuracy = np.mean(fold accuracies)
print("\nCross-validation Accuracies:")
for i, acc in enumerate(fold accuracies):
    print(f"Fold {i+1}: {acc:.4f}")
print(f"\nAverage Cross-validation Accuracy: {average_accuracy:.4f}")

model.eval()
with torch.no_grad():
    # Move test data to the same device as the model
    X_test_device = X_test.to(device)
    y_test_device = y_test.to(device)

    y_pred = model(X_test_device)
    y_pred_class = (y_pred >= 0.5).float()
    accuracy = (y_pred_class == y_test_device).float().mean()
    print(f"Test Accuracy: {accuracy:.4f}")

# Instantiate the best model with the best hyperparameters and optimizer
best_model = LungCancerNN(X_train.shape[1]).to(device)

# Use the best optimizer and its parameters
best_optimizer_config = None
for config in optimizer_configs:
    if config['name'] == best_optimizer_name:
        best_optimizer_config = config
        break

if best_optimizer_config is None:
    print("Error: Best optimizer configuration not found.")
else:
    best_optimizer = best_optimizer_config['optimizer'](best_model.parameters(), **best_optimizer_config['params'])

best_criterion = nn.BCELoss()

best_epochs = best_hyperparameters['epochs']
print(f"Training the best model with Optimizer: {best_optimizer_config['name']}, Parameters: {best_optimizer_config['params']}, Epochs: {best_epochs}")

# Training loop for the best model
for epoch in range(best_epochs):
    best_model.train()
    X_train_device = X_train.to(device)
    y_train_device = y_train.to(device)

    best_optimizer.zero_grad()
    outputs = best_model(X_train_device)
    loss = best_criterion(outputs, y_train_device)
    loss.backward()
    best_optimizer.step()

    if (epoch+1) % 10 == 0:
        print(f"Epoch [{epoch+1}/{best_epochs}], Loss: {loss.item():.4f}")

# Evaluate the best model on the test set
best_model.eval()
with torch.no_grad():
    X_test_device = X_test.to(device)
    y_test_device = y_test.to(device)
    y_pred_best = best_model(X_test_device)
    y_pred_class_best = (y_pred_best >= 0.5).float()
    accuracy_best = (y_pred_class_best == y_test_device).float().mean()
    print(f"\nFinal Best Model Test Accuracy: {accuracy_best:.4f}")

best_model.eval()
with torch.no_grad():
    X_test_device = X_test.to(device)
    y_pred_prob = best_model(X_test_device)

y_pred_prob_cpu = y_pred_prob.cpu().numpy()

print("Predicted survival probabilities (first 10):")
print(y_pred_prob_cpu[:10])

from sklearn.metrics import precision_score, recall_score, f1_score, confusion_matrix
import seaborn as sns
import matplotlib.pyplot as plt

y_test_cpu = y_test_device.cpu().numpy()
y_pred_class_cpu = y_pred_class_best.cpu().numpy()

precision = precision_score(y_test_cpu, y_pred_class_cpu)
recall = recall_score(y_test_cpu, y_pred_class_cpu)
f1 = f1_score(y_test_cpu, y_pred_class_cpu)

print(f"Precision: {precision:.4f}")
print(f"Recall: {recall:.4f}")
print(f"F1-score: {f1:.4f}")

# Confusion Matrix
cm = confusion_matrix(y_test_cpu, y_pred_class_cpu)

plt.figure(figsize=(8, 6))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=['Not Survived', 'Survived'], yticklabels=['Not Survived', 'Survived'])
plt.xlabel('Predicted')
plt.ylabel('Actual')

```

```

plt.title('Confusion Matrix')
plt.show()

import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np

plt.figure(figsize=(8, 6))
sns.histplot(y_pred_prob_cpu, bins=50, kde=True)
plt.title('Distribution of Predicted Survival Probabilities')
plt.xlabel('Predicted Probability of Survival')
plt.ylabel('Frequency')
plt.show()

from sklearn.metrics import precision_score, recall_score, f1_score, confusion_matrix
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np

# Trying a lower classification threshold
threshold = 0.3
y_pred_class_lower_threshold = (y_pred_prob_cpu >= threshold).astype(int)

# Calculate metrics with the new threshold
precision_lower_threshold = precision_score(y_test_cpu, y_pred_class_lower_threshold)
recall_lower_threshold = recall_score(y_test_cpu, y_pred_class_lower_threshold)
f1_lower_threshold = f1_score(y_test_cpu, y_pred_class_lower_threshold)

print(f"Evaluation with threshold = {threshold}:")
print(f"Precision: {precision_lower_threshold:.4f}")
print(f"Recall: {recall_lower_threshold:.4f}")
print(f"F1-score: {f1_lower_threshold:.4f}")

# Confusion Matrix with the new threshold
cm_lower_threshold = confusion_matrix(y_test_cpu, y_pred_class_lower_threshold)

plt.figure(figsize=(8, 6))
sns.heatmap(cm_lower_threshold, annot=True, fmt='d', cmap='Blues', xticklabels=['Not Survived', 'Survived'], yticklabels=['Not Survived', 'Survived'])
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title(f'Confusion Matrix with Threshold = {threshold}')
plt.show()

survived_count = df['survived'].sum()
print(f"Number of people who survived in the dataset: {int(survived_count)}")

total_people = len(df)
not_survived_count = total_people - survived_count
print(f"Number of people who did not survive in the dataset: {int(not_survived_count)}")

import torch

model_save_path = '/content/drive/My Drive/best_lung_cancer_model.pth'

torch.save(best_model.state_dict(), model_save_path)

print(f"Best model saved to {model_save_path}")

"""## Summary of Fine-tuning Process and Model Performance

We have performed several steps to fine-tune the initial neural network model for predicting lung cancer survival and evaluated its performance.

1. Data Loading and Preprocessing: We loaded the dataset, explored its features, and preprocessed the data by dropping irrelevant columns, encoding categorical variables, and splitting the data into training and testing sets.

2. Initial Model Training and Evaluation: We built and trained a basic neural network model and obtained an initial test accuracy.

3. Fine-tuning: We performed fine-tuning by:
    * Experimenting with different hyperparameters (learning rate, epochs, dropout rate) to find a better configuration. The best hyperparameters found were `{'learning_rate': 0.001, 'epochs': 10, 'dropout_rate': 0.5}`.
    * Comparing different optimizers (Adam, SGD, RMSprop) and found that RMSprop performed best with the chosen learning rate.
    * Exploring L2 regularization, which did not significantly improve performance in this case.
    * Using 5-fold cross-validation to obtain a more robust estimate of the model's performance, with an average cross-validation accuracy of 0.7797.

4. Final Model Training and Evaluation: We trained the best performing model configuration on the training data and evaluated it on the test set.
    * Initially, using a default classification threshold of 0.5, the model predicted 'Not Survived' for all instances, resulting in 0.0000 for Precision, Recall, and F1-score.
    * We investigated the distribution of predicted survival probabilities, which showed a skew towards lower values.
    * By lowering the classification threshold to 0.3, the model is now able to predict both survival outcomes. The evaluation metrics with this threshold are:
        * Precision: 0.2212
        * Recall: 0.8426
        * F1-score: 0.3504
    * The confusion matrix with the 0.3 threshold shows the breakdown of true positives, true negatives, false positives, and false negatives, indicating the model's performance.

Conclusion:
The fine-tuning process helped identify a model configuration that achieves a test accuracy of approximately 77.89%. However, the initial evaluation metrics revealed a significant bias towards predicting 'Not Survived'. This analysis provides a foundation for understanding the model's performance. Depending on the application, further work could involve exploring techniques to improve the model's ability to predict survival outcomes more accurately.
"""

```