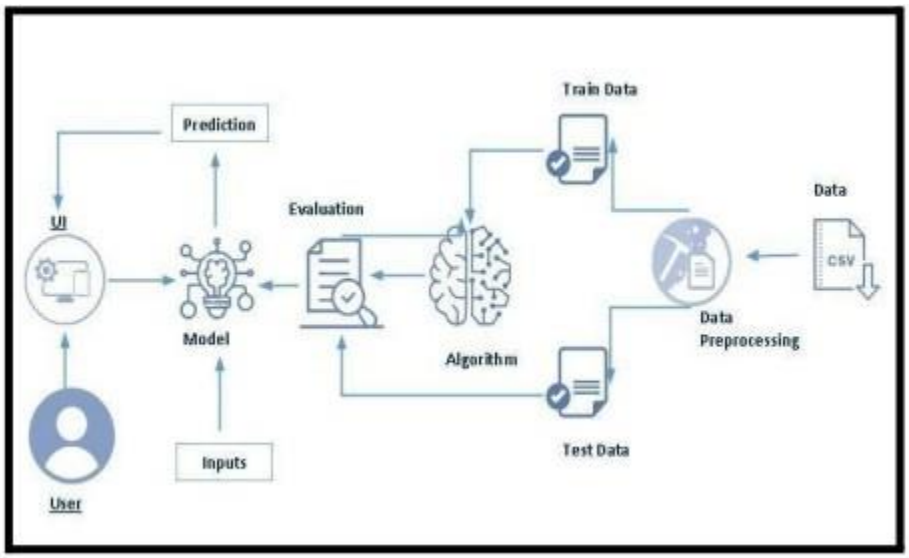
EARLY PREDICTION FOR CHRONIC KIDNEY DISEASE DETECTION:A PROGRESSIVE APPROACH TO HEALTH MANAGEMENT

OVERVIEW:

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 and 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.

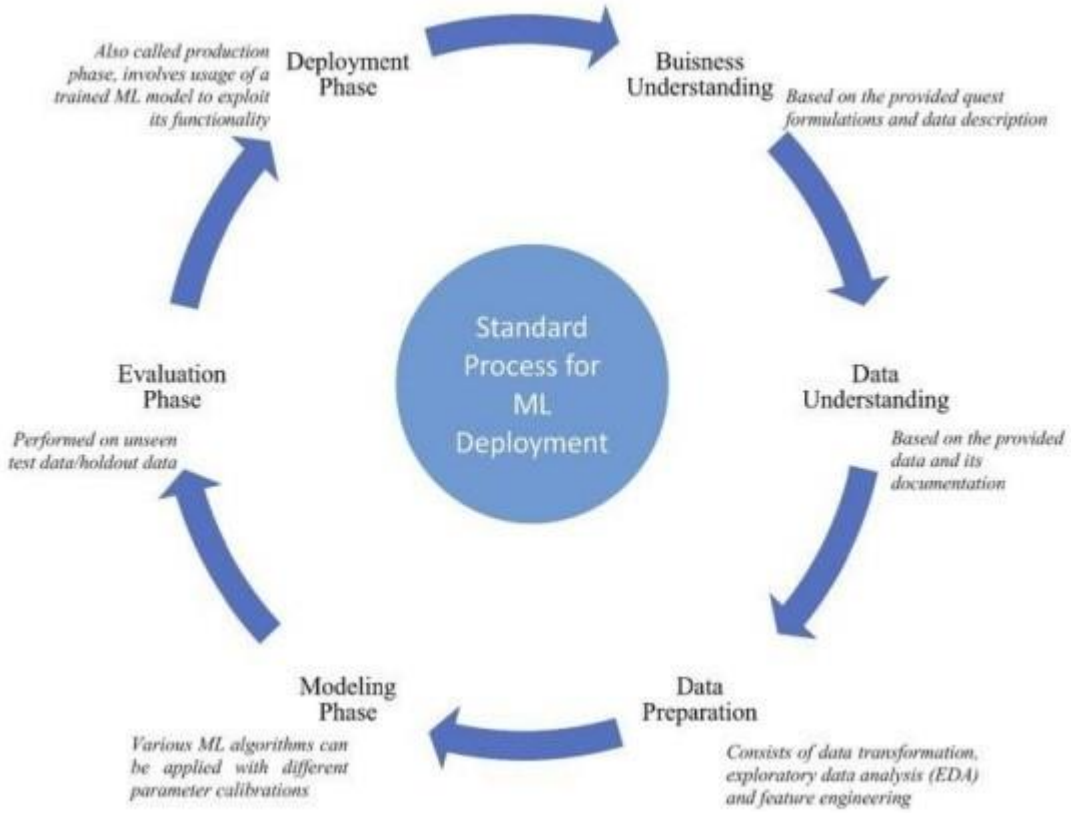
TECHINICAL ARCHITECTURE:



TECHINICAL ABOUT THE PROJECT:

Machine learnng is merely based on predictions madenbased onnexperience.It enables machines to make data-driven decisions,which is more efficient than explicitly programming to carry out certain tasks.These algorithms are designed

in a fashion that gives exposure to new data that can help organisations learn and improve their strategies.



A PROJECT DESCRIPTION:

Kidney diseases (acute and chronic) are an important public health problem, and chronic kidney disease (CKD) is a noncommunicable disease of global significance. CKD is defined by the presence of kidney damage or reduced kidney function for a period of at least 3 months, with implications for health. The level of disease severity has been used to classify CKD into various stages, from persistent kidney damage only with preserved kidney function (estimated glomerular filtration rate (eGFR) >90ml/min/1.73m2; stage 1) to persistent kidney damage accompanied by mild reduction in kidney function (eGFR 60-90; stage 2) to moderate to severe reduction in kidney function (eGFR 30-60; stage 3, and eGFR 15-30; stage 4). Stage 5 (eGFR <15) refers to the advanced stage of CKD also termed “kidney failure,” which can progress to end-stage kidney disease (ESKD), where dialysis therapy or kidney transplantation is essential to maintain life.

CDC’s Kidney Disease Surveillance System is the first surveillance system of its

kind developed in the United States to focus on tracking kidney disease prior to ESKD. It has a serious responsibility for serving as a timely and comprehensive surveillance and information system. Findings from this system highlighted on the project's website are intended to raise awareness of multiple facets of kidney disease (prevalence and incidence, risk factors, awareness, quality of care, health outcomes, and its social determinants of health), to spur individuals, communities, policymakers, researchers, clinicians, and health systems, to bring about incremental and sustainable improvements to reduce the impact of this often-neglected non-communicable disease.

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,

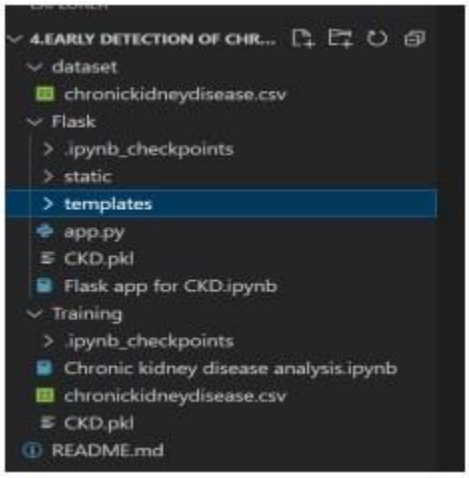
- Define Problem / Problem Understanding
  - Specify the business problem
  - Business requirements
  - Literature Survey
  - Social or Business Impact.
- Data Collection & Preparation
  - Collect the dataset
  - Data Preparation
- Exploratory Data Analysis
  - Descriptive statistical
  - Visual Analysis
- Model Building
  - Training the model in multiple algorithms

- Testing the model

- Performance Testing & Evaluate the results
  - Testing model with multiple evaluation metrics
  - Evaluate the results
- Model Deployment
  - Save the best model
  - Integrate with Web Framework
- Project Demonstration & Documentation
  - Record explanation Video for project end to end solution
  - Project Documentation-Step by step project development procedure

PROJECT STRUCTURE:

Create the Project folder which contains files as shown below



- We are building a flask application which needs HTML pages stored in the templates folde

PURPOSE:

There are limited data to describe academic achievement outcomes for children with mild to moderate pediatric chronic kidney disease (CKD). The objective of this study was to describe the prevalence of low academic achievement in patients with mild to moderate CKD.

Design, Setting, Participants, and Measurements:

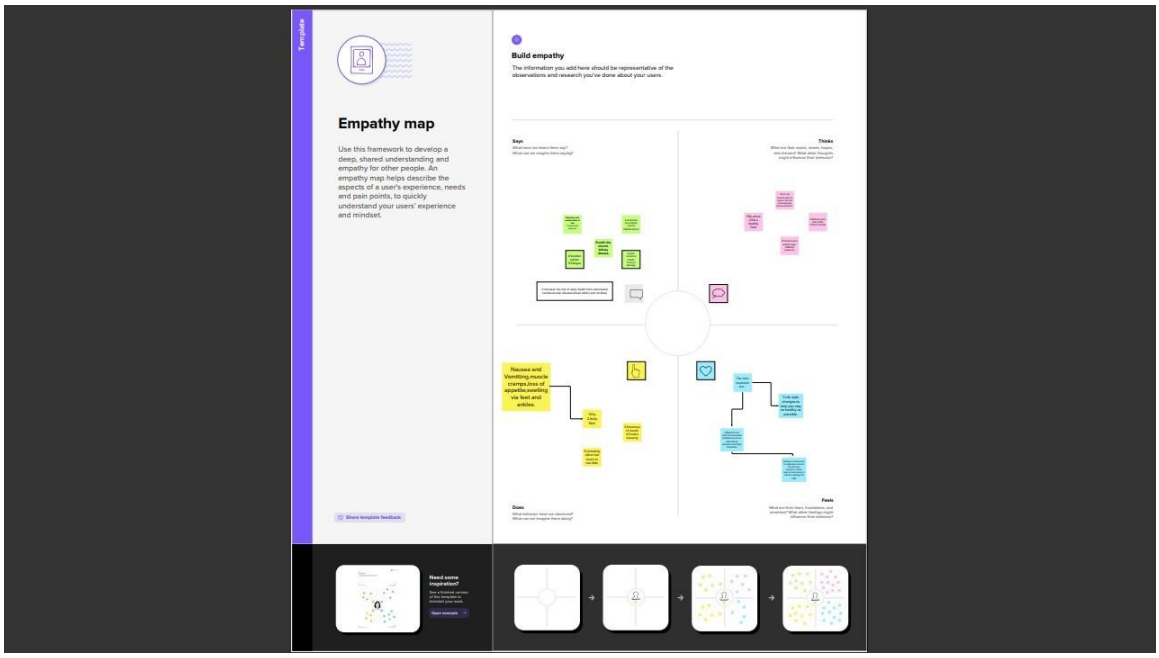
Wechsler Individual Achievement Test, Second Edition, Abbreviated (WIAT-II-A) data were collected at entry into the Chronic Kidney Disease in Children (CKiD) study. Achievement in basic reading, spelling, mathematics, and total achievement was evaluated with a focus on the effects of comorbid CKD-related variables, neurocognitive, and school-based characteristics on academic achievement.

The physical sequelae of pediatric chronic kidney disease (CKD) are well characterized [1]. Data support the parallel presence of subtle neurocognitive deficits in even mild to moderate pediatric CKD. Specifically, cognitive executive function, the neurocognitive ability to plan and make complex decisions, may be impaired in CKD [2]. As with executive function, behavioral concerns are reported by parents of children with CKD [3]. Although the specific mechanisms of neurocognitive and behavioral dysfunction associated with CKD are not fully understood, there is evidence to suggest that decline in renal function, early age of onset, and proteinuria increase the risk for neurocognitive and behavioral shortfalls even before the disease advances to the need for dialysis or transplantation [4].

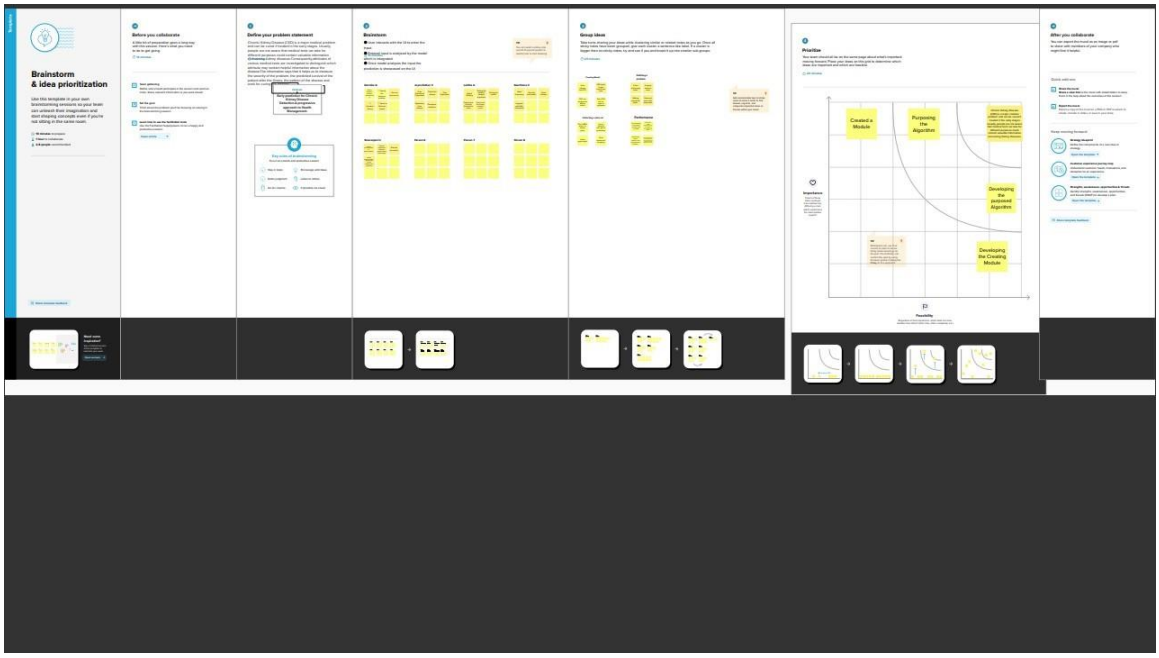
Problem Definition And Design Thinking :

Machine learning has become an increasingly popular tool in recent years ,given its ability to automatically detect patterns in data and make predictions about future events .this can be extremely useful for making decisions in a wide range of domains,from financial trading to medical diagnoses Empathy Map

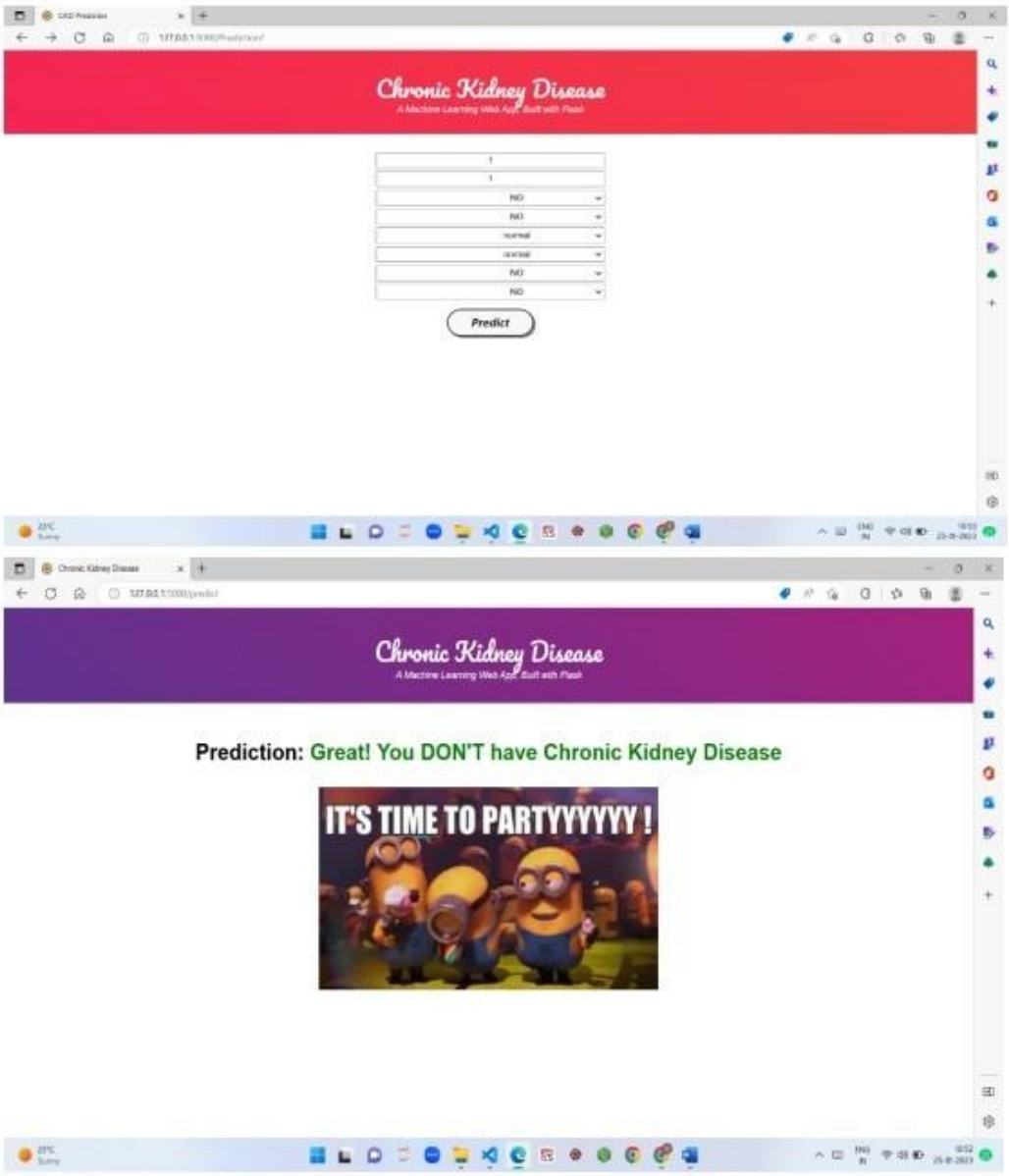
2.1 EMPATHY MAP:



2.2 Ideationand Brainstorming Map:



RESULT:



ADVANTAGE:

The number of patients on renal replacement therapy has doubled every decade since 1980, and prevalence of chronic kidney disease (CKD) in the early stages is also markedly increased.

In addition, CKD is a significant risk factor for cardiovascular morbidity and mortality. The only effective approach to this problem is prevention and early detection of CKD. In recent years, screening studies have been carried out in several countries

The findings have defined the scope of the problem and indicated which population

groups are at risk of developing CKD. The most numerous are patients with hypertension and diabetes. Also, these studies have indicated that screening should include measurement of serum creatinine for eGFR as well as urine albumin.

Early detection of CKD allows proper management that could slow down CKD progression, prevent cardiovascular and other comorbidities and enable timely initiation of dialysis. Screening for CKD could be best managed by partnership between primary care physicians and nephrologists. It is necessary to educate primary care physicians about CKD, its risk factors and associated co-morbidities.

Although multiple benefits of screening for CKD are doubtless, the results obtained by screening should be interpreted with caution, bearing in mind that screening detects only markers of kidney disease but not the disease itself.

DISADVANTAGES:

Having CKD increases the chances of having heart disease and stroke. Managing high blood pressure, blood sugar, and cholesterol levels—all factors that increase the risk for heart disease and stroke—is very important for people with CKD.

Anemia. This happens when your kidneys don't make enough erythropoietin (EPO), which affects their ability to make red blood cells. ...

Bone weakness. ...

Fluid retention. ...

Gout. ...

Heart disease. ...

High blood pressure (hypertension). ...

Hyperkalemia. ...

Metabolic acidosis.

APPLICATIONS:

The main treatments are: lifestyle changes – to help you stay as healthy as possible. medicine – to control associated problems, such as high blood pressure and high cholesterol. dialysis – treatment to replicate some of the kidney's functions, which may be necessary in advanced (stage 5) CKD.

Lifestyle changes

The following lifestyle measures are usually recommended for people with kidney disease:

stop smoking if you

smoke eat a healthy,

balanced diet
Medicine

There's no medicine specifically for CKD, but medicine can help control many of the problems that cause the condition and the complications that can happen as a result of it.

You may need to take medicine to treat or prevent the different problems caused by CKD.

High blood pressure

Good control of blood pressure is vital to protect the kidneys.

People with kidney disease should usually aim to get their blood pressure down to below
140/90mmHg, but you should aim to get it down to below 130/80mmHg if you also have diabetes

Most people know that a major function of the kidneys is to remove waste products and excess fluid from the body. These waste products and excess fluid are removed through the urine. The production of urine involves highly complex steps of excretion and re-absorption.

Tests of renal function can be used to assess overall renal function by direct measurement or estimation of the glomerular filtration rate. Estimation of the GFR is utilized to determine the presence of renal impairment.18-Jul-2022

The critical regulation of the body's salt, potassium and acid content is performed by the kidneys. The kidneys also produce hormones that affect the function of other organs. For example, a hormone produced by the kidneys stimulates red blood cell production

Nephrology (from Greek nephros "kidney", combined with the suffix -logy, "the study of") is a specialty of adult internal medicine and pediatric medicine that concerns the study of the kidneys, specifically normal kidney function (renal physiology) and kidney disease (renal pathophysiology), the preservation of kidney.

Dialysis is a treatment for people whose kidneys are failing. When you have kidney failure, your kidneys don't filter blood the way they should. As a result, wastes and toxins build up in your bloodstream. Dialysis does the work of your kidneys, removing waste products and excess fluid from the blood.

CONCLUSION:

Chronic renal failure represents a critical period in the evolution of chronic renal disease and is associated with complications and comorbidities that begin early in the course of the disease. These conditions are initially subclinical but progress relentlessly

and may eventually become symptomatic and irreversible. Early in the course of chronic renal failure, these conditions are amenable to interventions with relatively simple treatments that have the potential to prevent adverse outcomes. Fig Fig33 summarises strategies for effective management of chronic renal disease. By acknowledging these facts, we have an excellent opportunity to change the paradigm of management of chronic renal failure and improve patient outcomes.

The perception of advantages and disadvantages of APD differed between patients undergoing APD and CAPD; the former focus on the frequency of bag exchange, whereas the latter focused the size of device.

FUTURESCOPE:

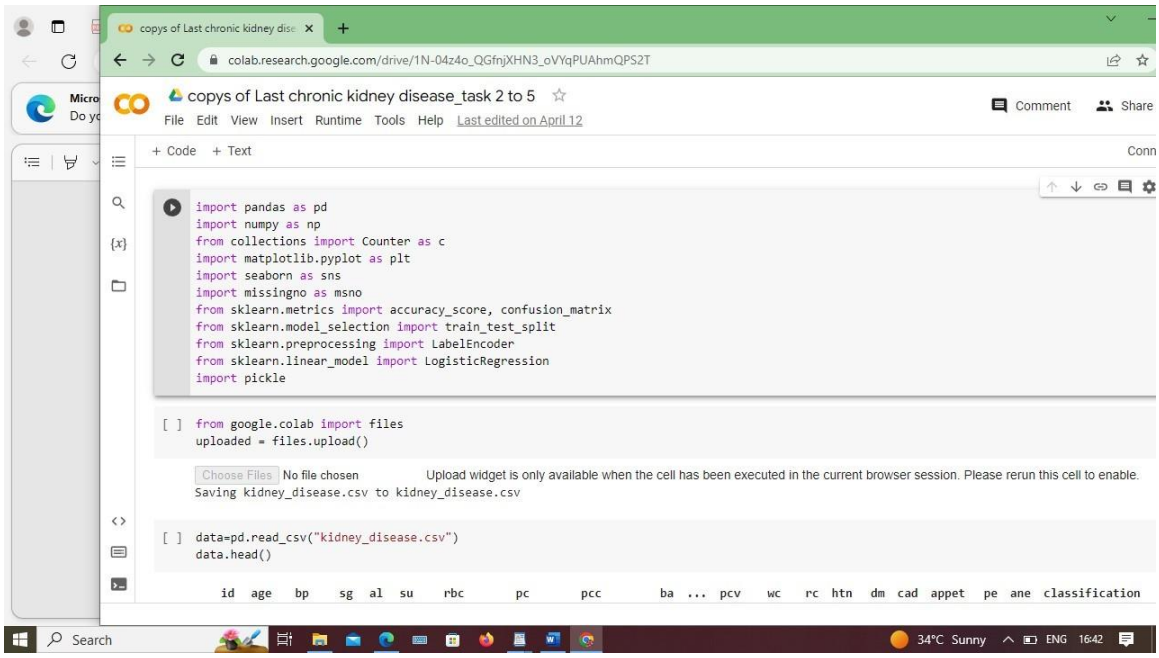
Imaging: assessing nephron number as a determinant of kidney disease and kidney fibrosis

Imaging techniques have the advantage of being non-invasive and, thus, may be safely repeated to evaluate changes, providing information for both kidneys and potentially combining functional with morphological information. The most interesting advances relate to estimation of nephron number, overall kidney functions, fibrosis and new functional magnetic resonance imaging (MRI), as well as ultrasound techniques such as diffusion-weighted MRI (DWI or DW-MRI), blood oxygenation level–dependent MRI (BOLD-MRI), perfusion MRI, hyperpolarized (HP) carbon 13 MRI (13C MRI) and contrast-enhanced ultrasound (CEUS).

CFE-MRI uses ferritin filled with an iron oxide future treatments for kidney disease

Novel therapeutic alternatives for ESRD include wearable artificial kidneys, xenotransplantation, stem cell–based therapy, and bioengineered and bio-artificial kidneys. Of note, one of the main objectives of these novel therapeutic approaches should be to maintain patients at home and to avoid dialysis.

APPENDIX: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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
[ ] from google.colab import files
uploaded = files.upload()
Choose Files No file chosen
Upload widget is only available when the cell has been executed in the current browser session. Please rerun this cell to enable.
Saving kidney_disease.csv to kidney_disease.csv
[ ] data=pd.read_csv("kidney_disease.csv")
data.head()
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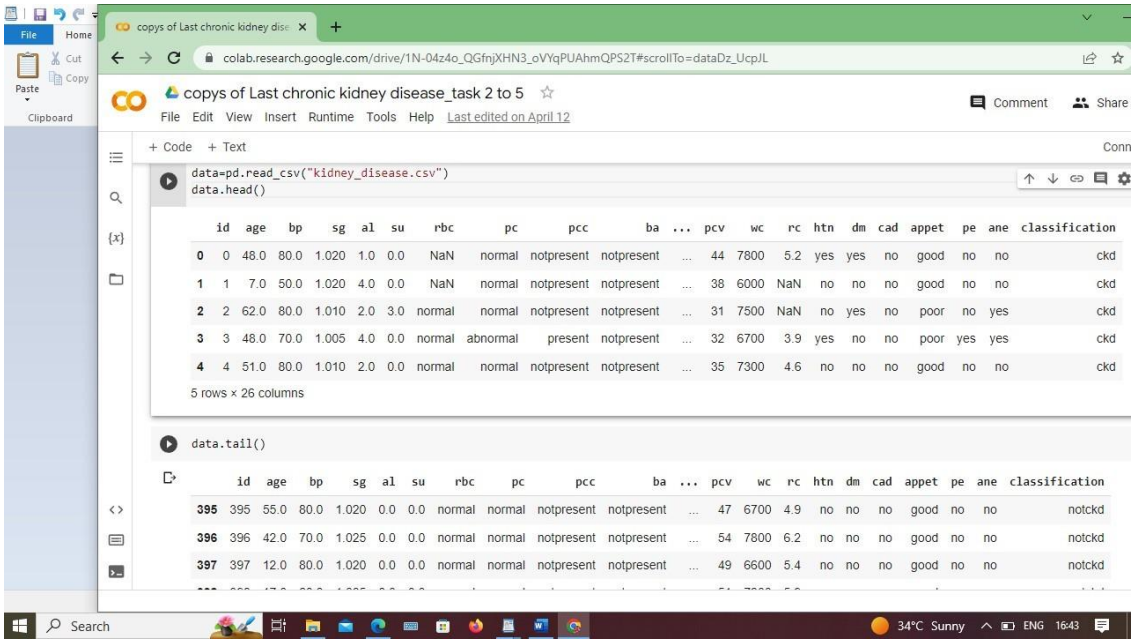
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data=pd.read_csv("kidney_disease.csv")
data.head()
id age bp sg al su rbc pc pcc ba ... pcv wc rc htn dm cad appet pe ane classification
0 0 48.0 80.0 1.020 1.0 0.0 NaN normal notpresent notpresent ... 44 7800 5.2 yes yes no good no no ckd
1 1 7.0 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
5 rows × 26 columns
data.tail()
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395 395 55.0 80.0 1.020 0.0 0.0 normal normal notpresent notpresent ... 47 6700 4.9 no no no good no no notckd
396 396 42.0 70.0 1.025 0.0 0.0 normal normal notpresent notpresent ... 54 7800 6.2 no no no good no no notckd
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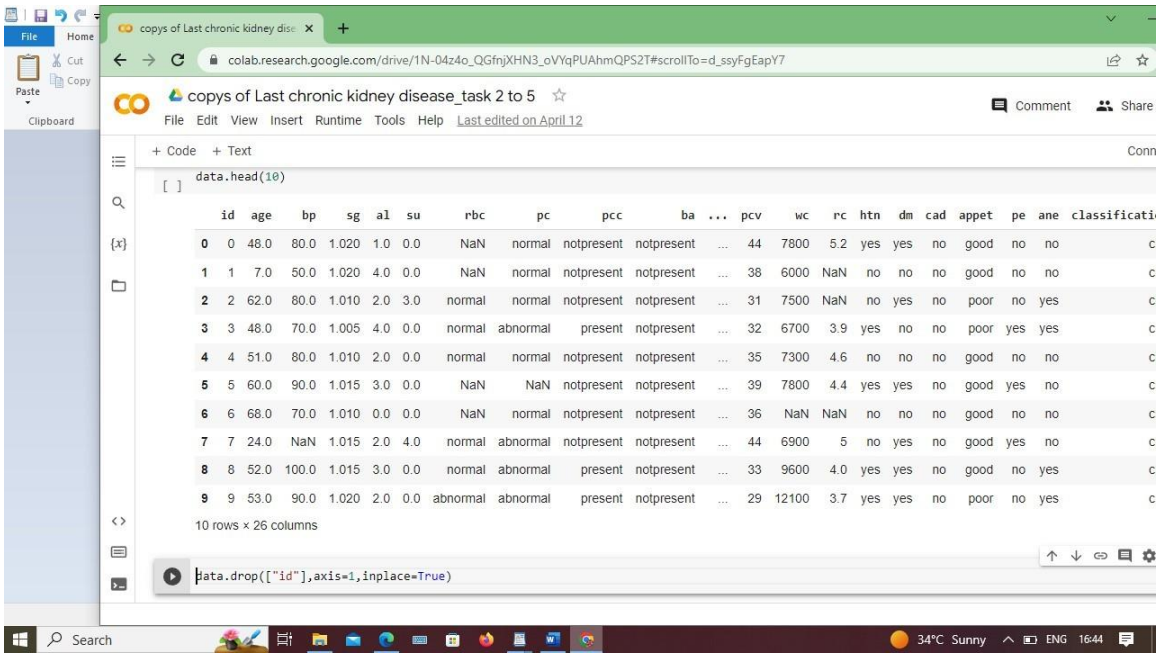
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0 0 48.0 80.0 1.020 1.0 0.0 NaN normal notpresent notpresent ... 44 7800 5.2 yes yes no good no no c
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2 2 62.0 80.0 1.010 2.0 3.0 normal normal notpresent notpresent ... 31 7500 NaN no yes no poor no yes c
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 c
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 c
5 5 60.0 90.0 1.015 3.0 0.0 NaN NaN notpresent notpresent ... 39 7800 4.4 yes yes no good yes no c
6 6 68.0 70.0 1.010 0.0 0.0 NaN normal notpresent notpresent ... 36 NaN NaN no no no good no no c
7 7 24.0 NaN 1.015 2.0 4.0 normal abnormal notpresent notpresent ... 44 6900 5 no yes no good yes no c
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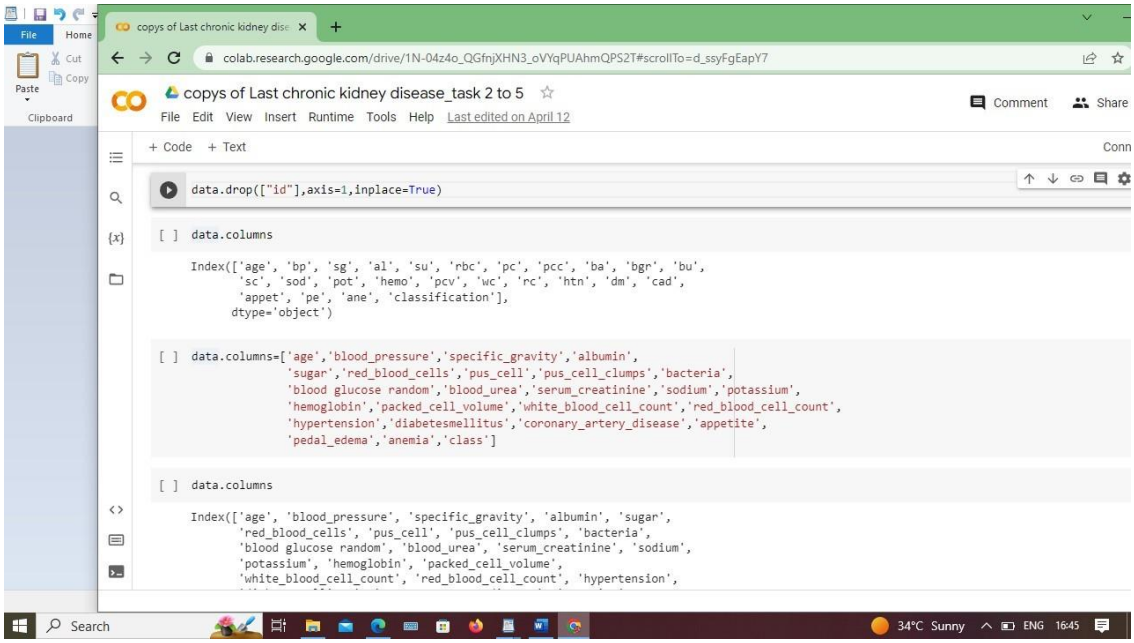
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'hemoglobin','packed_cell_volume','white_blood_cell_count','red_blood_cell_count',
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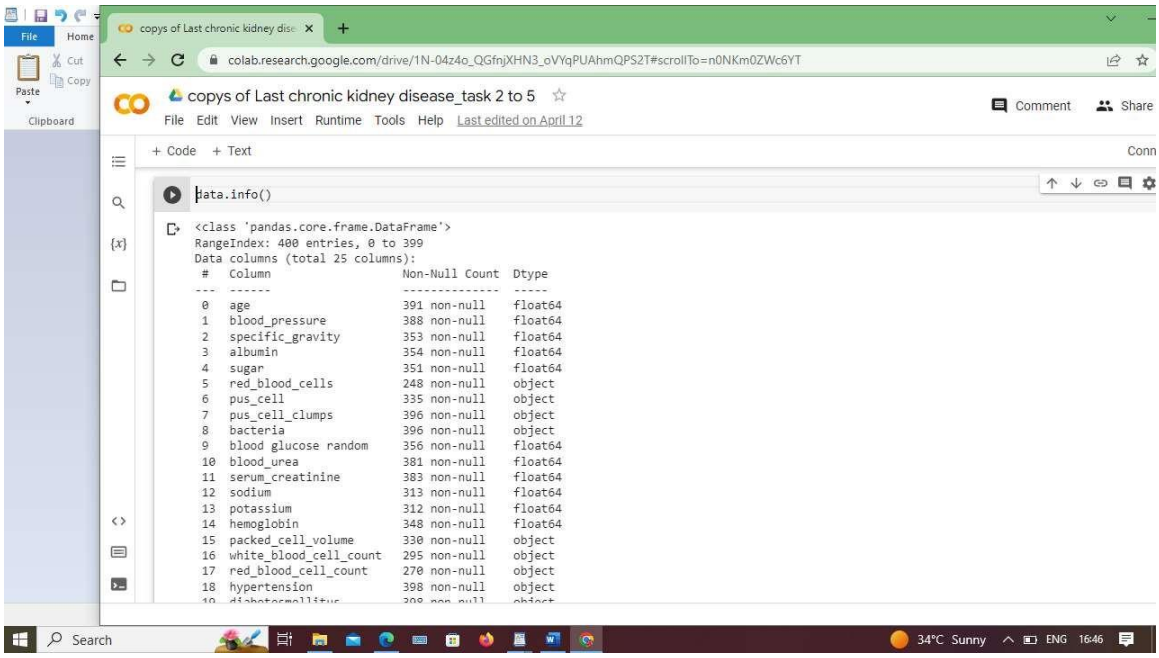
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1 blood_pressure 388 non-null float64
2 specific_gravity 353 non-null float64
3 albumin 354 non-null float64
4 sugar 351 non-null float64
5 red_blood_cells 248 non-null object
6 pus_cell 335 non-null object
7 pus_cell_clumps 396 non-null object
8 bacteria 396 non-null object
9 blood glucose random 356 non-null float64
10 blood_urea 381 non-null float64
11 serum_creatinine 383 non-null float64
12 sodium 313 non-null float64
13 potassium 312 non-null float64
14 hemoglobin 348 non-null float64
15 packed_cell_volume 330 non-null object
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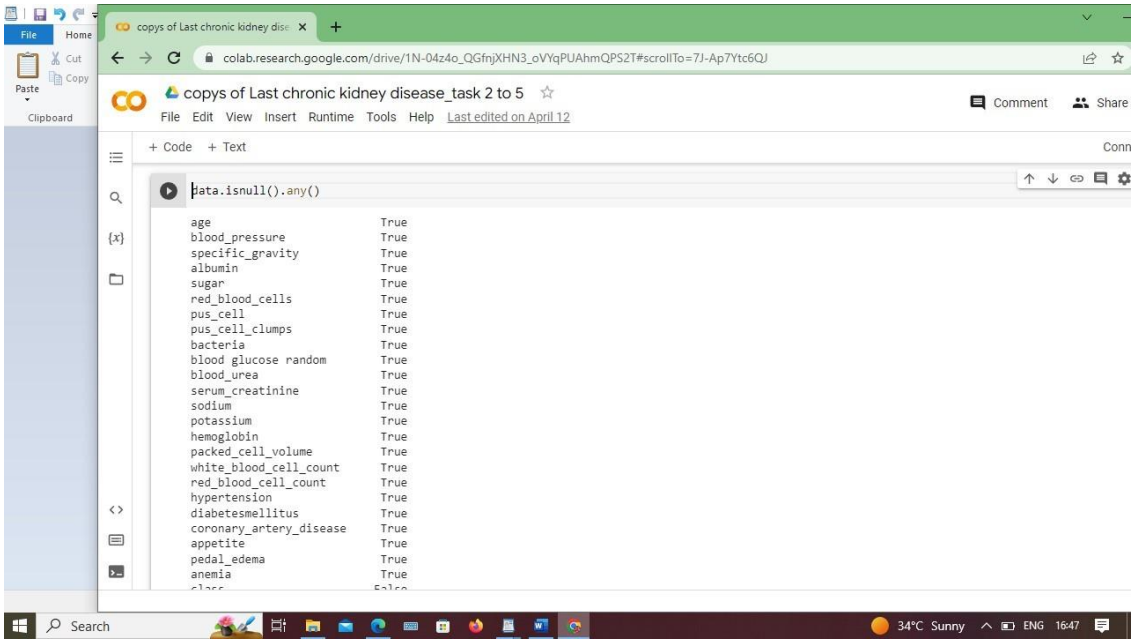
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data.isnull().any()
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specific_gravity True
albumin True
sugar True
red_blood_cells True
pus_cell True
pus_cell_clumps True
bacteria True
blood glucose random True
blood_urea True
serum_creatinine True
sodium True
potassium True
hemoglobin True
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white_blood_cell_count True
red_blood_cell_count True
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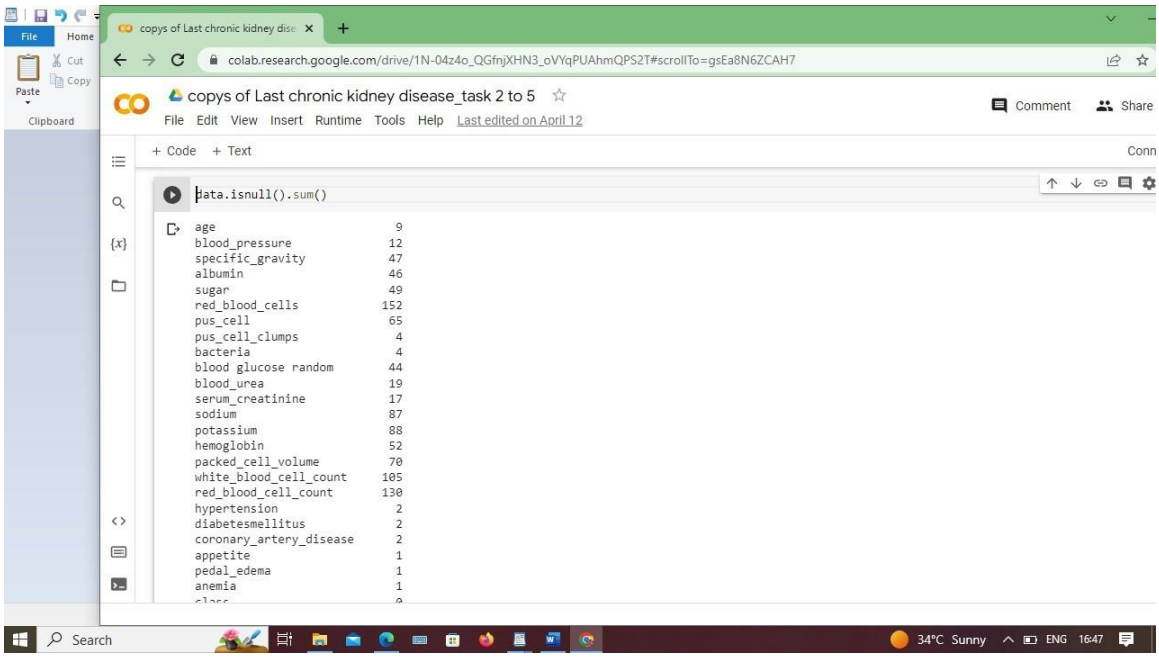

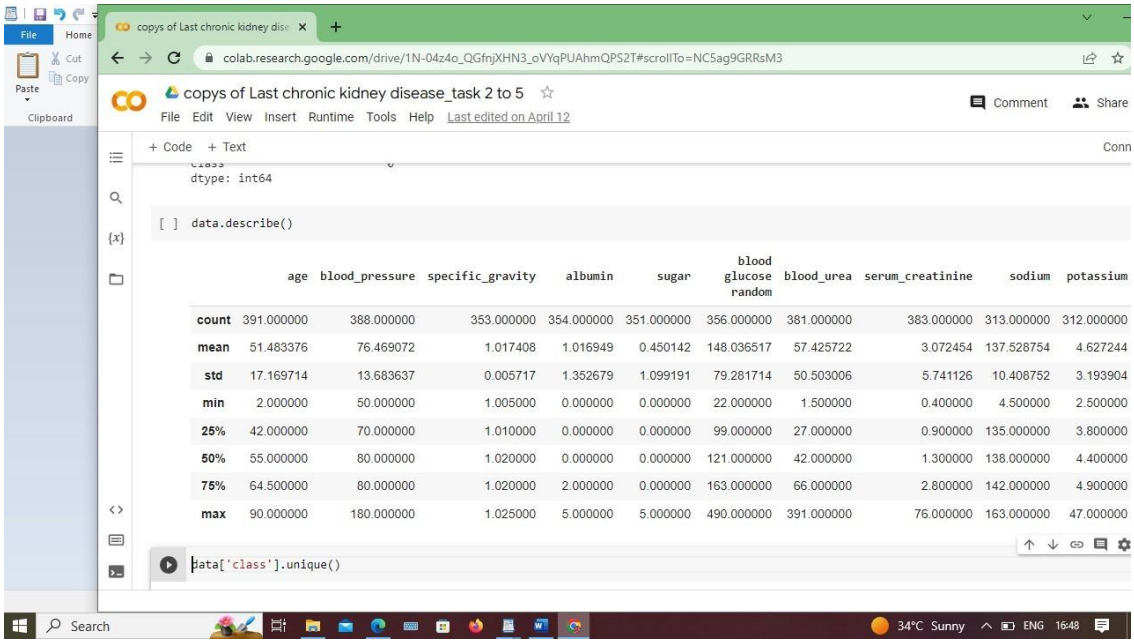

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mean	51.483376	76.469072	1.017408	1.016949	0.450142	148.036517	57.425722	3.072454	137.528754	4.627244
std	17.169714	13.683637	0.005717	1.352679	1.099191	79.281714	50.503006	5.741126	10.408752	3.193904
min	2.000000	50.000000	1.005000	0.000000	0.000000	22.000000	1.500000	0.400000	4.500000	2.500000
25%	42.000000	70.000000	1.010000	0.000000	0.000000	99.000000	27.000000	0.900000	135.000000	3.800000
50%	55.000000	80.000000	1.020000	0.000000	0.000000	121.000000	42.000000	1.300000	138.000000	4.400000
75%	64.500000	80.000000	1.020000	2.000000	0.000000	163.000000	66.000000	2.800000	142.000000	4.900000
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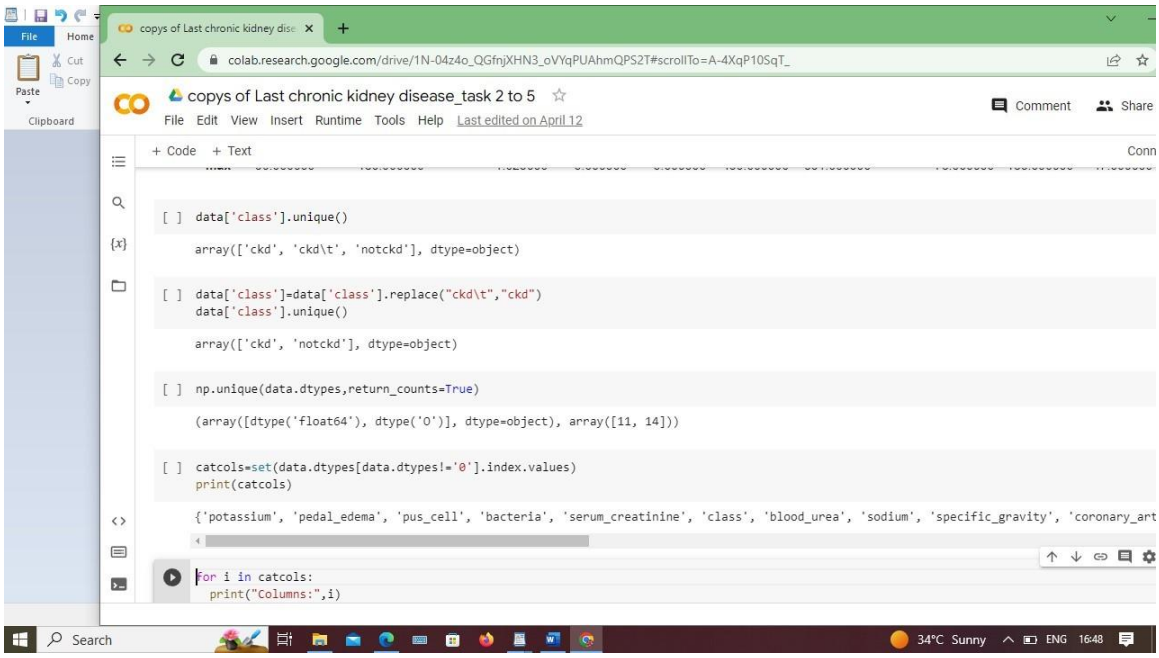
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print(catcols)
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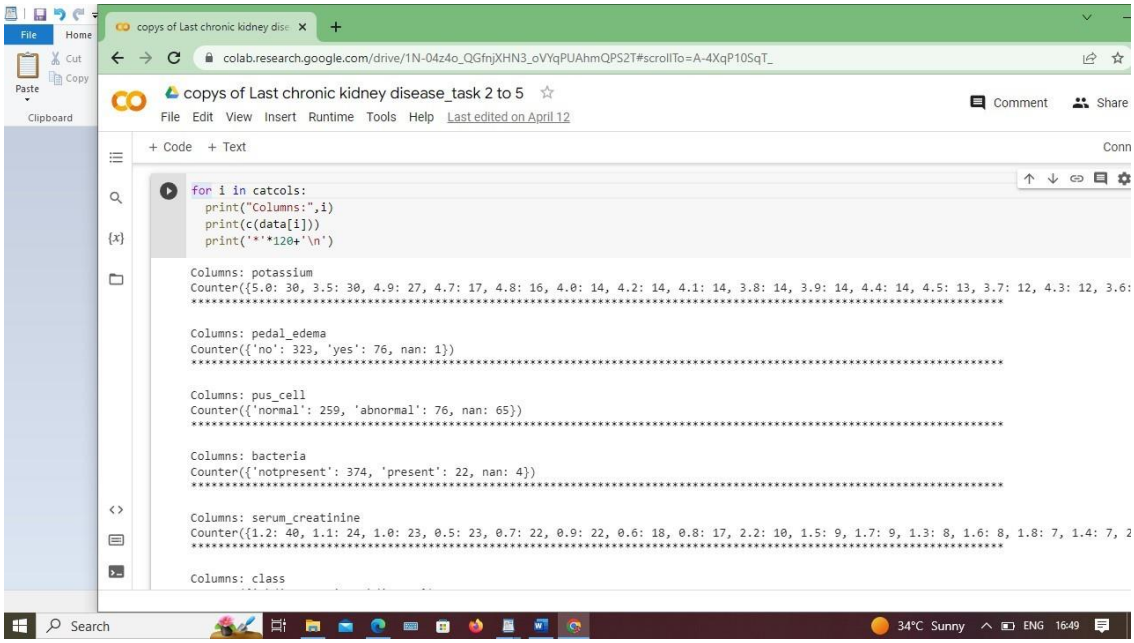
34°C Sunny
ENG 16:48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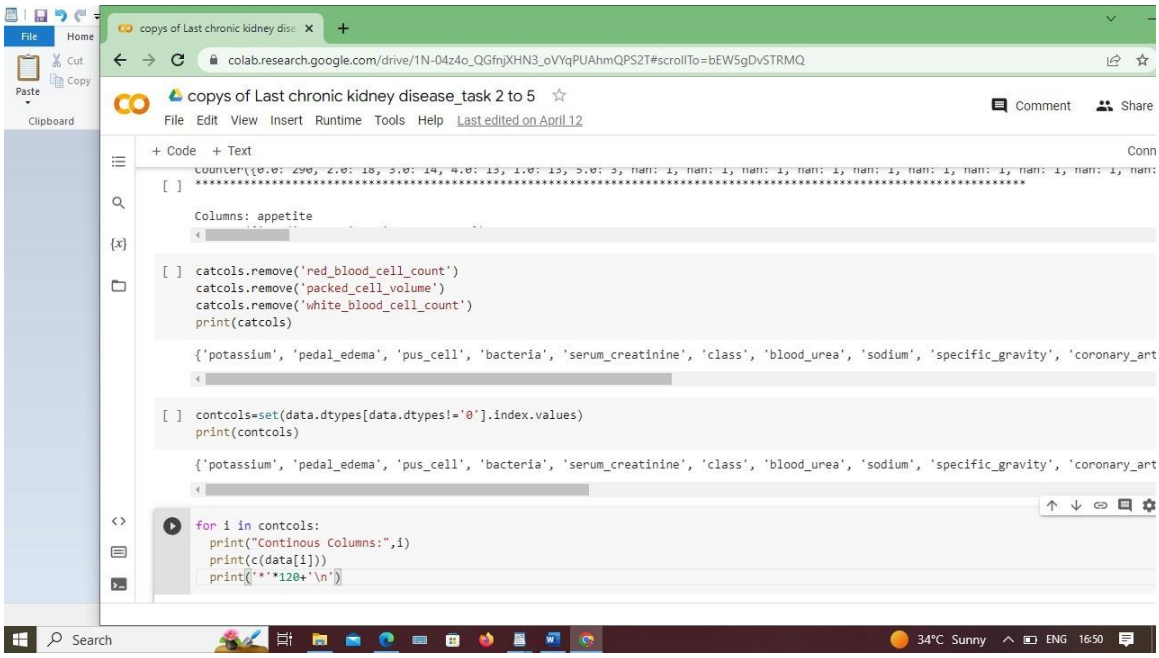
+ Code + Text
for i in catcols:
print("Columns:",i)
print(c(data[i]))
print('*'*120+'\n')
Columns: potassium
Counter({5.0: 30, 3.5: 30, 4.9: 27, 4.7: 17, 4.8: 16, 4.0: 14, 4.2: 14, 4.1: 14, 3.8: 14, 3.9: 14, 4.4: 14, 4.5: 13, 3.7: 12, 4.3: 12, 3.6:
Columns: pedal_edema
Counter({'no': 323, 'yes': 76, nan: 1})
Columns: pus_cell
Counter({'normal': 259, 'abnormal': 76, nan: 65})
Columns: bacteria
Counter({'notpresent': 374, 'present': 22, nan: 4})
Columns: serum_creatinine
Counter({1.2: 40, 1.1: 24, 1.0: 23, 0.5: 23, 0.7: 22, 0.9: 22, 0.6: 18, 0.8: 17, 2.2: 10, 1.5: 9, 1.7: 9, 1.3: 8, 1.6: 8, 1.8: 7, 1.4: 7,
Columns: class
Search
34°C Sunny
ENG 16:49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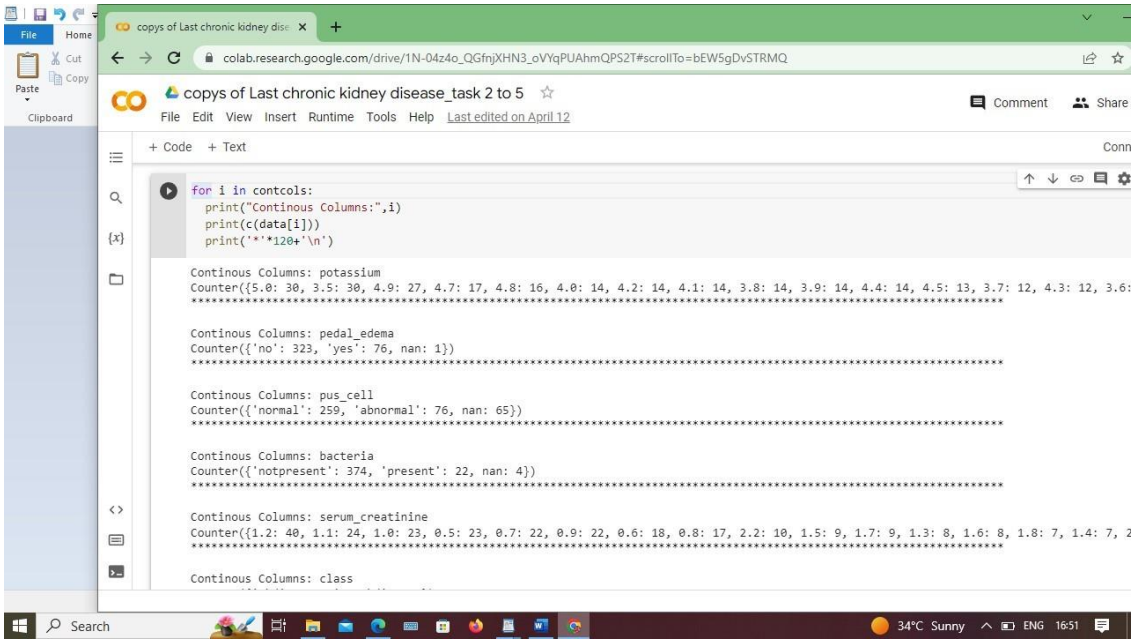
Columns: appetite
catcols.remove('red_blood_cell_count')
catcols.remove('packed_cell_volume')
catcols.remove('white_blood_cell_count')
print(catcols)
{'potassium', 'pedal_edema', 'pus_cell', 'bacteria', 'serum_creatinine', 'class', 'blood_urea', 'sodium', 'specific_gravity', 'coronary_art
contcols=set(data.dtypes[data.dtypes!='0'].index.values)
print(contcols)
{'potassium', 'pedal_edema', 'pus_cell', 'bacteria', 'serum_creatinine', 'class', 'blood_urea', 'sodium', 'specific_gravity', 'coronary_art
for i in contcols:
print("Continous Columns:",i)
print(c(data[i]))
print('*'*120+'\n')
Search
34°C Sunny
ENG
16:50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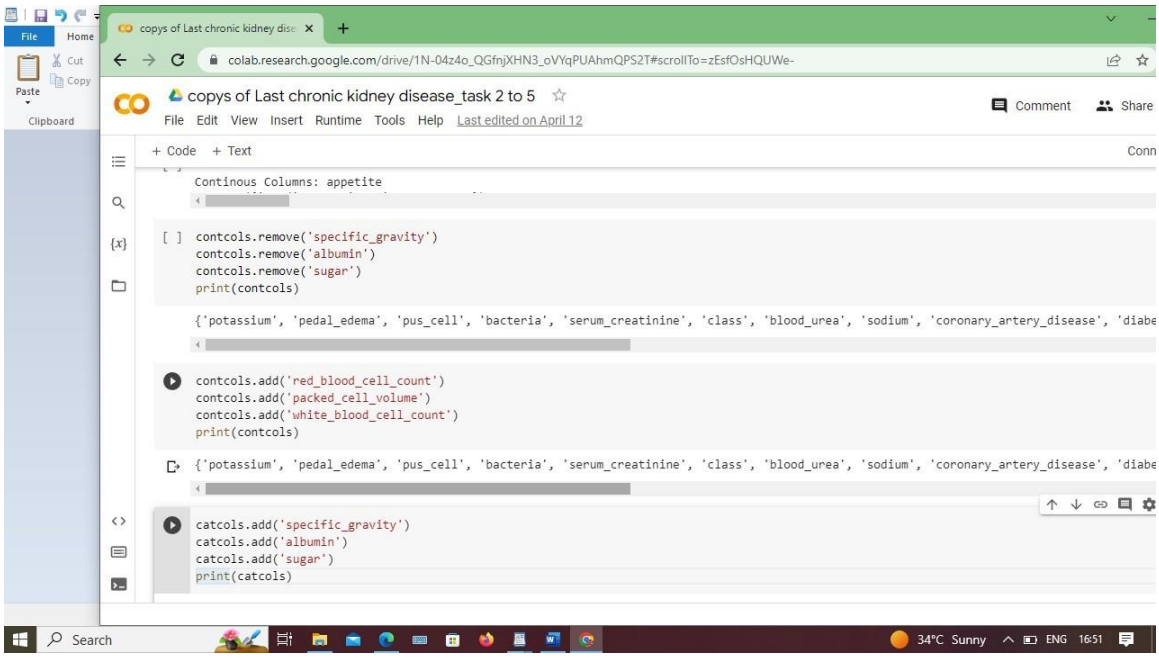
for i in contcols:
print("Continous Columns:",i)
print(c(data[i]))
print('*'*120+'\n')
Continous Columns: potassium
Counter({5.0: 30, 3.5: 30, 4.9: 27, 4.7: 17, 4.8: 16, 4.0: 14, 4.2: 14, 4.1: 14, 3.8: 14, 3.9: 14, 4.4: 14, 4.5: 13, 3.7: 12, 4.3: 12, 3.6:
Continous Columns: pedal_edema
Counter({'no': 323, 'yes': 76, nan: 1})
Continous Columns: pus_cell
Counter({'normal': 259, 'abnormal': 76, nan: 65})
Continous Columns: bacteria
Counter({'notpresent': 374, 'present': 22, nan: 4})
Continous Columns: serum_creatinine
Counter({1.2: 40, 1.1: 24, 1.0: 23, 0.5: 23, 0.7: 22, 0.9: 22, 0.6: 18, 0.8: 17, 2.2: 10, 1.5: 9, 1.7: 9, 1.3: 8, 1.6: 8, 1.8: 7, 1.4: 7, 2
Continous Columns: class
Search
34°C Sunny
ENG
16:51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colab.research.google.com/drive/1N-04z4o_QGfnjXHN3_oVYqPUAhmQPS2T#scrollTo=zEsfOsHQUWe-
copys of Last chronic kidney disease_task 2 to 5
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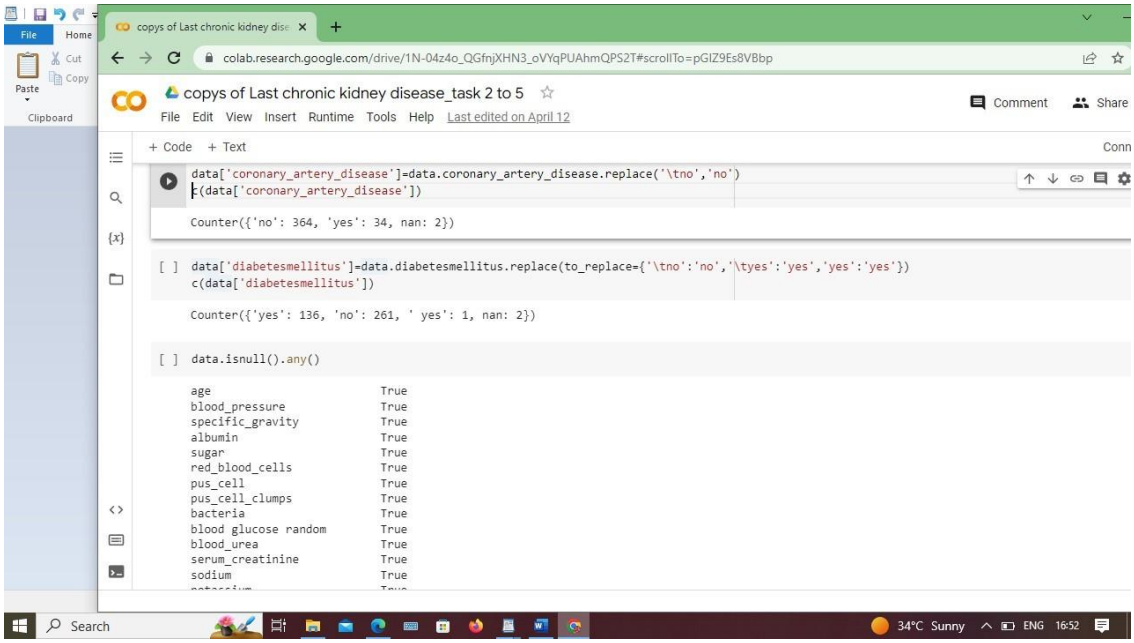
Continous Columns: appetite
contcols.remove('specific_gravity')
contcols.remove('albumin')
contcols.remove('sugar')
print(contcols)
{'potassium', 'pedal_edema', 'pus_cell', 'bacteria', 'serum_creatinine', 'class', 'blood_urea', 'sodium', 'coronary_artery_disease', 'diabe
contcols.add('red_blood_cell_count')
contcols.add('packed_cell_volume')
contcols.add('white_blood_cell_count')
print(contcols)
{'potassium', 'pedal_edema', 'pus_cell', 'bacteria', 'serum_creatinine', 'class', 'blood_urea', 'sodium', 'coronary_artery_disease', 'diabe
catcols.add('specific_gravity')
catcols.add('albumin')
catcols.add('sugar')
print(catcols)
Search
34°C Sunny
ENG 16:51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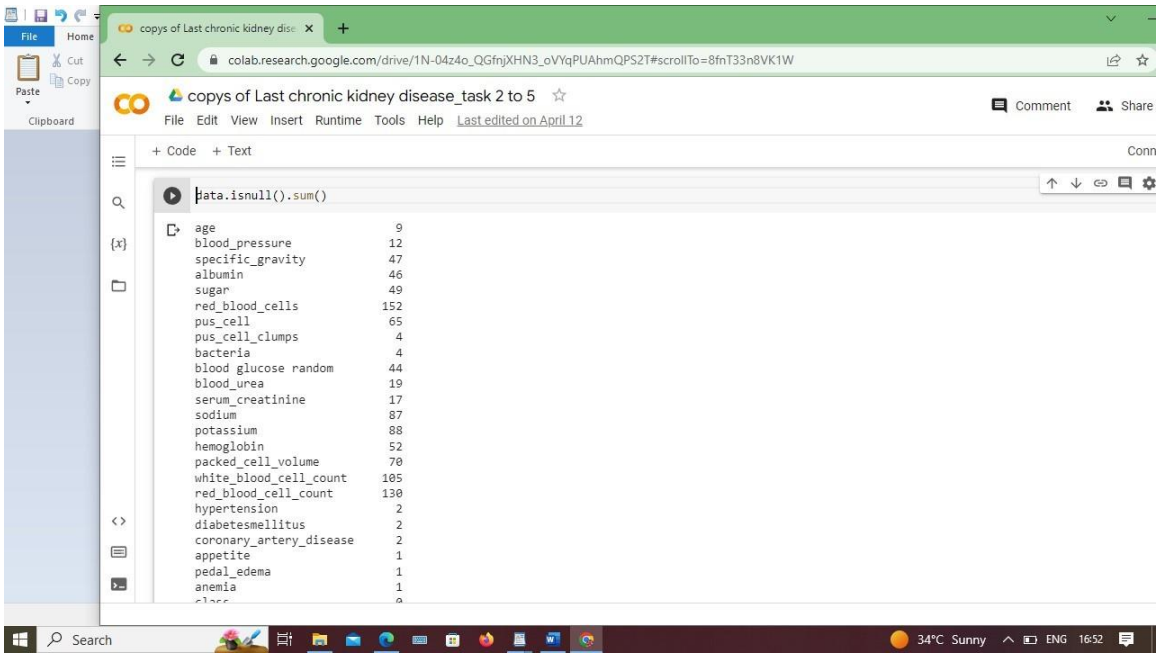
data['coronary_artery_disease']=data.coronary_artery_disease.replace('\tno','no')
c(data['coronary_artery_disease'])
Counter({'no': 364, 'yes': 34, nan: 2})
data['diabetesmellitus']=data.diabetesmellitus.replace(to_replace={'\tno':'no','\tyes':'yes','yes':'yes'})
c(data['diabetesmellitus'])
Counter({'yes': 136, 'no': 261, ' yes': 1, nan: 2})
data.isnull().any()
age True
blood_pressure True
specific_gravity True
albumin True
sugar True
red_blood_cells True
pus_cell True
pus_cell_clumps True
bacteria True
blood glucose random True
blood_urea True
serum_creatinine True
sodium True
Search
34°C Sunny
ENG 16:52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colab.research.google.com/drive/1N-04z4o_QGfnjXHN3_oVYqPUAhmQPS2T#scrollTo=8fnT33n8VK1W
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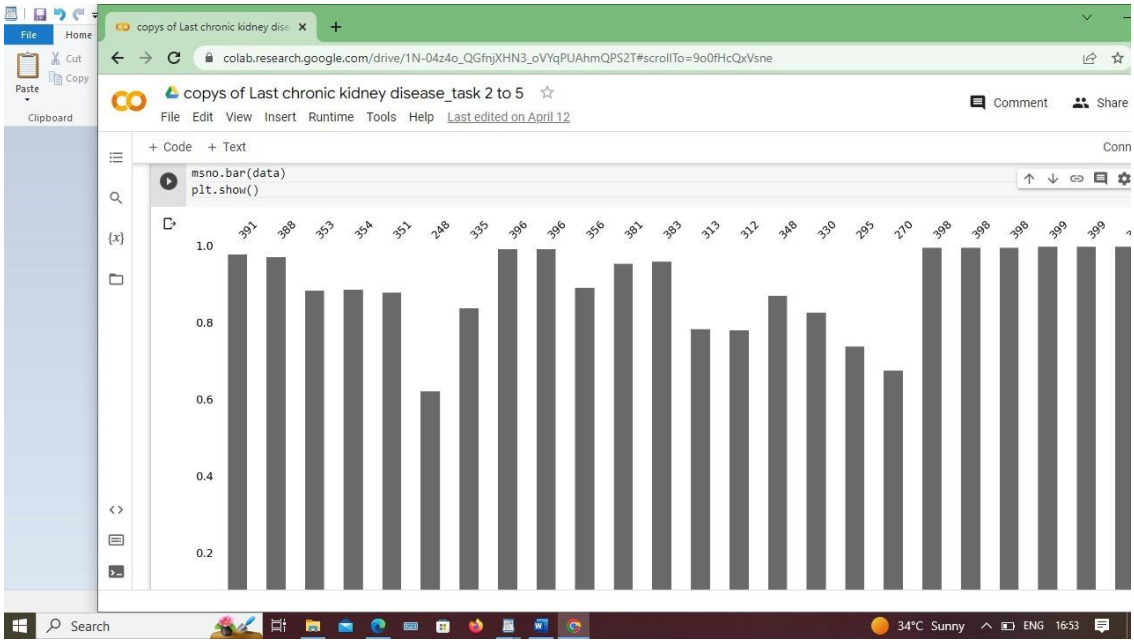
data.isnull().sum()
age 9
blood_pressure 12
specific_gravity 47
albumin 46
sugar 49
red_blood_cells 152
pus_cell 65
pus_cell_clumps 4
bacteria 4
blood glucose random 44
blood_urea 19
serum_creatinine 17
sodium 87
potassium 88
hemoglobin 52
packed_cell_volume 70
white_blood_cell_count 105
red_blood_cell_count 130
hypertension 2
diabetesmellitus 2
coronary_artery_disease 2
appetite 1
pedal_edema 1
anemia 1
34°C Sunny
ENG 16:52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colab.research.google.com/drive/1N-04z4o_QGfnjXHN3_oVYqPUAhmQPS2T#scrollTo=9o0fHcQxVsne
File Edit View Insert Runtime Tools Help Last edited on April 12
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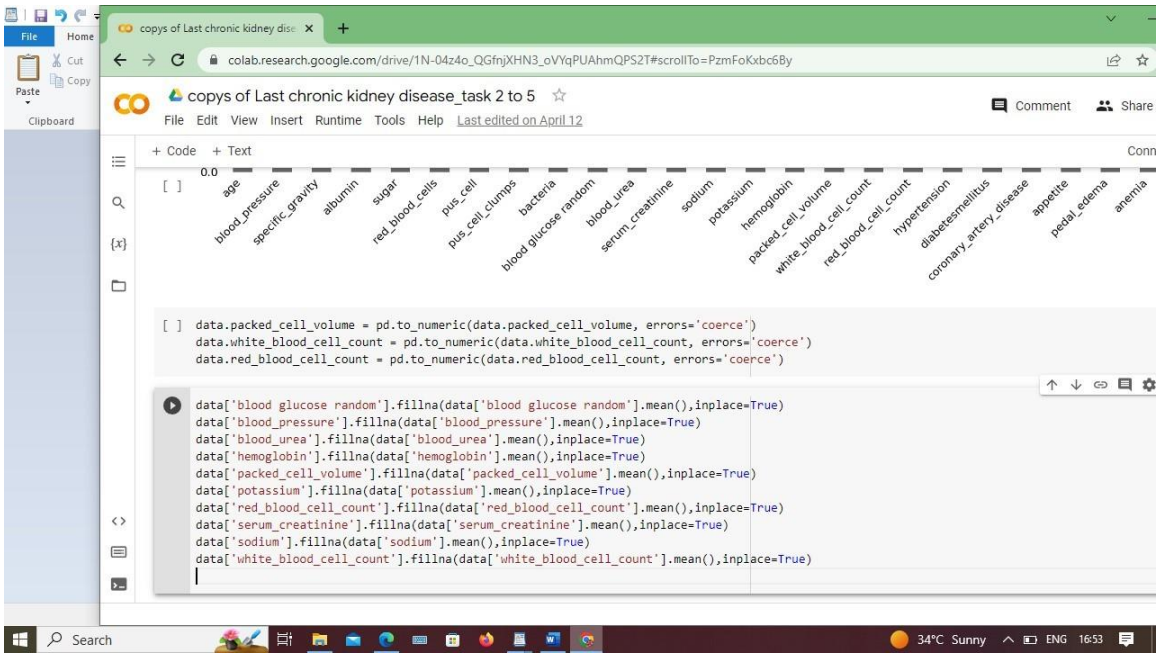
msno.bar(data)
plt.show()
391 388 353 354 351 248 335 396 396 356 381 383 313 312 348 330 295 270 398 398 398 399 399
1.0
0.8
0.6
0.4
0.2
34°C Sunny
ENG 16:53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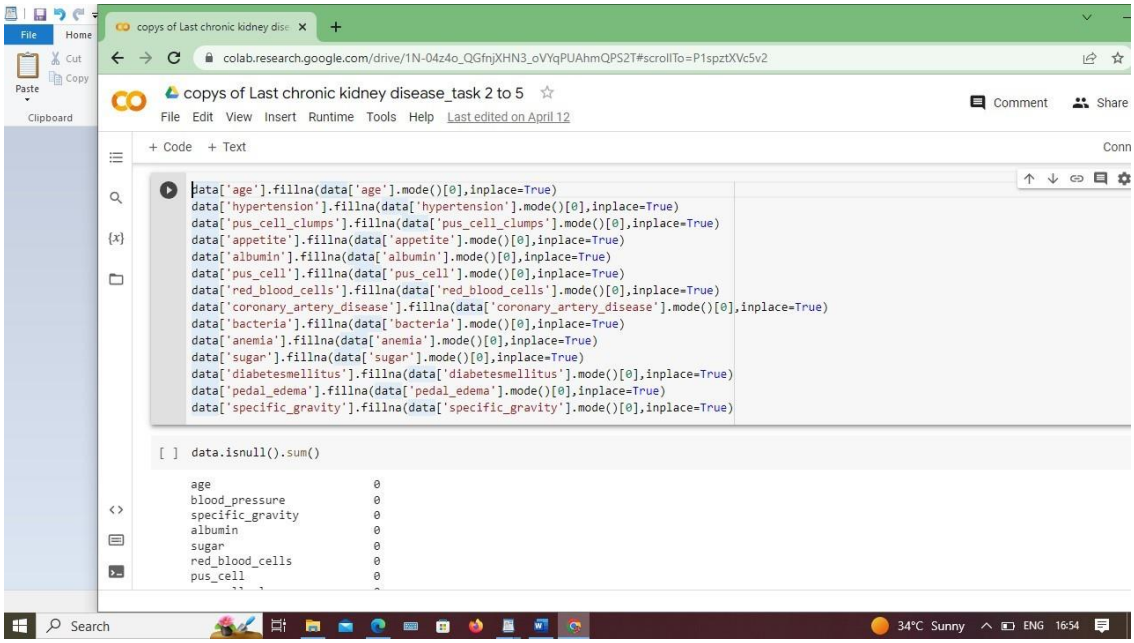
colab.research.google.com/drive/1N-04z4o_QGfnjXHN3_oVYqPUAhmQPS2T#scrollTo=PzmFoKxbc6By
0.0
age
blood_pressure
specific_gravity
albumin
sugar
red_blood_cells
pus_cell
pus_cell_clumps
bacteria
blood glucose random
blood_urea
serum_creatinine
sodium
potassium
hemoglobin
packed_cell_volume
white_blood_cell_count
red_blood_cell_count
hypertension
diabetesmellitus
coronary_artery_disease
appetite
pedal_edema
anemia
data.packed_cell_volume = pd.to_numeric(data.packed_cell_volume, errors='coerce')
data.white_blood_cell_count = pd.to_numeric(data.white_blood_cell_count, errors='coerce')
data.red_blood_cell_count = pd.to_numeric(data.red_blood_cell_count, errors='coerce')
data['blood glucose random'].fillna(data['blood glucose random'].mean(),inplace=True)
data['blood_pressure'].fillna(data['blood_pressure'].mean(),inplace=True)
data['blood_urea'].fillna(data['blood_urea'].mean(),inplace=True)
data['hemoglobin'].fillna(data['hemoglobin'].mean(),inplace=True)
data['packed_cell_volume'].fillna(data['packed_cell_volume'].mean(),inplace=True)
data['potassium'].fillna(data['potassium'].mean(),inplace=True)
data['red_blood_cell_count'].fillna(data['red_blood_cell_count'].mean(),inplace=True)
data['serum_creatinine'].fillna(data['serum_creatinine'].mean(),inplace=True)
data['sodium'].fillna(data['sodium'].mean(),inplace=True)
data['white_blood_cell_count'].fillna(data['white_blood_cell_count'].mean(),inplace=True)
Search
34°C Sunny
ENG
16:53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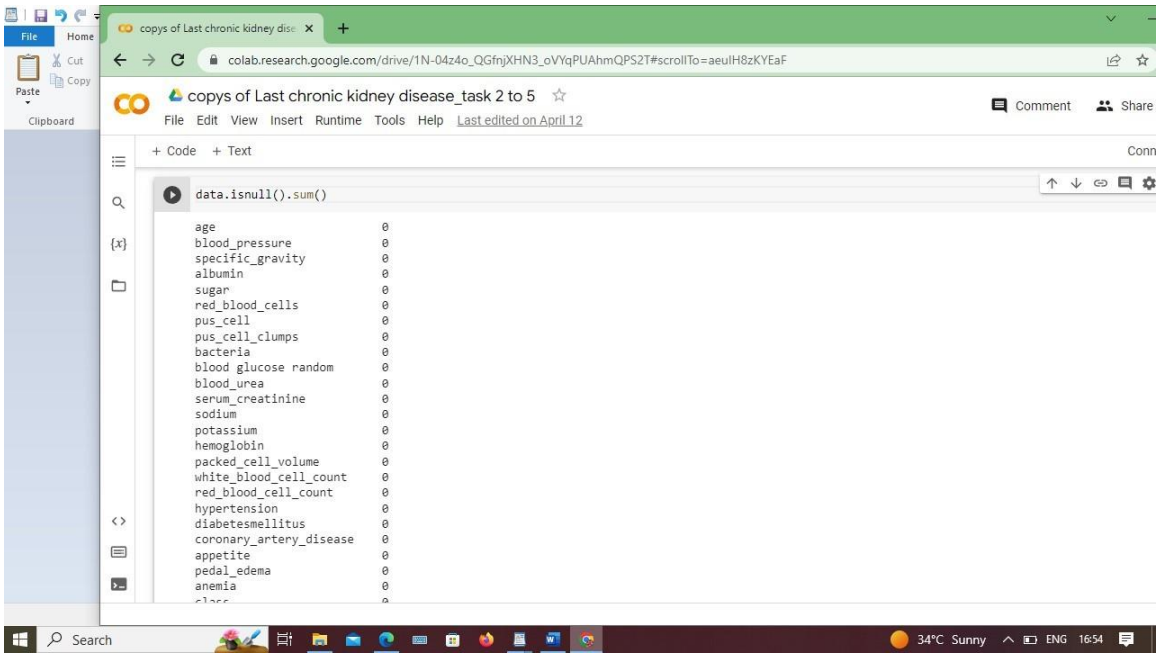
colab.research.google.com/drive/1N-04z4o_QGfnjXHN3_oVYqPUAhmQPS2T#scrollTo=P1spztXVc5v2
data['age'].fillna(data['age'].mode()[0],inplace=True)
data['hypertension'].fillna(data['hypertension'].mode()[0],inplace=True)
data['pus_cell_clumps'].fillna(data['pus_cell_clumps'].mode()[0],inplace=True)
data['appetite'].fillna(data['appetite'].mode()[0],inplace=True)
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)
data.isnull().sum()
age 0
blood_pressure 0
specific_gravity 0
albumin 0
sugar 0
red_blood_cells 0
pus_cell 0
Search
34°C Sunny
ENG
16:54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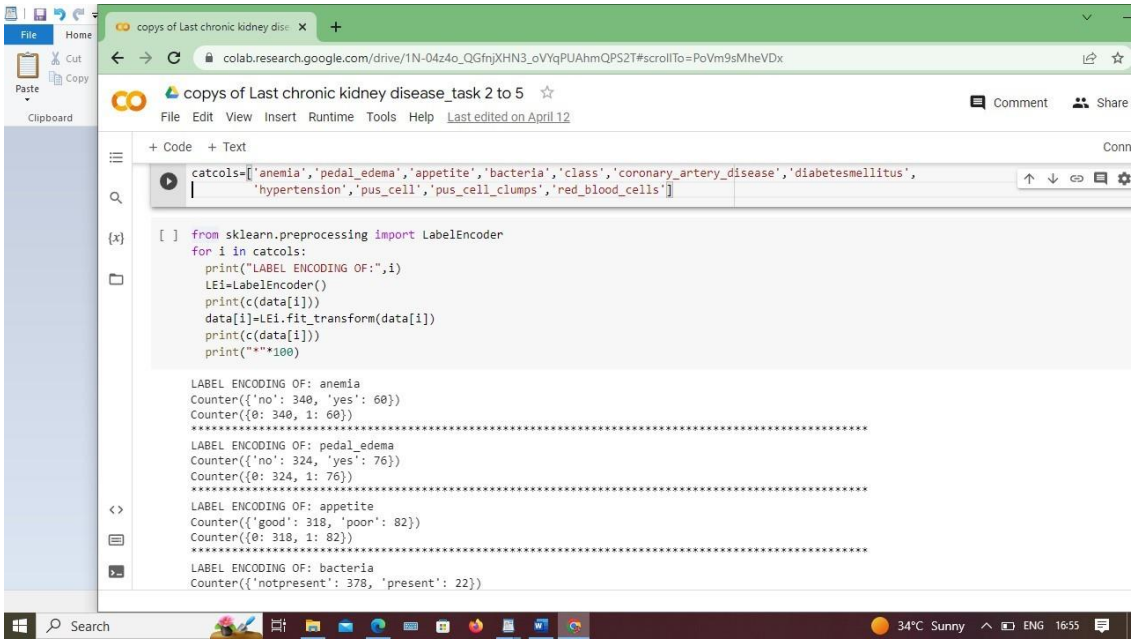
data.isnull().sum()
age 0
blood_pressure 0
specific_gravity 0
albumin 0
sugar 0
red_blood_cells 0
pus_cell 0
pus_cell_clumps 0
bacteria 0
blood glucose random 0
blood_urea 0
serum_creatinine 0
sodium 0
potassium 0
hemoglobin 0
packed_cell_volume 0
white_blood_cell_count 0
red_blood_cell_count 0
hypertension 0
diabetesmellitus 0
coronary_artery_disease 0
appetite 0
pedal_edema 0
anemia 0
Search
34°C Sunny
ENG 16:54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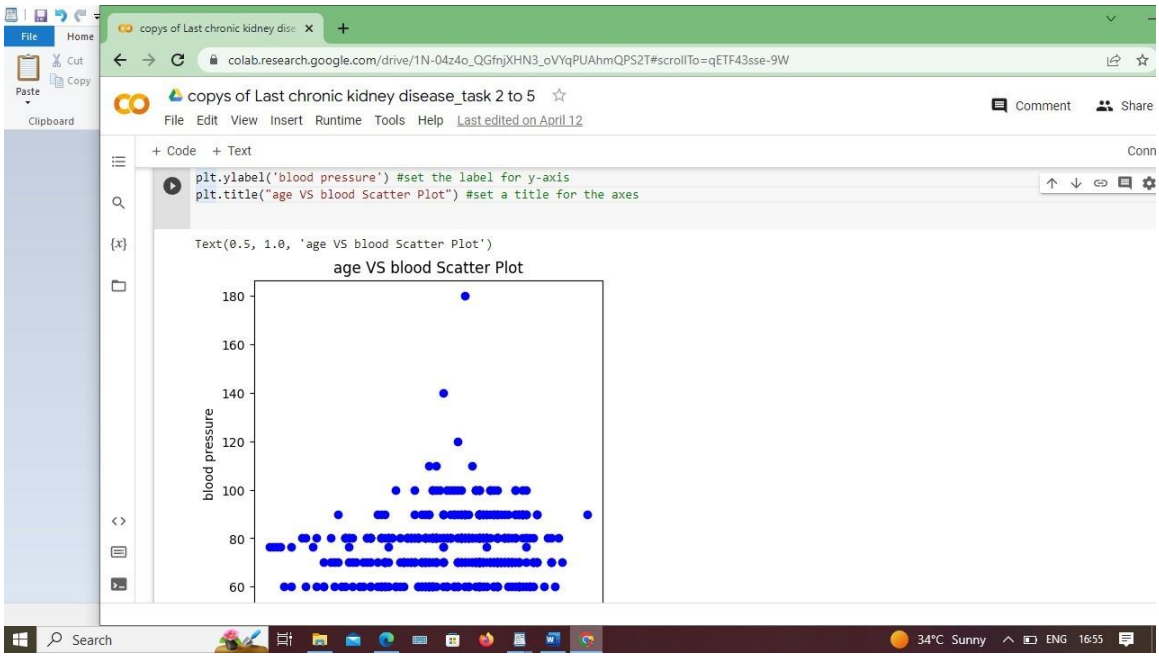
catcols=['anemia','pedal_edema','appetite','bacteria','class','coronary_artery_disease','diabetesmellitus',
'hypertension','pus_cell','pus_cell_clumps','red_blood_cells']
from sklearn.preprocessing import LabelEncoder
for i in catcols:
print("LABEL ENCODING OF:",i)
LEi=LabelEncoder()
print(c(data[i]))
data[i]=LEi.fit_transform(data[i])
print(c(data[i]))
print("*"*100)
LABEL ENCODING OF: anemia
Counter({'no': 340, 'yes': 60})
Counter({0: 340, 1: 60})
LABEL ENCODING OF: pedal_edema
Counter({'no': 324, 'yes': 76})
Counter({0: 324, 1: 76})
LABEL ENCODING OF: appetite
Counter({'good': 318, 'poor': 82})
Counter({0: 318, 1: 82})
LABEL ENCODING OF: bacteria
Counter({'notpresent': 378, 'present': 22})
Search
34°C Sunny
ENG 16:55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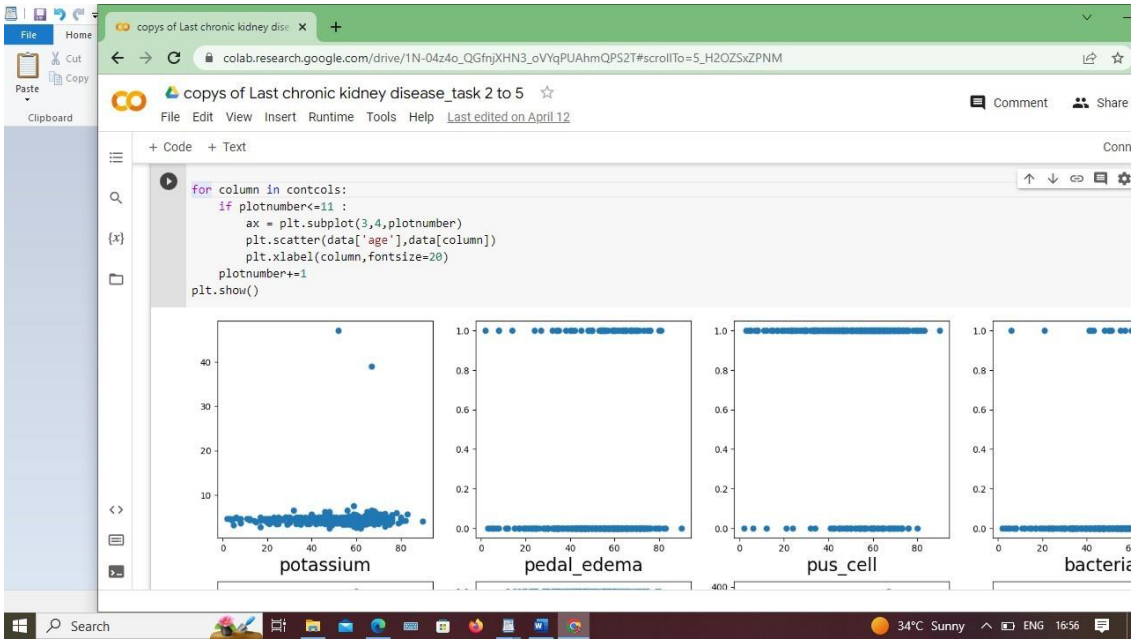
plt.ylabel('blood pressure') #set the label for y-axis
plt.title("age VS blood Scatter Plot") #set a title for the axes
Text(0.5, 1.0, 'age VS blood Scatter Plot')
age VS blood Scatter Plot
blood pressure
180
160
140
120
100
80
60
Search
34°C Sunny
ENG
16:55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for column in contcols:
if plotnumber<=11 :
ax = plt.subplot(3,4,plotnumber)
plt.scatter(data['age'],data[column])
plt.xlabel(column,fontsize=20)
plotnumber+=1
plt.show()
potassium
pedal_edema
pus_cell
Search
34°C Sunny
ENG
16:56


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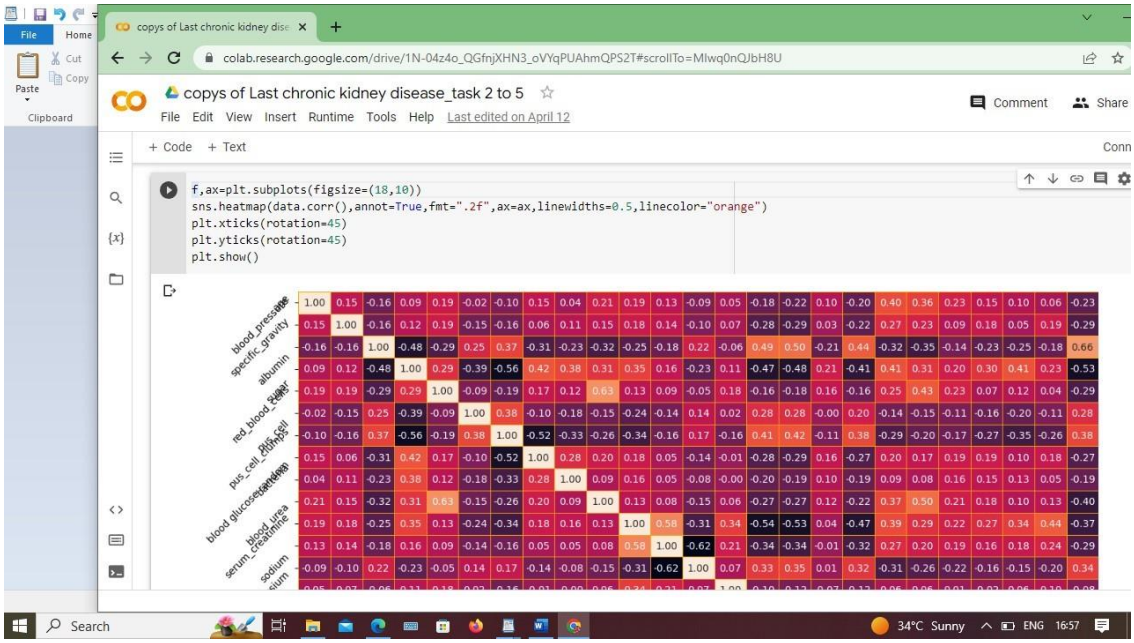
serum_creatinine
class
blood_urea
sodium
coronary_artery_disease
diabetesmellitus
blood glucose random
f,ax=plt.subplots(figsize=(18,10))
sns.heatmap(data.corr(),annot=True,fmt=".2f",ax=ax,linewidths=0.5,linecolor="orange")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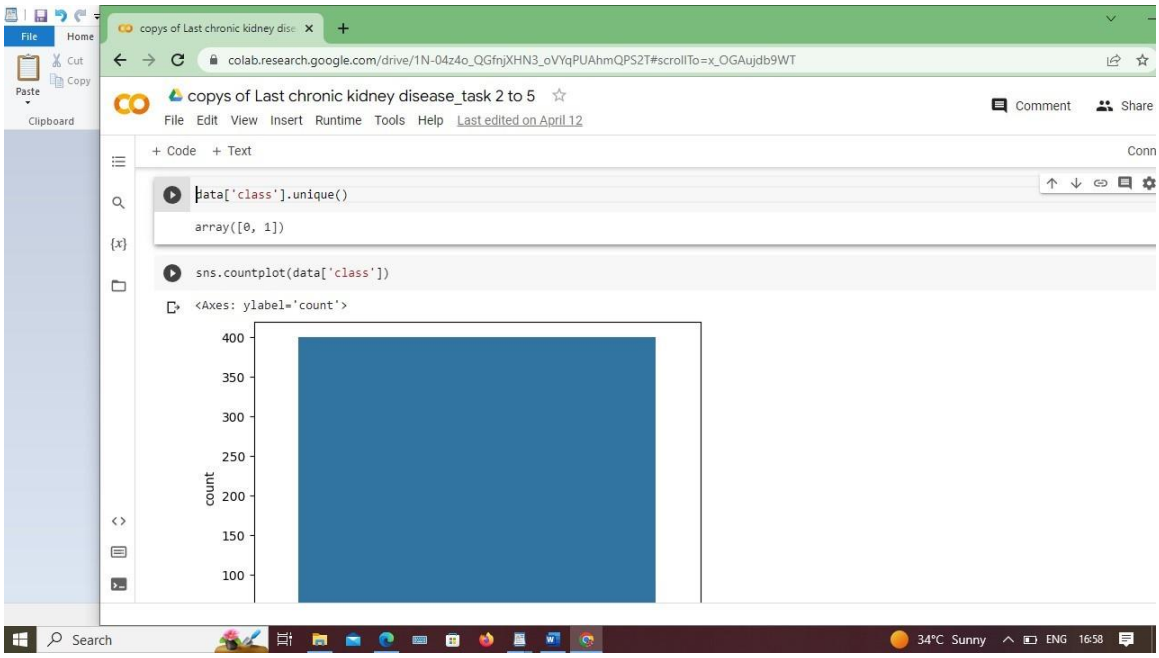
f,ax=plt.subplots(figsize=(18,10))
sns.heatmap(data.corr(),annot=True,fmt=".2f",ax=ax,linewidths=0.5,linecolor="orange")
plt.xticks(rotation=45)
plt.yticks(rotation=45)
plt.show()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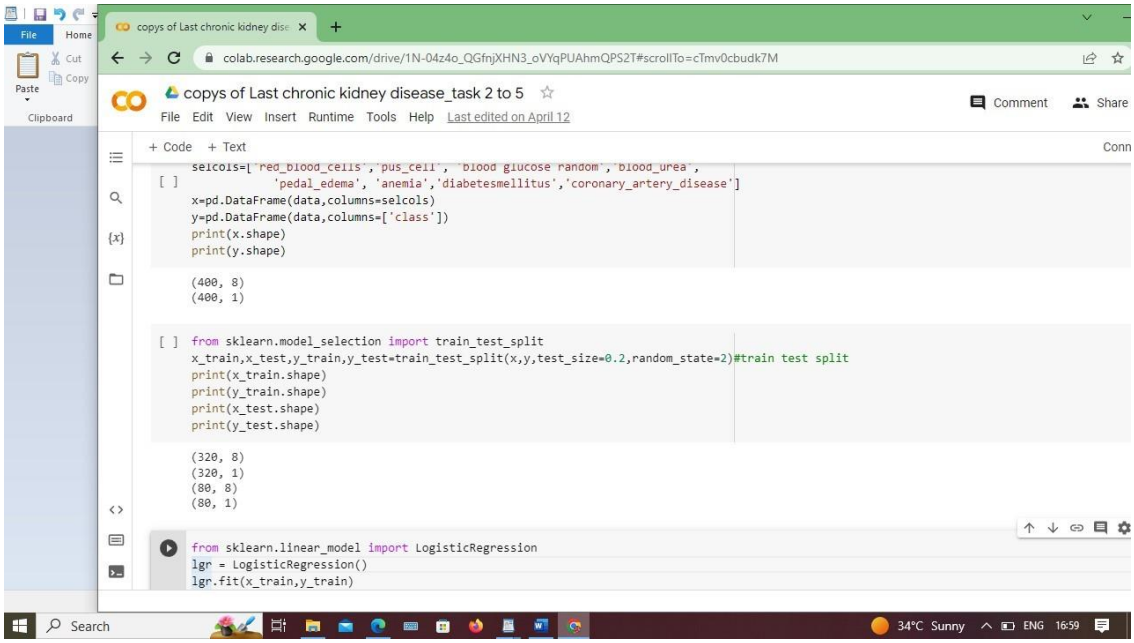
data['class'].unique()
array([0, 1])
sns.countplot(data['class'])
<Axes: ylabel='count'>
count
400
350
300
250
200
150
100
Search
34°C Sunny
ENG
16:58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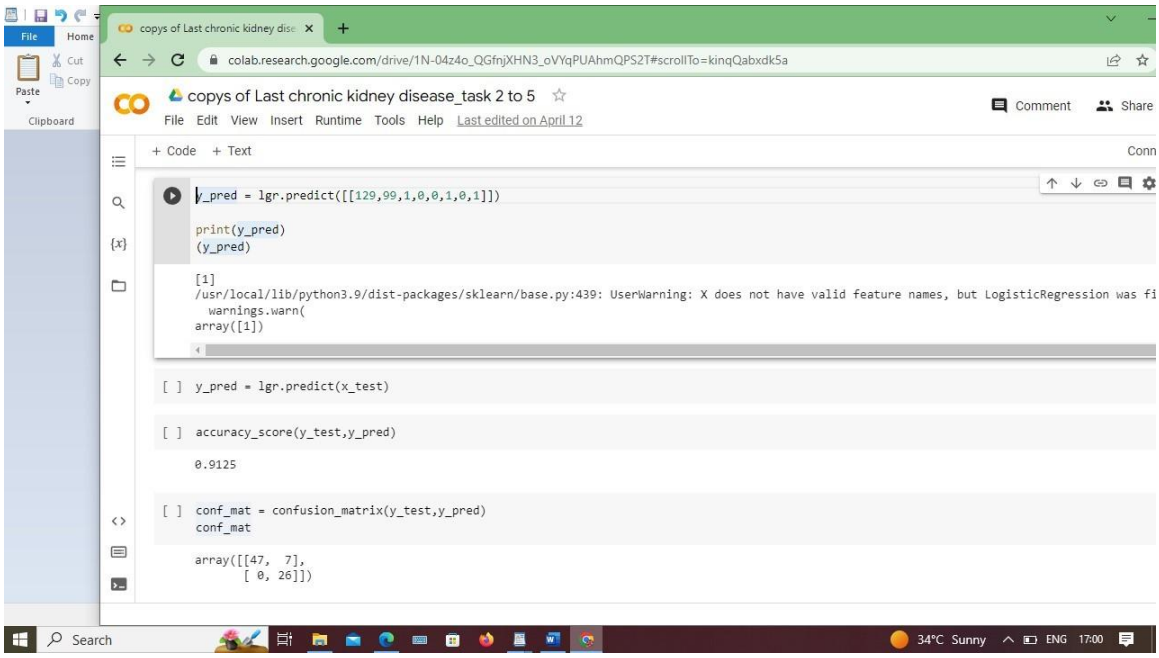
selcols=['red_blood_cells','pus_cell', 'blood glucose random','blood_urea',
'pedal_edema', 'anemia','diabetesmellitus','coronary_artery_disease']
x=pd.DataFrame(data,columns=selcols)
y=pd.DataFrame(data,columns=['class'])
print(x.shape)
print(y.shape)
(400, 8)
(400, 1)
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.2,random_state=2)#train test split
print(x_train.shape)
print(y_train.shape)
print(x_test.shape)
print(y_test.shape)
(320, 8)
(320, 1)
(80, 8)
(80, 1)
from sklearn.linear_model import LogisticRegression
lgr = LogisticRegression()
lgr.fit(x_train,y_train)
Search
34°C Sunny
ENG
16:59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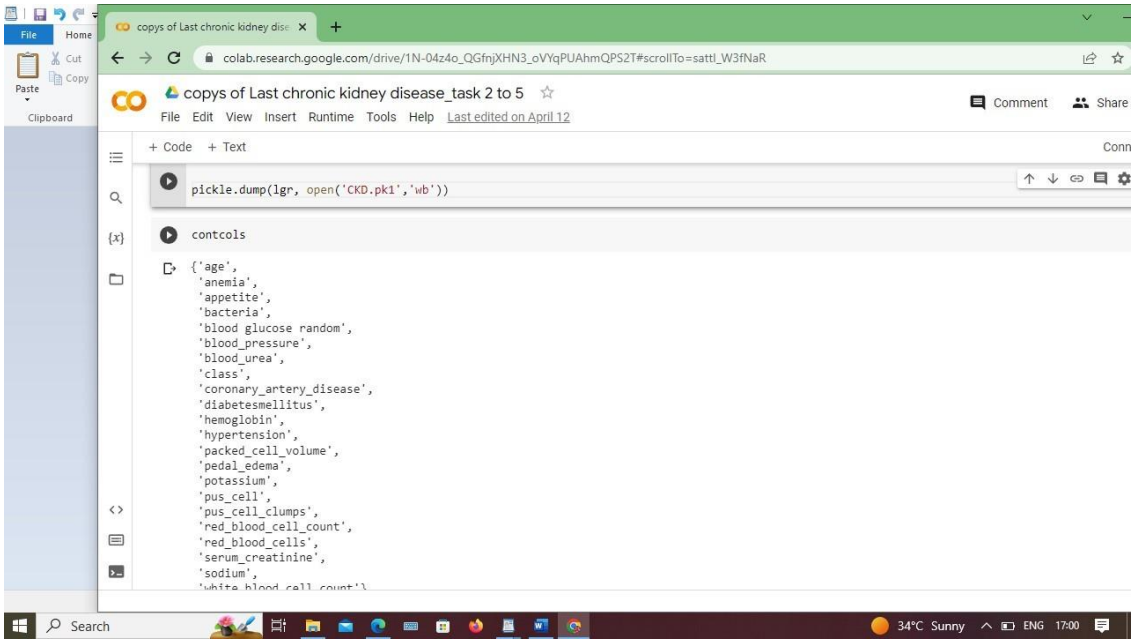
y_pred = lgr.predict([[129,99,1,0,0,1,0,1]])
print(y_pred)
(y_pred)
[1]
/usr/local/lib/python3.9/dist-packages/sklearn/base.py:439: UserWarning: X does not have valid feature names, but LogisticRegression was fi
warnings.warn(
array([1])
[ ] y_pred = lgr.predict(x_test)
[ ] accuracy_score(y_test,y_pred)
0.9125
[ ] conf_mat = confusion_matrix(y_test,y_pred)
conf_mat
array([[47, 7],
[0, 26]])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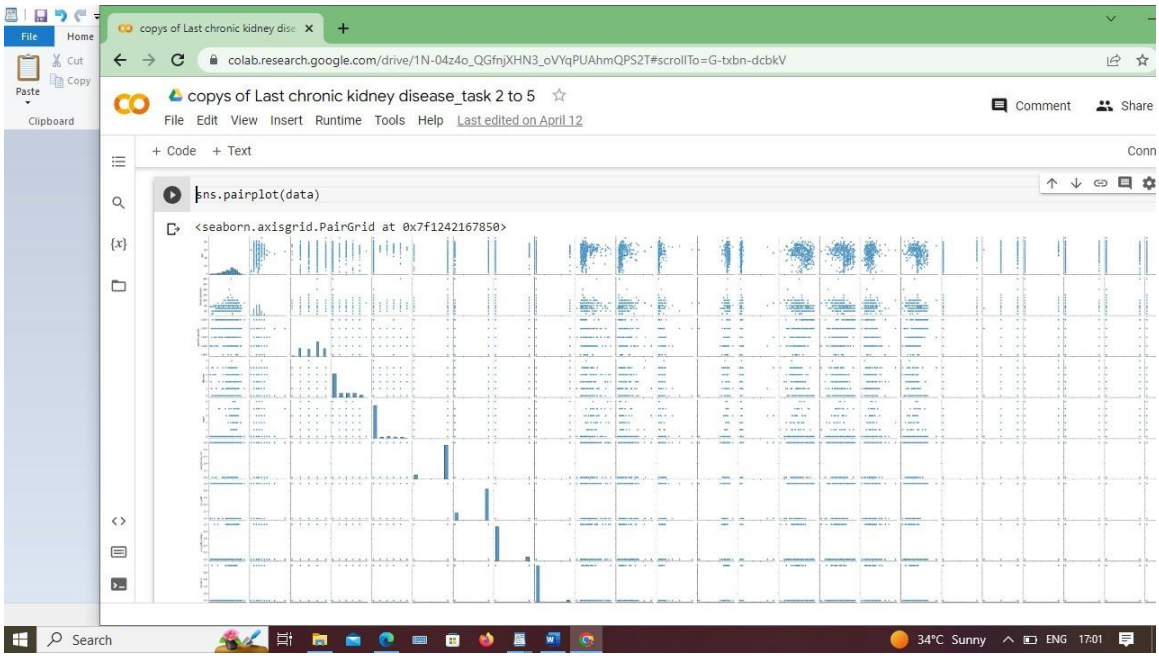
pickle.dump(lgr, open('CKD.pk1','wb'))
contcols
{'age',
'anemia',
'appetite',
'bacteria',
'blood glucose random',
'blood_pressure',
'blood_urea',
'class',
'coronary_artery_disease',
'diabetesmellitus',
'hemoglobin',
'hypertension',
'packed_cell_volume',
'pedal_edema',
'potassium',
'pus_cell',
'pus_cell_clumps',
'red_blood_cell_count',
'red_blood_cells',
'serum_creatinine',
'sodium',


copys of Last chronic kidney disease_task 2 to 5
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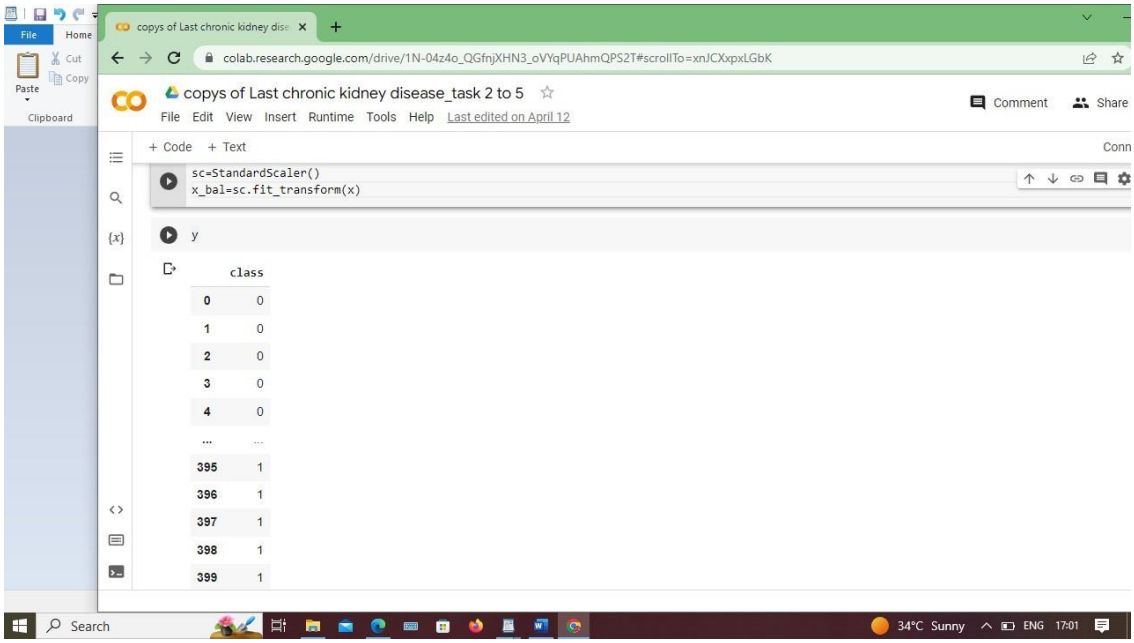
sns.pairplot(data)
<seaborn.axisgrid.PairGrid at 0x7f1242167850>


copys of Last chronic kidney disease_task 2 to 5
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Share
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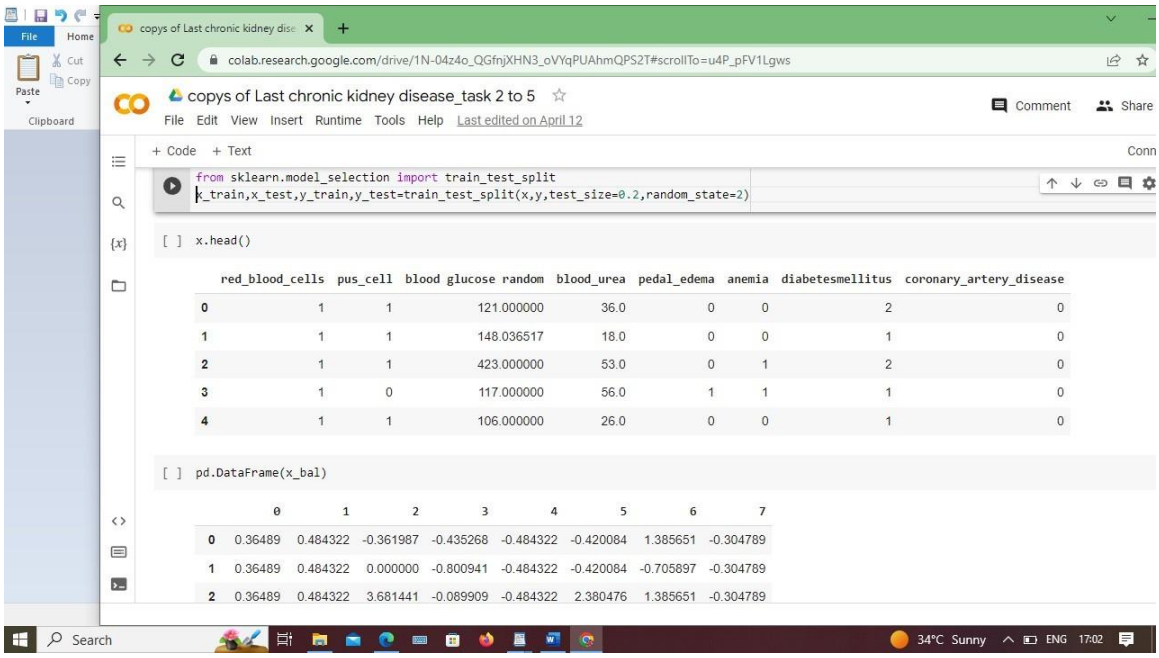
sc=StandardScaler()
x_bal=sc.fit_transform(x)
y
class
0 0
1 0
2 0
3 0
4 0
395 1
396 1
397 1
398 1
399 1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colab.research.google.com/drive/1N-04z4o_QGfnjXHN3_oVYqPUAhmQPS2T#scrollTo=u4P_pFV1Lgws
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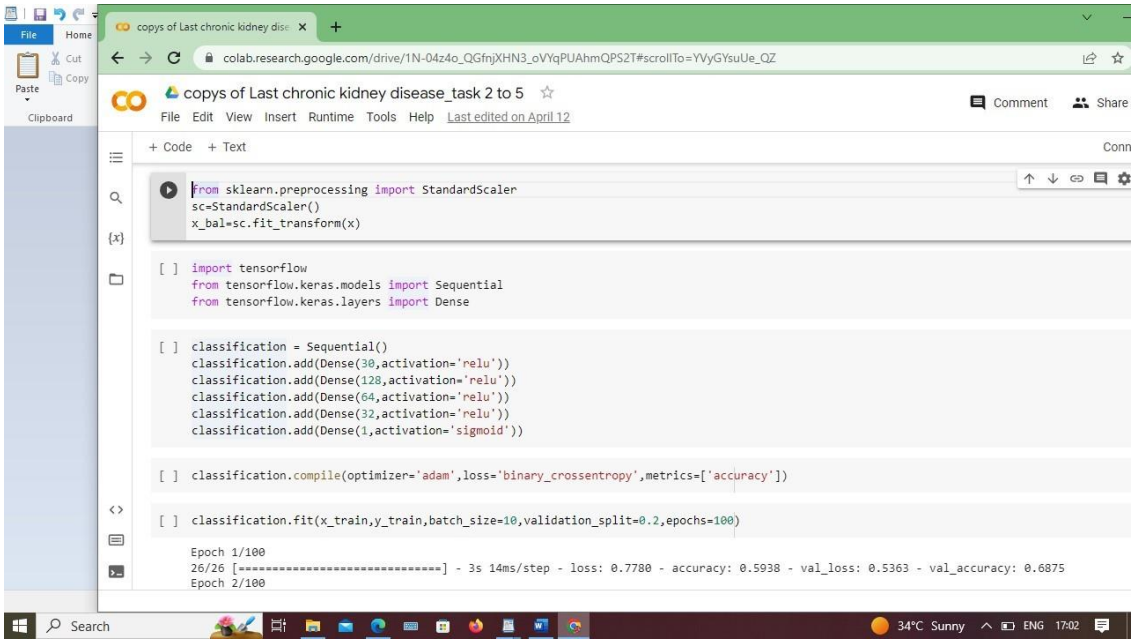
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=0.2,random_state=2)
[ ] x.head()
red_blood_cells pus_cell blood glucose random blood_urea pedal_edema anemia diabetesmellitus coronary_artery_disease
0 1 1 121.000000 36.0 0 0 2 0
1 1 1 148.036517 18.0 0 0 1 0
2 1 1 423.000000 53.0 0 1 2 0
3 1 0 117.000000 56.0 1 1 1 0
4 1 1 106.000000 26.0 0 0 1 0
[ ] pd.DataFrame(x_bal)
0 1 2 3 4 5 6 7
0 0.36489 0.484322 -0.361987 -0.435268 -0.484322 -0.420084 1.385651 -0.304789
1 0.36489 0.484322 0.000000 -0.800941 -0.484322 -0.420084 -0.705897 -0.304789
2 0.36489 0.484322 3.681441 -0.089909 -0.484322 2.380476 1.385651 -0.304789
Search
34°C Sunny
ENG 17:02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colab.research.google.com/drive/1N-04z4o_QGfnjXHN3_oVYqPUAhmQPS2T#scrollTo=YVyGYsuUe_QZ
copys of Last chronic kidney disease_task 2 to 5
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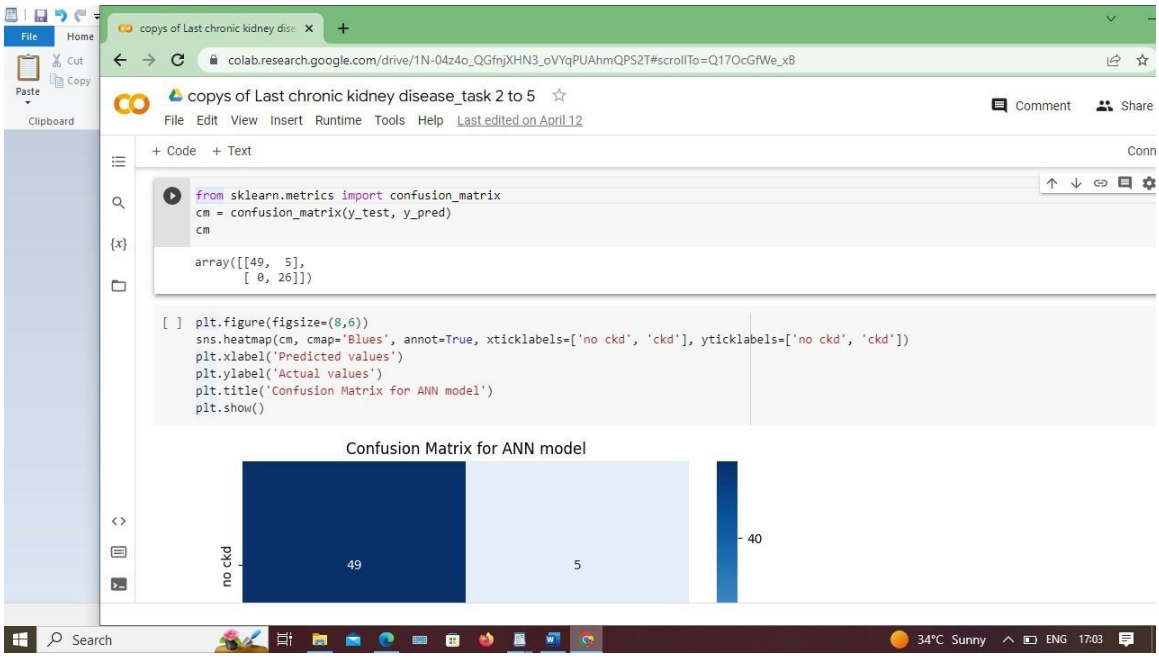
+ Code + Text
from sklearn.preprocessing import StandardScaler
sc=StandardScaler()
x_bal=sc.fit_transform(x)
[ ] import tensorflow
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense
[ ] classification = Sequential()
classification.add(Dense(30,activation='relu'))
classification.add(Dense(128,activation='relu'))
classification.add(Dense(64,activation='relu'))
classification.add(Dense(32,activation='relu'))
classification.add(Dense(1,activation='sigmoid'))
[ ] classification.compile(optimizer='adam',loss='binary_crossentropy',metrics=['accuracy'])
[ ] classification.fit(x_train,y_train,batch_size=10,validation_split=0.2,epochs=100)
Epoch 1/100
26/26 [==============================] - 3s 14ms/step - loss: 0.7780 - accuracy: 0.5938 - val_loss: 0.5363 - val_accuracy: 0.6875
Epoch 2/100
Search
34°C Sunny
ENG 17:02


copys of Last chronic kidney disease_task 2 to 5
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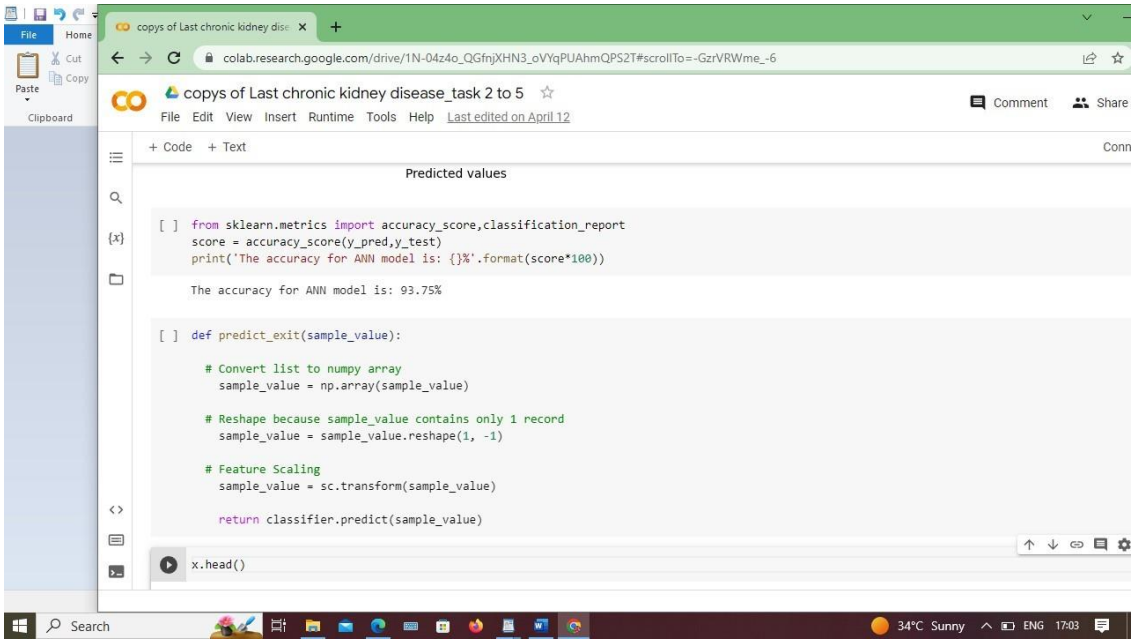
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test, y_pred)
cm
array([[49, 5],
[0, 26]])
plt.figure(figsize=(8,6))
sns.heatmap(cm, cmap='Blues', annot=True, xticklabels=['no ckd', 'ckd'], yticklabels=['no ckd', 'ckd'])
plt.xlabel('Predicted values')
plt.ylabel('Actual values')
plt.title('Confusion Matrix for ANN model')
plt.show()
Confusion Matrix for ANN model
no ckd
49
5
40
Search
34°C Sunny
ENG
17:03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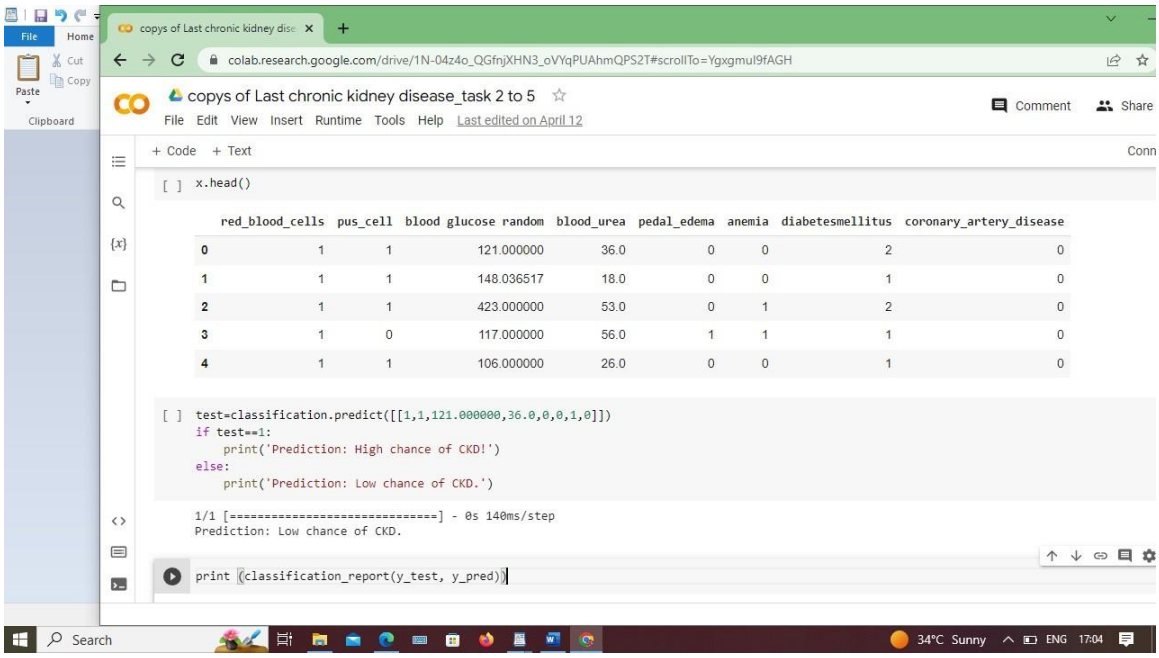
Predicted values
from sklearn.metrics import accuracy_score,classification_report
score = accuracy_score(y_pred,y_test)
print('The accuracy for ANN model is: {}%'.format(score*100))
The accuracy for ANN model is: 93.75%
def predict_exit(sample_value):
# Convert list to numpy array
sample_value = np.array(sample_value)
# 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)
x.head()
Search
34°C Sunny
ENG
17:03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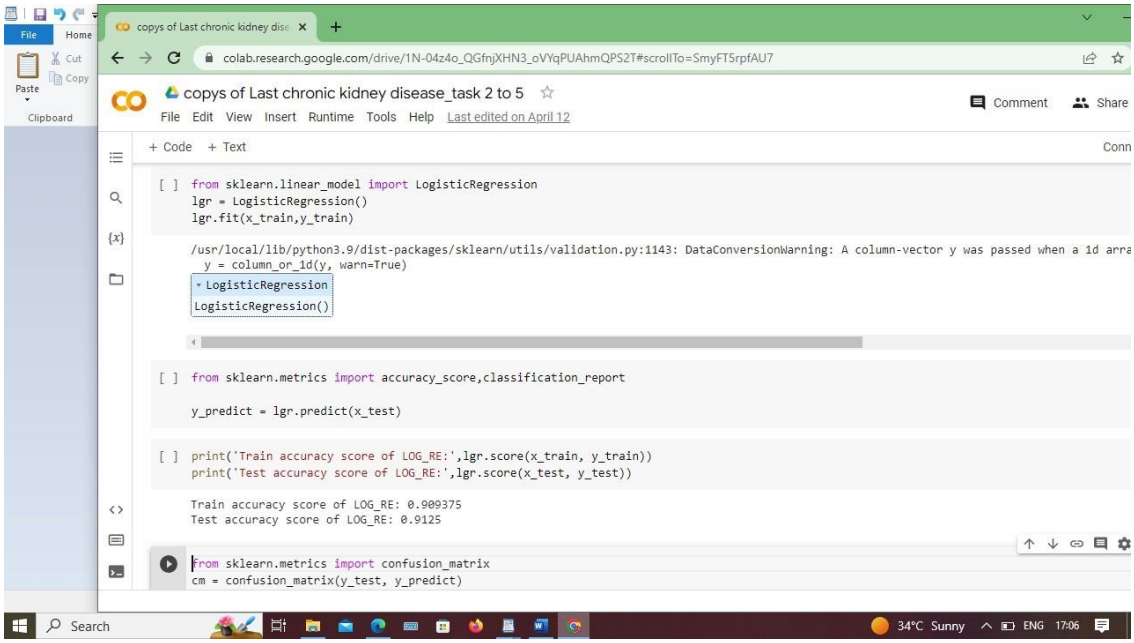
Conn
[ ] x.head()
red_blood_cells pus_cell blood glucose random blood_urea pedal_edema anemia diabetesmellitus coronary_artery_disease
0 1 1 121.000000 36.0 0 0 2 0
1 1 1 148.036517 18.0 0 0 1 0
2 1 1 423.000000 53.0 0 1 2 0
3 1 0 117.000000 56.0 1 1 1 0
4 1 1 106.000000 26.0 0 0 1 0
[ ] test=classification.predict([[1,1,121.000000,36.0,0,0,1,0]])
if test==1:
print('Prediction: High chance of CKD!')
else:
print('Prediction: Low chance of CKD.')
1/1 [==============================] - 0s 140ms/step
Prediction: Low chance of CKD.
print (classification_report(y_test, y_pred))
Search
34°C Sunny
ENG
17:04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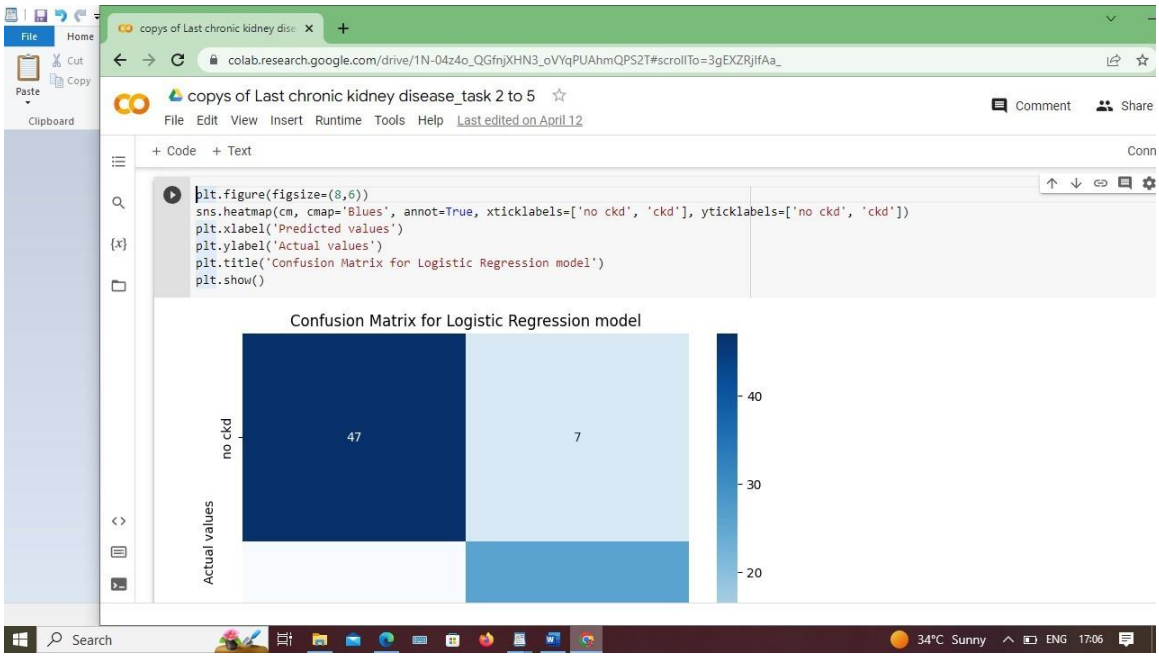
Conn
[ ] from sklearn.linear_model import LogisticRegression
lgr = LogisticRegression()
lgr.fit(x_train,y_train)
/usr/local/lib/python3.9/dist-packages/sklearn/utils/validation.py:1143: DataConversionWarning: A column-vector y was passed when a 1d arra
y = column_or_1d(y, warn=True)
LogisticRegression
LogisticRegression()
[ ] from sklearn.metrics import accuracy_score,classification_report
y_predict = lgr.predict(x_test)
[ ] print('Train accuracy score of LOG_RE:',lgr.score(x_train, y_train))
print('Test accuracy score of LOG_RE:',lgr.score(x_test, y_test))
Train accuracy score of LOG_RE: 0.909375
Test accuracy score of LOG_RE: 0.9125
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test, y_predict)
Search
34°C Sunny
ENG
17:06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colab.research.google.com/drive/1N-04z4o_QGfnjXHN3_oVYqPUAhmQPS2T#scrollTo=3gEXZRjIfAa_
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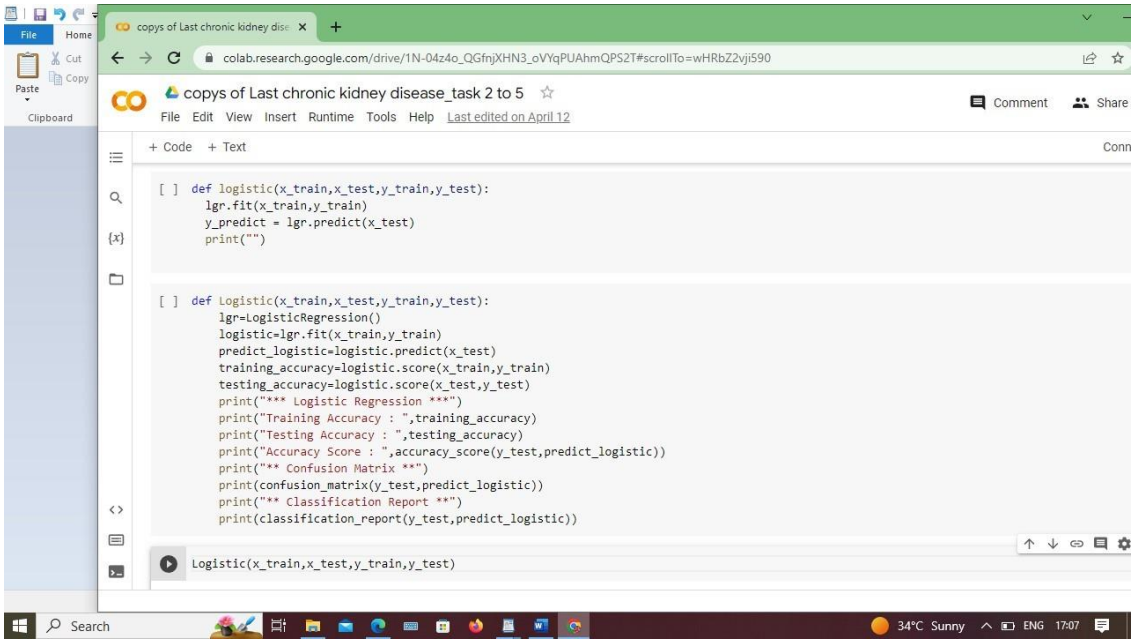
plt.figure(figsize=(8,6))
sns.heatmap(cm, cmap='Blues', annot=True, xticklabels=['no ckd', 'ckd'], yticklabels=['no ckd', 'ckd'])
plt.xlabel('Predicted values')
plt.ylabel('Actual values')
plt.title('Confusion Matrix for Logistic Regression model')
plt.show()
Confusion Matrix for Logistic Regression model
no ckd
Actual values
47
7
40
30
20
Search
34°C Sunny
ENG
17:06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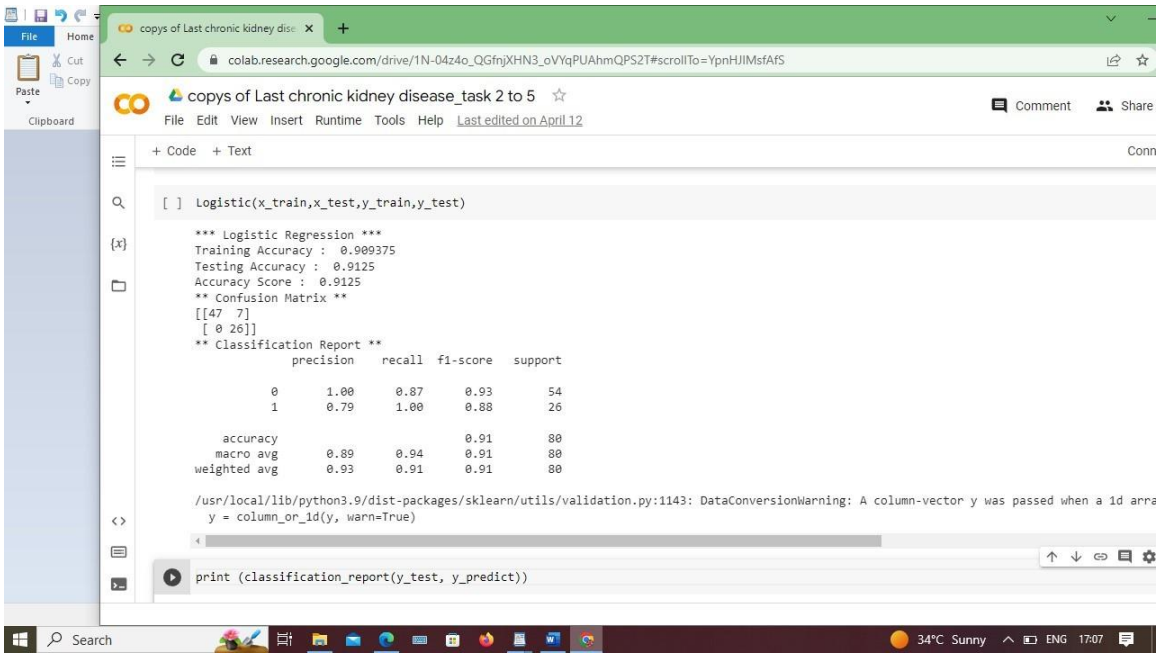
[ ] def logistic(x_train,x_test,y_train,y_test):
lgr.fit(x_train,y_train)
y_predict = lgr.predict(x_test)
print("")
[ ] def Logistic(x_train,x_test,y_train,y_test):
lgr=LogisticRegression()
logistic=lgr.fit(x_train,y_train)
predict_logistic=logistic.predict(x_test)
training_accuracy=logistic.score(x_train,y_train)
testing_accuracy=logistic.score(x_test,y_test)
print("*** Logistic Regression ***")
print("Training Accuracy : ",training_accuracy)
print("Testing Accuracy : ",testing_accuracy)
print("Accuracy Score : ",accuracy_score(y_test,predict_logistic))
print("** Confusion Matrix **")
print(confusion_matrix(y_test,predict_logistic))
print("** Classification Report **")
print(classification_report(y_test,predict_logistic))
Logistic(x_train,x_test,y_train,y_test)
Search
34°C Sunny
ENG
17:07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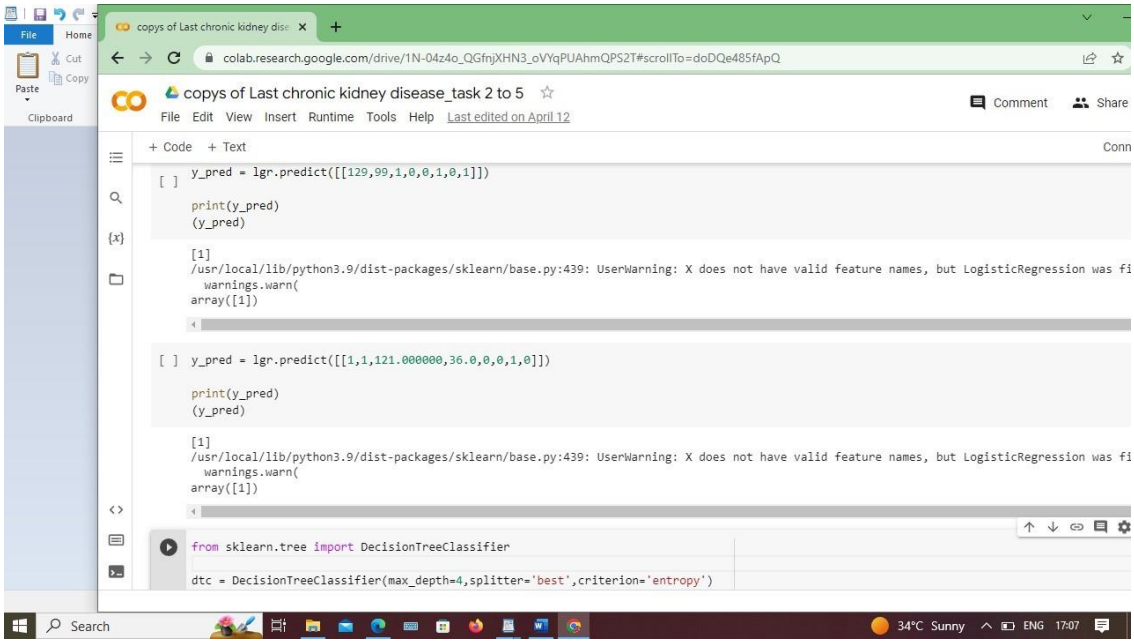
[ ] Logistic(x_train,x_test,y_train,y_test)
*** Logistic Regression ***
Training Accuracy : 0.909375
Testing Accuracy : 0.9125
Accuracy Score : 0.9125
** Confusion Matrix **
[[47 7]
[0 26]]
** Classification Report **
precision recall f1-score support
0 1.00 0.87 0.93 54
1 0.79 1.00 0.88 26
accuracy 0.91 80
macro avg 0.89 0.94 0.91 80
weighted avg 0.93 0.91 0.91 80
/usr/local/lib/python3.9/dist-packages/sklearn/utils/validation.py:1143: DataConversionWarning: A column-vector y was passed when a 1d arra
y = column_or_1d(y, warn=True)
print (classification_report(y_test, y_predict))
Search
34°C Sunny
ENG 17:07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colab.research.google.com/drive/1N-04z4o_QGfnjXHN3_oVYqPUAhmQPS2T#scrollTo=doDQe485fApQ
copys of Last chronic kidney disease_task 2 to 5
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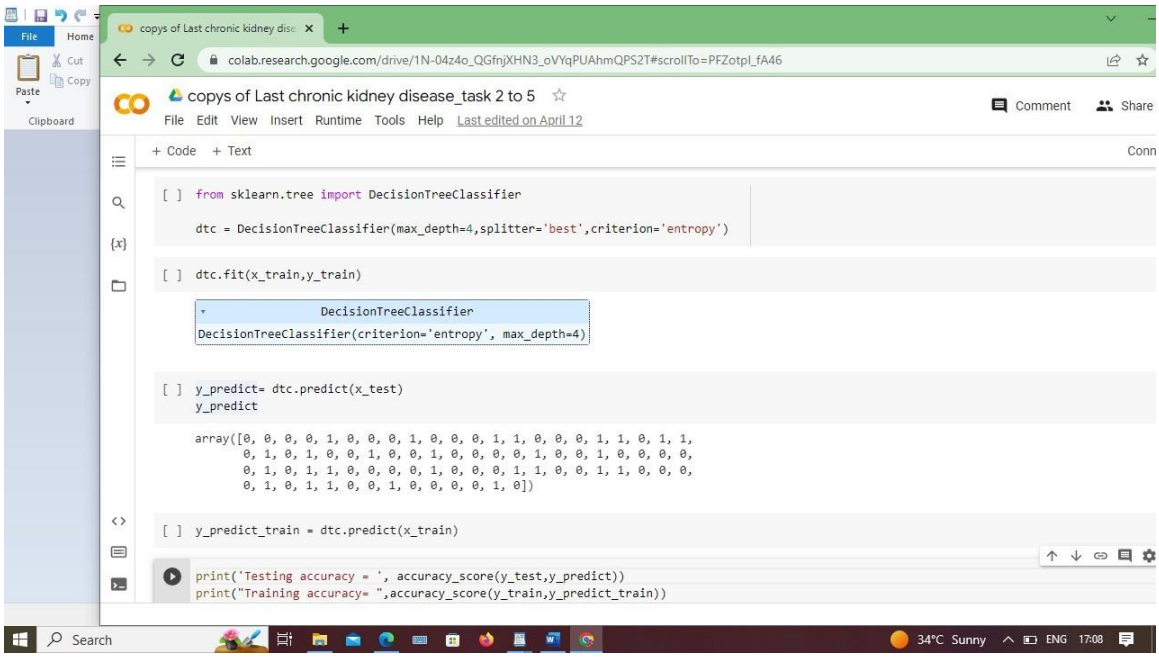
[ ] y_pred = lgr.predict([[129,99,1,0,0,1,0,1]])
print(y_pred)
(y_pred)
[1]
/usr/local/lib/python3.9/dist-packages/sklearn/base.py:439: UserWarning: X does not have valid feature names, but LogisticRegression was fi
warnings.warn(
array([1])
[ ] y_pred = lgr.predict([[1,1,121.000000,36.0,0,0,1,0]])
print(y_pred)
(y_pred)
[1]
/usr/local/lib/python3.9/dist-packages/sklearn/base.py:439: UserWarning: X does not have valid feature names, but LogisticRegression was fi
warnings.warn(
array([1])
from sklearn.tree import DecisionTreeClassifier
dtc = DecisionTreeClassifier(max_depth=4,splitter='best',criterion='entropy')
Search
34°C Sunny
ENG 17:07


copys of Last chronic kidney disease_task 2 to 5
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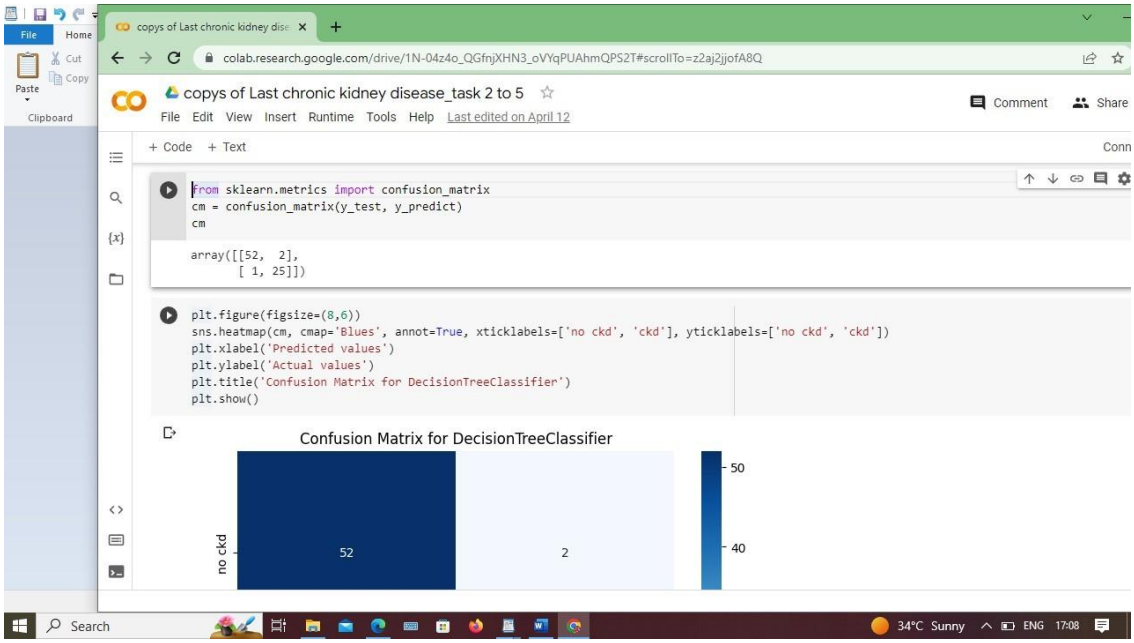
from sklearn.tree import DecisionTreeClassifier
dtc = DecisionTreeClassifier(max_depth=4,splitter='best',criterion='entropy')
dtc.fit(x_train,y_train)
DecisionTreeClassifier
DecisionTreeClassifier(criterion='entropy', max_depth=4)
y_predict= dtc.predict(x_test)
y_predict
array([0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1, 1, 0, 0, 0, 1, 1, 0, 1, 1,
0, 1, 0, 1, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0,
0, 1, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0, 0,
0, 1, 0, 1, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0])
y_predict_train = dtc.predict(x_train)
print('Testing accuracy = ', accuracy_score(y_test,y_predict))
print("Training accuracy= ",accuracy_score(y_train,y_predict_train))


copys of Last chronic kidney disease_task 2 to 5
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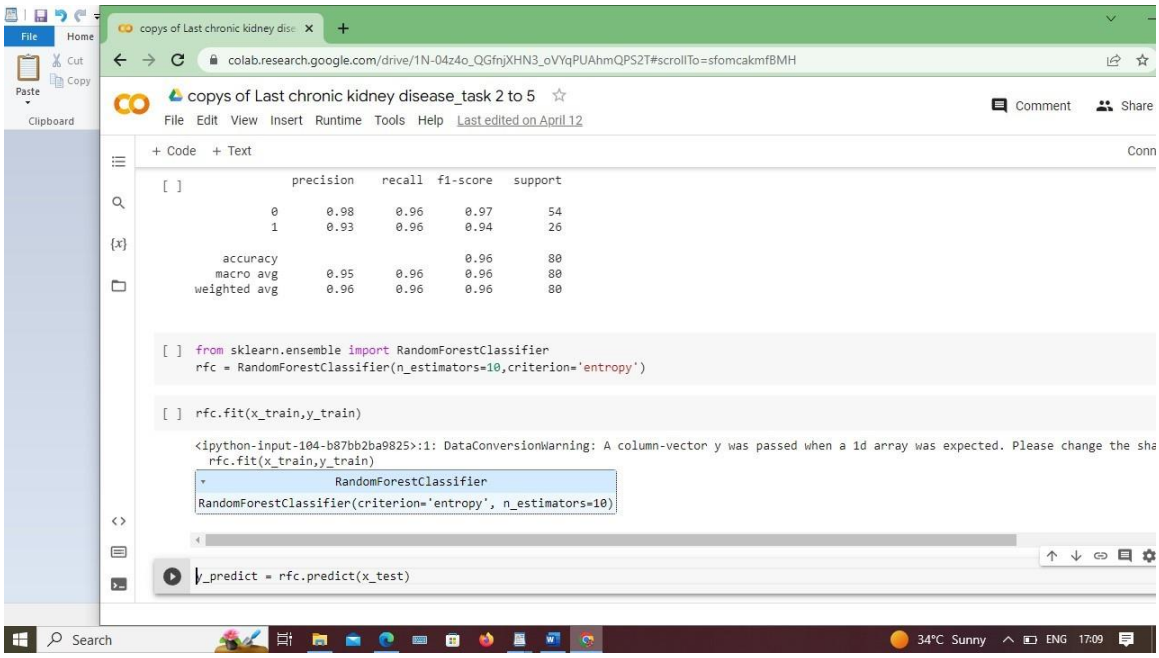
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test, y_predict)
cm
array([[52, 2],
[1, 25]])
plt.figure(figsize=(8,6))
sns.heatmap(cm, cmap='Blues', annot=True, xticklabels=['no ckd', 'ckd'], yticklabels=['no ckd', 'ckd'])
plt.xlabel('Predicted values')
plt.ylabel('Actual values')
plt.title('Confusion Matrix for DecisionTreeClassifier')
plt.show()
Confusion Matrix for DecisionTreeClassifier
no ckd
52
2
50
40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copys of Last chronic kidney disease_task 2 to 5
File Edit View Insert Runtime Tools Help Last edited on April 12
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Share
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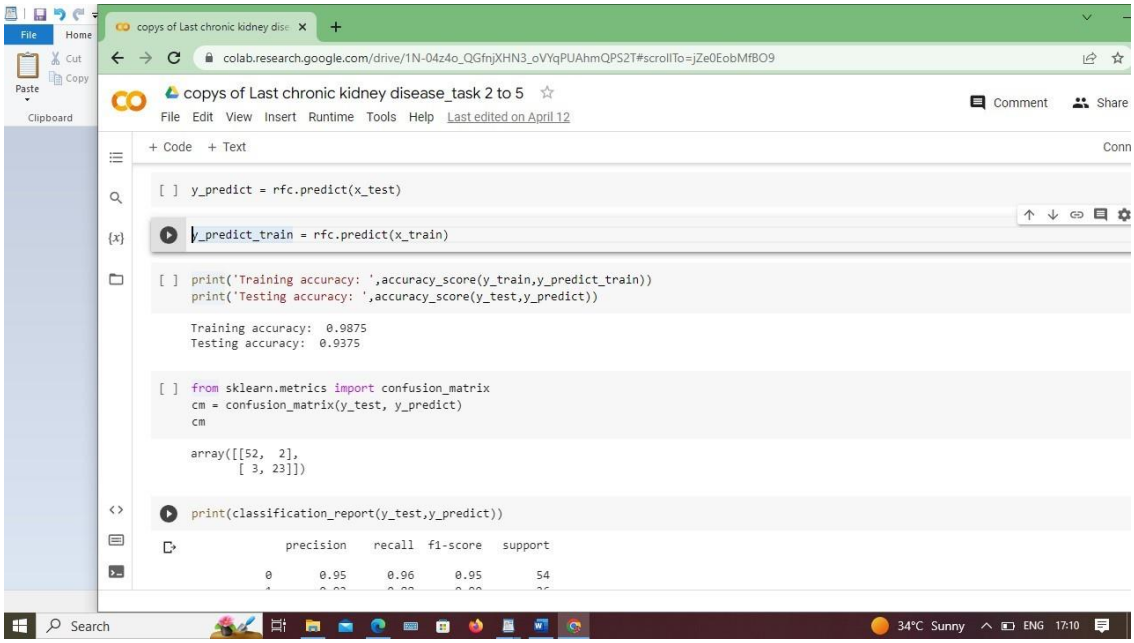
precision recall f1-score support
0 0.98 0.96 0.97 54
1 0.93 0.96 0.94 26
accuracy 0.96 80
macro avg 0.95 0.96 0.96 80
weighted avg 0.96 0.96 0.96 80
from sklearn.ensemble import RandomForestClassifier
rfc = RandomForestClassifier(n_estimators=10,criterion='entropy')
rfc.fit(x_train,y_train)
<ipython-input-104-b87bb2ba9825>:1: DataConversionWarning: A column-vector y was passed when a 1d array was expected. Please change the sha
rfc.fit(x_train,y_train)
RandomForestClassifier
RandomForestClassifier(criterion='entropy', n_estimators=10)
y_predict = rfc.predict(x_test)
Search
34°C Sunny
ENG
17:09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colab.research.google.com/drive/1N-04z4o_QGfnjXHN3_oVYqPUAhmQPS2T#scrollTo=jZe0EobMfBO9
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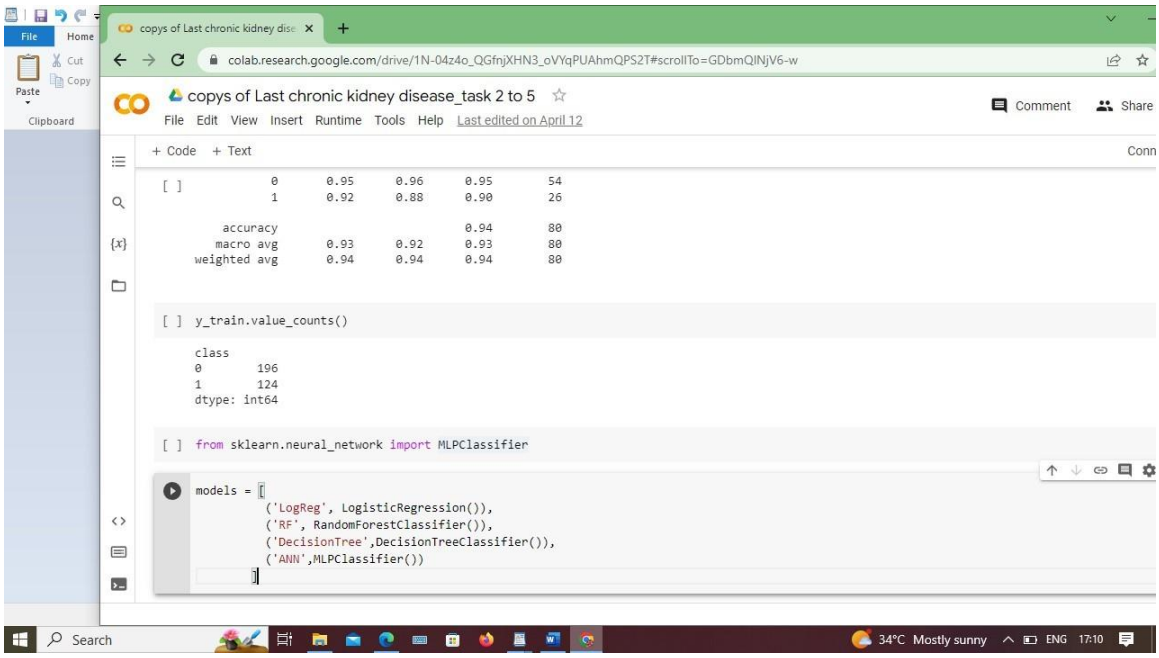
y_predict = rfc.predict(x_test)
y_predict_train = rfc.predict(x_train)
print('Training accuracy: ',accuracy_score(y_train,y_predict_train))
print('Testing accuracy: ',accuracy_score(y_test,y_predict))
Training accuracy: 0.9875
Testing accuracy: 0.9375
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(y_test, y_predict)
cm
array([[52, 2],
[3, 23]])
print(classification_report(y_test,y_predict))
precision recall f1-score support
0 0.95 0.96 0.95 54
Search
34°C Sunny
ENG
17:10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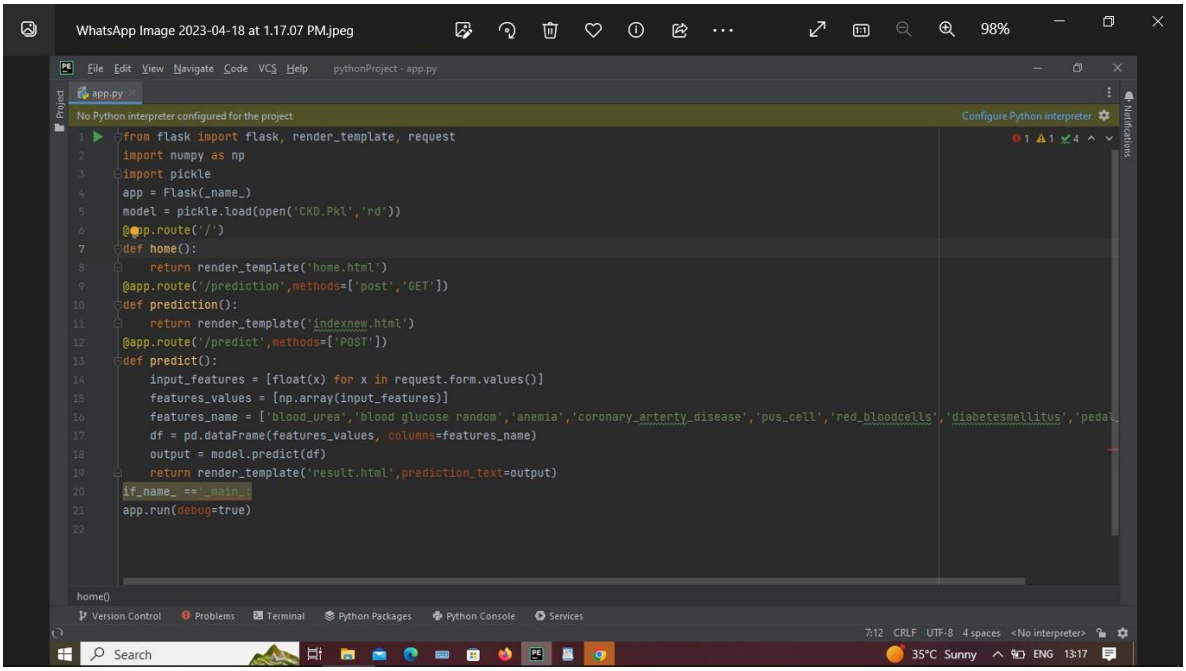
0 0.95 0.96 0.95 54
1 0.92 0.88 0.90 26
accuracy 0.94 80
macro avg 0.93 0.92 0.93 80
weighted avg 0.94 0.94 0.94 80
y_train.value_counts()
class
0 196
1 124
dtype: int64
from sklearn.neural_network import MLPClassifier
models = [
('LogReg', LogisticRegression()),
('RF', RandomForestClassifier()),
('DecisionTree',DecisionTreeClassifier()),
('ANN',MLPClassifier())
]
Search
34°C Mostly sunny
ENG 17:10


WhatsApp Image 2023-04-18 at 1.17.07 PM.jpeg
98%
pythonProject - app.py
app.py
No Python interpreter configured for the project
Configure Python interpreter
from flask import flask, render_template, request
import numpy as np
import pickle
app = Flask(_name_)
model = pickle.load(open('CKD.Pkl','rd'))
@app.route('/')
def home():
return render_template('home.html')
@app.route('/prediction',methods=['post','GET'])
def prediction():
return render_template('indexnew.html')
@app.route('/predict',methods=['POST'])
def predict():
input_features = [float(x) for x in request.form.values()]
features_values = [np.array(input_features)]
features_name = ['blood_urea','blood glucose random','anemia','coronary_arterty_disease','pus_cell','red_bloodcells','diabetesmellitus','pedal
df = pd.dataFrame(features_values, columns=features_name)
output = model.predict(df)
return render_template('result.html',prediction_text=output)
if_name_ =='_main_':
app.run(debug=true)
home()
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