

Files

sample_data
kidney_disease.csv

```
[ ] 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 X

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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```
+ Code + Text  
[ ] (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):  
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```

[ ] result= []
names=[]
scoring=['accuracy','precision_weighted','recall_weighted','f1'
target_names=['NO CKD','CKD']
for name,model in models:
    kfold=model_selection.KFold(n_splits=5, shuffle=True,random_s
    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.DataFrame(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
    
```

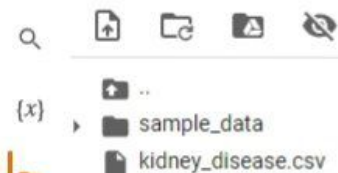
kidney_disease.csv X

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Files



+ Code + Text

```
[ ] 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_metrics)]
    results_long_nofit=results_long_nofit.sort_values(by='values')
    results_long_nofit=results_long_nofit.loc[results_long_nofit['metrics'].isin(time_metrics)]
    results_long_nofit=results_long_nofit.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,
```

RAM Disk

kidney_disease.csv X

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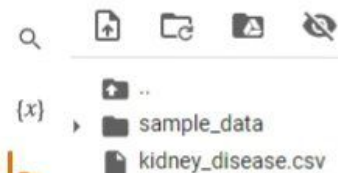
<>

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Disk 84.49 GB available

Files



+ Code + Text

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

```
File "<ipython-input-1-6c7888db3644>", line 2
sns.histmap(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

RAM Disk

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```
+ Code + Text

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

[ ] 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.title('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.heatmap(cm,cmap='Blues',annot=True, xticklabels=['no ckd','ckd'],ytickl
    plt.xlabel('predicted values')
    plt.ylabel('Actual values')
    plt.title('Confusion matrix for RandomForestClassifier')
    plt.show()
```

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

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[ ]  
[ ] 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.title('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  
  
[ ] 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)
```

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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_disease.replace('\tno',
c(data['cornary_artery_disease']))

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

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