SMU DataArts DS Task

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In [1]:
```
import requests
import json
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from datetime import datetime
```

1. Load Data

Description

COVID testing data provided by Johns Hopkins University to analyze cumulative COVID testing counts in New York state.

Task

- Access the JSON data that lives at this URL API call: https://jhucoronavirus.azureedge.net/api/v1/testing/daily.json (https://jhucoronavirus.azureedge.net/api/v1/testing/daily.json)
- Format the data into a dataframe (Python/R) to manipulate it for the following steps.

In [2]:
```
# Call the COVID testing data API filtered for New York data
response = requests.get('https://jhucoronavirus.azureedge.net/api/v1/testing/daily.json'
)
print(response.status_code) # 200 success
```

```
200
```

In [3]:
```
# Parse json format and convert to pandas dataframe
data = response.text
parse_json = json.loads(data)
df = pd.DataFrame(parse_json)
df.head()
```

Out[3]:

	date	state	people_viral_positive	tests_viral_positive	tests_viral_negative	encounters_viral_total	test
0	20200306	AK	NaN	NaN	NaN	NaN	
1	20200307	AK	NaN	NaN	NaN	NaN	
2	20200308	AK	NaN	NaN	NaN	NaN	
3	20200309	AK	NaN	NaN	NaN	NaN	
4	20200310	AK	NaN	NaN	NaN	NaN	

2. Data Exploration

Gather some basic information about the data that could include things like, number of observations, feature names, data types, memory usage, etc. Whatever you think helps someone understand the data at a high level.

In [4]:
```
df.shape # 36,628 records, 14 features
```

Out[4]:
```
(36628, 14)
```

In [5]:
```
df.columns # column names
```

Out[5]:
```
Index(['date', 'state', 'people_viral_positive', 'tests_viral_positive',
       'tests_viral_negative', 'encounters_viral_total', 'tests_viral_total',
       'people_viral_total', 'tests_combined_total', 'cases_conf_probable',
       'people_antigen_positive', 'people_antigen_total', 'cases_confirmed',
       'cases_probable'],
      dtype='object')
```

Data Quality Check

- The data has several columns that are missing values.
- The data consists of 14 variables - 12 variables have a float data type, 1 variable has an int data type, and 1 variable contains string values
- Memory usage 3.9 MB

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

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 36628 entries, 0 to 36627
Data columns (total 14 columns):
 #   Column                   Non-Null Count  Dtype  
---  ------                   --------------  -----  
 0   date                     36628 non-null  int64  
 1   state                    36628 non-null  object 
 2   people_viral_positive    33176 non-null  float64
 3   tests_viral_positive     17036 non-null  float64
 4   tests_viral_negative     10165 non-null  float64
 5   encounters_viral_total   9188 non-null   float64
 6   tests_viral_total        27846 non-null  float64
 7   people_viral_total       16198 non-null  float64
 8   tests_combined_total     36417 non-null  float64
 9   cases_conf_probable      36321 non-null  float64
 10  people_antigen_positive  1482 non-null   float64
 11  people_antigen_total     2165 non-null   float64
 12  cases_confirmed          13945 non-null  float64
 13  cases_probable           13944 non-null  float64
dtypes: float64(12), int64(1), object(1)
memory usage: 3.9+ MB
```

Categorical Data

One column has categorical state data. The states are abreviated. New York accounts for 654 records in the data.

```
In [7]: cat_cols = df.loc[:,df.dtypes=='object'].columns
        for column in cat_cols:
            print('Unique Values in ', column, df[column].unique())
            print(df[column].value_counts())
```

```
Unique Values in  state ['AK' 'AL' 'AR' 'AS' 'AZ' 'CA' 'CO' 'CT' 'DC' 'DE' 'FL' 'GA' 'G
U' 'HI'
 'IA' 'ID' 'IL' 'IN' 'KS' 'KY' 'LA' 'MA' 'MD' 'ME' 'MI' 'MN' 'MO' 'MP'
 'MS' 'MT' 'NC' 'ND' 'NE' 'NH' 'NJ' 'NM' 'NV' 'NY' 'OH' 'OK' 'OR' 'PA'
 'PR' 'RI' 'SC' 'SD' 'TN' 'TX' 'UT' 'VA' 'VI' 'VT' 'WA' 'WI' 'WV' 'WY']
WA    703
MA    694
VA    689
FL    687
NJ    675
NE    670
IN    658
CT    656
RI    655
WY    655
MI    655
NY    654
WI    653
TX    653
VT    653
PA    653
OR    652
NH    652
HI    652
CA    652
IL    652
GA    652
NC    652
SC    652
AZ    652
CO    652
NM    651
MD    651
DC    651
TN    651
OH    651
NV    651
KY    650
KS    650
AK    650
AR    650
DE    650
MN    650
IA    650
WV    650
MT    649
ME    649
OK    649
ND    649
LA    649
AL    649
MO    649
MS    649
UT    649
SD    649
ID    649
MP    640
PR    640
VI    640
AS    640
```

```
GU    640
Name: state, dtype: int64
```

Missing Values

- Columns people_antigen_positive and people_antigen_total are missing 90%+ of values.
- Columns encounters_viral_total, tests_viral_negative, cases_probable, cases_confirmed, people_viral_total, tests_viral_positive are missing between 50% and 75% of values.
- The remaining columns have less than 25% of values missing.

Some missing data can still be used in analysis. Columns where majority of the data exists already (> 49%) can be used with an imputation technique to predict the missing values. Imputing missing values can be done in several ways:

- Use mean/mode/median of column values to use where values are missing. While although this method is simple to explain and easy to implement, it is not as effective.
- Use an imputation algorithm like a random forest or K Nearest Neighbors. KNN finds missing values closest neighbors and imputes based on the surrounding data points. KNN and RF are computationally heavy but time and computation power can be afforded in this case since the dataset is small.

Missing data can be problematic when applying machine learning models. Simpler algorithms can not handle missing values. It's important to handle missing data effectively.

The sum of the missing values per variable are visualized below.

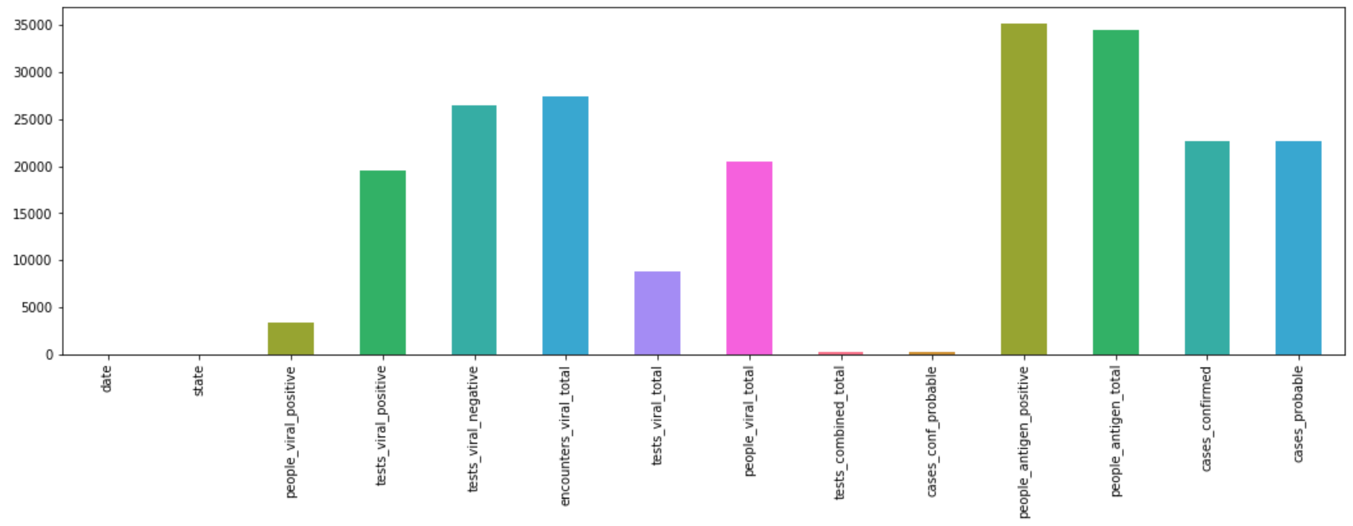
In [8]:
```
percent_missing = df.isnull().sum() * 100 / len(df)
missing_value_df = pd.DataFrame({'column_name': df.columns,
                                 'percent_missing': percent_missing})
missing_value_df.head()
missing_value_df.sort_values('percent_missing', ascending=False, inplace=True)
missing_value_df.head(30)
```

Out[8]:

	column_name	percent_missing
people_antigen_positive	people_antigen_positive	95.953915
people_antigen_total	people_antigen_total	94.089221
encounters_viral_total	encounters_viral_total	74.915365
tests_viral_negative	tests_viral_negative	72.248007
cases_probable	cases_probable	61.930763
cases_confirmed	cases_confirmed	61.928033
people_viral_total	people_viral_total	55.777001
tests_viral_positive	tests_viral_positive	53.489134
tests_viral_total	tests_viral_total	23.976193
people_viral_positive	people_viral_positive	9.424484
cases_conf_probable	cases_conf_probable	0.838157
tests_combined_total	tests_combined_total	0.576062
date	date	0.000000
state	state	0.000000

```
In [9]: plt.figure(figsize = (18,5))
        df.isnull().sum().plot(kind='bar',color=sns.color_palette("husl", 8))
```

```
Out[9]: <matplotlib.axes._subplots.AxesSubplot at 0x1928f50e518>
```



Descriptive Statistics

- On average 4,318,515 tests are positive, 3,790,848 people test positive, and 3,823,510 tests are negative

```
In [10]: df.describe()
```

Out[10]:

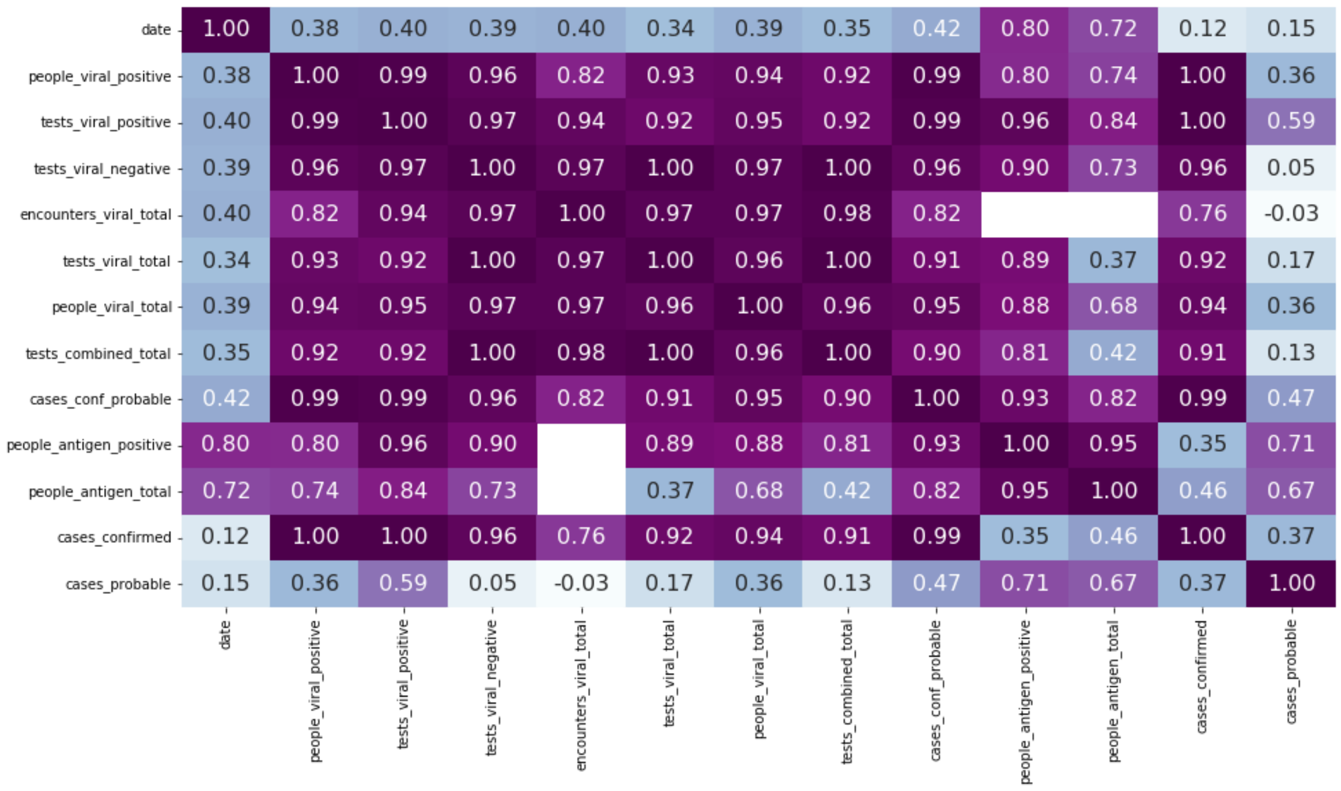
	date	people_viral_positive	tests_viral_positive	tests_viral_negative	encounters_viral_total	te
count	3.662800e+04	3.317600e+04	1.703600e+04	1.016500e+04	9.188000e+03	
mean	2.020604e+07	3.790848e+05	4.318515e+05	3.823510e+06	6.631937e+06	
std	4.937226e+03	6.275464e+05	6.738457e+05	5.487488e+06	1.172307e+07	
min	2.020011e+07	0.000000e+00	0.000000e+00	1.000000e+00	0.000000e+00	
25%	2.020081e+07	3.309925e+04	4.580800e+04	8.012060e+05	6.925688e+05	
50%	2.021012e+07	1.460960e+05	1.924800e+05	2.473541e+06	2.497510e+06	
75%	2.021070e+07	4.712642e+05	5.724602e+05	4.521318e+06	7.862398e+06	
max	2.021122e+07	4.896401e+06	4.393776e+06	4.024120e+07	8.388496e+07	

Correlation

The correlation plot below shows strong positive correlations with majority of the individual variables. The plot below suggests there is multicollinearity. Multicollinearity can cause issues in some machine learning models. Multicollinearity among independent variables will result in less reliable statistical inferences. The existence of multicollinearity in a data set can lead to less reliable results due to larger standard errors.

```
In [11]: plt.figure(figsize=(15,8))
         sns.heatmap(df.corr(),
                     cmap='BuPu',
                     annot=True,
                     fmt=".2f",
                     annot_kws={'size':16},
                     cbar=False)
```

```
Out[11]: <matplotlib.axes._subplots.AxesSubplot at 0x19290b63278>
```

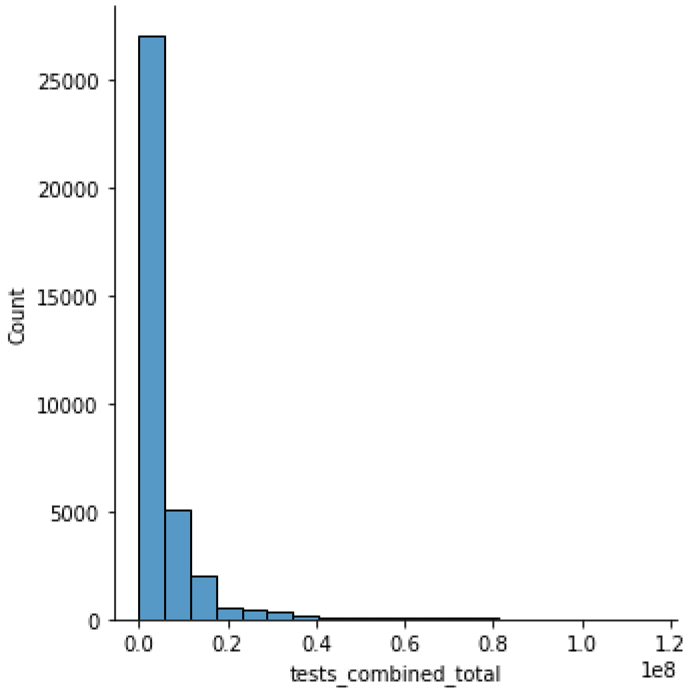


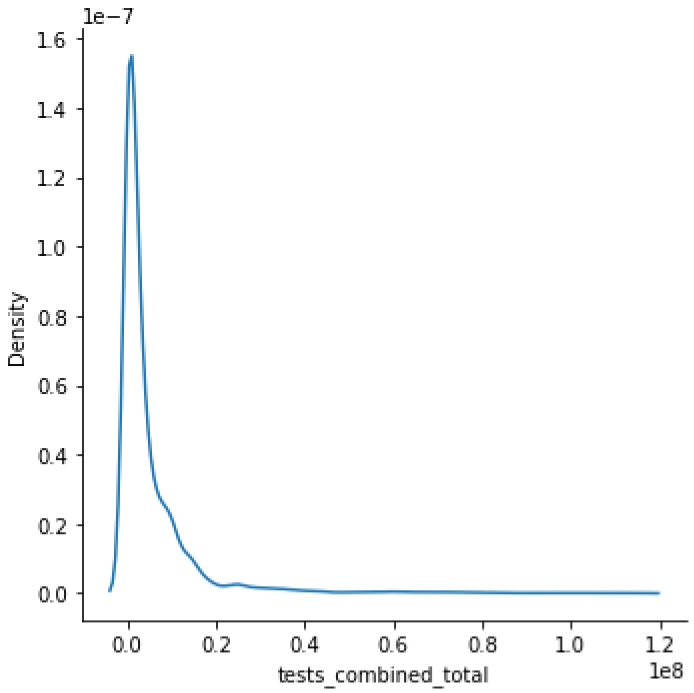
Histogram and Density Plots

The distribution of data suggests the data is skewed to the right. When data are skewed right, the mean is larger than the median. The histogram and density plot display a pareto distribution.

```
In [12]: sns.displot(df, x="tests_combined_total", bins=20)
         sns.displot(df, x="tests_combined_total", kind="kde")
```

```
Out[12]: <seaborn.axisgrid.FacetGrid at 0x19290d5b198>
```

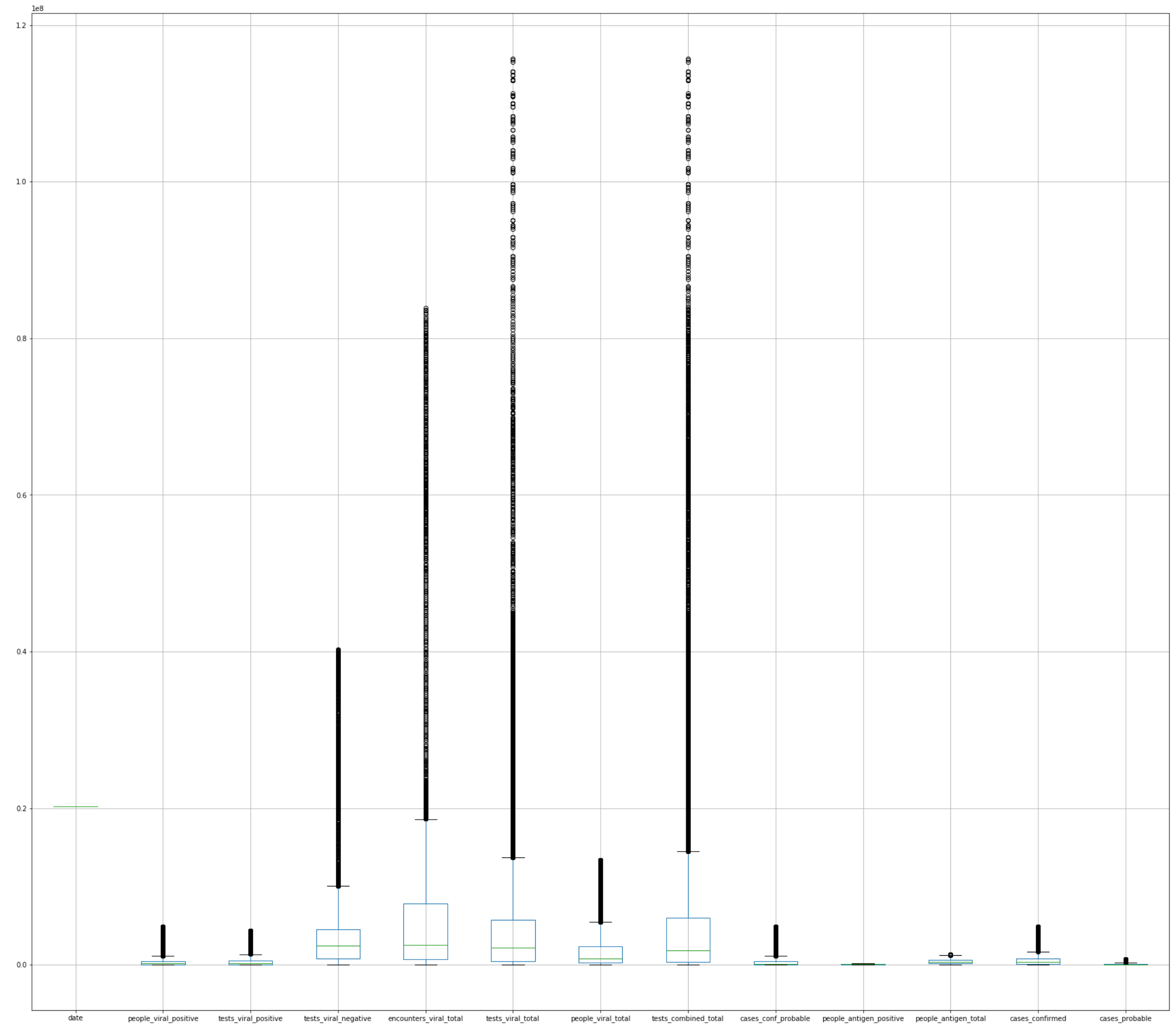




Box Plots

The variables tests_viral_total, tests_combined_total, encounters_viral_total have many outliers and a wider spread of data.

```
In [13]: plt.figure(figsize=(30,27))
         boxplot = df.boxplot()
```



Find the average for the variable tests_combined_total for the population

```
In [14]: print('Average Total Combined Tests',round(df["tests_combined_total"].mean(),2))
         print('Median Total Combined Tests ',round(df["tests_combined_total"].median(),2))
```

```
Average Total Combined Tests 5424406.35
Median Total Combined Tests  1845335.0
```

Convert Date from int to date time format

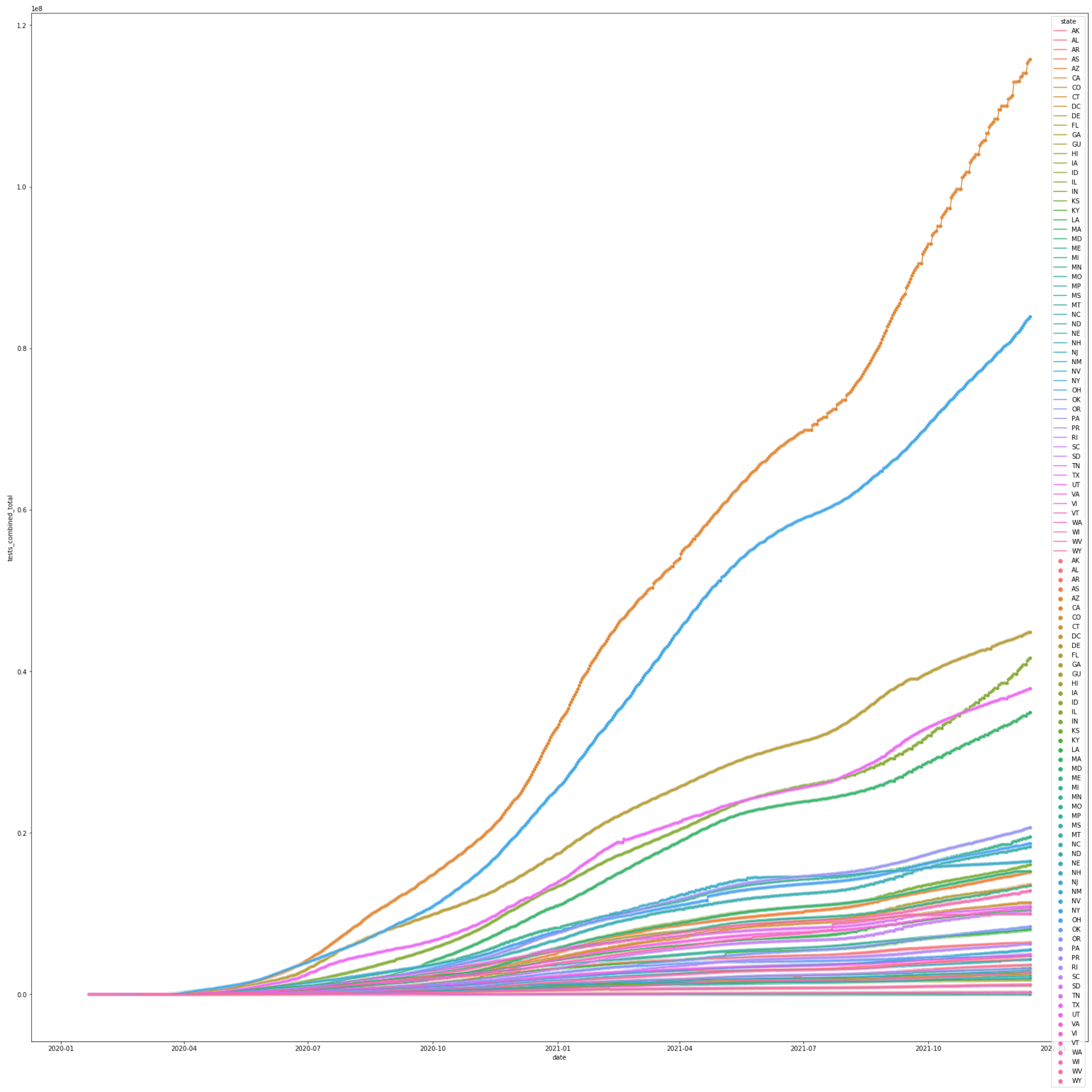
In [15]:
```
df['date'] = pd.to_datetime(df['date'], format="%Y%m%d")
df['date'].head()
```

Out[15]:
```
0    2020-03-06
1    2020-03-07
2    2020-03-08
3    2020-03-09
4    2020-03-10
Name: date, dtype: datetime64[ns]
```

Scatter Plot of Total Combined Tests Over Time by State

In [33]:
```
plt.figure(figsize=(30,30))
sns.scatterplot(data=df, x='date', y='tests_combined_total',hue="state")
sns.lineplot(data=df, x="date", y="tests_combined_total",hue="state")
```

Out[33]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x19297cb1cc0>
```



On Average the Top 10 States with the Most Total Tests Combined

The state of California, New York, Florida, Texas, Illinois, and Massachusetts rank as having on average the most total tests combined. This result is somewhat expected as several of these states have the largest populations in the nation.

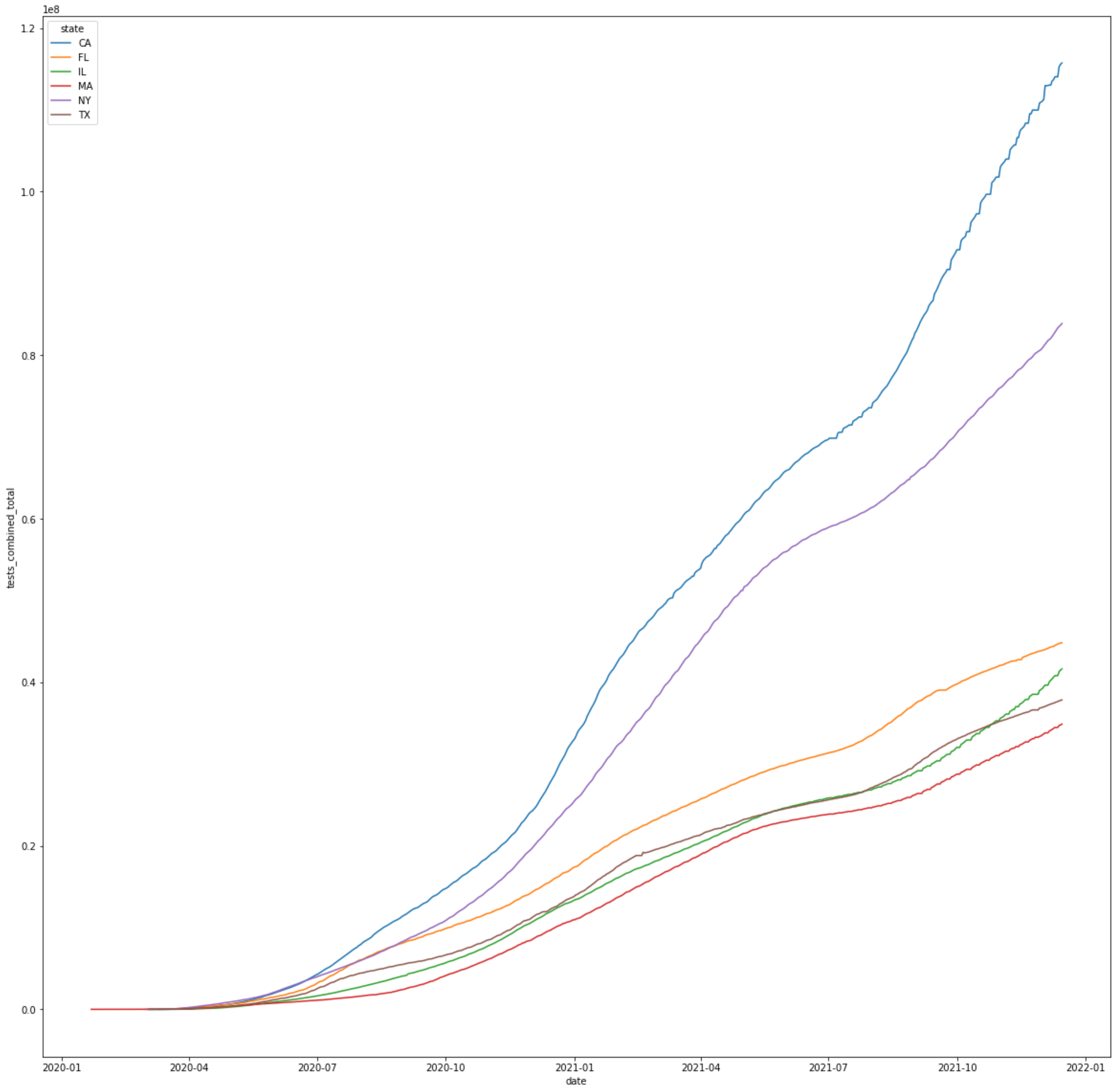
```
In [50]: avg_test_tot = df['tests_combined_total'].groupby(df['state']).mean().sort_values(ascend
         ing=False)
         avg_test_tot[0:6]
```

```
Out[50]: state
         CA    4.289986e+07
         NY    3.382254e+07
         FL    1.987543e+07
         TX    1.618458e+07
         IL    1.587493e+07
         MA    1.302128e+07
         Name: tests_combined_total, dtype: float64
```

Top 10 States on Average with the Most Total Tests Combined Visualized

In [53]:
```
plt.figure(figsize=(20,20))
top6=['CA','NY','FL','TX','IL','MA']
dfst=df[df['state'].isin(top6)]
sns.lineplot(data=dfst, x="date", y="tests_combined_total",hue="state")
```

Out[53]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x192991024e0>
```



3. Data Preparation: New York

Manipulate the data to only look at data for New York state. Save the NY data to a CSV. Gather some basic info about the NY data.

In [17]:
```
options = ['NY']

# Select NY rows
ny_df = df[df['state'].isin(options)]
ny_df.to_csv("NY_data.csv", index=False)
ny_df.head()
```

Out[17]:

	date	state	people_viral_positive	tests_viral_positive	tests_viral_negative	encounters_viral_total	tes
22327	2020-03-02	NY	0.0	NaN	NaN	0.0	
22328	2020-03-03	NY	1.0	NaN	NaN	1.0	
22329	2020-03-04	NY	1.0	NaN	NaN	10.0	
22330	2020-03-05	NY	3.0	NaN	NaN	30.0	
22331	2020-03-06	NY	25.0	NaN	NaN	122.0	

In [18]:
```
ny_df.shape # 654 records of NY data
```

Out[18]:
```
(654, 14)
```

NY Data Quality Check

- The data has several columns that are missing a majority or all values.
- The data consists of 14 variables - 12 variables have a float data type, 1 variable has an int data type, and 1 variable contains string values
- Memory usage 76.6 KB

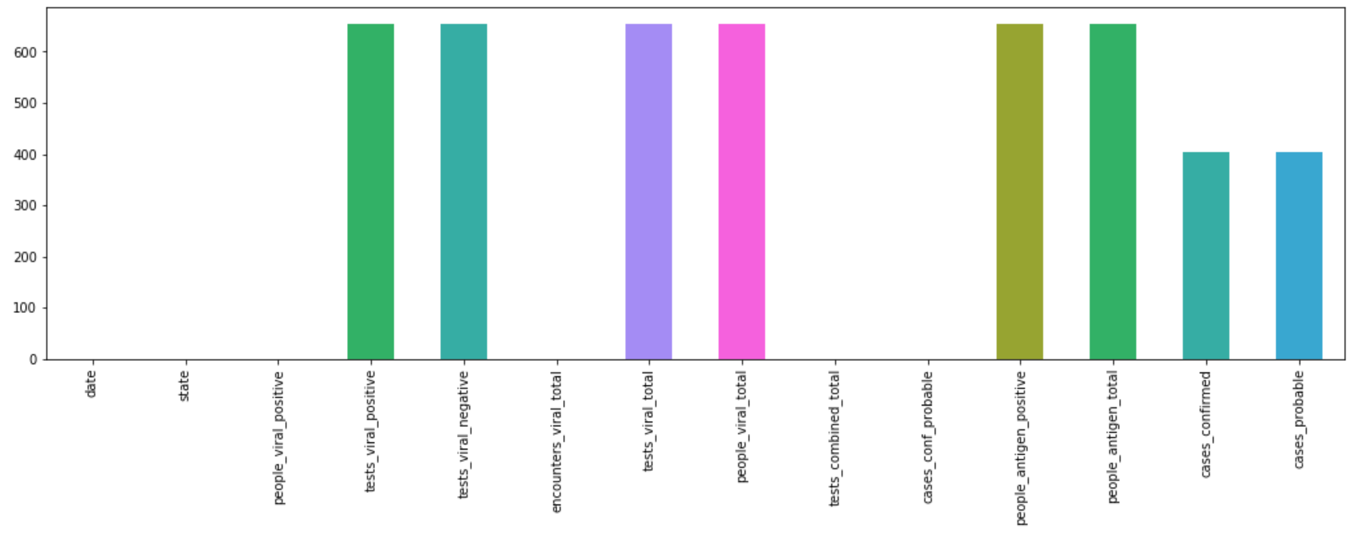
In [19]:
```
ny_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Int64Index: 654 entries, 22327 to 36609
Data columns (total 14 columns):
 #   Column                  Non-Null Count  Dtype         
---  ------                  --------------  -----         
 0   date                    654 non-null    datetime64[ns]
 1   state                   654 non-null    object        
 2   people_viral_positive   654 non-null    float64       
 3   tests_viral_positive    0 non-null      float64       
 4   tests_viral_negative    0 non-null      float64       
 5   encounters_viral_total  654 non-null    float64       
 6   tests_viral_total       0 non-null      float64       
 7   people_viral_total      0 non-null      float64       
 8   tests_combined_total    654 non-null    float64       
 9   cases_conf_probable     654 non-null    float64       
 10  people_antigen_positive 0 non-null      float64       
 11  people_antigen_total    0 non-null      float64       
 12  cases_confirmed         251 non-null    float64       
 13  cases_probable          251 non-null    float64       
dtypes: datetime64[ns](1), float64(12), object(1)
memory usage: 76.6+ KB
```

NY Missing Values

In [20]:
```
plt.figure(figsize = (18,5))
ny_df.isnull().sum().plot(kind='bar',color=sns.color_palette("husl", 8))
```

Out[20]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x19286c379b0>
```



NY Descriptive Statistics

- On average 2,275,027 cases were confirmed and 1,292,877 were confirmed probable
- On average a total of 3,382,254 viral encounters occurred in NY

In [21]:
```
ny_df.describe()
```

Out[21]:

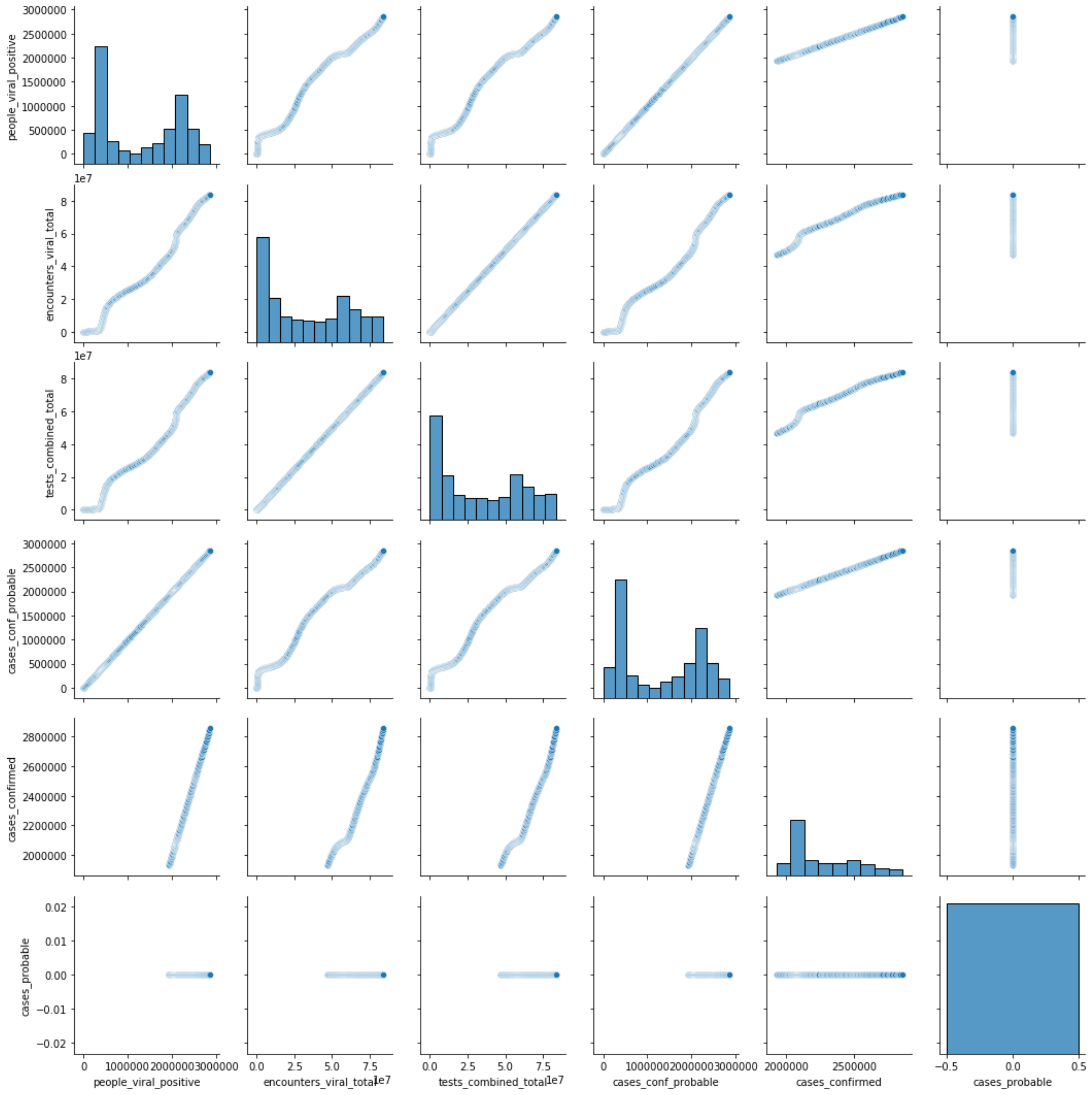
	people_viral_positive	tests_viral_positive	tests_viral_negative	encounters_viral_total	tests_viral_total
count	6.540000e+02	0.0	0.0	6.540000e+02	0.0
mean	1.292877e+06	NaN	NaN	3.382254e+07	NaN
std	8.909166e+05	NaN	NaN	2.727271e+07	NaN
min	0.000000e+00	NaN	NaN	0.000000e+00	NaN
25%	4.228872e+05	NaN	NaN	6.750456e+06	NaN
50%	1.307374e+06	NaN	NaN	3.016200e+07	NaN
75%	2.099584e+06	NaN	NaN	5.916881e+07	NaN
max	2.856505e+06	NaN	NaN	8.388496e+07	NaN

```
In [22]: ny_df.drop(columns=['tests_viral_positive', 'tests_viral_negative', 'tests_viral_total',
         'people_viral_total','people_antigen_positive','people_antigen_total'], inplace=True)
         sns.pairplot(ny_df)
```

```
C:\Users\mckee\Anaconda3\lib\site-packages\pandas\core\frame.py:3997: SettingWithCopyWa
rning:
A value is trying to be set on a copy of a slice from a DataFrame

See the caveats in the documentation: https://pandas.pydata.org/pandas-docs/stable/user
_guide/indexing.html#returning-a-view-versus-a-copy
  errors=errors,
```

```
Out[22]: <seaborn.axisgrid.PairGrid at 0x192918ce908>
```



4. Analyze the New York data for the tests_combined_total Feature

Find the average for the variable tests_combined_total for NY.

In [23]:
```
print('Average Total Combined Tests for New York',round(ny_df["tests_combined_total"].me
an(),2))
print('Median Total Combined Tests for New York ',round(ny_df["tests_combined_total"].me
dian(),2))
```

```
Average Total Combined Tests for New York 33822544.06
Median Total Combined Tests for New York  30162004.0
```

5. Visualize New York Data

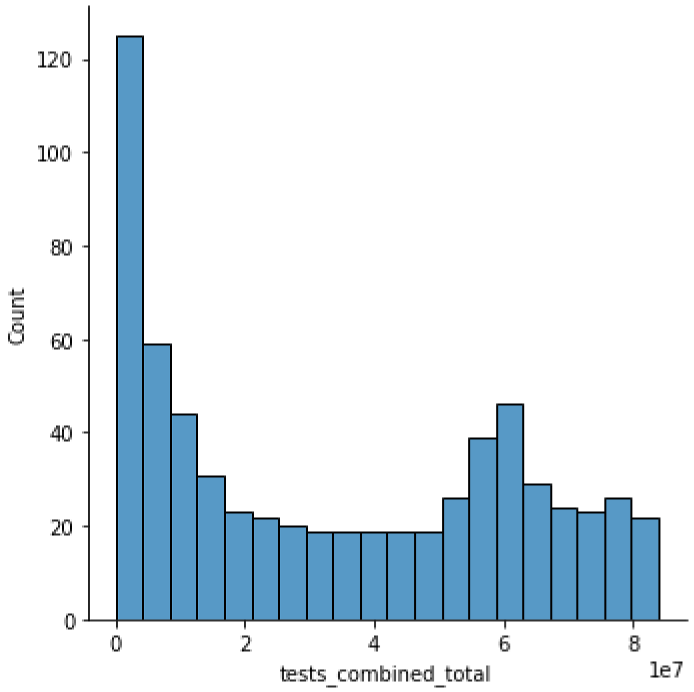
Create a visualization of the tests_combined_total variable for NY. Can be a static chart.

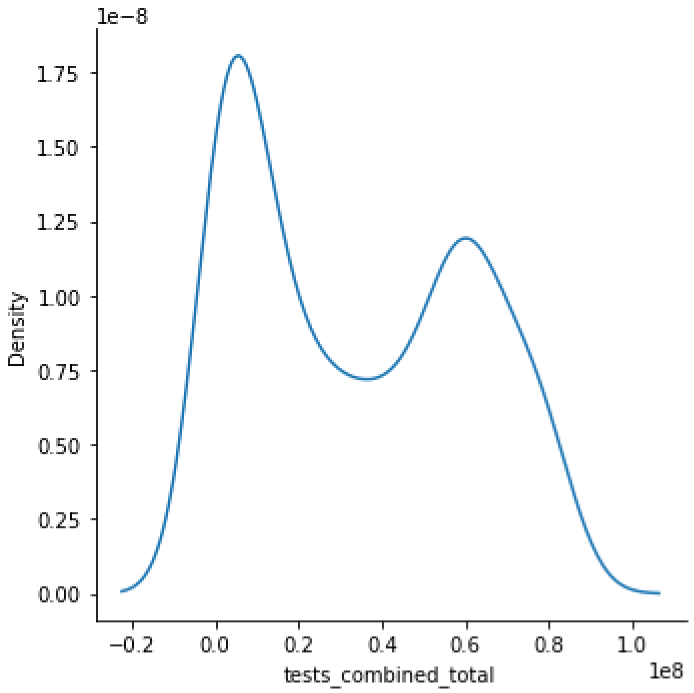
Histogram and Density Plots

The distribution of data suggests there are 2 distinct clusters of data. The histogram and density plot shows a bimodal curve.

```
In [28]: sns.displot(ny_df, x="tests_combined_total", bins=20)
         sns.displot(ny_df, x="tests_combined_total", kind="kde")

Out[28]: <seaborn.axisgrid.FacetGrid at 0x19293f0b828>
```



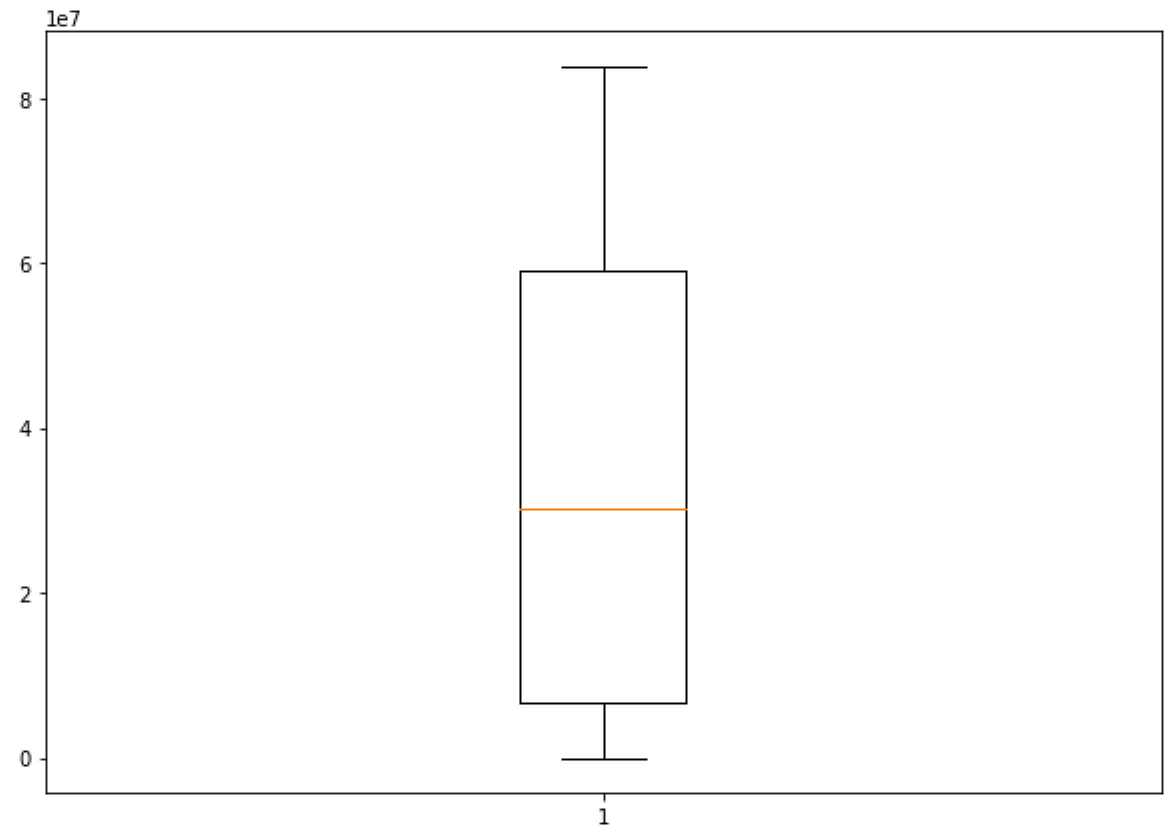


Box Plot

A box plot shows the spread and skewness groups of numerical data through their quartiles. It may also show outliers plotted as individual dots outside of the whiskers.

Majority of the data lies between 1,000,000 and 6,000,000 total combined tests.

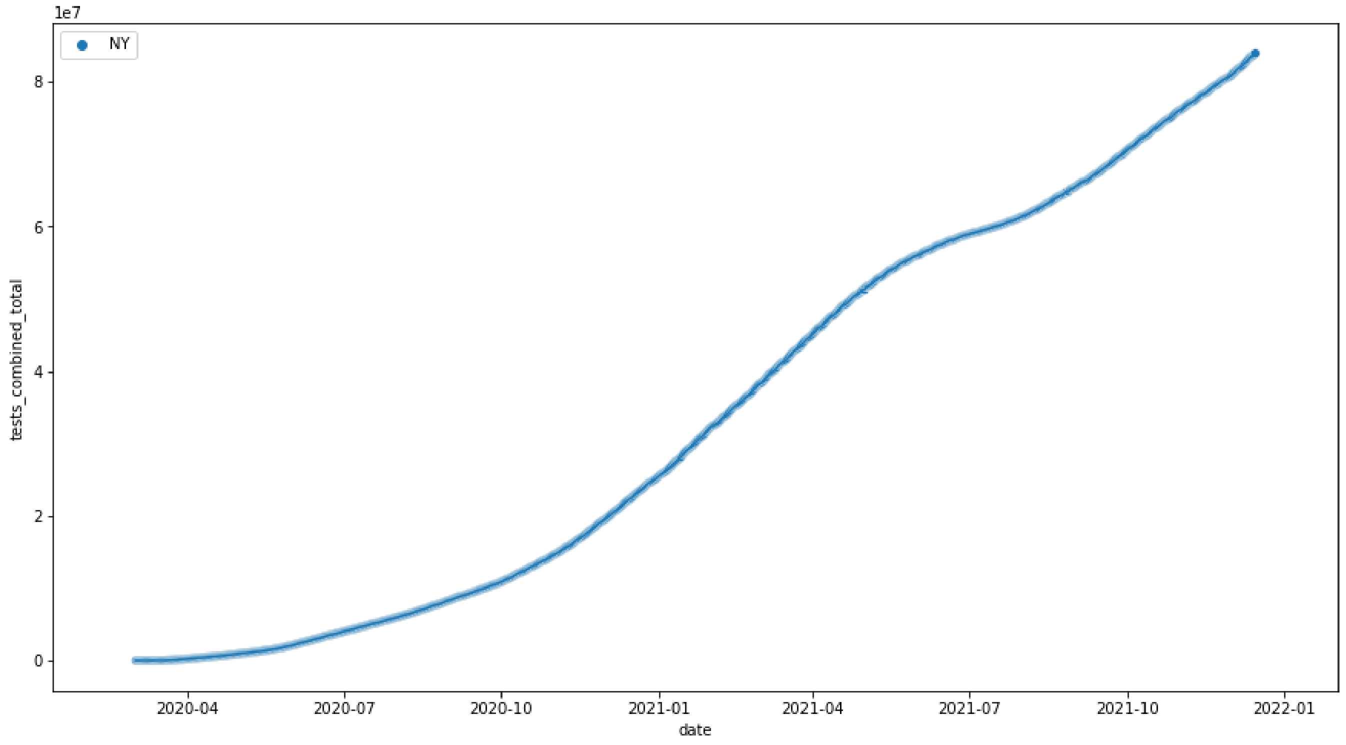
In [25]:
```
fig = plt.figure(figsize =(10, 7))
plt.boxplot(ny_df['tests_combined_total'])
plt.show()
```



Scatter Plot of Total Combined Tests Over Time for New York

```
In [32]: plt.figure(figsize=(15,8))
         sns.scatterplot(data=ny_df, x='date', y='tests_combined_total',hue="state")
         sns.lineplot(data=ny_df, x="date", y="tests_combined_total")

Out[32]: <matplotlib.axes._subplots.AxesSubplot at 0x19296360fd0>
```



6. Analysis Summary

Write a short description of the data and analysis based on what you've done above. Describe your process/choices briefly, and specifically note any steps in your process that are not expressed in your code. Essentially, if you were to create a short wiki page/GitHub repository about this data/analysis/process, what would it say?

Summary

This analysis was completed using COVID testing data provided by Johns Hopkins University to analyze cumulative COVID testing counts in the state of New York.

Load Data

The data was sourced from the Johns Hopkins coronavirus API and converted from a json format to a pandas dataframe.

Data Exploration

The data contains 36,628 records and 14 features where 12 variables have a float data type, 1 has an int data type, and 1 contains string values. 3.9 MB are used for memory of this data. Features: • date • state • people_viral_positive • tests_viral_positive • tests_viral_negative • encounters_viral_total • tests_viral_total • people_viral_total • tests_combined_total • cases_conf_probable • people_antigen_positive • people_antigen_total • cases_confirmed • cases_probable

The data has several columns that are missing values. The columns people_antigen_positive and people_antigen_total are missing 90%+ of values. The columns encounters_viral_total, tests_viral_negative, cases_probable, cases_confirmed, people_viral_total, and tests_viral_positive are missing between 50% and 75% of values. The remaining columns have less than 25% of values missing. Missing data can be problematic when applying machine learning models. Simpler algorithms cannot handle missing values. It's important to handle missing data effectively.

On average 4,318,515 tests are positive, 3,790,848 people test positive, and 3,823,510 tests are negative. There are strong positive correlations with majority of the individual variables. The correlation plot suggests there is multicollinearity. Multicollinearity among independent variables will result in less reliable statistical inferences. The existence of multicollinearity in a data set can lead to less reliable results due to larger standard errors. The variables tests_viral_total, tests_combined_total, and encounters_viral_total have many outliers and a wider spread of data.

The distribution of the tests_combined_total variable suggests the data is skewed to the right. When data is skewed right, the mean is larger than the median. The histogram and density plot display a pareto distribution and the mean is larger than the median. The average amount of total tests combined for the population equates to 5,424,406 tests. The median amount of total tests combined for the population equates to 1,845,335 tests.

The state of California, New York, Florida, Texas, Illinois, and Massachusetts rank as having on average the most total tests combined. This result is somewhat expected as several of these states have the largest populations in the nation.

Data Preparation and New York Exploration

The data contains 654 records and 14 features. A considerably smaller amount of memory is being used for the New York Data. 76.6 KB are allocated for memory of this data. The variables tests_viral_positive, tests_viral_negative, tests_viral_total, people_viral_total, people_antigen_positive, and people_antigen_total are missing 100% of values.

On average 2,275,027 cases were confirmed and 1,292,877 were confirmed probable. On average a total of 3,382,254 viral encounters occurred in New York.

New York Average tests_combined_total

The average amount of total tests combined for New York equates to 33,822,544 tests. The median amount of total tests combined for New York equates to 30,162,004 tests. Now let’s compare that to the population. The average amount of total tests combined for the population equates to 5,424,406 tests. The median amount of total tests combined for the population equates to 1,845,335 tests. New York well surpasses the population in the amount of testing.

New York tests_combined_total Visualized

Analyzing the distribution of the tests_combined_total variable further for the state of New York shows there are 2 distinct clusters of data. The histogram and density plot displays a bimodal curve. The box plot shows that the majority of the total combined tests variable lies between 1,000,000 and 6,000,000 total combined tests.