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sample_data

kidney_disease.csv

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```
[ ]  def predict_exit(sample_value):
       sample_value = np.array(sample_value)
       sample_value = sample_value.reshape(1,-1)
       sample_value=sc.transform(sample_value)
       return classifier.predict(sample_value)
```

```
[ ]  test=classification.predict([[1,1,121,000000,36.0,0,0,1,0]])
     if test==1;
     print('prediction:high chance of CKDI')
     else:
       print('prediction: low chance of CKD.')
```

```
[ ]  from sklearn import model_selection
```

```
[ ]        dfs = []
         models =[
                   ('LogReg, LogisticRegistaion()'),
                   ('RF',RandomForestClassifier()),
                   ('DecisionTree',DesitionTreeCladssifier()),
                 ]
         result= []
                 names=[]
                 scoring=['accuracy','precision_weighted','recall_weighted',f1
```

kidney_disease.csv

1 to 10 of 400 entries Filter

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

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```
[ ]  (y_pred)
```

```
[ ]  y_pred = dtc.predict([[1,1,121.000000,36.0,0,0,1,0]])
     print(y_pred)
     (y_pred)
```

```
[ ]  y_pred = rfc.predict([[1,1,121.000000,36.0,0,0,1,0]])
     print(y_pred)
     (y_pred)
```

```
[ ]  classification.save("ckd.h5")
```

```
[ ]  y_pred = classification.predict(x_test)
```

```
[ ]  y_pred
```

```
[ ]  y_pred=(y_pred>0.5)
     y_pred
```

```
[ ]  def predict_exit(sample_value):
       sample_value = np.array(sample_value)
```

kidney_disease.csv

1 to 10 of 400 entries Filter

id	age	bp	sg	al	su	rbc	pc	
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4	51.0	80.0	1.01	2.0	0.0	normal	normal	not
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6	68.0	70.0	1.01	0.0	0.0		normal	not
7	24.0		1.015	2.0	4.0	normal	abnormal	not
8	52.0	100.0	1.015	3.0	0.0	normal	abnormal	pre
9	53.0	90.0	1.02	2.0	0.0	abnormal	abnormal	pre

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                 ]
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```

kidney_disease.csv

1 to 10 of 400 entries Filter

id	age	bp	sg	al	su	rbc	pc	
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4	51.0	80.0	1.01	2.0	0.0	normal	normal	not
5	60.0	90.0	1.015	3.0	0.0			not
6	68.0	70.0	1.01	0.0	0.0		normal	not
7	24.0		1.015	2.0	4.0	normal	abnormal	not
8	52.0	100.0	1.015	3.0	0.0	normal	abnormal	pre
9	53.0	90.0	1.02	2.0	0.0	abnormal	abnormal	pre

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```
[ ]     result= []
            names=[]
            scoring=['accuracy','precision_weighted','recall_weighted',f1_
            target_names=['NO CKD','CKD']
            for name,mode1 in models:
              kflod=mode1_selection.KFold(n_splits=5, suffle=True,random_a
              cv_results=model_selection.cross_validate(model,x_train,y_tr
              clf = model.fit(x_train,y_train)
              y_pred==clf.predict(x_test)
              print(name)
              print(classification_report(y_test,y_pred,target_names=targe
              results.append(name)
              this_df=pd.DateFrame(cv_results)
              this _df=pd.DataFrame(cv_results)
              this _df['model']=name
              dfs.append(this_df)
          final=pd.concat(dfs,ignore_index=True)
          return final
```

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

kidney_disease.csv

1 to 10 of 400 entries Filter

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

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```
[ ]   bootstrap=model_df.sample(n=30,replace=true)
      bootstraps.append(bootstrap)
      bootstrap_df=pd.concat(bootstrap,ignore_index=true)
      results_long=pd.melt(bootstrap_df,id_vars=['metrics'].isin(time_metrics)
       time_metrics =['fit_time','score_time']
    results_long_nofit=results_long.loc[~results_long['metrics'].isin(time_met
    results_long_nofit=results_long_nofit.sort_values(by='values')
    results_long_nofit=results_long.loc[results_long['metrics'].isin(time_metr
    results_long_nofit=results_long_fit.sort_values(by='values')
```

```
[ ] import matplotlib.pyplot as plt
    import seaborn as sns
    plt.figure(figsize=(20,12))
    sns.set(font_scale=2.5)
    g=sns.boxplot(x="model",y="values",hue="metrics",data=results_long_nofit,
```

kidney_disease.csv

1 to 10 of 400 entries Filter

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

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```
[ ] plt.show()
```

```
  File "<ipython-input-1-6c7888db3644>", line 2
    sns.hestmap(cm,cmap'Blues',annot=True, xticklabels=['no
ckd','ckd'],yticklabels=['no ckd','ckd'])
                          ^
SyntaxError: invalid syntax
```

SEARCH STACK OVERFLOW

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

```
---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
<ipython-input-12-f0b0b49e64af> in <cell line: 2>()
      1 from sklearn.metrics import confusion_matrix
----> 2 cm = confusion_matrix(y_test,y_pred)
      3 cm

NameError: name 'y_test' is not defined
```

SEARCH STACK OVERFLOW

kidney_disease.csv

1 to 10 of 400 entries Filter

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

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

```
[ ]  plt.figure(figsize=(8,6))
     sns.hestmap(cm,cmap'Blues',annot=True, xticklabels=['no ckd','ckd'],ytick
     plt.xlabel('predicted values')
     plt.ylabel('Actual values')
     plt.titel('Confusion matrix for logistic Regression model')
     plt.show()
```

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

```
[ ]  plt.figure(figsize=(8,6))
     sns.hestmap(cm,cmap'Blues',annot=True, xticklabels=['no ckd','ckd'],ytick
     plt.xlabel('predicted values')
     plt.ylabel('Actual values')
     plt.titel('Confusion matrix for RandomForestClassifier')
     plt.show()
```

```
  File "<ipython-input-1-6c7888db3644>", line 2
```

kidney_disease.csv

1 to 10 of 400 entries Filter

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

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SEARCH STACK OVERFLOW

```
[ ]  plt.figure(figsize=(8,6))
     sns.heatmap(cm,cmap'Blues',annot=True, xticklabels=['no ckd','ckd'],ytickl
     plt.xlabel('predicted values')
     plt.ylabel('Actual values')
     plt.titel('Confusion matrix for DecisionTreeClassifier')
     plt.show()
```

```
  File "<ipython-input-8-1048d0a256fa>", line 2
    sns.hestmap(cm,cmap'Blues',annot=True, xticklabels=['no
ckd','ckd'],yticklabels=['no ckd','ckd'])
                         ^
SyntaxError: invalid syntax
```

SEARCH STACK OVERFLOW

```
[ ]  bootstraps=[]
     for model in list(set(final.model.values)):
       model_df=final.loc[final.model1==model]
       bootstrap=model_df.sample(n=30,replace=true)
       bootstraps.append(bootstrap)
       bootstrap_df=pd.concat(bootstrap,ignore_index=true)
```

kidney_disease.csv

1 to 10 of 400 entries Filter

id	age	bp	sg	al	su	rbc	pc	
0	48.0	80.0	1.02	1.0	0.0		normal	not
1	7.0	50.0	1.02	4.0	0.0		normal	not
2	62.0	80.0	1.01	2.0	3.0	normal	normal	not
3	48.0	70.0	1.005	4.0	0.0	normal	abnormal	pre
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SEARCH STACK OVERFLOW

```
[ ] contcols.add('red_blood_cell_count')
    contcols.add('packed_cell_volume')
    contcols.add('white_blood_cell_count')
    print(contcols)
```

```
{'dm', 'rc', 'rbc', 'white_blood_cell_count', 'bu', 'pcc', 'sc', 'al', 'bp
```

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

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

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

kidney_disease.csv

1 to 10 of 400 entries Filter

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