Smart Internz

Project Report Template

1 INTRODUCTION

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A brief description about your project

1.2 Purpose

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2 Problem Definition & Design Thinking

2.1Empathy Map

Paste the empathy map screenshot

2.2Ideation & Brainstorming Map

Paste the Ideation & brainstorming map screenshot

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Final findings (Output) of the project along with screenshots.

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List of advantages and disadvantages of the proposed solution

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The areas where this solution can be applied

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Conclusion summarizing the entire work and findings.

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8 APPENDIX A. Source Code Attach the code for the solution built.

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1 INTRODUCTION

1.1 Overview

A brief description of our project

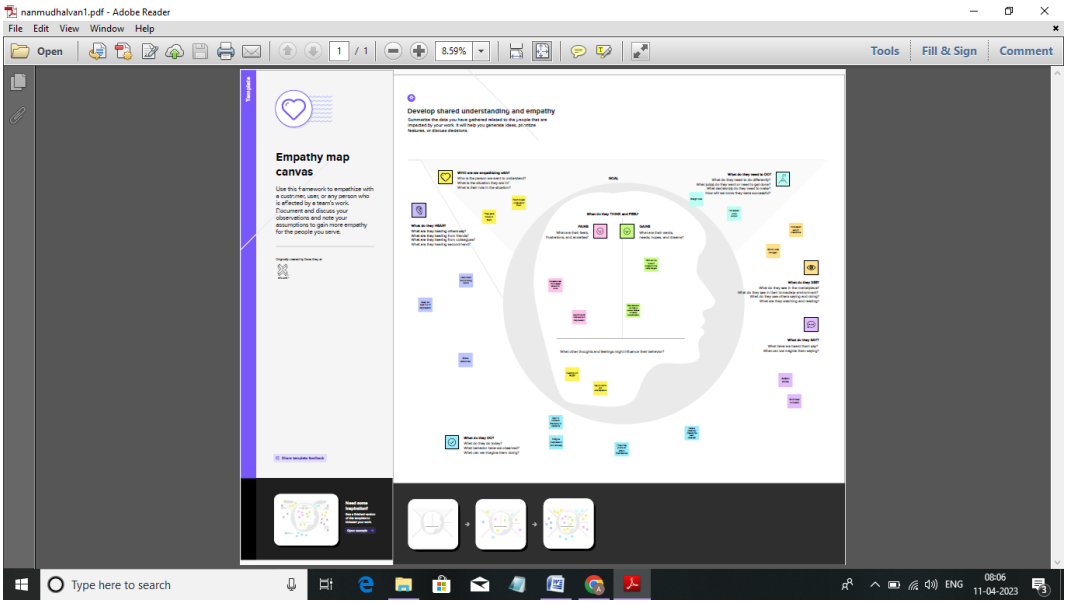
Chronic Kidney Disease (CKD) is a major medical problem and can be cured if treated in the early stages. Usually, people are not aware that medical tests we take for different purposes could containvaluable information concerning kidney diseases. Consequently, attributes of various medical tests are 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.

1.2 purpose

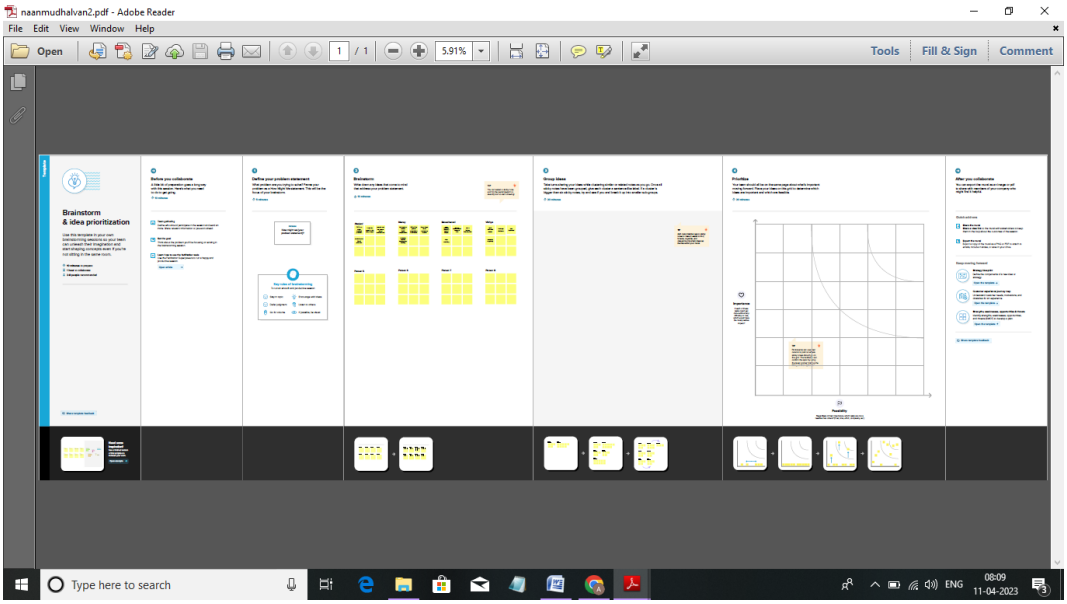
The business requirements for a machine learning model to predict chronic kidney disease include the ability to accurately predict the ckd based on given information, Minimise the number of false positives (predicting diseased) and false negatives (not diseased). Provide an explanation for the model's decision, to comply with regulations and improve transparency.

2.Problem definition & design thinking

2.1 Empathy map



2.2 Ideation & Brainstorming



3.Result

Importing Libaries

```
import pandas as pd #used for data manipulation
import numpy as np #used for numerical analysis
from collections import Counter as c # return counts of number of classess
import matplotlib.pyplot as plt #used for data Visualization
import seaborn as sns #data visualization library
import missingno as msno #finding missing values
from sklearn.metrics import accuracy_score, confusion_matrix#model performance
from sklearn.model_selection import train_test_split #splits data in random train and test array
from sklearn.preprocessing import LabelEncoder #encoding the levels of categorical features
from sklearn.linear_model import LogisticRegression #Classification ML algorithm
import pickle #Python object hierarchy is converted into a byte stream,
```

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

	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.columns #return all the column names
```

```
Index(['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')
```

```
data.columns=['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','class'] # manually giving the name  of the columns
data.columns
```

```
Index(['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', 'class'],
      dtype='object')
```

```
data.info() #info will give you a summary of dataset
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 400 entries, 0 to 399
Data columns (total 25 columns):
 #   Column                   Non-Null Count  Dtype
---  ------                   --------------  -----
 0   age                      391 non-null    float64
 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
 16  white_blood_cell_count   295 non-null    object
 17  red_blood_cell_count     270 non-null    object
 18  hypertension             398 non-null    object
 19  diabetesmellitus         398 non-null    object
 20  coronary_artery_disease  398 non-null    object
 21  appetite                 399 non-null    object
 22  pedal_edema              399 non-null    object
 23  anemia                   399 non-null    object
 24  class                    400 non-null    object
dtypes: float64(11), object(14)
memory usage: 78.2+ KB
```

```
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)
```

4 Advantages & disadvantages

Advantages

Increased recognition of CKD may facilitate implementation of therapeutic strategies to delay progression of kidney function decline or prevent CKD related metabolic complications and CVD. Inclusion of KTRs in a simple severity-based kidney disease classification schema may improve communication between clinicians, enhance public education and facilitate research. Finally, a uniform disease classification and action plan including all patients irrespective of the need or type of renal replacement therapy (i.e. dialysis or transplantation), may

enhance the continuity of patient care. These potential advantages should be weighed against the loss of precision inherent to adopting a generic disease classification system.

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

A history of CVD, albuminuria and advanced stages of CKD was associated with an **increased risk of mortality**. Each combination of these conditions further increased the risk of mortality. These results emphasize the importance of risk factors and cardiovascular and renal diabetes complications

6 .Conclusion

This summarized a detailed review on potential applications for early prediction for chronic kidney disease detection predicted survival of thepredicted survival of thepatient after the illness, the patte**rn of** thedisease and work for curing the disease

7.Future Scope

prevent or slow disease progression. promote physical and psychosocial well-being. monitor disease and treatment complications

8.APPENDIX

Source code

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```
Index(['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')
```

```
data.columns=['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',
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       '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')
```

```
catcols=set(data.dtypes[data.dtypes=='O'].index.values) # only fetch the object type columns
print(catcols)
```

```
{'hypertension', 'packed_cell_volume', 'class', 'coronary_artery_disease', 'anemia', 'red_blood_cell_count', 'red_blood_cells', 'bacteri
a', 'pedal_edema', 'appetite', 'pus_cell', 'diabetesmellitus', 'pus_cell_clumps', 'white_blood_cell_count'}
```