

Baseline-MDR-CaseCount

February 19, 2020

```
[1]: # Imports
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import matplotlib.ticker as ticker

[2]: def MDR_plot_genotype_freq(drug, drug_res):
    # Create Data Frame
    df = pd.read_csv(drug, sep='\t')
    # plot
    plt.plot(df['current_time'], df.iloc[:,0:150].filter(regex=drug_res,
    ↪axis=1).sum(axis=1))

[3]: def MDR_case_count(drug, drug_res):
    # Create Data Frame
    df = pd.read_csv(drug, sep='\t')
    # Total genotype count
    total = df.iloc[:,22:150].sum(axis=1).tail(1).values
    # Total population count
    total_pop = df['population'].tail(1).values
    # Filter out target genotypes
    mdr_count = df.iloc[:,0:150].filter(regex=drug_res, axis=1).sum(axis=1).
    ↪tail(1).values
    percentage = mdr_count[0] / total_pop[0] * 100
    return [mdr_count[0], total_pop[0], percentage]
```

1 Main Function

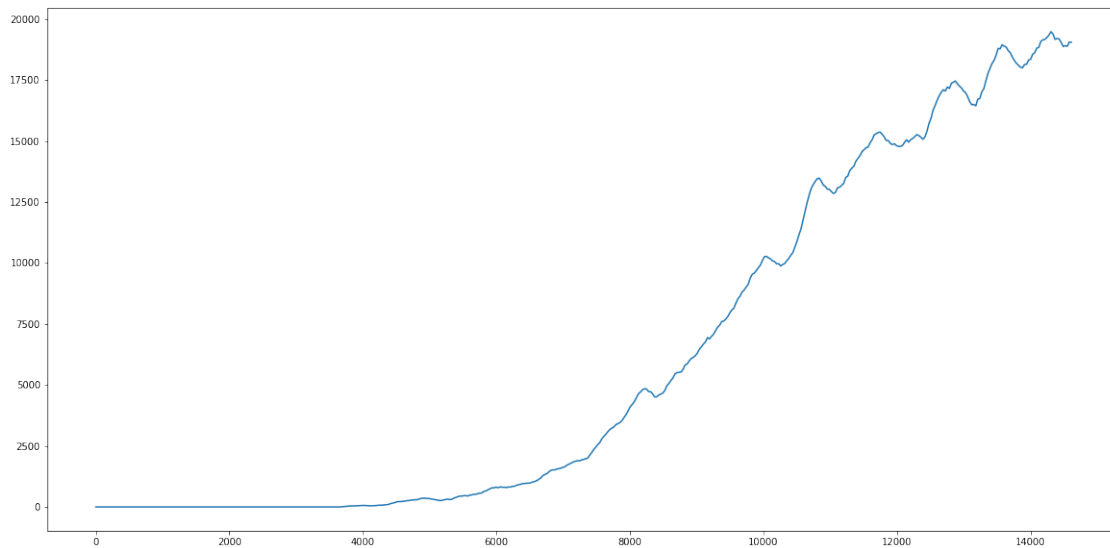
```
[5]: # Figure Size
plt.rcParams['figure.figsize'] = [20, 10]
```

1.1 AL

```
[6]: MDR_case_count('al.txt', '^(TYF|TNY|TNF|KYY|KYF|KNY|KNF)..Y..$')
```

```
[6]: [19044, 148249, 12.845955116054746]
```

```
[7]: MDR_plot_genotype_freq('al.txt', '^ (TYF|TNY|TNF|KYY|KYF|KNY|KNF) ..Y..$')
```

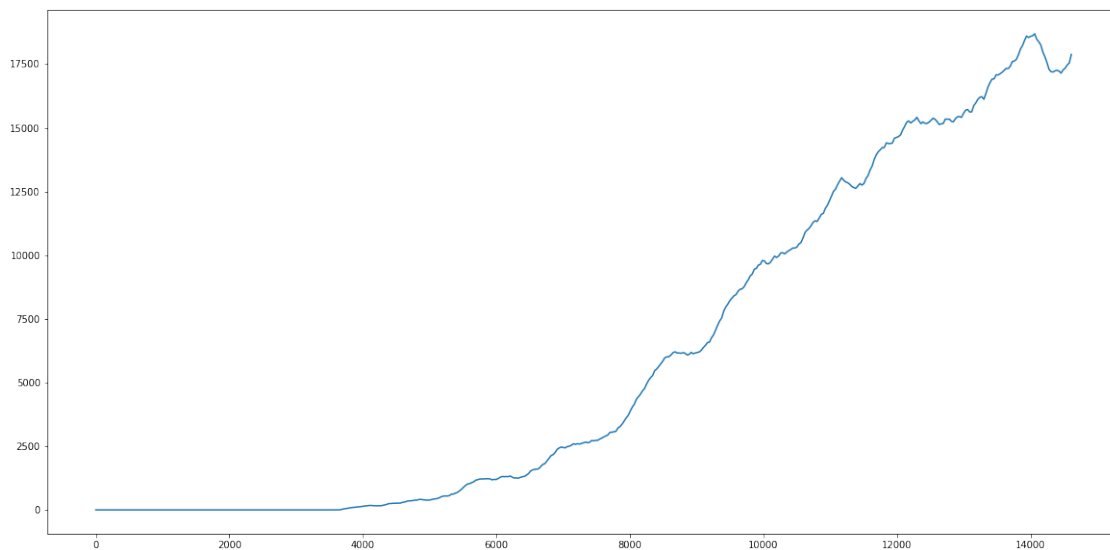


1.2 AS-AQ

```
[8]: MDR_case_count('asaq.txt', '^ (TYF|TNY|TNF|KYY|KYF|KNY|TYT) ..Y..$')
```

```
[8]: [17880, 149123, 11.990102130456066]
```

```
[9]: MDR_plot_genotype_freq('asaq.txt', '^ (TYF|TNY|TNF|KYY|KYF|KNY|TYT) ..Y..$')
```

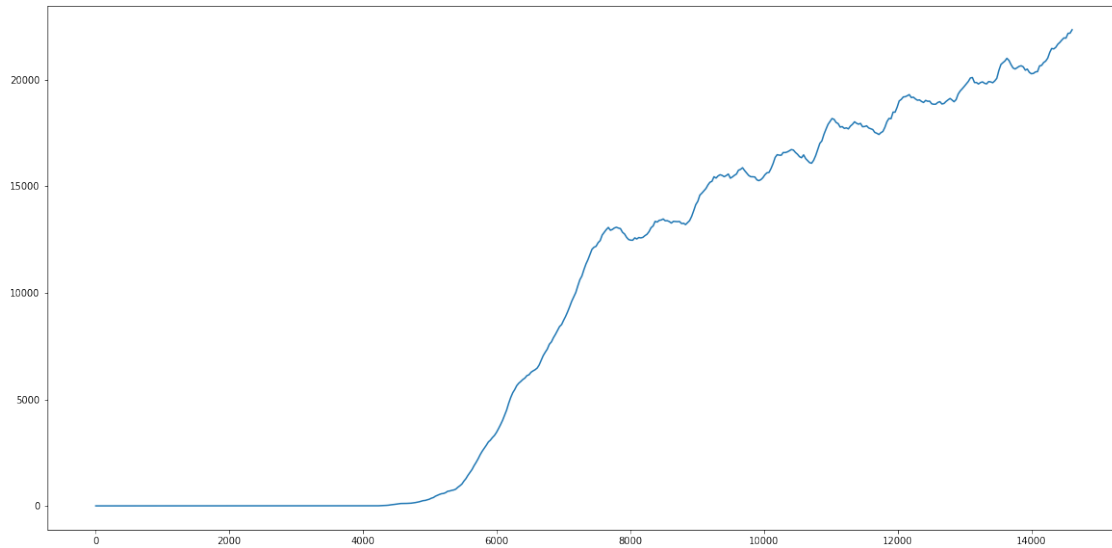


1.3 DHA-PPQ

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[10]: MDR_case_count('dhappq.txt', '^.....Y2.$')
```

```
[10]: [22344, 149582, 14.93762618496878]
```

```
[11]: MDR_plot_genotype_freq('dhappq.txt', '^.....Y2.$')
```



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[ ]:
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