```
import pandas as pd # Read data. This data represents the cumulative known cases to date (https://covidtracking.com/about-data/faq) wn != "https://raw.githubusercontent.com/COVID19Tracking/covid-tracking-data/master/data/states_daily_dpm_et.csv" df = pd.read_csv(wrl_index_col=0,parse_dates=[0])
              state positive negative pending hospitalizedCurrently hospitalizedCumulative inIcuCurrently inIcuCumulative onVentilatorCurrently onVentilatorCurrently recovered
                                                                                                                                                                                                      261.0 8915b2653b57fc004eaa5369881343ee1f984aa8 2020-05-
02T20:00:00Z 9.0
               AK 365.0 21034.0 NaN
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05-02
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02T20:00:00Z 0.0
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                                                                                                                                                                                                      1565.0 0eed79b0025a0cc44b30dfb01e4b3bb5a1148a5c 2020-05-02T20:00:00Z 348.0
              AZ 8364.0 69633.0 NaN
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Double-click (or enter) to edit
['iniculurrently', 'iniculumilative', 'onventilatorCumulative', 'hash', 'dateChecked', 'hospitalized', 'total', 'posNeg', 'fips', 'deathIncrease', 'hospitalizedIncrease', 'negativeIncrease', 'positiveIncrease', totalTestResultsIncrease'])
                  state positive negative pending hospitalizedCurrently hospitalizedCumulative recovered death totalTestResults
       2020-05-02
       2020-05-02
                             7434.0 84775.0
                                                    NaN
                                                                                               414.0 1987.0 73.0
       2020 05 02
                   AR 3372.0 48210.0 NaN
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       2020-05-02
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      2020-05-02 AZ 8364.0 69633.0
                                                   NaN
                                                                           718.0
                                                                                                     1339.0 1565.0 348.0
                                                                                                                                             77997.0
# Create new features
# Divide positive by totalTestResults to get positive_percent
df_drop["percent_positive"] = ""
df_drop["percent_positive"] = 100*df_drop["positive"]/df_drop["totalTestResults"]
df_drop.head()
                  state positive negative pending hospitalizedCurrently hospitalizedCumulative recovered death totalTestResults percent positive
      2020-05-02
                             365.0 21034.0
                                                                                                                   261.0 9.0
                                                                              10.0
       2020-05-02
                    AL 7434.0 84775.0
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                                                                                                                                             92209.0
                                                                                                                                                                 8.062120
                                                                                                     1023.0
                   AR 3372.0 48210.0 NaN
                                                                                                      414.0 1987.0 73.0
                                                                                                                                                                6.537164
                                                                             95.0
                                                                            718.0
# Divide hospitalized by positive to get hospitalized_percent
import numpy as np

df_drop("hospitalized_percent") = ""

df_drop("hospitalized_percent") = np.nammax(df_drop(['hospitalizedCurrently','hospitalizedCumulative']], axis=1)

df_drop("hospitalized_percent"] = 100*df_drop("hospitalized_percent")|df_drop("positive")|

df_drop_head()
 /usr/local/lib/python3.6/dist-packages/ipykernel_launcher.py:3: RuntimeWarning: All-NaN axis encountered
This is separate from the ipykernel package so we can avoid doing imports until
                   state positive negative pending hospitalizedCurrently hospitalizedCumulative recovered death totalTestResults percent_positive hospitalized_percent
       2020-05-02 AK
                             365.0 21034.0
                                                                                                                   261.0 9.0
      2020-05-02
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                                                                                                                                                                8 062120
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      2020-05-02 AR 3372.0 48210.0 NaN
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       2020-05-02 AZ 8364.0 69633.0 NaN
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                                                                                                                                             77997.0
                                                                                                                                                                10.723489
# Divide recovered by positive to get recovered_percent
df_drop["recovered_percent"] = ""
df_drop["recovered_percent"] = 190*df_drop["recovered"]/df_drop["positive"]
df_drop_head()
                  state positive negative pending hospitalizedCurrently hospitalizedCumulative recovered death totalTestResults percent positive hospitalized percent recovered percent
      2020-05-02 AK
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                                                                              10.0
                                                                                                        NaN
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                                                                                                                                              77997.0
                                                                                                                                                                10.723489
                                                                                                                                                                                        16.009087
                                                                                                                                                                                                             18.711143
# Divide death by positive to get death_percent
# Divide death by positive to get death_percent

df_drop["death_percent"] = ""

df_drop["death_percent"] = 100*df_drop["death"]/df_drop["positive"]

df_drop.head()
```

https://colab.research.google.com/drive/174WBhWYUOs5SthAgAGunrQfTLlfnLjfo#scrollTo=oAnjR4Sz932V&printMode=true

```
# Fetch the latest state population data (nst-est2019-01.csv)
from google.colab import files
uploaded = files.upload()

    Choose Fikes | nst-est2019-01 csv
    nst-est2019-01.csv(application/vnd.ms-excel) - 676 bytes, last modified: 4/13/2020 - 100%
    Saving nst-est2019-01.csv to nst-est2019-01.csv

# Load latest state population data
import io
import io
df_state_pop = pd.read_csv(io.StringIO(uploaded['nst-est2819-01.csv'].decode('utf-8')))
df_state_pop("Population"] = pd.to_numeric(df_state_pop("Population"))
df_state_po,head()
        State Population
        AK 731545.0
     1 AL 4903185.0
     2 AR 3017804.0
# Add column of state populations (population) to df_drop_total_posNeg # Need to sort rows by state using index numbering from state_list
df_drop["population"] = ""
df_drop[["population"]] = df_drop["population"].apply(pd.to_numeric)
df_drop.head()
                state positive negative pending hospitalizedCurrently hospitalizedCumulative recovered death totalTestResults percent positive hospitalized percent recovered percent death percent population
           date
      2020-05-02
                           365.0 21034.0
                                                                                                                                                                                                          2.465753
      2020-05-02
                         7434.0 84775.0 NaN
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# Normalize positive to state population
df_drop["positive_norm"] = ""
df_drop["positive_norm"] = df_drop["positive"]/df_drop["population"]
df_drop,head[
г
      2020-05-02
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                state positive negative pending hospitalizedCurrently hospitalizedCumulative recovered death totalTestResults percent positive hospitalized percent recovered percent death_percent population positive_norm hospitalized norm
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# Normalize recovered to state population
df_drop["recovered_norm"] = ""
df_drop["recovered_norm"] = df_drop["recovered"]/df_drop["population"]
df_drop.head()
                 state positive negative pending hospitalizedCurrently hospitalizedCurrently hospitalizedCurrently hospitalized_norm recovered_death totalTestResults percent_positive hospitalized_percent recovered_percent death_percent population positive_norm hospitalized_norm recovered_norm
                                                                                                                                                                                                                                      0.001117
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  Normalize death to state population
D+
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                                                                                                                                                                                                                                                                         0.000215
                                                                                                                                                                                                                                                                                    0.000048
```

```
C+ cclass 'pandas.core.frame.DataFrame'>
DatetimeIndex: 3265 entries, 2020-05-02 to 2020-01-22
Data columns (total 18 columns):

# Column Mon-Null Count Dtype
```

Get the unique values of 'state' column
state_list = df.state.unique()
state_list

D. array(['Ak', 'Ak', 'Ak', 'Ak', 'Ak', 'CA', 'CO', 'CT', 'DC', 'DE', 'FL', 'GA', 'GO', 'HI', 'IA', 'IB', 'II', 'IN', 'KS', 'KY', 'LA', 'MA', 'M

for key in df_state_dict.keys():
 df_state_dict[key] = df_drop[:][df_drop.state == key]

df_state_dict['AK'].head()

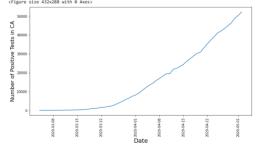
state positive negative pending hospitalizedCurrently hospitalizedCurrently hospitalizedCurrently hospitalized.morm recovered death totalTestResults percent_positive hospitalized_percent recovered_percent death_percent population positive_norm hospitalized_norm recovered_norm death_norm 2.472527 2020-05-01 AK 364.0 19961.0 NaN 25.0 NaN 254.0 9.0 20325.0 1.790898 6.868132 69.780220 731545.0 0.000498 0.000034 0.000347 0.000012 2020-04-30 AK 355.0 18764.0 NaN 19.0 NaN 252.0 9.0 19119.0 1.856792 5.352113 70.985915 2.535211 731545.0 0.000485 0.000026 0.000344 0.000012 2020-04-29 AK 355.0 18764.0 NaN 14.0 NaN 240.0 9.0 10110 0 1.856702 3.943662 67 605634 2.535211 731545.0 0.000485 0.000019 0.000328 0.000012 2020-04-28 AK 351.0 16738.0 NaN 16.0 228.0 9.0 17089 0 2 053953 4 558405 64 957265 2 564103 731545 0 0.000480 0.000022 0.000312 0.000012

df_state_dict['CA'].head()

□*		state	positive	negative	pending	${\tt hospitalizedCurrently}$	hospitalizedCumulative	recovered	death	totalTestResults	percent_positive	hospitalized_percent	recovered_percent	death_percent	population	positive_norm	hospitalized_norm	recovered_norm	death_norm
	date																		
	2020-05-02	CA	52197.0	634606.0	NaN	4722.0	NaN	NaN	2171.0	686803.0	7.599996	9.046497	NaN	4.159243	39512223.0	0.001321	0.000120	NaN	0.000055
	2020-05-01	CA	50442.0	604543.0	NaN	4706.0	NaN	NaN	2073.0	654985.0	7.701245	9.329527	NaN	4.109671	39512223.0	0.001277	0.000119	NaN	0.000052
	2020-04-30	CA	48917.0	576420.0	NaN	4981.0	NaN	NaN	1982.0	625337.0	7.822502	10.182554	NaN	4.051761	39512223.0	0.001238	0.000126	NaN	0.000050
	2020-04-29	CA	46500.0	556639.0	NaN	5011.0	NaN	NaN	1887.0	603139.0	7.709666	10.776344	NaN	4.058065	39512223.0	0.001177	0.000127	NaN	0.000048
	2020-04-28	CA	45031.0	532577.0	NaN	4983.0	NaN	NaN	1809.0	577608.0	7.796118	11.065710	NaN	4.017233	39512223.0	0.001140	0.000126	NaN	0.000046

from matplotlib import pyplot as plt

plt.plot(df_state_dict['CA'].positive)
plt.xticks(rotation='vertical')



plt.plot(df_state_dict['CA'].percent_positive)
plt.xticks(rotation='vertical')

plt.xlabel('Date', fontsize=18)
plt.ylabel('Percentage of Positive Tests in CA', fontsize=16)
plt.show()

D-

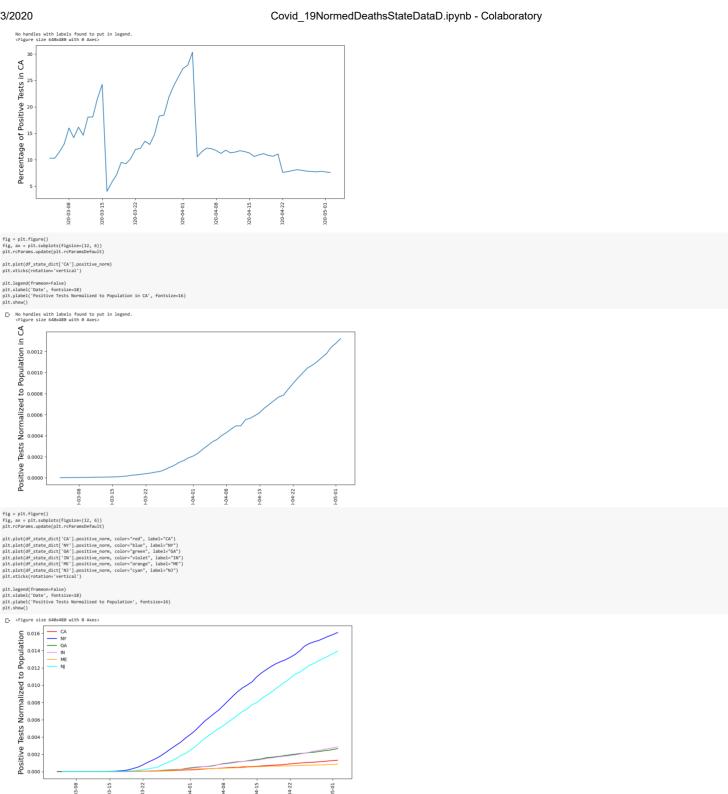
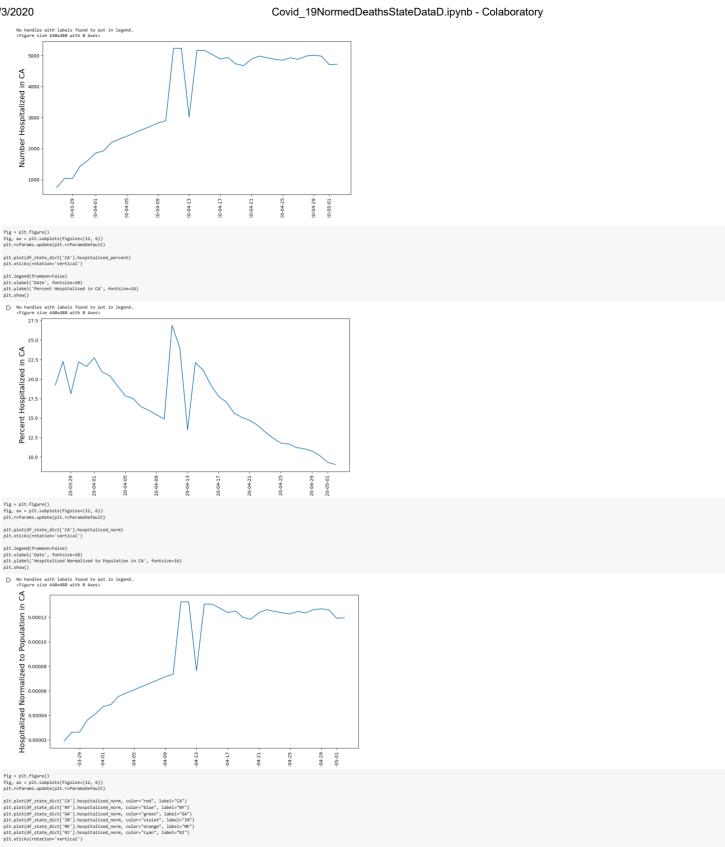
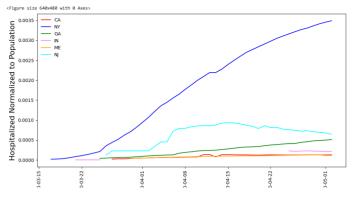


fig = plt.figure()
fig, ax = plt.subplots(figsize=(12, 6))
plt.rcParams.update(plt.rcParamsDefault) plt.plot(df_state_dict['CA'].hospitalizedCurrently)
plt.xticks(rotation='vertical') plt.legend(frameon=False)
plt.xlabel('Date', fontsize=18)
plt.ylabel('Number Hospitalized in CA', fontsize=16)

plt.show()





In several states, population normalized hospitalizations plateau, although population normalized death rate continues to grow

fig = plt.figure()
fig, ax = plt.subplots(figsize=(12, 6))
plt.rcParams.update(plt.rcParamsDefault)
plt.plot(df_state_dict['CA'].death)
plt.xticks(rotation='vertical')

plt.legend(frameon=False)
plt.xlabel('Date', fontsize=18)
plt.ylabel('Number Died in CA', fontsize=16)
plt.show()

No handles with labels found to put in legend. <Figure size 640x480 with 0 Axes>

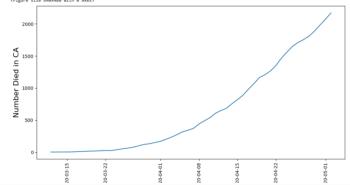


fig = plt.figure()
fig, ax = plt.subplots(figsize=(12, 6))
plt.rcParams.update(plt.rcParamsDefault)
plt.plot(df_state_dict['CA'].death_percent)
plt.xticks(rotation='vertical')

plt.xlabel('Date', fontsize=18)
plt.ylabel('Percent Death in CA', fontsize=16)
plt.show()

No handles with labels found to put in legend. <Figure size 640x480 with 0 Axes>

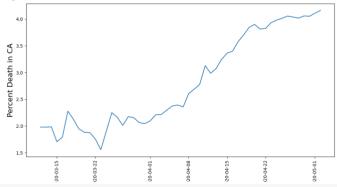


fig = plt.figure()
fig, ax = plt.subplots(figsize=(12, 6))
plt.rcParams.update(plt.rcParamsDefault)

plt.xticks(rotation='vertical')

plt.legend(frameon=False)
plt.xlabel('Date', fontsize=18)
plt.ylabel('Death Normalized to Population in CA', fontsize=16)
plt.show()

C+

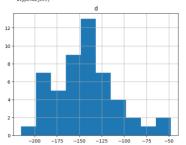
г

```
No handles with labels found to put in legend. 
<Figure size 640x480 with 0 Axes>
                     1e-5
          Death Normalized to Population in CA
plt.plot(df_state_dict['CA'].death_norm, color='red", label="CA")
plt.plot(df_state_dict['W'].death_norm, color='blue", label="W")
plt.plot(df_state_dict['W'].death_norm, color='green', label='WT)
plt.plot(df_state_dict['W'].death_norm, color='volot=', label='WT'
plt.plot(df_state_dict['W'].death_norm, color='volot=', label='WT'
plt.plot(df_state_dict['W'].death_norm, color='cyar', label='WT'
plt.plot(df_state_dict['W'].death_norm, color='cyar', label='WT')
plt.stick(cytotlor='vottcall')
plt.legend(frameon=False)
plt.xlabel('Date', fontsize=18)
plt.ylabel('Death Normalized to Population', fontsize=16)
plt.show()
C+ <Figure size 640x480 with 0 Axes>
             Normalized to Population
          Death 
Note how the population normalized death curves relate closely to population normalized postive test curves
# Curve fitting done at: \underline{\text{http://www.xuru.org/rt/NLR.asp\#CopyPaste}}
# Fetch the parameters for each state (CexpOx^-1.csv) that fit to positive_norm = a^*exp(b/x) # where x is the number of days from March 4, 2020 from goagle.colab import files uploaded = files.uploadef
[* Choose Files | CexpDx*-1.csv 
• CexpDx*-1.csv (application/wd.ms-excel) - 1680 bytes, last modified: 4/16/2020 - 100% done 
Saving CexpDx*-1.csv to CexpDx*-1.csv
# Load the parameters for each state (CexpDx^-1.csv) that fit to positive_norm = a^exp(b/x) inport to df_state_params = pd_read_csv(io.StringIO(uploaded['CexpDx^-1.csv'].decode('utf-8'))) df_state_params.head()
             State c (10^-4)
         0 AK 1.331139 -95.882596 2.0
1 AL 8.124937 -145.096536 1.0
                                 NaN
          4 AZ 4.374538 -129.204382
df_state_params.describe()
 C+
          count 51.000000 51.000000 51.000000
          mean 28.922502 -142.879078 2.098039
            std 53.235594 33.811201 2.156431
                       0.516899 -215.115296 1.000000
           25% 3.745253 -165.040649 1.000000
           50% 7.421743 -145.096536 1.000000
            max 231.216701 -47.945262 15.000000
```

array([[<matplotlib.axes, subplots.AxesSubplot object at 0x7f87007ee780>]]. High value outliers here are NJ (fit rank 1), NY, (fit rank 1), RI (fit rank 5), and SD (fit rank 4)

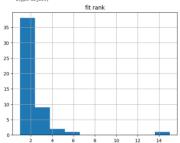
df_state_params.hist(column='d', bins=10)

array([[<matplotlib.axes._subplots.AxesSubplot object at 0x7f87007901d0>]],
dtyne=object)



Low value outliers here are RI (fit rank 5) and SD (fit rank 4).

df_state_params.hist(column='fit rank')



The A*exp(B/x) functional form works extremely well for thirty of the 52 states (57.7%).

Fetch static data for each state (CovidCompleteStateData.csv)
from google.colab import files
uploaded = files.upload()

Choose Files | CovidCompl...teData.csv

CovidCompleteStateData.csv(applica

CovidCompleteStateData.csv(application/vnd.ms-excel) - 60510 bytes, last modified: 4/20/2020 - 100% done Saving CovidCompleteStateData.csv to CovidCompleteStateData.csv

Load static data for each state (CovidCurrentStateData.csv) import io

df_state_data = pd.read_csv(io.StringIO(uploaded['CovidCompleteStateData.csv'].decode('utf-8')))
df_state_data.head()

Ŀ	State	Sum of NUM_Medicare_BEN	Sum of NUM_BEN_Age_Less_65	Sum of NUM_BEN_Age_65_to_74	Sum of NUM_BEN_Age_75_to_84	Sum of NUM_BEN_Age_Greater_84	Sum of NUM_Female_BEN	Sum of NUM_Male_BEN	Sum of NUM_Black_or_African_American_BEN	Sum of NUM_Asian_Pacific_Islander_BEN	Sum of NUM_Hispanic_BEN	Sum of NUM_American_IndianAlaska_Native_BEN NUM_BEN_With_
(AK.	1820384.0	270970.0	809516.0	468255.0	175296.0	1034762.0	760009.0	62311.0	76773.0	46525.0	147917.0
1	AL	10804823.0	2065353.0	4386595.0	2980828.0	1190504.0	6237445.0	4514041.0	1549811.0	30624.0	65500.0	5556.0
2	AR	15892716.0	2818665.0	6370265.0	4555468.0	1848506.0	9275039.0	6507151.0	1334245.0	19642.0	108428.0	62782.0
3	AS	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
4	AZ	10786064.0	886596.0	4861035.0	3377040.0	1294375.0	5944519.0	4747801.0	221183.0	61840.0	689880.0	179818.0
	44	C										

Feature Engineering
Land Area/Nater Area
Engineering
Land Area/Nater Area
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En

Capital Area Ratio = Capital Land Area/Capital Water Area
of state_data['Capital Area Ratio'] = of_state_data['Capital Land Area']/df_state_data['Capital Water Area']
of_state_data['Capital Land Area'] = of_state_data['Capital Land Area'].astype(float)
of_state_data['Capital Area Ratio'] = of_state_data['Capital Land Area'].divide(df_state_data['Capital Water Area'],

Boundaries = Number of boarding states + On Coast + Borders Another Country

of_state_data('Boundaries') = df_state_data('Number of bordering states') + df_state_data('On Coast') + df_state_data('Another of bordering states') + df_state_data('On Coast') + df_state_data('On Coast'

Laritude Difference to State Capital = Laritude - Capital Latitude df_state_data['Latitude Difference to State Capital'] = df_state_data['Latitude'] - df_state_data['Capital Latitude']

Longitude Difference to State Capital = Capital Longitude - Longitude

df_state_data['Longitude Difference to State Capital'] = df_state_data['Capital Longitude'] - df_state_data['Longitude']

Latitude Difference to DC = Latitude - DC Latitude df_state_data['Latitude Difference to DC'] = df_state_data['Latitude'] - 38.984722

Longitude Difference to DC = DC Longitude - Longitude df_state_data['Longitude bifference to DC'] = -77.016389 - df_state_data['Longitude']

Latitude Difference to US Center = Latitude - Center Latitude df_state_data['Latitude Difference to Center'] = df_state_data['Latitude'] - 39.833333

Longitude Different to US Center = Center Longitude - Longitude df_state_data['Longitude Difference to Center'] = -98.585522 - df_state_data['Longitude']

df state data.head()

□	State	Sum of NUM_Medicare_BEN		Sum of NUM_BEN_Age_65_to_74	Sum of NUM_BEN_Age_75_to_84	Sum of NUM_BEN_Age_Greater_84	Sum of NUM_Female_BEN	Sum of NUM_Male_BEN	Sum of NUM_Black_or_African_American_BEN	Sum of NUM_Asian_Pacific_Islander_BEN	Sum of NUM_Hispanic_BEN	Sum of NUM_American_IndianAlaska_Native_BEN NUM_BEN_With_
) AK	1820384.0	270970.0	809516.0	468255.0	175296.0	1034762.0	760009.0	62311.0	76773.0	46525.0	147917.0
	I AL	10804823.0	2065353.0	4386595.0	2980828.0	1190504.0	6237445.0	4514041.0	1549811.0	30624.0	65500.0	5556.0
	2 AR	15892716.0	2818665.0	6370265.0	4555468.0	1848506.0	9275039.0	6507151.0	1334245.0	19642.0	108428.0	62782.0
	a AS	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
	. AZ	10786064.0	886596.0	4861035.0	3377040.0	1294375.0	5944519.0	4747801.0	221183.0	61840.0	689880.0	179818.0
5	rows × 12	26 columns										

df_state_data.shape

D (56, 126)

Define variables for regression
df_temp1 = df_state_data.drop(df_state_data.index[[3, 12, 27, 42, 50, 55]])
X = df temp1.drop('State'. axis = 1)

df_temp2 = df_state_params.drop(df_state_data.index[[3, 12, 27, 42, 50, 55]])
y = df_temp2['d']

Look at correlation coefficients
pd.set_option('display.max_columns', None)
pd.set_option('display.max_rows', 1000)
X.corr()

D

	Sum of	Sum of	Sum of	Sum of	Sum of		Sum of	Sum of	Sum of	Sum of
	NUM_Medicare_BEN	NUM_BEN_Age_Less_65	NUM_BEN_Age_65_to_74	NUM_BEN_Age_75_to_84	NUM_BEN_Age_Greater_84	NUM_Female_BEN	NUM_Male_BEN	NUM_Black_or_African_American_BEN	NUM_Asian_Pacific_Islander_BEN	NUM_Hispanic_BEN NUM_A
Sum of NUM_Medicare_BEN	1.000000	0.981244	0.998612	0.998085	0.989852		0.999896	0.895536	0.524429	0.894417
Sum of NUM_BEN_Age_Less_65	0.981244		0.977935	0.969186	0.960258			0.925224	0.473716	0.829126
Sum of NUM_BEN_Age_65_to_74 Sum of NUM_BEN_Age_75_to_84	0.998612 0.998085		1.000000 0.996336	0.996336 1.000000					0.516336 0.528889	0.903356 0.900554
Sum of NUM_BEN_Age_Greater_84	0.989852		0.982527	0.992524	1.000000			0.863288	0.560359	0.880694
Sum of NUM_Female_BEN	0.999917	0.982419	0.998360	0.997902	0.989495	1.000000	0.999655	0.898089	0.522516	0.891099
Sum of NUM_Male_BEN	0.999896	0.979571	0.998622	0.998281	0.990300	0.999655	1.000000	0.892308	0.525905	0.896619
Sum of NUM_Black_or_African_American_BEN	0.895536	0.925224	0.894585	0.882970	0.863288		0.892308	1.000000	0.300440	0.726598
Sum of NUM_Asian_Pacific_Islander_BEN	0.524429	0.473716 0.829126	0.516336 0.903356	0.528889 0.900554	0.560359		0.525905	0.300440 0.726598	1.000000 0.633176	0.633176
Sum of NUM_Hispanic_BEN Sum of NUM_American_IndianAlaska_Native_BEN	0.894417		0.903356	0.900554					0.633176	0.128504
Sum of NUM_BEN_With_Race_Not_Elsewhere_Classified	0.821569		0.801707	0.830466			0.822968		0.740095	0.734077
Sum of NUM_Non-Hispanic_White_BEN	0.996809	0.978655	0.994347	0.996101	0.988772	0.997015	0.996718	0.887564	0.484280	0.866806
Sum of NUM_Minorities	0.958404	0.925675	0.961032	0.957614	0.944932	0.957333	0.958539	0.867684	0.645007	0.959572
Sum of Average_Age_of_BEN	0.678752		0.682844	0.659778	0.633311		0.674831	0.688783	0.128621	0.515698
Sum of NUM_BEN_Atrial_Fibrillation	0.990319	0.969220 0.979353	0.985453 0.991510	0.991337	0.990274		0.990716	0.888630 0.892110	0.458859 0.525949	0.852899
Sum of NUM_BEN_Asthma Sum of NUM_BEN_Cancer	0.995489	0.979353	0.991510	0.992852	0.991685		0.995563	0.892110	0.525949	0.882032
Sum of NUM_BEN_Heart_Failure	0.997108	0.985088	0.995323	0.993852	0.984794				0.483209	0.885584
Sum of NUM_BEN_Chronic_Kidney_Disease	0.997480	0.980181	0.997065	0.995383	0.984109	0.997259	0.997594	0.906086	0.484030	0.894095
Sum of NUM_BEN_Chronic_Obstructive_Pulmonary_Disease	0.986081	0.980417	0.981434	0.983841	0.977815	0.986841	0.985732	0.905511	0.428114	0.834249
Sum of NUM_BEN_Hyperlipidemia	0.996199	0.974138	0.994686	0.996386	0.987456	0.996064	0.996454	0.902110	0.475920	0.885160
Sum of NUM_BEN_Diabetes	0.997736	0.981117	0.996508	0.995642	0.985749	0.997730	0.997434	0.911839	0.493440	0.893757
Sum of NUM_BEN_Hypertension	0.998843	0.982162	0.998059	0.996914	0.985866	0.998953	0.998618	0.907127	0.491385	0.887840
Sum of NUM_BEN_Ischemic_Heart_Disease	0.993954	0.974989	0.991463	0.994045				0.905308	0.456240	0.877711
Sum of NUM_BEN_Stroke Sum of PCT_MEDICARE	0.990470 0.710503	0.971925 0.759188	0.988713 0.713882	0.989929 0.692945	0.980696		0.990562	0.918281	0.446318 0.138118	0.880341
% Urban Pop	0.710503	0.759188	0.713882	0.692945	0.667920			0.750005	0.138118	0.483164
Density (P/mi2)	-0.099963	-0.110703	-0.100658	-0.096325	-0.092020		-0.099698	-0.022034	-0.030915	-0.043443
Children 0-18	0.884945		0.874846	0.887257	0.911738	0.883447	0.886079	0.720117	0.776658	0.840977
Adults 19-25	0.864191	0.823977	0.851022	0.867408	0.899146	0.862807	0.865269	0.694892	0.785158	0.809783
Adults 26-34	0.846985	0.802138	0.833617	0.851409	0.884954		0.848432	0.664003	0.812162	0.808332
Adults 35-54 Adults 55-64	0.860076 0.838622		0.846322 0.819933	0.864281 0.843902	0.897686		0.861368	0.692402 0.674409	0.776687 0.735657	0.803974
Adults 55-64 65+	0.838622	0.799478	0.819933	0.843902	0.887867		0.840024	0.668530	0.735657	0.748042
Latitude	-0.395637	-0.392189	-0.398492	-0.402613	-0.376290		-0.394167	-0.444864	-0.181758	-0.282176
Longitude	0.036162	0.081918	0.023777	0.029848	0.047659	0.039383	0.032672	0.180157	-0.278308	-0.102843
Land Area	0.235431	0.200886	0.248419	0.236252	0.212046	0.232714	0.237349	0.134233	0.203781	0.344879
Water Area	0.038411		0.032297	0.034407					0.047097	0.042598
Mean Elevation Highest Elevation	-0.133770 -0.038246		-0.117766 -0.018904	-0.126100 -0.028611	-0.141332 -0.050574				0.122569 0.306550	0.060713 0.170534
Lowest elevation	-0.036246		-0.018904	-0.346722				-0.297556	-0.559828	-0.292318
Number of bordering states	0.092703		0.090523	0.073651	0.071016		0.089368	0.058746	-0.143034	-0.069825
On Coast	0.464164	0.497887	0.435913	0.455132	0.512184	0.464668	0.463205	0.505677	0.168436	0.270946
Borders Another Country	0.351913	0.303223	0.357825	0.350755	0.353612	0.345594	0.357028	0.180434	0.421510	0.499260
Capital Latitude	-0.386561	-0.391908	-0.392011	-0.390199				-0.462045	-0.135382	-0.268392
Capital Longitude Captial Land Area	0.018177 0.003972		0.005968 0.013931	0.010624 0.004629			0.014318		-0.302807 -0.015016	-0.121403 0.020859
Capital Water Area	-0.091118		-0.086948	-0.090518				-0.100670	-0.021996	-0.041502
Capital Mean Elevation	-0.166033		-0.154788	-0.163860		-0.169042	-0.162464		-0.114759	-0.033818
Capital is the Largest City	-0.154074	-0.128106	-0.149158	-0.156946	-0.178305	-0.151938	-0.155487	-0.115770	-0.123610	-0.183826
Largest City Latitude	-0.419120	-0.419459	-0.423088	-0.422919	-0.395974		-0.417371	-0.465860	-0.233447	-0.316075
Largest City Longitude	0.048321	0.092830	0.035728	0.041774	0.061209		0.044859	0.194353	-0.267233 0.096573	-0.086233 0.501717
Number of Counties Became a State	-0.126570		-0.115157	-0.112935	-0.129547	-0.130157	-0.122258	0.681011 -0.297191	0.096573	0.501717
DaysSinceStayatHomeOrder	-0.021086	-0.020186	-0.030817	-0.027800	0.007419		-0.019335	-0.046409	0.222069	0.052387
DaysSinceFirstPositive	0.357249	0.306142	0.355519	0.364255	0.380604	0.354390	0.360064	0.274180	0.255767	0.299965
DaysSinceTestStart	0.273593	0.219953	0.272942	0.282120	0.296656	0.271182	0.275880	0.213147	0.187346	0.237754
15-49yearsAllcauses	0.886884		0.873498	0.888773			0.887769	0.736622	0.737674	0.796260
15-49yearsAsthma 15-49yearsChronickidneydisease	0.822646 0.917925	0.785134 0.892317	0.805485 0.908566	0.825296 0.917956			0.823386	0.663701 0.803582	0.757688 0.715805	0.750738 0.829422
15-49yearsChronicobstructivepulmonarydisease	0.895564	0.892317	0.879172	0.917996					0.635855	0.829422
15-49yearsDiabetesmellitus	0.911319	0.879991	0.899800	0.913356			0.911822		0.693258	0.813431
15- 49yearsInterstitiallungdiseaseandpulmonarysarcoidosis	0.879916	0.862208	0.865322	0.878905	0.908126	0.879919	0.879735	0.780069	0.644763	0.739273
15-49yearsIschemicheartdisease	0.927678	0.926759	0.915842	0.922736	0.939065	0.928593	0.926497	0.847540	0.595987	0.766226
15-49yearsNeoplasms	0.886136		0.871628	0.887471					0.730821	0.786369
15-49yearsOtherchronicrespiratorydiseases	0.905560	0.883613	0.891223	0.905653	0.934091	0.905184	0.905799	0.782455	0.653038	0.776105
15-49yearsRheumaticheartdisease	0.902424		0.892262	0.897798					0.691629	0.786644
15-49yearsStroke	0.918867	0.897147	0.909310	0.918599				0.805987	0.703053	0.816330
50-69yearsAllcauses 50-69yearsAsthma	0.878744	0.853509 0.762340	0.861522 0.778773	0.880659 0.803715			0.879628	0.741745 0.636677	0.678456 0.742056	0.746293 0.706594
50-69yearsChronickidneydisease	0.916387	0.896945	0.904561	0.915572			0.916688	0.807095	0.676156	0.795122
50-69yearsChronicobstructivepulmonarydisease	0.877906	0.870963	0.859255	0.877419	0.911277	0.878288	0.878455	0.762080	0.542320	0.678790
50-69 years Diabetes mellitus	0.881134	0.855438	0.863901	0.883450	0.919693	0.880643	0.882016	0.750770	0.653836	0.744109
50- 69yearsInterstitiallungdiseaseandpulmonarysarcoidosis	0.861583	0.838312	0.844421	0.862487	0.900025	0.861105	0.862351	0.735721	0.674419	0.726896
50-69yearsIschemicheartdisease	0.904978	0.899635	0.888882	0.901757	0.930901	0.905480	0.904633	0.804866	0.618552	0.737135
50-69yearsNeoplasms	0.871034	0.851227	0.852407	0.872097	0.911177	0.870768	0.871794	0.742697	0.651344	0.720355
50-69 years Other chronic respiratory diseases	0.883753		0.866185	0.882303					0.570326	0.702496
50-69yearsRheumaticheartdisease	0.891423		0.879360	0.885632					0.641520	0.739209
50-69yearsStroke 70+yearsAllcauses	0.906978 0.847442	0.890724 0.816751	0.893997 0.826481	0.906473 0.852488			0.907337	0.798197 0.697071	0.657305 0.654330	0.765372 0.704089
70+yearsAllcauses 70+yearsAsthma	0.847442	0.816751	0.826481	0.852488			0.848827	0.697071	0.654330 0.747748	0.704089
70+yearsChronickidneydisease	0.875670		0.857657	0.876360			0.876558		0.643668	0.724464
70+yearsChronicobstructivepulmonarydisease	0.865156	0.840259	0.845077	0.869812	0.910486	0.864851	0.866648	0.717738	0.599882	0.699384
70+yearsDiabetesmellitus	0.843401		0.821754	0.849108					0.638607	0.695980
70+yearsInterstitiallungdiseaseandpulmonarysarcoidosis	0.831802		0.811884	0.837251			0.833566	0.671418	0.689938	0.706600
70+yearsIschemicheartdisease	0.839315 0.835509		0.816155 0.813851	0.842376 0.840697	0.892450 0.888696		0.840006	0.702589 0.685194	0.634217 0.648382	0.681467
70+yearsNeoplasms 70+yearsOtherchronicrespiratorydiseases	0.835509	0.857451	0.813851	0.840697			0.836996		0.586877	0.705416
70+yearsRheumaticheartdisease	0.842665	0.837198	0.824793	0.837776			0.843753	0.716967	0.626865	0.680450
70+yearsStroke	0.870071	0.847350	0.852618	0.871917	0.909247	0.869793	0.871222	0.729313	0.660317	0.721808

AllAgesAllcauses	0.878588	0.849145	0.861845	0.881318	0.917774	0.877905	0.879599	0.733191	0.695871	0.758571
AllAgesAsthma	0.831304	0.792231	0.813720	0.835086	0.877936	0.829823	0.832271	0.670182	0.749293	0.755115
AllAgesChronickidneydisease	0.904402	0.883840	0.890334	0.904351	0.932451	0.904221	0.904913	0.786269	0.672518	0.775388
AllAgesChronicobstructivepulmonarydisease	0.875803	0.858774	0.856544	0.878011	0.915264	0.875795	0.876810	0.742655	0.580530	0.697110
AllAgesDiabetesmellitus	0.878317	0.849967	0.860647	0.881652	0.919029	0.877785	0.879297	0.742684	0.658751	0.744450
AllAgesInterstitiallungdiseaseandpulmonarysarcoidosis	0.852165	0.823512	0.833849	0.855184	0.896166	0.851536	0.853348	0.710857	0.681959	0.721415
AllAgesIschemicheartdisease	0.882192	0.869062	0.862943	0.881839	0.920162	0.882348	0.882268	0.765407	0.628781	0.718536
AliAgesNeoplasms	0.863741	0.839097	0.844574	0.866307	0.907502	0.863308	0.864731	0.725375	0.663557	0.720556
AllAgesOtherchronicrespiratorydiseases	0.902524	0.884302	0.887253	0.902007	0.932378	0.902199	0.902973	0.782928	0.623094	0.754060
AllAgesRheumaticheartdisease	0.879079	0.873449	0.864765	0.873886	0.903225	0.878847	0.879647	0.764366	0.648372	0.728889
AllAgesStroke	0.894221	0.873914	0.879380	0.894925	0.924402	0.894172	0.894932	0.768243	0.667366	0.753694
AllAgesTotal	0.879105	0.851798	0.861916	0.881553	0.918458	0.878539	0.880046	0.737330	0.684312	0.751284
Airpollution	0.887961	0.886816	0.873716	0.881728	0.909727	0.888331	0.887745	0.777358	0.655261	0.730312
Highbody-massindex	0.892574	0.870891	0.875767	0.893521	0.928006	0.892269	0.893140	0.768343	0.661265	0.754688
Highfastingplasmaglucose	0.885519	0.868208	0.867475	0.886276	0.922271	0.885469	0.886040	0.770273	0.617289	0.725192
HighLDLcholesterol	0.892016	0.880761	0.874040	0.890927	0.925614	0.892300	0.891950	0.780580	0.627540	0.728204
Highsystolicbloodpressure	0.896298	0.880918	0.879042	0.896085	0.929809	0.896363	0.896543	0.785586	0.638860	0.742184
Impairedkidneyfunction	0.888684	0.870825	0.871779	0.888904	0.923102	0.888693	0.889102	0.770201	0.658349	0.741125
Noaccesstohandwashingfacility	0.876183	0.855685	0.860915	0.875209	0.908573	0.875653	0.876553	0.753540	0.668494	0.745193
Smoking	0.880256	0.864750	0.861340	0.881441	0.918294	0.880406	0.880814	0.757828	0.604253	0.706722
Log10Pop	0.730625	0.738162	0.716041	0.724834	0.750347	0.731527	0.730121	0.665876	0.425752	0.516893
DaysSinceInfection	0.412821	0.360632	0.410278	0.422147	0.434949	0.410914	0.414835	0.354265	0.259813	0.349814
Children0-18	0.170467	0.184747	0.184614	0.162743	0.122101	0.172944	0.167407	0.173000	0.050826	0.150062
Allriskfactors	0.881460	0.858902	0.864027	0.883001	0.919342	0.881097	0.882336	0.747372	0.661101	0.738270
State Area Ratio	-0.128550	-0.166800	-0.113602	-0.122087	-0.145833	-0.130919	-0.125230	-0.249270	-0.098980	-0.021322
Elevation Ratio	0.006435	-0.008386	0.016149	0.010278	-0.014214	0.007719	0.004657	0.117476	0.047721	0.006349
Capital Area Ratio	-0.107958	-0.139494	-0.098783	-0.101355	-0.113882	-0.109206	-0.106482	-0.160284	-0.071880	-0.046967
Boundaries	0.500872	0.558822	0.480645	0.479234	0.518677	0.501040	0.498998	0.456575	0.125069	0.276862
Latitude Difference to State Capital	-0.251296	-0.188306	-0.234552	-0.277897	-0.313035	-0.251254	-0.254554	-0.091516	-0.409883	-0.230231
Longitude Difference to State Capital	-0.132644	-0.120676	-0.128482	-0.139685	-0.144345	-0.132468	-0.134362	-0.089151	-0.102664	-0.103498
Latitude Difference to DC	-0.395637	-0.392189	-0.398492	-0.402613	-0.376290	-0.399287	-0.394167	-0.444864	-0.181758	-0.282176
Longitude Difference to DC	-0.036162	-0.081918	-0.023777	-0.029848	-0.047659	-0.039383	-0.032672	-0.180157	0.278308	0.102843
Latitude Difference to Center	-0.395637	-0.392189	-0.398492	-0.402613	-0.376290	-0.399287	-0.394167	-0.444864	-0.181758	-0.282176
Longitude Difference to Center	-0.036162	-0.081918	-0.023777	-0.029848	-0.047659	-0.039383	-0.032672	-0.180157	0.278308	0.102843

Select upper triangle of correlation matrix upper = corr_matrix.where(np.triu(np.ones(corr_matrix.shape), k=1).astype(np.bool))

Find index of feature columns with correlation greater than 0.95 to_drop = [column for column in upper.columns if any(upper[column] > 0.95)]

Ŀ	Sum of NUM_Medicare_BEN	Sum of NUM_Black_or_African_American_BEN	Sum of NUM_Asian_Pacific_Islander_BEN	Sum of NUM_Hispanic_BEN	Sum of NUM_American_IndianAlaska_Native_BEN	Sum of NUM_BEN_With_Race_Not_Elsewhere_Classified	Sum of Average_Age_of_BEN	Sum of U	% Jrban Pop	Density (P/mi2)	Children 0-18	Latitude	Longitude	Land Area
0	1820384.0	62311.0	76773.0	46525.0	147917.0	23372.0	996.298679	10.069041	66.0	1.2863	181405.17	61.370716	-152.404419	570665.0 §
1	10804823.0	1549811.0	30624.0	65500.0	5556.0	58660.0	3967.220634	51.254704	59.0	96.9221	1105570.08	32.806671	-86.791130	50644.0
2	15892716.0	1334245.0	19642.0	108428.0	62782.0	61250.0	3928.834167	94.570949	56.2	58.4030	686482.50	34.969704	-92.373123	52030.0
4	10786064.0	221183.0	61840.0	689880.0	179818.0	114903.0	1009.367955	14.075942	89.8	64.9550	1744612.56	33.729759	-111.431221	113595.0
5	42579588.0	2072012.0	3276415.0	5674776.0	113871.0	562214.0	4001.853612	63.398334	95.0 2	256.3727	9481941.36	36.116203	-119.681564	155766.0

C+ <class 'pandas.core.frame.DataFrame'>
Int64Index: 50 entries, 0 to 54

Data	columns (total 38 columns):		
#	Column	Non-Null Count	Dtype
0	Sum of NUM Medicare BEN	50 non-null	float64
1	Sum of NUM Black or African American BEN	50 non-null	float64
2	Sum of NUM Asian Pacific Islander BEN	50 non-null	float64
3	Sum of NUM Hispanic BEN	50 non-null	float64
4	Sum of NUM American IndianAlaska Native BEN	50 non-null	float64
5	Sum of NUM BEN With Race Not Elsewhere Classified	50 non-null	float64
6	Sum of Average Age of BEN	50 non-null	float64
7	Sum of PCT MEDICARE	50 non-null	float64
8	% Urban Pop	50 non-null	float64
9	Density (P/mi2)	50 non-null	float64
10	Children 0-18	50 non-null	float64
11	Latitude	50 non-null	float64
12	Longitude	50 non-null	float64
13	Land Area	50 non-null	float64
14	Water Area	50 non-null	float64
15	Mean Elevation	50 non-null	float64
16	Highest Elevation	50 non-null	float64
17	Lowest elevation	50 non-null	float64
18	Number of bordering states	50 non-null	float64
19	On Coast	50 non-null	float64
20	Borders Another Country	50 non-null	float64
21	Captial Land Area	50 non-null	float64
22	Capital Water Area	50 non-null	float64
23	Capital Mean Elevation	50 non-null	float64
24	Capital is the Largest City	50 non-null	float64
25	Became a State	50 non-null	float64
26	DaysSinceStayatHomeOrder	50 non-null	float64
27	DaysSinceFirstPositive	50 non-null	float64
28	DaysSinceTestStart	50 non-null	float64
29	Log10Pop	50 non-null	float64
30	DaysSinceInfection	50 non-null	float64
31	Children0-18	50 non-null	float64
32	State Area Ratio	50 non-null	float64
33	Elevation Ratio	50 non-null	float64
34	Capital Area Ratio	50 non-null	float64
35	Boundaries	50 non-null	float64
36	Latitude Difference to State Capital	50 non-null	float64
37	Longitude Difference to State Capital	50 non-null	float64
dtyp	es: float64(38)		
	ry usage: 15.2 KB		

D-	Sum of NUM_Medicare_BEN	Sum of NUM_Black_or_African_American_BEN	Sum of NUM_Asian_Pacific_Islander_BEN	Sum of NUM_Hispanic_BEN	Sum of NUM_American_IndianAlaska_Native_BEN	Sum of NUM_BEN_with_Race_Not_Elsewhere_Classified	Sum of Average_Age_of_BEN	Sum of PCT_MEDICARE	% Urban Pop	Density (P/mi2)	Children 0- 18	Latitude	Longit
count	5.000000e+01	5.000000e+01	5.000000e+01	5.000000e+01	50.000000	50.000000	50.000000	50.000000	50.000000	50.000000	5.000000e+01	50.000000	50.0000
mean	1.057661e+07	9.653450e+05	1.439833e+05	5.412557e+05	39027.080000	88021.940000	3574.438430	52.910339	74.294000	440.074918	1.513864e+06	39.399000	-93.060
std	1.317051e+07	1.280319e+06	4.765951e+05	1.644850e+06	88090.522177	115323.411288	2527.939135	46.730862	14.976518	1662.815407	1.772177e+06	6.112752	19.379€
min	1.655870e+05	2.960000e+02	1.660000e+02	4.130000e+02	0.000000	1693.000000	70.002893	0.972106	38.700000	1.286300	1.160123e+05	21.094318	-157.4983
25%	2.518838e+06	6.328700e+04	6.770500e+03	3.269350e+04	2929.750000	19717.000000	1529.891773	13.039638	66.025000	56.532925	4.596994e+05	35.659511	-99.697
50%	6.848160e+06	3.978665e+05	2.777200e+04	1.050865e+05	7558.000000	58749.500000	3752.318846	52.406965	74.400000	110.435050	1.059542e+06	39.583974	-89.3010
75%	1.479523e+07	1.548688e+06	7.370350e+04	2.012818e+05	28748.250000	100639.500000	5216.766839	79.721735	87.725000	226.003700	1.728603e+06	43.052506	-78.5790
max	7.644909e+07	7.011107e+06	3.276415e+06	1.007620e+07	560433.000000	562214.000000	13644.965980	219.756971	100.000000	11814.541000	9.481941e+06	61.370716	-69.381!

```
from sklearn.model selection import train test split
 X_train, X_val, y_train, y_val = train_test_split(X, y, test_size = 0.25, random_state = 42)
 X train.shape, y train.shape, X val.shape, y val.shape
  [+ ((37, 38), (37,), (13, 38), (13,))
  Г÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Density Children Θ-
(P/mi2) 18 Latitude Longiti
                                              Sum of Su
                                                                                                                                                                                       3 700000e+01
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                         std
                                                            1 384476e+07
                                                                                                                                                                                  1.398898e+06
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                         min
                                                            1.655870e+05
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                                                                                                                                                                                 1.057920e+05 12709.000000
5.217080e+05 30624.000000
1.693845e+06 76800.000000
7.011107e+06 783067.000000
                       25%
                                                            3.242760e+06
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5.217080e+05
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                         50%
                                                                                                                                                                                                                                                                                                                                                                       1.112130e+05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3926.277651 54.780620 74.600000 112.820400 1.140729e+06 39.063946 -86.791
                                                            8.517210e+06
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                         75%
                                                            1.629170e+07
                                                                                                                                                                                                                                                                                                                                                                     2.027260e+05
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                                                                                                                                                                             7.011107e+06
                                                            7.644909e+07
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 # Optimizing Hyperparameters
from sklearn.model_selection import GridSearchCV
from sklearn.ensemble import RandomForestRegress
 # Parameters to fit
max_depth = [2, 3, 4]

n_estimators = [28, 29, 30]

min_samples_split = [1.5, 2, 2.5]

min_samples_leaf = [3.5, 4, 4.5]

max_leaf_nodes = [None]

max_features = ['auto']

ccp_alpha = [0.0, 0.00625, 0.0125]
 min weight fraction leaf = [0.0, 0.00625, 0.0125]
 hyperf = dict(n_estimators = n_estimators, max_depth = max_depth,
min_samples_split = min_samples_split,
min_samples_tel = min_samples_tel,
max_leaf_nodes = max_leaf_nodes,
max_features = max_leaf_nodes,
ccp_alphasccp_alpha,
min_weight_fraction_leaf=min_weight_fraction_leaf)
# Output best accuracy and best parameters
print('The score achieved with the best parameters = ', gridF.best_score_, '\n')
print('The parameters are:', gridF.best_params_)
               nt('The score achieved with the best parameters = ', gridf. best_score_, '\n')

nt('The parameters are', 'gridf-best_params.)

Fitting 1 folds for each of 729 candidates, totalling 2HP fits

Favallel(n_jobs-1): bone based of 729 candidates, totalling 2HP fits

Favallel(n_jobs-1): bone 1 tasks | elapsed: 1.6s

[Favallel(n_jobs-1): bone 1 tasks | elapsed: 1.6s

[Favallel(n_jobs-1): bone 9 tasks | elapsed: 1.6s

[Favallel(n_jobs-1): bone 9 tasks | elapsed: 1.5s

[Favallel(n_jobs-1): bone 9 tasks | elapsed: 1.5s

[Favallel(n_jobs-1): batch computation too fast (0.1863.) Setting batch_size-2.

[Favallel(n_jobs-1): batch computation too fast (0.1863.) Setting batch_size-2.

[Favallel(n_jobs-1): bone 5 tasks | elapsed: 1.5s

[Favallel(n_jobs-1): bone 5 tasks | elapsed: 2.6s

[Favallel(n_jobs-1): bone 5 tasks | elapsed: 3.9s

[Favallel(n_jobs-1): bone 5 tasks | elapsed: 3.9s

[Favallel(n_jobs-1): bone 5 tasks | elapsed: 3.7s

[Favallel(n_jobs-1): bone 5 tasks | elapsed: 4.7s

[Favallel(n_jobs-1): bone 5 tasks | elapsed: 1.6s

[Favallel(n_jobs-1): bone 5 tasks | elapsed: 2.4s

[Favallel(n_jobs-1): bone 150 tasks | elapsed: 2.4s

[Favallel(n_jobs-1): bone 150 tasks | elapsed: 2.4.5

[F
                    The parameters are: {'ccp_alpha': 0.0, 'max_depth': 3, 'max_features': 'auto', 'max_leaf_nodes': None, 'min_samples_leaf': 4, 'min_samples_split': 2, 'min_weight_fraction_leaf': 0.0, 'n_estimators': 29}
[Parallel(n_jobs=1)]: Done 2187 out of 2187 | elapsed: 36.65 finished
sted.org/packages/6e/a1/f7a22f144f33be78afeb86bfa78478e8284a64263a3c09b1ef54e673841e/category encoders-2.0.0-pv2.pv3-none-any.whl (87kB)
 from sklearn.ensemble import RandomForestRegressor
from sklearn.pipeline import make_pipeline
import category_encoders as ce
from sklearn.impute import SimpleImputer
  pipeline1 = make_pipeline(
             ellne1 make_pipeline(
cc.Oneiotincoder(use_cat_names=True),
SimpleImputer(strategy="mean"),
RandomForestRegressor(bcotstrap=True, ccp_alpha=0.0, criterion="mse",
max_depth=3, max_features="auto", max_leaf_nodes=hone,
max_samples=hone, min_impurity_decreas=e0.0,
min_impurity_split=Nome, min_impurity_split=Nome, min_impurity_split=Nome,
min_impurity_split=Nome, min_impurity_split=Nome,
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min_impurity_split=Nome,
min_impurity_sp
  # Get the model's training accuracy
print("Training Accurary: R^2 = ", pipelinel.score(X_train,y_train))
            Set the model's validation accuracy
int('Validation Accuracy: R^2 = ', pipeline1.score(X_val, y_val))
  Training Accurary: R^2 = 0.6195488363328325
Validation Accuracy: R^2 = 0.48283160859213214
  print(pipeline1.steps[2][1].feature importances )
               Feature Laportances = [0. 0. 0.0751305 0.0953321 0.0953321 0.0953321 0.0953321 0.0953321 0.0953321 0.0953321 0.0953321 0.09535321 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.0953525 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.0953576 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.0953517 0.09535569 0.09535569 0.0953517 0.09535569 0.09535569 0.0953517 0.09535569 0.09535569 0.0953517 0.09535569 0.09535569 0.0953517 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.0953569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.09535569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.0953569 0.09
```

```
%matplotlib inline
import matplotlib.ppplot as plt
# Get feature importances
encoder = pipelinel.named_steps['onehotencoder']
encoded = encoder.transform(X_train)
rf = pipelinel.named_steps['randomforestregressor']
importances! = pd.Series(rf.feature_importances_, encoded.columns)
# Plot feature importances
# Plot feature importances
      n = 12
plt.figure(figsize=(10,n/2))
plt.title(f'Top {n} features pipeline1')
importances1.sort_values()[-n:].plot.barh(color='grey');
                                                                            Density (P(mi2) -
                                                                        Canital Area Ratio -
                                                                        Highest Elevatio
                                                                                % Urban Pop
                                        Longitude Difference to State Capital
                                                                               Children0-18
                                                                                                                          0.02
    # Generate validation curves

**Mmatplotlib inline

import numpy as np

import matplotlib.pyplot as plt

from sklearn.model_selection imp

impeline2 = make_pipeline(

ce.OrdinalEncoder(),

cimnleTmouter(),
                                                                               import validation_curve
     depth = range(1, 10, 2)
train_scores, val_scores = validation_curve(
    pipeline2, X_train, y_train,
    param_name='randomforestregressor_max_depth',
    param_range=depth,
    cv=3,
    n_jobs=-1
     plt.figure(dpi=158)
plt.plc(depth, np.mean(train_scores, axis=1), color='blue', label='training error')
plt.plc(depth, np.mean(val_scores, axis=1), color='red', label='validation error')
plt.title('validation Curve')
plt.xlabel('model complexity: RandomForestRegressor max_depth')
plt.ylabel('model complexity: RandomForestRegressor max_depth')
plt.ylabel('model score: Accuracy')
plt.lapen(0);
                                                                                                                                      Validation Curve
                                      0.8
                                      0.6
                                      0.4
                                                                                                                                                                                                                              training error
                                      0.2
                                                                                                                                                                                                                              validation error
                                      0.0
                       model
                                 -0.2
                                   -0.4
                                                                          model\ complexity:\ Random Forest Regressor\ max\_depth
# Get drop-column importances
column = 'Density (P/mi2)'
     # Fit without column
pipeline3.fit(%_train.drop(columns=column), y_train)
score_without = pipeline3.score(%_val.drop(columns=column), y_val)
print(f'Validation Accuracy without {column}: {score_without}')
      # Compare the error with & without column
print(f'Drop-Column Importance for {column}: {score_with - score_without}')
       C→ Validation Accuracy without Density (P/mi2): 0.5809375902676718
Validation Accuracy with Density (P/mi2): 0.48283160859213214
Drop-Column Importance for Density (P/mi2): -0.018105981675539673
      # Using Eli5 library which does not work with pipelines
transformers = make_pipeline(
   ce.OmetoHznoder(use_caf_names=True),
   SimpleImputer(strategy='most_frequent')
      X_train_transformed = transformers.fit_transform(X_train)
X_val_transformed = transformers.transform(X_val)
                                     RandomForestRegressor(bootstrap=True, ccp_alpha=0.15, criterion='nse',
max_depth=3, max_features='auto', max_leaf_nodes=None,
max_samples=None, min_supurity_decress=0.0,
min_impurity_split=None, min_samples_leaf=4,
min_samples_split=2, min_weight_fraction_leaf=0,
n_estimators=20, n_jobs=None, oob_score=False,
random_estate=0, verbes=0, varm_start=False)
      model1.fit(X train transformed, y train)
      P. RandomforestRegressor(bootstrap=True, ccp_alpha=0.15, criterion='mse',
max_depth=3, max_features='auto', max_leaf_node=None,
max_samples=None, min_impurtty_decrease=0.0,
min_impurity_split=None, min_samples_leaf=4,
min_samples_split=2, min_esimple_fraction_leaf=0,
m_estimator=<20, n_jobs=None, oob_score=False,
random_crate=0, wrent=cee, warm_tart=false)
      # Get permutation importances
! pip install eli5
from eli5.sklearn import PermutationImportance
import eli5
```

```
model1,
scoring='r2',
n_iter=2,
random_state=42
     permuter.fit(X_val_transformed, y_val)
feature_names = X_val.columns.tolist()
    elis.show_weights(
    permuter,
    top=None, # show permutation importances for all features
    feature_names=feature_names
regioner, a how prematation injurances for all features feature, general processing injury and processing inju
     from sklearn.metrics import mean_squared_error, r2_score
     # Coefficient of determination r2 for the training set
pipeline_score = permuter.score(X_train_transformed,y_train)
print("Coefficient of determination r2 for the training set.: ", pipeline_score)
     # Coefficient of determination r2 for the validation set
pipeline_score = permuter.score(X_val_transformed,y_val)
print("Coefficient of determination r2 for the validation set.: ", pipeline_score)
     """
y_pred = permuter.predict(X_val_transformed)
print("Mean squared error: %.2f"% mean_squared_error(y_val, y_pred))
      Coefficient of determination r2 for the training set.: 0.6195488363328325
Coefficient of determination r2 for the validation set.: 0.48283160859213214
Mean squared error: 528.60
     # Thus, Density remains important according to feature permutation than according to feature importance in the Rando
# Use importances for feature selection
print("Shape before removing features:', X_train.shape)
      C. Shape before removing features: (37, 38)
    # Coefficient of determination r2 for the training set
pipeline_score = pipeline4.score(X_train,y_train)
print("Coefficient of determination r2 for the training set.: ", pipeline_score)
     # Coefficient of determination r2 for the validation set
pipeline_score = pipeline4.score(X_val,y_val)
print("Coefficient of determination r2 for the validation set.: ", pipeline_score)
      w The mean squared error
y_pred = pipeline4.predict(X_val)
print("Mean squared error: %.2f"% mean_squared_error(y_val, y_pred))
       Coefficient of determination r2 for the training set.: 0.6266222750237471
Coefficient of determination r2 for the validation set.: 0.4897612195667084
Mean sourced error: 521.52
    pipeline4.fit(X_val, y_val)
# Plot of features
%matplotlib inline
import matplotlib.pyplot as plt
    # Get feature importances
encoder = pipeline4.named_steps['onehotencoder']
encoded = encoded.transform(X_val)
rf = pipeline4.named_steps['randomforestregressor']
importances2 = pd.Series(rf.feature_importances_, encoded.columns)
     n = b
plt.figure(figsize=(10,n/2))
plt.title(f'Top {n} features pipeline4')
importances2.sort_values()[-n:].plot.barh(color='grey');
```

```
5/3/2020
                                                                                                                                                                                      Covid_19NormedDeathsStateDataD.ipynb - Colaboratory
        Б
                                                                                                                    Top 6 features pipeline4
                                                 Capital Area Ratio
                 Sum of NUM American IndianAlaska Native BEN
       # Gradient boosting using XGboost with 15 estimators
from xgboost import XGBRegressor
pipelines = make pipeline(
ce.ordinalEncoder(),
XGBRegressor(n_estimators15,
max_depth=1,
learning_rate=0.41, # try a higher learning rate
random_trate=0.41, # try a higher learning rate
       pipeline5.fit(X_train, y_train);
        [] [19:45:31] WARNING: /workspace/src/objective/regression_obj.cu:152: reg:linear is now deprecated in favor of reg:squarederror
       # Coefficient of determination r2 for the training set
pipeline_score = pipelineS.score(X_train,y_train)
print("Coefficient of determination r2 for the training set.: ", pipeline_score)
       # Coefficient of determination r2 for the validation set
pipeline_score = pipeline5.score(X_val,y_val)
print("Coefficient of determination r2 for the validation set.: ", pipeline_score)
       # The mean squared error
y_pred = pipelines.predict(X_val)
print("Mean squared error: %.2f"% mean_squared_error(y_val, y_pred))
         Coefficient of determination r2 for the training set.: 0.7838756216629406
Coefficient of determination r2 for the validation set.: 0.606786244166149
Mean squared error: 402.93
       The best validation score (0.605786) and lowest MSE (402.93) comes from using Gradient Boosting with 13 estimators.
       pipeline5.fit(X_val, y_val)
# Plot of features
%matplotlib inline
import matplotlib.pyplot as plt
       # Get feature importances
encoder = pipelineS.named.steps['ordinalencoder']
encoded = encodect.transform(K_val)
rf = pipelineS.named_steps['xgbregressor']
importances2 = of.Series(fr.f.Seture_Importances_, encoded.columns)
       # Plot feature importances
n = 6
       n = b
plt.figure(figsize=(10,n/2))
plt.title(f'Top (n) features pipeline5')
importances3.sort_values()[-n:].plot.barh(color='grey');
       [3:45:31] WARNING: /workspace/src/objective/regression_obj.cu:152: reg:linear is now deprecated in favor of reg:squarederror.

Top 6 features pipeline5
                 Sum of NUM_American_IndianAlaska_Native_BEN
                                                   Density (P/mi2)
                                                          Land Area - 0.00 0.05
                                                                                                                   0.15
                                                                                               0.10
                                                                                                                                  0.20
                                                                                                                                                  0.25
                                                                                                                                                                   0.30
       # Gradient boosting using XGboost with 1000 estimators encoder = ce.OrdinalEncoder()
X.train_encoded = encoder.fit_transform(X_train)
X.val_encoded = encoder.transform(X_val)
X.train_encoded = encoder.transform(X_val)
```

[+ ((37, 22), (13, 22), (37, 22), (13, 22))

model2 = XGBRegressor(
 n_estimators=1800, # <= 1800 trees, depends on early stopping
 max_depth=1,
 learning_rate=0.41, # try higher learning_rate
 n_jobs=1)</pre> $\label{eq:model2.fit} $$ \mbox{model2.fit}(X_{train_encoded}, \mbox{y_t-rain}, \mbox{eval_set=eval_set}, \mbox{ eval_metric='rmse'}, \\ \mbox{early_stopping_rounds=50} $$ \mbox{} $$$

г

```
[19:45:31] WARNING: /workspace/src/objective/regression_obj.cu:152: reg:linear is now deprecated in favor of reg:squarederror.
[8] validation_0-mes:91.5887 validation_1-mes:92.8396
Wiltiple eval metrics have been passed: 'validation_1-mes' vali be used for early stopping.
                                                                                                                   essor(base_score=0.5, booster='gbtree', colsample_bylevel=1, colsample_bynode=1, colsample_byree=1, gamma=0, importance_type='gbin', learning_rate=0.41, max_elta_step=0, max_depth=1, min_child_weight=1, missing=None, n_estimators=18000 n_iobs=-1, inthread-None, objective='regilinear', random_state=0, reg_alpha=0, reg_lambda=1, scale_pos_weight=1, seed=None, silen=twone, subsample=1, verbosity=1)
   # Plot the results result() results = model2.evals_result() train_error = results['validation_8']['rmse'] val_error = results['validation_1']['rmse'] epoch = rame(cf, lem(train_error)_1) plt.plot(epoch, train_error, label='rmin') plt.plot(epoch, val_error, label='validation') plt.plot(epoch, val_error, label='validation') plt.ylabel('806 Error') plt.ylabel('806 Error') # plt.ylabel('806 Complexty (o_nestimators)') # plt.ylabel('806 
         plt.legend();
      # Plot log classification error versus model complexity import numpy as no results - model zenals_result() log_train_error = np.log(results['validation_0'']['rmse']) log_train_error = np.log(results['validation_1'']['rmse']) epoch = range(j, len(train_error)*1) plt.plot(epoch, log_train_error, label='validation') plt.plot(epoch, log_train_error, label='validation') plt.plate(plot, log_train_error, label='validation') plt.plate() (so gNB Error') plt.valbe('(log_NB Error') plt.
                D+
                                                                        4.0
gb.fit(X_train, y_train)
             #y_pred = gb.predict(X_val)
#print('Gradient Boosting R^2', r2_score(y_val, y_pred))
                Б
```

```
('xgbregressor's,'
XGBRegressor(base_score=0.5, booster='gbtree',
colsample_byteve=1, 
  # Coefficient of determination r2 for the training set 
#pipellne_score = gb.score(X_train,y_train) 
y_train_pred = gb.predic(T_C_train,y_train) 
pipeline_score = r2_score(y_train,y_train_pred) 
print(TCoefficient of determination r2 for the training set.: ", pipeline_score)
  # Coefficient of determination r2 for the validation set 
#pipeline_score = gb.score(X_val,y_val) 
y_val_pred = gb.predict(X_val) 
pipeline_score = r2_score(y_val, y_val_pred) 
print("Coefficient of determination r2 for the validation set.: ", pipeline_score)
      Coefficient of determination r2 for the training set.: 0.7838756216629406

Coefficient of determination r2 for the validation set.: 0.606786244166149

Mean squared error: 402.93
    # Get feature importances
encoder = gb.named_steps['ordinalencoder']
encoded = encodec_transform(X_val)
rf = gb.named_steps['vgbregressor']
importances = pd.Sertes(rf.feature_importances_, encoded.columns)
    n = 6
plt.figure(figsize=(10,n/2))
splt.title(f'Top {n} features pipelines')
plt.title(f'Top {n} features Gradient Boosting')
importances4.sort_values()[-n:].plot.barh(color='grey');
                                                                              Longitude Difference to State Capital
                                                                                                                                                            Density (P/mi2)
                                                                                                                                                                                     Land Area 0.00 0.05
[ptp install pdpbox Demindence of the public of the public
    !pip install pdpbox
  pdp interact plot(interaction, plot type='grid', feature names=features2);
                           findfont: Font family ['Arial'] not found. Falling back to DejaVu Sans. findfont: Font family ['Arial'] not found. Falling back to DejaVu Sans. findfont: Font family ['Arial'] not found. Falling back to DejaVu Sans. findfont: Font family ['Arial'] not found. Falling back to DejaVu Sans.
                                                                           PDP interact for "Latitude" and "Longitude Difference to State Capital"
                                                                                                                                                                                                                                                                                                                                                                                                      -140.72
                                                                                                                                                                                                     \label{eq:index} $$\inf(x)=1, x\in \mathbb{R}^{n}$ index properties of the 
    import plotly.graph_objs as go
    target = 'Value of d parameter
```

```
yaxis=dict(title=features2[1]),
zaxis=dict(title=target)
 fig = go.Figure(surface, layout)
fig.show()
 г
                                                                                                                                                                                                                                                                                                                              -120
                                                                                                                                                                                                                                                                                                                              -130
                                                                                                                                                                                                                                                                                                                             -135
  In order to establish feature importances. Shapley Force Plots are used. SHAP is both consistent and accurate as a way to allocate feature
                                ces. The details are in a recent paper by Lundberg and Lee (papers.nips.cc/paper/7062-a-unified-approach-to-interpreting-model
        Created wheel for shale: Tilenamesnape-8.33.0-typo-typos-linux_now_s-mm. sactored in directory: root_cache/plyheals/97/79/f79/f79/80808678930808030816472-f796b123516bc224c

Successfully built shap

Successfully built shap

Successfully built shap

Book of the state of the state
                  RESTART RUNTIME
  # Local Interpretation using SHAP (for prediction at State # = 4, row 32)
      odel_shap = XGBRegressor(n_estimators=15,
objectives-reg:squarederror',
max_depth=1, # try deeper trees because of high cardinality categoricals
learning_rate=0.41, # try a higher learning rate
random_tate=22,
n_106s=-1)
   shap.initjs()

Mexplainer = shap.TreeExplainer(model2)

explainer = shap.TreeExplainer(model_shap)

mshap_values = explainer.shap_values(X_train_shap_enc_shap_values = explainer.shap_values(X_train_shap_enc_shap_values = explainer.shap_values(X_train_shap_enc_shap_values = explainer.shap_values(X_train_shap_enc_shap_values = explainer.shap_values(X_train_shap_enc_shap_values = explainer.shap_values(X_train_shap_enc_shap_values)
```

```
i = 32
shap.force_plot(explainer.expected.value,
shap.values[i],

# features_X_train_shap_encoded.loc[i],
features_X_train_loc[i],
# feature_anes_X_train_shap_encoded.columns)
feature_names=X_train_columns)
   [] validation_0-rmse:91.9687 validation_1-rmse:92.6396
Multiple eval metrics have been passed: 'validation_1-rmse' will be used for early stopping.
               Multiple eval metrics have been passed: 'validation_1-rmse' will b

Will train until validation_1-rmse hasn't improved in 50 rounds.

1] validation_0-mes:55.8496
validation_1-rmse:59.3736

(2] validation_0-rmse:10.6495
validation_1-rmse:20.57376

(3] validation_0-rmse:20.6295
validation_1-rmse:20.77771
validation_0-rmse:22.411
validation_0-rmse:22.411
validation_0-rmse:22.411
validation_0-rmse:23.944
validation_1-rmse:23.9450
validation_1-rmse:23.9450
validation_1-rmse:23.9450
validation_0-rmse:19.1823
validation_0-rmse:19.1823
validation_0-rmse:19.1823
validation_0-rmse:19.5841
validation_0-rmse:19.5851
validation_0-rmse:19.5852
validation_0-rmse:23.9530
validation_0-rmse:19.5851
validation_0-rmse:10.5852
validation_0-rmse:23.9530
validation_0-rmse:23.9530
validation_0-rmse:23.9530
validation_0-rmse:23.9530
validation_0-rmse:23.9530
validation_0-rmse:23.9530
validation_0-rmse:23.9530
validation_0-rmse:23.9530
validation_1-rmse:23.8532
validation_1-rmse:23.8532
validation_1-rmse:23.8532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (js)
X_train_processed = processor.fit_transform(X_train)
column_names = X_train.columns
shap_values_array = pd.DataFrame(columns = column_names)
for i in range(len(y.train)):
    row x train.loc[[i]]
    rop and train.loc[[i]]
    replainer = shep.TreeExplainer(model_shap)
    row processed = processor.transform(row)
    shap values input = explainer.shap values(row.processed)
    shap.values_array = np.concatenate((shap.values_array, shap.values_input), axis=0)
# Create a 3D plot of force as a function of state curve displacement from mean curve and features for validation sai 
# A two feature partical dependence plot in 3D 
import plotly.graph_objs as go 
surface = go.Surface(x=column_names, 
y=y_train, 
z=shap_values_array)
fig = go.Figure(surface, layout)
fig.show()
D+
```