Create a New Repository from jo | kidney dieases - Colaboratory

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kidney dieases

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Files

..
sample_data
kidney_disease.csv

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```
for i in catcols:
    print("Columns :",i)
    print(c(data[i]))
    print('*'*120+'\n')
```

```
Columns : dm
Counter({'no': 258, 'yes': 134, '\tno': 3, '\tyes': 2, nan: 2, ' yes': 1})
************************************************************************************************************************

Columns : rc
Counter({nan: 130, '5.2': 18, '4.5': 16, '4.9': 14, '4.7': 11, '3.9': 10,
************************************************************************************************************************

Columns : pe
Counter({'no': 323, 'yes': 76, nan: 1})
************************************************************************************************************************

Columns : rbc
Counter({'normal': 201, nan: 152, 'abnormal': 47})
************************************************************************************************************************

Columns : htn
Counter({'no': 251, 'yes': 147, nan: 2})
************************************************************************************************************************

Columns : cad
Counter({'no': 362, 'yes': 34, '\tno': 2, nan: 2})
```

kidney_disease.csv

1 to 10 of 400 entries Filter

id	age	bp	sg	al	su	rbc	pc	
0	48.0	80.0	1.02	1.0	0.0		normal	not
1	7.0	50.0	1.02	4.0	0.0		normal	not
2	62.0	80.0	1.01	2.0	3.0	normal	normal	not
3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	pre
4	51.0	80.0	1.01	2.0	0.0	normal	normal	not
5	60.0	90.0	1.015	3.0	0.0			not
6	68.0	70.0	1.01	0.0	0.0		normal	not
7	24.0		1.015	2.0	4.0	normal	abnormal	not
8	52.0	100.0	1.015	3.0	0.0	normal	abnormal	pre
9	53.0	90.0	1.02	2.0	0.0	abnormal	abnormal	pre

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kidney diseases

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sample_data

kidney_disease.csv

```
import pandas as pd
import numpy as np
from collections import Counter as c
import matplotlib.pyplot as plt
import seaborn as sns
import missingno as msno
from sklearn.metrics import accuracy_score, confusion_matrix
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
from sklearn.linear_model import LogisticRegression
import pickle
```

```
data=pd.read_csv("\content\kidney_disease.csv")#loading the csv data
data.head()#return you the first 5 rows values
```

	id	age	bp	sg	al	su	rbc	pc	pcc	ba	...
0	0	48.0	80.0	1.020	1.0	0.0	NaN	normal	notpresent	notpresent	..
1	1	7.0	50.0	1.020	4.0	0.0	NaN	normal	notpresent	notpresent	..
2	2	62.0	80.0	1.010	2.0	3.0	normal	normal	notpresent	notpresent	..
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	present	notpresent	..
4	4	51.0	80.0	1.010	2.0	0.0	normal	normal	notpresent	notpresent	..

kidney_disease.csv

1 to 10 of 400 entries Filter

	id	age	bp	sg	al	su	rbc	pc	
0	0	48.0	80.0	1.02	1.0	0.0		normal	not
1	1	7.0	50.0	1.02	4.0	0.0		normal	not
2	2	62.0	80.0	1.01	2.0	3.0	normal	normal	not
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	pre
4	4	51.0	80.0	1.01	2.0	0.0	normal	normal	not
5	5	60.0	90.0	1.015	3.0	0.0			not
6	6	68.0	70.0	1.01	0.0	0.0		normal	not
7	7	24.0		1.015	2.0	4.0	normal	abnormal	not
8	8	52.0	100.0	1.015	3.0	0.0	normal	abnormal	pre
9	9	53.0	90.0	1.02	2.0	0.0	abnormal	abnormal	pre

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Files

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kidney_disease.csv

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```
data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 26 columns):
 #   Column          Non-Null Count  Dtype  
---  ------          --------------  -----  
 0   id              400 non-null    int64  
 1   age             391 non-null    float64
 2   bp              388 non-null    float64
 3   sg              353 non-null    float64
 4   al              354 non-null    float64
 5   su              351 non-null    float64
 6   rbc             248 non-null    object 
 7   pc              335 non-null    object 
 8   pcc             396 non-null    object 
 9   ba              396 non-null    object 
 10  bgr             356 non-null    float64
 11  bu              381 non-null    float64
 12  sc              383 non-null    float64
 13  sod             313 non-null    float64
 14  pot             312 non-null    float64
 15  hemo            348 non-null    float64
 16  pcv             330 non-null    object 
 17  wc              295 non-null    object 
 18  rc              270 non-null    object 
 19  htn             398 non-null    object 
```

kidney_disease.csv

1 to 10 of 400 entries Filter

id	age	bp	sg	al	su	rbc	pc	
0	48.0	80.0	1.02	1.0	0.0		normal	not
1	7.0	50.0	1.02	4.0	0.0		normal	not
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6	68.0	70.0	1.01	0.0	0.0		normal	not
7	24.0		1.015	2.0	4.0	normal	abnormal	not
8	52.0	100.0	1.015	3.0	0.0	normal	abnormal	pre
9	53.0	90.0	1.02	2.0	0.0	abnormal	abnormal	pre

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Files

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sample_data
kidney_disease.csv

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```
contcols.add('specific_gravity')
contcols.add('albumin')
contcols.add('sugar')
print(catcols)
```

```
data['coronary_artery_disease']=data.cornary_artery_diease.replace('\tno',
c(data['cornary_artery_disease'])
```

```
data['diabetesmellitus']=data.diabetesmellitus.replace{'\tno':'no','\types
c(data['diabetesmellitus'])
```

```
  File "<ipython-input-6-aa1607572f48>", line 1

data['diabetesmellitus']=data.diabetesmellitus.replace{'\tno':'no','\types
                                                       ^
SyntaxError: invalid syntax
```

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```
data.describe()
```

kidney_disease.csv

1 to 10 of 400 entries Filter

id	age	bp	sg	al	su	rbc	pc	
0	48.0	80.0	1.02	1.0	0.0		normal	not
1	7.0	50.0	1.02	4.0	0.0		normal	not
2	62.0	80.0	1.01	2.0	3.0	normal	normal	not
3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	pre
4	51.0	80.0	1.01	2.0	0.0	normal	normal	not
5	60.0	90.0	1.015	3.0	0.0			not
6	68.0	70.0	1.01	0.0	0.0		normal	not
7	24.0		1.015	2.0	4.0	normal	abnormal	not
8	52.0	100.0	1.015	3.0	0.0	normal	abnormal	pre
9	53.0	90.0	1.02	2.0	0.0	abnormal	abnormal	pre

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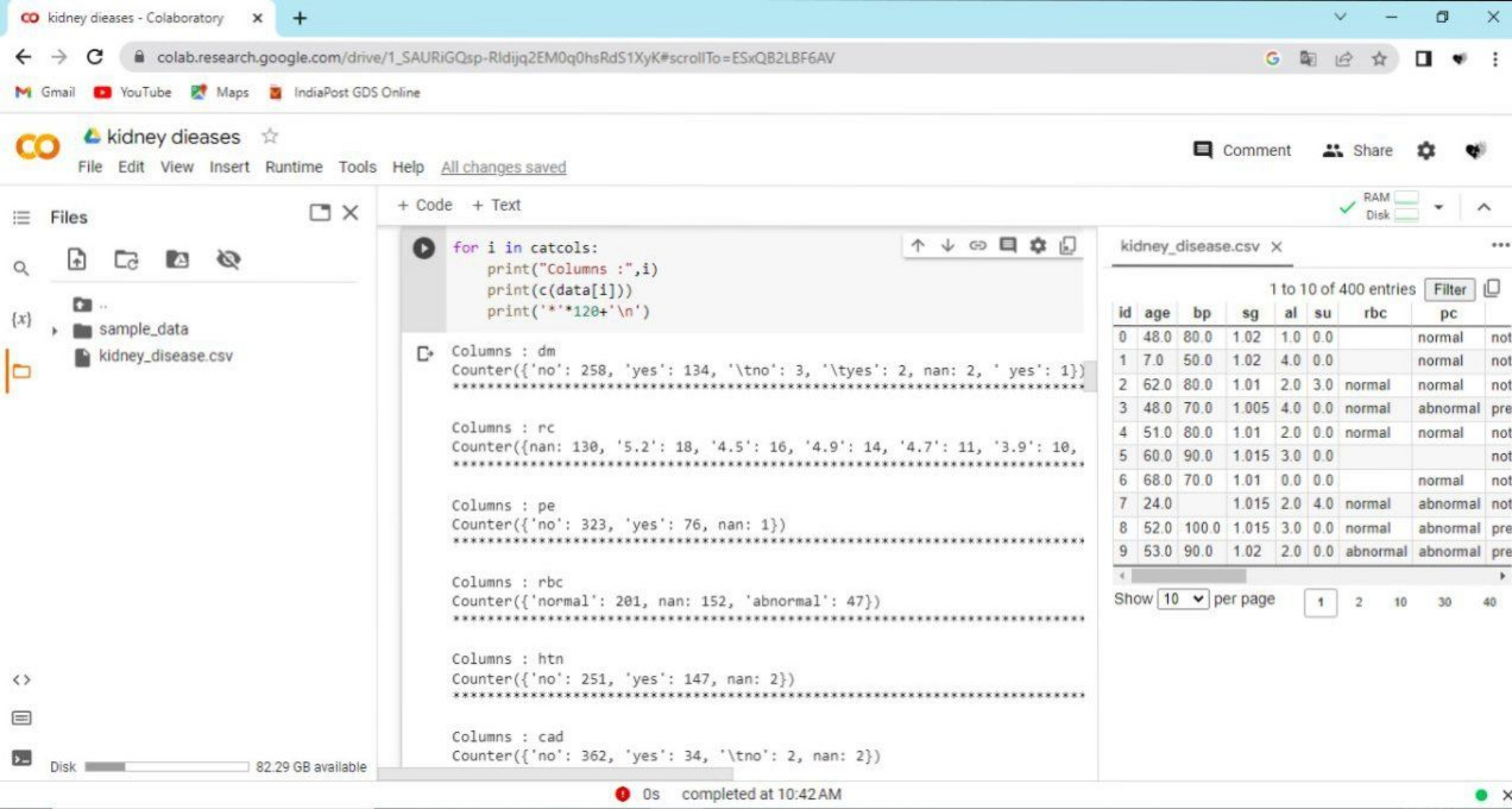
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kidney dieases
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RAM
Disk
for i in catcols:
print("Columns :",i)
print(c(data[i]))
print('*'*120+'\n')
Columns : dm
Counter({'no': 258, 'yes': 134, '\tno': 3, '\tyes': 2, nan: 2, ' yes': 1})
Columns : rc
Counter({nan: 130, '5.2': 18, '4.5': 16, '4.9': 14, '4.7': 11, '3.9': 10,
Columns : pe
Counter({'no': 323, 'yes': 76, nan: 1})
Columns : rbc
Counter({'normal': 201, nan: 152, 'abnormal': 47})
Columns : htn
Counter({'no': 251, 'yes': 147, nan: 2})
Columns : cad
Counter({'no': 362, 'yes': 34, '\tno': 2, nan: 2})
sample_data
kidney_disease.csv
Disk 82.29 GB available
kidney_disease.csv
1 to 10 of 400 entries Filter
id age bp sg al su rbc pc
0 48.0 80.0 1.02 1.0 0.0 normal not
1 7.0 50.0 1.02 4.0 0.0 normal not
2 62.0 80.0 1.01 2.0 3.0 normal normal not
3 48.0 70.0 1.005 4.0 0.0 normal abnormal pre
4 51.0 80.0 1.01 2.0 0.0 normal normal not
5 60.0 90.0 1.015 3.0 0.0 not
6 68.0 70.0 1.01 0.0 0.0 normal not
7 24.0 1.015 2.0 4.0 normal abnormal not
8 52.0 100.0 1.015 3.0 0.0 normal abnormal pre
9 53.0 90.0 1.02 2.0 0.0 abnormal abnormal pre
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```
for i in contcols:
    print("Continous Columns :",i)
    print(c(data[i]))
    print('*'*120+'\n')
```

```
Continous Columns : dm
Counter({'no': 258, 'yes': 134, '\tno': 3, '\tyes': 2, nan: 2, ' yes': 1})
************************************************************************************************************************

Continous Columns : rc
Counter({nan: 130, '5.2': 18, '4.5': 16, '4.9': 14, '4.7': 11, '3.9': 10,
************************************************************************************************************************

Continous Columns : rbc
Counter({'normal': 201, nan: 152, 'abnormal': 47})
************************************************************************************************************************

Continous Columns : bu
Counter({46.0: 15, 25.0: 13, 19.0: 11, 40.0: 10, 18.0: 9, 50.0: 9, 15.0: 9
************************************************************************************************************************

Continous Columns : pcc
Counter({'notpresent': 354, 'present': 42, nan: 4})
************************************************************************************************************************

Continous Columns : sc
```

kidney_disease.csv

1 to 10 of 400 entries Filter

id	age	bp	sg	al	su	rbc	pc	
0	48.0	80.0	1.02	1.0	0.0		normal	not
1	7.0	50.0	1.02	4.0	0.0		normal	not
2	62.0	80.0	1.01	2.0	3.0	normal	normal	not
3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	pre
4	51.0	80.0	1.01	2.0	0.0	normal	normal	not
5	60.0	90.0	1.015	3.0	0.0			not
6	68.0	70.0	1.01	0.0	0.0		normal	not
7	24.0		1.015	2.0	4.0	normal	abnormal	not
8	52.0	100.0	1.015	3.0	0.0	normal	abnormal	pre
9	53.0	90.0	1.02	2.0	0.0	abnormal	abnormal	pre

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	id	age	bp	sg		
count	400.000000	391.000000	388.000000	353.000000	354.000000	351.00000
mean	199.500000	51.483376	76.469072	1.017408	1.016949	0.45014
std	115.614301	17.169714	13.683637	0.005717	1.352679	1.09919
min	0.000000	2.000000	50.000000	1.005000	0.000000	0.00000
25%	99.750000	42.000000	70.000000	1.010000	0.000000	0.00000
50%	199.500000	55.000000	80.000000	1.020000	0.000000	0.00000
75%	299.250000	64.500000	80.000000	1.020000	2.000000	0.00000
max	399.000000	90.000000	180.000000	1.025000	5.000000	5.00000

kidney_disease.csv

1 to 10 of 400 entries Filter

	id	age	bp	sg	al	su	rbc	pc	
0	0	48.0	80.0	1.02	1.0	0.0		normal	not
1	1	7.0	50.0	1.02	4.0	0.0		normal	not
2	2	62.0	80.0	1.01	2.0	3.0	normal	normal	not
3	3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	pre
4	4	51.0	80.0	1.01	2.0	0.0	normal	normal	not
5	5	60.0	90.0	1.015	3.0	0.0			not
6	6	68.0	70.0	1.01	0.0	0.0		normal	not
7	7	24.0		1.015	2.0	4.0	normal	abnormal	not
8	8	52.0	100.0	1.015	3.0	0.0	normal	abnormal	pre
9	9	53.0	90.0	1.02	2.0	0.0	abnormal	abnormal	pre

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```
[ ] sns.displot(data.age)

[ ] import matplotlib.pyplot as plt
    fig=plt.figure(figsize=(5,5))
    plt.scatter(data['age'],data['blood pressure'],color='blue')
```

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sample_data
kidney_disease.csv

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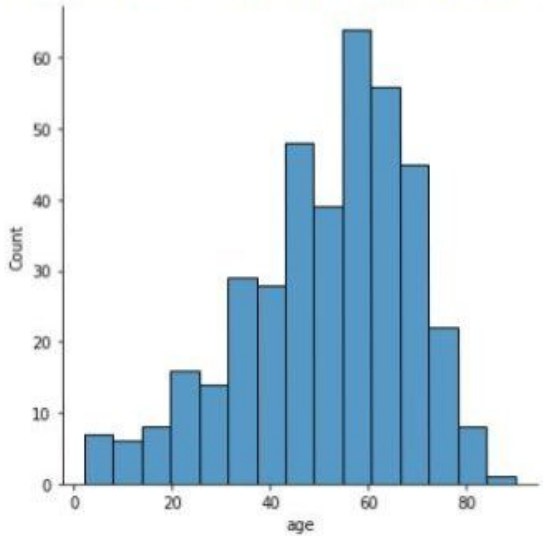
```
sns.displot(data.age)
```

```
<seaborn.axisgrid.FacetGrid at 0x7fa81d9477f0>
```



kidney_disease.csv

1 to 10 of 400 entries Filter

id	age	bp	sg	al	su	rbc	pc	
0	48.0	80.0	1.02	1.0	0.0		normal	not
1	7.0	50.0	1.02	4.0	0.0		normal	not
2	62.0	80.0	1.01	2.0	3.0	normal	normal	not
3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	pre
4	51.0	80.0	1.01	2.0	0.0	normal	normal	not
5	60.0	90.0	1.015	3.0	0.0			not
6	68.0	70.0	1.01	0.0	0.0		normal	not
7	24.0		1.015	2.0	4.0	normal	abnormal	not
8	52.0	100.0	1.015	3.0	0.0	normal	abnormal	pre
9	53.0	90.0	1.02	2.0	0.0	abnormal	abnormal	pre

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