

## Lab Assignment 2: Data Preprocessing Pipeline

Aim: To implement a data preprocessing pipeline, including data cleaning, feature engineering, and basic classification, using the Heart Disease UCI dataset.

### Task 1: Load and Explore the Dataset

1. Load the Heart Disease UCI dataset using pandas.

```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
%matplotlib inline
import warnings
warnings.filterwarnings('ignore')
```

```
df = pd.read_csv('heart_disease_uci.csv')
df.head()
```

	id	age	sex	dataset	cp	trestbps	chol	fbs
0	1	63	Male	Cleveland	typical angina	145.0	233.0	True
1	2	67	Male	Cleveland	asymptomatic	160.0	286.0	False
2	3	67	Male	Cleveland	asymptomatic	120.0	229.0	False
3	4	37	Male	Cleveland	non-anginal	130.0	250.0	False
4	5	41	Female	Cleveland	atypical angina	130.0	204.0	False

	restecg	thalch	exang	oldpeak	slope	ca
0	lv hypertrophy	150.0	False	2.3	downsloping	0.0
1	lv hypertrophy	108.0	True	1.5	flat	3.0
2	lv hypertrophy	129.0	True	2.6	flat	2.0
3	normal	187.0	False	3.5	downsloping	0.0
4	lv hypertrophy	172.0	False	1.4	upsloping	0.0

	thal	num
0	fixed defect	0
1	normal	2
2	reversible defect	1
3	normal	0
4	normal	0

## 2. Display dataset characteristics:

– Number of records and features

```
df.shape  
  
(920, 16)
```

– Data types of columns

```
df.dtypes  
  
id          int64  
age         int64  
sex         object  
dataset     object  
cp          object  
trestbps    float64  
chol        float64  
fbs         object  
restecg     object  
thalch      float64  
exang       object  
oldpeak     float64  
slope       object  
ca          float64  
thal        object  
num         int64  
dtype: object
```

– Summary statistics (mean, median, standard deviation, etc.).

```
df.describe()  
  
      id      age  trestbps      chol      thalch  
oldpeak \  
count  920.000000  920.000000  861.000000  890.000000  865.000000  
858.000000  
mean   460.500000   53.510870  132.132404  199.130337  137.545665  
0.878788  
std    265.725422    9.424685   19.066070  110.780810   25.926276  
1.091226  
min     1.000000   28.000000    0.000000    0.000000   60.000000 -  
2.600000  
25%    230.750000   47.000000   120.000000   175.000000   120.000000  
0.000000  
50%    460.500000   54.000000   130.000000   223.000000   140.000000  
0.500000  
75%    690.250000   60.000000   140.000000   268.000000   157.000000  
1.500000  
max     920.000000   77.000000   200.000000   603.000000   202.000000  
6.200000
```

```
id      460.5
age      54.0
trestbps 130.0
chol     223.0
thalch    140.0
oldpeak    0.5
ca        0.0
num       1.0
dtype: float64
```

[illegible]

False

	thalch	exang	oldpeak	slope	ca	thal	num
0	False	False	False	False	False	False	False
1	False	False	False	False	False	False	False
2	False	False	False	False	False	False	False
3	False	False	False	False	False	False	False
4	False	False	False	False	False	False	False
...	...	...	...	...	...	...	...
915	False	False	False	True	True	True	False
916	True	True	True	True	True	True	False
917	False	False	False	True	True	False	False
918	True	True	True	True	True	True	False
919	False	False	False	True	True	True	False

[920 rows x 16 columns]

```
df.isnull().sum()
```

```
id          0
age         0
sex         0
dataset     0
cp          0
trestbps   59
chol       30
fbs       90
restecg     2
thalch     55
exang      55
oldpeak    62
slope     309
ca        611
thal     486
num        0
dtype: int64
```

```
df.duplicated().sum()
```

```
0
```

## Task 2: Data Cleaning

### 1. Handle missing values using:

Mean/median/mode imputation for numerical columns.

```
numeric = df.select_dtypes(include=['float64', 'int64']).columns
df[numeric] = df[numeric].fillna(df[numeric].median())
```

Most frequent category imputation for categorical columns.

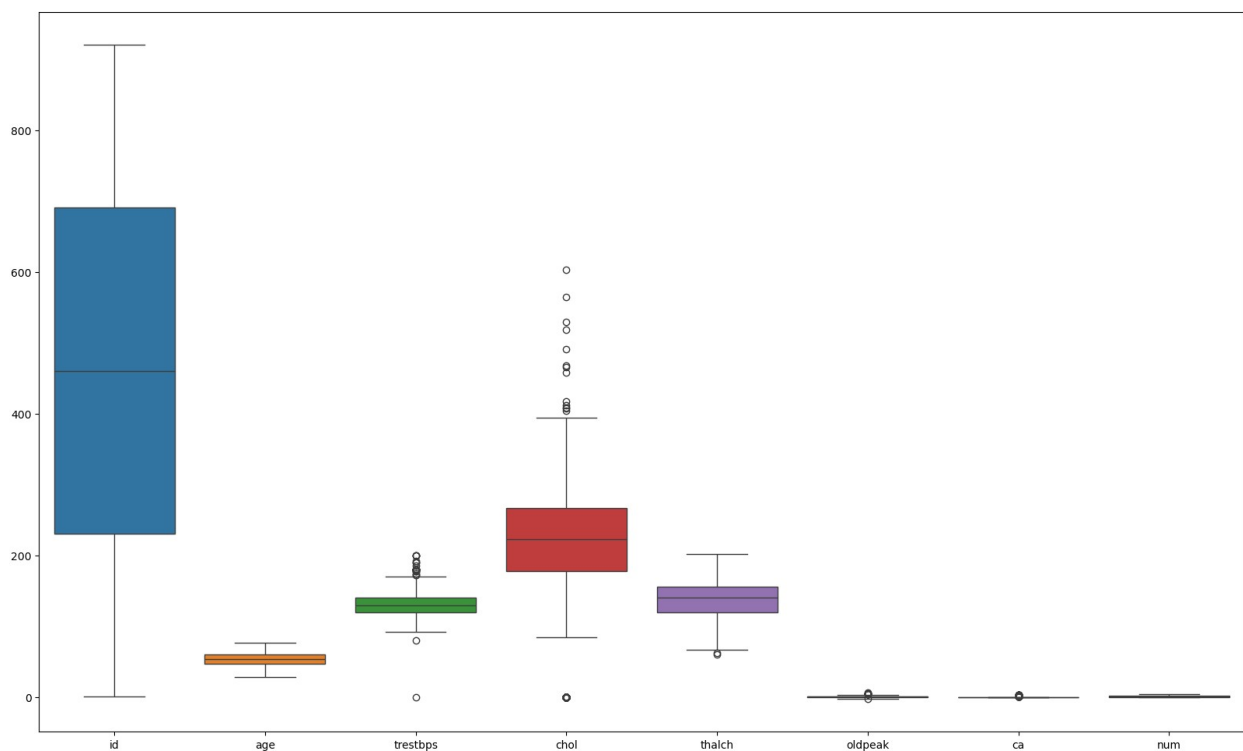
```
categoric = df.select_dtypes(include=['object']).columns
df[categoric] = df[categoric].fillna(df[categoric].mode())
```

```
df.isnull().sum()
```

### 3. Detect and handle outliers using:

– Box plots

```
num_columns = df.select_dtypes(include=['float64', 'int64']).columns
plt.figure(figsize = (20,12))
sns.boxplot(data=df[num_columns])
plt.show()
```



– Z-score method

```
from scipy.stats import zscore
z_scores = df[numeric].apply(zscore)

zero_outliers = df[(z_scores < 3).all(axis=1)]
df = zero_outliers

df_shape = df.shape
print('Data after removing outliers:',df_shape)

Data after removing outliers: (887, 16)
```

## Task 3: Feature Engineering

### 1. Convert categorical features into numerical format using:

– One-hot encoding

```
df = pd.get_dummies(df, columns=categoric, drop_first=True)
```

```
df.head()
```

	id	age	trestbps	chol	thalch	oldpeak	ca	num	sex_Male \
0	1	63	145.0	233.0	150.0	2.3	0.0	0	True
2	3	67	120.0	229.0	129.0	2.6	2.0	1	True
3	4	37	130.0	250.0	187.0	3.5	0.0	0	True
4	5	41	130.0	204.0	172.0	1.4	0.0	0	False
5	6	56	120.0	236.0	178.0	0.8	0.0	0	True

	dataset_Hungary ...	cp_non-anginal	cp_typical	angina
0	False ...	False	True	True
2	False ...	False	False	False
3	False ...	True	False	False
4	False ...	False	False	False
5	False ...	False	False	False

	restecg_normal	restecg_st-t	abnormality	exang_True	slope_flat \
0	False		False	False	False
2	False		False	True	True
3	True		False	False	False
4	False		False	False	False
5	True		False	False	False

	slope_upsloping	thal_normal	thal_reversable	defect
0	False	False		False
2	False	False		True
3	False	True		False
4	True	True		False
5	True	True		False

```
[5 rows x 23 columns]
```

– Label encoding

```
from sklearn.preprocessing import LabelEncoder  
categoric = df.select_dtypes(include=['object']).columns
```

```
label_encoder = LabelEncoder()
```

```

for col in categoric:
    if col in df.columns:
        df[col] = label_encoder.fit_transform(df[col])
    else:
        print(f"Column '{col}' not found in the dataset.")

```

## 2. Normalize numerical features using:

– Min-Max Scaling

```

from sklearn.preprocessing import MinMaxScaler

scaler = MinMaxScaler()
df[numeric] = scaler.fit_transform(df[numeric])

```

– Standardization

```

from sklearn.preprocessing import StandardScaler

scaler = StandardScaler()
df[numeric] = scaler.fit_transform(df[numeric])

```

## 3. Analyse feature importance using correlation analysis.

```

corr= df.corr()
corr

```

	id	age	trestbps	chol
thalch \				
id	1.000000	0.269867	0.052029	-0.367751
0.446318				
age	0.269867	1.000000	0.232077	-0.098067
0.361037				
trestbps	0.052029	0.232077	1.000000	0.102173
0.102014				
chol	-0.367751	-0.098067	0.102173	1.000000
0.231315				
thalch	-0.446318	-0.361037	-0.102014	0.231315
1.000000				
oldpeak	0.055014	0.231706	0.144652	0.026499
0.157453				
ca	-0.363204	0.208402	0.002857	0.127913
0.063583				
num	0.318765	0.332769	0.078398	-0.264661
0.359543				
sex_Male	0.287763	0.069513	0.008305	-0.203249
0.179379				
dataset_Hungary	-0.047275	-0.400148	0.032937	0.322291
0.036979				
dataset_Switzerland	0.286409	0.077934	-0.051838	-0.729107
0.249525				

dataset_VA Long Beach	0.716469	0.342518	0.032815	-0.087155	-
0.225492					
cp_atypical angina	-0.167262	-0.217299	-0.052948	0.162080	
0.247820					
cp_non-anginal	-0.096052	-0.011819	-0.030240	0.000786	
0.142558					
cp_typical angina	-0.068768	0.033895	0.042978	0.018260	
0.100555					
fbs_True	0.160651	0.227493	0.148356	0.076576	-
0.028136					
restecg_normal	-0.042409	-0.215523	-0.096619	-0.024756	
0.015796					
restecg_st-t abnormality	0.391885	0.147810	0.090487	-0.127878	-
0.135210					
exang_True	0.169577	0.162084	0.150267	-0.038586	-
0.364215					
slope_flat	-0.039195	0.111591	0.064928	-0.039741	-
0.240757					
slope_upsloping	-0.333088	-0.010953	-0.051488	-0.004160	
0.304255					
thal_normal	-0.481388	-0.031038	-0.041228	0.125905	
0.295141					
thal_reversable defect	-0.169329	0.124124	0.070475	-0.109566	-
0.104733					

	oldpeak	ca	num	sex_Male	\
id	0.055014	-0.363204	0.318765	0.287763	
age	0.231706	0.208402	0.332769	0.069513	
trestbps	0.144652	0.002857	0.078398	0.008305	
chol	0.026499	0.127913	-0.264661	-0.203249	
thalch	-0.157453	0.063583	-0.359543	-0.179379	
oldpeak	1.000000	0.173369	0.406139	0.116991	
ca	0.173369	1.000000	0.204365	-0.047612	
num	0.406139	0.204365	1.000000	0.288093	
sex_Male	0.116991	-0.047612	0.288093	1.000000	
dataset_Hungary	-0.168533	-0.239184	-0.375735	-0.119723	
dataset_Switzerland	-0.065446	-0.082028	0.295718	0.132948	
dataset_VA Long Beach	0.147164	-0.185516	0.266000	0.238220	
cp_atypical angina	-0.242570	-0.090715	-0.345873	-0.174806	
cp_non-anginal	-0.110003	-0.036527	-0.152485	-0.069607	
cp_typical angina	0.028843	0.060215	-0.046499	-0.006461	
fbs_True	0.038580	0.037424	0.127674	0.081332	
restecg_normal	-0.080490	-0.114772	-0.151280	-0.019056	
restecg_st-t abnormality	0.028249	-0.153849	0.143632	0.063101	
exang_True	0.422426	0.053196	0.357586	0.155638	
slope_flat	0.402720	0.133087	0.245719	0.028297	
slope_upsloping	-0.098867	0.156733	-0.140298	-0.102855	
thal_normal	-0.112379	0.150625	-0.232888	-0.300040	
thal_reversable defect	0.124522	0.238635	0.268577	0.145117	



	dataset_Hungary	...	cp_non-anginal	\
id	-0.047275	...	-0.096052	
age	-0.400148	...	-0.011819	
trestbps	0.032937	...	-0.030240	
chol	0.322291	...	0.000786	
thalch	0.036979	...	0.142558	
oldpeak	-0.168533	...	-0.110003	
ca	-0.239184	...	-0.036527	
num	-0.375735	...	-0.152485	
sex_Male	-0.119723	...	-0.069607	
dataset_Hungary	1.000000	...	-0.057715	
dataset_Switzerland	-0.275589	...	-0.085929	
dataset_VA Long Beach	-0.372920	...	0.018223	
cp_atypical angina	0.295872	...	-0.261126	
cp_non-anginal	-0.057715	...	1.000000	
cp_typical angina	-0.039617	...	-0.123526	
fbs_True	-0.158002	...	0.008646	
restecg_normal	0.276094	...	0.007164	
restecg_st-t abnormality	-0.037100	...	-0.041412	
exang_True	-0.094440	...	-0.178894	
slope_flat	-0.090696	...	-0.099093	
slope_upsloping	-0.300994	...	0.079916	
thal_normal	-0.318365	...	0.180820	
thal_reversable defect	-0.277215	...	-0.074065	
	cp_typical angina	fbs_True	restecg_normal	\
id	-0.068768	0.160651	-0.042409	
age	0.033895	0.227493	-0.215523	
trestbps	0.042978	0.148356	-0.096619	
chol	0.018260	0.076576	-0.024756	
thalch	0.100555	-0.028136	0.015796	
oldpeak	0.028843	0.038580	-0.080490	
ca	0.060215	0.037424	-0.114772	
num	-0.046499	0.127674	-0.151280	
sex_Male	-0.006461	0.081332	-0.019056	
dataset_Hungary	-0.039617	-0.158002	0.276094	
dataset_Switzerland	-0.032011	-0.118266	0.070449	

dataset_VA Long Beach	-0.025810	0.289114	-0.226524
cp_atypical angina	-0.112977	-0.057066	0.105877
cp_non-anginal	-0.123526	0.008646	0.007164
cp_typical angina	1.000000	0.049457	-0.066759
fbs_True	0.049457	1.000000	-0.169721
restecg_normal	-0.066759	-0.169721	1.000000
restecg_st-t abnormality	-0.011967	0.137522	-0.619193
exang_True	-0.121568	-0.008873	-0.034914
slope_flat	-0.006279	-0.012723	-0.003383
slope_upsloping	0.024789	-0.068045	-0.026165
thal_normal	0.068662	-0.058917	-0.052210
thal_reversable defect	-0.024247	0.026848	-0.030992
	restecg_st-t abnormality	exang_True	
slope_flat \			
id	0.391885	0.169577	-
0.039195			
age	0.147810	0.162084	
0.111591			
trestbps	0.090487	0.150267	
0.064928			
chol	-0.127878	-0.038586	-
0.039741			
thalch	-0.135210	-0.364215	-
0.240757			
oldpeak	0.028249	0.422426	
0.402720			
ca	-0.153849	0.053196	
0.133087			
num	0.143632	0.357586	
0.245719			
sex_Male	0.063101	0.155638	
0.028297			
dataset_Hungary	-0.037100	-0.094440	-
0.090696			
dataset_Switzerland	0.041107	0.061012	
0.104798			
dataset_VA Long Beach	0.362643	0.120947	-

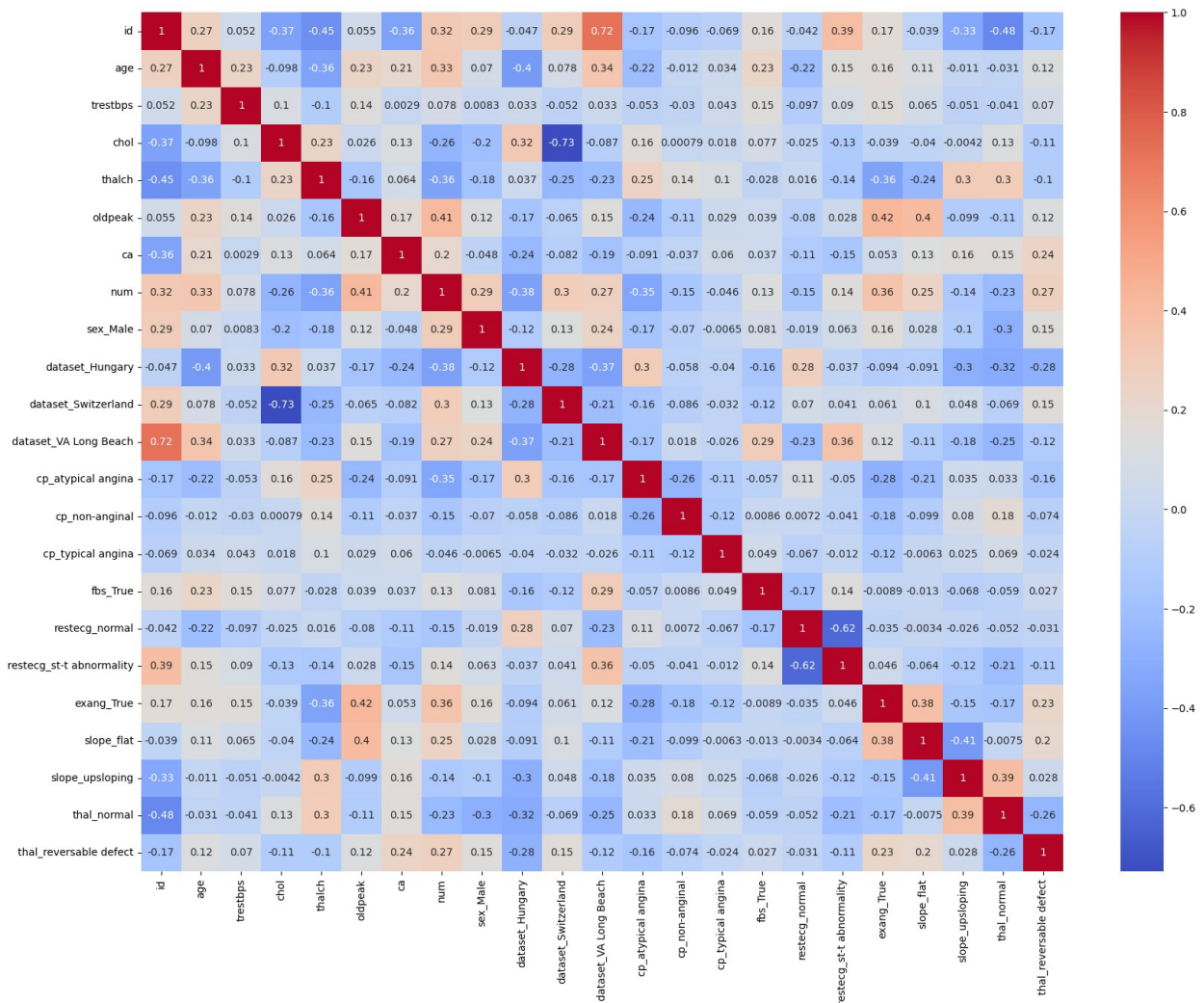
0.114072			
cp_atypical angina	-0.049661	-0.280743	-
0.213498			
cp_non-anginal	-0.041412	-0.178894	-
0.099093			
cp_typical angina	-0.011967	-0.121568	-
0.006279			
fbs_True	0.137522	-0.008873	-
0.012723			
restecg_normal	-0.619193	-0.034914	-
0.003383			
restecg_st-t abnormality	1.000000	0.046468	-
0.063775			
exang_True	0.046468	1.000000	
0.378427			
slope_flat	-0.063775	0.378427	
1.000000			
slope_upsloping	-0.116223	-0.145074	-
0.408309			
thal_normal	-0.209606	-0.168888	-
0.007478			
thal_reversable defect	-0.111694	0.225334	
0.202500			

	slope_upsloping	thal_normal	
thal_reversable defect			
id	-0.333088	-0.481388	-
0.169329			
age	-0.010953	-0.031038	
0.124124			
trestbps	-0.051488	-0.041228	
0.070475			
chol	-0.004160	0.125905	-
0.109566			
thalch	0.304255	0.295141	-
0.104733			
oldpeak	-0.098867	-0.112379	
0.124522			
ca	0.156733	0.150625	
0.238635			
num	-0.140298	-0.232888	
0.268577			
sex_Male	-0.102855	-0.300040	
0.145117			
dataset_Hungary	-0.300994	-0.318365	-
0.277215			
dataset_Switzerland	0.048412	-0.069489	
0.149621			
dataset_VA Long Beach	-0.183338	-0.252464	-

0.117226			
cp_atypical angina	0.034525	0.033261	-
0.156105			
cp_non-anginal	0.079916	0.180820	-
0.074065			
cp_typical angina	0.024789	0.068662	-
0.024247			
fbs_True	-0.068045	-0.058917	
0.026848			
restecg_normal	-0.026165	-0.052210	-
0.030992			
restecg_st-t abnormality	-0.116223	-0.209606	-
0.111694			
exang_True	-0.145074	-0.168888	
0.225334			
slope_flat	-0.408309	-0.007478	
0.202500			
slope_upsloping	1.000000	0.386556	
0.028169			
thal_normal	0.386556	1.000000	-
0.257110			
thal_reversable defect	0.028169	-0.257110	
1.000000			

[23 rows x 23 columns]

```
plt.figure(figsize=(20, 15))
sns.heatmap(corr, annot=True, cmap="coolwarm")
plt.show()
```



## Task 4: Basic Classification using k-Nearest Neighbors (kNN)

1. Split the dataset into training (80%) and testing (20%) sets.

```
from sklearn.model_selection import train_test_split

X = df.drop('num',axis=1)
y = df['num']

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

y_train = y_train.astype(int)
y_test = y_test.astype(int)

print("Unique values in y_train:", y_train.unique())

Unique values in y_train: [1 0 2]
```

2. Train a k-Nearest Neighbors (kNN) classifier using Scikit-learn.

```
from sklearn.neighbors import KNeighborsClassifier

KNN = KNeighborsClassifier(n_neighbors=5)
KNN.fit(X_train, y_train)

KNeighborsClassifier()
```

3. Evaluate the model's performance using:

```
from sklearn.metrics import accuracy_score, classification_report,
confusion_matrix
y_pred = KNN.predict(X_test)
accuracy = accuracy_score(y_test, y_pred)
print(accuracy)
```

0.8595505617977528

```
cr = classification_report(y_test, y_pred)
print(cr)
```

	precision	recall	f1-score	support
0	0.88	0.97	0.92	155
1	0.33	0.10	0.15	20
2	0.00	0.00	0.00	3
accuracy			0.86	178
macro avg	0.40	0.36	0.36	178
weighted avg	0.80	0.86	0.82	178

```
cm = confusion_matrix(y_test, y_pred)
print(cm)
```

```
[[151  4  0]
 [ 18  2  0]
 [  3  0  0]]
```