Background

The World Health Organization (WHO) characterized the COVID-19, caused by the SARS-CoV-2, as a pandemic on March 11, while the exponential increase in the number of cases was risking to overwhelm health systems around the world with a demand for ICU beds far above the existing capacity, with regions of Italy being prominent examples.

Brazil recorded the first case of SARS-CoV-2 on February 26, and the virus transmission evolved from imported cases only, to local and finally community transmission very rapidly, with the federal government declaring nationwide community transmission on March 20.

Until March 27, the state of São Paulo had recorded 1,223 confirmed cases of COVID-19, with 68 related deaths, while the county of São Paulo, with a population of approximately 12 million people and where Hospital Israelita Albert Einstein is located, had 477 confirmed cases and 30 associated death, as of March 23. Both the state and the county of São Paulo decided to establish quarantine and social distancing measures, that will be enforced at least until early April, in an effort to slow the virus spread.

One of the motivations for this challenge is the fact that in the context of an overwhelmed health system with the possible limitation to perform tests for the detection of SARS-CoV-2, testing every case would be impractical and tests results could be delayed even if only a target subpopulation would be tested.

Dataset

This dataset contains anonymized data from patients seen at the Hospital Israelita Albert Einstein, at São Paulo, Brazil, and who had samples collected to perform the SARS-CoV-2 RT-PCR and additional laboratory tests during a visit to the hospital.

All data were anonymized following the best international practices and recommendations. All clinical data were standardized to have a mean of zero and a unit standard deviation.

AIM

Studying the variables associated with Covid-19 and use different machine learning algorithms to classify a positive case vs. a negative case.

Loading required libraries

In [178]:
```
#pip install graphviz
#pip install pydotplus
```

In [148]:
```
import pandas as pd
import numpy as np
import seaborn as sns
import pydotplus
import graphviz
import matplotlib.pyplot as plt
from sklearn import tree
from sklearn import metrics
from sklearn.metrics import roc_curve, auc
from sklearn.ensemble import RandomForestRegressor
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import  classification_report, confusion_matrix
from sklearn.tree import export_graphviz
from sklearn.externals.six import StringIO
from IPython.display import Image
```

Loading the data

In [149]:
```
df=pd.read_excel('dataset.xlsx')
```

In [150]:
```
df.head()
```

Out[150]:

	Patient ID	Patient age quantile	SARS-Cov-2 exam result	Patient addmited to regular ward (1=yes, 0=no)	Patient addmited to semi-intensive unit (1=yes, 0=no)	Patient addmited to intensive care unit (1=yes, 0=no)	Hematocrit	Hemoglobin	Platelets	Mean platelet volume	...	Hb saturation (arterial blood gases)	pCO2 (arterial blood gas analysis)
0	44477f75e8169d2	13	negative	0	0	0	NaN	NaN	NaN	NaN	...	NaN	NaN
1	126e9dd13932f68	17	negative	0	0	0	0.236515	-0.02234	-0.517413	0.010677	...	NaN	NaN
2	a46b4402a0e5696	8	negative	0	0	0	NaN	NaN	NaN	NaN	...	NaN	NaN
3	f7d619a94f97c45	5	negative	0	0	0	NaN	NaN	NaN	NaN	...	NaN	NaN
4	d9e41465789c2b5	15	negative	0	0	0	NaN	NaN	NaN	NaN	...	NaN	NaN

5 rows × 111 columns

Studying the data

In [151]:
```
print(f"Num rows: {len(df)}")
print(f"Num columns: {len(df.columns)}")
```

```
Num rows: 5644
Num columns: 111
```

In [152]:
```
df.groupby("SARS-Cov-2 exam result").count()
```

Out[152]:

SARS-Cov-2 exam result	Patient ID	Patient age quantile	Patient addmited to regular ward (1=yes, 0=no)	Patient addmited to semi-intensive unit (1=yes, 0=no)	Patient addmited to intensive care unit (1=yes, 0=no)	Hematocrit	Hemoglobin	Platelets	Mean platelet volume	Red blood Cells	...	Hb saturation (arterial blood gases)	pCO2 (arterial blood gas analysis)	Bas exces (arteri bloo ga analysi
negative	5086	5086	5086	5086	5086	520	520	519	518	519	...	14	14	1
positive	558	558	558	558	558	83	83	83	81	83	...	13	13	1

2 rows × 110 columns

In [153]:
```
df.dtypes
```

Out[153]:
```
Patient ID                                                 object
Patient age quantile                                        int64
SARS-Cov-2 exam result                                     object
Patient addmited to regular ward (1=yes, 0=no)              int64
Patient addmited to semi-intensive unit (1=yes, 0=no)       int64
Patient addmited to intensive care unit (1=yes, 0=no)       int64
Hematocrit                                                float64
Hemoglobin                                                float64
Platelets                                                 float64
Mean platelet volume                                      float64
Red blood Cells                                           float64
Lymphocytes                                               float64
Mean corpuscular hemoglobin concentration (MCHC)          float64
Leukocytes                                                float64
Basophils                                                 float64
Mean corpuscular hemoglobin (MCH)                         float64
Eosinophils                                               float64
Mean corpuscular volume (MCV)                             float64
Monocytes                                                 float64
Red blood cell distribution width (RDW)                   float64
Serum Glucose                                             float64
Respiratory Syncytial Virus                                object
Influenza A                                                object
Influenza B                                                object
Parainfluenza 1                                            object
CoronavirusNL63                                            object
Rhinovirus/Enterovirus                                     object
Mycoplasma pneumoniae                                     float64
Coronavirus HKU1                                           object
Parainfluenza 3                                            object
                                                           ...
Urine - Sugar                                             float64
Urine - Leukocytes                                         object
Urine - Crystals                                           object
Urine - Red blood cells                                   float64
Urine - Hyaline cylinders                                  object
Urine - Granular cylinders                                 object
Urine - Yeasts                                             object
Urine - Color                                              object
Partial thromboplastin time (PTT)                         float64
Relationship (Patient/Normal)                             float64
International normalized ratio (INR)                      float64
Lactic Dehydrogenase                                      float64
Prothrombin time (PT), Activity                           float64
Vitamin B12                                               float64
Creatine phosphokinase (CPK)                              float64
Ferritin                                                  float64
Arterial Lactic Acid                                      float64
Lipase dosage                                             float64
D-Dimer                                                   float64
Albumin                                                   float64
Hb saturation (arterial blood gases)                      float64
pCO2 (arterial blood gas analysis)                        float64
Base excess (arterial blood gas analysis)                 float64
pH (arterial blood gas analysis)                          float64
Total CO2 (arterial blood gas analysis)                   float64
HCO3 (arterial blood gas analysis)                        float64
pO2 (arterial blood gas analysis)                         float64
Arteiral Fio2                                             float64
Phosphor                                                  float64
ctO2 (arterial blood gas analysis)                        float64
Length: 111, dtype: object
```

In [154]:
```
# understand data
df.describe(include="all").T
```

Out[154]:

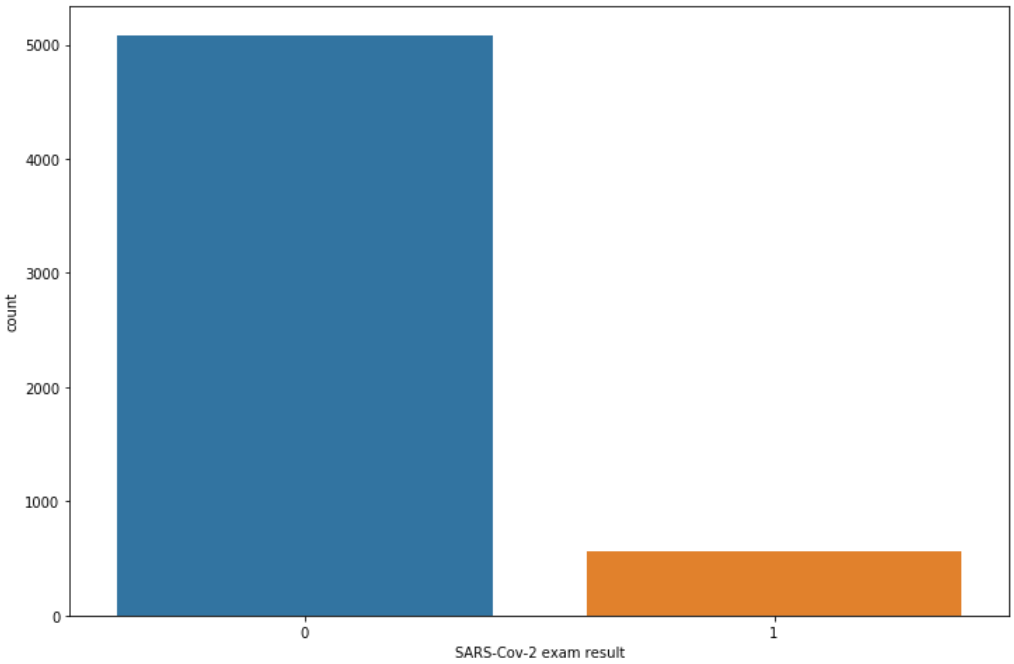
	count	unique	top	freq	mean	std	min	25%	50%	75%	max
Patient ID	5644	5644	fa1f502c1dc9cc7	1	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Patient age quantile	5644	NaN	NaN	NaN	9.31839	5.7779	0	4	9	14	19
SARS-Cov-2 exam result	5644	2	negative	5086	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Patient addmited to regular ward (1=yes, 0=no)	5644	NaN	NaN	NaN	0.0139972	0.117489	0	0	0	0	1
Patient addmited to semi-intensive unit (1=yes, 0=no)	5644	NaN	NaN	NaN	0.00885897	0.0937125	0	0	0	0	1
Patient addmited to intensive care unit (1=yes, 0=no)	5644	NaN	NaN	NaN	0.00726435	0.0849286	0	0	0	0	1
Hematocrit	603	NaN	NaN	NaN	-2.18621e-09	1.00083	-4.50142	-0.518807	0.053407	0.717175	2.6627
Hemoglobin	603	NaN	NaN	NaN	-1.60132e-08	1.00083	-4.3456	-0.586244	0.040316	0.729532	2.67187
Platelets	602	NaN	NaN	NaN	-3.535e-10	1.00083	-2.55243	-0.605346	-0.121716	0.531498	9.53203
Mean platelet volume	599	NaN	NaN	NaN	7.43814e-09	1.00084	-2.45757	-0.662483	-0.101517	0.683835	3.71305
Red blood Cells	602	NaN	NaN	NaN	8.42445e-09	1.00083	-3.97061	-0.56795	0.0138521	0.666176	3.64571
Lymphocytes	602	NaN	NaN	NaN	-7.86674e-09	1.00083	-1.86507	-0.730707	-0.014267	0.597692	3.7641
Mean corpuscular hemoglobin concentration (MCHC)	602	NaN	NaN	NaN	1.01486e-09	1.00083	-5.43181	-0.552476	-0.0545852	0.642463	3.33107
Leukocytes	602	NaN	NaN	NaN	6.21583e-09	1.00083	-2.0203	-0.637255	-0.212879	0.454295	4.52204
Basophils	602	NaN	NaN	NaN	-6.63374e-09	1.00083	-1.14014	-0.529226	-0.223767	0.387152	11.0782
Mean corpuscular hemoglobin (MCH)	602	NaN	NaN	NaN	-3.45301e-09	1.00083	-5.9376	-0.501356	0.125903	0.596348	4.09855
Eosinophils	602	NaN	NaN	NaN	7.20615e-09	1.00083	-0.835508	-0.66695	-0.329835	0.344395	8.35088
Mean corpuscular volume (MCV)	602	NaN	NaN	NaN	-4.15537e-09	1.00083	-5.10158	-0.514813	0.0660446	0.626871	3.41098
Monocytes	601	NaN	NaN	NaN	-3.22011e-09	1.00083	-2.16372	-0.614192	-0.115191	0.488863	4.5334
Red blood cell distribution width (RDW)	602	NaN	NaN	NaN	1.02043e-08	1.00083	-1.59809	-0.625073	-0.18279	0.347948	6.98218
Serum Glucose	208	NaN	NaN	NaN	7.06999e-09	1.00241	-1.10975	-0.504062	-0.29207	0.139483	7.00649
Respiratory Syncytial Virus	1354	2	not_detected	1302	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Influenza A	1354	2	not_detected	1336	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Influenza B	1354	2	not_detected	1277	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Parainfluenza 1	1352	2	not_detected	1349	NaN	NaN	NaN	NaN	NaN	NaN	NaN
CoronavirusNL63	1352	2	not_detected	1307	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Rhinovirus/Enterovirus	1352	2	not_detected	973	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Mycoplasma pneumoniae	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Coronavirus HKU1	1352	2	not_detected	1332	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Parainfluenza 3	1352	2	not_detected	1342	NaN	NaN	NaN	NaN	NaN	NaN	NaN
...	...	...	...	...	...	...	...	...	...	...	...
Urine - Sugar	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Urine - Leukocytes	70	31	3000	9	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Urine - Crystals	70	5	Ausentes	65	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Urine - Red blood cells	70	NaN	NaN	NaN	7.55702e-09	1.00722	-0.202297	-0.202297	-0.193921	-0.166071	7.82199
Urine - Hyaline cylinders	67	1	absent	67	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Urine - Granular cylinders	69	1	absent	69	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Urine - Yeasts	70	1	absent	70	NaN	NaN	NaN	NaN	NaN	NaN	NaN

	count	unique	top	freq	mean	std	min	25%	50%	75%	max
Urine - Color	70	4	yellow	55	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Partial thromboplastin time (PTT)	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Relationship (Patient/Normal)	91	NaN	NaN	NaN	-9.82494e-10	1.00554	-2.35135	-0.496616	-0.0894807	0.453368	4.70568
International normalized ratio (INR)	133	NaN	NaN	NaN	-4.73364e-09	1.00378	-1.79715	-0.665422	-0.156144	0.296546	7.36984
Lactic Dehydrogenase	101	NaN	NaN	NaN	1.73355e-09	1.00499	-1.35858	-0.699774	-0.33084	0.472908	2.95003
Prothrombin time (PT), Activity	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Vitamin B12	3	NaN	NaN	NaN	-1.98682e-08	1.22474	-1.40061	-0.434897	0.530811	0.700303	0.869795
Creatine phosphokinase (CPK)	104	NaN	NaN	NaN	-6.48344e-09	1.00484	-0.515714	-0.376967	-0.22475	0.0352306	7.21636
Ferritin	23	NaN	NaN	NaN	7.28861e-09	1.02247	-0.627529	-0.559897	-0.358466	0.119507	3.84575
Arterial Lactic Acid	27	NaN	NaN	NaN	-1.65568e-09	1.01905	-1.09107	-0.694761	-0.298454	0.229956	3.00411
Lipase dosage	8	NaN	NaN	NaN	-3.72529e-09	1.06904	-1.19223	-0.547022	-0.350655	0.182341	1.72522
D-Dimer	0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
Albumin	13	NaN	NaN	NaN	-5.73122e-09	1.04083	-2.29016	-0.53886	-0.03849	0.46188	1.96299
Hb saturation (arterial blood gases)	27	NaN	NaN	NaN	-1.37974e-10	1.01905	-1.99956	-1.12257	0.267769	0.73835	1.33726
pCO2 (arterial blood gas analysis)	27	NaN	NaN	NaN	8.4164e-09	1.01905	-1.24482	-0.53481	-0.21208	0.0230521	3.23652
Base excess (arterial blood gas analysis)	27	NaN	NaN	NaN	-1.65568e-09	1.01905	-3.08267	-0.330867	-0.0118167	0.666165	1.70308
pH (arterial blood gas analysis)	27	NaN	NaN	NaN	4.13921e-10	1.01905	-3.56888	-0.0921058	0.294202	0.5115	1.04267
Total CO2 (arterial blood gas analysis)	27	NaN	NaN	NaN	-7.47214e-09	1.01905	-2.92562	-0.511772	0.0774348	0.438561	1.94009
HCO3 (arterial blood gas analysis)	27	NaN	NaN	NaN	6.07084e-09	1.01905	-2.98559	-0.539721	0.0563319	0.50851	2.02947
pO2 (arterial blood gas analysis)	27	NaN	NaN	NaN	-2.46973e-08	1.01905	-1.17591	-0.81699	-0.159955	0.450009	2.20537
Arteiral Fio2	20	NaN	NaN	NaN	4.65661e-09	1.02598	-1.53293	-0.121498	-0.0117437	-0.0117437	2.84186
Phosphor	20	NaN	NaN	NaN	6.33299e-09	1.02598	-1.48053	-0.55273	-0.138182	0.276365	2.86235
ctO2 (arterial blood gas analysis)	27	NaN	NaN	NaN	5.243e-09	1.01905	-2.90025	-0.485279	0.182693	0.593753	1.82693

111 rows × 11 columns

In [155]:
```
plt.figure(figsize=(12,8))
df['SARS-Cov-2 exam result'] = df['SARS-Cov-2 exam result'].replace(['negative','positive'], [0,1])
sns.countplot(df['SARS-Cov-2 exam result'])
```

Out[155]: <matplotlib.axes._subplots.AxesSubplot at 0x1a1e562550>



In [156]:
```
print(f"Num positive cases: {len(df[df['SARS-Cov-2 exam result'] == 1])}")
print(f"Num negative cases: {len(df[df['SARS-Cov-2 exam result'] == 0])}")
```

```
Num positive cases: 558
Num negative cases: 5086
```

In [157]:
```
print("There are {}% target values with 1".format(100 * df['SARS-Cov-2 exam result'].value_counts()[1]/df.shape[0]))
```

```
There are 9.886605244507441% target values with 1
```

The data is unbalanced (approximatly 90%-10% negative-positive), which will bias any statistical model.

Let's look at the number and percentage of missing values in each column

In [158]:
```
def missing_data(data):
    total = data.isnull().sum()
    percent = (data.isnull().sum()/data.isnull().count()*100)
    tt = pd.concat([total, percent], axis=1, keys=['Total', 'Percent'])
    types = []
    for col in data.columns:
        dtype = str(data[col].dtype)
        types.append(dtype)
    tt['Types'] = types
    return(np.transpose(tt))
```

In [159]:
```
missing_data(df)
```

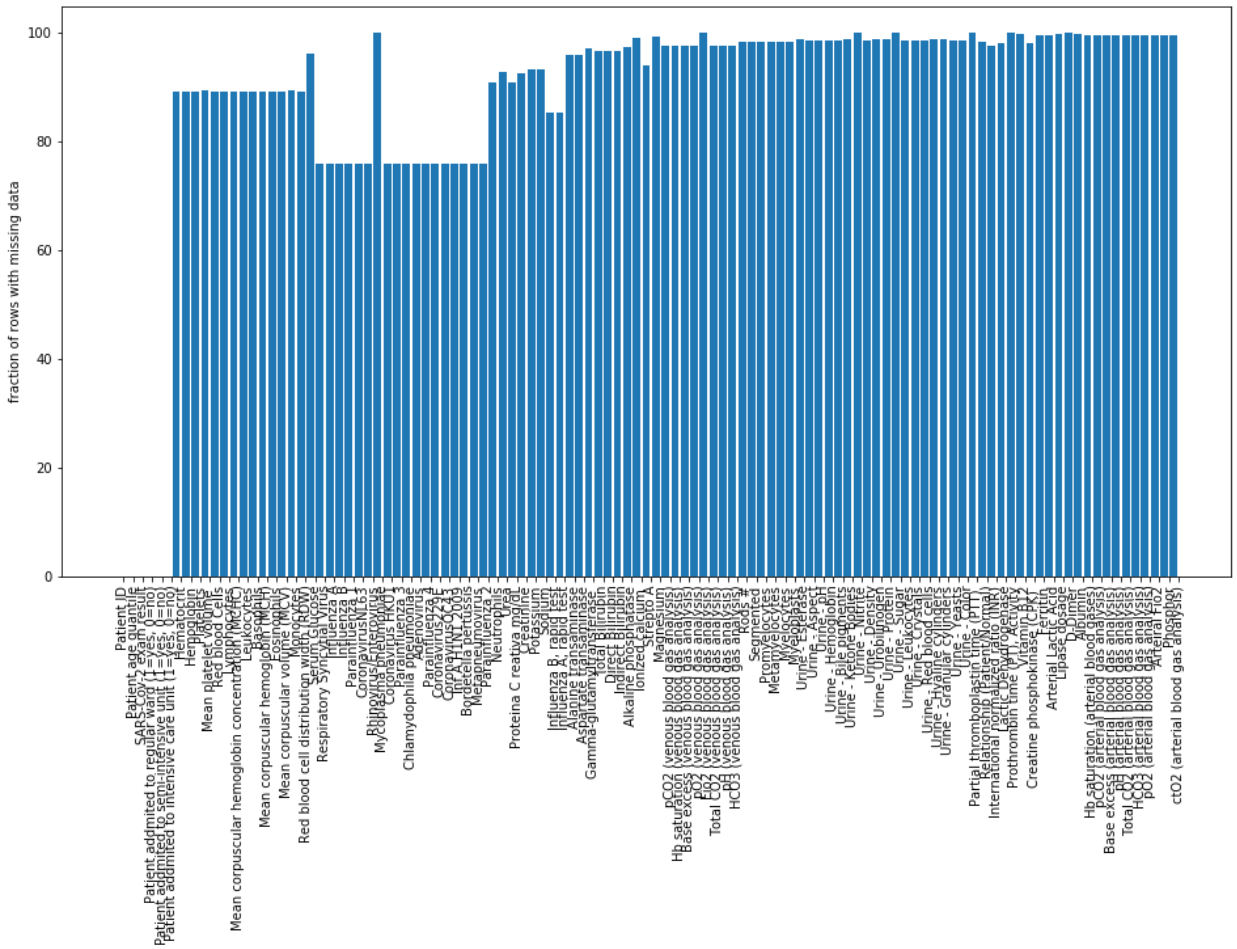
Out[159]:

	Patient ID	Patient age quantile	SARS-Cov-2 exam result	Patient addmited to regular ward (1=yes, 0=no)	Patient addmited to semi-intensive unit (1=yes, 0=no)	Patient addmited to intensive care unit (1=yes, 0=no)	Hematocrit	Hemoglobin	Platelets	Mean platelet volume	...	Hb saturation (arterial blood gases)	pCO2 (arterial blood gas analysis)	Bas exces (arteri bloo ga analysi
Total	0	0	0	0	0	0	5041	5041	5042	5045	...	5617	5617	561
Percent	0	0	0	0	0	0	89.3161	89.3161	89.3338	89.387	...	99.5216	99.5216	99.521
Types	object	int64	int64	int64	int64	int64	float64	float64	float64	float64	...	float64	float64	float6

3 rows × 111 columns

Plotting the percentage of missing data variable wise

In [160]:
```
null_perc = df.isnull().sum()*100/len(df)
plt.figure(figsize=(16,8))
plt.xticks(np.arange(len(null_perc))+0.5,null_perc.index,rotation='vertical')
plt.ylabel('fraction of rows with missing data')
plt.bar(np.arange(len(null_perc)),null_perc)
plt.show()
```



Based on this plot, It's clear that this dataset has a lot of missing values. Only 6 columns have no null values. There are features with 100% NULL.

In [118]:
```
df1=df.copy()
df1['count'] = 1
```

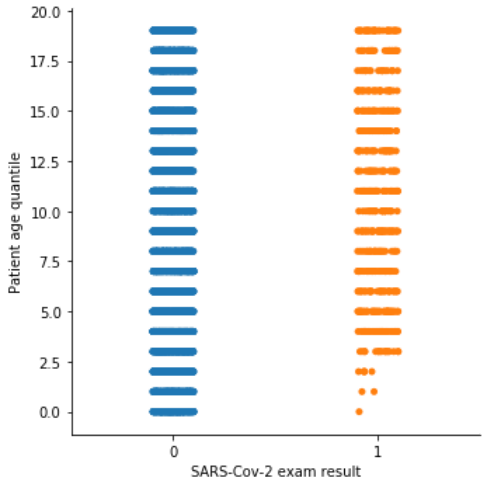
In [122]:
```
df1.groupby("Patient addmited to intensive care unit (1=yes, 0=no)").agg({'count': 'sum'})
```

Out[122]:

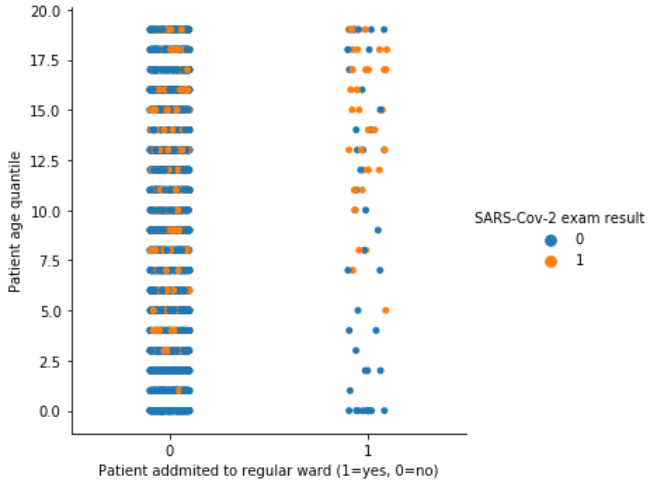
Patient addmited to intensive care unit (1=yes, 0=no)	count
0	5603
1	41

The number of possible positive tested patients is equally distributed across age quantiles, except for the first two quantiles.

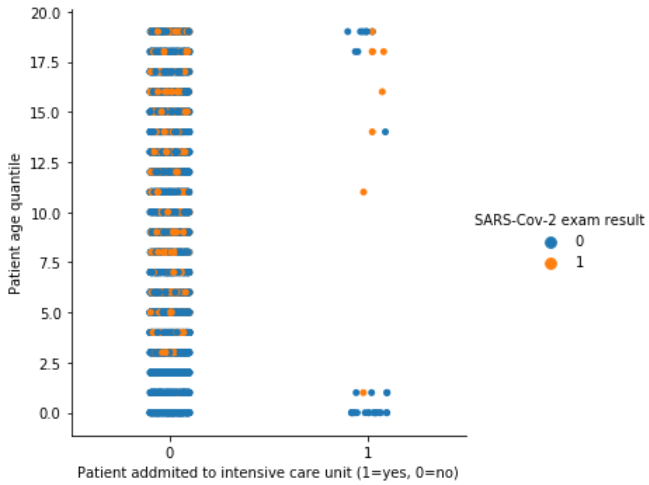
In [123]:
```
sns.catplot(x='SARS-Cov-2 exam result', y="Patient age quantile", data=df1);
```



In [124]:
```
sns.catplot(x='Patient addmited to regular ward (1=yes, 0=no)', y="Patient age quantile", hue="SARS-Cov-2
 exam result", data=df1);
```



In [125]:
```
sns.catplot(x='Patient addmited to intensive care unit (1=yes, 0=no)', y="Patient age quantile", hue="SARS
-Cov-2 exam result", data=df1);
```



Most of the patients were not admitted to the regular ward, which is expected. On the other hand, most of the patients that were admitted to the regular ward are older and most them tested positive.

Checking Correlation between variables

In [161]:
```
plt.figure(figsize=(25, 15))
matrix = np.triu(df.corr())
sns.heatmap(df.corr(), mask=matrix)
```

Out[161]: <matplotlib.axes._subplots.AxesSubplot at 0x1a22c0c470>

We see that although there are many variables, most of them are not very highly correlated while few of them don't have any correlation.

First try...

We will check the columns that have full datas and are not null to build a model.

In [162]:
```
data_null=df.isna().sum()
(data_null/df.shape[0]*100).round(2)
#collect columns with good data
good_columns = data_null[data_null==0].reset_index()
good_columns
```

Out[162]:

	index	0
0	Patient ID	0
1	Patient age quantile	0
2	SARS-Cov-2 exam result	0
3	Patient addmited to regular ward (1=yes, 0=no)	0
4	Patient addmited to semi-intensive unit (1=yes...	0
5	Patient addmited to intensive care unit (1=yes...	0

In [163]:
```
#create a new dataframe with good columns
data1=df[good_columns['index']]
data1.head()
```

Out[163]:

	Patient ID	Patient age quantile	SARS-Cov-2 exam result	Patient addmited to regular ward (1=yes, 0=no)	Patient addmited to semi-intensive unit (1=yes, 0=no)	Patient addmited to intensive care unit (1=yes, 0=no)
0	44477f75e8169d2	13	0	0	0	0
1	126e9dd13932f68	17	0	0	0	0
2	a46b4402a0e5696	8	0	0	0	0
3	f7d619a94f97c45	5	0	0	0	0
4	d9e41465789c2b5	15	0	0	0	0

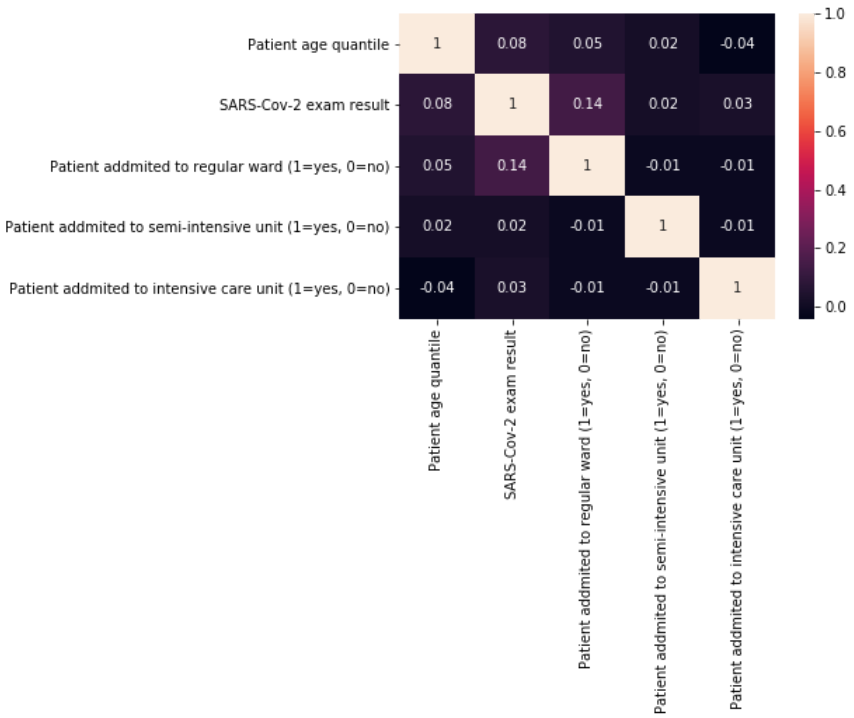
Checing correlation amoong these variables

In [164]:
```
#check correlation
data1.corr()
```

Out[164]:

	Patient age quantile	SARS-Cov-2 exam result	Patient addmited to regular ward (1=yes, 0=no)	Patient addmited to semi-intensive unit (1=yes, 0=no)	Patient addmited to intensive care unit (1=yes, 0=no)
Patient age quantile	1.000000	0.075244	0.046166	0.015736	-0.035772
SARS-Cov-2 exam result	0.075244	1.000000	0.142437	0.019364	0.027586
Patient addmited to regular ward (1=yes, 0=no)	0.046166	0.142437	1.000000	-0.011264	-0.010192
Patient addmited to semi-intensive unit (1=yes, 0=no)	0.015736	0.019364	-0.011264	1.000000	-0.008087
Patient addmited to intensive care unit (1=yes, 0=no)	-0.035772	0.027586	-0.010192	-0.008087	1.000000

In [165]:
```
# check correlation with graphics...
ax = sns.heatmap(data1.corr().round(2), annot=True)
plt.show()
```



It is evident that these variables don't have any positive or negative correlation among themselves. Let's try to build our model using only these features.

Logistic Regression

In [166]:
```
# dropping the non numeical column as it will not be used in the modelling process.
data1 = data1.drop([
    "Patient ID",], axis=1)
```

In [167]:
```
# get the target variable
target = data1['SARS-Cov-2 exam result']
```

In [168]:
```
# all the other columns for training the model
expl = data1.drop(columns='SARS-Cov-2 exam result')
```

In [40]:
```
feature_cols = ['Patient age quantile','Patient addmited to regular ward (1=yes, 0=no)','Patient addmited
 to semi-intensive unit (1=yes, 0=no)','Patient addmited to intensive care unit (1=yes, 0=no)']
```

In [50]:
```
#split into training and testing
X_treino, X_teste, Y_treino, Y_teste = train_test_split(expl, target, test_size=0.3, random_state=30)
```

In [51]:
```
#fit model
model_lr = LogisticRegression()
model_lr.fit(X_treino, Y_treino)
```

```
/anaconda3/lib/python3.7/site-packages/sklearn/linear_model/logistic.py:432: FutureWarning: Default solve
r will be changed to 'lbfgs' in 0.22. Specify a solver to silence this warning.
  FutureWarning)
```

Out[51]:
```
LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=True,
                   intercept_scaling=1, l1_ratio=None, max_iter=100,
                   multi_class='warn', n_jobs=None, penalty='l2',
                   random_state=None, solver='warn', tol=0.0001, verbose=0,
                   warm_start=False)
```

Validating the model

In [52]:
```
#check score training data
print(round(model_lr.score(X_treino, Y_treino)*100,2), '%')
```

```
90.25 %
```

In [53]:
```
#check score test data
print(round(model_lr.score(X_teste, Y_teste)*100,2),'%')
```

```
89.79 %
```

In [54]:
```
#check confusion matrix

confusion_matrix(Y_teste, model_lr.predict(X_teste))
```

Out[54]:
```
array([[1521,    0],
       [ 173,    0]])
```

In [170]:
```
Y_pred_lr=model_lr.predict(X_teste)
print("Classification Report")
print(metrics.classification_report(Y_test, Y_pred_lr,digits=4))
```

```
Classification Report
              precision    recall  f1-score   support

           0     0.8979    1.0000    0.9462      1521
           1     0.0000    0.0000    0.0000       173

    accuracy                         0.8979      1694
   macro avg     0.4489    0.5000    0.4731      1694
weighted avg     0.8062    0.8979    0.8496      1694


/anaconda3/lib/python3.7/site-packages/sklearn/metrics/classification.py:1437: UndefinedMetricWarning: Pr
ecision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples.
  'precision', 'predicted', average, warn_for)
/anaconda3/lib/python3.7/site-packages/sklearn/metrics/classification.py:1437: UndefinedMetricWarning: Pr
ecision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples.
  'precision', 'predicted', average, warn_for)
/anaconda3/lib/python3.7/site-packages/sklearn/metrics/classification.py:1437: UndefinedMetricWarning: Pr
ecision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples.
  'precision', 'predicted', average, warn_for)
```

Decision Trees

In [56]:
```
model_tree = tree.DecisionTreeClassifier()
model_tree.fit(X_treino, Y_treino)
```

Out[56]:
```
DecisionTreeClassifier(class_weight=None, criterion='gini', max_depth=None,
                       max_features=None, max_leaf_nodes=None,
                       min_impurity_decrease=0.0, min_impurity_split=None,
                       min_samples_leaf=1, min_samples_split=2,
                       min_weight_fraction_leaf=0.0, presort=False,
                       random_state=None, splitter='best')
```

Model validation

In [174]:
```
#check score training data
print(round(model_tree.score(X_treino, Y_treino)*100,2), '%')
```

```
90.63 %
```

In [175]:
```
#check score test data
print(round(model_tree.score(X_teste, Y_teste)*100,2),'%')
```

```
89.79 %
```

In [176]:
```
#check confusion matrix

confusion_matrix(Y_teste, model_tree.predict(X_teste))
```

Out[176]:
```
array([[1515,    6],
       [ 167,    6]])
```

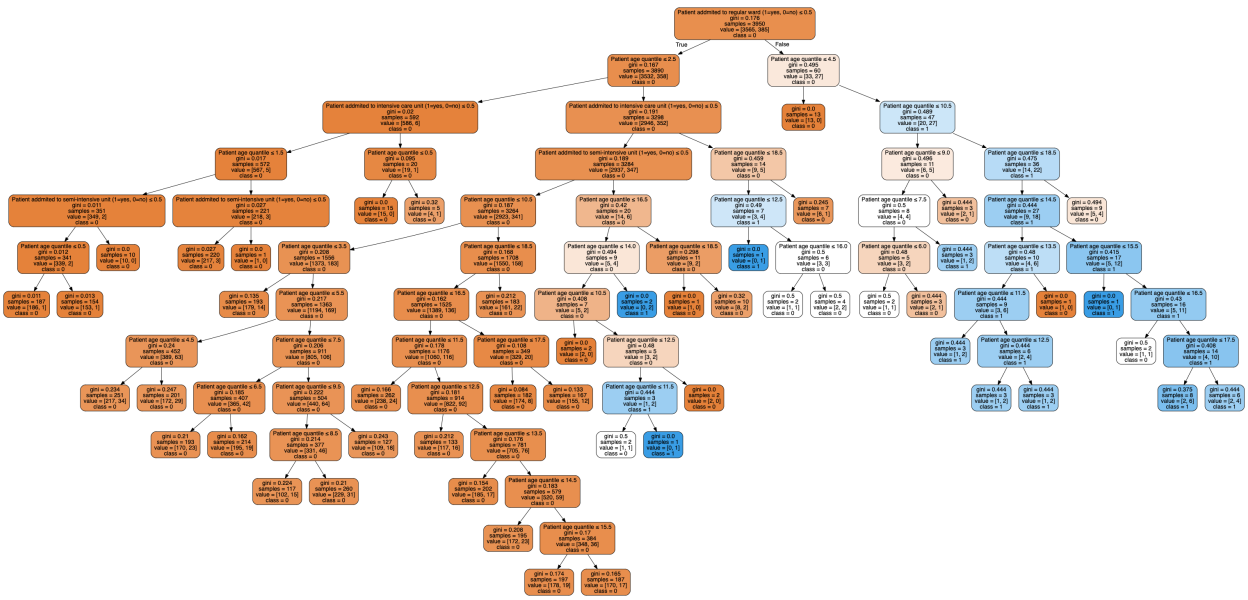
In [177]:
```
Y_pred_tree=model_tree.predict(X_teste)
print("Classification Report")
print(metrics.classification_report(Y_test, Y_pred_tree,digits=4))
```

```
Classification Report
              precision    recall  f1-score   support

           0     0.9007    0.9961    0.9460      1521
           1     0.5000    0.0347    0.0649       173

    accuracy                         0.8979      1694
   macro avg     0.7004    0.5154    0.5054      1694
weighted avg     0.8598    0.8979    0.8560      1694
```

Plotting the decision tree

In [61]:
```
dot_data = StringIO()
export_graphviz(model_tree, out_file=dot_data,
                filled=True, rounded=True,
                special_characters=True,feature_names = feature_cols,class_names=['0','1'])
graph = pydotplus.graph_from_dot_data(dot_data.getvalue())
graph.write_png('diabetes.png')
Image(graph.create_png())
```

Out[61]:



Random Forest

In [179]:
```
# Instantiate model with 1000 decision trees
rf = RandomForestRegressor(n_estimators = 1000, random_state = 42)
# Train the model on training data
rf.fit(X_treino, Y_treino);
```

In [180]:
```
# Use the forest's predict method on the test data
predictions = rf.predict(X_teste)
# Calculate the absolute errors
errors = abs(predictions - Y_teste)
# Print out the mean absolute error (mae)
print('Mean Absolute Error:', round(np.mean(errors), 2), 'degrees.')
```

```
Mean Absolute Error: 0.17 degrees.
```

Validating the model

In [182]:
```
y_pred = rf.predict(X_teste)
```

In [183]:
```
print('Mean Absolute Error:', metrics.mean_absolute_error(Y_teste, y_pred))
print('Mean Squared Error:', metrics.mean_squared_error(Y_teste, y_pred))
print('Root Mean Squared Error:', np.sqrt(metrics.mean_squared_error(Y_teste, y_pred)))
```

```
Mean Absolute Error: 0.16876975928622384
Mean Squared Error: 0.0879112903475432
Root Mean Squared Error: 0.29649838169464465
```

In [240]:
```
print("Accuracy:",metrics.accuracy_score(Y_teste, y_pred.round()))
```

```
Accuracy: 0.898465171192444
```

In [248]:
```
#check confusion matrix

confusion_matrix(Y_teste, y_pred.round())
```

Out[248]:
```
array([[1515,    6],
       [ 166,    7]])
```

In [249]:
```
print("Classification Report")
print(metrics.classification_report(Y_test, y_pred.round(),digits=4))
```

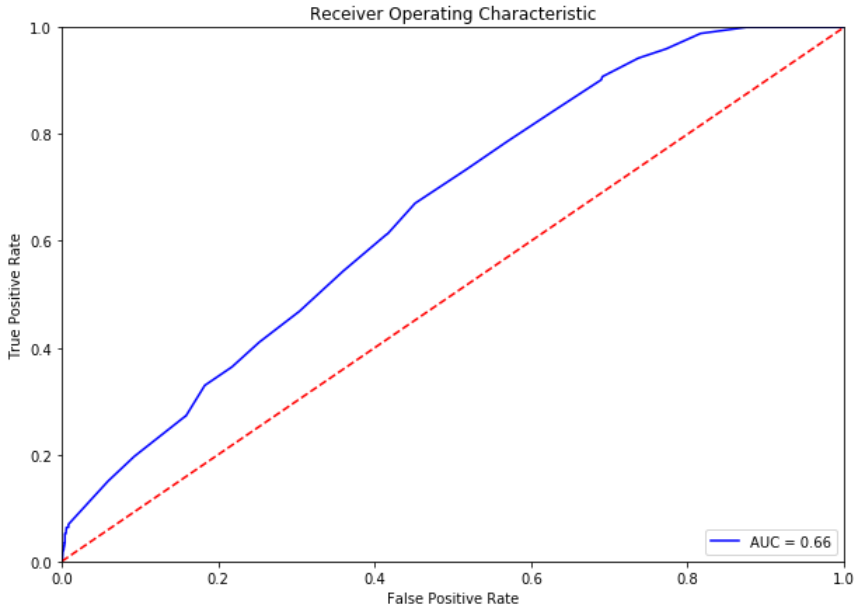
```
Classification Report
              precision    recall  f1-score   support

           0     0.9012    0.9961    0.9463      1521
           1     0.5385    0.0405    0.0753       173

    accuracy                         0.8985      1694
   macro avg     0.7199    0.5183    0.5108      1694
weighted avg     0.8642    0.8985    0.8573      1694
```

Random Forest performs the best in the first scenario, by a small margin. Whereas Logistic regression and Decision trees have the same performance accuracy.

Plotting the ROC curve and checking AUC

In [184]:
```
def plot_roc_curve(y_true, y_pred):
    fpr, tpr, threshold = roc_curve(y_true, y_pred)
    roc_auc = auc(fpr, tpr)
    fig, ax = plt.subplots(figsize=(10,7))
    ax.set_title('Receiver Operating Characteristic')
    ax.plot(fpr, tpr, 'b', label = 'AUC = %0.2f' % roc_auc)
    ax.legend(loc = 'lower right')
    ax.plot([0, 1], [0, 1],'r--')
    ax.set_xlim([0, 1])
    ax.set_ylim([0, 1])
    ax.set_ylabel('True Positive Rate')
    ax.set_xlabel('False Positive Rate')
    return ax


plot_roc_curve(Y_teste, y_pred)
```

Out[184]: <matplotlib.axes._subplots.AxesSubplot at 0x1a19bcf470>



In [185]:
```
roc_auc_score(Y_teste, y_pred)
```

Out[185]: 0.6570308551188943

Second try...

We will check the data of all columns and do some steps:

1) fix it if necessary.

2) remove some columns with there are not relevance.

3) create dummy variable

In [186]:
```
#create a list of columns with datatype == 'object'
x1=[]
for c in df.columns:
    x=df[c].dtype
    if x == 'object' and c != 'Patient ID':
        x1.append(c)
print(x1)
```

```
['Respiratory Syncytial Virus', 'Influenza A', 'Influenza B', 'Parainfluenza 1', 'CoronavirusNL63', 'Rhin
ovirus/Enterovirus', 'Coronavirus HKU1', 'Parainfluenza 3', 'Chlamydophila pneumoniae', 'Adenovirus', 'Pa
rainfluenza 4', 'Coronavirus229E', 'CoronavirusOC43', 'Inf A H1N1 2009', 'Bordetella pertussis', 'Metapne
umovirus', 'Parainfluenza 2', 'Influenza B, rapid test', 'Influenza A, rapid test', 'Strepto A', 'Urine -
Esterase', 'Urine - Aspect', 'Urine - pH', 'Urine - Hemoglobin', 'Urine - Bile pigments', 'Urine - Ketone
Bodies', 'Urine - Nitrite', 'Urine - Urobilinogen', 'Urine - Protein', 'Urine - Leukocytes', 'Urine - Cry
stals', 'Urine - Hyaline cylinders', 'Urine - Granular cylinders', 'Urine - Yeasts', 'Urine - Color']
```

In [187]:
```
#check unique values on list
for a in x1:
    print('analyzing column: ', a)
    print(df[a].unique())
    print()
```

```
analyzing column:  Respiratory Syncytial Virus
[nan 'not_detected' 'detected']

analyzing column:  Influenza A
[nan 'not_detected' 'detected']

analyzing column:  Influenza B
[nan 'not_detected' 'detected']

analyzing column:  Parainfluenza 1
[nan 'not_detected' 'detected']

analyzing column:  CoronavirusNL63
[nan 'not_detected' 'detected']

analyzing column:  Rhinovirus/Enterovirus
[nan 'detected' 'not_detected']

analyzing column:  Coronavirus HKU1
[nan 'not_detected' 'detected']

analyzing column:  Parainfluenza 3
[nan 'not_detected' 'detected']

analyzing column:  Chlamydophila pneumoniae
[nan 'not_detected' 'detected']

analyzing column:  Adenovirus
[nan 'not_detected' 'detected']

analyzing column:  Parainfluenza 4
[nan 'not_detected' 'detected']

analyzing column:  Coronavirus229E
[nan 'not_detected' 'detected']

analyzing column:  CoronavirusOC43
[nan 'not_detected' 'detected']

analyzing column:  Inf A H1N1 2009
[nan 'not_detected' 'detected']

analyzing column:  Bordetella pertussis
[nan 'not_detected' 'detected']

analyzing column:  Metapneumovirus
[nan 'not_detected' 'detected']

analyzing column:  Parainfluenza 2
[nan 'not_detected']

analyzing column:  Influenza B, rapid test
[nan 'negative' 'positive']

analyzing column:  Influenza A, rapid test
[nan 'negative' 'positive']

analyzing column:  Strepto A
[nan 'positive' 'negative' 'not_done']

analyzing column:  Urine - Esterase
[nan 'absent' 'not_done']

analyzing column:  Urine - Aspect
[nan 'clear' 'cloudy' 'altered_coloring' 'lightly_cloudy']

analyzing column:  Urine - pH
[nan '6.5' '6.0' 'Não Realizado' '5.0' '7.0' '5' '5.5' '7.5' '6' '8.0' 6
 6.5 7 5 5.5]

analyzing column:  Urine - Hemoglobin
[nan 'absent' 'present' 'not_done']

analyzing column:  Urine - Bile pigments
[nan 'absent' 'not_done']

analyzing column:  Urine - Ketone Bodies
[nan 'absent' 'not_done']

analyzing column:  Urine - Nitrite
[nan 'not_done']

analyzing column:  Urine - Urobilinogen
[nan 'normal' 'not_done']

analyzing column:  Urine - Protein
[nan 'absent' 'not_done']
```

```
analyzing column:  Urine - Leukocytes
[nan '38000' '5942000' '32000' '22000' '<1000' '3000' '16000' '7000'
 '5300' '1000' '4000' '5000' '10600' '6000' '2500' '2600' '23000' '124000'
 '8000' '29000' '2000' '624000' '40000' '3310000' '229000' '19000' '28000'
 '10000' '4600' '77000' '43000']

analyzing column:  Urine - Crystals
[nan 'Ausentes' 'Urato Amorfo --+' 'Oxalato de Cálcio +++'
 'Oxalato de Cálcio -++' 'Urato Amorfo +++']

analyzing column:  Urine - Hyaline cylinders
[nan 'absent']

analyzing column:  Urine - Granular cylinders
[nan 'absent']

analyzing column:  Urine - Yeasts
[nan 'absent']

analyzing column:  Urine - Color
[nan 'light_yellow' 'yellow' 'orange' 'citrus_yellow']
```

In [188]:
```
#replace some datas
df=df.replace(['positive','negative','not_detected','detected','not_done','absent','Não Realizado','presen
t','normal'],
                    [1,0,0,1,np.nan,0,np.nan,1,0])
df['Urine - Leukocytes'].replace('<1000', '999', inplace=True)
df['Urine - pH'] = df['Urine - pH'].astype("float64")
df['Urine - Leukocytes'] = df['Urine - Leukocytes'].astype("float64")
df['Urine - Urobilinogen'] = df['Urine - Urobilinogen'].astype("float64")
```

In [189]:
```
#replace nan by 0
df = df.fillna(0)
```

In [190]:
```
# Making dummies variable from categorical

#create dataframe with dummies
data_dummies=pd.get_dummies(df[df.dtypes[(df.dtypes == "object")].drop("Patient ID").index])
data_dummies.head()
```

Out[190]:

	Urine - Aspect_0	Urine - Aspect_altered_coloring	Urine - Aspect_clear	Urine - Aspect_cloudy	Urine - Aspect_lightly_cloudy	Urine - Crystals_0	Urine - Crystals_Ausentes	Urine - Crystals_Oxalato de Cálcio +++	Cryst de
0	1	0	0	0	0	1	0	0	
1	1	0	0	0	0	1	0	0	
2	1	0	0	0	0	1	0	0	
3	1	0	0	0	0	1	0	0	
4	1	0	0	0	0	1	0	0	

In [191]:
```
#create dataframe without dtypes object
data2=pd.concat([df["Patient ID"], df[df.dtypes[(df.dtypes != "object")].index]], axis=1)
```

In [192]:
```
#concate dummies with not-dummies and target
df=pd.concat([data_dummies,data2], axis=1)
```

In [193]:
```
#check if have columns empty
df.describe(include="all").T.round().sort_values('max', ascending=True)
```

Out[193]:

	count	unique	top	freq	mean	std	min	25%	50%	75%	max
Urine - Ketone Bodies	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Fio2 (venous blood gas analysis)	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Myeloblasts	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Urine - Esterase	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Urine - Bile pigments	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Urine - Nitrite	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Urine - Urobilinogen	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Mycoplasma pneumoniae	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Urine - Protein	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Urine - Hyaline cylinders	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Urine - Granular cylinders	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Urine - Yeasts	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Partial thromboplastin time (PTT)	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Prothrombin time (PT), Activity	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
D-Dimer	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Urine - Sugar	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Parainfluenza 2	5644	NaN	NaN	NaN	0	0	0	0	0	0	0
Vitamin B12	5644	NaN	NaN	NaN	-1.05607e-11	0.0230571	-1.40061	0	0	0	0.869795
Parainfluenza 3	5644	NaN	NaN	NaN	0.00177179	0.0420591	0	0	0	0	1
Coronavirus HKU1	5644	NaN	NaN	NaN	0.00354359	0.0594277	0	0	0	0	1
Urine - Aspect_0	5644	NaN	NaN	NaN	0.987597	0.110684	0	1	1	1	1
CoronavirusNL63	5644	NaN	NaN	NaN	0.00797307	0.0889432	0	0	0	0	1
Parainfluenza 1	5644	NaN	NaN	NaN	0.000531538	0.023051	0	0	0	0	1
Chlamydophila pneumoniae	5644	NaN	NaN	NaN	0.00159461	0.0399043	0	0	0	0	1
Rhinovirus/Enterovirus	5644	NaN	NaN	NaN	0.067151	0.250305	0	0	0	0	1
Adenovirus	5644	NaN	NaN	NaN	0.00230333	0.047942	0	0	0	0	1
Strepto A	5644	NaN	NaN	NaN	0.0060241	0.0773878	0	0	0	0	1
Coronavirus229E	5644	NaN	NaN	NaN	0.00159461	0.0399043	0	0	0	0	1
CoronavirusOC43	5644	NaN	NaN	NaN	0.00141743	0.0376255	0	0	0	0	1
Inf A H1N1 2009	5644	NaN	NaN	NaN	0.0173636	0.130633	0	0	0	0	1
...	...	...	...	...	...	...	...	...	...	...	...
Sodium	5644	NaN	NaN	NaN	7.36609e-10	0.256062	-5.24695	0	0	0	4.09693
Mean corpuscular hemoglobin (MCH)	5644	NaN	NaN	NaN	-3.68305e-10	0.32662	-5.9376	0	0	0	4.09855
Leukocytes	5644	NaN	NaN	NaN	6.62993e-10	0.32662	-2.0203	0	0	0	4.52204
Monocytes	5644	NaN	NaN	NaN	-3.42893e-10	0.326349	-2.16372	0	0	0	4.5334
Relationship (Patient/Normal)	5644	NaN	NaN	NaN	-1.58411e-11	0.126989	-2.35135	0	0	0	4.70568
Total Bilirubin	5644	NaN	NaN	NaN	-8.9766e-11	0.179589	-1.09317	0	0	0	5.0286
Creatinine	5644	NaN	NaN	NaN	-5.01799e-10	0.274112	-2.39	0	0	0	5.05357
pCO2 (venous blood gas analysis)	5644	NaN	NaN	NaN	-4.66321e-10	0.155244	-2.70501	0	0	0	5.67952
Metamyelocytes	5644	NaN	NaN	NaN	1.4785e-10	0.131108	-0.315965	0	0	0	6.13638
Myelocytes	5644	NaN	NaN	NaN	2.37616e-10	0.131109	-0.233126	0	0	0	6.55085
Indirect Bilirubin	5644	NaN	NaN	NaN	9.76866e-11	0.179589	-0.771034	0	0	0	6.61466
Red blood cell distribution width (RDW)	5644	NaN	NaN	NaN	1.08841e-09	0.32662	-1.59809	0	0	0	6.98218
Direct Bilirubin	5644	NaN	NaN	NaN	3.88766e-10	0.179589	-1.16972	0	0	0	6.9959
Serum Glucose	5644	NaN	NaN	NaN	2.60553e-10	0.191989	-1.10975	0	0	0	7.00649
Creatine phosphokinase (CPK)	5644	NaN	NaN	NaN	-1.19468e-10	0.135757	-0.515714	0	0	0	7.21636
Aspartate transaminase	5644	NaN	NaN	NaN	-2.17815e-11	0.200124	-0.704122	0	0	0	7.23117
International normalized ratio (INR)	5644	NaN	NaN	NaN	-1.11547e-10	0.153522	-1.79715	0	0	0	7.36984
Urine - Red blood cells	5644	NaN	NaN	NaN	9.37263e-11	0.111377	-0.202297	0	0	0	7.82199
Alanine transaminase	5644	NaN	NaN	NaN	1.08412e-10	0.199681	-0.641951	0	0	0	7.93066
Urine - pH	5644	NaN	NaN	NaN	0.0727321	0.660712	0	0	0	0	8
Proteina C reativa mg/dL	5644	NaN	NaN	NaN	2.49208e-10	0.299447	-0.535362	0	0	0	8.02667
Eosinophils	5644	NaN	NaN	NaN	7.68622e-10	0.32662	-0.835508	0	0	0	8.35088

	count	unique	top	freq	mean	std	min	25%	50%	75%	max
Gamma-glutamyltransferase	5644	NaN	NaN	NaN	-4.00977e-11	0.164661	-0.476607	0	0	0	8.50795
Platelets	5644	NaN	NaN	NaN	-3.7705e-11	0.32662	-2.55243	0	0	0	9.53203
Promyelocytes	5644	NaN	NaN	NaN	1.26729e-10	0.131109	-0.102062	0	0	0	9.79796
Basophils	5644	NaN	NaN	NaN	-7.07568e-10	0.32662	-1.14014	0	0	0	11.0782
Urea	5644	NaN	NaN	NaN	-4.69539e-10	0.265241	-1.63041	0	0	0	11.2466
Patient age quantile	5644	NaN	NaN	NaN	9.31839	5.7779	0	4	9	14	19
Urine - Leukocytes	5644	NaN	NaN	NaN	1925.34	90989.2	0	0	0	0	5.942e+06
Patient ID	5644	5644	fa1f502c1dc9cc7	1	NaN	NaN	NaN	NaN	NaN	NaN	NaN

124 rows × 11 columns

In [194]:
```
#remove columns without data

#create a list of columns
list_empty=df[df.sum()[(df.sum() == 0)].index].columns
print(list_empty)
```

```
Index(['Mycoplasma pneumoniae', 'Parainfluenza 2',
       'Fio2 (venous blood gas analysis)', 'Myeloblasts', 'Urine - Esterase',
       'Urine - Bile pigments', 'Urine - Ketone Bodies', 'Urine - Nitrite',
       'Urine - Urobilinogen', 'Urine - Protein', 'Urine - Sugar',
       'Urine - Hyaline cylinders', 'Urine - Granular cylinders',
       'Urine - Yeasts', 'Partial thromboplastin time (PTT) ',
       'Prothrombin time (PT), Activity', 'D-Dimer'],
      dtype='object')
```

In [195]:
```
#create a dataframe without empty data
df=df.drop(list_empty,axis=1)
df.shape
```

Out[195]: (5644, 107)

In [196]:
```
df.head()
```

Out[196]:

	Urine - Aspect_0	Urine - Aspect_altered_coloring	Urine - Aspect_clear	Urine - Aspect_cloudy	Urine - Aspect_lightly_cloudy	Urine - Crystals_0	Urine - Crystals_Ausentes	Urine - Crystals_Oxalato de Cálcio +++	Cryst d
0	1	0	0	0	0	1	0	0	
1	1	0	0	0	0	1	0	0	
2	1	0	0	0	0	1	0	0	
3	1	0	0	0	0	1	0	0	
4	1	0	0	0	0	1	0	0	

5 rows × 107 columns

Logistic Regression

In [197]:
```
# remove some columns
data3 = df.drop([
    "Patient ID",
    'Patient addmited to regular ward (1=yes, 0=no)',
    'Patient addmited to semi-intensive unit (1=yes, 0=no)',
    'Patient addmited to intensive care unit (1=yes, 0=no)'
], axis=1)
```

In [198]:
```
data3.head()
```

Out[198]:

	Urine - Aspect_0	Urine - Aspect_altered_coloring	Urine - Aspect_clear	Urine - Aspect_cloudy	Urine - Aspect_lightly_cloudy	Urine - Crystals_0	Urine - Crystals_Ausentes	Urine - Crystals_Oxalato de Cálcio +++	Cryst d
0	1	0	0	0	0	1	0	0	
1	1	0	0	0	0	1	0	0	
2	1	0	0	0	0	1	0	0	
3	1	0	0	0	0	1	0	0	
4	1	0	0	0	0	1	0	0	

5 rows × 103 columns

In [199]:
```
# get target
target = df['SARS-Cov-2 exam result']
```

In [200]:
```
expl2 = data3.drop(columns='SARS-Cov-2 exam result')
```

In [201]:
```
#split into training and testing
X_train, X_test, Y_train, Y_test = train_test_split(expl2, target, test_size=0.3, random_state=30)
```

In [202]:
```
#fit model
model_lr2 = LogisticRegression()
model_lr2.fit(X_train, Y_train)
```

```
/anaconda3/lib/python3.7/site-packages/sklearn/linear_model/logistic.py:432: FutureWarning: Default solve
r will be changed to 'lbfgs' in 0.22. Specify a solver to silence this warning.
  FutureWarning)
```

Out[202]:
```
LogisticRegression(C=1.0, class_weight=None, dual=False, fit_intercept=True,
                   intercept_scaling=1, l1_ratio=None, max_iter=100,
                   multi_class='warn', n_jobs=None, penalty='l2',
                   random_state=None, solver='warn', tol=0.0001, verbose=0,
                   warm_start=False)
```

In [243]:
```
#check score training data
print(round(model_lr2.score(X_train, Y_train)*100,2), '%')
```

```
90.71 %
```

In [244]:
```
#check score test data
print(round(model_lr2.score(X_test, Y_test)*100,2),'%')
```

```
90.5 %
```

In [245]:
```
#check confusion matrix

confusion_matrix(Y_test, model_lr2.predict(X_test))
```

Out[245]:
```
array([[1521,    0],
       [ 161,   12]])
```

In [206]:
```
Y_pred_logistic = model_lr2.predict(X_test)
```

In [207]:
```
print("Classification Report")
print(metrics.classification_report(Y_test, Y_pred_logistic,digits=4))
```

```
Classification Report
              precision    recall  f1-score   support

           0     0.9043    1.0000    0.9497      1521
           1     1.0000    0.0694    0.1297       173

    accuracy                         0.9050      1694
   macro avg     0.9521    0.5347    0.5397      1694
weighted avg     0.9141    0.9050    0.8660      1694
```

The performance has increased by approximately 2% compared to the previous logistic model.

Decision Trees

In [209]:
```
model_tree2 = tree.DecisionTreeClassifier()
model_tree2.fit(X_train, Y_train)
Y_pred_tree = model_tree2.predict(X_test)
```

In [210]:
```
#check score training data
print(round(model_tree2.score(X_train, Y_train)*100,2), '%')
```

```
91.9 %
```

In [211]:
```
#check score test data
print(round(model_tree2.score(X_test, Y_test)*100,2),'%')
```

```
89.49 %
```

In [212]:
```
#check confusion matrix

confusion_matrix(Y_test, model_tree2.predict(X_test))
```

Out[212]:
```
array([[1505,   16],
       [ 162,   11]])
```

In [213]:
```
print("Classification Report")
print(metrics.classification_report(Y_test, Y_pred_tree,digits=4))
```

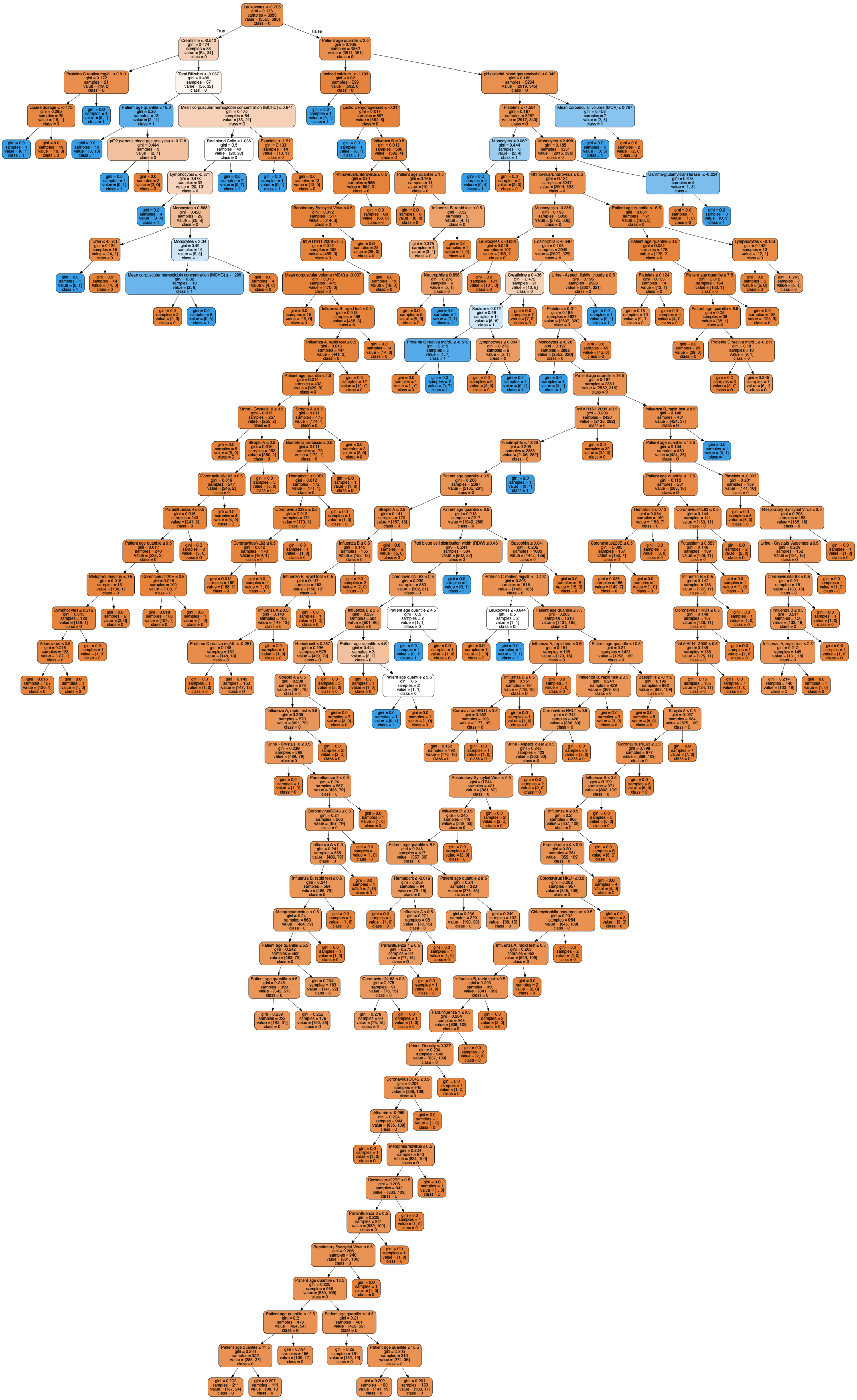
```
Classification Report
              precision    recall  f1-score   support

           0     0.9028    0.9895    0.9442      1521
           1     0.4074    0.0636    0.1100       173

    accuracy                         0.8949      1694
   macro avg     0.6551    0.5265    0.5271      1694
weighted avg     0.8522    0.8949    0.8590      1694
```

Decison trees performance has gone a little down and was not expected. Let's plot our tree and check.

In [214]:
```
feature_cols2 = list(expl2.columns.values)
```

In [215]:
```
dot_data = StringIO()
export_graphviz(model_tree2, out_file=dot_data,
                filled=True, rounded=True,
                special_characters=True,feature_names = feature_cols2,class_names=['0','1'])
graph = pydotplus.graph_from_dot_data(dot_data.getvalue())
graph.write_png('covid2.png')
Image(graph.create_png())
```

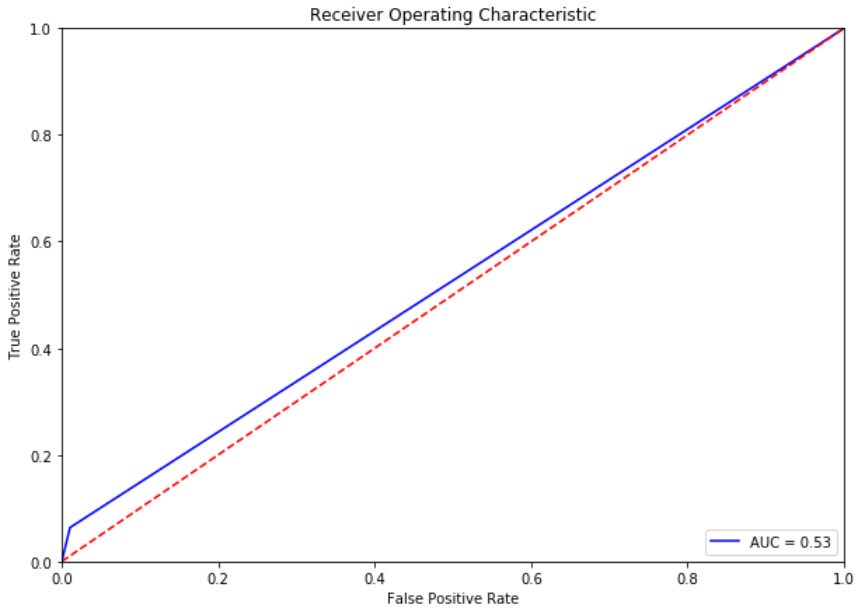
Out[215]:



Although this tree is more extensive, it performs lightly poor than than the previous one. Let's check the ROC and AUC.

In [217]:
```
plot_roc_curve(Y_test, Y_pred_tree)
```

Out[217]: <matplotlib.axes._subplots.AxesSubplot at 0x1a1b6ff358>



Feature importance

In [134]:
```
model_tree2.fit(X_train.values, Y_train.values)
feat_importances = pd.Series(model_tree2.feature_importances_, index=X_train.columns)
feat_importances.nlargest(20).plot(kind='barh', figsize=(6, 8), alpha=0.5)
```

Out[134]: <matplotlib.axes._subplots.AxesSubplot at 0x1a22d67160>

Random Forest

In [219]:
```
# Instantiate model with 1000 decision trees
rf2 = RandomForestRegressor(n_estimators = 1000, random_state = 42)
# Train the model on training data
rf2.fit(X_train, Y_train);
```

In [221]:
```
# Use the forest's predict method on the test data
predictions2 = rf2.predict(X_test)
# Calculate the absolute errors
errors2 = abs(predictions2 - Y_test)
# Print out the mean absolute error (mae)
print('Mean Absolute Error:', round(np.mean(errors2), 2), 'degrees.')
```

```
Mean Absolute Error: 0.17 degrees.
```

In [222]:
```
y_pred2 = rf2.predict(X_test)
```

In [224]:
```
print('Mean Absolute Error:', metrics.mean_absolute_error(Y_test, y_pred2))
print('Mean Squared Error:', metrics.mean_squared_error(Y_test, y_pred2))
print('Root Mean Squared Error:', np.sqrt(metrics.mean_squared_error(Y_test, y_pred2)))
```

```
Mean Absolute Error: 0.16843778279462324
Mean Squared Error: 0.08467292379673967
Root Mean Squared Error: 0.2909861230312189
```

In [239]:
```
print("Accuracy:",metrics.accuracy_score(Y_test, y_pred2.round()))
```

```
Accuracy: 0.9020070838252656
```

In [247]:
```
#check confusion matrix

confusion_matrix(Y_test, y_pred2.round())
```

Out[247]:
```
array([[1517,    4],
       [ 162,   11]])
```

In [242]:
```
print("Classification Report")
print(metrics.classification_report(Y_test, y_pred2.round(),digits=4))
```

```
Classification Report
              precision    recall  f1-score   support

           0     0.9035    0.9974    0.9481      1521
           1     0.7333    0.0636    0.1170       173

    accuracy                         0.9020      1694
   macro avg     0.8184    0.5305    0.5326      1694
weighted avg     0.8861    0.9020    0.8632      1694
```

Logistic regression performs the best in this scenario followed by Random Forest and Decision trees.

In [ ]:
```
```