04_baseline_model_revised

March 10, 2024

1 Revised Baseline Model

2 Import Modules

[27]:
```
import numpy as np
import pandas as pd
import statsmodels.api as sm
from statsmodels.tools import eval_measures
import statsmodels.formula.api as smf

%matplotlib inline
import matplotlib.pyplot as plt
plt.style.use("dark_background")
import seaborn as sns

from warnings import filterwarnings
filterwarnings('ignore')
```

3 Load Data

[28]:
```
# load the provided data
train_features = pd.read_csv('../data/dengue_features_train.csv',
                             index_col=[0,1,2])

train_labels = pd.read_csv('../data/dengue_labels_train.csv',
                           index_col=[0,1,2])
```

4 Split Data

[29]:
```
# Seperate data for San Juan
sj_train_features = train_features.loc['sj']
sj_train_labels = train_labels.loc['sj']

# Separate data for Iquitos
iq_train_features = train_features.loc['iq']
iq_train_labels = train_labels.loc['iq']
```

[30]:
```
print('San Juan')
print('features: ', sj_train_features.shape)
print('labels   : ', sj_train_labels.shape)

print('\nIquitos')
print('features: ', iq_train_features.shape)
print('labels   : ', iq_train_labels.shape)
```

```
San Juan
features:  (936, 21)
labels   :  (936, 1)

Iquitos
features:  (520, 21)
labels   :  (520, 1)
```

5 Feature Engineering

[31]:
```
# Remove `week_start_date` string.
sj_train_features.drop('week_start_date', axis=1, inplace=True)
iq_train_features.drop('week_start_date', axis=1, inplace=True)
```

6 Check for Missing Values

[32]:
```
# Null check
pd.isnull(sj_train_features).any()
```

[32]:
```
ndvi_ne                                  True
ndvi_nw                                  True
ndvi_se                                  True
ndvi_sw                                  True
precipitation_amt_mm                     True
reanalysis_air_temp_k                    True
reanalysis_avg_temp_k                    True
reanalysis_dew_point_temp_k              True
reanalysis_max_air_temp_k                True
reanalysis_min_air_temp_k                True
reanalysis_precip_amt_kg_per_m2          True
reanalysis_relative_humidity_percent     True
reanalysis_sat_precip_amt_mm             True
reanalysis_specific_humidity_g_per_kg    True
reanalysis_tdtr_k                        True
station_avg_temp_c                       True
station_diur_temp_rng_c                  True
station_max_temp_c                       True
station_min_temp_c                       True
```

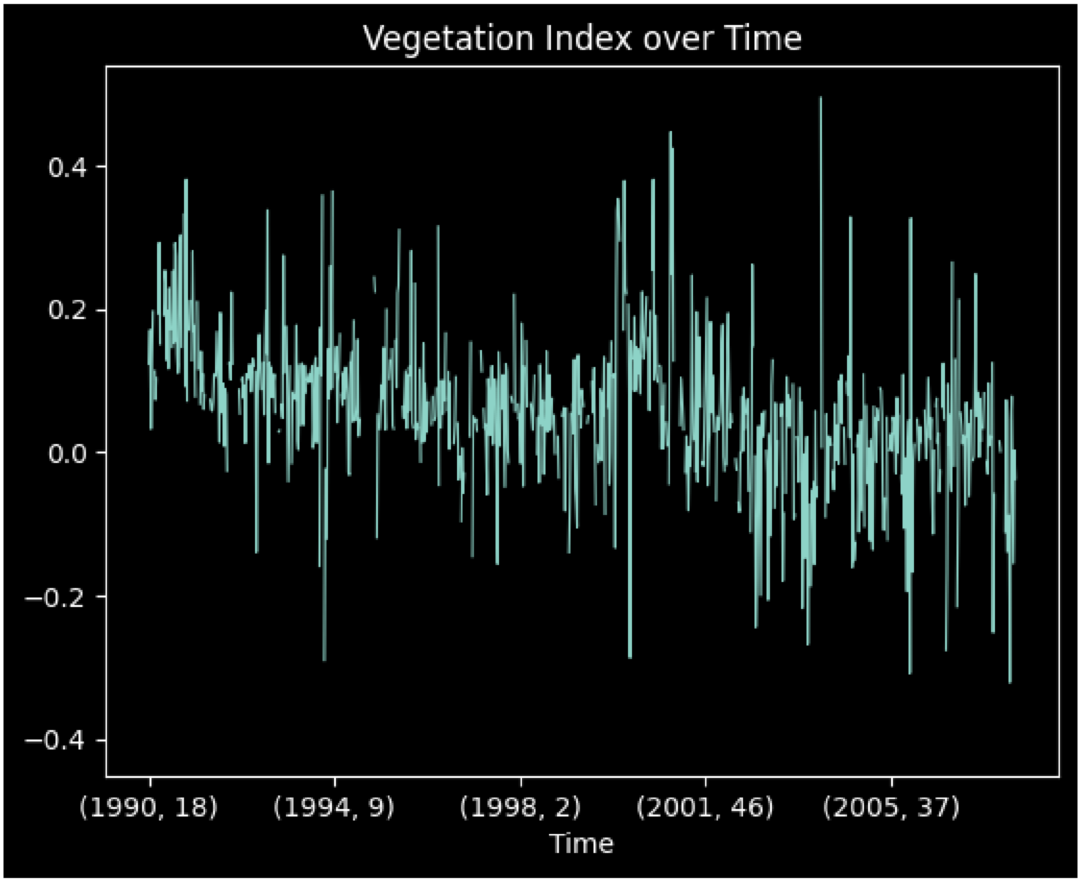
```
station_precip_mm                         True
dtype: bool
```

7 Plot to Check Missing Values

[33]:
```
(sj_train_features
     .ndvi_ne
     .plot
     .line(lw=0.8))

plt.title('Vegetation Index over Time')
plt.xlabel('Time')
```

[33]:
```
Text(0.5, 0, 'Time')
```



8 Fill Missing Values

Replace `NA` values with most recent value

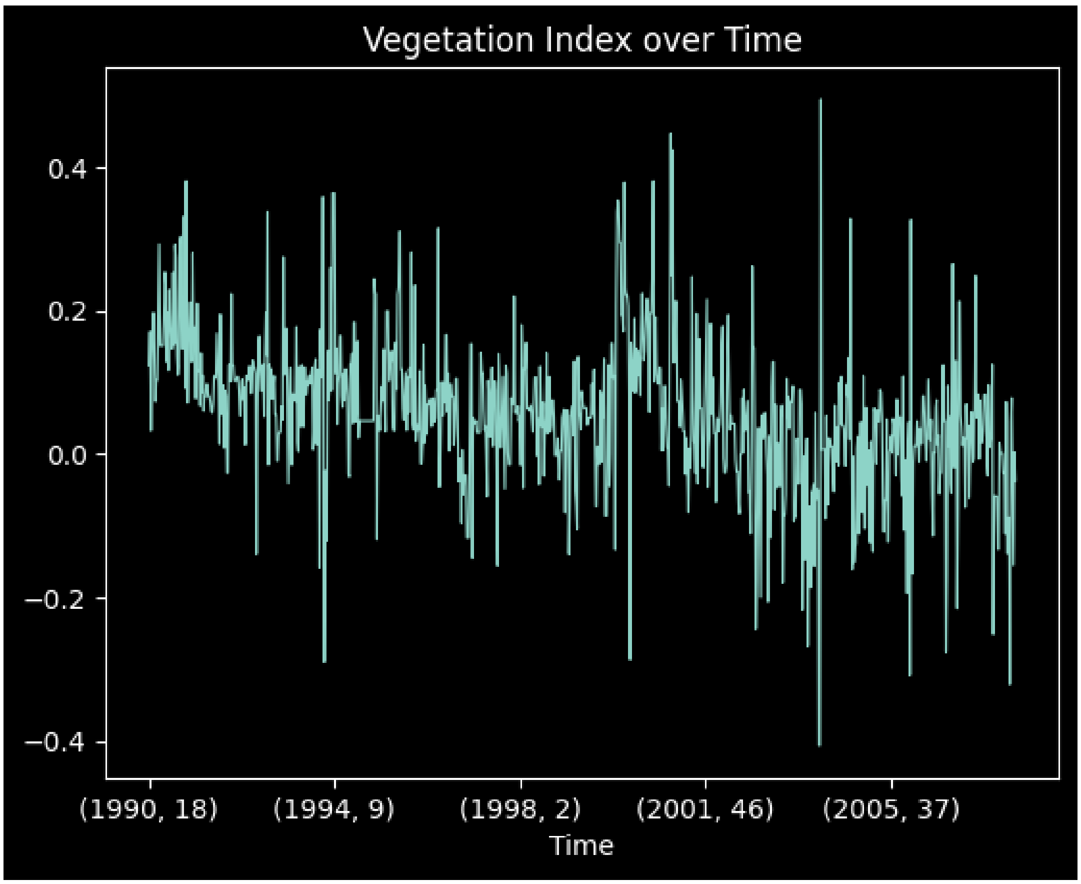
[34]:
```
sj_train_features.fillna(method='ffill', inplace=True)
iq_train_features.fillna(method='ffill', inplace=True)
```

9 Plot to Check Filled Values

[35]:
```
(sj_train_features
     .ndvi_ne
     .plot
     .line(lw=0.8))

plt.title('Vegetation Index over Time')
plt.xlabel('Time')
```

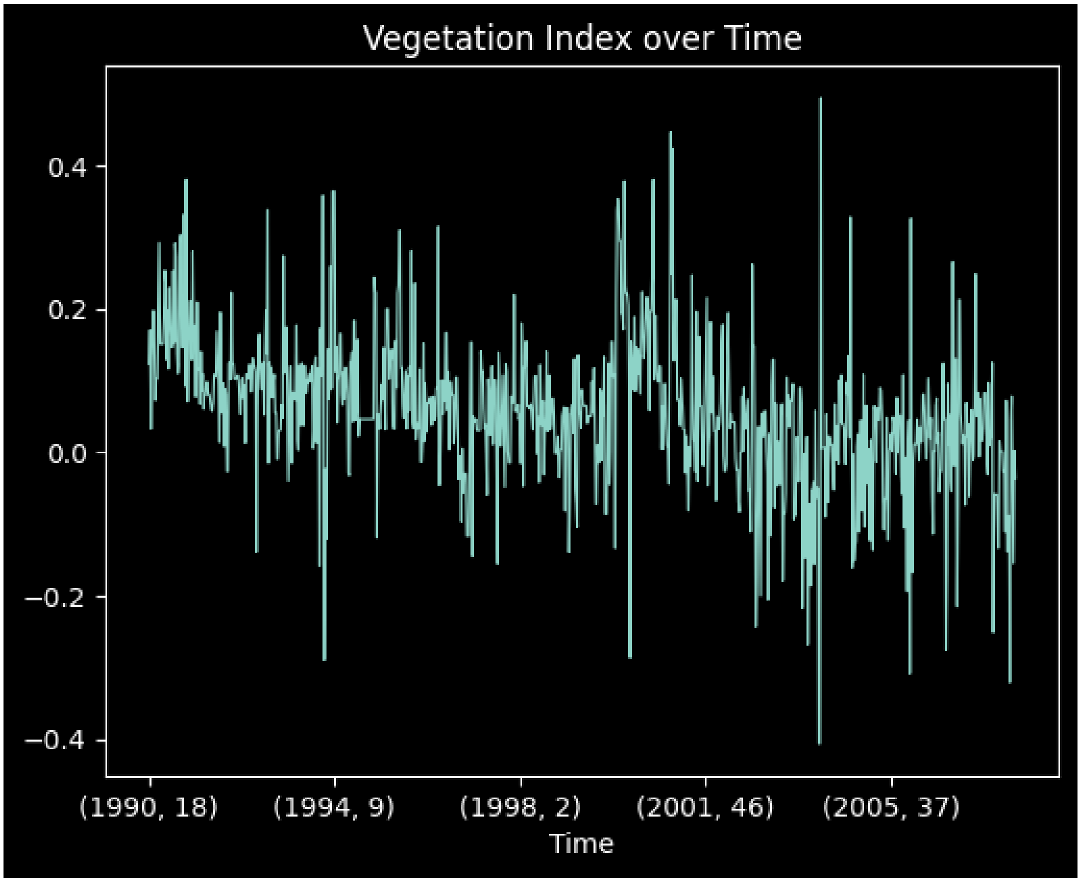
[35]: Text(0.5, 0, 'Time')



[36]:
```
(sj_train_features
     .ndvi_ne
     .plot
     .line(lw=0.8))
```

```
plt.title('Vegetation Index over Time')
plt.xlabel('Time')
```

[36]: Text(0.5, 0, 'Time')



10 Choose Model

- Poisson regression: assumes mean and variance of population distributions are equal
- Negative binomial regression: preferred if the variance is much larger than the mean

The variance is larger than the mean for both cities, so we'll use Negative Binomial Regression.

[37]:
```
print('San Juan')
print('mean: ', sj_train_labels.mean()[0])
print('var :', sj_train_labels.var()[0])

print('\nIquitos')
print('mean: ', iq_train_labels.mean()[0])
print('var :', iq_train_labels.var()[0])
```

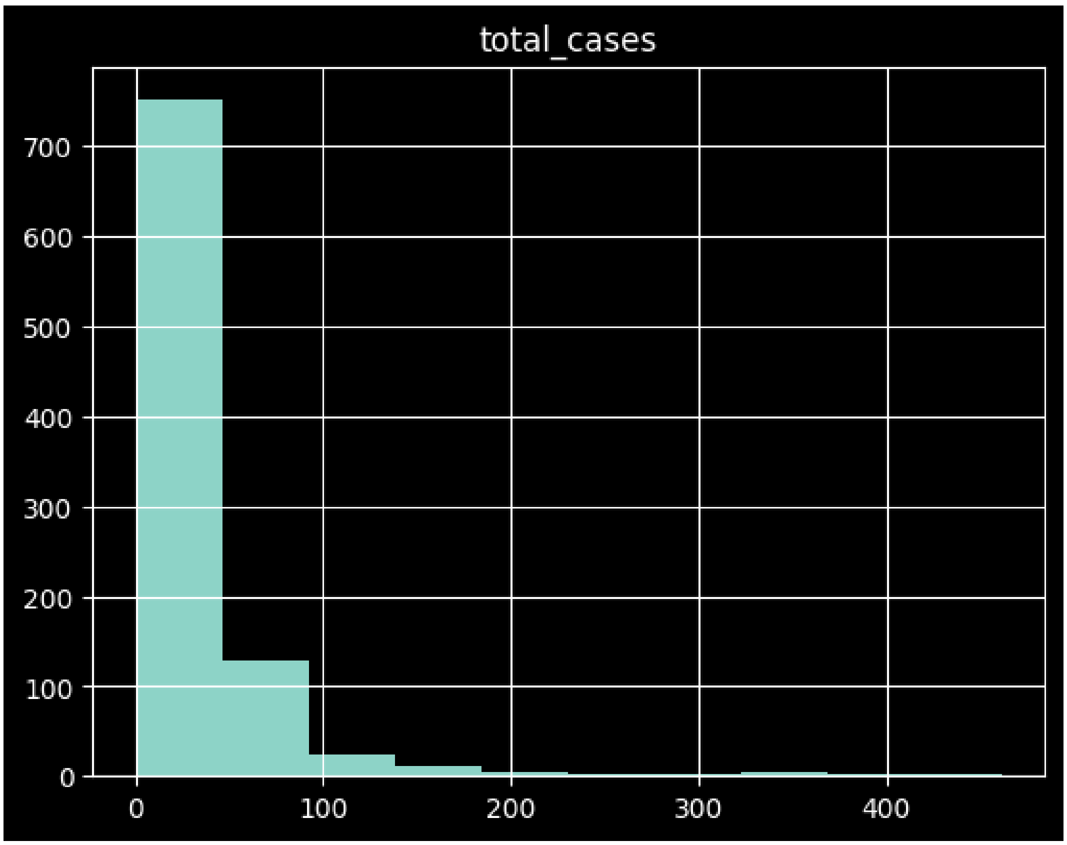
```
San Juan
mean:  34.18055555555556
var : 2640.0454396910277

Iquitos
mean:  7.565384615384615
var : 115.89552393656439
```

11 Plot Target Values

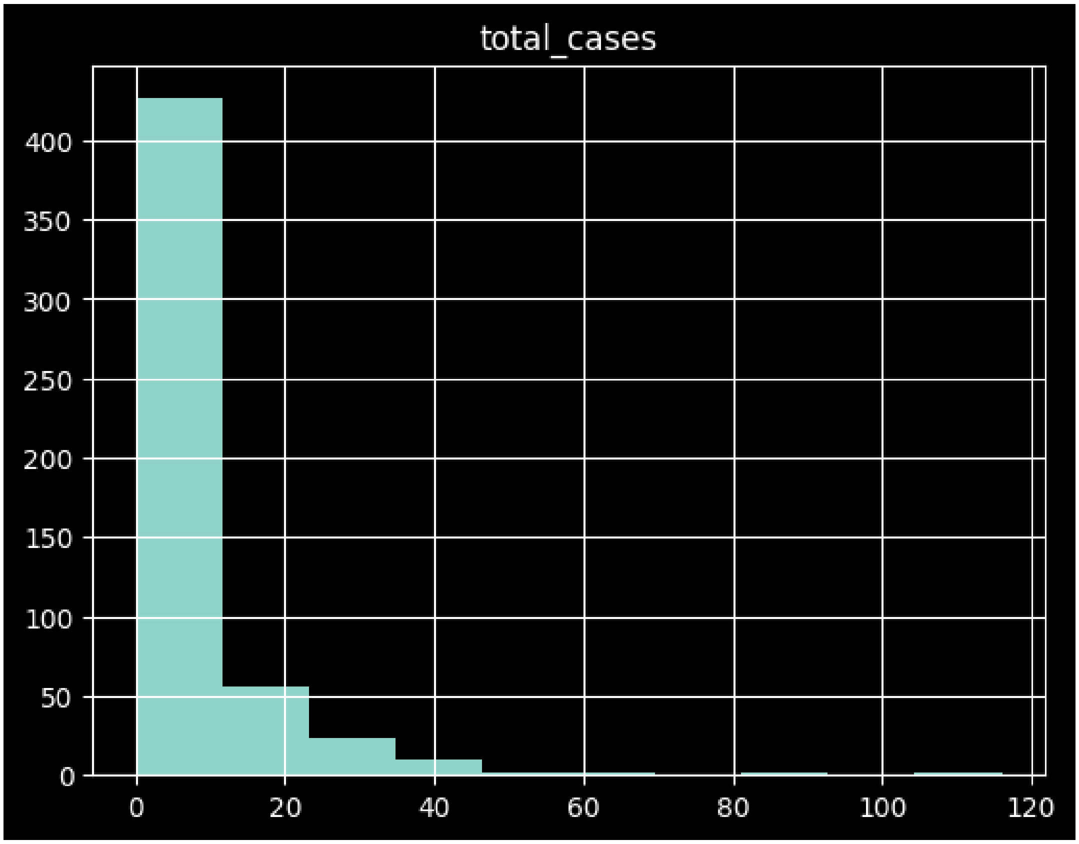
[38]:
```
sj_train_labels.hist()
```

[38]:
```
array([[<Axes: title={'center': 'total_cases'}>]], dtype=object)
```



[39]:
```
iq_train_labels.hist()
```

[39]:
```
array([[<Axes: title={'center': 'total_cases'}>]], dtype=object)
```



12 Find Features vs Target Correlations

12.1 Add Target to Features DataFrames

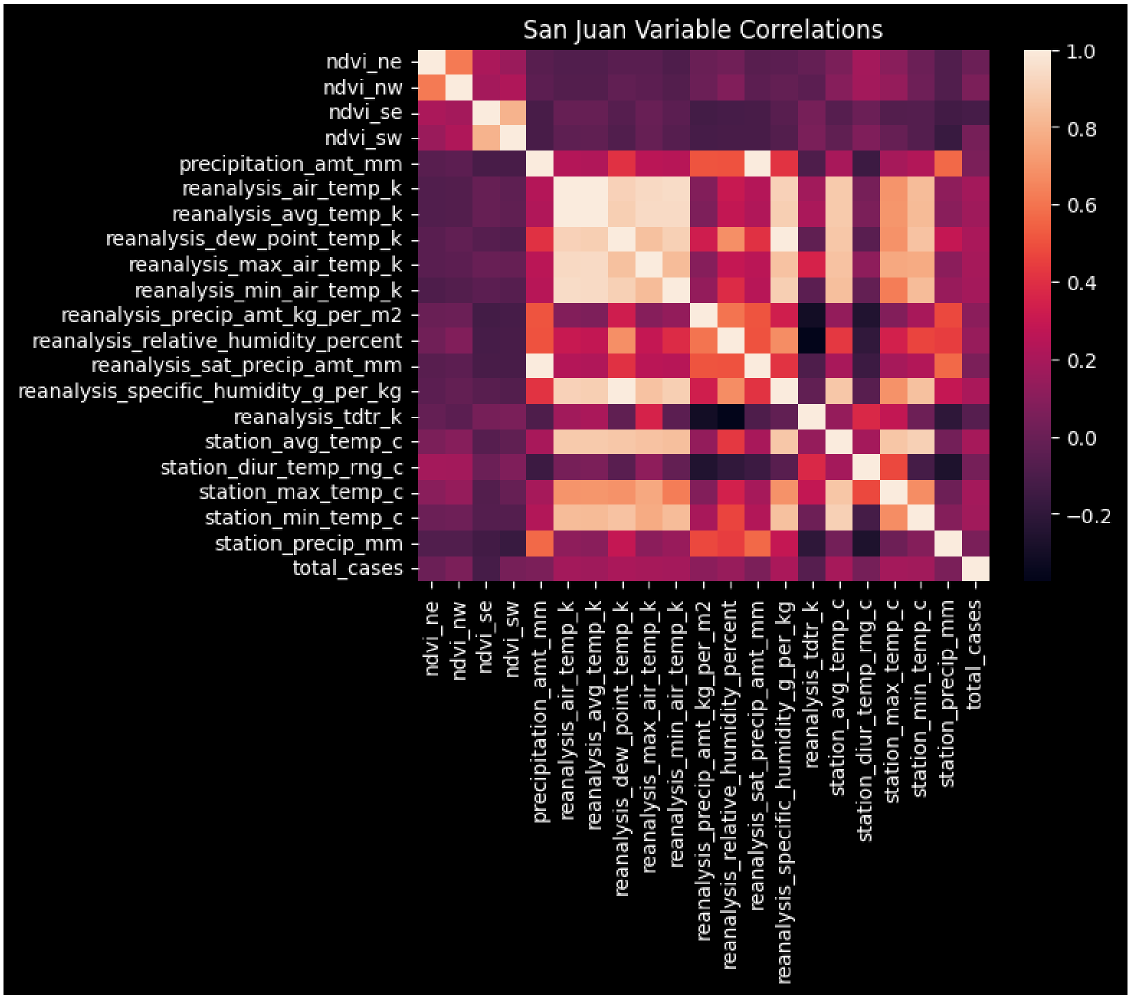
[40]:
```
sj_train_features['total_cases'] = sj_train_labels.total_cases
iq_train_features['total_cases'] = iq_train_labels.total_cases
```

12.2 Plot Correlation Heatmaps

[41]:
```
# compute the correlations
sj_correlations = sj_train_features.corr()
iq_correlations = iq_train_features.corr()
```

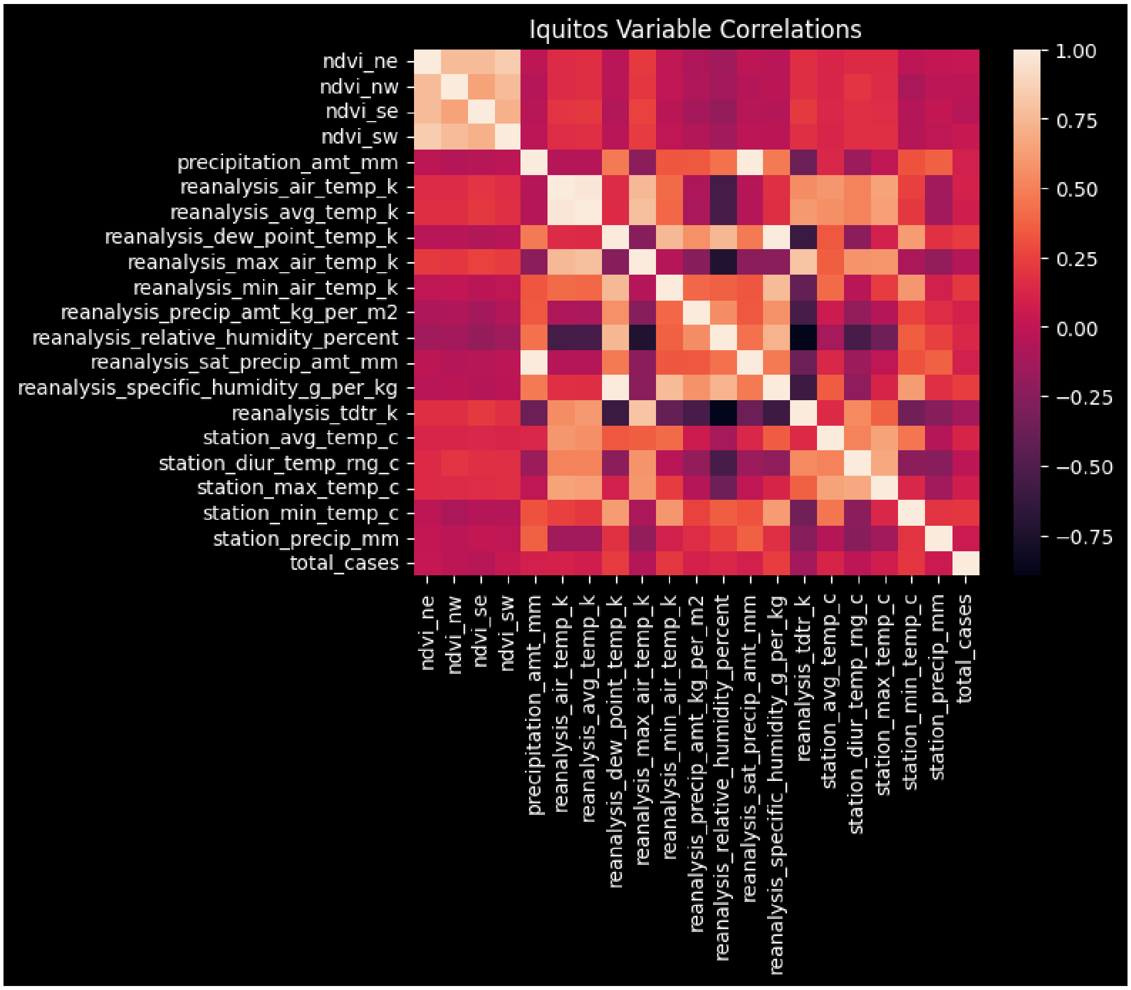
[42]:
```
# plot san juan
sj_corr_heat = sns.heatmap(sj_correlations)
plt.title('San Juan Variable Correlations')
```

[42]:
```
Text(0.5, 1.0, 'San Juan Variable Correlations')
```



[43]:
```
# plot iquitos
iq_corr_heat = sns.heatmap(iq_correlations)
plt.title('Iquitos Variable Correlations')
```

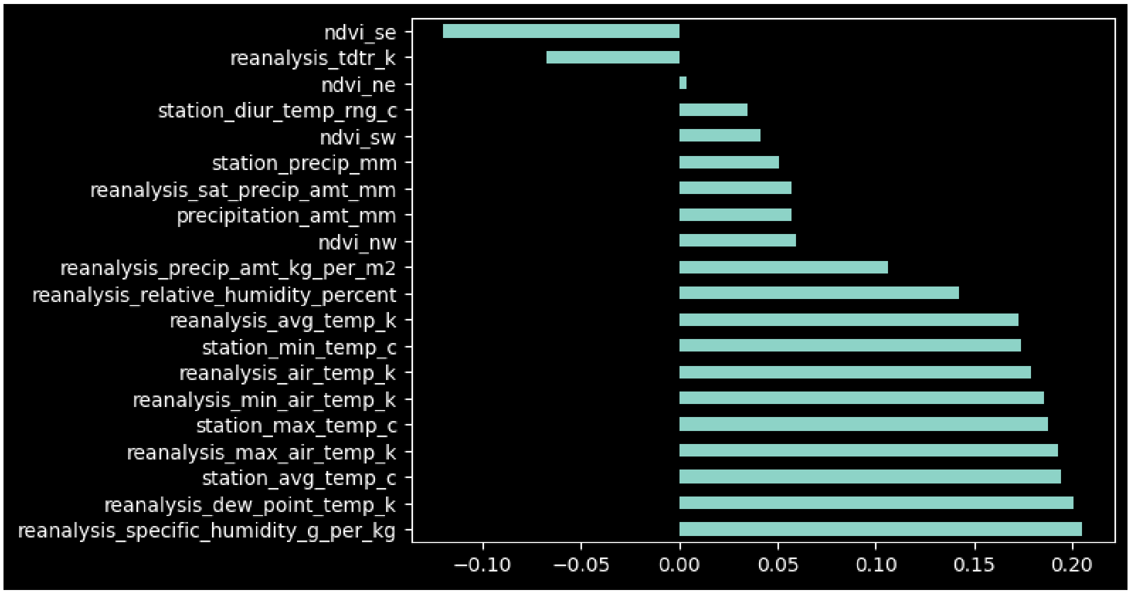
[43]: `Text(0.5, 1.0, 'Iquitos Variable Correlations')`



12.3 Bar Plots of Correlations

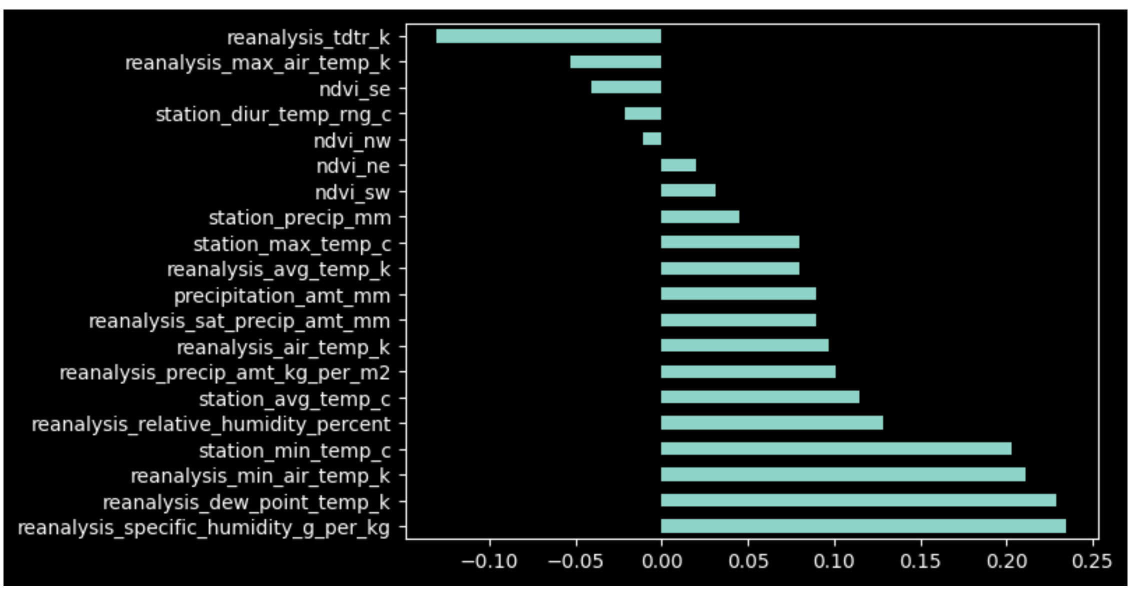
[44]:
```python
# San Juan
(sj_correlations
     .total_cases
     .drop('total_cases') # don't compare with myself
     .sort_values(ascending=False)
     .plot
     .barh()) # horizontal bar plot
```

[44]: <Axes: >



[45]:
```python
# Iquitos
(iq_correlations
     .total_cases
     .drop('total_cases') # don't compare with myself
     .sort_values(ascending=False)
     .plot
     .barh()) # horizontal bar plot
```

[45]: <Axes: >



13 Observations

Wet and warm climates are correlated with cases of Dengue fever.

- `reanalysis_specific_humidity_g_per_kg` and `reanalysis_dew_point_temp_k` are most strongly correlated with `total_cases`
- `reanalysis_min_air_temp` and `station_min_temp` are also strongly correlated with `total_cases`

We'll use these features for our model!

14 Preprocess Data

We create a smaller dataset to train our model.

[46]:
```
def preprocess_data(data_path, labels_path=None):
    # load data and set index to city, year, weekofyear
    df = pd.read_csv(data_path, index_col=[0, 1, 2])

    # select features we want
    features = ['reanalysis_specific_humidity_g_per_kg',
                'reanalysis_dew_point_temp_k',
                'station_avg_temp_c',
                'station_min_temp_c']
    df = df[features]

    # fill missing values
    df.fillna(method='ffill', inplace=True)

    # add labels to dataframe
    if labels_path:
        labels = pd.read_csv(labels_path, index_col=[0, 1, 2])
        df = df.join(labels)

    # separate san juan and iquitos
    sj = df.loc['sj']
    iq = df.loc['iq']

    return sj, iq
```

[47]:
```
sj_train, iq_train = preprocess_data('../data/dengue_features_train.csv',
                                    labels_path="../data/dengue_labels_train.
 ↪csv")
```

[48]:
```
sj_train.describe()
```

[48]:

```
       reanalysis_specific_humidity_g_per_kg  reanalysis_dew_point_temp_k  \
count                             936.000000                   936.000000
mean                               16.547535                   295.104736
std                                 1.560663                     1.570075
min                                11.715714                   289.642857
25%                                15.233571                   293.843929
50%                                16.835000                   295.451429
75%                                17.854286                   296.415714
max                                19.440000                   297.795714

       station_avg_temp_c  station_min_temp_c  total_cases
count          936.000000          936.000000   936.000000
mean            26.999191           22.594017    34.180556
std              1.415079            1.506281    51.381372
min             22.842857           17.800000     0.000000
25%             25.842857           21.700000     9.000000
50%             27.214286           22.800000    19.000000
75%             28.175000           23.900000    37.000000
max             30.071429           25.600000   461.000000
```

[49]:

```
iq_train.describe()
```

[49]:

```
       reanalysis_specific_humidity_g_per_kg  reanalysis_dew_point_temp_k  \
count                             520.000000                   520.000000
mean                               17.102019                   295.498723
std                                 1.443048                     1.414360
min                                12.111429                   290.088571
25%                                16.121429                   294.596429
50%                                17.428571                   295.852143
75%                                18.180357                   296.557143
max                                20.461429                   298.450000

       station_avg_temp_c  station_min_temp_c  total_cases
count          520.000000          520.000000   520.000000
mean            27.506331           21.210385     7.565385
std              0.908973            1.257734    10.765478
min             21.400000           14.700000     0.000000
25%             26.957500           20.600000     1.000000
50%             27.587500           21.400000     5.000000
75%             28.075000           22.000000     9.000000
max             30.800000           24.200000   116.000000
```

15 Split Datasets

For a time series model, we'll use a strict-future holdout (validation) set when splitting our train set and test set.

[50]:
```python
sj_train_subtrain = sj_train.head(800)
sj_train_subtest = sj_train.tail(sj_train.shape[0] - 800)

iq_train_subtrain = iq_train.head(400)
iq_train_subtest = iq_train.tail(iq_train.shape[0] - 400)
```

16 Fit Model on Training Set

We'll use a **Negative Binomial Regression** model, suitable for **count** data, where the **variance is larger than the mean**.

This function finds the best model parameters using a Generalized Linear Model (`GLM`) with a Negative Binomial distribution.

This is particularly useful in epidemiology for modeling **count** data that follows a distribution with **over-dispersion**, meaning the variance is greater than the mean, which is a common occurrence in infectious disease counts.

While it can model over-dispersed count data better than Poisson regression, it is less flexible in capturing complex nonlinear relationships compared to Random Forest, used for our first baseline model.

To evaluate the performance of the model, we again use the Mean Absolutel Error (`MAE`) between the predicted and actual total cases. The **alpha** value that results in the lowest `MAE` is considered the best. The **alpha** value is the over-dispersion parameter. The best model is then refitted on the entire dataset.

For the first dataset (San Juan), the best score, or the lowest `MAE` achieved, was approximately `22.08`, while for the second dataset (Iquitos), it was approximately `6.47`. These scores give an indication of how far off the predictions are from the actual values, on average, in terms of the total number of cases.

[51]:
```python
def get_best_model(train, test):
    # Step 1: specify the form of the model
    model_formula = "total_cases ~ 1 + " \
                    "reanalysis_specific_humidity_g_per_kg + " \
                    "reanalysis_dew_point_temp_k + " \
                    "station_min_temp_c + " \
                    "station_avg_temp_c"

    grid = 10 ** np.arange(-8, -3, dtype=np.float64)

    best_alpha = []
    best_score = 1000

    # Step 2: Find the best hyper parameter, alpha
    for alpha in grid:
        model = smf.glm(formula=model_formula,
                        data=train,
```

```
                         family=sm.families.NegativeBinomial(alpha=alpha))

        results = model.fit()
        predictions = results.predict(test).astype(int)
        score = eval_measures.meanabs(predictions, test.total_cases)

        if score < best_score:
            best_alpha = alpha
            best_score = score

    print('best alpha = ', best_alpha)
    print('best score = ', best_score)

    # Step 3: refit on entire dataset
    full_dataset = pd.concat([train, test])
    model = smf.glm(formula=model_formula,
                    data=full_dataset,
                    family=sm.families.NegativeBinomial(alpha=best_alpha))

    fitted_model = model.fit()
    return fitted_model

sj_best_model = get_best_model(sj_train_subtrain, sj_train_subtest)
iq_best_model = get_best_model(iq_train_subtrain, iq_train_subtest)
```

```
best alpha =  1e-08
best score =  22.080882352941178
best alpha =  1e-08
best score =  6.466666666666667
```

17 Evaluate Model: Plot Predicted vs Actual Cases

We can notice the following from the plots below:

- The model does seem to predict the seasonal patterns in Dengue cases
- The model does not predict the spikes in cases

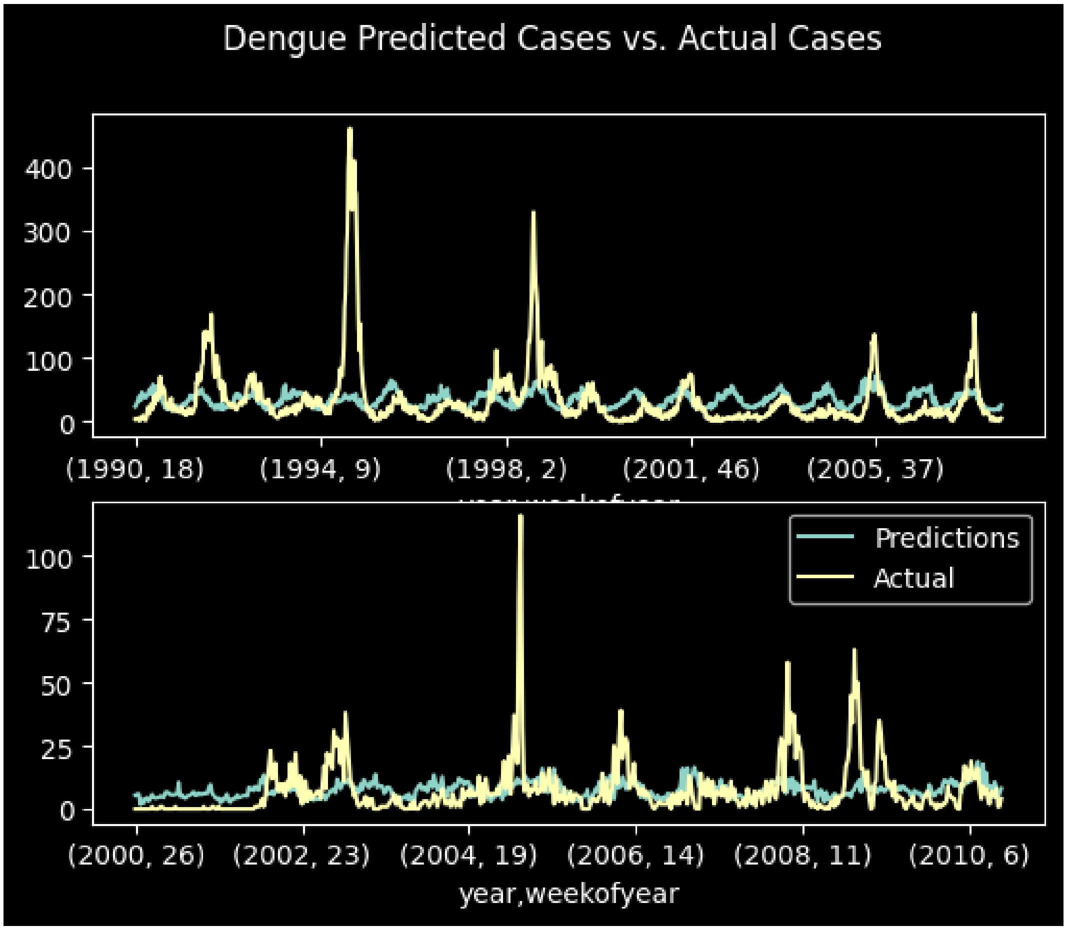
[52]:
```
figs, axes = plt.subplots(nrows=2, ncols=1)

# plot sj
sj_train['fitted'] = sj_best_model.fittedvalues
sj_train.fitted.plot(ax=axes[0], label="Predictions")
sj_train.total_cases.plot(ax=axes[0], label="Actual")

# plot iq
iq_train['fitted'] = iq_best_model.fittedvalues
iq_train.fitted.plot(ax=axes[1], label="Predictions")
iq_train.total_cases.plot(ax=axes[1], label="Actual")
```

```
plt.suptitle("Dengue Predicted Cases vs. Actual Cases")
plt.legend()
```

[52]: <matplotlib.legend.Legend at 0x7778372ebaf0>



18 Make Third Submission

We made our third submission to DrivenData using this revised pipeline and received a Mean Absolute Error (`MAE`) score of `25.8173`.

In the context of our model, which predicts total cases of Dengue fever, an `MAE` of `25.8173` means that, on average, our predictions are about `25.8173` cases away from the actual number of cases.

So, despite the changes made to this pipeline between the first and second submissions, our third and final model did not improve on our first and second submissions! Our best score was `25.6875` using a **Random Forest** regressor.

[53]:
```python
sj_test, iq_test = preprocess_data('../data/dengue_features_test.csv')

sj_predictions = sj_best_model.predict(sj_test).astype(int)
iq_predictions = iq_best_model.predict(iq_test).astype(int)

submission = pd.read_csv("../data/submission_format.csv",
                         index_col=[0, 1, 2])

submission.total_cases = np.concatenate([sj_predictions, iq_predictions])
submission.to_csv("../submissions/benchmark.csv")
```

19 Reflections

The main differences between our first and second attempts and this third and final attempt were:

- We filled `NA` values with most recent values in the time series
- We **split** the data set between cities, San Juan and Iquitos
- We used a **Negative Binomial** regression model

While we made several fundamental changes to our pipeline, our best score was for our second attempting, using a Random Forest regressor.

Given these results, it appears that while our model performed reasonably well on the validation set, there's a discrepancy between the validation `MAE` and the score on the test set, which is more than double. This could be due to several reasons:

- **Overfitting to the validation set**: Our model might have learned specific patterns in the validation set that don't generalize to the test set.
- **Differences between validation and test sets**: If the test set contains different patterns or a different distribution of cases, this could lead to a higher error rate.
- **Model Limitations**: The model may not capture all the complexities of the data, or there may be influential features or interactions that the model is not considering.

19.1 Future Work

To improve our model, we could consider the following steps:

- **Feature Engineering**: Create new features or transform existing ones to better capture the relationships in the data.
- **Hyperparameter Tuning**: Optimize the model's hyperparameters to improve performance.
- **Cross-Validation**: Implement **k-fold cross-validation** to ensure that the model's performance is consistent across different subsets of the data.
- **Ensemble Methods**: Combine different models to improve predictions and reduce the likelihood of overfitting.
- **Leakage Check**: Ensure there's no leakage of information from the test set into the training process.