

Random Forest for COVID Case Study

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Random Forest is an ensemble of Decision Trees. With a few exceptions, a `RandomForestClassifier` has all the hyperparameters of a `DecisionTreeClassifier` (to control how trees are grown), plus all the hyperparameters of a `BaggingClassifier` (re: [sklearn.ensemble.BaggingClassifier](#)) to control the ensemble itself.

The Random Forest algorithm introduces extra randomness when growing trees; instead of searching for the very best feature when splitting a node, it searches for the best feature among a random subset of features. This results in a greater tree diversity, which (once again) trades a higher bias for a lower variance, generally yielding an overall better model. The `BaggingClassifier` (commented out below) is roughly equivalent to the previous `RandomForestClassifier`. Run the cell below to visualize a single estimator from a random forest model (or uncomment the `BaggingClassifier` and comment out the `RandomForestClassifier`), using the Iris dataset to classify the data into the appropriate species.

```
In [1]: from sklearn.datasets import load_iris
iris = load_iris()

# Model (can also use single decision tree)
from sklearn.ensemble import RandomForestClassifier
from sklearn.ensemble import BaggingClassifier
model = RandomForestClassifier(n_estimators=10, random_state = 0)
# model = BaggingClassifier(n_estimators=10, random_state = 0)

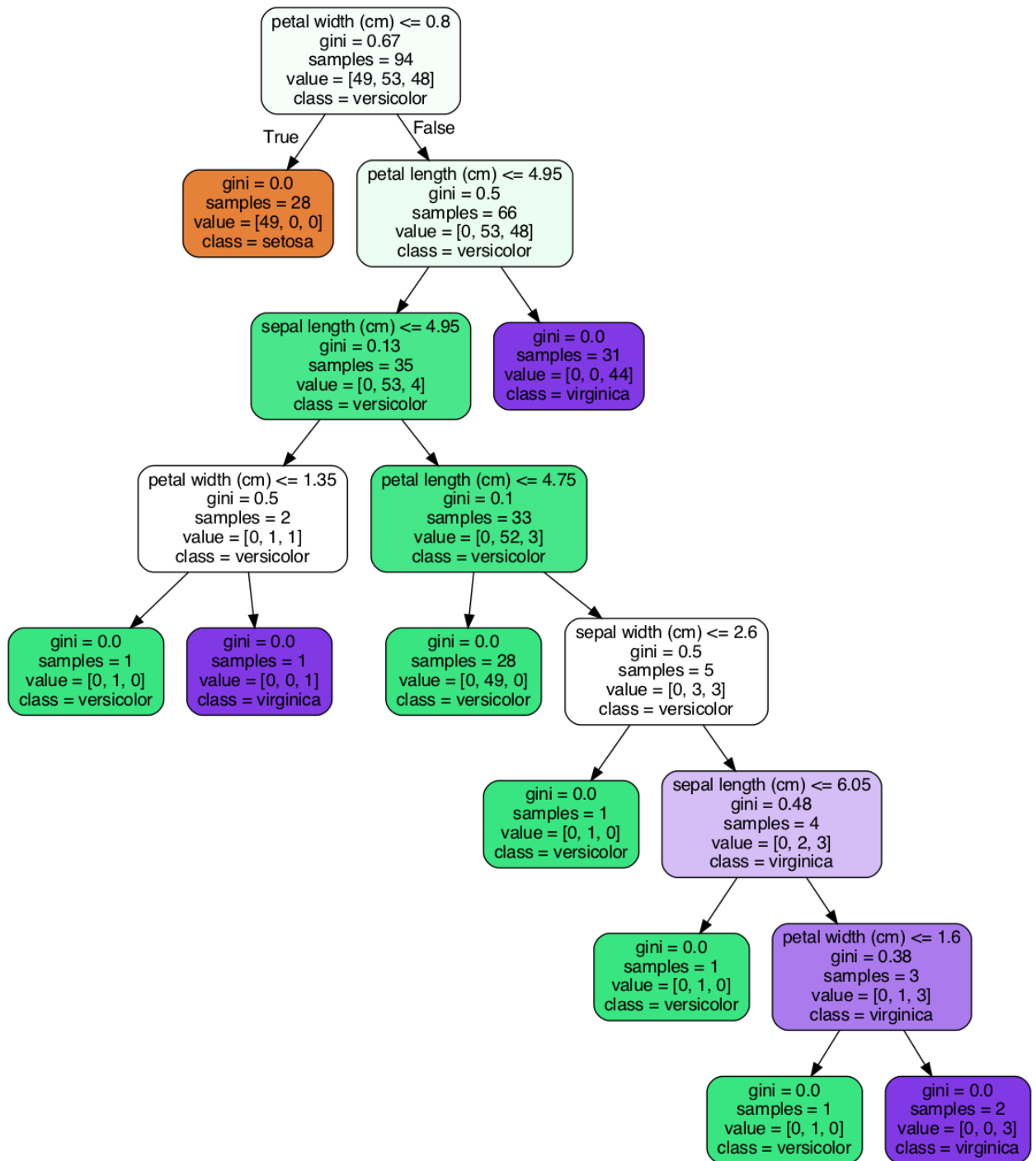
# Train
model.fit(iris.data, iris.target)
# Extract single tree
estimator = model.estimators_[5]

from sklearn.tree import export_graphviz
# Export as dot file
export_graphviz(estimator, out_file='tree.dot',
                feature_names = iris.feature_names,
                class_names = iris.target_names,
                rounded = True, proportion = False,
                precision = 2, filled = True)

# Convert to png using system command (requires Graphviz)
from subprocess import call
# call(['dot', '-Tpng', 'tree.dot', '-o', 'tree.png', '-Gdpi=600'])
call(['dot', '-Tpng', 'tree.dot', '-o', 'tree.png', '-Gdpi=100'])

# Display in jupyter notebook
from IPython.display import Image
Image(filename = 'tree.png')
```

Out [1]:



Notice how each split separates the data into buckets of similar observations. This is a single tree and a relatively simple classification dataset, but the same method is used in a more complex dataset with greater depth to the trees.

Coronavirus

Coronavirus disease (COVID-19) is an infectious disease caused by a new virus. The disease causes respiratory illness (like the flu) with symptoms such as a cough, fever, and in more severe cases, difficulty breathing. There is a detailed guideline of preventive actions against COVID-19 available now (Ref: [CDC guidelines](#)). An outbreak of COVID-19 started in December 2019 and is

still continuing throughout the world. An excellent [spatial dashboard](#) built by Johns Hopkins shows the daily confirmed cases by country.

This case study is designed to drive home the important role that data science plays in real-world situations like this pandemic. This case study uses the Random Forest Classifier and a dataset from the South Korean cases of COVID-19. The goal of this work is to build a Random Forest Classifier to predict the 'state' of the patient.

Imports

First, please load the needed packages and modules into Python. Next, load the data into a pandas dataframe for ease of use.

```
In [2]: import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
import numpy as np
%matplotlib inline

from sklearn.ensemble import RandomForestClassifier

from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score, f1_score
from sklearn.metrics import confusion_matrix, classification_report

import itertools
```

Load and Explore Data

```
In [3]: file = 'SouthKoreacoronavirusdataset/PatientInfo.csv'
# df = pd.read_csv(url)
df = pd.read_csv(file, parse_dates = ['symptom_onset_date', 'confirmed_date', 'release_date'])
df.head()
```

```
Out[3]:
```

	patient_id	global_num	sex	birth_year	age	country	province	city	disease	infection_status
0	1000000001	2.0	male	1964.0	50s	Korea	Seoul	Gangseo-gu	NaN	overseas
1	1000000002	5.0	male	1987.0	30s	Korea	Seoul	Junghnang-gu	NaN	overseas
2	1000000003	6.0	male	1964.0	50s	Korea	Seoul	Jongno-gu	NaN	contacted
3	1000000004	7.0	male	1991.0	20s	Korea	Seoul	Mapo-gu	NaN	overseas
4	1000000005	9.0	female	1992.0	20s	Korea	Seoul	Seongbuk-gu	NaN	contacted

```
In [4]: df.shape
```

```
Out[4]: (2218, 18)
```

```
In [5]: # #Counts of null values
# na_df=pd.DataFrame(df.isnull().sum().sort_values(ascending=False)).reset_index()
# na_df.columns = ['VarName', 'NullCount']
# na_df[(na_df['NullCount']>0)]

#Counts of null values
def count_null_values(data):
    na_df=pd.DataFrame(data.isnull().sum().sort_values(ascending=False)).reset_index()
    na_df.columns = ['VarName', 'NullCount']
    na_df = na_df[(na_df['NullCount']>0)]
    return na_df

count_null_values(df)
```

Out[5]:

	VarName	NullCount
0	disease	2199
1	deceased_date	2186
2	infection_order	2176
3	symptom_onset_date	2025
4	released_date	1995
5	contact_number	1807
6	infected_by	1749
7	infection_case	1055
8	global_num	904
9	birth_year	454
10	age	261
11	sex	145
12	confirmed_date	141
13	state	88
14	city	65

```
In [6]: #counts of response variable values
df.state.value_counts(dropna = False)
```

```
Out[6]: isolated    1791
released    307
NaN         88
deceased    32
Name: state, dtype: int64
```

Create a new column named 'n_age' which is the calculated age based on the birth year column.

```
In [7]: df['birth_year'].info()
```

```

<class 'pandas.core.series.Series'>
RangeIndex: 2218 entries, 0 to 2217
Series name: birth_year
Non-Null Count  Dtype
-----
1764 non-null   float64
dtypes: float64(1)
memory usage: 17.5 KB

```

```
In [8]: df['confirmed_date'].info()
```

```

<class 'pandas.core.series.Series'>
RangeIndex: 2218 entries, 0 to 2217
Series name: confirmed_date
Non-Null Count  Dtype
-----
2077 non-null   datetime64[ns]
dtypes: datetime64[ns](1)
memory usage: 17.5 KB

```

```
In [9]: # df['n_age'] = df['birth_year'].apply(lambda x: date.today().year - x)
df['n_age'] = (df['confirmed_date'].dt.year.astype('float64')) - df['birth_year']
df.n_age
```

```

Out[9]: 0      56.0
1      33.0
2      56.0
3      29.0
4      28.0
...
2213   30.0
2214   22.0
2215   22.0
2216   48.0
2217   46.0
Name: n_age, Length: 2218, dtype: float64

```

Handle Missing Values

Print the number of missing values by column.

```
In [10]: count_null_values(df)
```

Out[10]:

	VarName	NullCount
0	disease	2199
1	deceased_date	2186
2	infection_order	2176
3	symptom_onset_date	2025
4	released_date	1995
5	contact_number	1807
6	infected_by	1749
7	infection_case	1055
8	global_num	904
9	n_age	455
10	birth_year	454
11	age	261
12	sex	145
13	confirmed_date	141
14	state	88
15	city	65

In [11]: `df.info()`

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2218 entries, 0 to 2217
Data columns (total 19 columns):
#   Column                Non-Null Count  Dtype
---  -
0   patient_id            2218 non-null   int64
1   global_num            1314 non-null   float64
2   sex                   2073 non-null   object
3   birth_year            1764 non-null   float64
4   age                   1957 non-null   object
5   country               2218 non-null   object
6   province              2218 non-null   object
7   city                  2153 non-null   object
8   disease               19 non-null     object
9   infection_case        1163 non-null   object
10  infection_order        42 non-null     float64
11  infected_by            469 non-null     float64
12  contact_number         411 non-null     float64
13  symptom_onset_date     193 non-null     datetime64[ns]
14  confirmed_date         2077 non-null     datetime64[ns]
15  released_date          223 non-null     datetime64[ns]
16  deceased_date          32 non-null     datetime64[ns]
17  state                  2130 non-null   object
18  n_age                  1763 non-null   float64
dtypes: datetime64[ns](4), float64(6), int64(1), object(8)
memory usage: 329.4+ KB
```

`disease` column

Fill the 'disease' missing values with 0 and remap the True values to 1.

```
In [12]: df.disease = df.disease.map({True:1, np.nan:0})
df.disease.value_counts()
```

```
Out[12]: 0    2199
         1      19
         Name: disease, dtype: int64
```

```
In [13]: df.disease.isnull().sum()
```

```
Out[13]: 0
```

`birth_year` column

Since we already have `age` and `n_age` column, let's drop the `birth_year` column.

```
In [14]: df.drop(['birth_year'], axis=1, inplace=True)
```

`global number`, `infection order`, `infected by` and `contact number` columns

Fill null values in the following columns with their mean: 'global_number', 'infection_order', 'infected_by' and 'contact_number'

```
In [15]: features = ['global_num', 'infection_order', 'infected_by', 'contact_number']

df[features] = df[features].fillna(df[features].mean())
```

```
In [16]: print(f"global_num\n\n{df.global_num.value_counts()}\n\n")
         print(f"infection_order\n\n{df.infection_order.value_counts()}\n\n")
         print(f"infected_by\n\n{df.infected_by.value_counts()}\n\n")
         print(f"contact_number\n\n{df.contact_number.value_counts()}\n\n")
```

```

global_num

4664.816591    904
1753.000000     2
8476.000000     2
2769.000000     2
7103.000000     2
...
392.000000      1
649.000000      1
565.000000      1
574.000000      1
5534.000000      1
Name: global_num, Length: 1304, dtype: int64

```

```

infection_order

2.285714    2176
2.000000     19
1.000000     11
3.000000      6
5.000000      3
4.000000      2
6.000000      1
Name: infection_order, dtype: int64

```

```

infected_by

2.600789e+09    1749
2.000000e+09     44
4.100000e+09     27
4.100000e+09     21
2.000000e+09     17
...
2.000000e+09      1
2.000000e+09      1
2.000000e+09      1
2.002000e+09      1
6.113000e+09      1
Name: infected_by, Length: 207, dtype: int64

```

```

contact_number

24.128954    1807
0.000000     47
2.000000     44
3.000000     42
1.000000     34
...
450.000000      1
65.000000      1
156.000000      1
39.000000      1
84.000000      1
Name: contact_number, Length: 73, dtype: int64

```

Remove date columns from the data.


```
In [17]: df = df.drop(['symptom_onset_date', 'confirmed_date', 'released_date', 'deceased_date'])
```

Check for any remaining null values.

```
In [18]: count_null_values(df)
```

```
Out[18]:
```

	VarName	NullCount
0	infection_case	1055
1	n_age	455
2	age	261
3	sex	145
4	state	88
5	city	65

Fill the rest of the missing values with any method.

`age` and `n_age` columns

```
In [19]: df.age.info()

<class 'pandas.core.series.Series'>
RangeIndex: 2218 entries, 0 to 2217
Series name: age
Non-Null Count  Dtype
-----
1957 non-null   object
dtypes: object(1)
memory usage: 17.5+ KB
```

```
In [20]: age_keys = list(df.age.value_counts().index)
age_keys
```

```
Out[20]: ['20s', '50s', '40s', '30s', '60s', '70s', '80s', '10s', '0s', '90s', '100s']
```

Remove the 's' from the end and convert the datatype from `object` to `int` for the `age` column.

```
In [21]: age_values = [x[:-1] for x in age_keys]
age_values = [int(i) for i in age_values]
age_values
```

```
Out[21]: [20, 50, 40, 30, 60, 70, 80, 10, 0, 90, 100]
```

```
In [22]: # using zip() to create a dictionary to use in `.replace` function
age_dict = dict(zip(age_keys, age_values))
age_dict
```

```
Out[22]: {'20s': 20,
          '50s': 50,
          '40s': 40,
          '30s': 30,
          '60s': 60,
          '70s': 70,
          '80s': 80,
          '10s': 10,
          '0s': 0,
          '90s': 90,
          '100s': 100}
```

```
In [23]: df["age"].replace(age_dict, inplace=True)
df["age"] = df["age"].astype('Int64')
df.age.info()
```

```
<class 'pandas.core.series.Series'>
RangeIndex: 2218 entries, 0 to 2217
Series name: age
Non-Null Count  Dtype
-----
1957 non-null   Int64
dtypes: Int64(1)
memory usage: 19.6 KB
```

```
In [24]: df.n_age.info()
```

```
<class 'pandas.core.series.Series'>
RangeIndex: 2218 entries, 0 to 2217
Series name: n_age
Non-Null Count  Dtype
-----
1763 non-null   float64
dtypes: float64(1)
memory usage: 17.5 KB
```

Note: We see that the `age` column has 1957 entries while the newly created `n_age` column has 1763 entries. We need to get some of the missing values of `n_age` from `age` column.

Replace the missing values of `n_age` by the available values of the `age` column.

```
In [25]: index_missing_nage = df[['age', 'n_age']].loc[df.n_age.isnull()].index
df[['age', 'n_age']].iloc[index_missing_nage]
```

```
Out[25]:
```

	age	n_age
446	40	NaN
447	20	NaN
448	30	NaN
449	30	NaN
450	30	NaN
...
2128	0	NaN
2136	70	NaN
2159	<NA>	NaN
2160	<NA>	NaN
2161	<NA>	NaN

455 rows × 2 columns

```
In [26]: df.n_age.fillna(df.age, inplace=True)
df[['age', 'n_age']].iloc[index_missing_nage]
```

```
Out[26]:
```

	age	n_age
446	40	40.0
447	20	20.0
448	30	30.0
449	30	30.0
450	30	30.0
...
2128	0	0.0
2136	70	70.0
2159	<NA>	<NA>
2160	<NA>	<NA>
2161	<NA>	<NA>

455 rows × 2 columns

```
In [27]: df[['age', 'n_age']].isnull().sum()
```

```
Out[27]: age      261
n_age    151
dtype: int64
```

We can now drop the `age` column.

```
In [28]: df.drop(['age'], axis=1, inplace=True)
```

Fill null values of `n_age` column by its mean.

```
In [29]: df['n_age'] = df['n_age'].fillna(df['n_age'].mean())
```

```
In [30]: df.n_age.isnull().sum()
```

```
Out[30]: 0
```

`sex` column

```
In [31]: df.sex.info()
```

```
<class 'pandas.core.series.Series'>
RangeIndex: 2218 entries, 0 to 2217
Series name: sex
Non-Null Count  Dtype
-----
2073 non-null   object
dtypes: object(1)
memory usage: 17.5+ KB
```

```
In [32]: df.sex.value_counts(dropna = False)
```

```
Out[32]: female    1171
male           902
NaN            145
Name: sex, dtype: int64
```

```
In [33]: df.sex.mode()
```

```
Out[33]: 0    female
Name: sex, dtype: object
```

We will use `mode` value to impute the `sex` column.

```
In [34]: df.sex = df.sex.fillna('female')
```

```
In [35]: df.sex.isnull().sum()
```

```
Out[35]: 0
```

`city` column

```
In [36]: df.city.info()
```

```
<class 'pandas.core.series.Series'>
RangeIndex: 2218 entries, 0 to 2217
Series name: city
Non-Null Count  Dtype
-----
2153 non-null   object
dtypes: object(1)
memory usage: 17.5+ KB
```

Note that there is no missing values for `province`.

```
In [37]: df.province.isnull().sum()
```

Out[37]: 0

Replace the missing values of `city` by the corresponding values of the `province` column.

```
In [38]: df.city.fillna(df.province, inplace=True)
```

```
In [39]: df.city.isnull().sum()
```

Out[39]: 0

'infection case' column

```
In [40]: df.infection_case.info()
```

```
<class 'pandas.core.series.Series'>
RangeIndex: 2218 entries, 0 to 2217
Series name: infection_case
Non-Null Count  Dtype
-----
1163 non-null   object
dtypes: object(1)
memory usage: 17.5+ KB
```

```
In [41]: df.infection_case.value_counts(dropna = False)
```

```
Out[41]: NaN                                1055
contact with patient                        530
etc                                         220
Guro-gu Call Center                       102
Shincheonji Church                        86
overseas inflow                           61
Onchun Church                             33
gym facility in Cheonan                    30
Ministry of Oceans and Fisheries           27
Cheongdo Daenam Hospital                   21
Dongan Church                             17
Eunpyeong St. Mary's Hospital              14
Seongdong-gu APT                           13
gym facility in Sejong                      4
Suyeong-gu Kindergarten                   3
River of Grace Community Church            1
Pilgrimage to Israel                       1
Name: infection_case, dtype: int64
```

```
In [42]: df.infection_case.mode()
```

```
Out[42]: 0    contact with patient
Name: infection_case, dtype: object
```

We will use `mode` value to impute the `infection_case` column.

```
In [43]: df.infection_case = df.infection_case.fillna('contact with patient')
```

```
In [44]: df.infection_case.isnull().sum()
```

Out[44]: 0

```
In [45]: df.infection_case.value_counts(dropna = False)
```

```
Out[45]: contact with patient      1585
etc                               220
Guro-gu Call Center              102
Shincheonji Church              86
overseas inflow                  61
Onchun Church                    33
gym facility in Cheonan          30
Ministry of Oceans and Fisheries 27
Cheongdo Daenam Hospital         21
Dongan Church                    17
Eunpyeong St. Mary's Hospital   14
Seongdong-gu APT                 13
gym facility in Sejong           4
Suyeong-gu Kindergarten          3
River of Grace Community Church  1
Pilgrimage to Israel             1
Name: infection_case, dtype: int64
```

`state` column

Replace null values in the `state` column with `missing`.

```
In [46]: df.state = df.state.fillna('missing')
```

Check for any remaining null values.

```
In [47]: count_null_values(df)
```

```
Out[47]: VarName  NullCount
```

All missing values are now replaced.

```
In [48]: df.head()
```

```
Out[48]:
```

	patient_id	global_num	sex	country	province	city	disease	infection_case	infection
0	1000000001	2.0	male	Korea	Seoul	Gangseo-gu	0	overseas inflow	
1	1000000002	5.0	male	Korea	Seoul	Junghang-gu	0	overseas inflow	
2	1000000003	6.0	male	Korea	Seoul	Jongno-gu	0	contact with patient	
3	1000000004	7.0	male	Korea	Seoul	Mapo-gu	0	overseas inflow	
4	1000000005	9.0	female	Korea	Seoul	Seongbuk-gu	0	contact with patient	

```
In [49]: df.info()
```

```

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 2218 entries, 0 to 2217
Data columns (total 13 columns):
 #   Column                Non-Null Count  Dtype
---  -
 0   patient_id            2218 non-null   int64
 1   global_num            2218 non-null   float64
 2   sex                   2218 non-null   object
 3   country               2218 non-null   object
 4   province              2218 non-null   object
 5   city                  2218 non-null   object
 6   disease               2218 non-null   int64
 7   infection_case        2218 non-null   object
 8   infection_order       2218 non-null   float64
 9   infected_by           2218 non-null   float64
10   contact_number        2218 non-null   float64
11   state                 2218 non-null   object
12   n_age                 2218 non-null   Float64
dtypes: Float64(1), float64(4), int64(2), object(6)
memory usage: 227.6+ KB

```

Review the count of unique values by column.

```
In [50]: print(df.nunique())
```

```

patient_id      2218
global_num      1304
sex              2
country          4
province        17
city            139
disease          2
infection_case   16
infection_order  7
infected_by     207
contact_number   73
state            4
n_age           97
dtype: int64

```

Review the percent of unique values by column.

```
In [51]: print(df.nunique()/df.shape[0])
```

```

patient_id      1.000000
global_num      0.587917
sex             0.000902
country         0.001803
province        0.007665
city            0.062669
disease         0.000902
infection_case  0.007214
infection_order 0.003156
infected_by     0.093327
contact_number  0.032913
state           0.001803
n_age           0.043733
dtype: float64

```

Review the range of values per column.

```
In [52]: df.describe().T
```

```
Out[52]:
```

	count	mean	std	min	25%	50%
patient_id	2218.0	4.014678e+09	2.192419e+09	1.000000e+09	1.700000e+09	6.001000e+09
global_num	2218.0	4.664817e+03	2.211785e+03	1.000000e+00	4.205250e+03	4.664817e+03
disease	2218.0	8.566276e-03	9.217769e-02	0.000000e+00	0.000000e+00	0.000000e+00
infection_order	2218.0	2.285714e+00	1.706622e-01	1.000000e+00	2.285714e+00	2.285714e+00
infected_by	2218.0	2.600789e+09	7.216328e+08	1.000000e+09	2.600789e+09	2.600789e+09
contact_number	2218.0	2.412895e+01	3.917141e+01	0.000000e+00	2.412895e+01	2.412895e+01
n_age	2218.0	4.420416e+01	1.877212e+01	0.000000e+00	2.800000e+01	4.420416e+01

```
In [53]: df.describe(include=[object]).T
```

```
Out[53]:
```

	count	unique	top	freq
sex	2218	2	female	1316
country	2218	4	Korea	2206
province	2218	17	Gyeongsangbuk-do	1054
city	2218	139	Gyeongsan-si	535
infection_case	2218	16	contact with patient	1585
state	2218	4	isolated	1791

Check for duplicated rows

```
In [54]: duplicateRowsDF = df[df.duplicated()]
duplicateRowsDF
```

```
Out[54]:
```

patient_id	global_num	sex	country	province	city	disease	infection_case	infection_order	infec
------------	------------	-----	---------	----------	------	---------	----------------	-----------------	-------

Print the categorical columns and their associated levels.

```
In [55]: dfo = df.select_dtypes(include=['object'], exclude=['datetime'])
print(f"dfo.shape: {dfo.shape}")

#get levels for all variables
vn = pd.DataFrame(dfo.nunique().reset_index())
vn.columns = ['VarName', 'LevelsCount']
vn.sort_values(by='LevelsCount', ascending =False)
vn

dfo.shape: (2218, 6)
```


Out[55]:

	VarName	LevelsCount
0	sex	2
1	country	4
2	province	17
3	city	139
4	infection_case	16
5	state	4

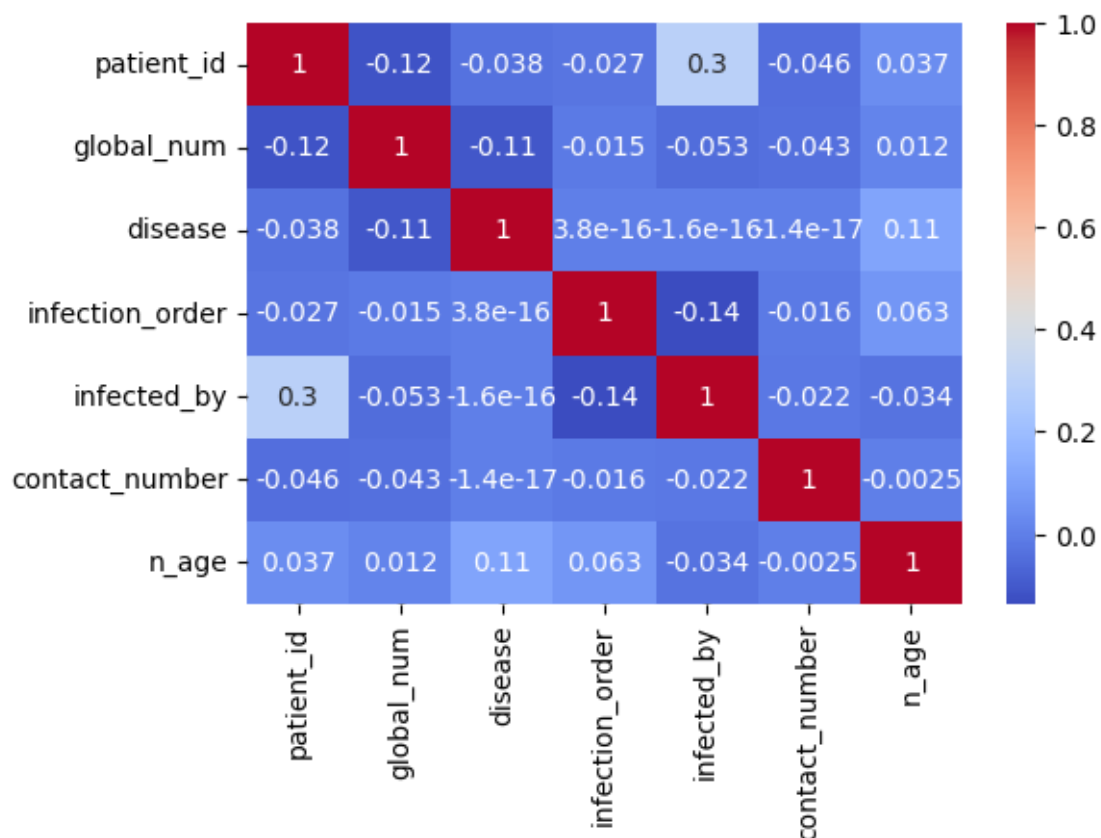
Plot the correlation heat map for the features.

```
In [56]: # Make a heatmap of the data
plt.figure(dpi = 100)

ax = sns.heatmap(df.corr(), cmap="coolwarm", annot=True, annot_kws={"fontsize": 10})

ax.set_xticklabels(ax.get_xmajorticklabels(), fontsize = 10, rotation=90);
ax.set_yticklabels(ax.get_ymajorticklabels(), fontsize = 10);

ax.collections[0].colorbar.ax.tick_params(labelsize=10)
```



We see that the **numerical features are only weakly correlated** to each other. So, we need to consider all these features as input variables for our random forest classifier.

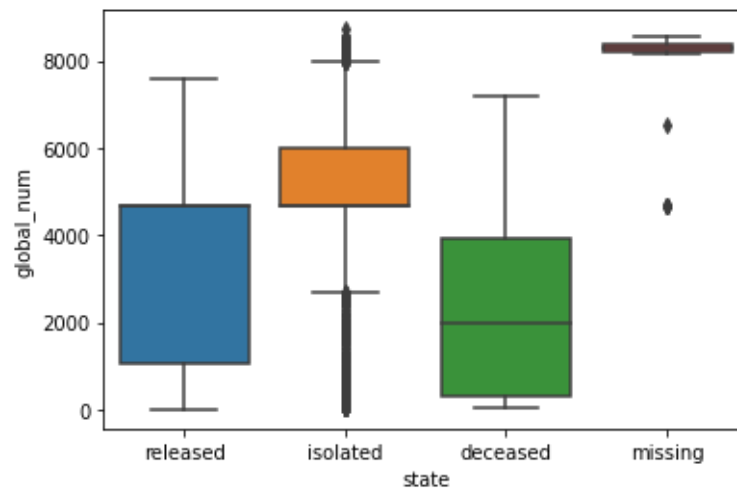
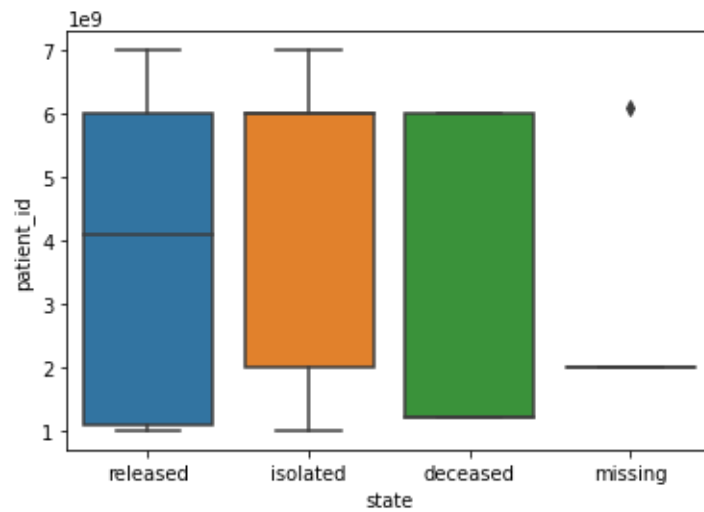
Plot the boxplots to check for outliers.

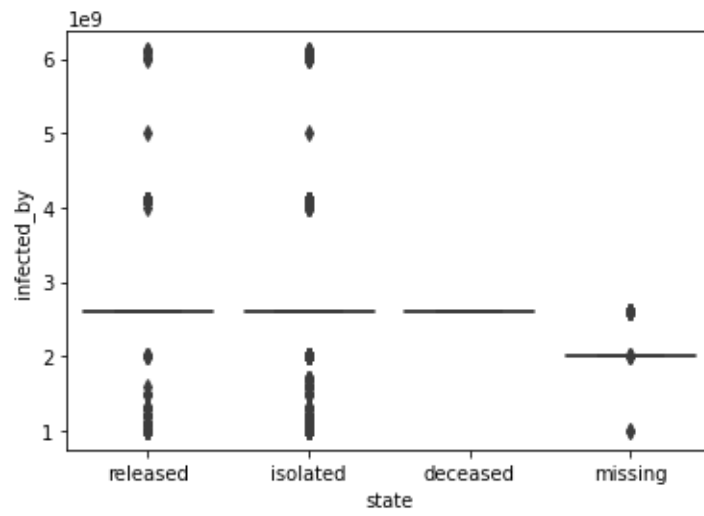
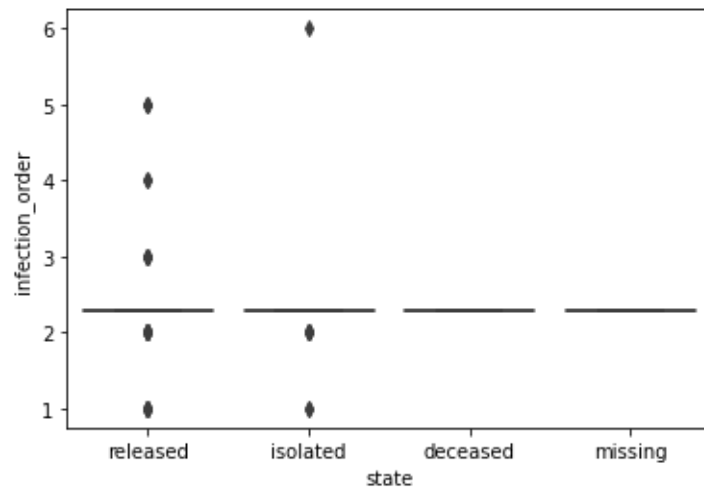
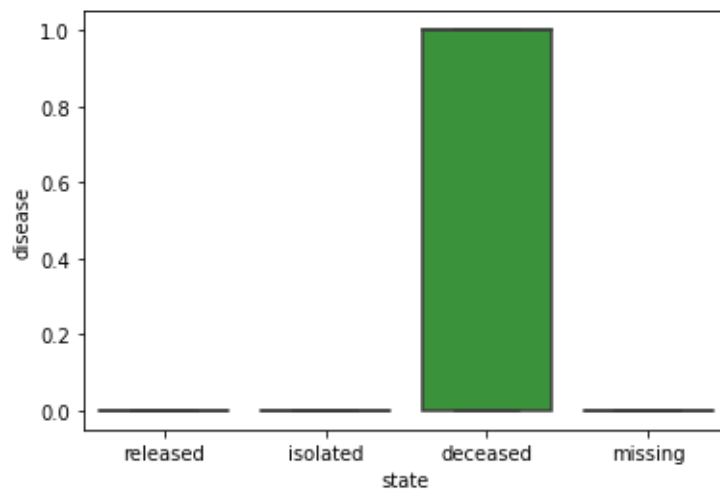
```
In [57]: df1 = df.select_dtypes(include=['int', 'float'])
df1_list = list(df1.columns.values)
```

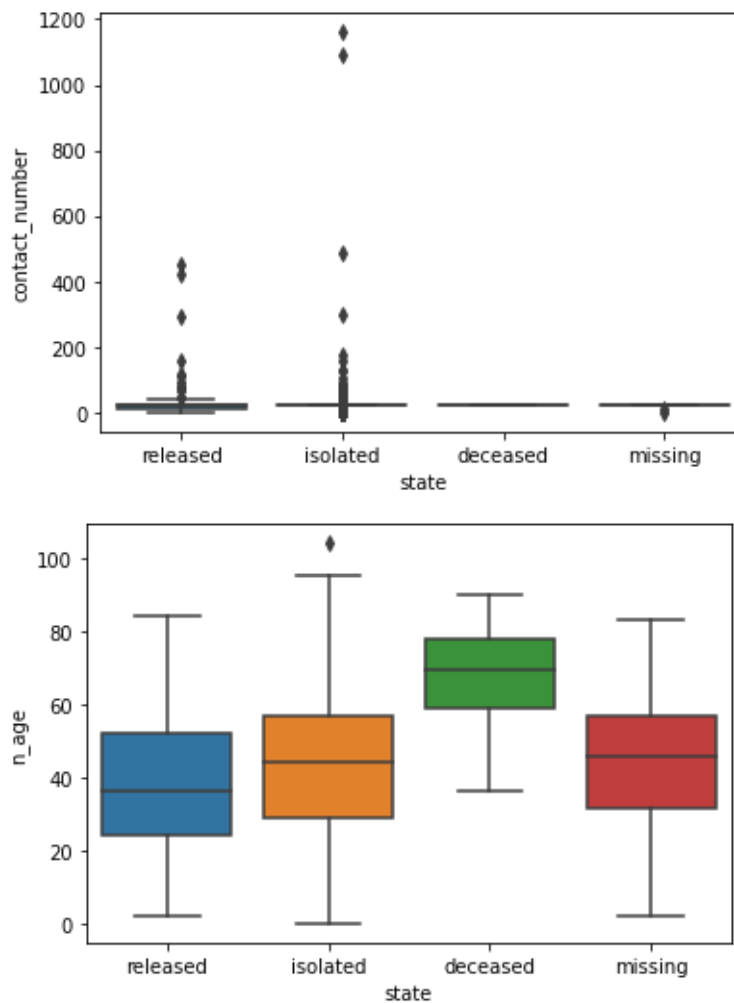
```
df1_list
```

```
Out[57]: ['patient_id',  
          'global_num',  
          'disease',  
          'infection_order',  
          'infected_by',  
          'contact_number',  
          'n_age']
```

```
In [58]: for feature in df1_list:  
          plt.figure()  
          sns.boxplot(x='state', y=feature, data=df);
```







Let's count the number of outliers of each numerical columns. See this [stackoverflow response](#).

```
In [59]: Q1 = df1.quantile(0.25)
Q3 = df1.quantile(0.75)
IQR = Q3 - Q1
```

```
In [60]: print(f"\nNumber of outliers:")
((df1 < (Q1 - 1.5 * IQR)) | (df1 > (Q3 + 1.5 * IQR))).sum()
```

```
Number of outliers:
Out[60]: patient_id      0
global_num    331
disease       19
infection_order 42
infected_by   469
contact_number 411
n_age         1
dtype: int64
```

Create dummy features for object type features.

Note: A random forest classifier is a meta estimator that fits a number of decision tree classifiers on various sub-samples of the dataset and uses averaging to improve the predictive accuracy and control over-fitting (re: [sklearn.ensemble.RandomForestClassifier](#)).

Decision tree classifier can handle both numerical and categorical data. However, the `scikit-learn` implementation does not support categorical variables for now (re: [Decision Trees](#)).

Therefore, we will convert our categorical variables into dummy/indicator variables (re: [pandas.get_dummies](#)) using one-hot-encoding.

```
In [61]: X = pd.get_dummies(df.drop('state', axis=1))
print(f"X.shape: {X.shape}")
X.head()
```

X.shape: (2218, 185)

```
Out[61]:
```

	patient_id	global_num	disease	infection_order	infected_by	contact_number	n_age	sex_fer
0	1000000001	2.0	0	1.0	2.600789e+09	75.0	56.0	
1	1000000002	5.0	0	1.0	2.600789e+09	31.0	33.0	
2	1000000003	6.0	0	2.0	2.002000e+09	17.0	56.0	
3	1000000004	7.0	0	1.0	2.600789e+09	9.0	29.0	
4	1000000005	9.0	0	2.0	1.000000e+09	2.0	28.0	

5 rows × 185 columns

```
In [62]: y = df['state']
print(f"\ny.shape: {y.shape}\n")
y.value_counts()
```

y.shape: (2218,)

```
Out[62]: isolated    1791
released    307
missing      88
deceased     32
Name: state, dtype: int64
```

Split the data into test and train subsamples

Make sure you also pass `stratify = y` to split the data in a stratified fashion.

```
In [63]: # dont forget to define your X and y

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=.2, random_stat
```

Scaling of Data

The random forest classification algorithm is based on multiple decision tree classifiers, and the decision tree classifier requires little data preparation (re: [Decision Trees](#)). The decision tree classifier uses partitioning, i.e., a set of if-then-else decision rules; see [Decision Trees](#). Even if you apply feature scaling, the result would still be the same. Hence, we will **not apply any scaling on our data**.

Side Note: Note that the feature scaling slightly affects the results of the random forest regressors (see this [article](#)). But, the results are practically same.

```
In [64]: #scale data
# from sklearn import preprocessing
# import numpy as np
# # build scaler based on training data and apply it to test data to then also scale
# scaler = preprocessing.StandardScaler().fit(X_train)
# X_train_scaled=scaler.transform(X_train)
# X_test_scaled=scaler.transform(X_test)
```

Fit Random Forest Classifier

```
In [65]: clf = RandomForestClassifier(n_estimators=300, random_state = 1,n_jobs=-1)
model_res = clf.fit(X_train, y_train)
y_pred = model_res.predict(X_test)
y_pred_prob = model_res.predict_proba(X_test)
lr_probs = y_pred_prob[:,1]
ac = accuracy_score(y_test, y_pred)

f1 = f1_score(y_test, y_pred, average='weighted')
cm = confusion_matrix(y_test, y_pred)

print('Random Forest: Accuracy=%.3f' % (ac))

print('Random Forest: f1-score=%.3f' % (f1))
```

```
Random Forest: Accuracy=0.865
Random Forest: f1-score=0.854
```

The fit model shows an overall accuracy of 86.5% with a f1-score of 0.854. This is great and indicates our model was effectively able to identify the status of a patients in the South Korea dataset.

Create Confusion Matrix Plots

Confusion matrices are great ways to review your model performance for a multi-class classification problem. Being able to identify which class the misclassified observations end up in is a great way to determine if you need to build additional features to improve your overall model. In the example below we plot a regular counts confusion matrix as well as a weighted percent confusion matrix. The percent confusion matrix is particularly helpful when you have unbalanced class sizes.

```
In [66]: # class_names = ['isolated','released','missing','deceased'] # name of classes
class_names = list(y_train.value_counts(dropna = False).index)
class_names
```

```
Out[66]: ['isolated', 'released', 'missing', 'deceased']
```

```
In [67]: y_train.value_counts(dropna = False)
```

```
Out[67]: isolated    1432
         released    246
         missing      70
         deceased     26
         Name: state, dtype: int64
```

```
In [68]: def plot_confusion_matrix(cm, classes,
                                   normalize=False,
                                   title='Confusion matrix',
                                   cmap=plt.cm.Blues):

    """
    This function prints and plots the confusion matrix.
    Normalization can be applied by setting `normalize=True`.
    """

    if normalize:
        cm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]
        print("Normalized confusion matrix")
    else:
        print('Confusion matrix, without normalization')

    print(cm)

    plt.imshow(cm, interpolation='nearest', cmap=cmap)
    plt.title(title)
    plt.colorbar()
    tick_marks = np.arange(len(classes))
    plt.xticks(tick_marks, classes, rotation=45)
    plt.yticks(tick_marks, classes)

    fmt = '.2f' if normalize else 'd'
    thresh = cm.max() / 2.
    for i, j in itertools.product(range(cm.shape[0]), range(cm.shape[1])):
        plt.text(j, i, format(cm[i, j], fmt),
                 horizontalalignment="center",
                 color="white" if cm[i, j] > thresh else "black")

    plt.ylabel('True label')
    plt.xlabel('Predicted label')
    plt.tight_layout()

# Compute confusion matrix
cnf_matrix = confusion_matrix(y_test, y_pred)
np.set_printoptions(precision=2)

# Plot non-normalized confusion matrix
plt.figure()
plot_confusion_matrix(cnf_matrix, classes=class_names,
                      title='Confusion matrix, without normalization')
#plt.savefig('figures/RF_cm_multi_class.png')

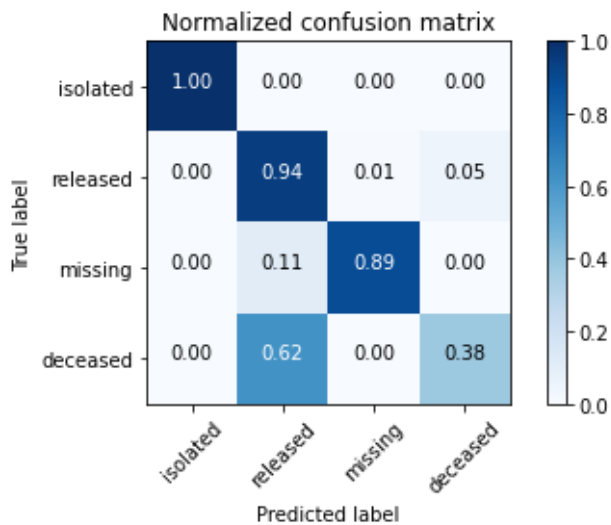
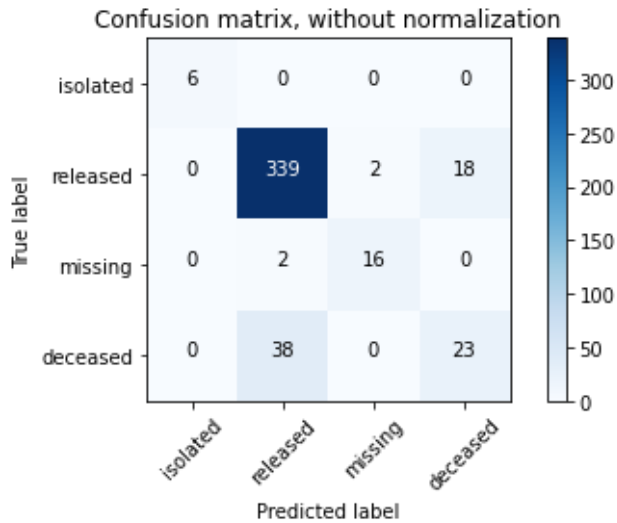
# Plot normalized confusion matrix
plt.figure()
plot_confusion_matrix(cnf_matrix, classes=class_names, normalize=True,
                      title='Normalized confusion matrix')
#plt.savefig('figures/RF_cm_proportion_multi_class.png', bbox_inches="tight")
plt.show()
```

Confusion matrix, without normalization

```
[[ 6  0  0  0]
 [ 0 339  2 18]
 [ 0  2 16  0]
 [ 0 38  0 23]]
```

Normalized confusion matrix

```
[[1.  0.  0.  0. ]
 [0.  0.94 0.01 0.05]
 [0.  0.11 0.89 0.  ]
 [0.  0.62 0.  0.38]]
```



Even though our model has a fairly good overall accuracy of 86.5% and a f1-score of 0.854, it could not classify the `deceased` state well. It has a very low recall score for the `deceased` state (38% -- see below), which is possibly of significant concern.

```
In [69]: print(classification_report(y_test, y_pred, target_names = class_names))
```


	precision	recall	f1-score	support
isolated	1.00	1.00	1.00	6
released	0.89	0.94	0.92	359
missing	0.89	0.89	0.89	18
deceased	0.56	0.38	0.45	61
accuracy			0.86	444
macro avg	0.84	0.80	0.81	444
weighted avg	0.85	0.86	0.85	444

Plot feature importances

The random forest algorithm can be used as a regression or classification model. In either case it tends to be a bit of a black box, where understanding what's happening under the hood can be difficult. Plotting the feature importances is one way that you can gain a perspective on which features are driving the model predictions.

```
In [70]: feature_importance = clf.feature_importances_
len(feature_importance)
```

```
Out[70]: 185
```

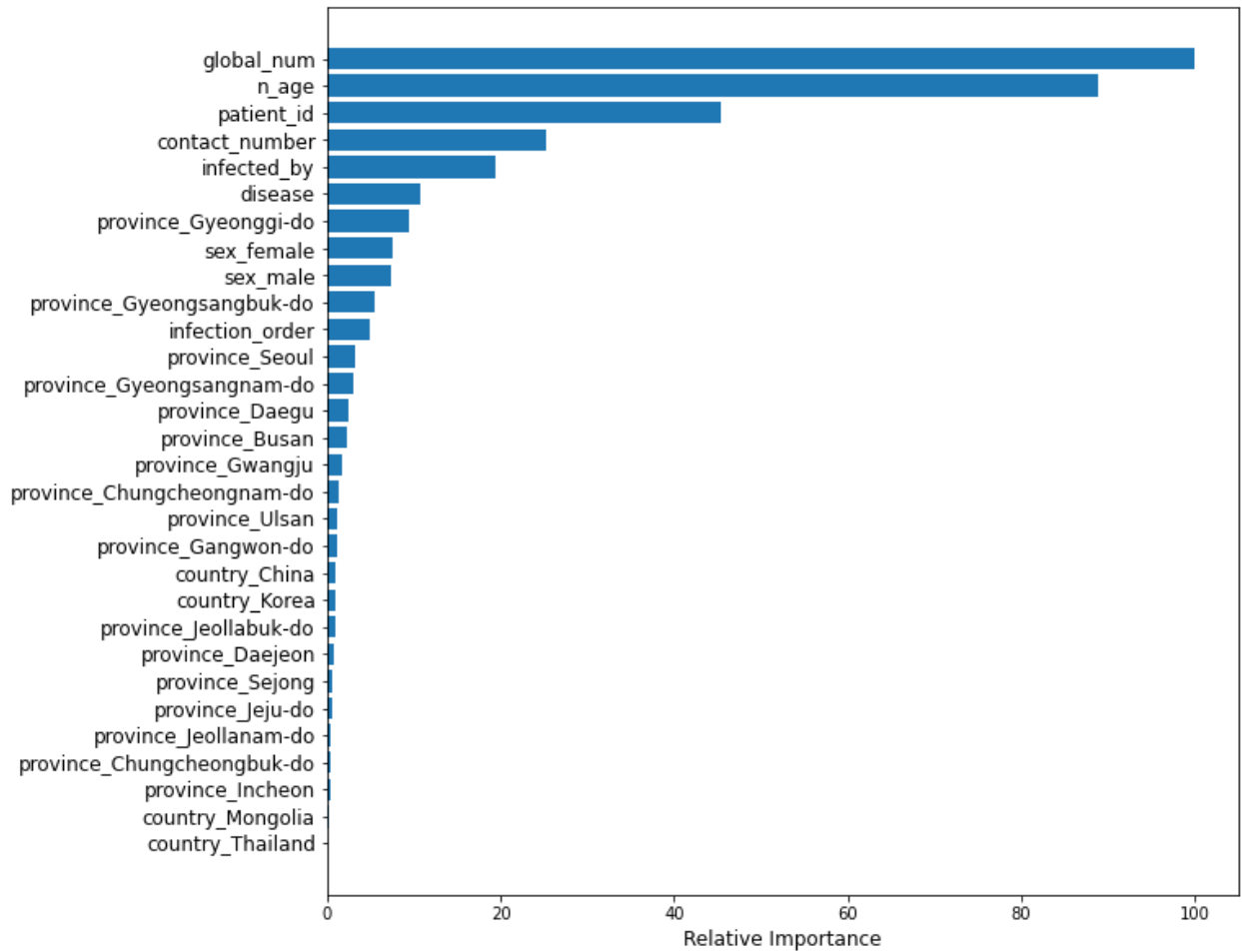
```
In [71]: n_feature_importance = 30 # Plot for top 30 important features

# make importances relative to max importance
feature_importance = 100.0 * (feature_importance / feature_importance.max())[:n_feature_importance]
sorted_idx = np.argsort(feature_importance)[::-n_feature_importance]

pos = np.arange(sorted_idx.shape[0]) + .5

plt.figure(figsize=(10,10))
plt.barh(pos, feature_importance[sorted_idx], align='center')
plt.yticks(pos, X.columns[sorted_idx], fontsize = 12)
plt.xlabel('Relative Importance', fontsize = 12)
plt.suptitle('Variable Importance', fontsize = 18)
plt.show()
```

Variable Importance



The popularity of random forest is primarily due to how well it performs in a multitude of data situations. It tends to handle highly correlated features well, where as a linear regression model would not. In this case study we demonstrate the performance ability even with only a few features and almost all of them being highly correlated with each other. Random Forest is also used as an efficient way to investigate the importance of a set of features with a large data set. Consider random forest to be one of your first choices when building a decision tree, especially for multiclass classifications.