EsraKantarci_DMMT21

October 22, 2021

1 Esra Kantarcı - 2021

Google Colab Version of Notebook: Link

First, we are importing the main machine learning, plotting and data processing libraries:

[219]:
```
## for data
import pandas as pd
import numpy as np

## for plotting
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
import plotly.express as px
import plotly
plotly.offline.init_notebook_mode (connected = True)
!pip install pygal

## for statistical tests
import scipy
import statsmodels.formula.api as smf
import statsmodels.api as sm

## for machine learning
from sklearn import svm, tree, ensemble, discriminant_analysis, gaussian_process
from xgboost import XGBClassifier
from sklearn.model_selection import train_test_split
from sklearn.tree import DecisionTreeClassifier
from sklearn import feature_selection
from sklearn import model_selection
from sklearn import metrics

## for encoding
from sklearn.preprocessing import OneHotEncoder, LabelEncoder
```

```
Requirement already satisfied: pygal in /usr/local/lib/python3.7/dist-packages
(2.4.0)
```

2 Business Understanding:

The first task according to CRISP-DM methodology is business understanding in a data mining project. So, before starting anything, we need to understand the problem, detail it and decide where to begin or where to stop.

2.1 Task:

The dataset obtained from CDC Covid Data and has the following headers.

cdc_case_earliest_dt,cdc_report_dt,pos_spec_dt,onset_dt,current_status,sex,age_group, race_ethnicity_combined, hosp_yn, icu_yn, death_yn, medcond_yn

Among the fields, cdc_report_dt,pos_spec_dt,onset_dt,current_status fields may be ignored. You may have to deal with some missing/unknown data the way you like it. You may also need to reduce the race_ethnicity_combined to fewer nominal choices.

Some of the things you could do with this data (but should not be limitted):

- *Being able to print the intensity of pandemic by month*
- *Age group, race, medical condition effect on Death Rate*
- *Recognition of some strong relationship between certain fields*
- *Construction of a Decission Tree*

In it you should attached screenshot of your knime workflow and pandas code and charts with a story that explains your findings.

Python and Knime may solve different part of the problem. I want you to experience both of these technologies and take advantages of either depending on the part that you are dealing with.

2.2 First Evaluation of the Problem:

- We have CDC Covid Data and we are asked to analysis the data freely.
- Some data rows need to be processed due to missing values.
- Some columns can be ignored.
- We can group or re-define the nominal classes for better use.
- We need to provide charts of analysis
- Use both KNIME and python

So, it is better to check the column and the values they represent, then find the relationships of the data by using plots, heatmaps, correlations.

```
[220]: df = pd.read_csv('CovidSurveillance.csv')
       df.head()
```

```
[220]:   cdc_case_earliest_dt cdc_report_dt pos_spec_dt  ... icu_yn death_yn medcond_yn
       0           2020/11/14    2021/02/08         NaN  ...     No       No         No
       1           2020/07/15    2020/08/20         NaN  ...     No       No         No
       2           2020/06/23    2020/09/01         NaN  ...     No       No         No
       3           2020/05/09    2020/08/13         NaN  ...     No       No         No
       4           2020/10/20    2020/10/30         NaN  ...     No       No         No
```

```
[5 rows x 12 columns]
```

[221]:
```
print(df.columns.values)
```

```
['cdc_case_earliest_dt' 'cdc_report_dt' 'pos_spec_dt' 'onset_dt'
 'current_status' 'sex' 'age_group' 'race_ethnicity_combined' 'hosp_yn'
 'icu_yn' 'death_yn' 'medcond_yn']
```

3 Data Understanding:

So we have these columns which are represented above. For the better understanding of the data, we need to check CDC website for the details.

CDC Website explains these column values and also provides helpful histograms for insights. You can check them out from the source.

As we know in the data there are vague values like "unknown" of the data according to histogram in the official website, but as I do not know the heatmap yet, I want to keep other columns as well. However, I want to drop cdc_report_dt, post_spec_dt and onset_dt beforehand and do not waste time to filter/manipulate these column values.

So, as the task suggest, we need to use KNIME as well. This is why, getting the strong sides of the both part, I want to use KNIME for big data evaluation with built-in features. But python's visualization is better and there are many options for evaluation, too.

I will check out the interactive histograms in KNIME, manipulate the data with python (not because it is better, but I find it faster since I am used to it) and evaluate outputs in both platform.

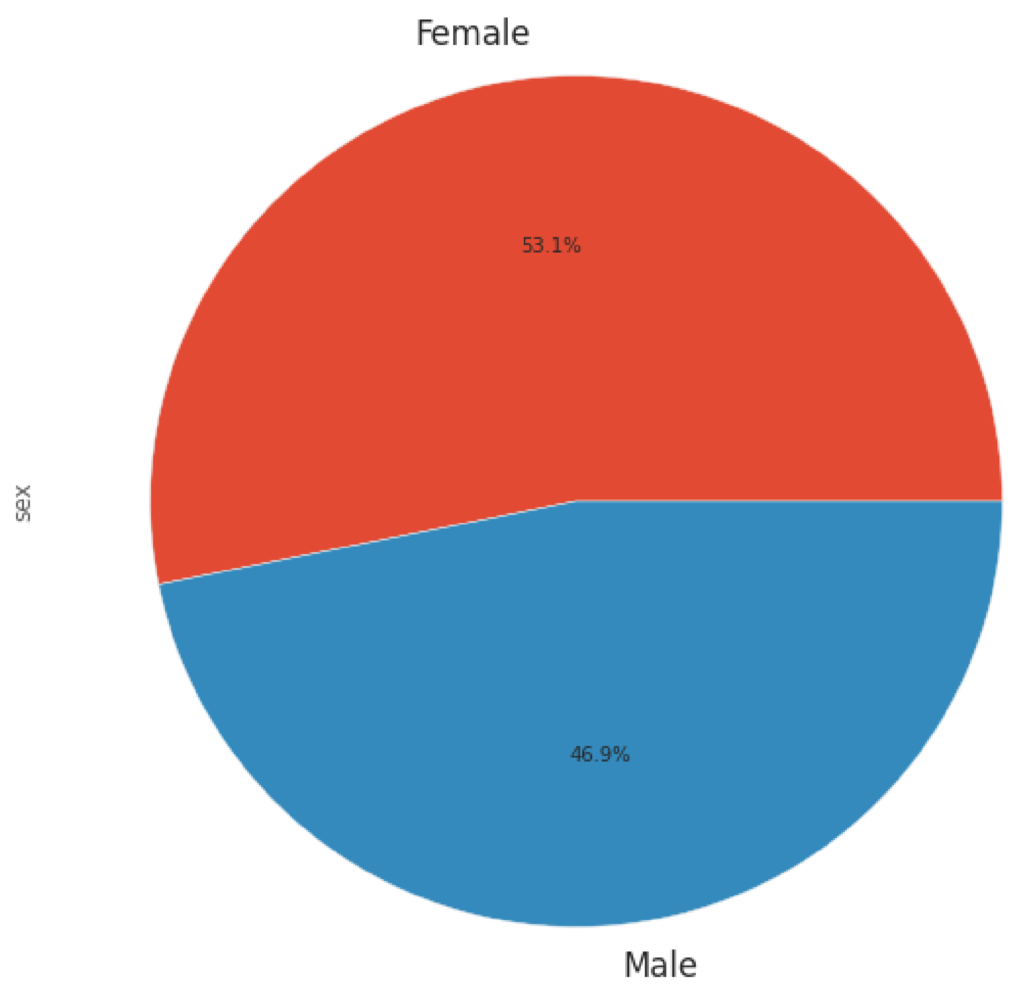
Now, let's see the data.

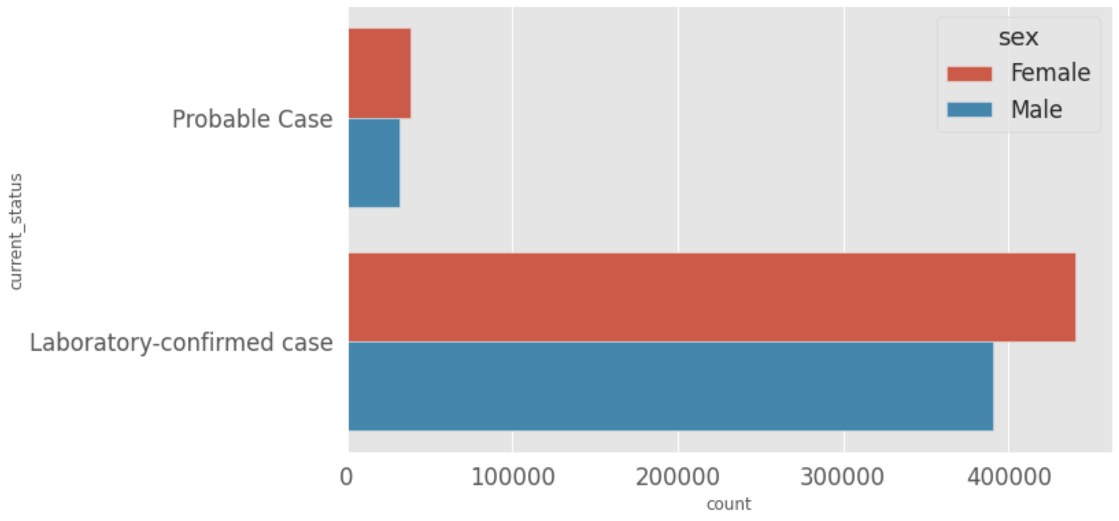
[222]:
```
df.info()

plt.figure(figsize=(20, 10))
plt.style.use("ggplot")

df['sex'].value_counts().plot.pie(autopct="%1.1f%%")

plt.figure(figsize=(10,6))
sns.countplot(y="current_status",hue ='sex',data=df)

plt.figure(figsize=(10,6))
sns.countplot(y="death_yn",hue ='sex',data=df)
```

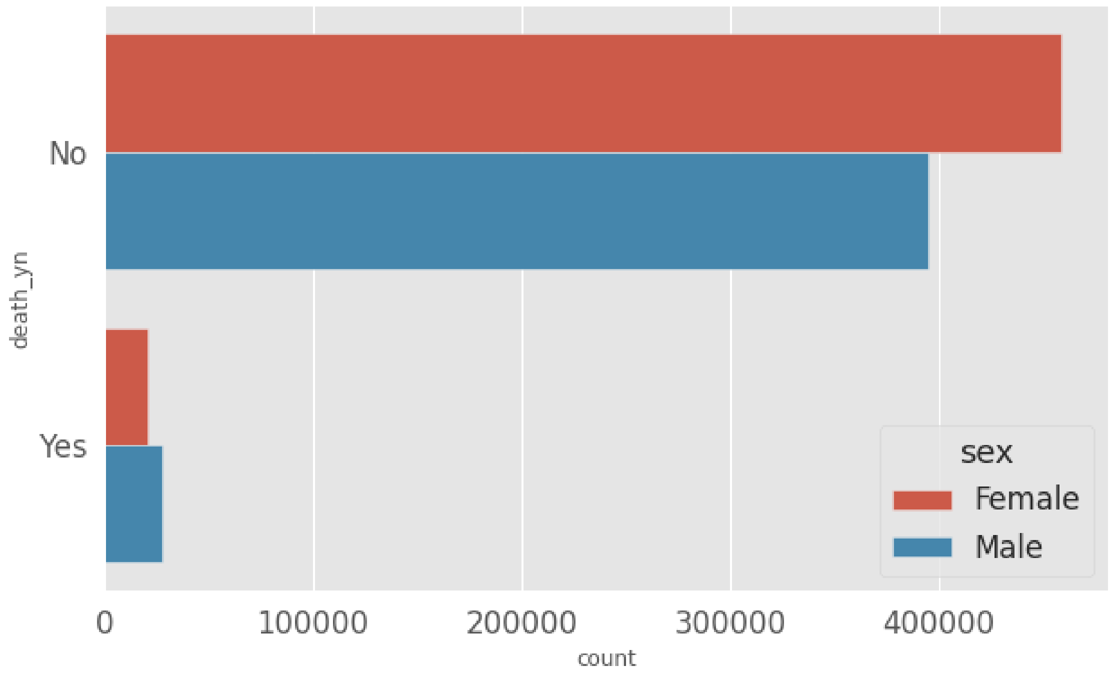
```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 901599 entries, 0 to 901598
Data columns (total 12 columns):
 #   Column                   Non-Null Count   Dtype
---  ------                   --------------   -----
```

```
 0   cdc_case_earliest_dt     901599 non-null  object
 1   cdc_report_dt            901599 non-null  object
 2   pos_spec_dt              586023 non-null  object
 3   onset_dt                 836668 non-null  object
 4   current_status           901599 non-null  object
 5   sex                      901599 non-null  object
 6   age_group                901599 non-null  object
 7   race_ethnicity_combined  901599 non-null  object
 8   hosp_yn                  901599 non-null  object
 9   icu_yn                   901599 non-null  object
 10  death_yn                 901599 non-null  object
 11  medcond_yn               901599 non-null  object
dtypes: object(12)
memory usage: 82.5+ MB
```

```
[222]: <matplotlib.axes._subplots.AxesSubplot at 0x7f8e8029c990>
```







3.1 Initial Findings - 1:

Even though there are more female patients than males, the death count of the male seems higher than females as you can see the graphs above.

3.2 Initial Findings - 2 :

Below this section, you see there are null values in specific columns. pos_spec_dt stands for date of first positive specimen collection and onset_dt is symptom onset date, if the patient is symptomatic. We will not use these labels in our evaluation so, I will drop these columns.

[223]:
```
df.isnull().sum()
```

[223]:
```
cdc_case_earliest_dt            0
cdc_report_dt                   0
pos_spec_dt                315576
onset_dt                    64931
current_status                  0
sex                             0
age_group                       0
race_ethnicity_combined         0
hosp_yn                         0
icu_yn                          0
death_yn                        0
medcond_yn                      0
dtype: int64
```

[224]:
```
# Dropping the columns
columns_to_drop = ["cdc_report_dt", "pos_spec_dt", "onset_dt"]
df = df.drop(columns=columns_to_drop)
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 901599 entries, 0 to 901598
Data columns (total 9 columns):
 #   Column                   Non-Null Count   Dtype
---  ------                   --------------   -----
 0   cdc_case_earliest_dt     901599 non-null  object
 1   current_status           901599 non-null  object
 2   sex                      901599 non-null  object
 3   age_group                901599 non-null  object
 4   race_ethnicity_combined  901599 non-null  object
 5   hosp_yn                  901599 non-null  object
 6   icu_yn                   901599 non-null  object
 7   death_yn                 901599 non-null  object
 8   medcond_yn               901599 non-null  object
dtypes: object(9)
memory usage: 61.9+ MB
```

[225]:
```
# Removing missing values
df = df.dropna()
df.describe().T
```

[225]:
```
                          count  unique                      top    freq
cdc_case_earliest_dt     901599     471               2020/11/09    5865
current_status           901599       2  Laboratory-confirmed case  830822
sex                      901599       2                   Female  479010
age_group                901599      10            20 - 29 Years  149512
race_ethnicity_combined  901599       9      White, Non-Hispanic  470395
hosp_yn                  901599       4                       No  746708
icu_yn                   901599       2                       No  856413
death_yn                 901599       2                       No  853653
medcond_yn               901599       2                       No  520132
```

4 Data Preprocessing

First, cdc_case_earliest_dt is in String format, we can use this column to analyze by time (not as time series though). So let's change this to DateTime format.

4.1 String Manipulation and Encoding

I also stored the original dataframe in anycase.

I also mapped age_group, race_ethnicity and hosp_yn columns to prefferable chunks to tune the data before model training.

4.1.1 Age Group:

The mode shows that the mean value of the column was 20-29 years. I wanted to fill the missing values with the most frequent value to prevent data loss. After that, I decided to use the average values of each age gap for the label.

4.1.2 Race Ethnicity:

Heuristically I decided to remove ethnicity and only use the race value. Afterwards it is ready to encode the race column for the process.

4.1.3 Hospitalized:

There are vague values such as Missing and Unknown labels. However, it is highly possible that if these values are not entered, it means not hospitalized according the rates and frequency. Also due to buerocratic reasons, if the person is hospitalized, there should be paper-work, which ends up in the Yes value.

After these processes, other than the date values, every column is encoded by using LabelEncoder. We could do this in KNIME, too.

[226]:
```python
# String manipulation and encoding

# Column data-types:
df["cdc_case_earliest_dt"] = pd.to_datetime(df["cdc_case_earliest_dt"])
df.info()
df.head()

# Before encoding, I want to store original df in another dataframe
df_origin = df
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 901599 entries, 0 to 901598
Data columns (total 9 columns):
 #   Column                    Non-Null Count   Dtype
---  ------                    --------------   -----
 0   cdc_case_earliest_dt      901599 non-null  datetime64[ns]
 1   current_status            901599 non-null  object
 2   sex                       901599 non-null  object
 3   age_group                 901599 non-null  object
 4   race_ethnicity_combined  901599 non-null  object
 5   hosp_yn                   901599 non-null  object
 6   icu_yn                    901599 non-null  object
 7   death_yn                  901599 non-null  object
 8   medcond_yn                901599 non-null  object
dtypes: datetime64[ns](1), object(8)
memory usage: 68.8+ MB
```

[227]:
```
print(df.age_group.unique())
df.age_group.mode()
```

```
['0 - 9 Years' '10 - 19 Years' '20 - 29 Years' '30 - 39 Years'
 '40 - 49 Years' '50 - 59 Years' '60 - 69 Years' '70 - 79 Years'
 '80+ Years' 'Missing']
```

[227]:
```
0    20 - 29 Years
dtype: object
```

[228]:
```
# I want to map age gaps into chunks of their median value.
# mode shows 20-29 Years is the most frequent one, I will fill missing values
# with 20-29 years.

mapping={
        '0 - 9 Years': 5,
        '10 - 19 Years': 15,
        '20 - 29 Years': 25,
        '30 - 39 Years': 35,
        '40 - 49 Years': 45,
        '50 - 59 Years': 55,
        '60 - 69 Years': 65,
        '70 - 79 Years': 75,
        '80+ Years': 85,
        'Missing': 25
        }

df['age_chunks'] = df['age_group'].map(mapping)
df.head()
```

[228]:
```
  cdc_case_earliest_dt             current_status  ... medcond_yn age_chunks
0           2020-11-14              Probable Case  ...         No          5
1           2020-07-15  Laboratory-confirmed case  ...         No          5
2           2020-06-23              Probable Case  ...         No          5
3           2020-05-09              Probable Case  ...         No          5
4           2020-10-20              Probable Case  ...         No          5

[5 rows x 10 columns]
```

[229]:
```
# I also want to remove ethnicity and just use race
print(df.race_ethnicity_combined.unique())

df.race_ethnicity_combined.mode()
```

```
['American Indian/Alaska Native, Non-Hispanic' 'Unknown' 'Hispanic/Latino'
 'Black, Non-Hispanic' 'Asian, Non-Hispanic' 'Missing'
 'Multiple/Other, Non-Hispanic'
 'Native Hawaiian/Other Pacific Islander, Non-Hispanic'
 'White, Non-Hispanic']
```

[229]:
```
0    White, Non-Hispanic
dtype: object
```

[230]:
```
mapping={
        'American Indian/Alaska Native, Non-Hispanic': 'Native Indian',
         'Hispanic/Latino': 'Latino',
        'Black, Non-Hispanic':'Black',
        'Asian, Non-Hispanic': 'Asian',
        'Multiple/Other, Non-Hispanic': 'Mixed',
        'Native Hawaiian/Other Pacific Islander, Non-Hispanic': 'Native␣
 ↪Islander',
        'White, Non-Hispanic': 'White',
        'Missing': 'White',
        'Unknown': 'White'
        }

df['race'] = df['race_ethnicity_combined'].map(mapping)
df.head()
```

[231]:
```
print(df.hosp_yn.unique())

mapping={'Unknown': 0,
         'Missing': 0,
         'No': 0,
         'Yes': 1
        }
df['hosp_yn_encoded'] = df['hosp_yn'].map(mapping)
```

```
['Unknown' 'No' 'Missing' 'Yes']
```

[232]:
```
# Encoding

encoder=LabelEncoder()

df['current_status_encoded']=encoder.fit_transform(df['current_status'])
df['icu_yn_encoded']=encoder.fit_transform(df['icu_yn'])
df['medcond_yn_encoded']=encoder.fit_transform(df['medcond_yn'])
df['death_encoded']=encoder.fit_transform(df['death_yn'])
df['sex_encoded']=encoder.fit_transform(df['sex'])
df['race_encoded']=encoder.fit_transform(df['race'])
```

5 Data Analysis

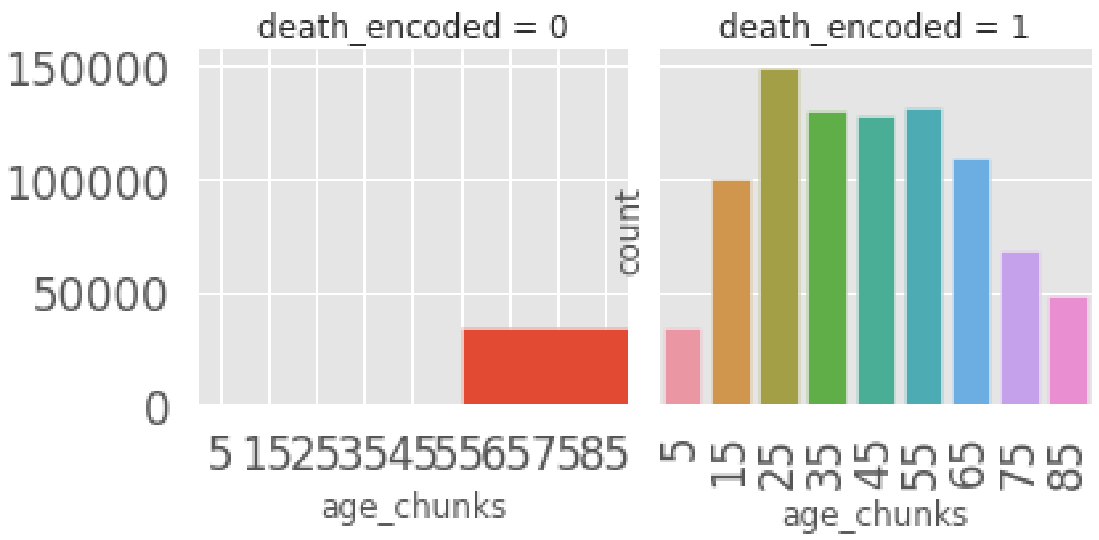
When COVID-19 is mentioned, everyone thinks the death rate and risks. So, at the first step of the analysis, I will consider death risks and risky groups.

According to age chunks - death chart, even though there are more patients between 5 and 55 years old, the death rate is visible and uncomfortable after age 55.

[233]:
```
## Let's analyze the data
plt.figure(figsize=(7, 9))
plt.style.use("ggplot")

g = sns.FacetGrid(df, col='death_encoded')
g.map(plt.hist, 'age_chunks', bins=20)
plt.xticks(rotation=90)
sns.countplot('age_chunks',data=df)
```

[233]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x7f8e5de3d650>
```

```
<Figure size 504x648 with 0 Axes>
```

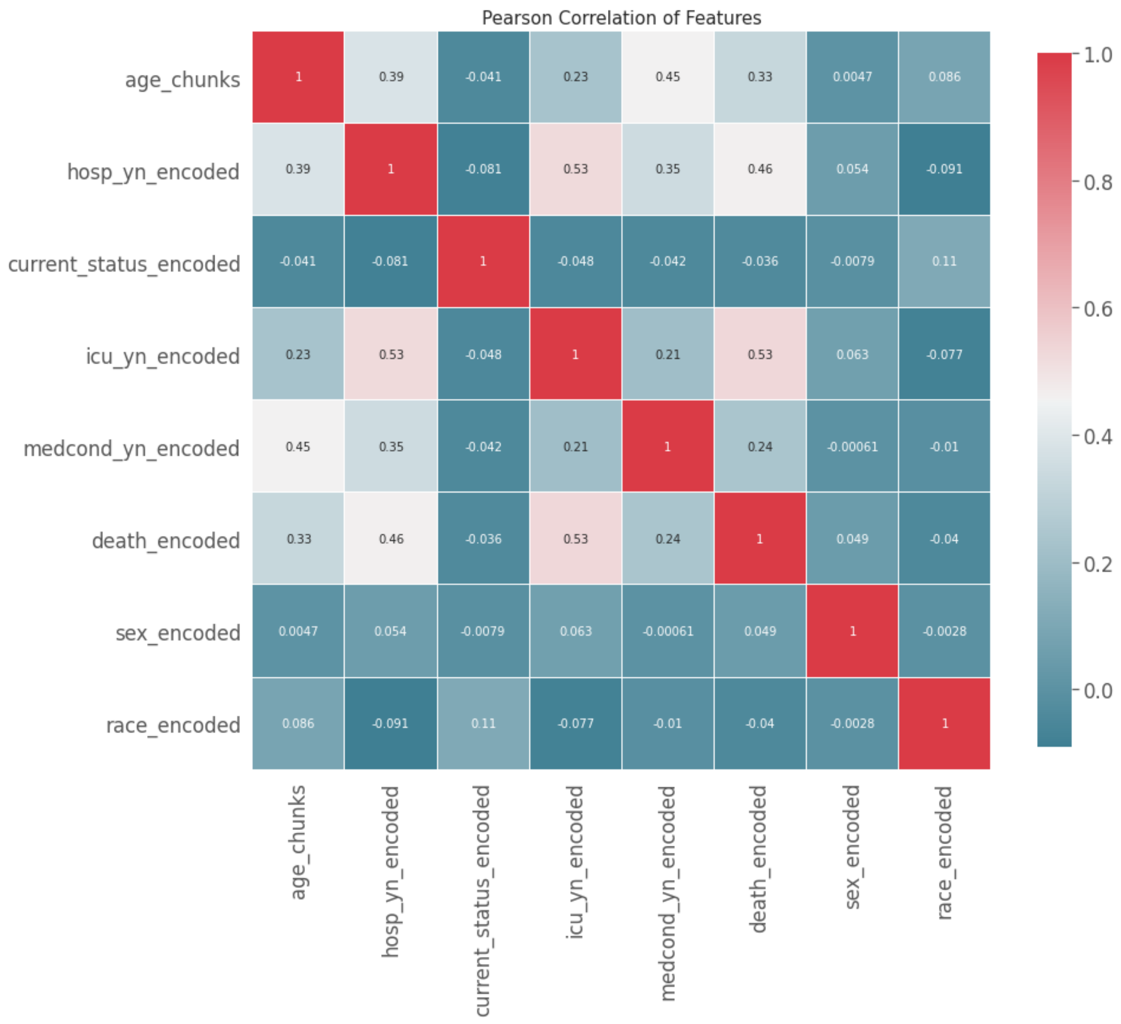


5.1 Correlation Heatmap

Using Seaborn's heatmap facility, we can see the relationship between hospitalized - intensive care - age and death. Also, having medical condition also has high relationship with age pair and moderate effect on hospitalization and death.

When we think about the COVID-19's nature and process, it is only normal to have these kind of relationship.

[234]:
```python
def correlation_heatmap(df):
    _ , ax = plt.subplots(figsize =(14, 12))
    colormap = sns.diverging_palette(220, 10, as_cmap = True)

    _ = sns.heatmap(
        df.corr(),
        cmap = colormap,
        square=True,
        cbar_kws={'shrink':.9 },
        ax=ax,
        annot=True,
        linewidths=0.1,vmax=1.0, linecolor='white',
    )

    plt.title('Pearson Correlation of Features', y=1.05, size=15)

correlation_heatmap(df)
```



5.1.1 Insights of Hospitalization and Intensive Care Unit Relationship:

As you can see, many of patients were not hospitalized and therefore not put under intensive care. We can analyze the ICU and age relationship in our training as well. Because I believe everyone is doing the same analysis for the death. But it is major thing to do, so I will also do it.

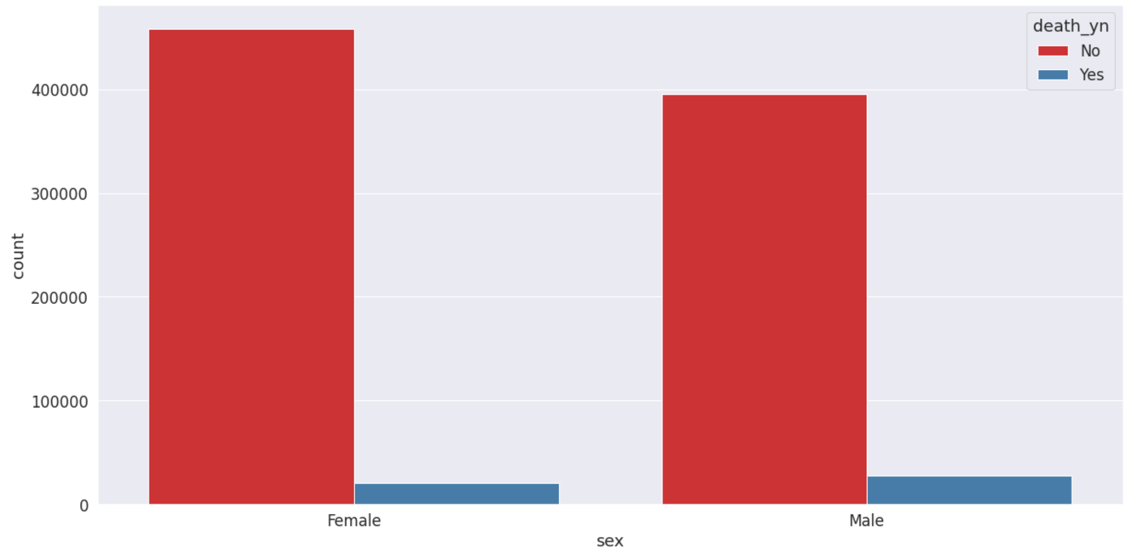
[235]:
```
crosstable=pd.crosstab(df['hosp_yn_encoded'],df['icu_yn_encoded'])
crosstable
```

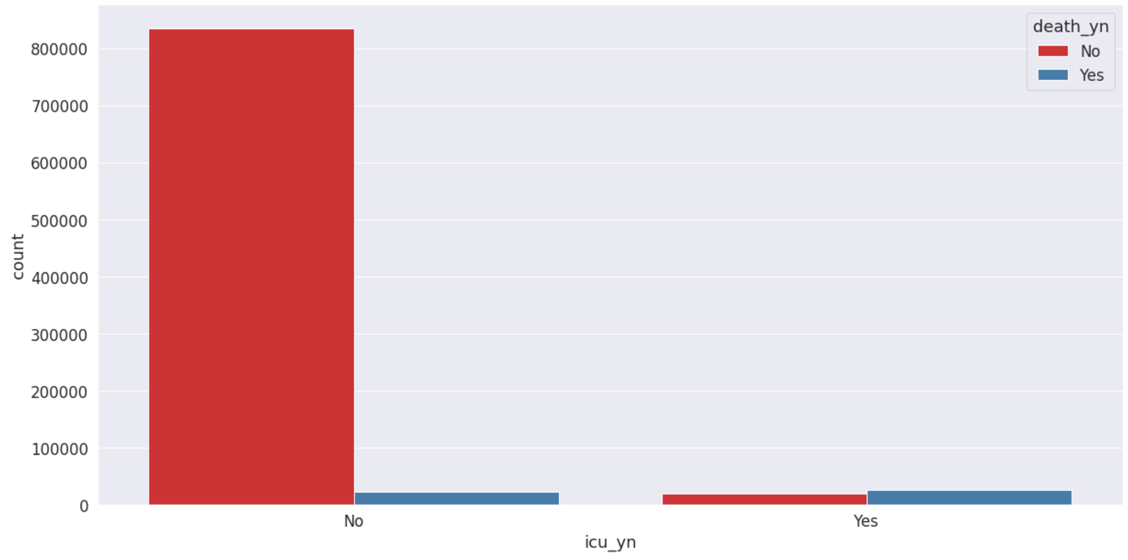
[235]:
```
icu_yn_encoded        0      1
hosp_yn_encoded
0                761184    707
1                 95229  44479
```

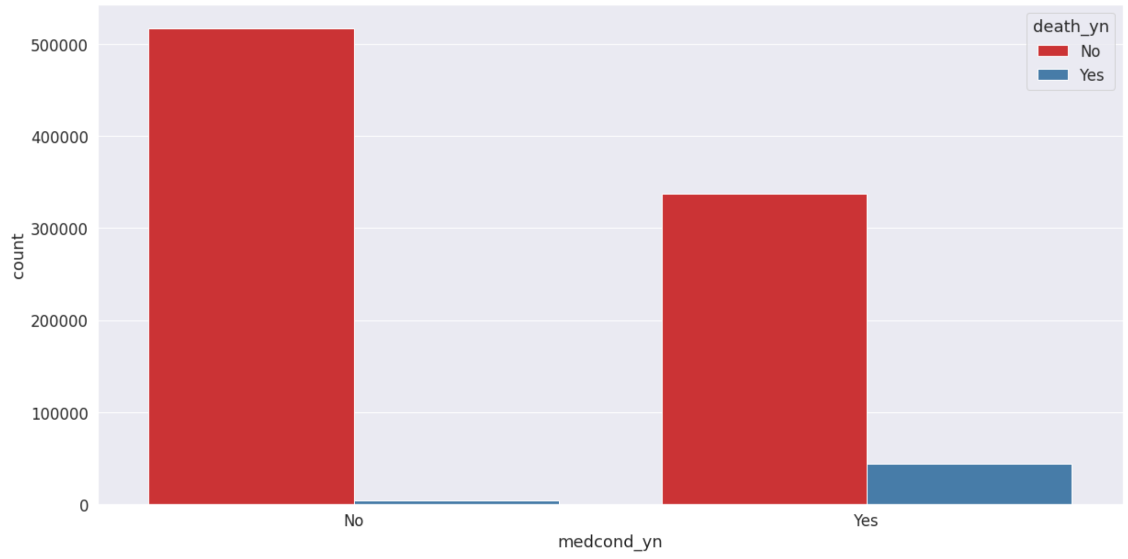
5.2 Data Analysis Graphs for Death Relationships

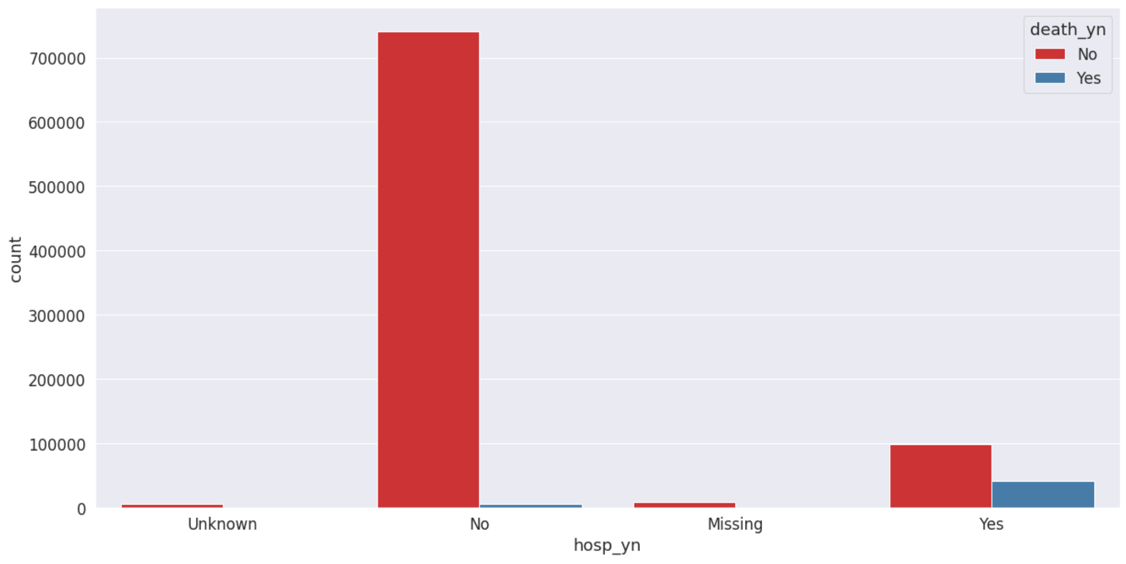
```
[236]: # Reference: https://www.kaggle.com/accountstatus/covid-data-analysis
df['month']=pd.DatetimeIndex(df['cdc_case_earliest_dt']).month
df['year']=pd.DatetimeIndex(df['cdc_case_earliest_dt']).year
df.head()

# Reference: https://www.kaggle.com/artyomkolas/
 ↪covid-19-case-surveillance-public-use-dataset

target_column = ['death_yn']
columns_to_use = ['age_chunks', 'current_status',␣
 ↪'hosp_yn','icu_yn','medcond_yn','sex', 'race']
predictors = list(set(columns_to_use)-set(target_column))

plt.figure(figsize=(9, 7))
plt.style.use("ggplot")

sns.set(font_scale=1.5)

for el in predictors:
    plt.figure(figsize=(20, 10))
    plot_data = df[['death_yn', el]]
    try:
        sns.countplot(x=el, hue='death_yn', data=plot_data, palette='Set1')
    except:
        pass
```

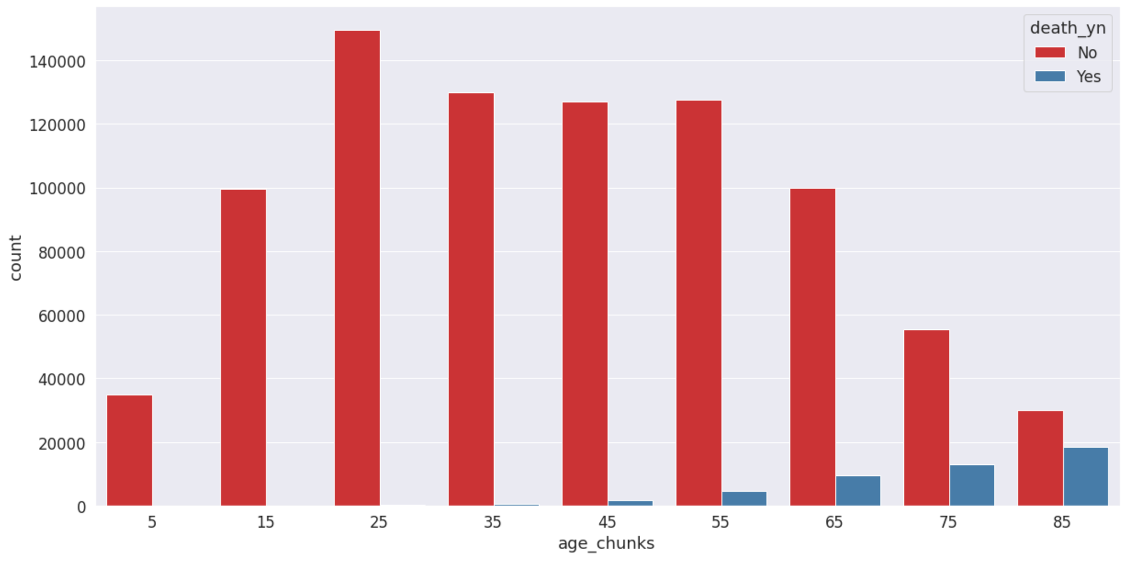
```
<Figure size 648x504 with 0 Axes>
```

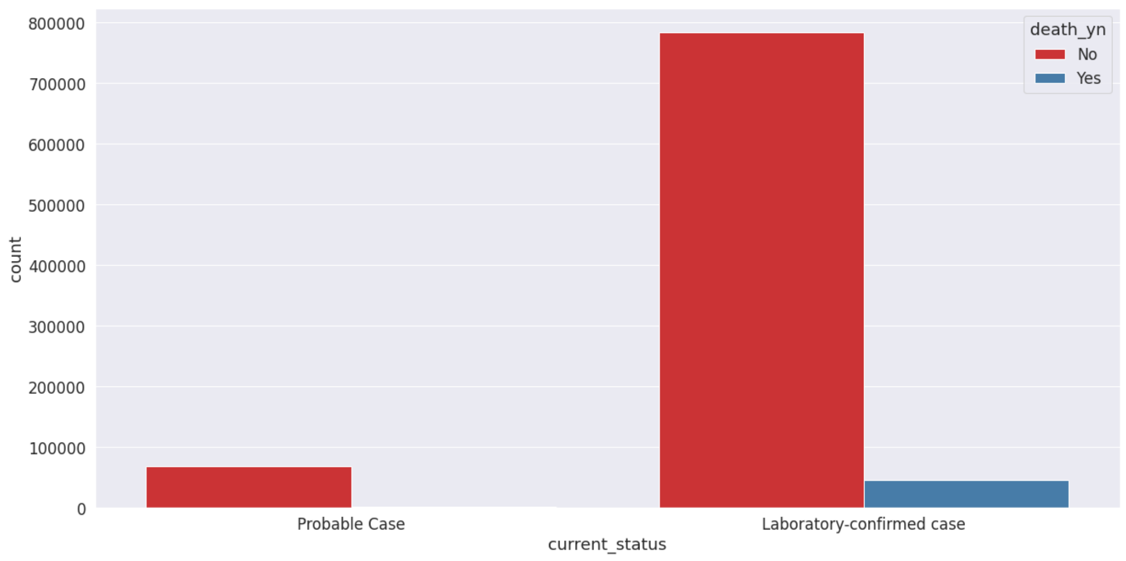


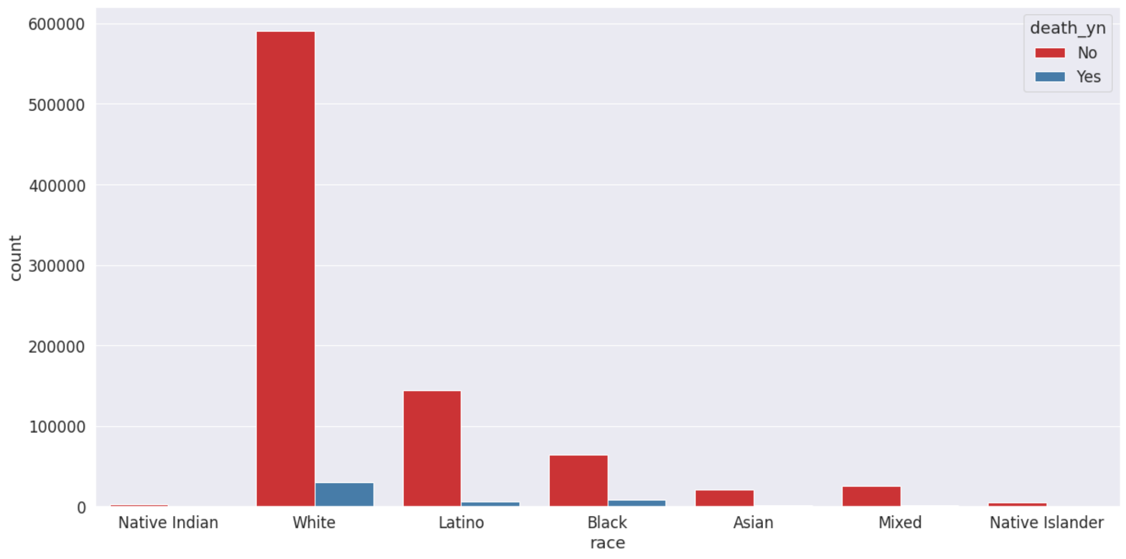

death_yn
No
Yes
count
800000
700000
600000
500000
400000
300000
200000
100000
0
No
Yes
icu_yn


death_yn
No
Yes
count
500000
400000
300000
200000
100000
0
No
Yes
medcond_yn


death_yn
No
Yes
count
700000
600000
500000
400000
300000
200000
100000
0
Unknown
No
Missing
Yes
hosp_yn


death_yn
No
Yes
count
140000
120000
100000
80000
60000
40000
20000
0
5
15
25
35
45
55
65
75
85
age_chunks



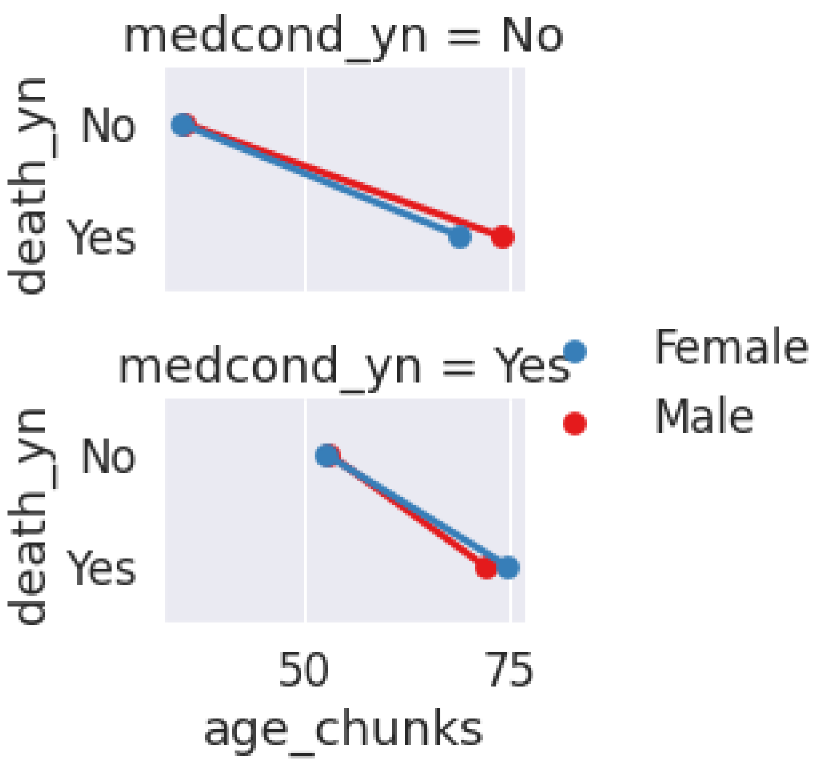


[237]:
```python
grid = sns.FacetGrid(df, row='medcond_yn', height=2.2, aspect=1.6)
grid.map(sns.pointplot, 'age_chunks', 'death_yn', 'sex', palette='Set1')
grid.add_legend()
```

```
/usr/local/lib/python3.7/dist-packages/seaborn/axisgrid.py:643: UserWarning:

Using the pointplot function without specifying `order` is likely to produce an
incorrect plot.

/usr/local/lib/python3.7/dist-packages/seaborn/axisgrid.py:648: UserWarning:
```

```
Using the pointplot function without specifying `hue_order` is likely to produce
an incorrect plot.
```

[237]:
```
<seaborn.axisgrid.FacetGrid at 0x7f8e620e0810>
```



[238]:
```
crosstable=pd.crosstab(df['age_chunks'],df['death_yn'])
crosstable
```

[238]:
```
death_yn        No    Yes
age_chunks
5            34797     28
15           99515     44
25          149440    225
35          129881    628
45          126999   1663
55          127618   4523
65           99836   9427
75           55398  12920
85           30169  18488
```

5.3 Interesting Graph On Month-Death Relationship:

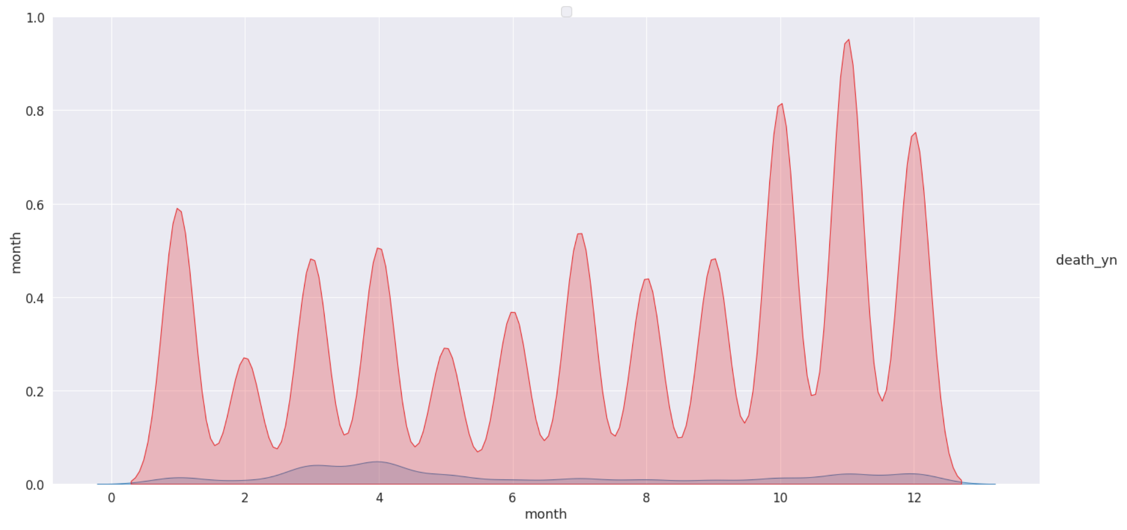
Even though patient count was higher than the earlier times of the year, as the time goes death rate was diminished. This might be due to vaccination, or the medical progress as we understand the nature of the illness and medications by the time goes. Interesting.

[239]:
```
# Reference: https://www.kaggle.com/artyomkolas/
↪covid-19-case-surveillance-public-use-dataset

plt.figure(figsize=(20, 10))
plot_data = df[['death_yn', 'month']]

g = sns.pairplot(plot_data, hue='death_yn', palette='Set1', height=10, aspect=2)

handles = g._legend_data.values()
labels = g._legend_data.keys()
g.fig.legend(handles=handles, labels=labels, loc='upper center', ncol=1)
```

```
No handles with labels found to put in legend.
```

[239]:
```
<matplotlib.legend.Legend at 0x7f8e65350c50>
```

```
<Figure size 1440x720 with 0 Axes>
```

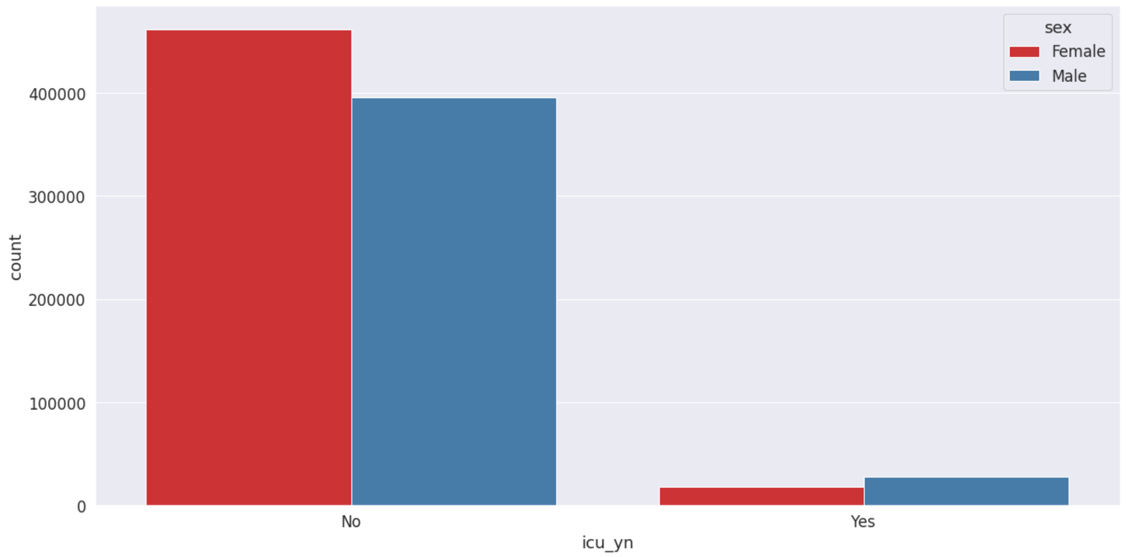


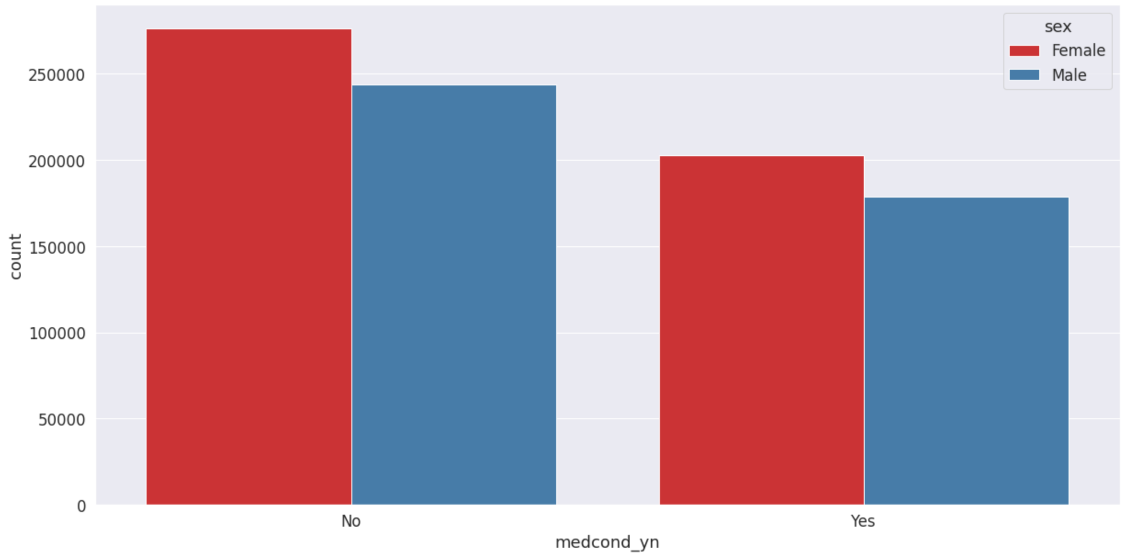
5.4 Interesting Analysis on Sex:

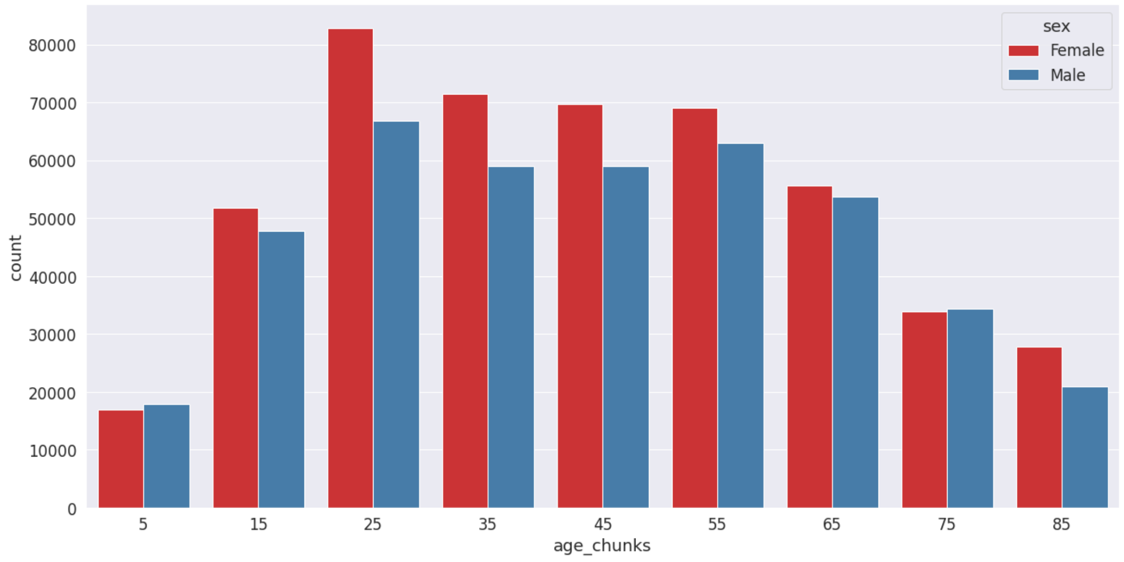
Even though there are more female patients and where the medical condition rate is almost the same, males are more likely to be hospitalized, put under intensive care unit or die.

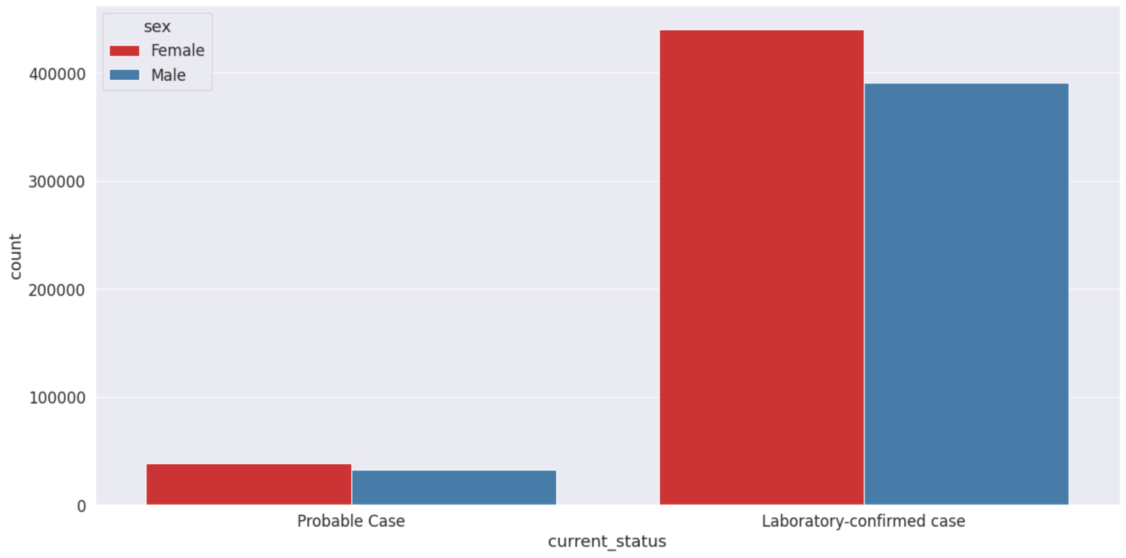
```
[272]: target_column = ['sex']
       columns_to_use = ['age_chunks', 'current_status',␣
        ↪'hosp_yn_encoded','icu_yn','medcond_yn','death_yn', 'race']
       predictors = list(set(columns_to_use)-set(target_column))

       plt.figure(figsize=(9, 7))
       plt.style.use("ggplot")

       sns.set(font_scale=1.5)

       for el in predictors:
           plt.figure(figsize=(20, 10))
           plot_data = df[['sex', el]]
           try:
               sns.countplot(x=el, hue='sex', data=plot_data, palette='Set1')
           except:
               pass
```

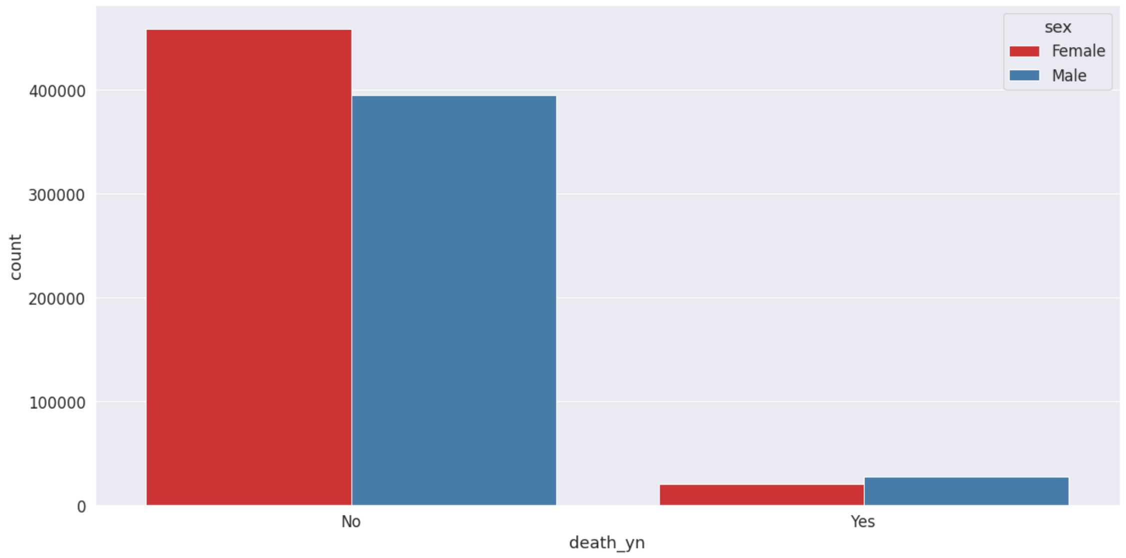
```
<Figure size 648x504 with 0 Axes>
```

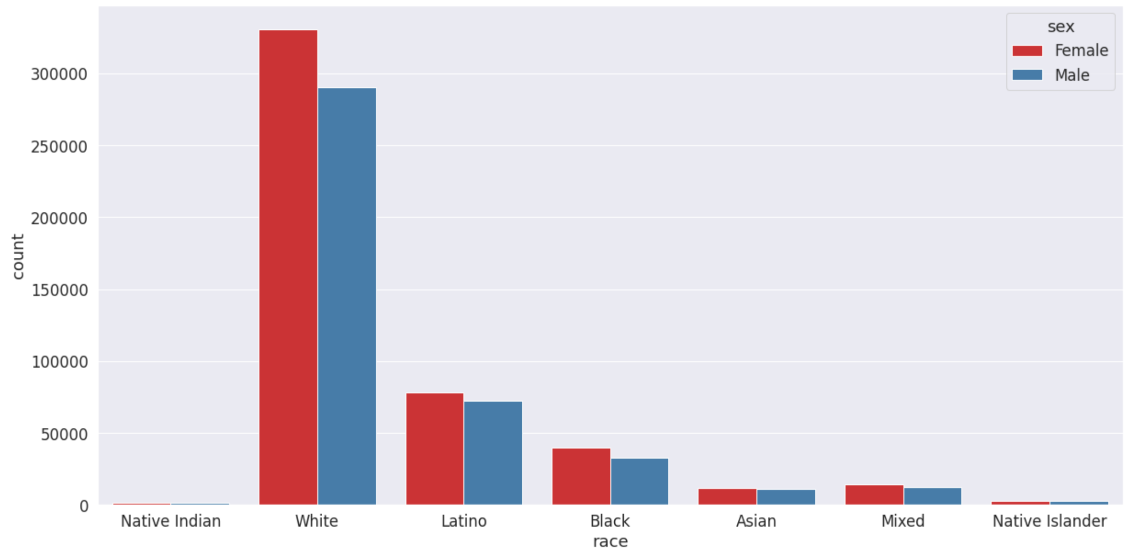


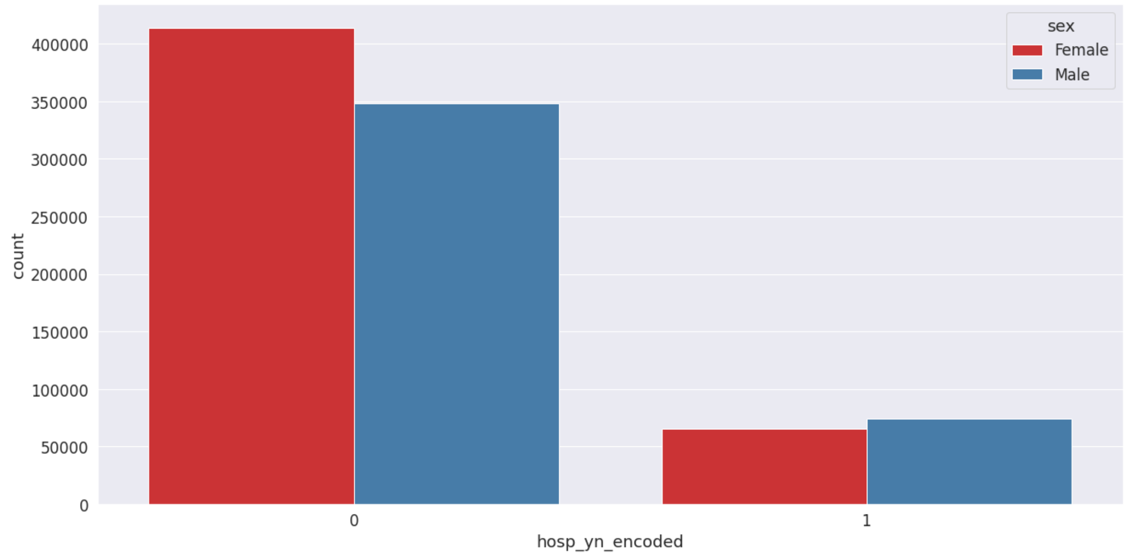

sex
Female
Male
count
250000
200000
150000
100000
50000
0
No
Yes
medcond_yn


sex
Female
Male
count
80000
70000
60000
50000
40000
30000
20000
10000
0
5
15
25
35
45
55
65
75
85
age_chunks


sex
Female
Male
count
0
100000
200000
300000
400000
Probable Case
Laboratory-confirmed case
current_status


sex
Female
Male
count
0
100000
200000
300000
400000
No
Yes
death_yn





[240]:
```
df.info()

columns_for_x = ['month','year','age_chunks','race_encoded', 'sex_encoded',
                  'current_status_encoded', 'hosp_yn_encoded','icu_yn_encoded',␣
 ↪'medcond_yn_encoded']
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 901599 entries, 0 to 901598
Data columns (total 20 columns):
 #   Column                   Non-Null Count   Dtype
```

```
---  ------                    --------------   -----
 0   cdc_case_earliest_dt      901599 non-null  datetime64[ns]
 1   current_status            901599 non-null  object
 2   sex                       901599 non-null  object
 3   age_group                 901599 non-null  object
 4   race_ethnicity_combined   901599 non-null  object
 5   hosp_yn                   901599 non-null  object
 6   icu_yn                    901599 non-null  object
 7   death_yn                  901599 non-null  object
 8   medcond_yn                901599 non-null  object
 9   age_chunks                901599 non-null  int64
 10  race                      901599 non-null  object
 11  hosp_yn_encoded           901599 non-null  int64
 12  current_status_encoded    901599 non-null  int64
 13  icu_yn_encoded            901599 non-null  int64
 14  medcond_yn_encoded        901599 non-null  int64
 15  death_encoded             901599 non-null  int64
 16  sex_encoded               901599 non-null  int64
 17  race_encoded              901599 non-null  int64
 18  month                     901599 non-null  int64
 19  year                      901599 non-null  int64
dtypes: datetime64[ns](1), int64(10), object(9)
memory usage: 184.5+ MB
```

6 Model Training

First I needed to sample the data by 0.3 because it is so big and takes time. Since our time is limited, I wanted to be faster. If you want to check out with the full data, just make df_sample = df change and nothing to do more.

Actually before training, we might have use uint coded datatype to get smaller data type to evaluate. I also standardized the values in anycase, but the data is somewhat standart enough.

After that, I chosed encoded columns and date for features and death as the target value and splitted the dataset using train test split method by 0.25 - 0.75.

[241]:
```python
df_sample = df.sample(frac=0.30)

X = df_sample[columns_for_x]
y = df_sample['death_encoded']
```

[242]:
```python
# Standardizing
from sklearn.preprocessing import StandardScaler

scaler=StandardScaler()
X=scaler.fit_transform(X)
```

```
[243]: X_train,X_test,y_train,y_test = train_test_split(X,y,test_size=0.
        ↪25,random_state=0)
```

6.1 Decision Tree:

As it was suggested, my first model to train was Decision Tree. The accuracy rate was so high so I tried to run the confusion matrix to check out the overfitting and true/false negatives/positives.

Actually it seems like not overfitting by the numbers, but when we see the decision tree, we can easily say that it is way too overfit to data. Please see Google Colab for bigger graph. Let's move on some other choices.

```
[244]: decision_tree = DecisionTreeClassifier()
       clf = decision_tree.fit(X_train, y_train)
       y_pred = decision_tree.predict(X_test)
       acc_decision_tree = round(decision_tree.score(X_train, y_train) * 100, 2)
       acc_decision_tree
```

```
[244]: 96.4
```

```
[245]: from sklearn.metrics import confusion_matrix

       pd.DataFrame(
           confusion_matrix(y_test, y_pred),
           columns=['Predicted Not Dead', 'Predicted Dead'],
           index=['True Not Dead', 'True Dead']
       )
```

```
[245]:                Predicted Not Dead  Predicted Dead
       True Not Dead               63046             903
       True Dead                    1890            1781
```

```
[246]: from sklearn.tree import export_graphviz
       from sklearn.externals.six import StringIO
       from IPython.display import Image
       import pydotplus

       dot_data = StringIO()
       export_graphviz(clf, out_file=dot_data,
                       filled=True, rounded=True,
                       special_characters=True,feature_names =␣
        ↪columns_for_x,class_names=['0','1'])
       graph = pydotplus.graph_from_dot_data(dot_data.getvalue())
       graph.write_png('diabetes.png')
       Image(graph.create_png())
```

```
dot: graph is too large for cairo-renderer bitmaps. Scaling by 0.134779 to fit
```

```
dot: graph is too large for cairo-renderer bitmaps. Scaling by 0.134779 to fit
```

6.2 XGBoost:

Since XGBoost is pretty popular and high performanced classifier, I wanted to use it as second model and also for the validation purposes, added kFold cross validation into the training.

The results were also good and was faster than decision tree.

[247]:
```
from sklearn.model_selection import KFold, train_test_split, cross_val_predict,␣
 ↪cross_val_score
import xgboost

# CV model
model = xgboost.XGBClassifier()
kfold = KFold(n_splits=10)
results = cross_val_score(model, X, y, cv=kfold)
print("Accuracy: %.2f%% (%.2f%%)" % (results.mean()*100, results.std()*100))
```

```
Accuracy: 96.05% (0.09%)
```

[248]:
```
clf = model.fit(X_train, y_train)
y_pred = model.predict(X_test)
pd.DataFrame(
    confusion_matrix(y_test, y_pred),
    columns=['Predicted Not Dead', 'Predicted Dead'],
    index=['True Not Dead', 'True Dead']
)
```

[248]:
```
               Predicted Not Dead  Predicted Dead
True Not Dead               63040             909
True Dead                    1783            1888
```

6.3 Ada Boost:

Standart deviation is just 0.01 higher than XGBoost:

[249]:
```
model = ensemble.AdaBoostClassifier()
kfold = KFold(n_splits=10)
results = cross_val_score(model, X, y, cv=kfold)
print("Accuracy: %.2f%% (%.2f%%)" % (results.mean()*100, results.std()*100))
```

```
Accuracy: 95.91% (0.10%)
```

[250]:
```
clf = model.fit(X_train, y_train)
y_pred = model.predict(X_test)
pd.DataFrame(
    confusion_matrix(y_test, y_pred),
    columns=['Predicted Not Dead', 'Predicted Dead'],
    index=['True Not Dead', 'True Dead']
)
```

[250]:
```
               Predicted Not Dead  Predicted Dead
True Not Dead               63123             826
True Dead                    1952            1719
```

6.4 Logistic Regression:

Did not really think that accuracy would be that high because it does not really suitable for the problem in my opinion. Interesting.

[251]:
```
model = LogisticRegression()
kfold = KFold(n_splits=10)
results = cross_val_score(model, X, y, cv=kfold)
print("Accuracy: %.2f%% (%.2f%%)" % (results.mean()*100, results.std()*100))
```

```
Accuracy: 95.91% (0.11%)
```

[252]:
```
clf = model.fit(X_train, y_train)
y_pred = model.predict(X_test)
pd.DataFrame(
    confusion_matrix(y_test, y_pred),
    columns=['Predicted Not Dead', 'Predicted Dead'],
    index=['True Not Dead', 'True Dead']
)
```

[252]:
```
               Predicted Not Dead  Predicted Dead
True Not Dead               63158             791
True Dead                    1995            1676
```

[253]:
```
## All the Machine Learning Algorithms in a Chunk:

# Reference: https://www.programmersought.com/article/61551504484/

MLA = [
    #Ensemble Methods
    ensemble.AdaBoostClassifier(),
    ensemble.BaggingClassifier(),
    ensemble.ExtraTreesClassifier(),
    ensemble.GradientBoostingClassifier(),
    ensemble.RandomForestClassifier(),

    #Gaussian Processes
    gaussian_process.GaussianProcessClassifier(),
    #GLM
    linear_model.LogisticRegressionCV(),
    linear_model.PassiveAggressiveClassifier(),
    linear_model.RidgeClassifierCV(),
    linear_model.SGDClassifier(),
    linear_model.Perceptron(),

    #Navies Bayes
    naive_bayes.BernoulliNB(),
    naive_bayes.GaussianNB(),

    #Nearest Neighbor
    neighbors.KNeighborsClassifier(),

    #SVM
    svm.SVC(probability=True),
    svm.NuSVC(probability=True),
    svm.LinearSVC(),

    #Trees
    tree.DecisionTreeClassifier(),
    tree.ExtraTreeClassifier(),

    #Discriminant Analysis
    discriminant_analysis.LinearDiscriminantAnalysis(),
    discriminant_analysis.QuadraticDiscriminantAnalysis(),


    #xgboost: http://xgboost.readthedocs.io/en/latest/model.html
    XGBClassifier()
    ]
```

I just added these for the future usage, we can check these in our free time. Now I want to analyze other kind of target values for more interesting results.

---

7 Intensive Care Unit Prediction

In this section, I will be just adjusting a little bit and checkout the results. I will not use death column because the intensive care unit happens before death. So, we want to learn whether people are under risk before death happens.

So, the accuracy is slightly less than death prediction.

```
[254]: columns_for_x = ['month','year','age_chunks','race_encoded', 'sex_encoded',
                        'current_status_encoded', 'hosp_yn_encoded',␣
         ↪'medcond_yn_encoded']
       X = df_sample[columns_for_x]
       y = df_sample['icu_yn_encoded']
       X_train,X_test,y_train,y_test = train_test_split(X,y,test_size=0.
         ↪25,random_state=0)
```

```
[255]: # CV model
       model = xgboost.XGBClassifier()
       kfold = KFold(n_splits=10)
       results = cross_val_score(model, X, y, cv=kfold)
       print("Accuracy: %.2f%% (%.2f%%)" % (results.mean()*100, results.std()*100))
```

```
Accuracy: 95.04% (0.14%)
```

```
[256]: clf = model.fit(X_train, y_train)
       y_pred = model.predict(X_test)
       pd.DataFrame(
           confusion_matrix(y_test, y_pred),
           columns=['Predicted Not ICUd', 'Predicted ICUd'],
           index=['True Not ICUd', 'True ICUd']
       )
```

```
[256]:               Predicted Not ICUd  Predicted ICUd
        True Not ICUd               64039             162
        True ICUd                    3219             200
```

7.1 The Impact of Variables:

XGBoost have many false-negatives on ICUd: 3111 ICUd patients, only 230 of them was marked. Logistic was even worse. Not preferable. And decision tree gave the same result with logistic. Let's try the ICU analysis on KNIME!

```
[257]: columns_for_x = ['age_chunks','race_encoded', 'sex_encoded',
                        'hosp_yn_encoded', 'medcond_yn_encoded']
       X = df_sample[columns_for_x]
       y = df_sample['icu_yn_encoded']
       X_train,X_test,y_train,y_test = train_test_split(X,y,test_size=0.
         ↪25,random_state=0)
```

```
[258]: # CV model
       model = xgboost.XGBClassifier()
       kfold = KFold(n_splits=10)
       results = cross_val_score(model, X, y, cv=kfold)
       print("Accuracy: %.2f%% (%.2f%%)" % (results.mean()*100, results.std()*100))
```

```
Accuracy: 95.01% (0.13%)
```

[259]:
```
clf = model.fit(X_train, y_train)
y_pred = model.predict(X_test)
pd.DataFrame(
    confusion_matrix(y_test, y_pred),
    columns=['Predicted Not ICUd', 'Predicted ICUd'],
    index=['True Not ICUd', 'True ICUd']
)
```

[259]:
```
               Predicted Not ICUd  Predicted ICUd
True Not ICUd               64039             162
True ICUd                    3225             194
```

[260]:
```
model = LogisticRegression()
kfold = KFold(n_splits=10)
results = cross_val_score(model, X, y, cv=kfold)
print("Accuracy: %.2f%% (%.2f%%)" % (results.mean()*100, results.std()*100))
```

```
Accuracy: 94.96% (0.14%)
```

[261]:
```
clf = model.fit(X_train, y_train)
y_pred = model.predict(X_test)
pd.DataFrame(
    confusion_matrix(y_test, y_pred),
    columns=['Predicted Not ICUd', 'Predicted ICUd'],
    index=['True Not ICUd', 'True ICUd']
)
```

[261]:
```
               Predicted Not ICUd  Predicted ICUd
True Not ICUd               64118              83
True ICUd                    3342              77
```

[261]:
```
decision_tree = DecisionTreeClassifier()
clf = decision_tree.fit(X_train, y_train)
y_pred = decision_tree.predict(X_test)
acc_decision_tree = round(decision_tree.score(X_train, y_train) * 100, 2)
```

[262]:
```
acc_decision_tree
```

[262]:
```
96.4
```

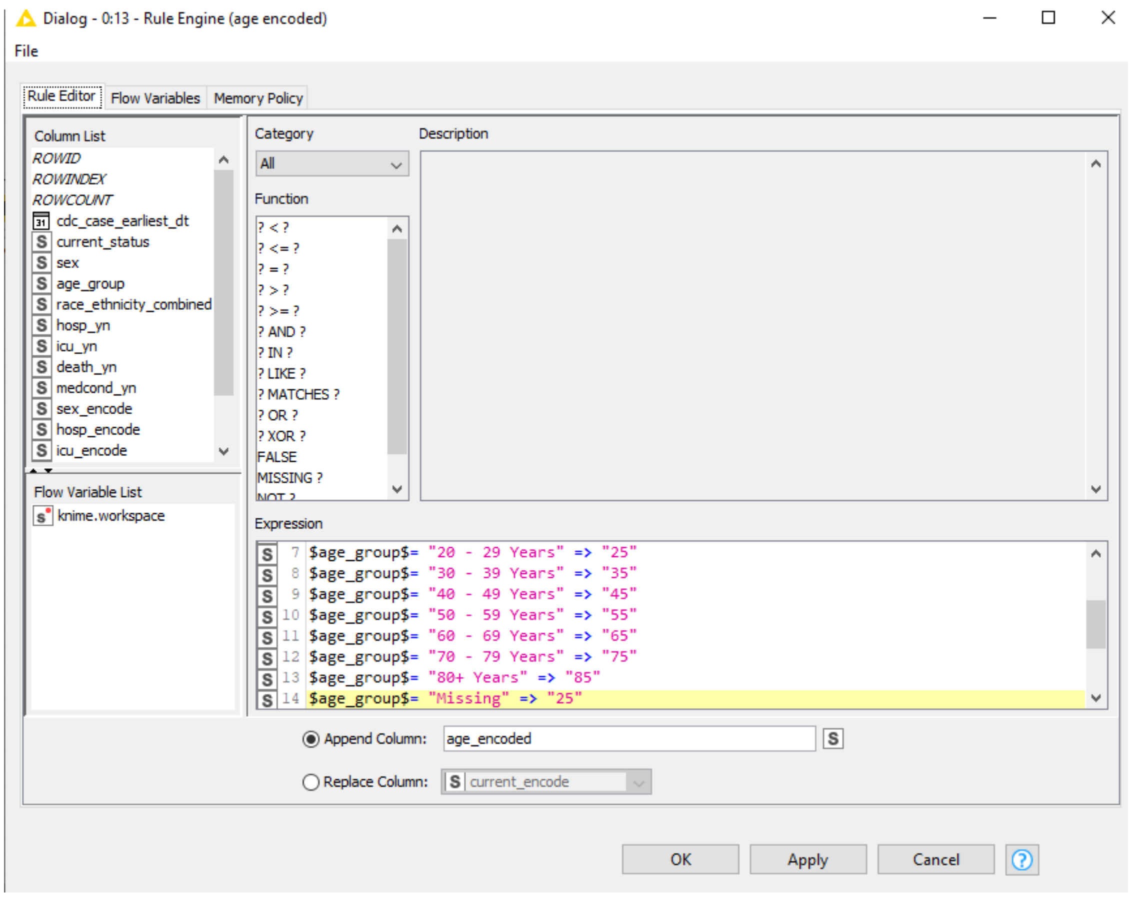
[263]:
```
pd.DataFrame(
    confusion_matrix(y_test, y_pred),
    columns=['Predicted Not ICUd', 'Predicted ICUd'],
    index=['True Not ICUd', 'True ICUd']
)
```

```
[263]:                 Predicted Not ICUd  Predicted ICUd
       True Not ICUd                64118              83
       True ICUd                     3342              77
```

```
[269]:
```

8 KNIME PART

I had recreated the string manipulation and filtering process on KNIME, actually it was faster than I imagined. I think KNIME was better for data preprocessing.

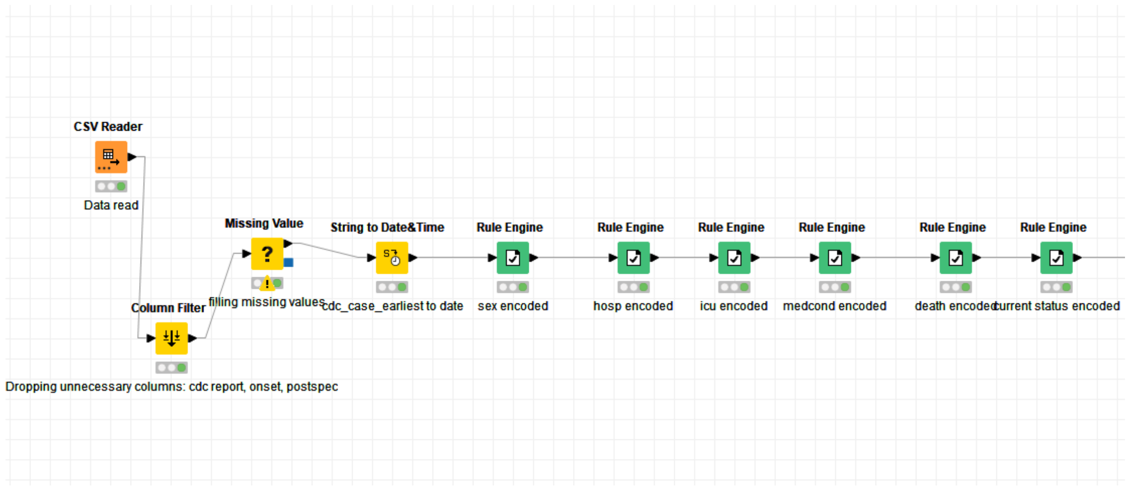


```
$age_group$= "20 - 29 Years" => "25"
$age_group$= "30 - 39 Years" => "35"
$age_group$= "40 - 49 Years" => "45"
$age_group$= "50 - 59 Years" => "55"
$age_group$= "60 - 69 Years" => "65"
$age_group$= "70 - 79 Years" => "75"
$age_group$= "80+ Years" => "85"
$age_group$= "Missing" => "25"
```

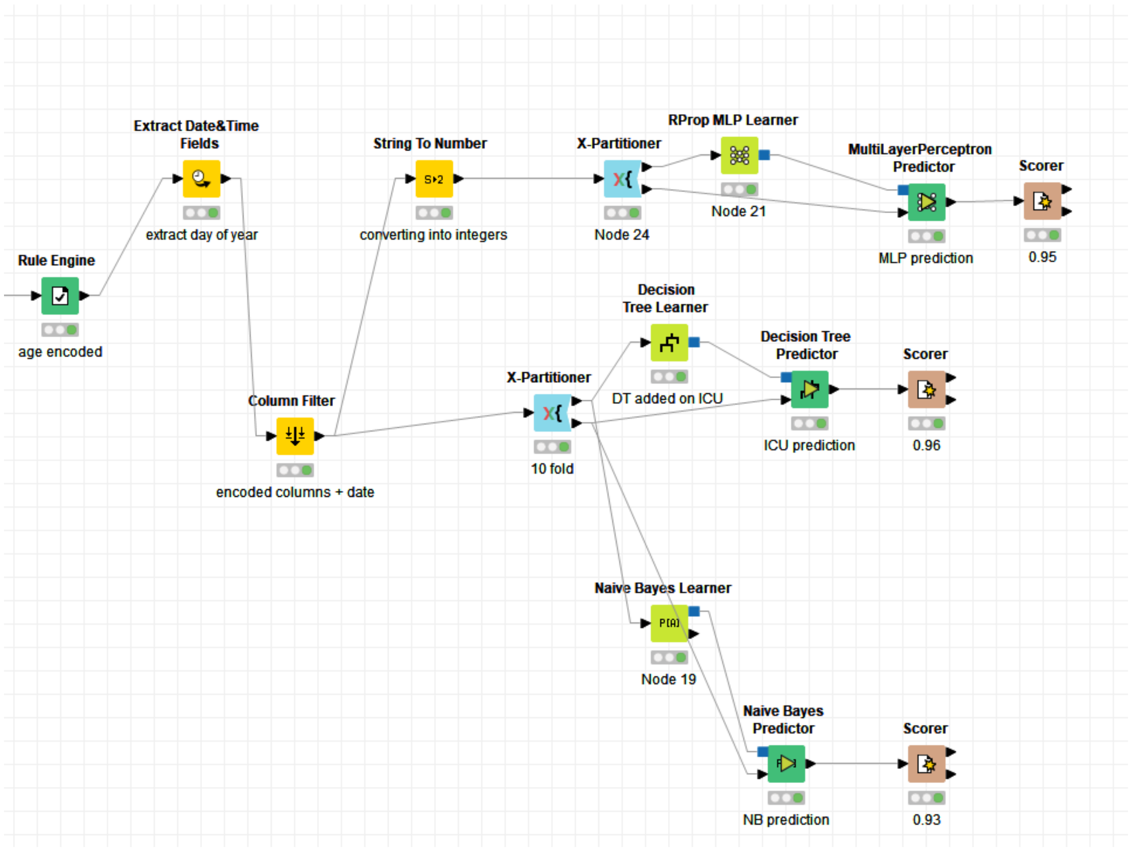
[✓ Append Column:] age_encoded

Replace Column: current_encode

Here is the schema of the workflow:



Part 2:


Extract Date&Time Fields
String To Number
X-Partitioner
RProp MLP Learner
MultiLayerPerceptron Predictor
Scorer
extract day of year
converting into integers
Node 24
Node 21
MLP prediction
0.95
Rule Engine
age encoded
Decision Tree Learner
Decision Tree Predictor
Scorer
X-Partitioner
DT added on ICU
Column Filter
ICU prediction
0.96
10 fold
encoded columns + date
Naive Bayes Learner
Node 19
Naive Bayes Predictor
Scorer
NB prediction
0.93

9 Conclusions:

In KNIME, it is easy to use tools to manipulate or encode data. So it is a suitable tool for data preprocessing. However, the visualization and ML Kits are more preferable in Python.

As the expected, death risk is getting higher and higher with age. There is positive correlation between death, age, putting under intensive care unit, hospitalization and medical condiiton.

Race has almost no effect. However sex is important, graphs show that males are more likely to have problems with COVID-19, where females are more likely to get better sooner.

Even though the number of cases got increased by the time, the death rate seems to be get lowered. This may be caused by vaccination or learning how to fight with this disease by time passes.

All the models seem to be working quite good, however they are more likely to overfit. Using cross validation methods and then checking the confusion matrices show us the XGBoost had the best results for right classification of the negative samples.

The models were more successful on predicting the death rather than the intensive care unit status.

We can use more and more models if we had time and consider the different relationships of these columns.

```
[ ]:
```

10 Bibliography

* Model Fitting on Titanic Dataset - Link

* CDC COVID-19 Case Surveillance Public Dataset Data Profile - Link

* A Data Science Framework: To Achieve %99 Accuracy - Link

* Machine Learning with Python: Complete Tutorial - Link

* Kaggle: Covid-19 Case Surveillance - Classification - Link

* Kaggle: Covid-19 Case Surveillance + Modelling - Link

* Kaggle: Just A Bunch of Interactive Charts, Nothing New - Link

* Kaggle: Covid19-2020 year - Link