EARLY PREDICTION FOR CHRONIC KIDNEY DISEASE DETECTION: A PROGRESSIVE APPROACH TO HEALTH MANAGEMENT

1.INTRODUCTION

OVERVIEW:

DESCRIPTION

Chronic Kidney Disease (CKD) is a major medical problem and can be cured if treated in the early stages. Usually , people are not aware that medical tests we take for different purposes could contain valuable information concerning kidney diseases. Consequently, attributes of various medical tests are investigated to distinguish which attributes may contain helpful information about the disease. The information says that it helps us to measure the severity of the problem, the predicted survival of

the patient after the illness, the pattern of the disease ad work for curing the disease.

In todays world as we know most of the people are facing so many disease and as this can be cured if we treat people in early stages this project can use a pretrained model to predict the Chronic kidney Disease which can help in treatments of peoples who are suffer from this disease.

CKD is a condition in which the kidneys are damaged and cannot filter blood as well as they should. Because of this, excess fluid and waste from blood remain in the body and may cause other health problems, such as heart disease and stroke.

Project flow:

- User interacts with the UI to enter the input.
- Entered input is analysed by the model which is integrated.
- Once model analyses the input the prediction is showcased on the UI

To accomplish this, we have to complete all the activities listed below,

- Define Problem/Problem Understanding
- Data collection & Preparation
- Exploratory Data Analysis
- Model Building
- Performance Testing & Evaluate this results
- Model Deployment
- Project Demonstration & Documentation

PURPOSE

Your kidneys remove wastes and extra fluid from your body. Your kidneys also remove acid that is produced by the cells of your body and maintain a healthy balance of water, salts, and minerals—such as sodium, calcium, phosphorus, and potassium—in your blood.

Without this balance, nerves, muscles, and other tissues in your body may not work normally.

Your kidneys also make hormones that help

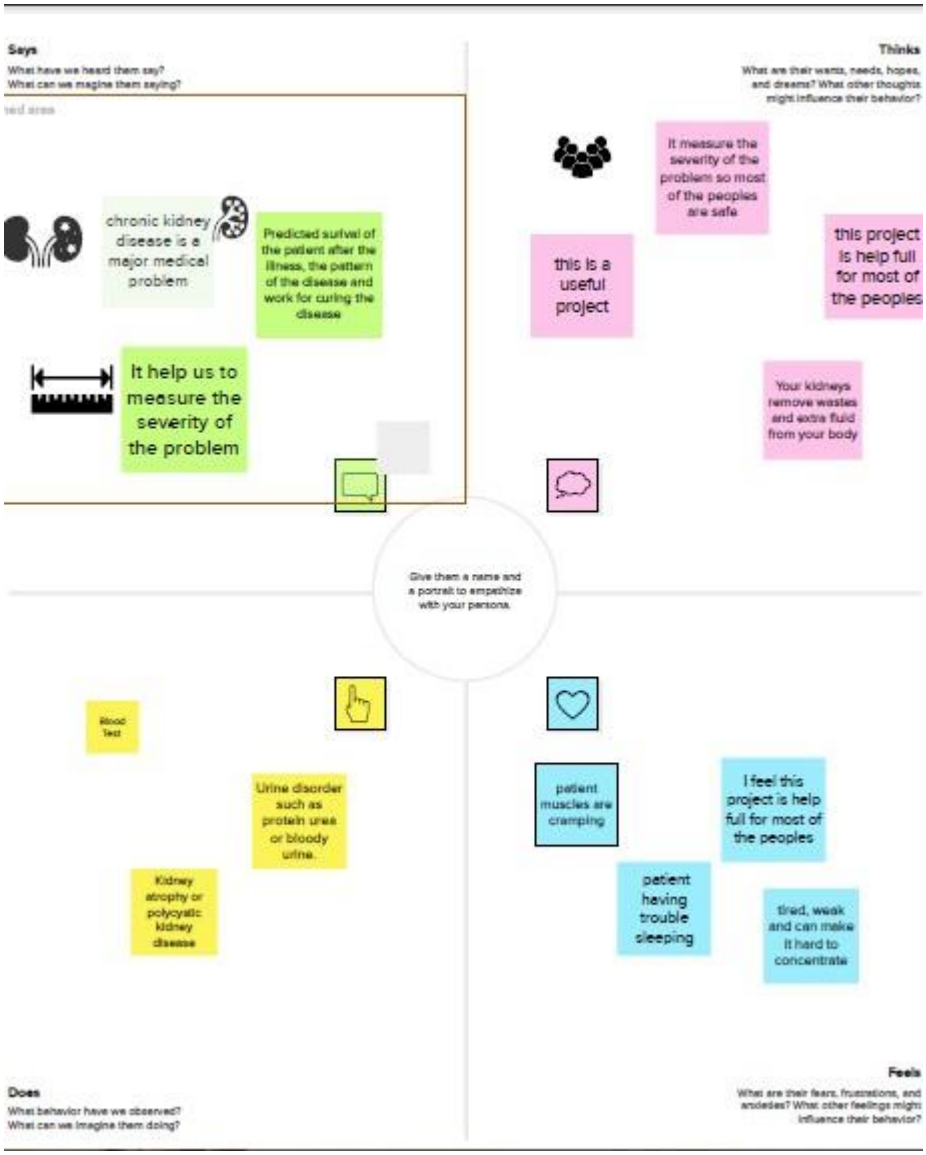
- Control your blood pressure
- Make red blood cells
- Keep your bone strong and healthy

ACHIVEMENT

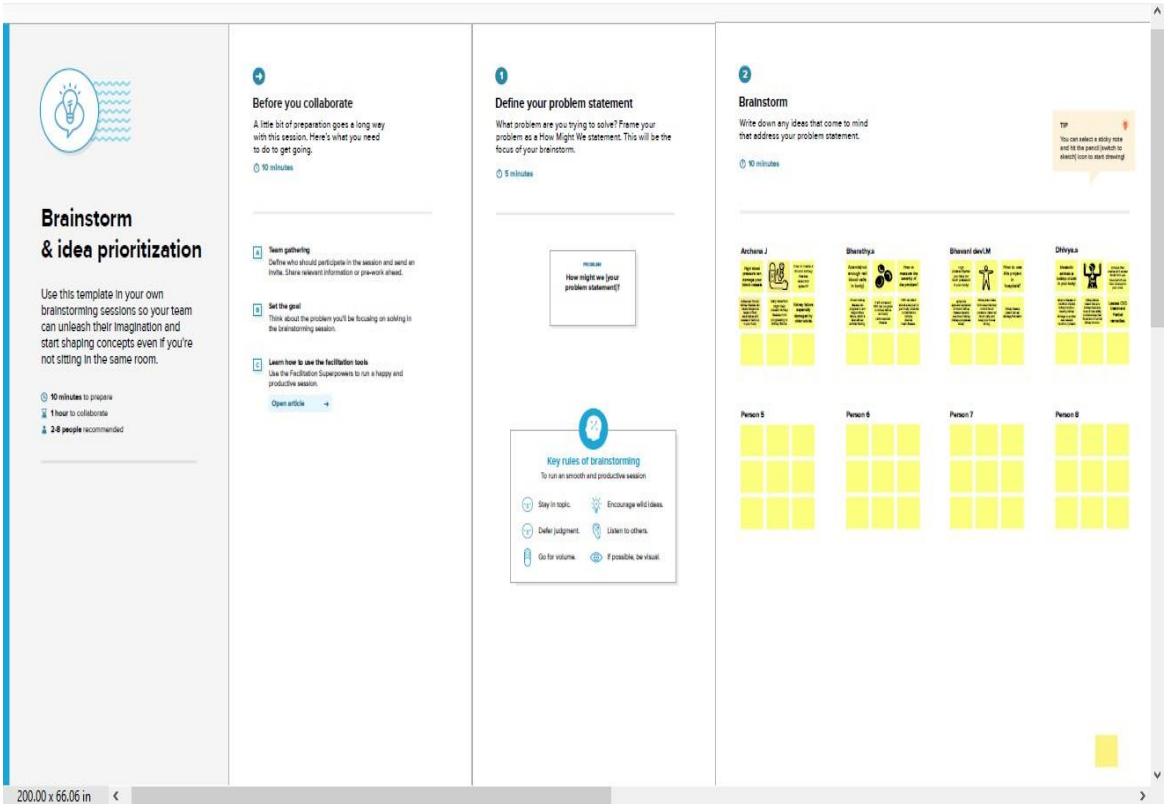
- The main of treatment is to prevent progression of CKD to complete kidney failure.
- The best way to do this is to diagnose CKD early and control the underlying cause.
- The symptoms, evaluation and management of CKD will be reviewed here.
- Kidney transplantation, peritoneal dialysis and hemodialysis are discussed separately.

2.PROBLEM DEFINITION & DESIGN THINKING

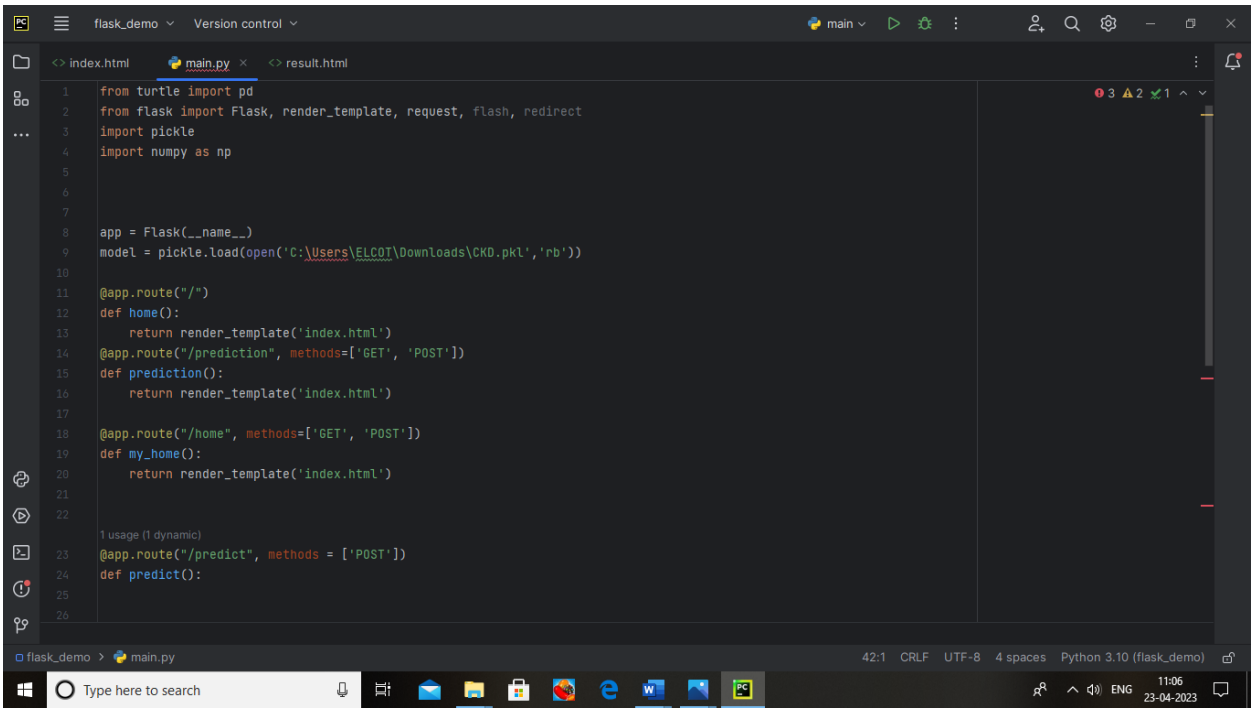
1. Empathy Map

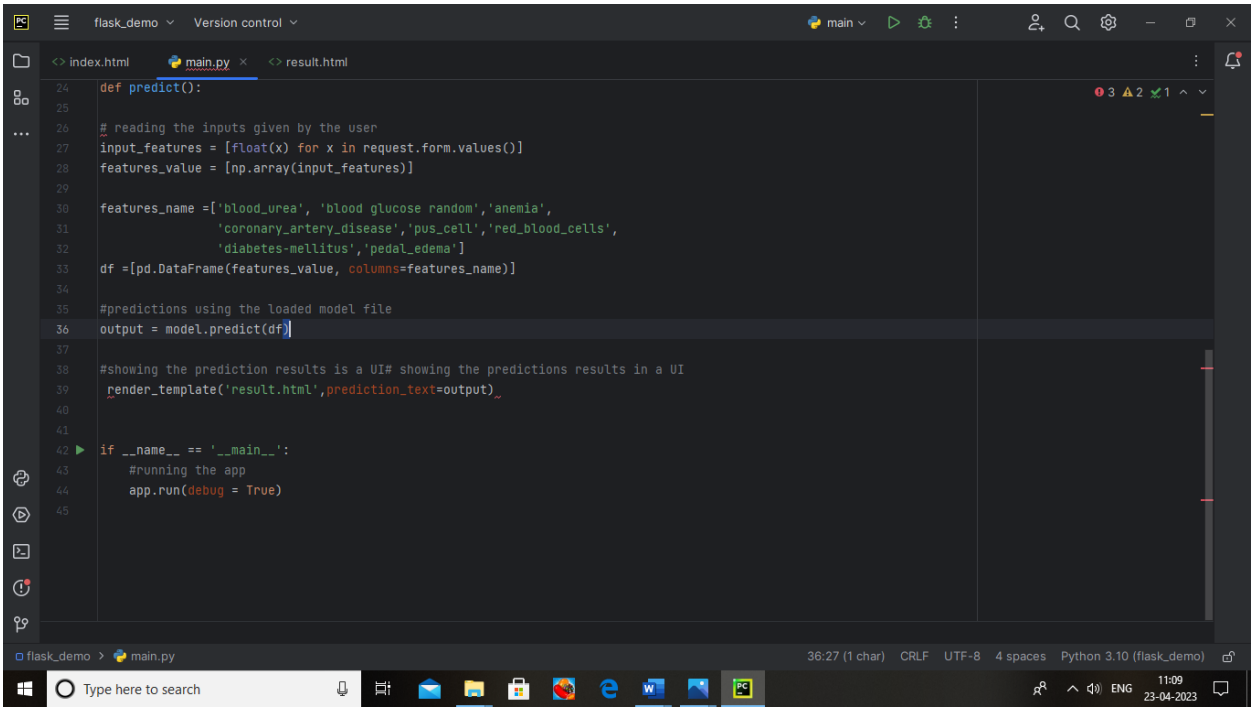


2. Ideation & Brainstorming Map

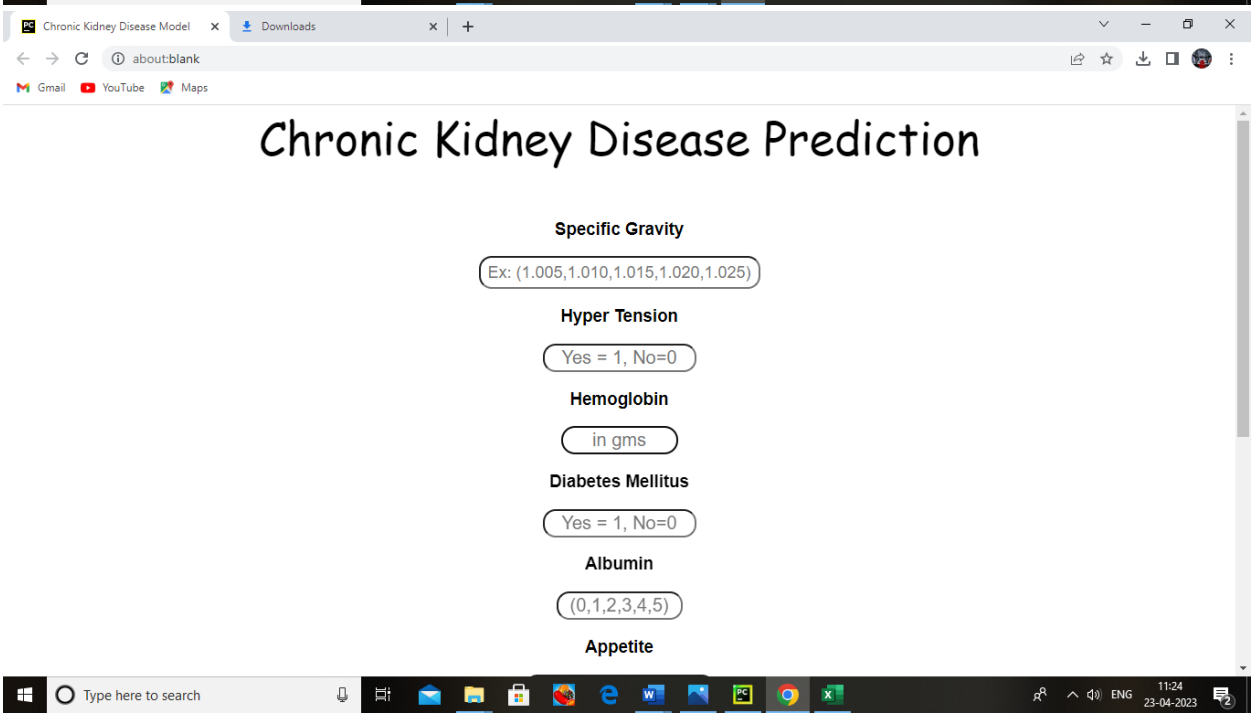


3.RESULT:





```
def predict():

# reading the inputs given by the user
input_features = [float(x) for x in request.form.values()]
features_value = [np.array(input_features)]

features_name =['blood_urea', 'blood glucose random','anemia',
                'coronary_artery_disease','pus_cell','red_blood_cells',
                'diabetes-mellitus','pedal_edema']
df =[pd.DataFrame(features_value, columns=features_name)]

#predictions using the loaded model file
output = model.predict(df)

#showing the prediction results is a UI# showing the predictions results in a UI
 render_template('result.html',prediction_text=output)


if __name__ == '__main__':
    #running the app
    app.run(debug = True)
```



Chronic Kidney Disease Prediction

Specific Gravity

Ex: (1.005,1.010,1.015,1.020,1.025)

Hyper Tension

Yes = 1, No=0

Hemoglobin

in gms

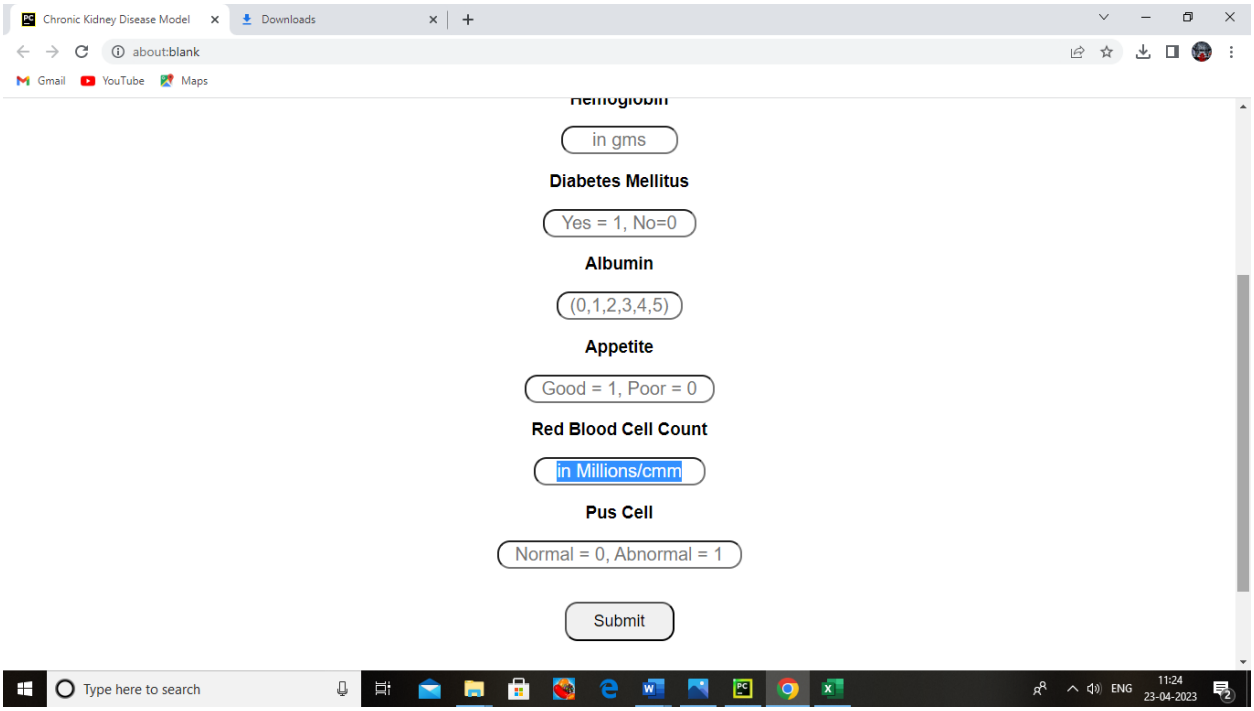
Diabetes Mellitus

Yes = 1, No=0

Albumin

(0,1,2,3,4,5)

Appetite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Downloads
about:blank
Gmail
YouTube
Maps
Hemoglobin
in gms
Diabetes Mellitus
Yes = 1, No=0
Albumin
(0,1,2,3,4,5)
Appetite
Good = 1, Poor = 0
Red Blood Cell Count
in Millions/cmm
Pus Cell
Normal = 0, Abnormal = 1
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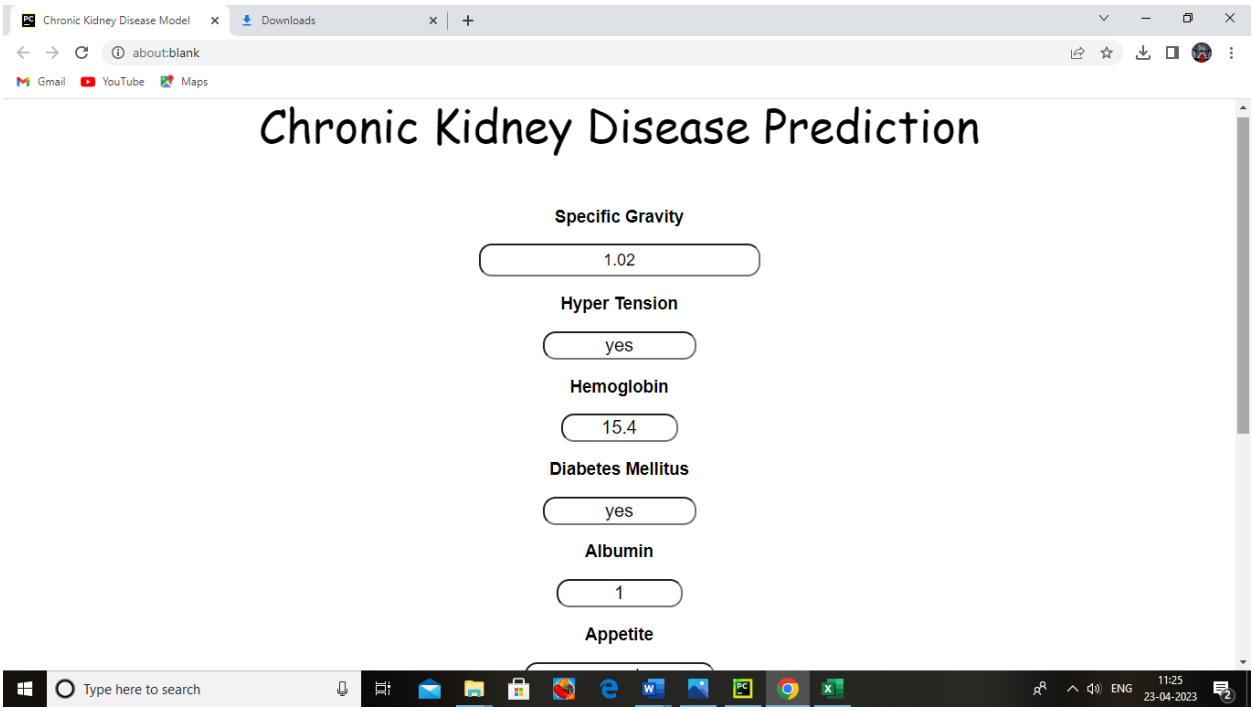
23-04-2023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Maps
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Diabetes Mellitus
yes
Albumin
1
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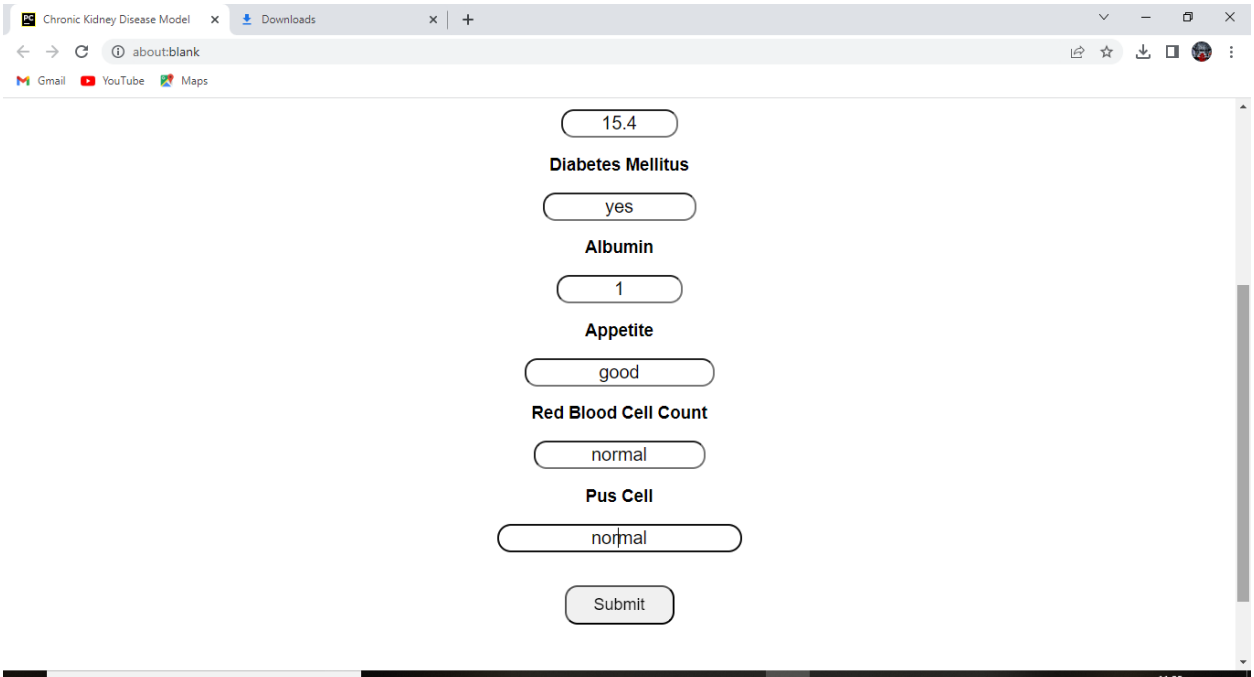
Chronic Kidney Disease Model
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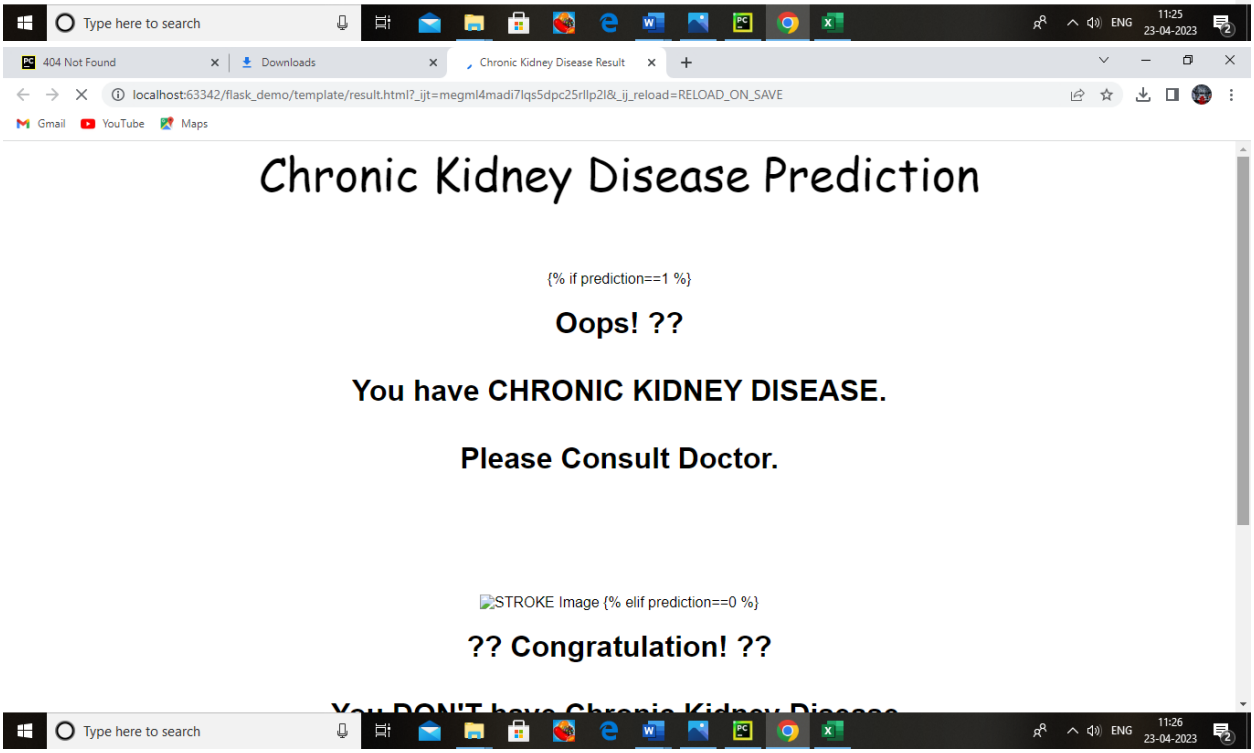
Albumin
1
Appetite
good
Red Blood Cell Count
normal
Pus Cell
normal
Submit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Chronic Kidney Disease Result
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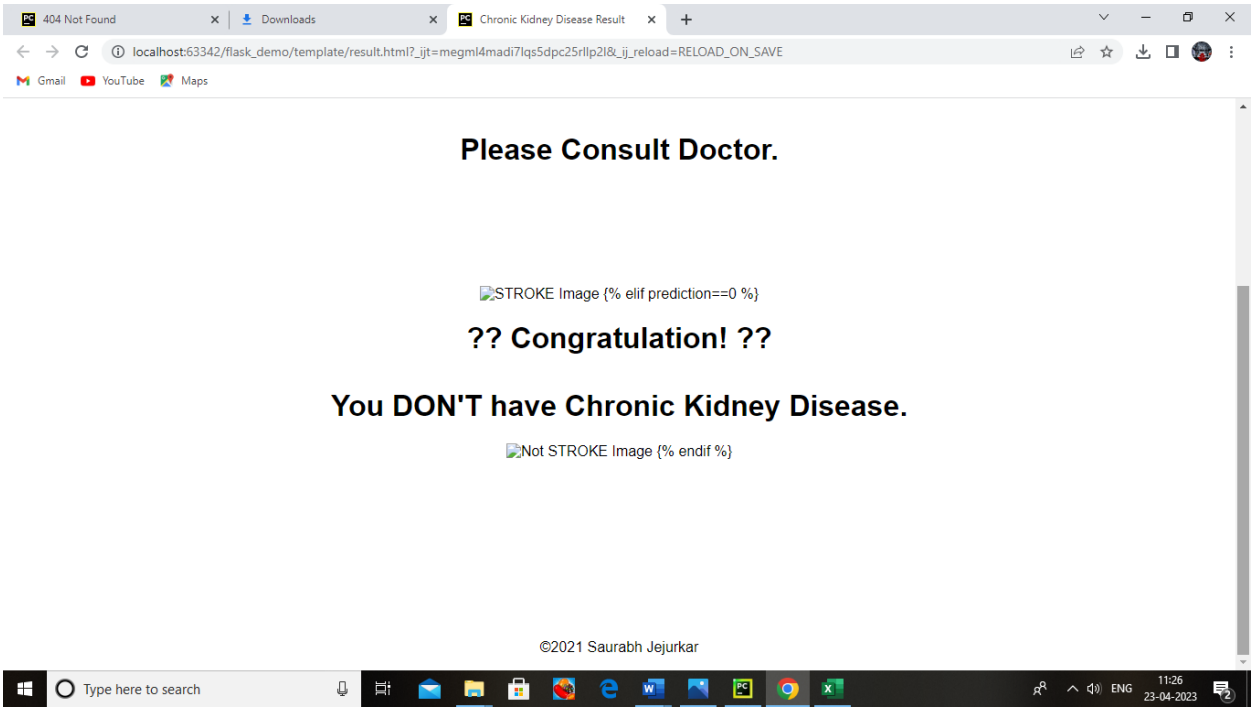
Gmail
YouTube
Maps
Chronic Kidney Disease Prediction
{% if prediction==1 %}
Oops! ??
You have CHRONIC KIDNEY DISEASE.
Please Consult Doctor.
STROKE Image {% elif prediction==0 %}
?? Congratulation! ??



4.ADVANTAGE & DISADVANTAGES:

The Proposed System is an mechanism for predicting Chronic Kidney Disease using different classification techniques. CKD ca e classified according to it severeness using machine learning process.

ADVANTAGES:

- One of the main advantages of PD over hemodialysis is that the procedure can be carried out in the comfort of the patients' home.

- For most, all that is required is a washroom with fresh running water, a sterile area of the house for the procedure to take place, and space to store the fluid for dialysis.
- This is also allow patients to travel.
- For elderly patients who may be unable to administer the procedure themselves, assistance may be given by a trained carer or community nurse.
- Additionally, the procedure can even be run while the patient sleeps.

DISADVANTAGES:

- Anemia or low red Blood cell count, which can cause fatigue and weakness.
- Extra fluid in the body, which can cause high blood pressure, swelling in the legs, or shortness of breath.
- A weakened immune system, which make it easier to develop infections.

5.APPLICATIONS:

- ✓Chronic Kidney disease (CKD) poses a great burden to global public health as current therapies are generally ineffective.
- ✓Early detection and effective therapy are crucial for the future prevention and progression of CKD.
- ✓Nanoparticles (NPs) vary by particle size, shape, charge and the density of targeting ligands and are associated with enhancement of the pharmacokinetic properties, targetablility, or the bioavailability of drugs.

6. CONCLUSIONS

In this paper, we employed a web application which can predict CKD , a comparative analysis was performed between KNN yield a better result. From the result obtained it is observed that overall precision, F-measure, recall is 0.971, 0.985, 1 and accuracy is 97.18 percentage respectively.

This shows that KNN yields better result when compared with Naïve Bayes. So medical practitioner can use KNN for prediction of CKD stage predication

is done by using GFR, depending on stage diet is recommended by the doctor and they can also upload patient's treatment details. Patients can access uploaded treatment and recommended diet by the doctor.

The proposed model uses a single algorithm to predict CKD, accuracy of the present work can be enhanced by using hybrid machine leaning algorithms, which gives better accuracy compared with KNN algorithm. Along with this additional feature could be added to enhance our web application in future.

7.FUTURE SCOPE

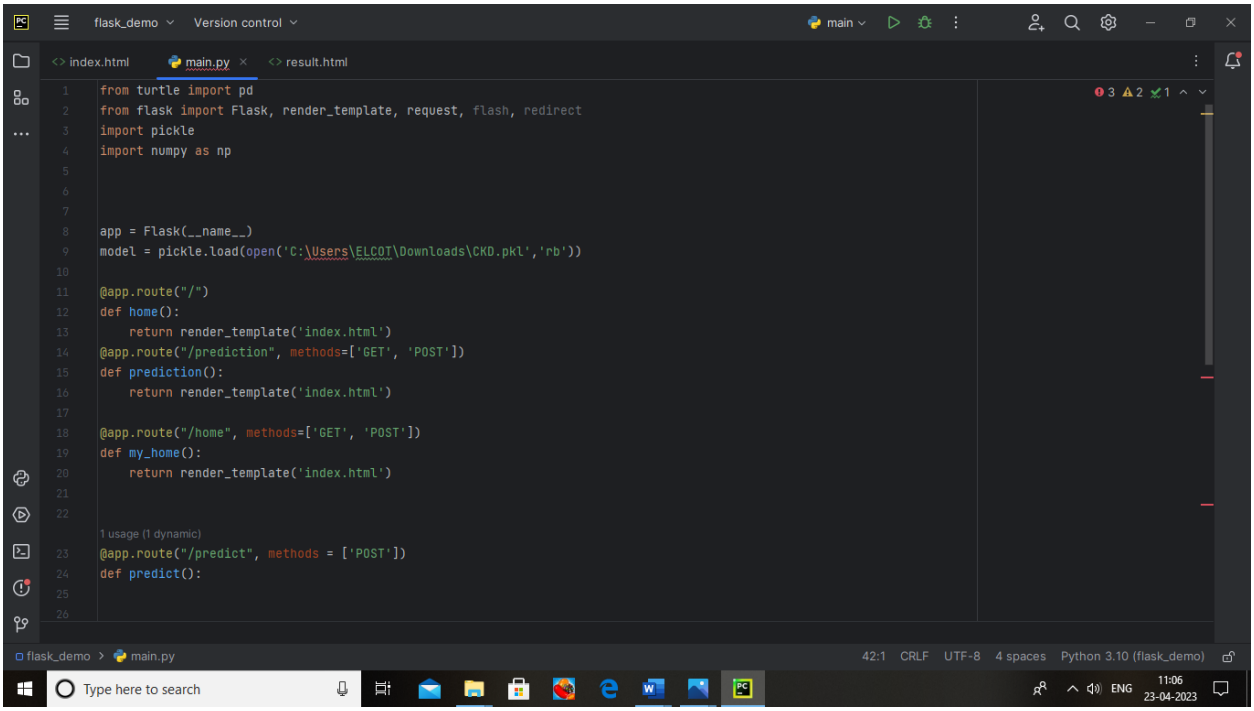
- Dialysis artificially removes waste products and extra fluid from your blood when your kidneys can no longer do this. In hemodialysis, a machine filters waste and excess fluids from your blood.
- In peritoneal dialysis, a thin tube inserted into your abdomen fills your abdominal cavity with a

dialysis solution that absorbs waste and excess fluids.

- After a time, the dialysis solution drains from your body, carrying the waste with it.
- A kidney transplant involves surgically placing a healthy kidney from a donor into your body.
- Transplanted kidneys can come from deceased or living donors.

8.APPENDIX

Source code: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Version control
main
index.html
main.py
result.html
from turtle import pd
from flask import Flask, render_template, request, flash, redirect
import pickle
import numpy as np
app = Flask(__name__)
model = pickle.load(open('C:\Users\ELCOT\Downloads\CKD.pkl','rb'))
@app.route("/")
def home():
return render_template('index.html')
@app.route("/prediction", methods=['GET', 'POST'])
def prediction():
return render_template('index.html')
@app.route("/home", methods=['GET', 'POST'])
def my_home():
return render_template('index.html')
1 usage (1 dynamic)
@app.route("/predict", methods = ['POST'])
def predict():
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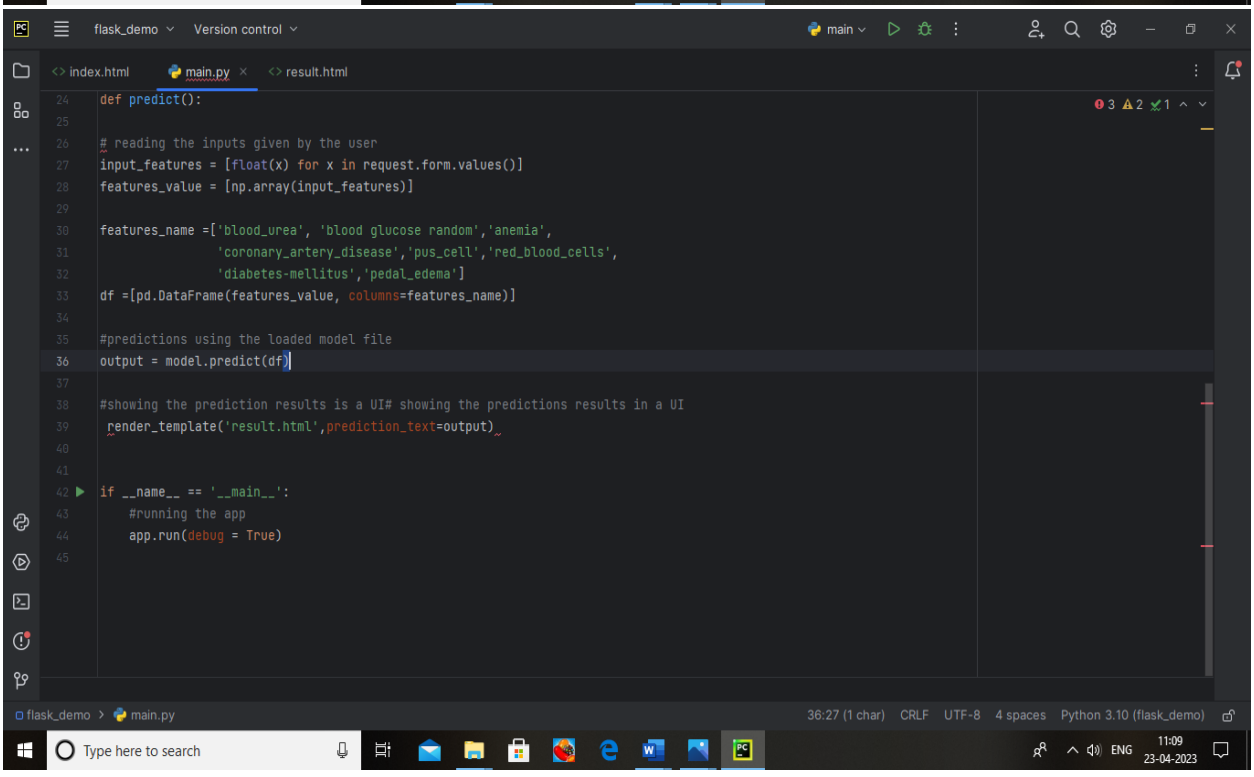
flask_demo
Version control
main
index.html
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result.html
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'diabetes-mellitus','pedal_edema']
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#predictions using the loaded model file
output = model.predict(df)
#showing the prediction results is a UI# showing the predictions results in a UI
render_template('result.html',prediction_text=output)
if __name__ == '__main__':
#running the app
app.run(debug = True)
flask_demo
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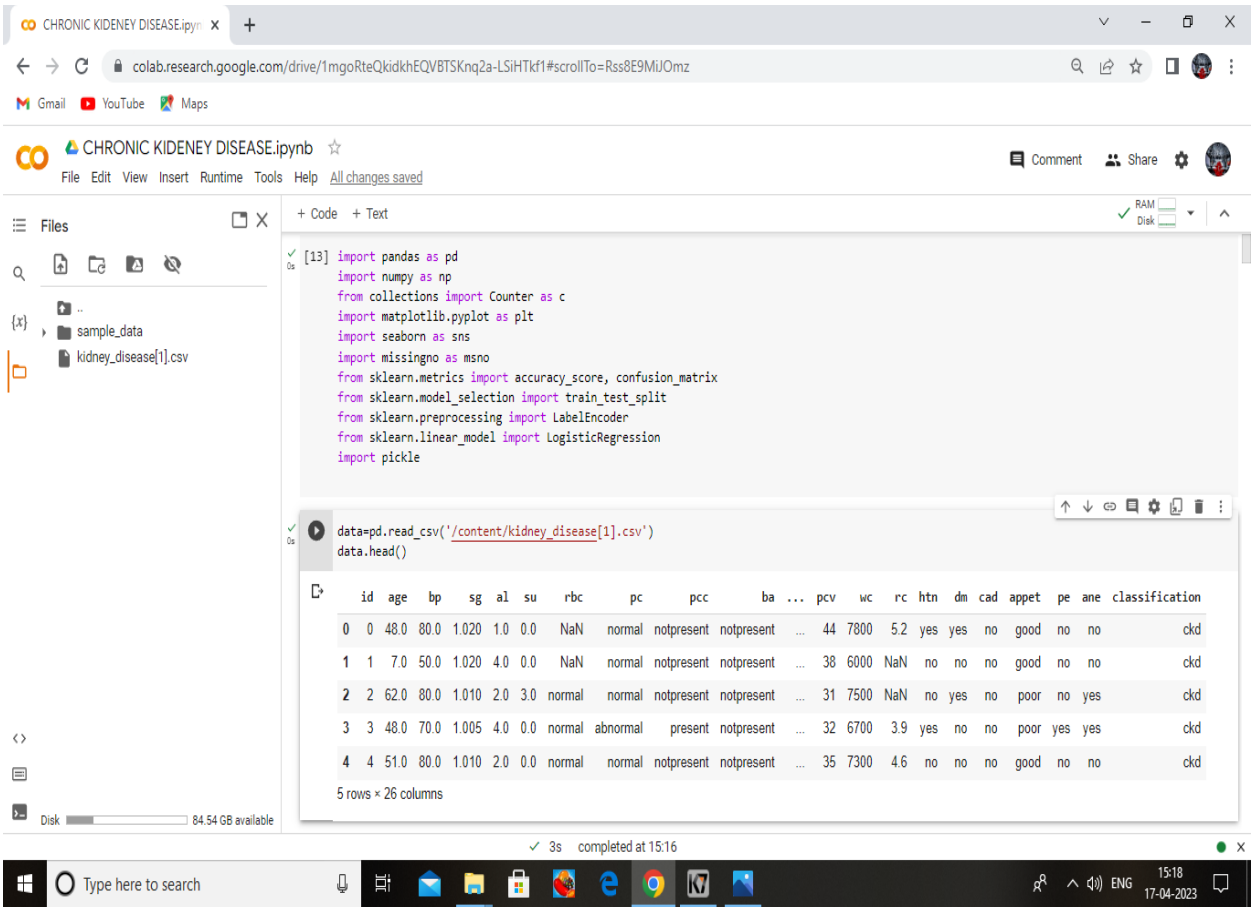
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File Edit View Insert Runtime Tools Help All changes saved
Comment
Share
Files
sample_data
kidney_disease[1].csv
Disk 84.54 GB available
+ Code + Text
RAM
Disk
[13] import pandas as pd
import numpy as np
from collections import Counter as c
import 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[1].csv')
data.head()
id age bp sg al su rbc pc pcc ba ... pcv wc rc htn dm cad appet pe ane classification
0 0 48.0 80.0 1.020 1.0 0.0 NaN normal notpresent notpresent ... 44 7800 5.2 yes yes no good no no ckd
1 1 7.0 50.0 1.020 4.0 0.0 NaN normal notpresent notpresent ... 38 6000 NaN no no no good no no ckd
2 2 62.0 80.0 1.010 2.0 3.0 normal normal notpresent notpresent ... 31 7500 NaN no yes no poor no yes ckd
3 3 48.0 70.0 1.005 4.0 0.0 normal abnormal present notpresent ... 32 6700 3.9 yes no no poor yes yes ckd
4 4 51.0 80.0 1.010 2.0 0.0 normal normal notpresent notpresent ... 35 7300 4.6 no no no good no no ckd
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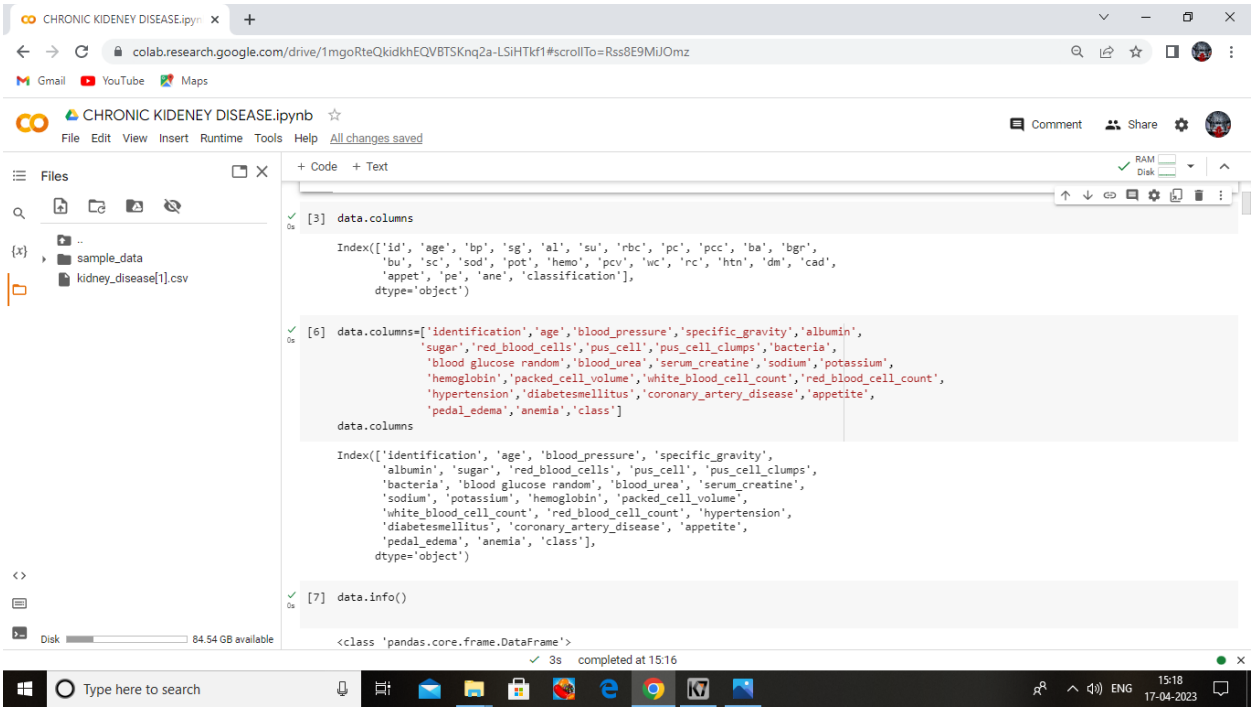
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Comment
Share
Files
sample_data
kidney_disease[1].csv
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[3] data.columns
Index(['id', 'age', 'bp', 'sg', 'al', 'su', 'rbc', 'pc', 'pcc', 'ba', 'bgr',
'bu', 'sc', 'sod', 'pot', 'hemo', 'pcv', 'wc', 'rc', 'htn', 'dm', 'cad',
'appet', 'pe', 'ane', 'classification'],
dtype='object')
[6] data.columns=['identification','age','blood_pressure','specific_gravity','albumin',
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'blood glucose random','blood_urea','serum_creatine','sodium','potassium',
'hemoglobin','packed_cell_volume','white_blood_cell_count','red_blood_cell_count',
'hypertension','diabetesmellitus','coronary_artery_disease','appetite',
'pedal_edema','anemia','class']
data.columns
Index(['identification', 'age', 'blood_pressure', 'specific_gravity',
'albumin', 'sugar', 'red_blood_cells', 'pus_cell', 'pus_cell_clumps',
'bacteria', 'blood glucose random', 'blood_urea', 'serum_creatine',
'sodium', 'potassium', 'hemoglobin', 'packed_cell_volume',
'white_blood_cell_count', 'red_blood_cell_count', 'hypertension',
'diabetesmellitus', 'coronary_artery_disease', 'appetite',
'pedal_edema', 'anemia', 'class'],
dtype='object')
[7] data.info()
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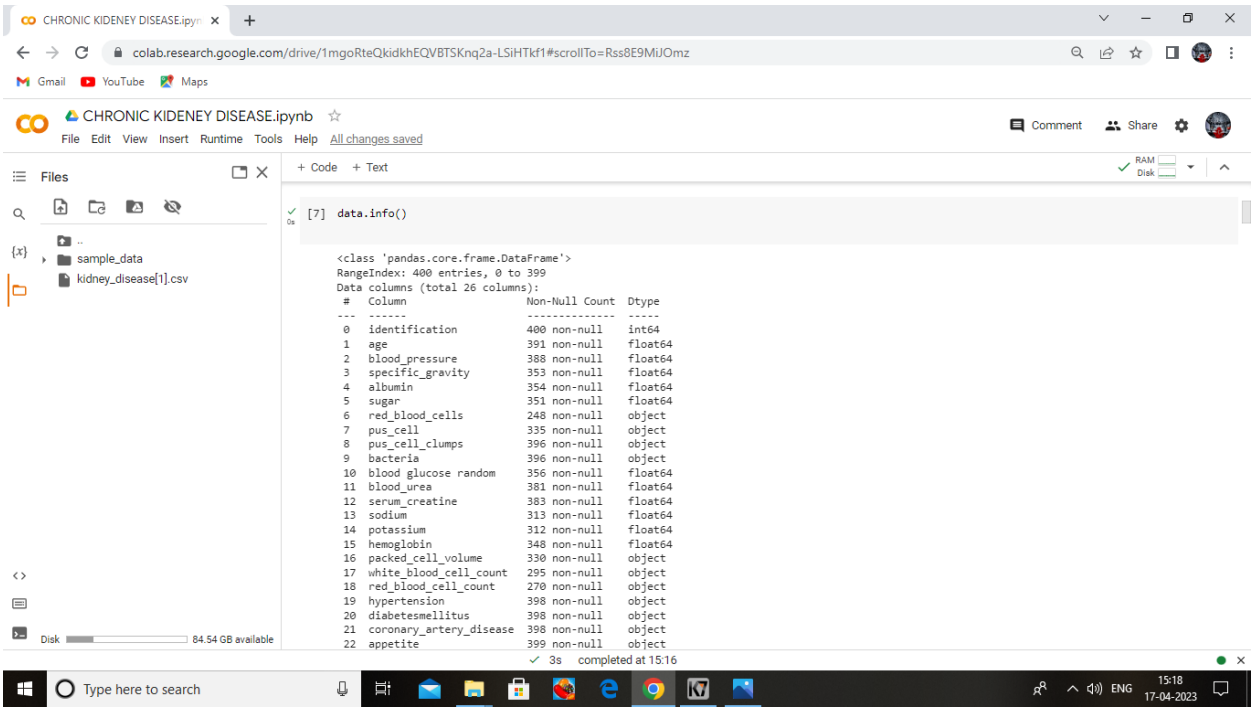
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File Edit View Insert Runtime Tools Help All changes saved
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Share
Files
sample_data
kidney_disease[1].csv
+ Code + Text
RAM
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[7] data.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 26 columns):
Column Non-Null Count Dtype
--- ------ -------------- -----
0 identification 400 non-null int64
1 age 391 non-null float64
2 blood_pressure 388 non-null float64
3 specific_gravity 353 non-null float64
4 albumin 354 non-null float64
5 sugar 351 non-null float64
6 red_blood_cells 248 non-null object
7 pus_cell 335 non-null object
8 pus_cell_clumps 396 non-null object
9 bacteria 396 non-null object
10 blood glucose random 356 non-null float64
11 blood_urea 381 non-null float64
12 serum_creatine 383 non-null float64
13 sodium 313 non-null float64
14 potassium 312 non-null float64
15 hemoglobin 348 non-null float64
16 packed_cell_volume 330 non-null object
17 white_blood_cell_count 295 non-null object
18 red_blood_cell_count 270 non-null object
19 hypertension 398 non-null object
20 diabetesmellitus 398 non-null object
21 coronary_artery_disease 398 non-null object
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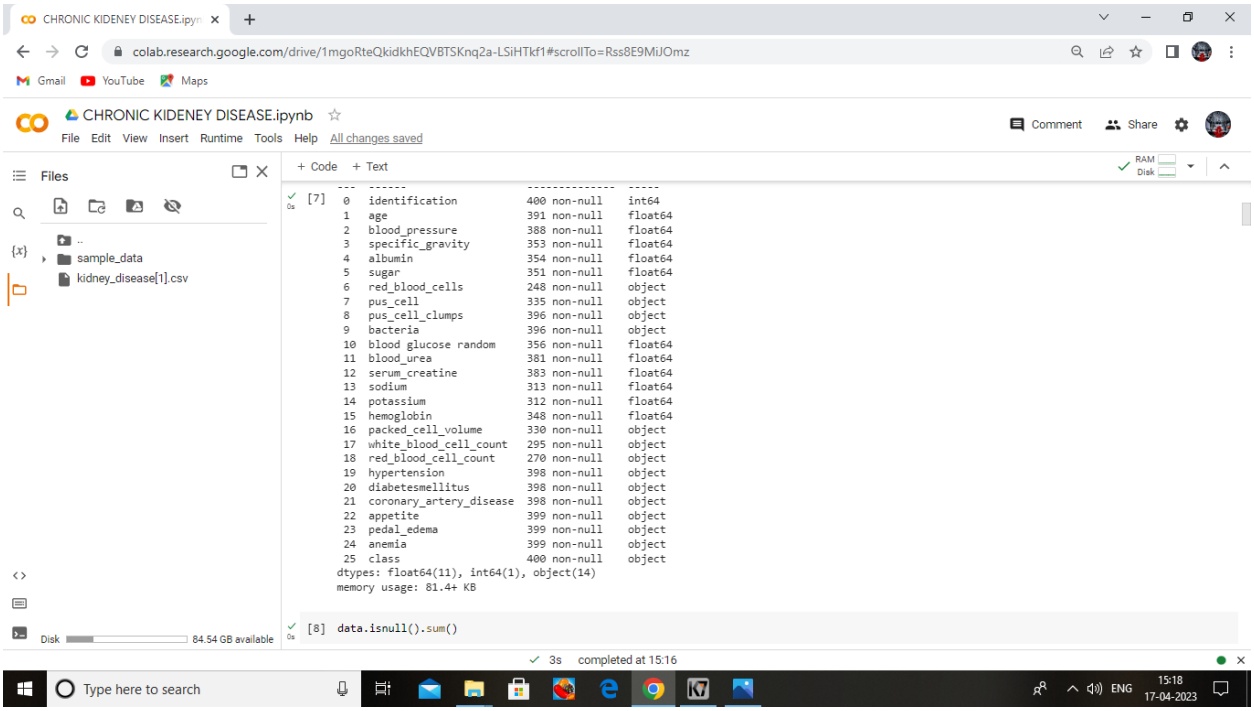
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2 blood_pressure 388 non-null float64
3 specific_gravity 353 non-null float64
4 albumin 354 non-null float64
5 sugar 351 non-null float64
6 red_blood_cells 248 non-null object
7 pus_cell 335 non-null object
8 pus_cell_clumps 396 non-null object
9 bacteria 396 non-null object
10 blood glucose random 356 non-null float64
11 blood_urea 381 non-null float64
12 serum_creatine 383 non-null float64
13 sodium 313 non-null float64
14 potassium 312 non-null float64
15 hemoglobin 348 non-null float64
16 packed_cell_volume 330 non-null object
17 white_blood_cell_count 295 non-null object
18 red_blood_cell_count 270 non-null object
19 hypertension 398 non-null object
20 diabetesmellitus 398 non-null object
21 coronary_artery_disease 398 non-null object
22 appetite 399 non-null object
23 pedal_edema 399 non-null object
24 anemia 399 non-null object
25 class 400 non-null object
dtypes: float64(11), int64(1), object(14)
memory usage: 81.4+ KB
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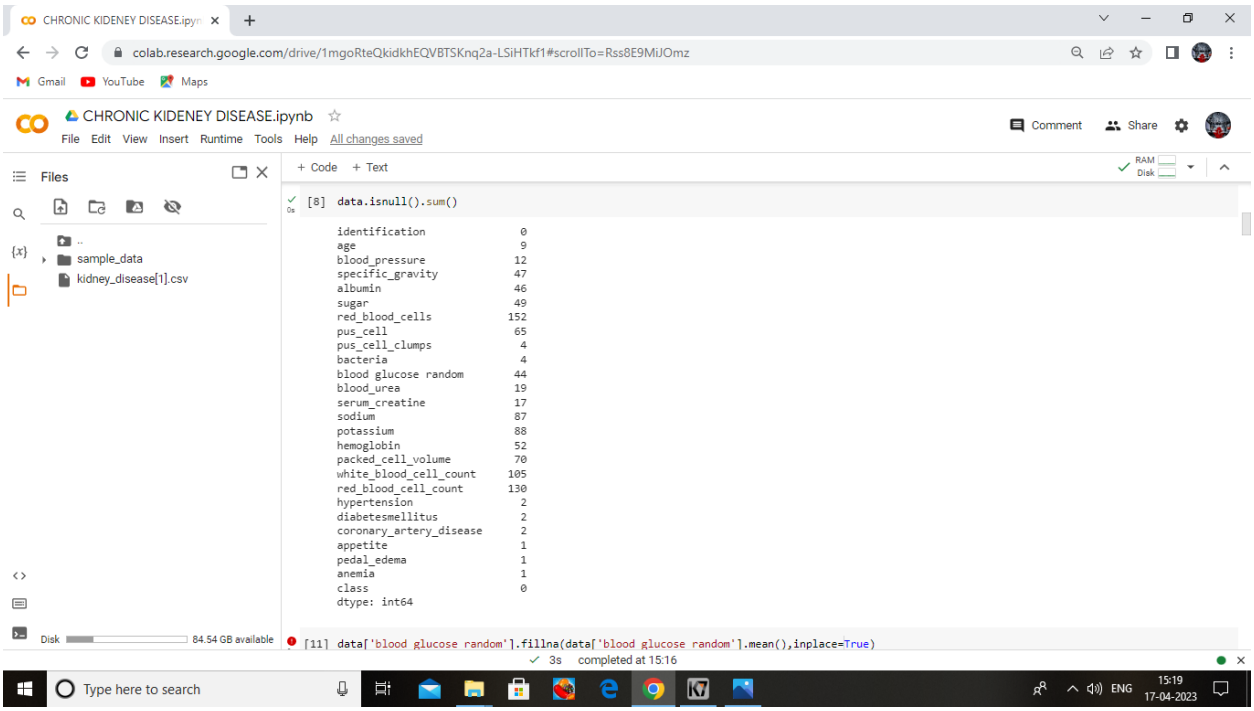
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kidney_disease[1].csv
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specific_gravity 47
albumin 46
sugar 49
red_blood_cells 152
pus_cell 65
pus_cell_clumps 4
bacteria 4
blood glucose random 44
blood_urea 19
serum_creatine 17
sodium 87
potassium 88
hemoglobin 52
packed_cell_volume 70
white_blood_cell_count 105
red_blood_cell_count 130
hypertension 2
diabetesmellitus 2
coronary_artery_disease 2
appetite 1
pedal_edema 1
anemia 1
class 0
dtype: int64
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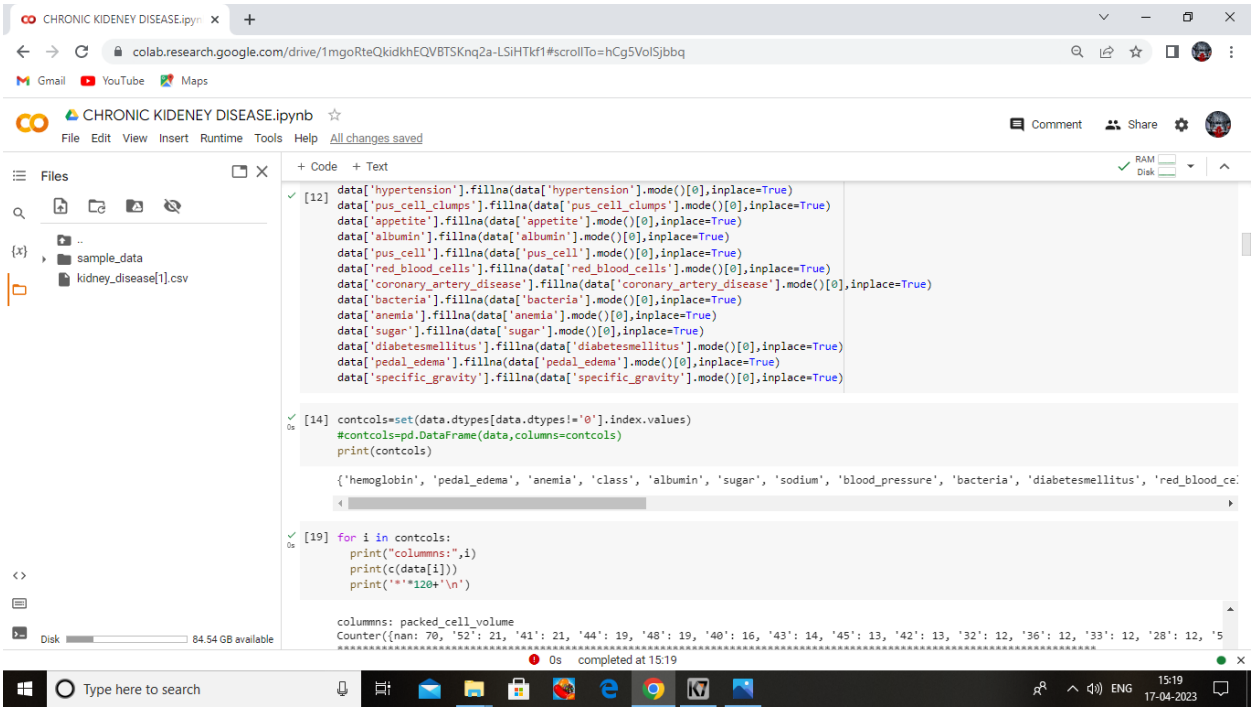
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Gmail
YouTube
Maps
CHRONIC KIDENEY DISEASE.ipynb
File Edit View Insert Runtime Tools Help All changes saved
Comment
Share
Files
sample_data
kidney_disease[1].csv
Disk 84.54 GB available
+ Code + Text
RAM
Disk
[12] data['hypertension'].fillna(data['hypertension'].mode()[0],inplace=True)
data['pus_cell_clumps'].fillna(data['pus_cell_clumps'].mode()[0],inplace=True)
data['appetite'].fillna(data['appetite'].mode()[0],inplace=True)
data['albumin'].fillna(data['albumin'].mode()[0],inplace=True)
data['pus_cell'].fillna(data['pus_cell'].mode()[0],inplace=True)
data['red_blood_cells'].fillna(data['red_blood_cells'].mode()[0],inplace=True)
data['coronary_artery_disease'].fillna(data['coronary_artery_disease'].mode()[0],inplace=True)
data['bacteria'].fillna(data['bacteria'].mode()[0],inplace=True)
data['anemia'].fillna(data['anemia'].mode()[0],inplace=True)
data['sugar'].fillna(data['sugar'].mode()[0],inplace=True)
data['diabetesmellitus'].fillna(data['diabetesmellitus'].mode()[0],inplace=True)
data['pedal_edema'].fillna(data['pedal_edema'].mode()[0],inplace=True)
data['specific_gravity'].fillna(data['specific_gravity'].mode()[0],inplace=True)
[14] contcols=set(data.dtypes[data.dtypes!='0'].index.values)
#contcols=pd.DataFrame(data,columns=contcols)
print(contcols)
{'hemoglobin', 'pedal_edema', 'anemia', 'class', 'albumin', 'sugar', 'sodium', 'blood_pressure', 'bacteria', 'diabetesmellitus', 'red_blood_ce
[19] for i in contcols:
print("columnns:",i)
print(c(data[i]))
print('*'*120+'\n')
columnns: packed_cell_volume
Counter({nan: 70, '52': 21, '41': 21, '44': 19, '48': 19, '40': 16, '43': 14, '45': 13, '42': 13, '32': 12, '36': 12, '33': 12, '28': 12, '5
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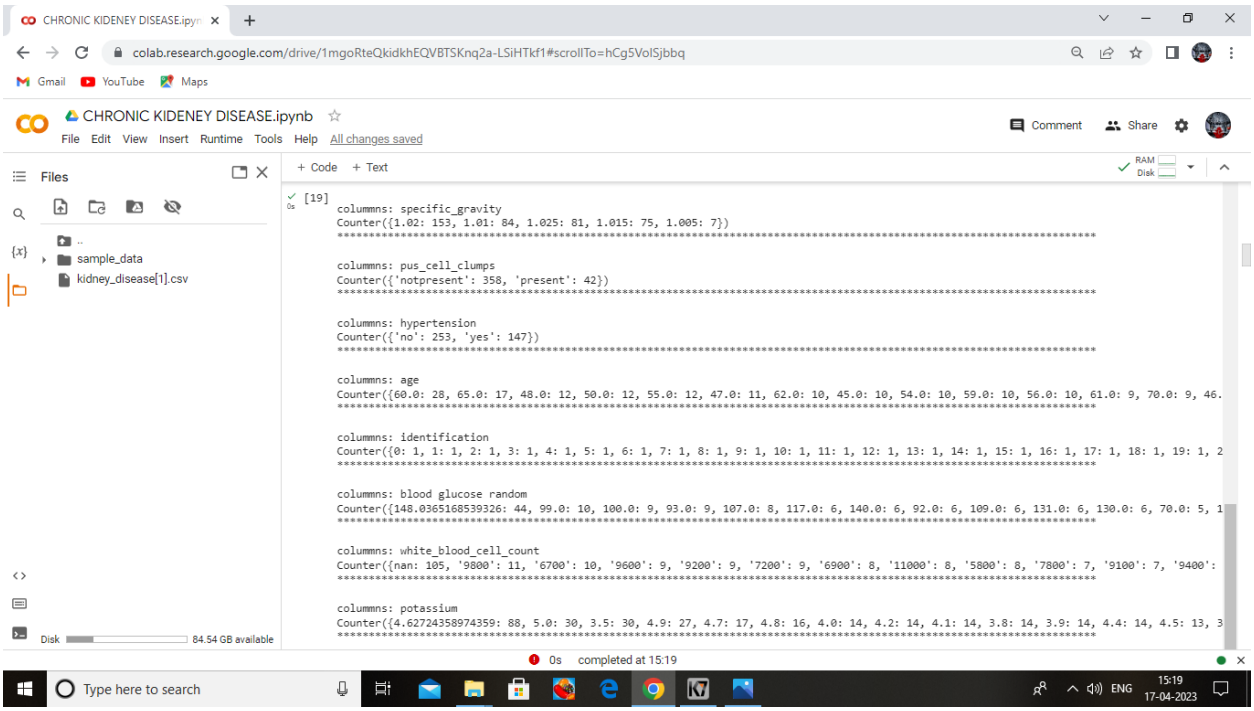
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sample_data
kidney_disease[1].csv
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[19]
columnns: specific_gravity
Counter({1.02: 153, 1.01: 84, 1.025: 81, 1.015: 75, 1.005: 7})
columnns: pus_cell_clumps
Counter({'notpresent': 358, 'present': 42})
columnns: hypertension
Counter({'no': 253, 'yes': 147})
columnns: age
Counter({60.0: 28, 65.0: 17, 48.0: 12, 50.0: 12, 55.0: 12, 47.0: 11, 62.0: 10, 45.0: 10, 54.0: 10, 59.0: 10, 56.0: 10, 61.0: 9, 70.0: 9, 46.
columnns: identification
Counter({0: 1, 1: 1, 2: 1, 3: 1, 4: 1, 5: 1, 6: 1, 7: 1, 8: 1, 9: 1, 10: 1, 11: 1, 12: 1, 13: 1, 14: 1, 15: 1, 16: 1, 17: 1, 18: 1, 19: 1, 2
columnns: blood glucose random
Counter({148.0365168539326: 44, 99.0: 10, 100.0: 9, 93.0: 9, 107.0: 8, 117.0: 6, 140.0: 6, 92.0: 6, 109.0: 6, 131.0: 6, 130.0: 6, 70.0: 5, 1
columnns: white_blood_cell_count
Counter({nan: 105, '9800': 11, '6700': 10, '9600': 9, '9200': 9, '7200': 9, '6900': 8, '11000': 8, '5800': 8, '7800': 7, '9100': 7, '9400':
columnns: potassium
Counter({4.62724358974359: 88, 5.0: 30, 3.5: 30, 4.9: 27, 4.7: 17, 4.8: 16, 4.0: 14, 4.2: 14, 4.1: 14, 3.8: 14, 3.9: 14, 4.4: 14, 4.5: 13, 3
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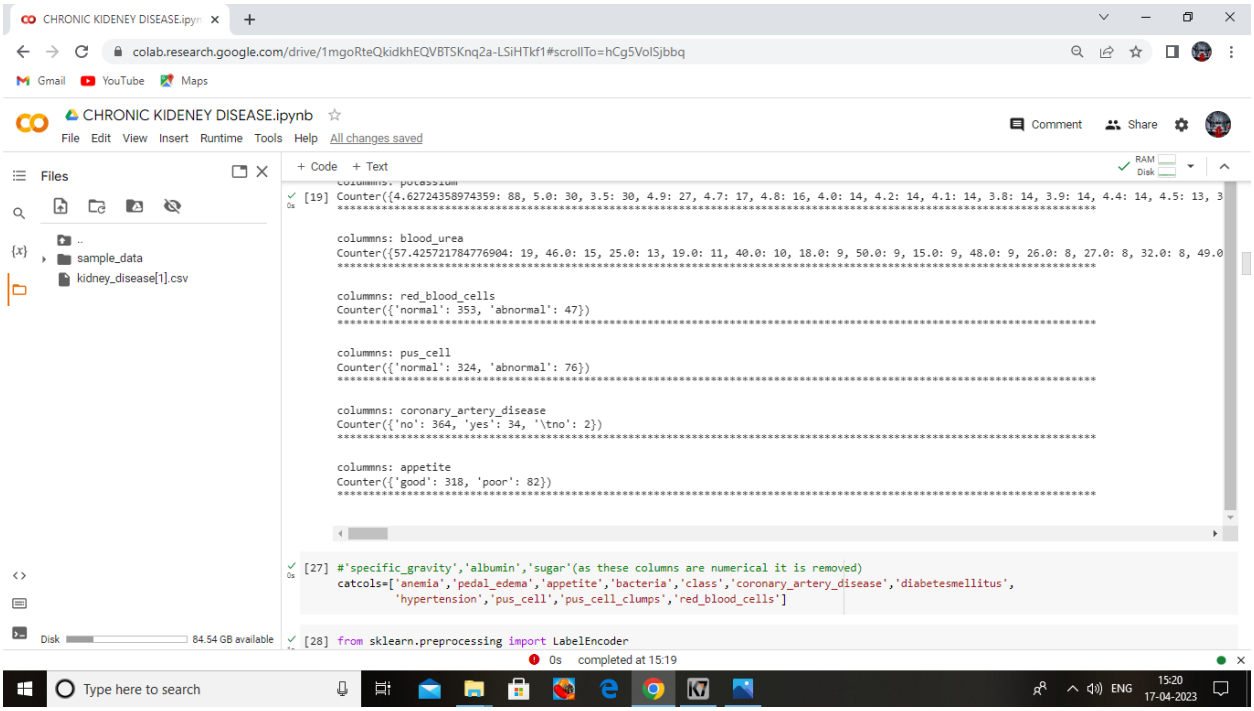
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[19] Counter({4.627243589743 59: 88, 5.0: 30, 3.5: 30, 4.9: 27, 4.7: 17, 4.8: 16, 4.0: 14, 4.2: 14, 4.1: 14, 3.8: 14, 3.9: 14, 4.4: 14, 4.5: 13, 3
columnns: blood_urea
Counter({57.425721784776904: 19, 46.0: 15, 25.0: 13, 19.0: 11, 40.0: 10, 18.0: 9, 50.0: 9, 15.0: 9, 48.0: 9, 26.0: 8, 27.0: 8, 32.0: 8, 49.0
columnns: red_blood_cells
Counter({'normal': 353, 'abnormal': 47})
columnns: pus_cell
Counter({'normal': 324, 'abnormal': 76})
columnns: coronary_artery_disease
Counter({'no': 364, 'yes': 34, '\tno': 2})
columnns: appetite
Counter({'good': 318, 'poor': 82})
[27] #'specific_gravity','albumin','sugar'(as these columns are numerical it is removed)
catcols=['anemia','pedal_edema','appetite','bacteria','class','coronary_artery_disease','diabetesmellitus',
'hypertension','pus_cell','pus_cell_clumps','red_blood_cells']
[28] from sklearn.preprocessing import LabelEncoder
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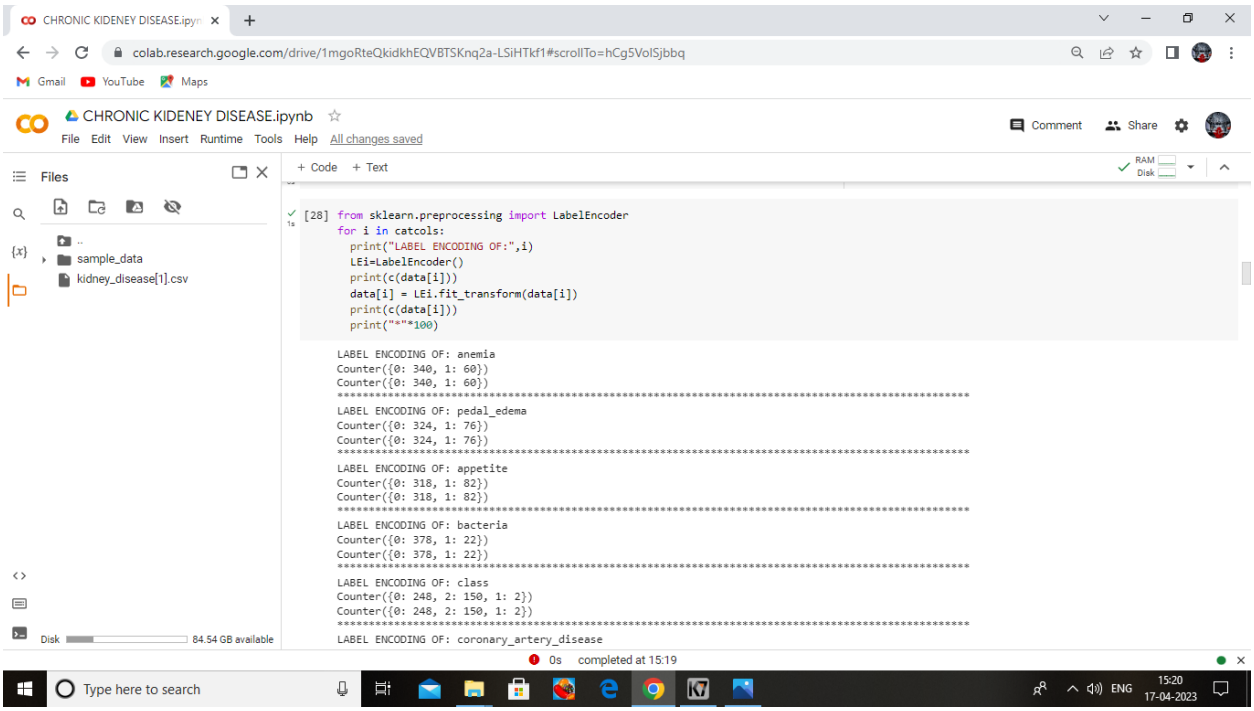
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[28] from sklearn.preprocessing import LabelEncoder
for i in catcols:
print("LABEL ENCODING OF:",i)
LEi=LabelEncoder()
print(c(data[i]))
data[i] = LEi.fit_transform(data[i])
print(c(data[i]))
print("*"*100)
LABEL ENCODING OF: anemia
Counter({0: 340, 1: 60})
Counter({0: 340, 1: 60})
LABEL ENCODING OF: pedal_edema
Counter({0: 324, 1: 76})
Counter({0: 324, 1: 76})
LABEL ENCODING OF: appetite
Counter({0: 318, 1: 82})
Counter({0: 318, 1: 82})
LABEL ENCODING OF: bacteria
Counter({0: 378, 1: 22})
Counter({0: 378, 1: 22})
LABEL ENCODING OF: class
Counter({0: 248, 2: 150, 1: 2})
Counter({0: 248, 2: 150, 1: 2})
LABEL ENCODING OF: coronary_artery_disease
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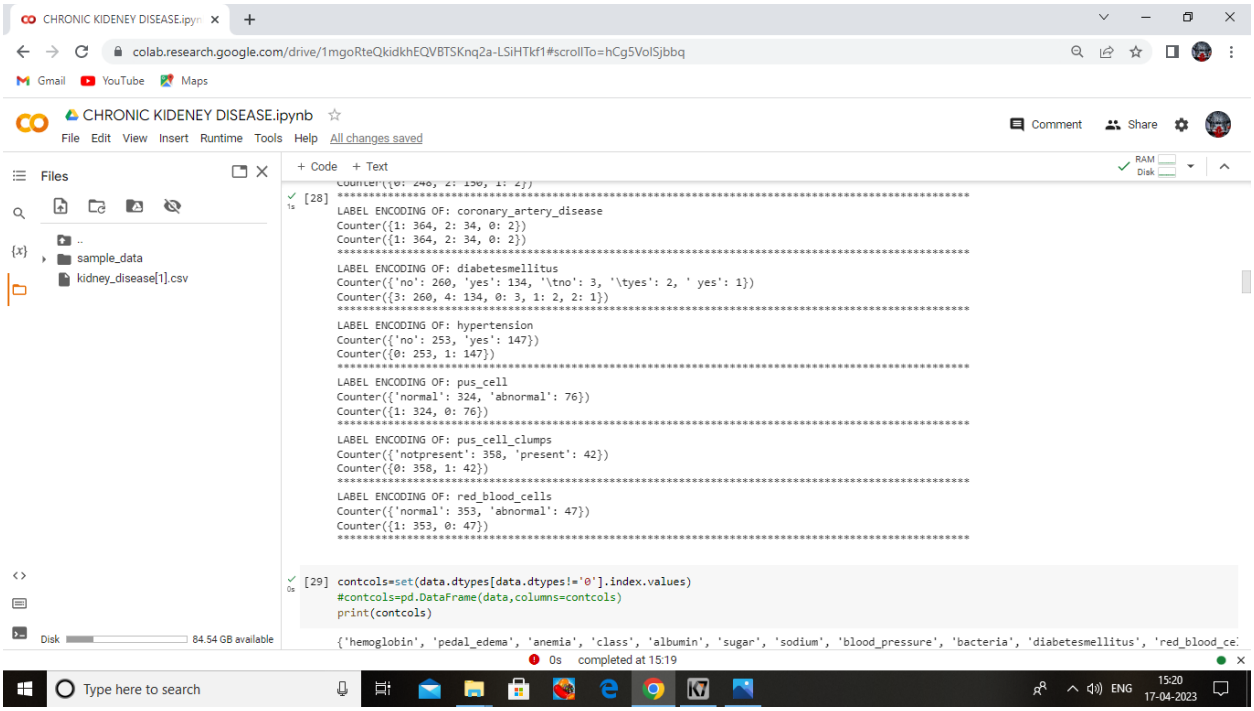
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[28]
LABEL ENCODING OF: coronary_artery_disease
Counter({1: 364, 2: 34, 0: 2})
Counter({1: 364, 2: 34, 0: 2})
LABEL ENCODING OF: diabetesmellitus
Counter({'no': 260, 'yes': 134, '\tno': 3, '\tyes': 2, ' yes': 1})
Counter({3: 260, 4: 134, 0: 3, 1: 2, 2: 1})
LABEL ENCODING OF: hypertension
Counter({'no': 253, 'yes': 147})
Counter({0: 253, 1: 147})
LABEL ENCODING OF: pus_cell
Counter({'normal': 324, 'abnormal': 76})
Counter({1: 324, 0: 76})
LABEL ENCODING OF: pus_cell_clumps
Counter({'notpresent': 358, 'present': 42})
Counter({0: 358, 1: 42})
LABEL ENCODING OF: red_blood_cells
Counter({'normal': 353, 'abnormal': 47})
Counter({1: 353, 0: 47})
[29] contcols=set(data.dtypes[data.dtypes!='0'].index.values)
#contcols=pd.DataFrame(data,columns=contcols)
print(contcols)
{'hemoglobin', 'pedal_edema', 'anemia', 'class', 'albumin', 'sugar', 'sodium', 'blood_pressure', 'bacteria', 'diabetesmellitus', 'red_blood_ce
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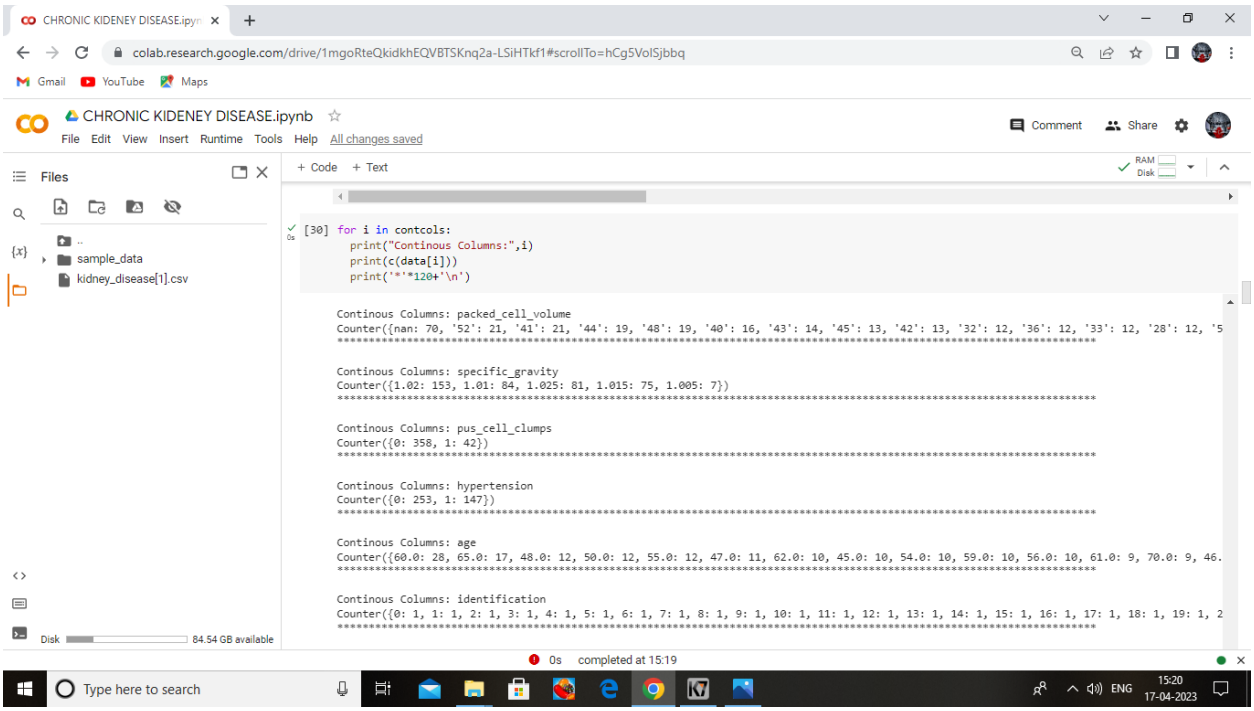
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[30] for i in contcols:
print("Continous Columns:",i)
print(c(data[i]))
print('*'*120+'\n')
Continous Columns: packed_cell_volume
Counter({nan: 70, '52': 21, '41': 21, '44': 19, '48': 19, '40': 16, '43': 14, '45': 13, '42': 13, '32': 12, '36': 12, '33': 12, '28': 12, '5
Continous Columns: specific_gravity
Counter({1.02: 153, 1.01: 84, 1.025: 81, 1.015: 75, 1.005: 7})
Continous Columns: pus_cell_clumps
Counter({0: 358, 1: 42})
Continous Columns: hypertension
Counter({0: 253, 1: 147})
Continous Columns: age
Counter({60.0: 28, 65.0: 17, 48.0: 12, 50.0: 12, 55.0: 12, 47.0: 11, 62.0: 10, 45.0: 10, 54.0: 10, 59.0: 10, 56.0: 10, 61.0: 9, 70.0: 9, 46.
Continous Columns: identification
Counter({0: 1, 1: 1, 2: 1, 3: 1, 4: 1, 5: 1, 6: 1, 7: 1, 8: 1, 9: 1, 10: 1, 11: 1, 12: 1, 13: 1, 14: 1, 15: 1, 16: 1, 17: 1, 18: 1, 19: 1, 2
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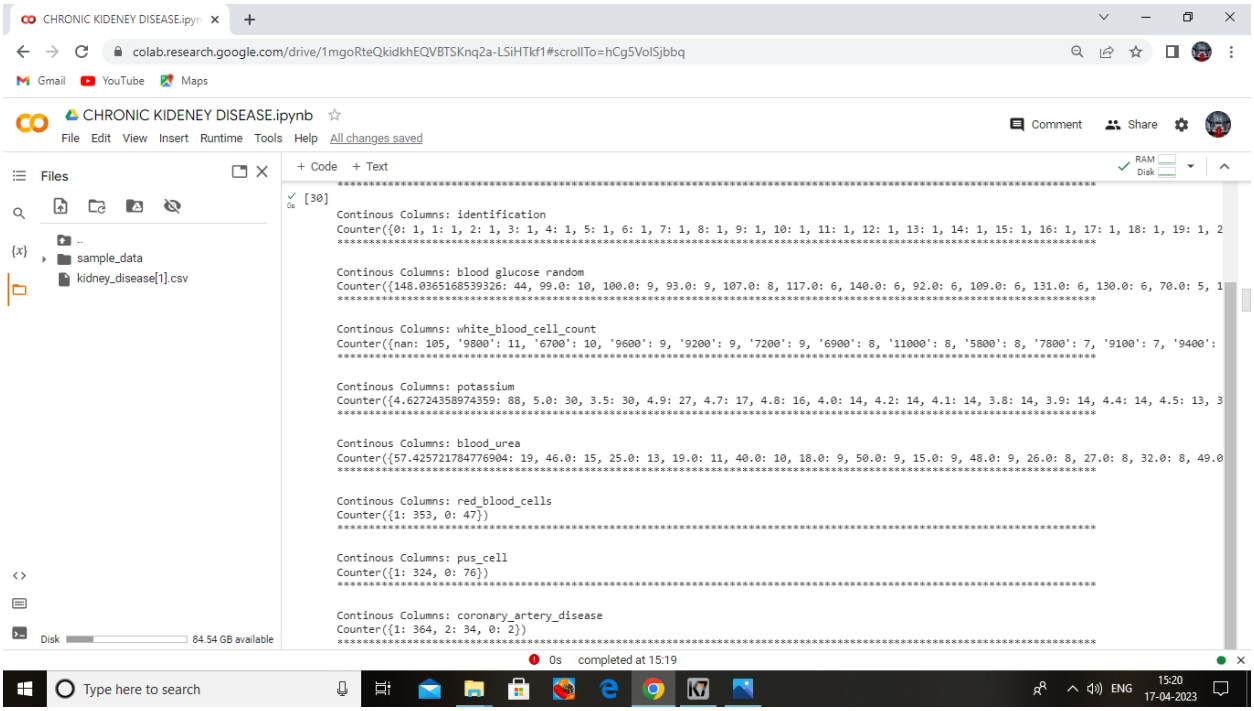
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kidney_disease[1].csv
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[30]
Continous Columns: identification
Counter({0: 1, 1: 1, 2: 1, 3: 1, 4: 1, 5: 1, 6: 1, 7: 1, 8: 1, 9: 1, 10: 1, 11: 1, 12: 1, 13: 1, 14: 1, 15: 1, 16: 1, 17: 1, 18: 1, 19: 1, 2
Continous Columns: blood glucose random
Counter({148.0365168539326: 44, 99.0: 10, 100.0: 9, 93.0: 9, 107.0: 8, 117.0: 6, 140.0: 6, 92.0: 6, 109.0: 6, 131.0: 6, 130.0: 6, 70.0: 5, 1
Continous Columns: white_blood_cell_count
Counter({nan: 105, '9800': 11, '6700': 10, '9600': 9, '9200': 9, '7200': 9, '6900': 8, '11000': 8, '5800': 8, '7800': 7, '9100': 7, '9400':
Continous Columns: potassium
Counter({4.627243589743359: 88, 5.0: 30, 3.5: 30, 4.9: 27, 4.7: 17, 4.8: 16, 4.0: 14, 4.2: 14, 4.1: 14, 3.8: 14, 3.9: 14, 4.4: 14, 4.5: 13, 3
Continous Columns: blood_urea
Counter({57.425721784776904: 19, 46.0: 15, 25.0: 13, 19.0: 11, 40.0: 10, 18.0: 9, 50.0: 9, 15.0: 9, 48.0: 9, 26.0: 8, 27.0: 8, 32.0: 8, 49.0
Continous Columns: red_blood_cells
Counter({1: 353, 0: 47})
Continous Columns: pus_cell
Counter({1: 324, 0: 76})
Continous Columns: coronary_artery_disease
Counter({1: 364, 2: 34, 0: 2})
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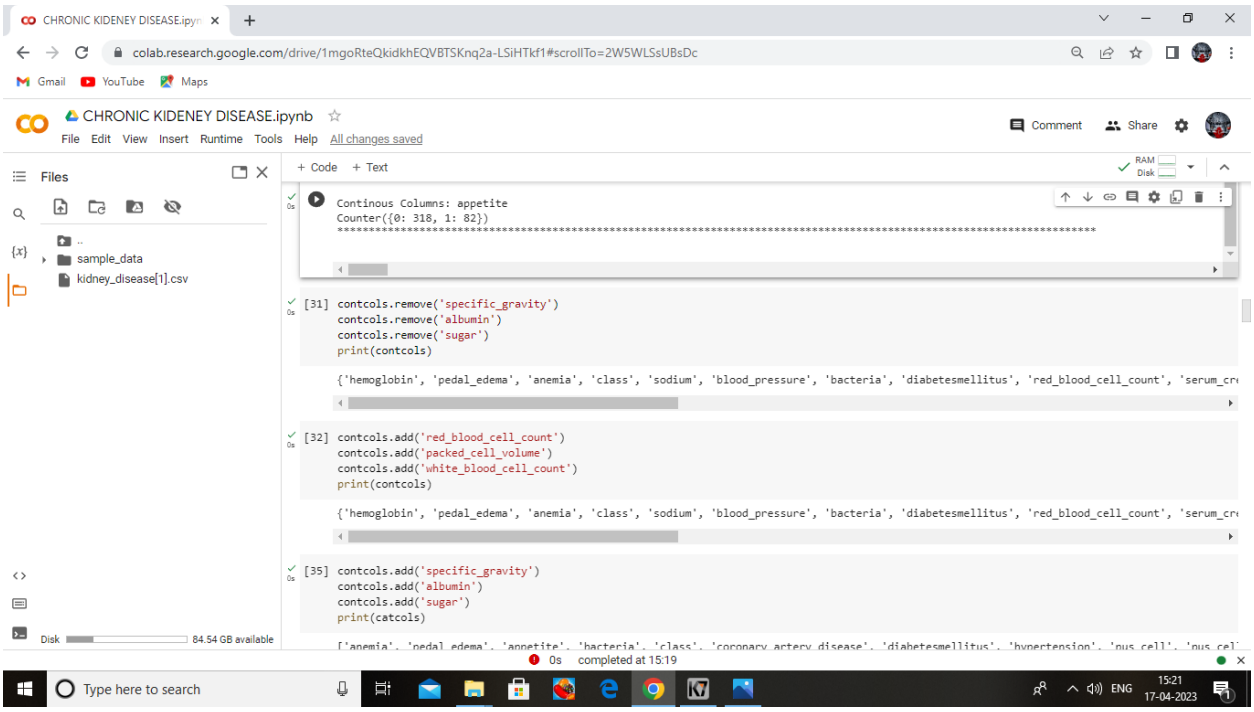
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sample_data
kidney_disease[1].csv
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Continous Columns: appetite
Counter({0: 318, 1: 82})
[31] contcols.remove('specific_gravity')
contcols.remove('albumin')
contcols.remove('sugar')
print(contcols)
{'hemoglobin', 'pedal_edema', 'anemia', 'class', 'sodium', 'blood_pressure', 'bacteria', 'diabetesmellitus', 'red_blood_cell_count', 'serum_cr
[32] contcols.add('red_blood_cell_count')
contcols.add('packed_cell_volume')
contcols.add('white_blood_cell_count')
print(contcols)
{'hemoglobin', 'pedal_edema', 'anemia', 'class', 'sodium', 'blood_pressure', 'bacteria', 'diabetesmellitus', 'red_blood_cell_count', 'serum_cr
[35] contcols.add('specific_gravity')
contcols.add('albumin')
contcols.add('sugar')
print(catcols)
['anemia', 'pedal_edema', 'appetite', 'bacteria', 'class', 'coronary_artery_disease', 'diabetesmellitus', 'hypertension', 'pus_cell', 'pus_cel
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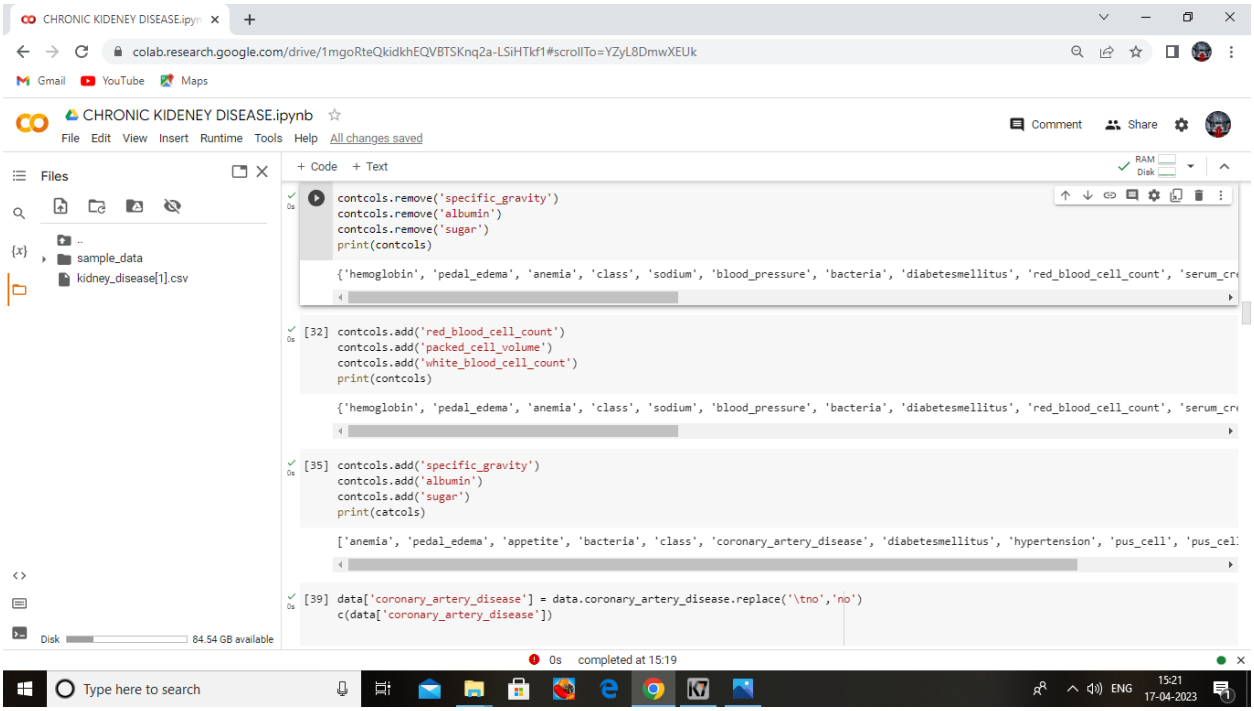
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contcols.remove('specific_gravity')
contcols.remove('albumin')
contcols.remove('sugar')
print(contcols)
{'hemoglobin', 'pedal_edema', 'anemia', 'class', 'sodium', 'blood_pressure', 'bacteria', 'diabetesmellitus', 'red_blood_cell_count', 'serum_cr
[32] contcols.add('red_blood_cell_count')
contcols.add('packed_cell_volume')
contcols.add('white_blood_cell_count')
print(contcols)
{'hemoglobin', 'pedal_edema', 'anemia', 'class', 'sodium', 'blood_pressure', 'bacteria', 'diabetesmellitus', 'red_blood_cell_count', 'serum_cr
[35] contcols.add('specific_gravity')
contcols.add('albumin')
contcols.add('sugar')
print(catcols)
['anemia', 'pedal_edema', 'appetite', 'bacteria', 'class', 'coronary_artery_disease', 'diabetesmellitus', 'hypertension', 'pus_cell', 'pus_cel
[39] data['coronary_artery_disease'] = data.coronary_artery_disease.replace('\tno','no')
c(data['coronary_artery_disease'])
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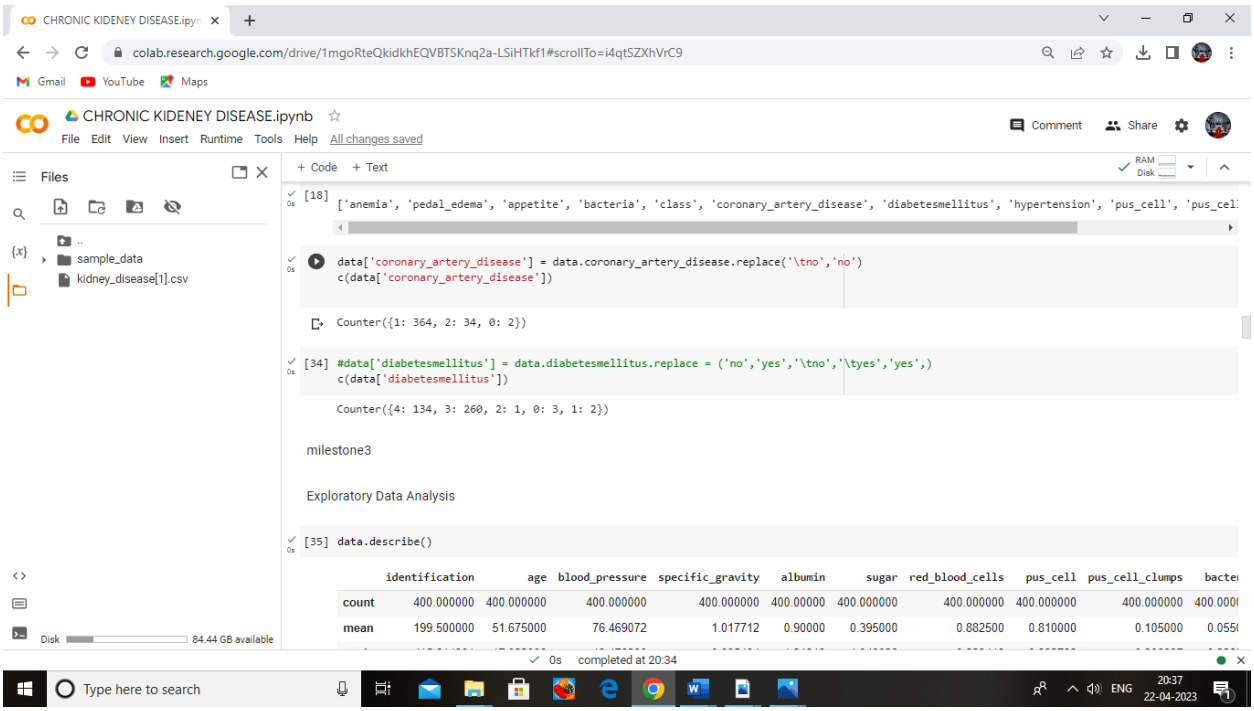
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[18] ['anemia', 'pedal_edema', 'appetite', 'bacteria', 'class', 'coronary_artery_disease', 'diabetesmellitus', 'hypertension', 'pus_cell', 'pus_cel
data['coronary_artery_disease'] = data.coronary_artery_disease.replace('\tno','no')
c(data['coronary_artery_disease'])
Counter({1: 364, 2: 34, 0: 2})
[34] #data['diabetesmellitus'] = data.diabetesmellitus.replace = ('no','yes','\tno','\tyes','yes',)
c(data['diabetesmellitus'])
Counter({4: 134, 3: 260, 2: 1, 0: 3, 1: 2})
milestone3
Exploratory Data Analysis
[35] data.describe()
identification age blood_pressure specific_gravity albumin sugar red_blood_cells pus_cell pus_cell_clumps
count 400.000000 400.000000 400.000000 400.000000 400.00000 400.000000 400.000000 400.000000 400.000000
mean 199.500000 51.675000 76.469072 1.017712 0.90000 0.395000 0.882500 0.810000 0.105000
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[35]

	identification	age	blood_pressure	specific_gravity	albumin	sugar	red_blood_cells	pus_cell	pus_cell_clumps	bacte
count	400.000000	400.000000	400.000000	400.000000	400.000000	400.000000	400.000000	400.000000	400.000000	400.000
mean	199.500000	51.675000	76.469072	1.017712	0.90000	0.395000	0.882500	0.810000	0.105000	0.055
std	115.614301	17.022008	13.476298	0.005434	1.31313	1.040038	0.322418	0.392792	0.306937	0.228
min	0.000000	2.000000	50.000000	1.005000	0.00000	0.000000	0.000000	0.000000	0.000000	0.000
25%	99.750000	42.000000	70.000000	1.015000	0.00000	0.000000	1.000000	1.000000	0.000000	0.000
50%	199.500000	55.000000	78.234536	1.020000	0.00000	0.000000	1.000000	1.000000	0.000000	0.000
75%	299.250000	64.000000	80.000000	1.020000	2.00000	0.000000	1.000000	1.000000	0.000000	0.000
max	399.000000	90.000000	180.000000	1.025000	5.00000	5.000000	1.000000	1.000000	1.000000	1.000

8 rows × 23 columns

Age distribution

[36]
```
sns.distplot(data.age)
```

```
<ipython-input-36-868c85374ad7>:1: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.
```

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kidney_disease[1].csv

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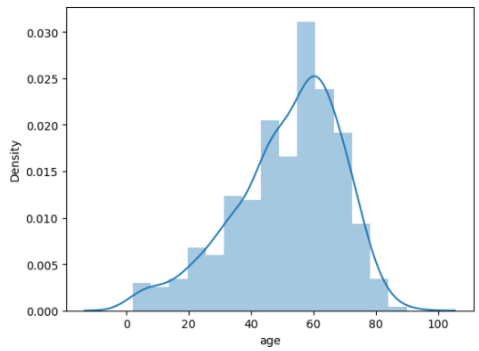
[36]
```
For a guide to updating your code to use the new functions, please see
https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

  sns.distplot(data.age)
<Axes: xlabel='age', ylabel='Density'>
```



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sample_data

kidney_disease[1].csv

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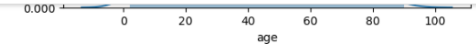
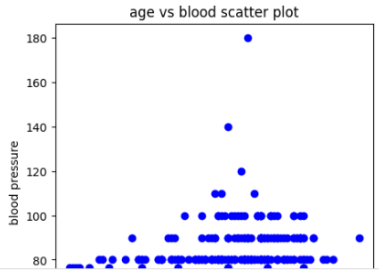
[36]



[37]

```
import matplotlib.pyplot as plt
fig=plt.figure(figsize=(5,5))
plt.scatter(data['age'],data['blood_pressure'],color='blue')
plt.xlabel('age')
plt.ylabel('blood pressure')
plt.title("age vs blood scatter plot")
```

```
Text(0.5, 1.0, 'age vs blood scatter plot')
```



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[37]

[38]

```
plt.figure(figsize=(20,15),facecolor='white')
plotnumber=1
```

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kidney_disease[1].csv

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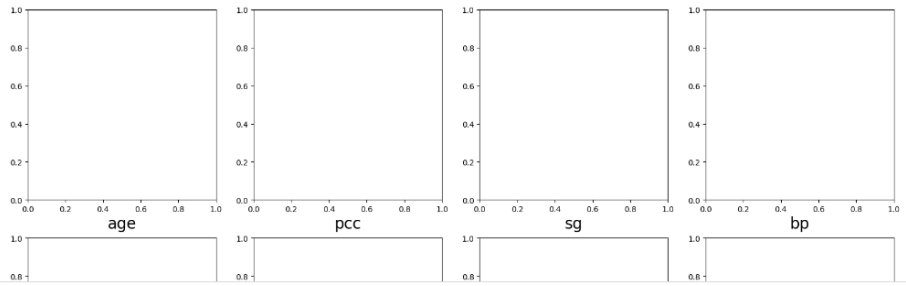
[38]
```
plotnumber=1

for column in contcols:
  if plotnumber<=11:
    ax=plt.subplot(3,4,plotnumber)
    plt.xlabel(column,fontsize=20)

    plotnumber+=1

plt.show()
```



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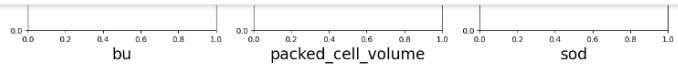
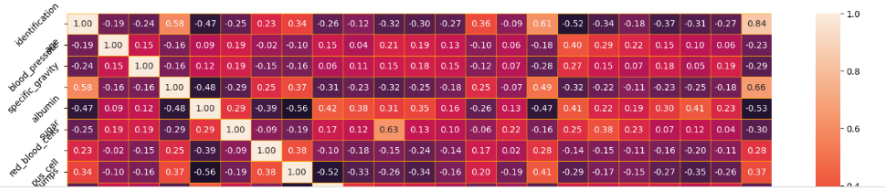
[38]



Finding correlation between the independent Columns

[39]
```
#HEAT MAP #correlation of parameters
f,ax=plt.subplots(figsize=(18,10))
sns.heatmap(data.corr(),annot=True,fmt=".2f",ax=ax,linewidths=0.5,linecolor="orange")
plt.xticks(rotation=45)
plt.yticks(rotation=45)
plt.show()
```

```
<ipython-input-39-9d5ae916c1e3>:3: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it w
  sns.heatmap(data.corr(),annot=True,fmt=".2f",ax=ax,linewidths=0.5,linecolor="orange")
```



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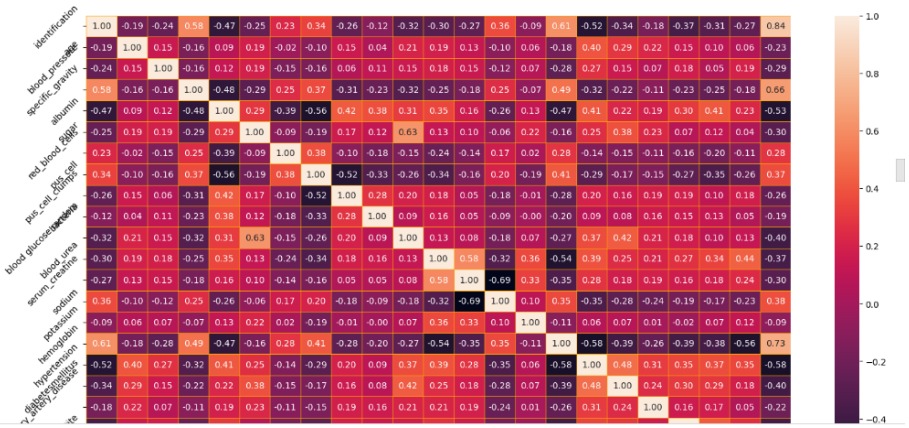
[39] <ipython-input-39-9d5ae916c1e3>:3: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it w
sns.heatmap(data.corr(),annot=True,fmt=".2f",ax=ax,linewidths=0.5,linecolor="orange")



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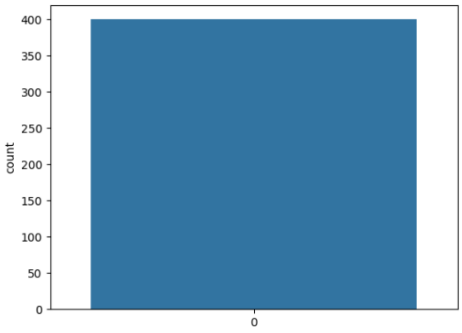
[40] sns.countplot(data['class'])

<Axes: ylabel='count'>



[41] # perfroming feature scaling operation using standard scaller on X part of the dataset because
there different type of values in the columns

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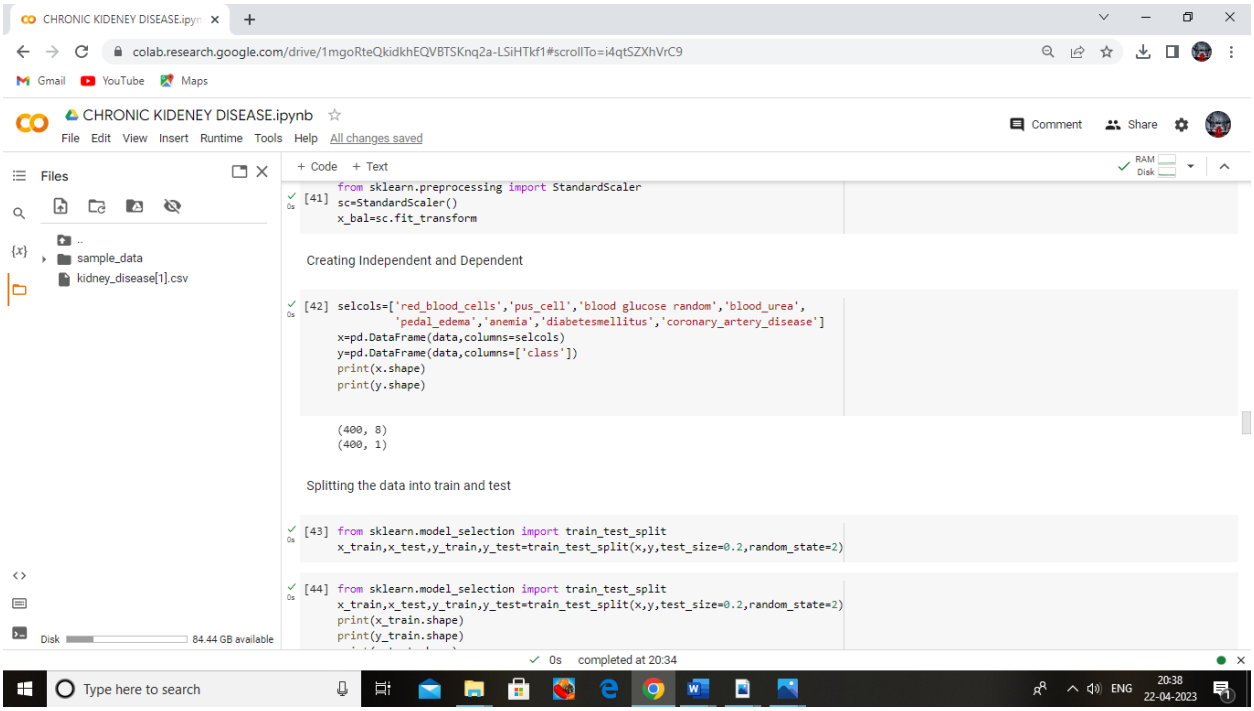
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RAM
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[41] from sklearn.preprocessing import StandardScaler
sc=StandardScaler()
x_bal=sc.fit_transform
Creating Independent and Dependent
[42] selcols=['red_blood_cells','pus_cell','blood glucose random','blood_urea',
'pedal_edema','anemia','diabetesmellitus','coronary_artery_disease']
x=pd.DataFrame(data,columns=selcols)
y=pd.DataFrame(data,columns=['class'])
print(x.shape)
print(y.shape)
(400, 8)
(400, 1)
Splitting the data into train and test
[43] from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.2,random_state=2)
[44] from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.2,random_state=2)
print(x_train.shape)
print(y_train.shape)
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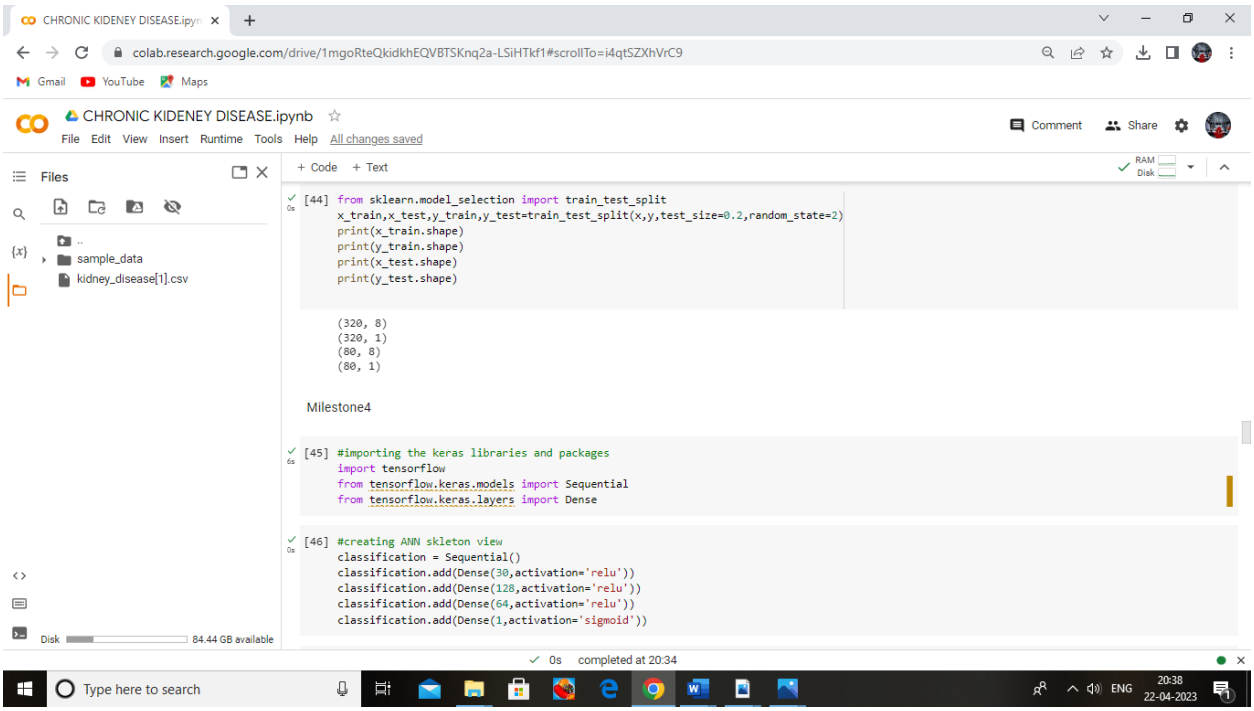
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[44] from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.2,random_state=2)
print(x_train.shape)
print(y_train.shape)
print(x_test.shape)
print(y_test.shape)
(320, 8)
(320, 1)
(80, 8)
(80, 1)
Milestone4
[45] #importing the keras libraries and packages
import tensorflow
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense
[46] #creating ANN skleton view
classification = Sequential()
classification.add(Dense(30,activation='relu'))
classification.add(Dense(128,activation='relu'))
classification.add(Dense(64,activation='relu'))
classification.add(Dense(1,activation='sigmoid'))
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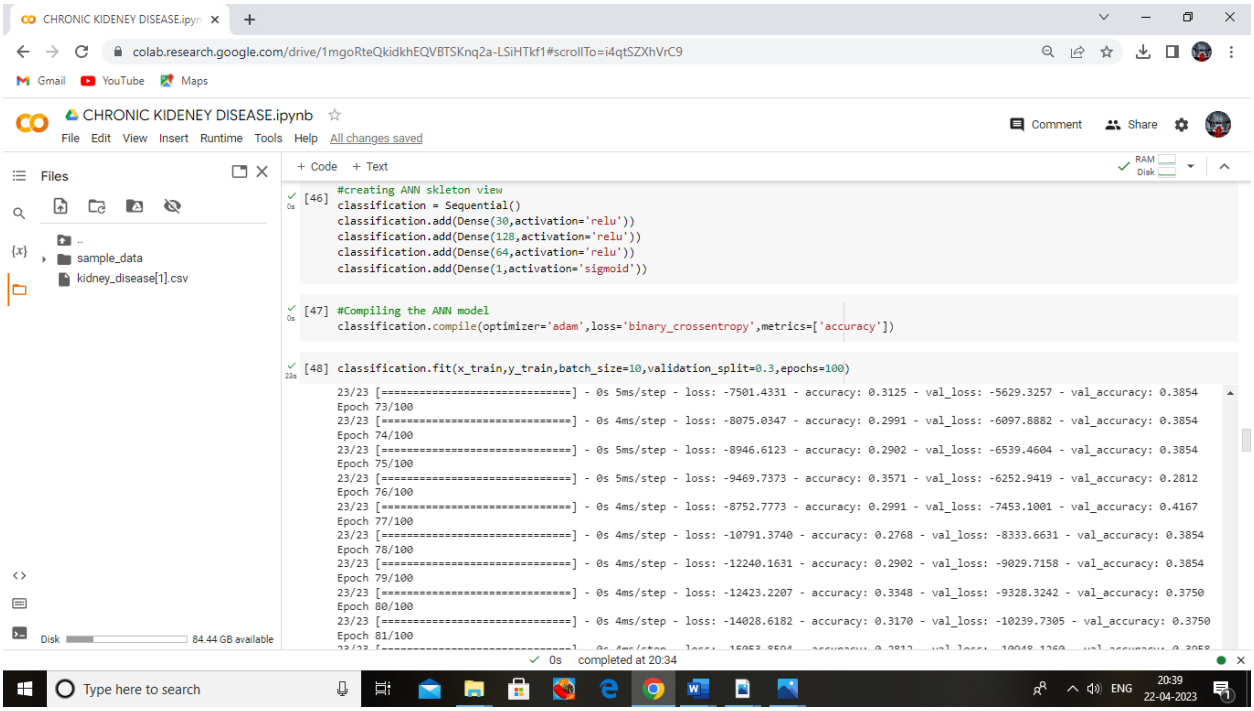
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kidney_disease[1].csv
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[46] #creating ANN skleton view
classification = Sequential()
classification.add(Dense(30,activation='relu'))
classification.add(Dense(128,activation='relu'))
classification.add(Dense(64,activation='relu'))
classification.add(Dense(1,activation='sigmoid'))
[47] #Compiling the ANN model
classification.compile(optimizer='adam',loss='binary_crossentropy',metrics=['accuracy'])
[48] classification.fit(x_train,y_train,batch_size=10,validation_split=0.3,epochs=100)
23/23 [==============================] - 0s 5ms/step - loss: -7501.4331 - accuracy: 0.3125 - val_loss: -5629.3257 - val_accuracy: 0.3854
Epoch 73/100
23/23 [==============================] - 0s 4ms/step - loss: -8075.0347 - accuracy: 0.2991 - val_loss: -6097.8882 - val_accuracy: 0.3854
Epoch 74/100
23/23 [==============================] - 0s 5ms/step - loss: -8946.6123 - accuracy: 0.2902 - val_loss: -6539.4604 - val_accuracy: 0.3854
Epoch 75/100
23/23 [==============================] - 0s 5ms/step - loss: -9469.7373 - accuracy: 0.3571 - val_loss: -6252.9419 - val_accuracy: 0.2812
Epoch 76/100
23/23 [==============================] - 0s 4ms/step - loss: -8752.7773 - accuracy: 0.2991 - val_loss: -7453.1001 - val_accuracy: 0.4167
Epoch 77/100
23/23 [==============================] - 0s 4ms/step - loss: -10791.3740 - accuracy: 0.2768 - val_loss: -8333.6631 - val_accuracy: 0.3854
Epoch 78/100
23/23 [==============================] - 0s 4ms/step - loss: -12240.1631 - accuracy: 0.2902 - val_loss: -9029.7158 - val_accuracy: 0.3854
Epoch 79/100
23/23 [==============================] - 0s 4ms/step - loss: -12423.2207 - accuracy: 0.3348 - val_loss: -9328.3242 - val_accuracy: 0.3750
Epoch 80/100
23/23 [==============================] - 0s 4ms/step - loss: -14028.6182 - accuracy: 0.3170 - val_loss: -10239.7305 - val_accuracy: 0.3750
Epoch 81/100
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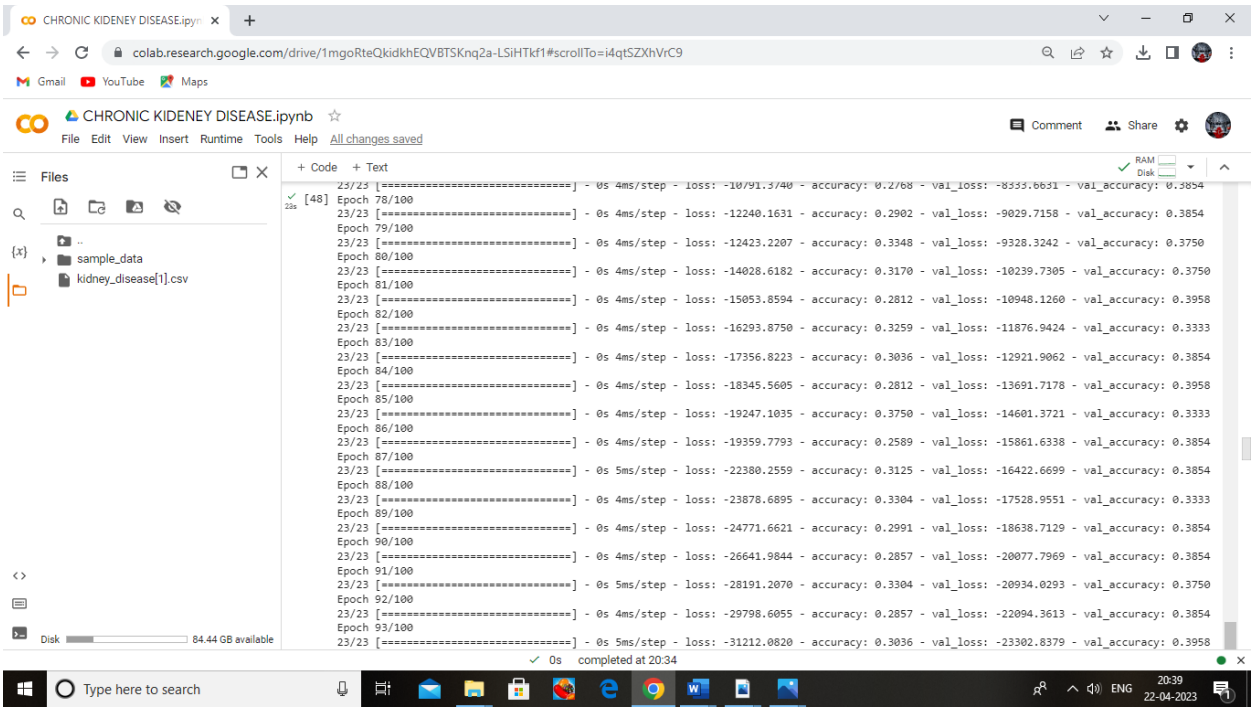
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kidney_disease[1].csv
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[48] Epoch 78/100
23/23 [==============================] - 0s 4ms/step - loss: -12240.1631 - accuracy: 0.2902 - val_loss: -9029.7158 - val_accuracy: 0.3854
Epoch 79/100
23/23 [==============================] - 0s 4ms/step - loss: -12423.2207 - accuracy: 0.3348 - val_loss: -9328.3242 - val_accuracy: 0.3750
Epoch 80/100
23/23 [==============================] - 0s 4ms/step - loss: -14028.6182 - accuracy: 0.3170 - val_loss: -10239.7305 - val_accuracy: 0.3750
Epoch 81/100
23/23 [==============================] - 0s 4ms/step - loss: -15053.8594 - accuracy: 0.2812 - val_loss: -10948.1260 - val_accuracy: 0.3958
Epoch 82/100
23/23 [==============================] - 0s 4ms/step - loss: -16293.8750 - accuracy: 0.3259 - val_loss: -11876.9424 - val_accuracy: 0.3333
Epoch 83/100
23/23 [==============================] - 0s 4ms/step - loss: -17356.8223 - accuracy: 0.3036 - val_loss: -12921.9062 - val_accuracy: 0.3854
Epoch 84/100
23/23 [==============================] - 0s 4ms/step - loss: -18345.5605 - accuracy: 0.2812 - val_loss: -13691.7178 - val_accuracy: 0.3958
Epoch 85/100
23/23 [==============================] - 0s 4ms/step - loss: -19247.1035 - accuracy: 0.3750 - val_loss: -14601.3721 - val_accuracy: 0.3333
Epoch 86/100
23/23 [==============================] - 0s 4ms/step - loss: -19359.7793 - accuracy: 0.2589 - val_loss: -15861.6338 - val_accuracy: 0.3854
Epoch 87/100
23/23 [==============================] - 0s 5ms/step - loss: -22380.2559 - accuracy: 0.3125 - val_loss: -16422.6699 - val_accuracy: 0.3854
Epoch 88/100
23/23 [==============================] - 0s 4ms/step - loss: -23878.6895 - accuracy: 0.3304 - val_loss: -17528.9551 - val_accuracy: 0.3333
Epoch 89/100
23/23 [==============================] - 0s 4ms/step - loss: -24771.6621 - accuracy: 0.2991 - val_loss: -18638.7129 - val_accuracy: 0.3854
Epoch 90/100
23/23 [==============================] - 0s 4ms/step - loss: -26641.9844 - accuracy: 0.2857 - val_loss: -20077.7969 - val_accuracy: 0.3854
Epoch 91/100
23/23 [==============================] - 0s 5ms/step - loss: -28191.2070 - accuracy: 0.3304 - val_loss: -20934.0293 - val_accuracy: 0.3750
Epoch 92/100
23/23 [==============================] - 0s 4ms/step - loss: -29798.6055 - accuracy: 0.2857 - val_loss: -22094.3613 - val_accuracy: 0.3854
Epoch 93/100
23/23 [==============================] - 0s 5ms/step - loss: -31212.0820 - accuracy: 0.3036 - val_loss: -23302.8379 - val_accuracy: 0.3958
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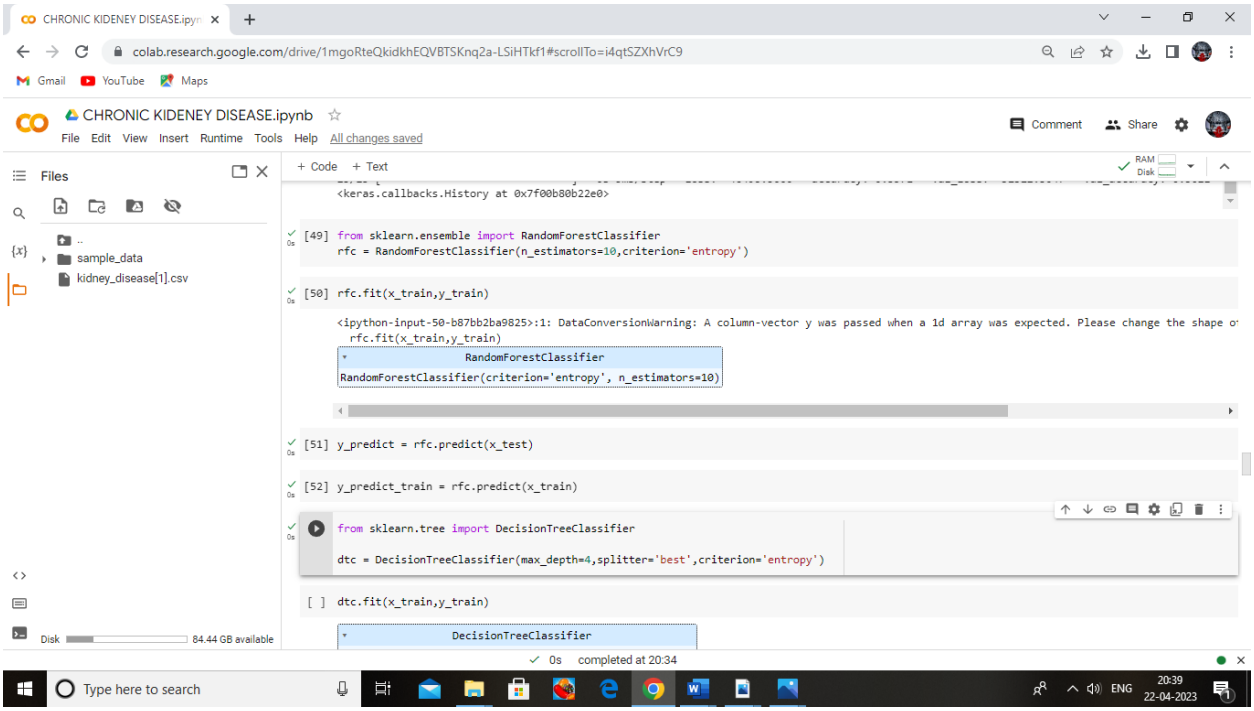
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<keras.callbacks.History at 0x7f00b80b22e0>
[49] from sklearn.ensemble import RandomForestClassifier
rfc = RandomForestClassifier(n_estimators=10,criterion='entropy')
[50] rfc.fit(x_train,y_train)
<ipython-input-50-b87bb2ba9825>:1: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the shape of
rfc.fit(x_train,y_train)
RandomForestClassifier
RandomForestClassifier(criterion='entropy', n_estimators=10)
[51] y_predict = rfc.predict(x_test)
[52] y_predict_train = rfc.predict(x_train)
from sklearn.tree import DecisionTreeClassifier
dtc = DecisionTreeClassifier(max_depth=4,splitter='best',criterion='entropy')
[ ] dtc.fit(x_train,y_train)
DecisionTreeClassifier
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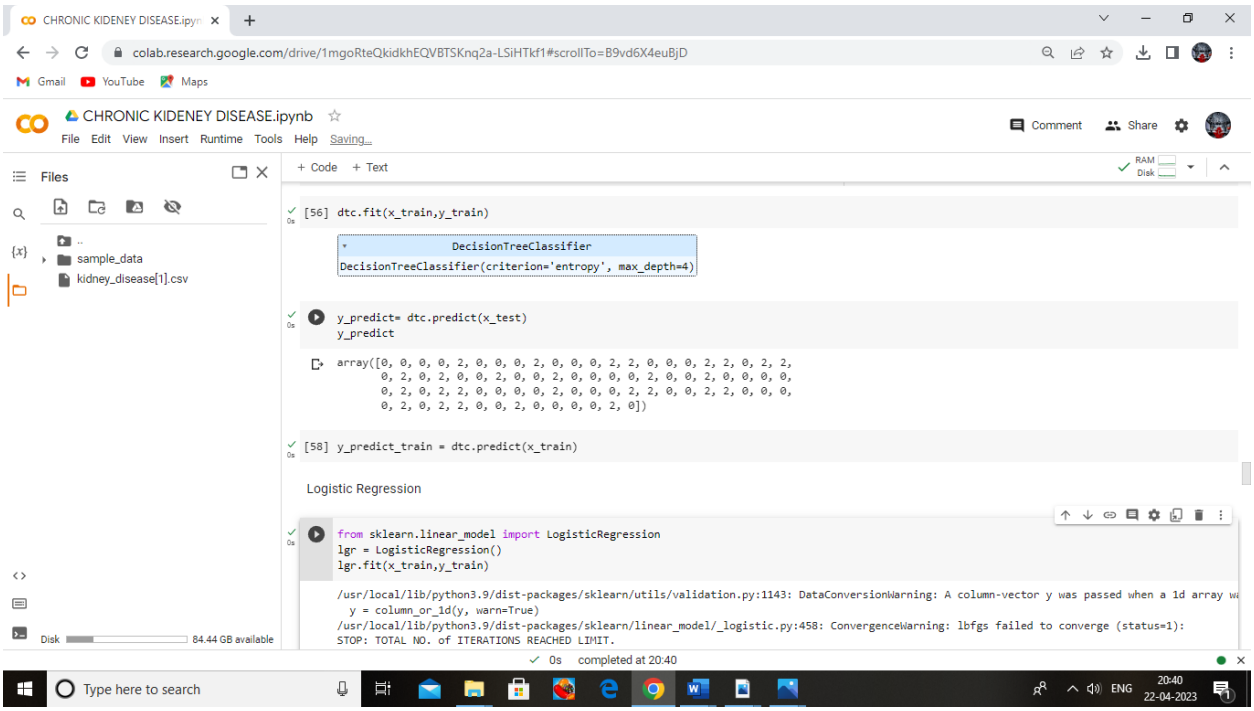
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kidney_disease[1].csv
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[56] dtc.fit(x_train,y_train)
DecisionTreeClassifier
DecisionTreeClassifier(criterion='entropy', max_depth=4)
y_predict= dtc.predict(x_test)
y_predict
array([0, 0, 0, 0, 2, 0, 0, 0, 2, 0, 0, 0, 2, 2, 0, 0, 0, 2, 2, 0, 2, 2,
0, 2, 0, 2, 0, 0, 2, 0, 0, 2, 0, 0, 0, 0, 2, 0, 0, 2, 0, 0, 0, 0,
0, 2, 0, 2, 2, 0, 0, 0, 0, 2, 0, 0, 0, 2, 2, 0, 0, 2, 2, 0, 0, 0,
0, 2, 0, 2, 2, 0, 0, 2, 0, 0, 0, 0, 2, 0])
[58] y_predict_train = dtc.predict(x_train)
Logistic Regression
from sklearn.linear_model import LogisticRegression
lgr = LogisticRegression()
lgr.fit(x_train,y_train)
/usr/local/lib/python3.9/dist-packages/sklearn/utils/validation.py:1143: DataConversionWarning: A column-vector y was passed when a 1d array wa
y = column_or_1d(y, warn=True)
/usr/local/lib/python3.9/dist-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
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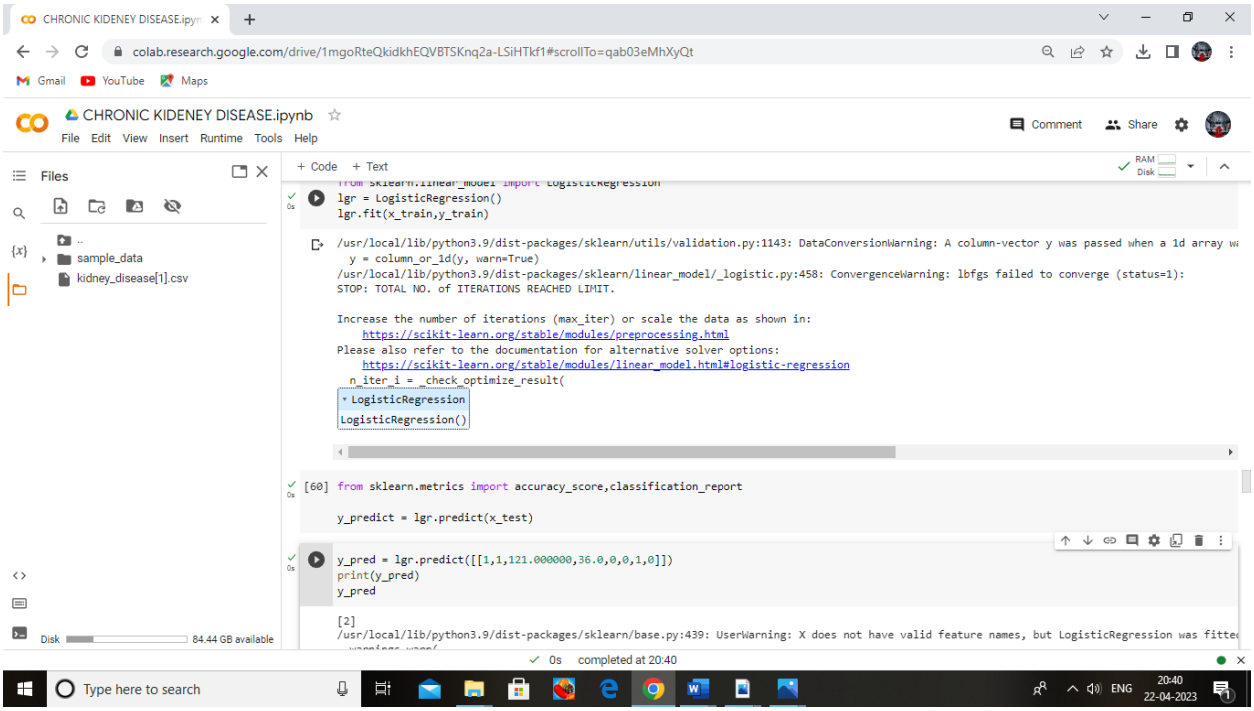
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lgr = LogisticRegression()
lgr.fit(x_train,y_train)
/usr/local/lib/python3.9/dist-packages/sklearn/utils/validation.py:1143: DataConversionWarning: A column-vector y was passed when a 1d array wa
y = column_or_1d(y, warn=True)
/usr/local/lib/python3.9/dist-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
Increase the number of iterations (max_iter) or scale the data as shown in:
https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
n_iter_i = _check_optimize_result(
LogisticRegression
LogisticRegression()
[60] from sklearn.metrics import accuracy_score,classification_report
y_predict = lgr.predict(x_test)
y_pred = lgr.predict([[1,1,121.000000,36.0,0,0,1,0]])
print(y_pred)
y_pred
[2]
/usr/local/lib/python3.9/dist-packages/sklearn/base.py:439: UserWarning: X does not have valid feature names, but LogisticRegression was fitte
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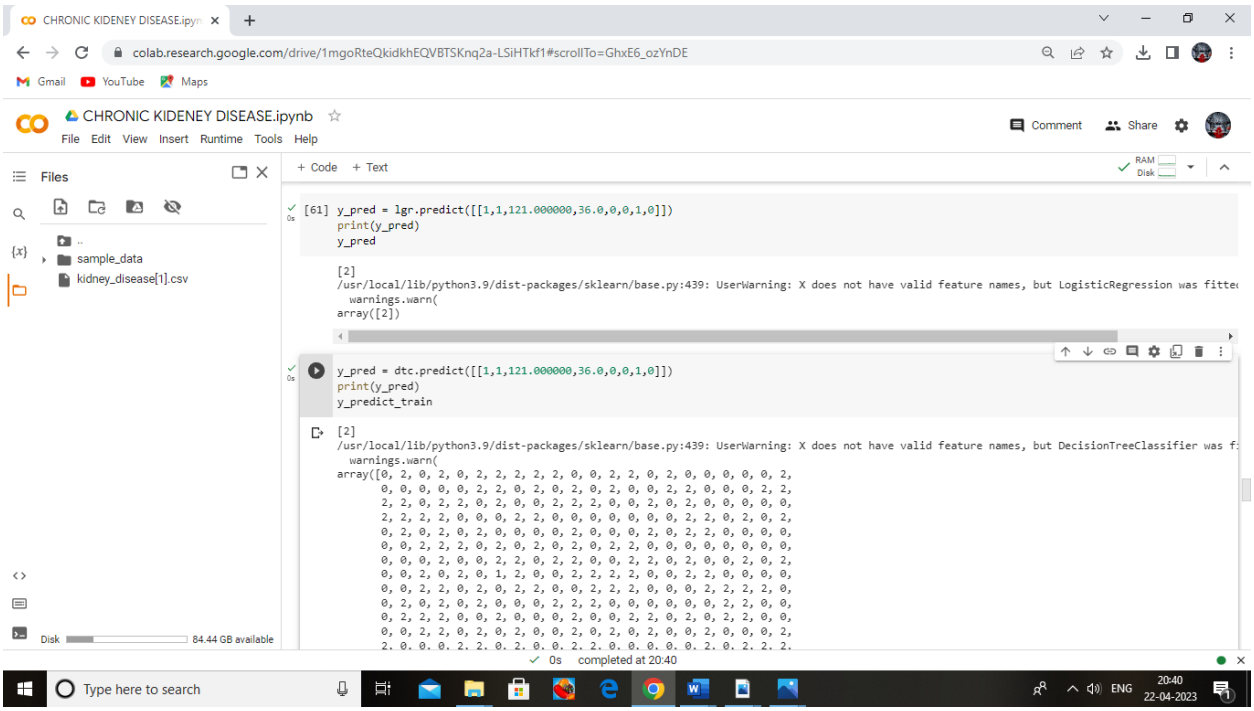
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[61] y_pred = lgr.predict([[1,1,121.000000,36.0,0,0,1,0]])
print(y_pred)
y_pred
[2]
/usr/local/lib/python3.9/dist-packages/sklearn/base.py:439: UserWarning: X does not have valid feature names, but LogisticRegression was fitte
warnings.warn(
array([2])
y_pred = dtc.predict([[1,1,121.000000,36.0,0,0,1,0]])
print(y_pred)
y_predict_train
[2]
/usr/local/lib/python3.9/dist-packages/sklearn/base.py:439: UserWarning: X does not have valid feature names, but DecisionTreeClassifier was f
warnings.warn(
array([0, 2, 0, 2, 0, 2, 2, 2, 2, 2, 0, 0, 2, 2, 0, 2, 0, 0, 0, 0, 0, 2,
0, 0, 0, 0, 0, 2, 2, 0, 2, 0, 2, 0, 2, 0, 2, 0, 0, 0, 2, 2,
2, 2, 0, 2, 2, 0, 2, 0, 0, 0, 2, 2, 2, 0, 0, 2, 0, 2, 0, 0,
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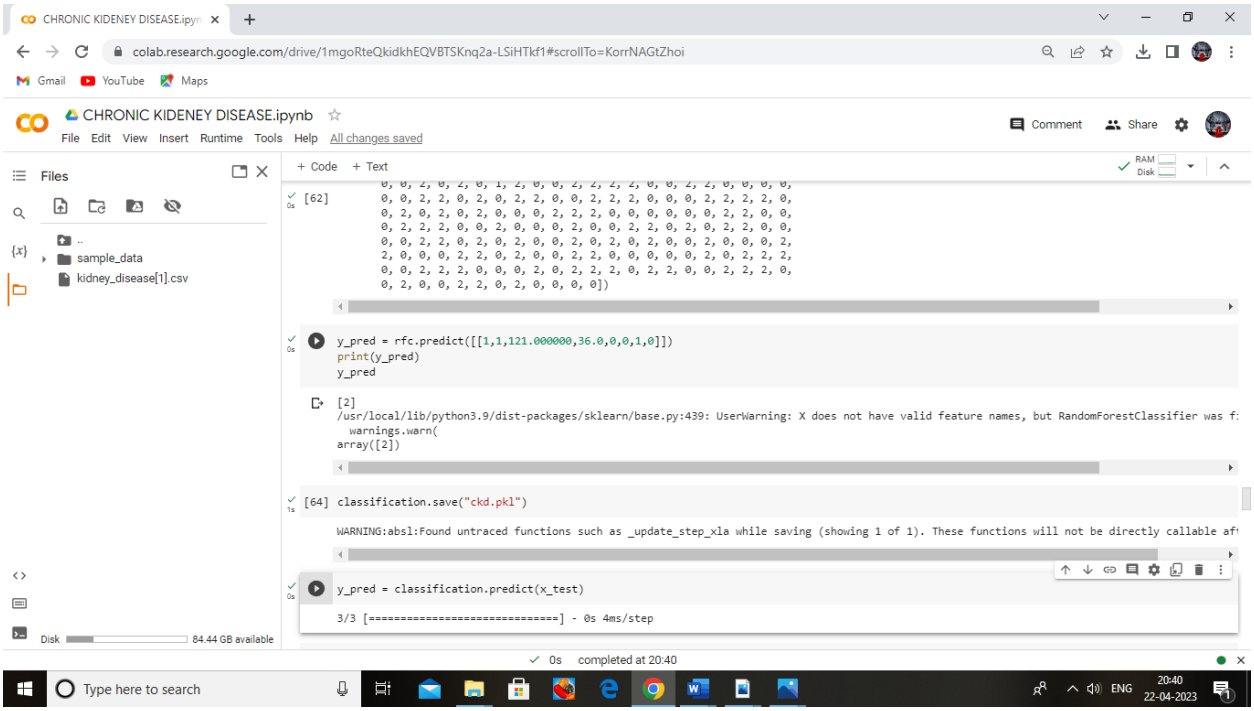
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[62]
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y_pred = rfc.predict([[1,1,121.000000,36.0,0,0,1,0]])
print(y_pred)
y_pred
[2]
/usr/local/lib/python3.9/dist-packages/sklearn/base.py:439: UserWarning: X does not have valid feature names, but RandomForestClassifier was f
warnings.warn(
array([2])
[64] classification.save("ckd.pkl")
WARNING:absl:Found untraced functions such as _update_step_xla while saving (showing 1 of 1). These functions will not be directly callable af
y_pred = classification.predict(x_test)
3/3 [==============================] - 0s 4ms/step
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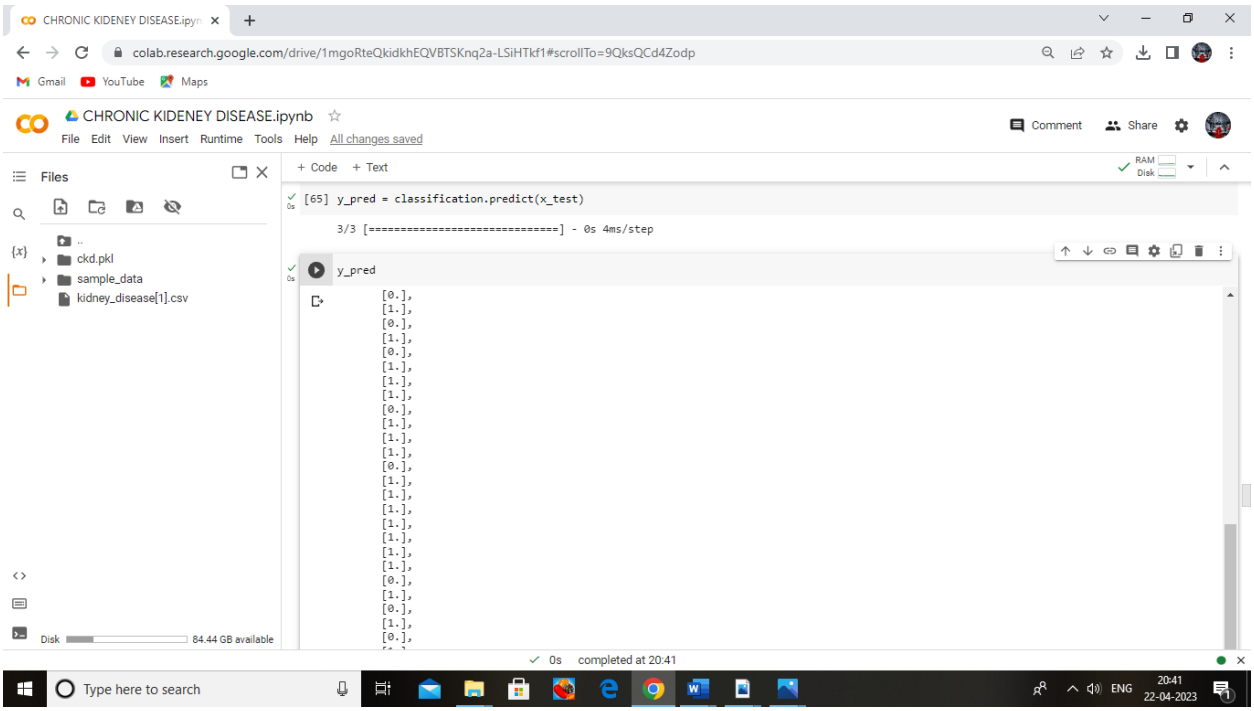
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[65] y_pred = classification.predict(x_test)
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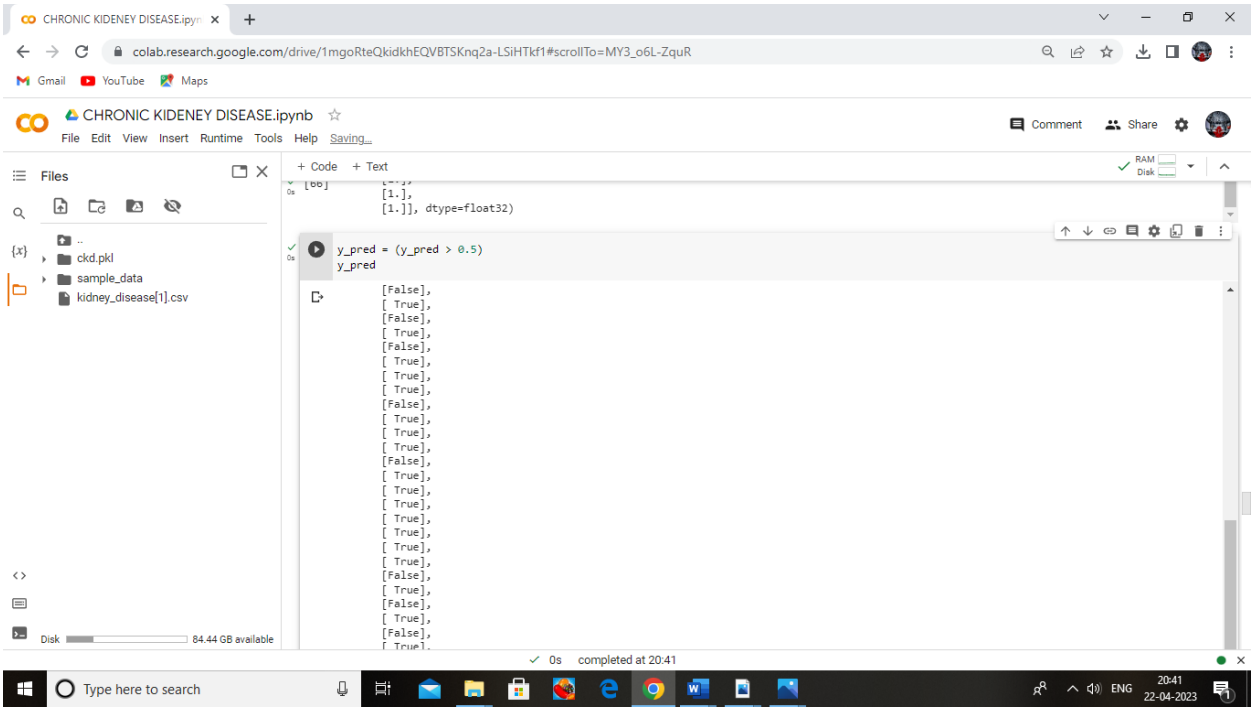
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[1.],
[1.]], dtype=float32)
y_pred = (y_pred > 0.5)
y_pred
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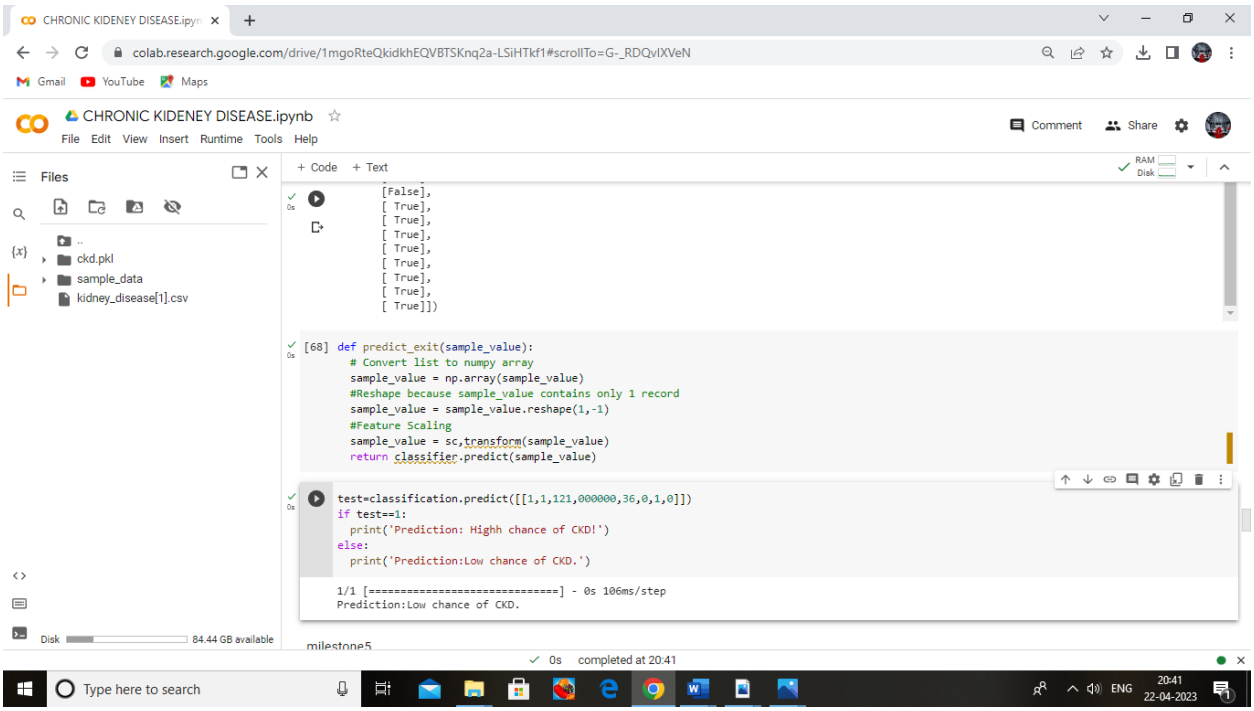
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[False],
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[True],
[True],
[True],
[True]])
[68] def predict_exit(sample_value):
# Convert list to numpy array
sample_value = np.array(sample_value)
#Reshape because sample_value contains only 1 record
sample_value = sample_value.reshape(1,-1)
#Feature Scaling
sample_value = sc.transform(sample_value)
return classifier.predict(sample_value)
test=classification.predict([[1,1,121,000000,36,0,1,0]])
if test==1:
print('Prediction: Highh chance of CKD!')
else:
print('Prediction:Low chance of CKD.')
1/1 [==============================] - 0s 106ms/step
Prediction:Low chance of CKD.
milestone5
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```
[68] def predict_exit(sample_value):
       # Convert list to numpy array
       sample_value = np.array(sample_value)
       #Reshape because sample_value contains only 1 record
       sample_value = sample_value.reshape(1,-1)
       #Feature Scaling
       sample_value = sc.transform(sample_value)
       return classifier.predict(sample_value)
```

```
test=classification.predict([[1,1,121,000000,36,0,1,0]])
if test==1:
  print('Prediction: Highh chance of CKD!')
else:
  print('Prediction:Low chance of CKD.')
```

```
1/1 [==============================] - 0s 106ms/step
Prediction:Low chance of CKD.
```

milestone5

```
from sklearn import model_selection
```

```
[ ]     dfs =[]
models =[
          ('LogReg',LogisticRegression()),
          ('RF', RandomForestClassifier())
```

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```
[72] from sklearn.metrics import confusion_matrix
     cm = confusion_matrix(y_test,y_predict)
     cm
```

```
array([[48,  0,  5],
       [ 1,  0,  0],
       [ 0,  0, 26]])
```

```
# Plotting confusion matrix
plt.figure(figsize=(8,6))
sns.heatmap(cm, cmap='Blues',annot=True,xticklabels=['no ckd','ckd'],yticklabels=['no,ckd','ckd'])
plt.xlabel('predicted values')
plt.ylabel('Actual values')
plt.title('Confusion Matrix for Logistic Regression model')
plt.show()
```

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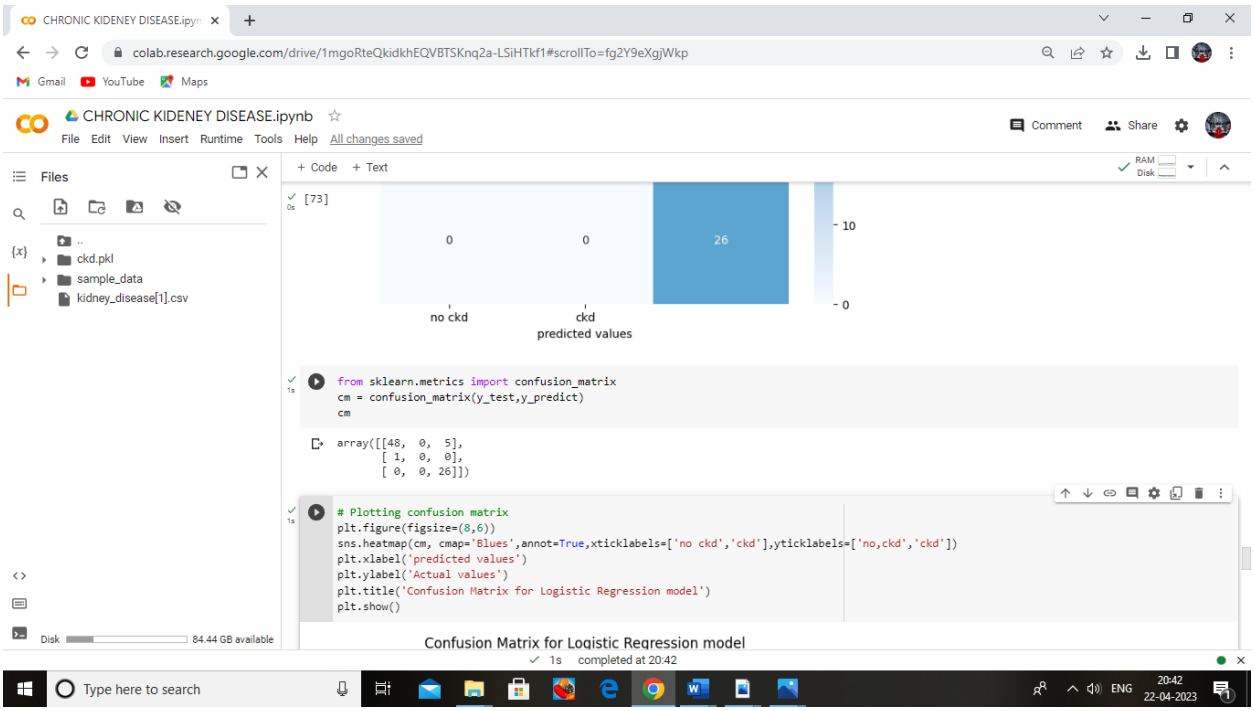
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from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test,y_predict)
cm
array([[48, 0, 5],
[1, 0, 0],
[0, 0, 26]])
# Plotting confusion matrix
plt.figure(figsize=(8,6))
sns.heatmap(cm, cmap='Blues',annot=True,xticklabels=['no ckd','ckd'],yticklabels=['no,ckd','ckd'])
plt.xlabel('predicted values')
plt.ylabel('Actual values')
plt.title('Confusion Matrix for Logistic Regression model')
plt.show()
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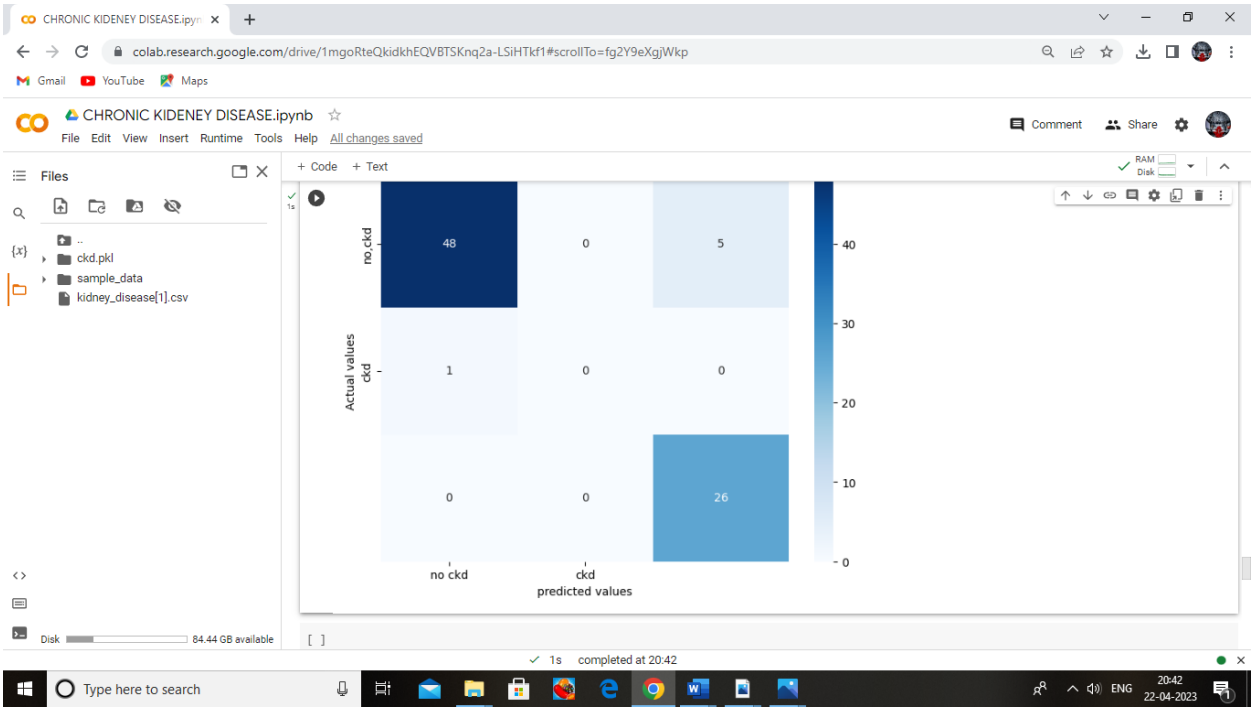
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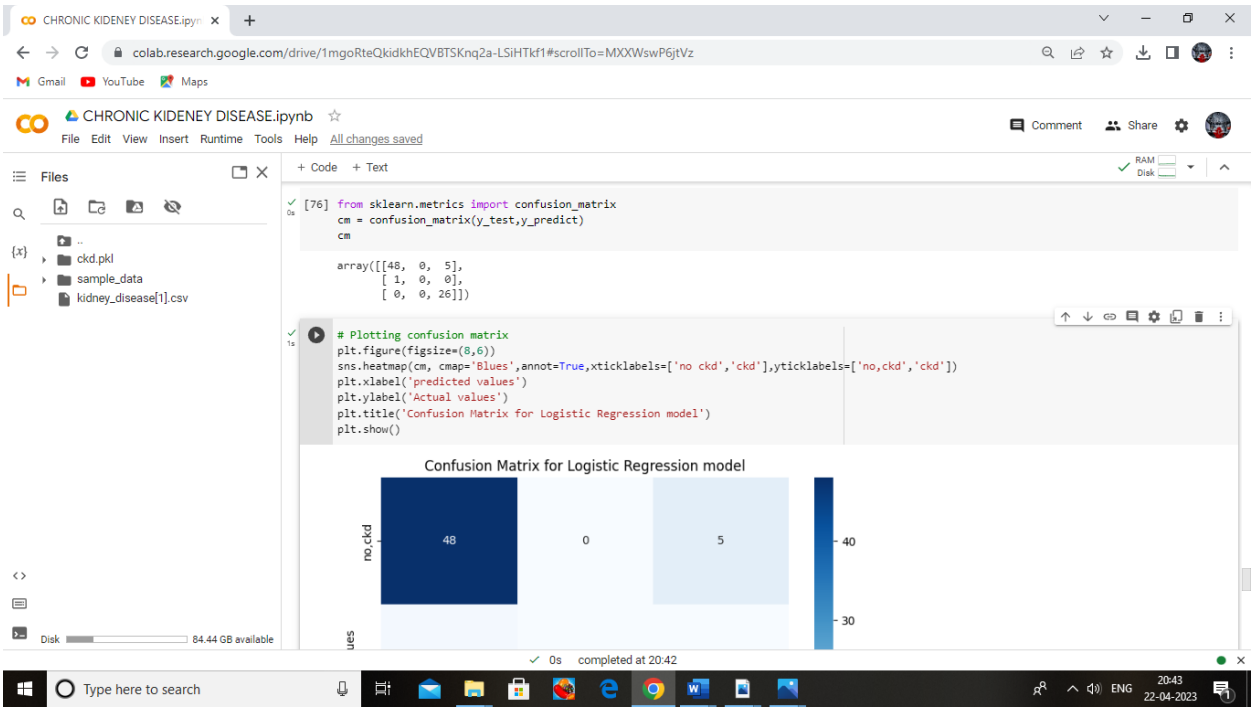
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[76] from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test,y_predict)
cm
array([[48, 0, 5],
[1, 0, 0],
[0, 0, 26]])
# Plotting confusion matrix
plt.figure(figsize=(8,6))
sns.heatmap(cm, cmap='Blues',annot=True,xticklabels=['no ckd','ckd'],yticklabels=['no,ckd','ckd'])
plt.xlabel('predicted values')
plt.ylabel('Actual values')
plt.title('Confusion Matrix for Logistic Regression model')
plt.show()
Confusion Matrix for Logistic Regression model
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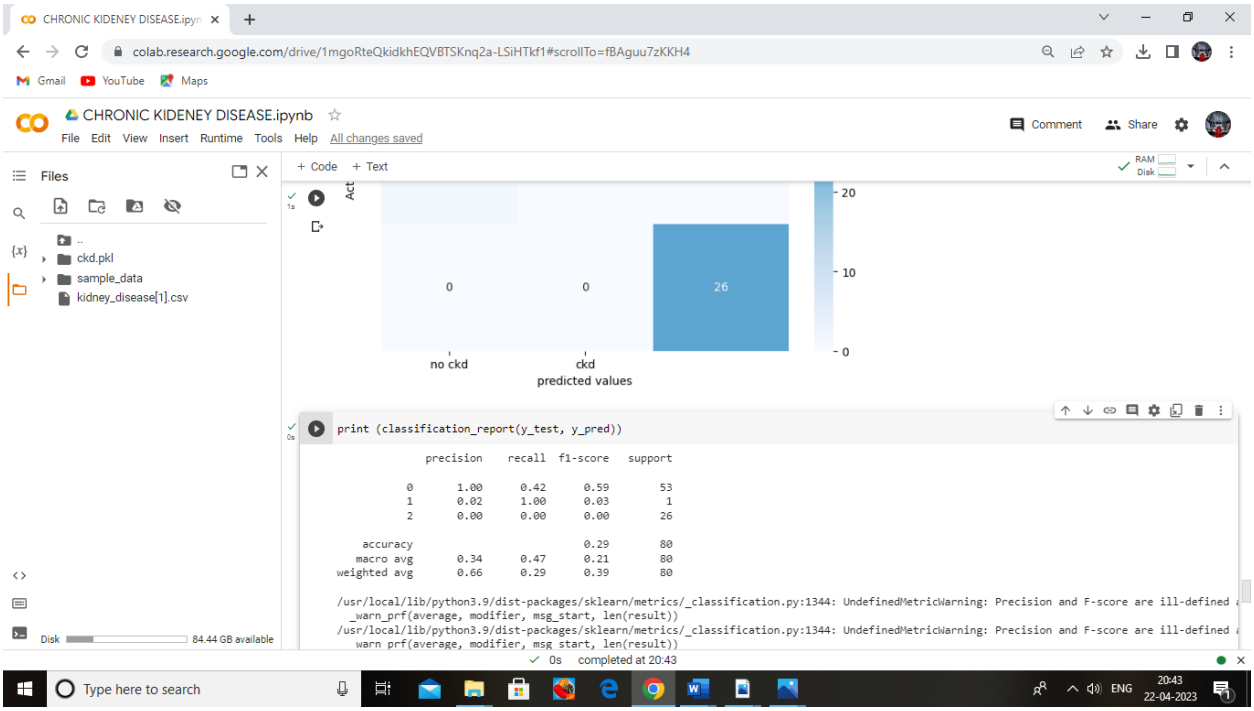
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predicted values
print (classification_report(y_test, y_pred))
precision recall f1-score support
0 1.00 0.42 0.59 53
1 0.02 1.00 0.03 1
2 0.00 0.00 0.00 26
accuracy 0.29 80
macro avg 0.34 0.47 0.21 80
weighted avg 0.66 0.29 0.39 80
/usr/local/lib/python3.9/dist-packages/sklearn/metrics/_classification.py:1344: UndefinedMetricWarning: Precision and F-score are ill-defined
_warn_prf(average, modifier, msg_start, len(result))
/usr/local/lib/python3.9/dist-packages/sklearn/metrics/_classification.py:1344: UndefinedMetricWarning: Precision and F-score are ill-defined
warn_prf(average, modifier, msg_start, len(result))
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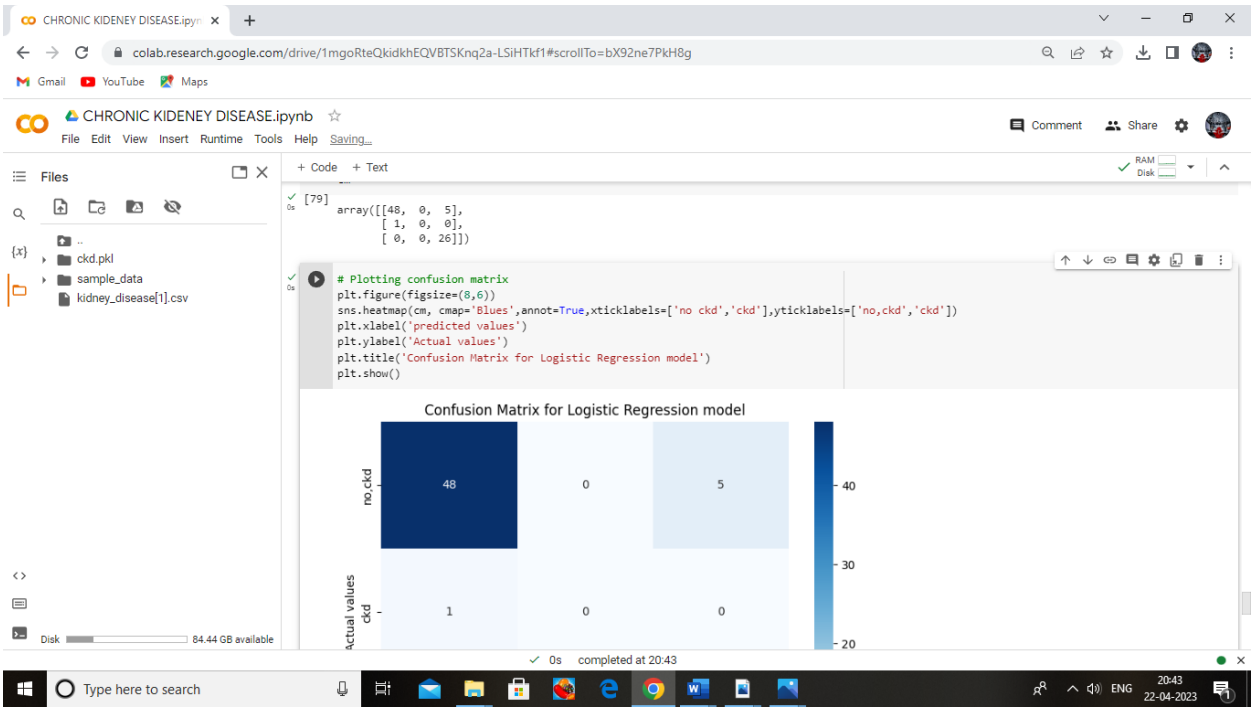
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[79]
array([[48, 0, 5],
[1, 0, 0],
[0, 0, 26]])
# Plotting confusion matrix
plt.figure(figsize=(8,6))
sns.heatmap(cm, cmap='Blues',annot=True,xticklabels=['no ckd','ckd'],yticklabels=['no,ckd','ckd'])
plt.xlabel('predicted values')
plt.ylabel('Actual values')
plt.title('Confusion Matrix for Logistic Regression model')
plt.show()
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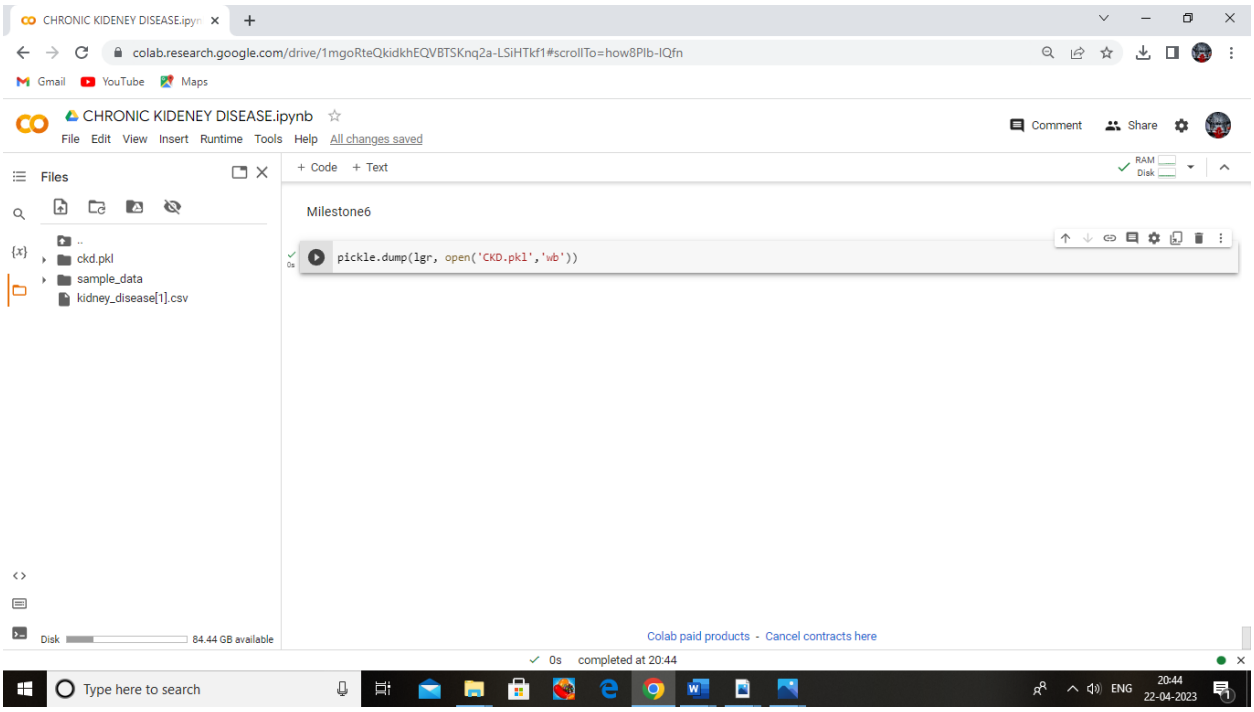
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