Predicting Chronic Kidney Disease based on health records

Given 24 health related attributes taken in 2-month period of 400 patients, using the information of the 158 patients with complete records to predict the outcome (i.e. whether one has chronic kidney disease) of the remaining 242 patients (with missing values in their records).

Summary of Results

With proper tuning of parameters using cross-validation in the training set, the Random Forest Classfier achieves an accuracy of 88.8% and an ROC AUC of 99.2%. Lesson learnt: It happens that some pruning helps improve the performance of RF a lot. (http:)

Load Modules and helper functions

In [1]:
```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.metrics import roc_curve, auc, confusion_matrix, classification_repo
from sklearn.ensemble import RandomForestClassifier
import warnings
warnings.filterwarnings('ignore')
%matplotlib inline

def auc_scorer(clf, X, y, model): # Helper function to plot the ROC curve
    if model=='RF':
        fpr, tpr, _ = roc_curve(y, clf.predict_proba(X)[:,1])
    elif model=='SVM':
        fpr, tpr, _ = roc_curve(y, clf.decision_function(X))
    roc_auc = auc(fpr, tpr)

    plt.figure()    # Plot the ROC curve
    plt.plot(fpr, tpr, label='ROC curve from '+model+' model (area = %0.3f)' % ro
    plt.plot([0, 1], [0, 1], 'k--')
    plt.xlim([0.0, 1.0])
    plt.ylim([0.0, 1.05])
    plt.xlabel('False Positive Rate')
    plt.ylabel('True Positive Rate')
    plt.title('ROC Curve')
    plt.legend(loc="lower right")
    plt.show()

    return fpr,tpr,roc_auc

# from subprocess import check_output
# print(check_output(["ls", "../input"]).decode("utf8"))
```

Load files

In [3]:
```
df = pd.read_csv('kidney_disease.csv')
```

Cleaning and preprocessing of data for training a classifier

In [4]:
```
# Map text to 1/0 and do some cleaning
df[['htn','dm','cad','pe','ane']] = df[['htn','dm','cad','pe','ane']].replace(to_
df[['rbc','pc']] = df[['rbc','pc']].replace(to_replace={'abnormal':1,'normal':0})
df[['pcc','ba']] = df[['pcc','ba']].replace(to_replace={'present':1,'notpresent':
df[['appet']] = df[['appet']].replace(to_replace={'good':1,'poor':0,'no':np.nan})
df['classification'] = df['classification'].replace(to_replace={'ckd':1.0,'ckd\t'
df.rename(columns={'classification':'class'},inplace=True)
```

In [5]:
```
# Further cleaning
df['pe'] = df['pe'].replace(to_replace='good',value=0) # Not having pedal edema i
df['appet'] = df['appet'].replace(to_replace='no',value=0)
df['cad'] = df['cad'].replace(to_replace='\tno',value=0)
df['dm'] = df['dm'].replace(to_replace={'\tno':0,'\tyes':1,' yes':1, '':np.nan})
df.drop('id',axis=1,inplace=True)
```

In [6]:
```
df.head()
```

Out[6]:

	age	bp	sg	al	su	rbc	pc	pcc	ba	bgr	...	pcv	wc	rc	htn	dm	cad	appe
0	48.0	80.0	1.020	1.0	0.0	NaN	0.0	0.0	0.0	121.0	...	44	7800	5.2	1.0	1.0	0.0	1.
1	7.0	50.0	1.020	4.0	0.0	NaN	0.0	0.0	0.0	NaN	...	38	6000	NaN	0.0	0.0	0.0	1.
2	62.0	80.0	1.010	2.0	3.0	0.0	0.0	0.0	0.0	423.0	...	31	7500	NaN	0.0	1.0	0.0	0.
3	48.0	70.0	1.005	4.0	0.0	0.0	1.0	1.0	0.0	117.0	...	32	6700	3.9	1.0	0.0	0.0	0.
4	51.0	80.0	1.010	2.0	0.0	0.0	0.0	0.0	0.0	106.0	...	35	7300	4.6	0.0	0.0	0.0	1.

5 rows × 25 columns

Check the portion of rows with NaN

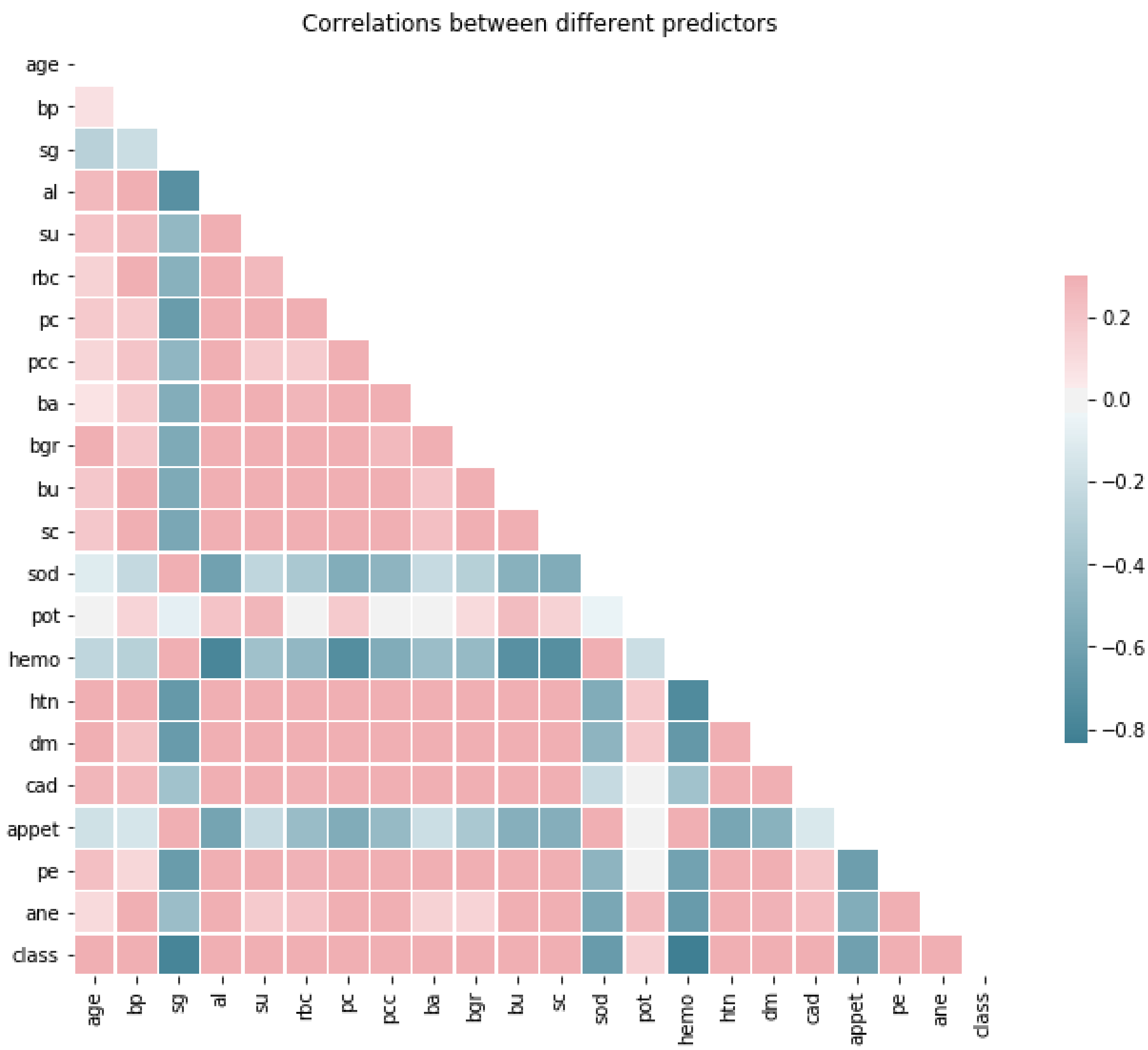
- Now the data is cleaned with improper values labelled NaN. Let's see how many NaNs are there.
- Drop all the rows with NaN values, and build a model out of this dataset (i.e. df2)

In [7]:
```
df2 = df.dropna(axis=0)
df2['class'].value_counts()
```

Out[7]:
```
0.0    115
1.0     43
Name: class, dtype: int64
```

Examine correlations between different features

In [8]:
```
corr_df = df2.corr()

# Generate a mask for the upper triangle
mask = np.zeros_like(corr_df, dtype=np.bool)
mask[np.triu_indices_from(mask)] = True

# Set up the matplotlib figure
f, ax = plt.subplots(figsize=(11, 9))

# Generate a custom diverging colormap
cmap = sns.diverging_palette(220, 10, as_cmap=True)

# Draw the heatmap with the mask and correct aspect ratio
sns.heatmap(corr_df, mask=mask, cmap=cmap, vmax=.3, center=0,
            square=True, linewidths=.5, cbar_kws={"shrink": .5})
plt.title('Correlations between different predictors')
plt.show()
```



Split the set for training models further into a (sub-)training set and testing set.

In [9]:
```
X_train, X_test, y_train, y_test = train_test_split(df2.iloc[:,:-1], df2['class']
                                                     test_size = 0.33, random_stat
                                                    stratify= df2['class'] )
```

In [10]:
```
print(X_train.shape)
print(X_test.shape)
```

```
(105, 24)
(53, 24)
```

In [11]:
```
y_train.value_counts()
```

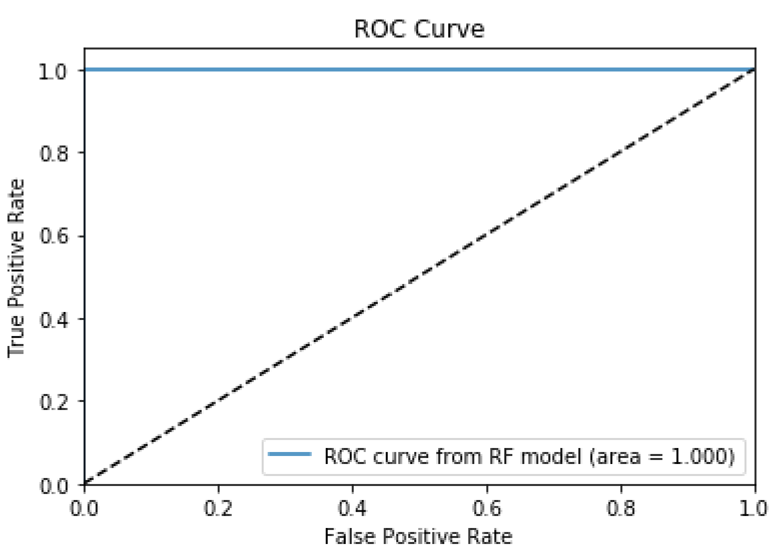
Out[11]:
```
0.0    76
1.0    29
Name: class, dtype: int64
```

Choosing parameters with GridSearchCV with 10-fold cross validations.

(Suggestion for next time: try using Bayesian model selection method)

In [12]:
```
tuned_parameters = [{'n_estimators':[7,8,9,10,11,12,13,14,15,16],'max_depth':[2,3
                     'class_weight':[None,{0: 0.33,1:0.67},'balanced'],'random_st
clf = GridSearchCV(RandomForestClassifier(), tuned_parameters, cv=10,scoring='f1'
clf.fit(X_train, y_train)

print("Detailed classification report:")
y_true, lr_pred = y_test, clf.predict(X_test)
print(classification_report(y_true, lr_pred))

confusion = confusion_matrix(y_test, lr_pred)
print('Confusion Matrix:')
print(confusion)

# Determine the false positive and true positive rates
fpr,tpr,roc_auc = auc_scorer(clf, X_test, y_test, 'RF')

print('Best parameters:')
print(clf.best_params_)
clf_best = clf.best_estimator_
```

```
Detailed classification report:
              precision    recall  f1-score   support

         0.0       1.00      1.00      1.00        39
         1.0       1.00      1.00      1.00        14

    accuracy                           1.00        53
   macro avg       1.00      1.00      1.00        53
weighted avg       1.00      1.00      1.00        53

Confusion Matrix:
[[39  0]
 [ 0 14]]
```



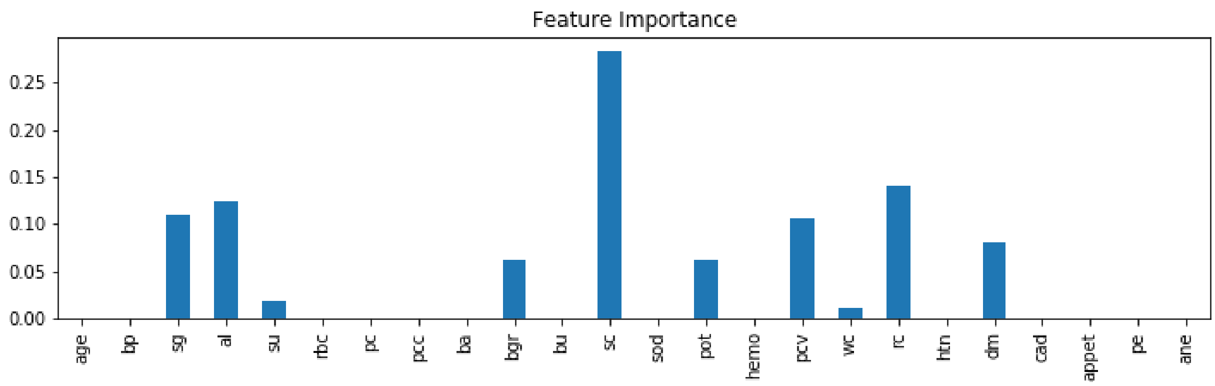

```
Best parameters:
{'class_weight': None, 'max_depth': 2, 'n_estimators': 8, 'random_state': 42}
```

Examine feature importance

Since I pruned the forest (*max_depth*=2) and decrease the number of trees (*n_estimators*=8), not all features are used.

In [13]:
```
plt.figure(figsize=(12,3))
features = X_test.columns.values.tolist()
importance = clf_best.feature_importances_.tolist()
feature_series = pd.Series(data=importance,index=features)
feature_series.plot.bar()
plt.title('Feature Importance')
```

Out[13]:
```
Text(0.5, 1.0, 'Feature Importance')
```



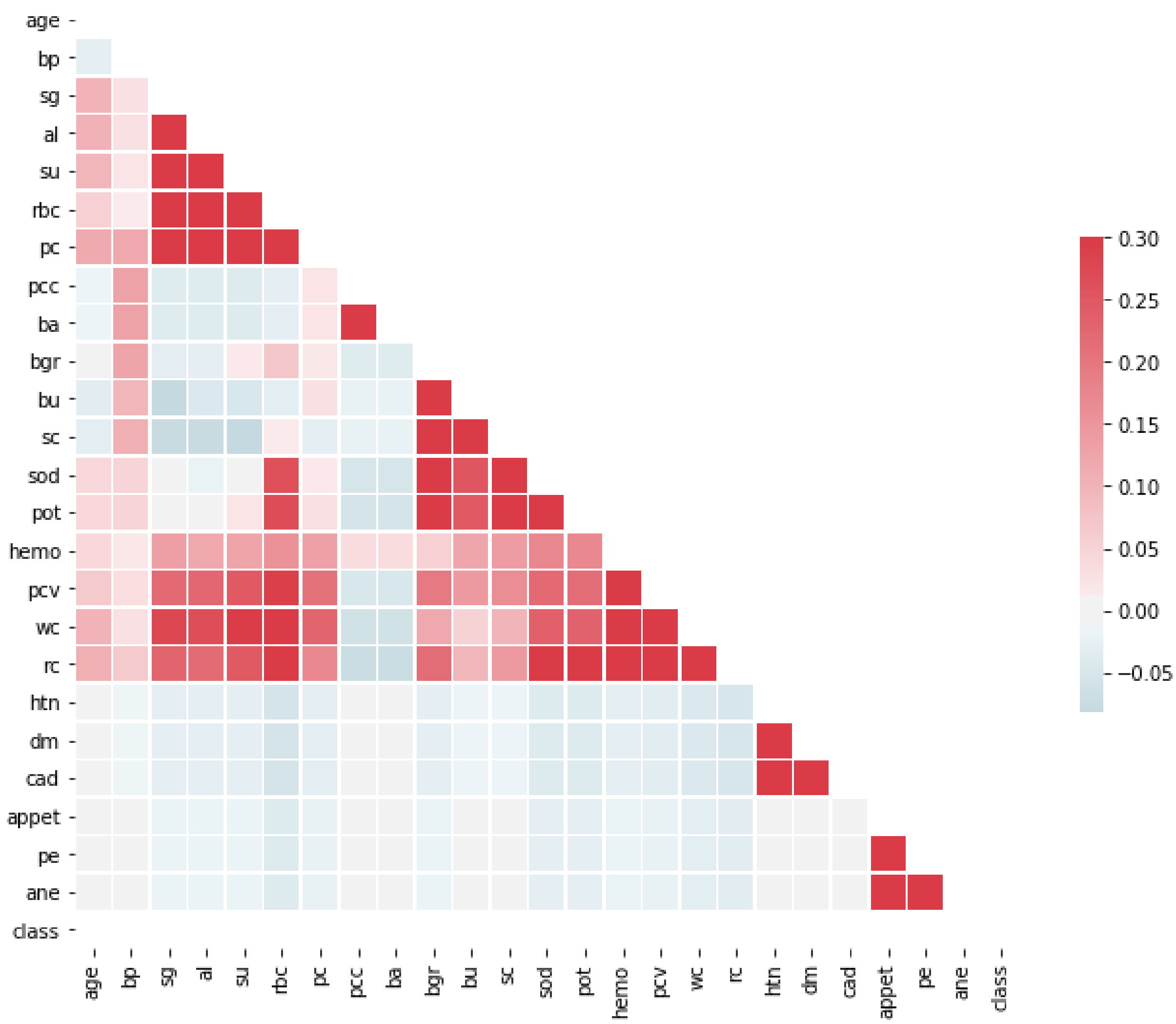
In [14]:
```
list_to_fill = X_test.columns[feature_series>0]
print(list_to_fill)
```

```
Index(['sg', 'al', 'su', 'bgr', 'sc', 'pot', 'pcv', 'wc', 'rc', 'dm'], dtype='o
bject')
```

Next, I examine the rest of the dataset (with missing values across the rows)

Are there correlations between occurence of missing values in a row? The plot suggests, seems no.

In [15]:
```
# Are there correlation in missing values?
corr_df = pd.isnull(df).corr()

# Generate a mask for the upper triangle
mask = np.zeros_like(corr_df, dtype=np.bool)
mask[np.triu_indices_from(mask)] = True

# Set up the matplotlib figure
f, ax = plt.subplots(figsize=(11, 9))

# Generate a custom diverging colormap
cmap = sns.diverging_palette(220, 10, as_cmap=True)

# Draw the heatmap with the mask and correct aspect ratio
sns.heatmap(corr_df, mask=mask, cmap=cmap, vmax=.3, center=0,
            square=True, linewidths=.5, cbar_kws={"shrink": .5})
plt.show()
```



Make predictions with the best model selected above

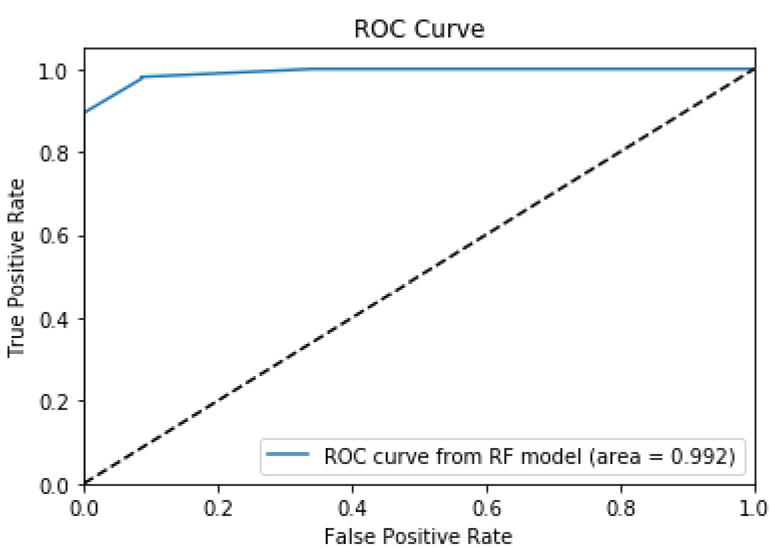
I filled in all NaN with 0 and pass it to the trained classifier. The results are as follows:

- True positive = 180
- True negative = 35
- False positive = 0
- False negative = 27

- Accuracy = 88.8%
- ROC AUC = 99.2%

In [16]:
```
df2 = df.dropna(axis=0)
no_na = df2.index.tolist()
some_na = df.drop(no_na).apply(lambda x: pd.to_numeric(x,errors='coerce'))
some_na = some_na.fillna(0) # Fill up all Nan by zero.

X_test = some_na.iloc[:,:-1]
y_test = some_na['class']
y_true = y_test
lr_pred = clf_best.predict(X_test)
print(classification_report(y_true, lr_pred))

confusion = confusion_matrix(y_test, lr_pred)
print('Confusion Matrix:')
print(confusion)

print('Accuracy: %3f' % accuracy_score(y_true, lr_pred))
# Determine the false positive and true positive rates
fpr,tpr,roc_auc = auc_scorer(clf_best, X_test, y_test, 'RF')
```

```
              precision    recall  f1-score   support

         0.0       0.56      1.00      0.72        35
         1.0       1.00      0.87      0.93       207

    accuracy                           0.89       242
   macro avg       0.78      0.93      0.83       242
weighted avg       0.94      0.89      0.90       242

Confusion Matrix:
[[ 35   0]
 [ 27 180]]
Accuracy: 0.888430
```



In [ ]: