change-cyc-yr-Copy1

July 1, 2019

```python
In [1]: ##### Comparisons between different plots
```

```python
In [3]: import pandas as pd
        import numpy as np
        import matplotlib.pyplot as plt
        import matplotlib.ticker as ticker
```

```python
In [4]: plt.rcParams['figure.figsize'] = [20, 15]
```

```python
In [5]: df = pd.read_csv('0.txt', sep='\t') # convert tsv to pandas data frame
        df1 = pd.read_csv('1.txt', sep='\t')
        df2 = pd.read_csv('2.txt', sep='\t')
```

```python
In [6]: # scale func to show x-axis in years
        scale_x = 12
        ticks_x = ticker.FuncFormatter(lambda x, pos: '{0:g}'.format(x/scale_x))
```

```python
In [2]: # 0 - 5yr, 3-drug-rotation, 70%-tcr
        # 1 - 5yr, 2-drug-rotation, 70%-tcr (ASAQ, AL)
        # 2 - 3yr, 3-drug-rotation, 70%-tcr
```

```python
In [13]: # blood_slide_prevalence plot
         fig = plt.figure()
         ax1 = fig.add_subplot(211)
         ax1.plot(df['blood_slide_prev'])
         ax1.xaxis.set_major_locator(ticker.MultipleLocator(12*5))
         ax1.xaxis.set_major_formatter(ticks_x)
         ax1.set_xlabel('years')
         ax1.set_ylabel('blood slide prev')
         ax1.set_title('Blood Slide Prev. Plot #0')

         # sum up total num of parasites in the silumation
         tot_para = df.iloc[:,22:150].sum(axis=1)
         # parasite freq plot
         ax2 = fig.add_subplot(212)
         # grouped comparisons for DHA-PPQ resistance
         ax2.plot(df.iloc[:,0:151].filter(regex='.....C1.', axis=1).sum(axis=1)/tot_para, label
         ax2.plot(df.iloc[:,0:151].filter(regex='.....C2.', axis=1).sum(axis=1)/tot_para, label
```

```
ax2.plot(df.iloc[:,0:151].filter(regex='.....Y1.', axis=1).sum(axis=1)/tot_para, label
ax2.plot(df.iloc[:,0:151].filter(regex='.....Y2.', axis=1).sum(axis=1)/tot_para, label
ax2.plot(df.iloc[:,0:151].filter(regex='TY......', axis=1).sum(axis=1)/tot_para, label
ax2.plot(df.iloc[:,0:151].filter(regex='KN......', axis=1).sum(axis=1)/tot_para, label

# format x-axis
ax2.xaxis.set_major_locator(ticker.MultipleLocator(12*5))
ax2.xaxis.set_major_formatter(ticks_x)
# format y-axis
#ax2.yaxis.set_major_formatter(ticker.PercentFormatter(xmax=1.0))
ax2.set_xlabel('years')
ax2.set_ylabel('parasite freq')
ax2.set_title('Parasite Freq. Plot #0')
ax2.legend()
```
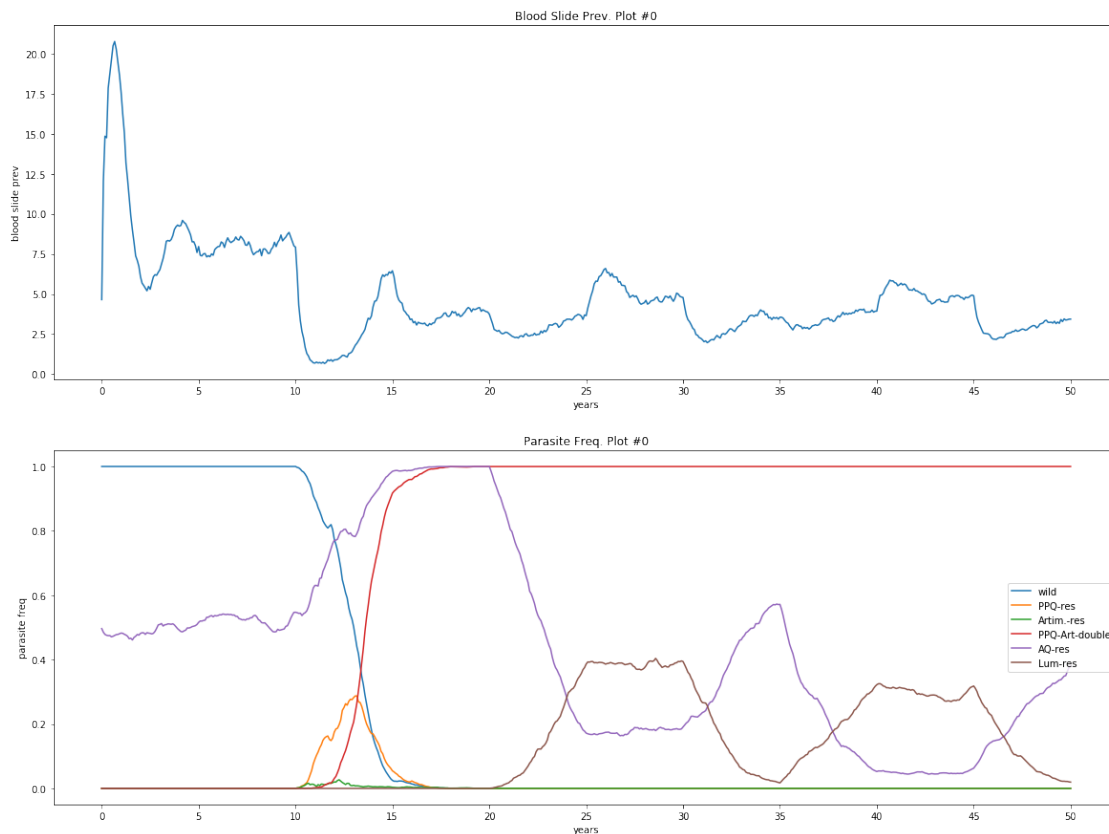
Out[13]: <matplotlib.legend.Legend at 0x1210e2b38>

In [8]: #

In [9]: # plot 1s
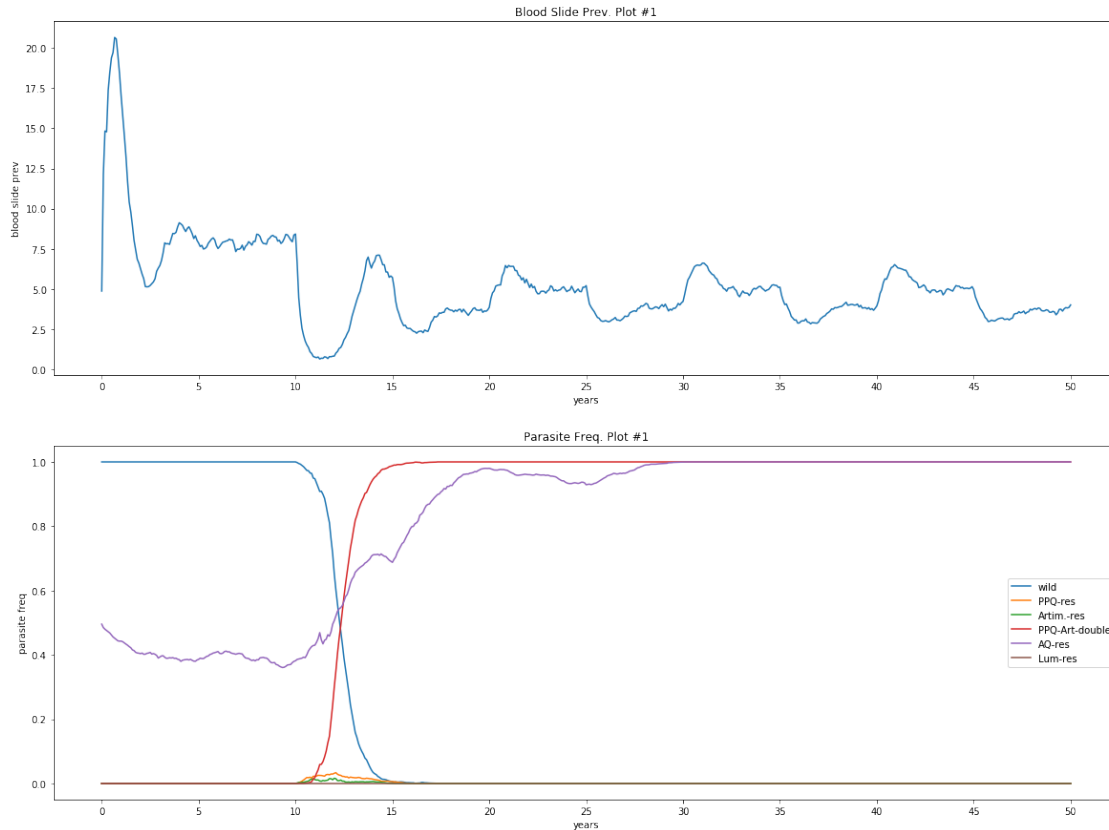   # blood_slide_prevalence plot

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```python
fig = plt.figure()
ax1 = fig.add_subplot(211)
ax1.plot(df1['blood_slide_prev'])
ax1.xaxis.set_major_locator(ticker.MultipleLocator(60))
ax1.xaxis.set_major_formatter(ticks_x)
ax1.set_xlabel('years')
ax1.set_ylabel('blood slide prev')
ax1.set_title('Blood Slide Prev. Plot #1')

# sum up total num of parasites in the silumation
tot_para = df1.iloc[:,22:150].sum(axis=1)
# parasite freq plot
ax2 = fig.add_subplot(212)
# grouped comparisons for DHA-PPQ resistance
ax2.plot(df1.iloc[:,0:151].filter(regex='.....C1.', axis=1).sum(axis=1)/tot_para, label
ax2.plot(df1.iloc[:,0:151].filter(regex='.....C2.', axis=1).sum(axis=1)/tot_para, label
ax2.plot(df1.iloc[:,0:151].filter(regex='.....Y1.', axis=1).sum(axis=1)/tot_para, label
ax2.plot(df1.iloc[:,0:151].filter(regex='.....Y2.', axis=1).sum(axis=1)/tot_para, label
ax2.plot(df1.iloc[:,0:151].filter(regex='TY......', axis=1).sum(axis=1)/tot_para, label
ax2.plot(df1.iloc[:,0:151].filter(regex='KN......', axis=1).sum(axis=1)/tot_para, label

# format x-axis
ax2.xaxis.set_major_locator(ticker.MultipleLocator(12*5))
ax2.xaxis.set_major_formatter(ticks_x)
# format y-axis
#ax2.yaxis.set_major_formatter(ticker.PercentFormatter(xmax=1.0))
ax2.set_xlabel('years')
ax2.set_ylabel('parasite freq')
ax2.set_title('Parasite Freq. Plot #1')
ax2.legend()
```

Out[9]: <matplotlib.legend.Legend at 0x122b13e10>

Blood Slide Prev. Plot #1

Parasite Freq. Plot #1

In [10]: #

In [11]: ```python
# plot 2s
# blood_slide_prevalence plot
majors = [10,13,16,19,22,25,28,31,34,37,40,43,46,49]
fig = plt.figure()
ax1 = fig.add_subplot(211)
ax1.plot(df2['blood_slide_prev'])
ax1.xaxis.set_major_locator(ticker.FixedLocator([i*12 for i in majors])) # 3-yr rotat
ax1.xaxis.set_major_formatter(ticks_x)
ax1.set_xlabel('years')
ax1.set_ylabel('blood slide prev')
ax1.set_title('Blood Slide Prev. Plot #2')

# sum up total num of parasites in the silumation
tot_para = df2.iloc[:,22:150].sum(axis=1)
# parasite freq plot
ax2 = fig.add_subplot(212)
# grouped comparisons for DHA-PPQ resistance
ax2.plot(df2.iloc[:,0:151].filter(regex='.....C1.', axis=1).sum(axis=1)/tot_para, labe
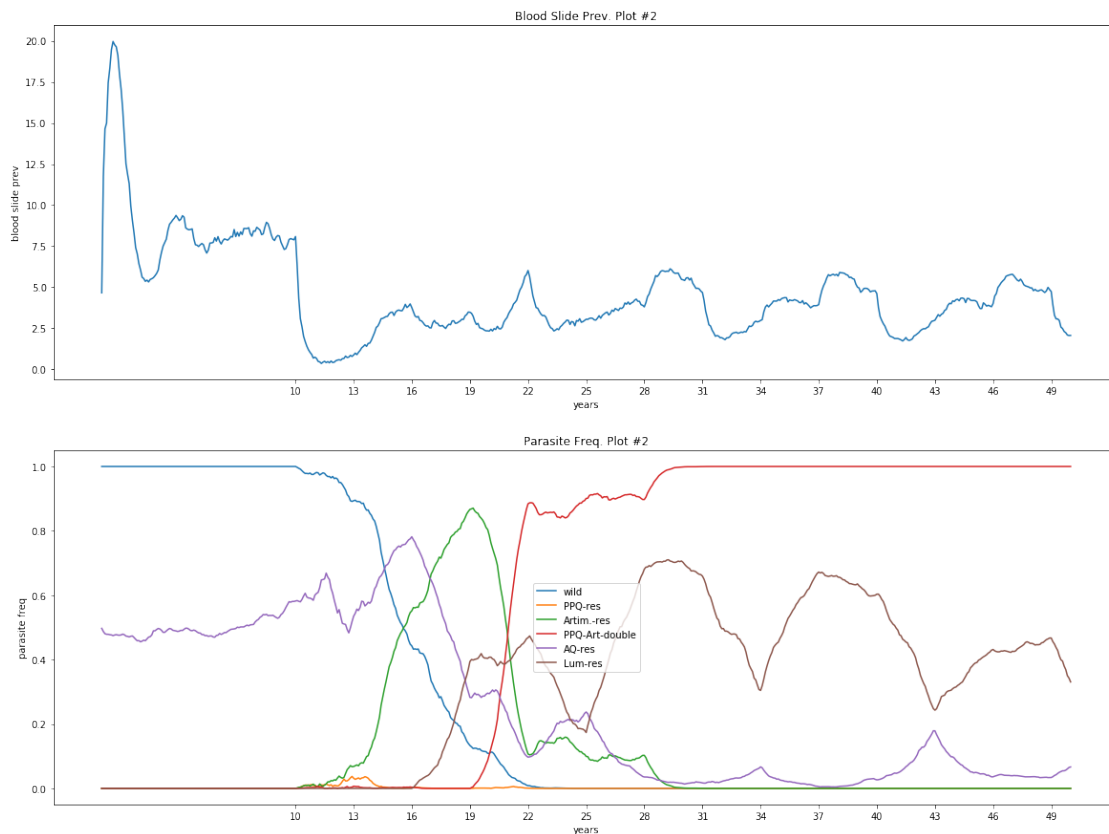ax2.plot(df2.iloc[:,0:151].filter(regex='.....C2.', axis=1).sum(axis=1)/tot_para, labe
```

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```
ax2.plot(df2.iloc[:,0:151].filter(regex='.....Y1.', axis=1).sum(axis=1)/tot_para, labe
ax2.plot(df2.iloc[:,0:151].filter(regex='.....Y2.', axis=1).sum(axis=1)/tot_para, labe
ax2.plot(df2.iloc[:,0:151].filter(regex='TY......', axis=1).sum(axis=1)/tot_para, labe
ax2.plot(df2.iloc[:,0:151].filter(regex='KN......', axis=1).sum(axis=1)/tot_para, labe

# format x-axis
ax2.xaxis.set_major_locator(ticker.FixedLocator([i*12 for i in majors])) # 3-yr rotat
ax2.xaxis.set_major_formatter(ticks_x)
# format y-axis
#ax2.yaxis.set_major_formatter(ticker.PercentFormatter(xmax=1.0))
ax2.set_xlabel('years')
ax2.set_ylabel('parasite freq')
ax2.set_title('Parasite Freq. Plot #2')
ax2.legend()
```

Out[11]: <matplotlib.legend.Legend at 0x120fd2cc0>

In [12]: #

In [ ]: