

Untitled

January 26, 2017

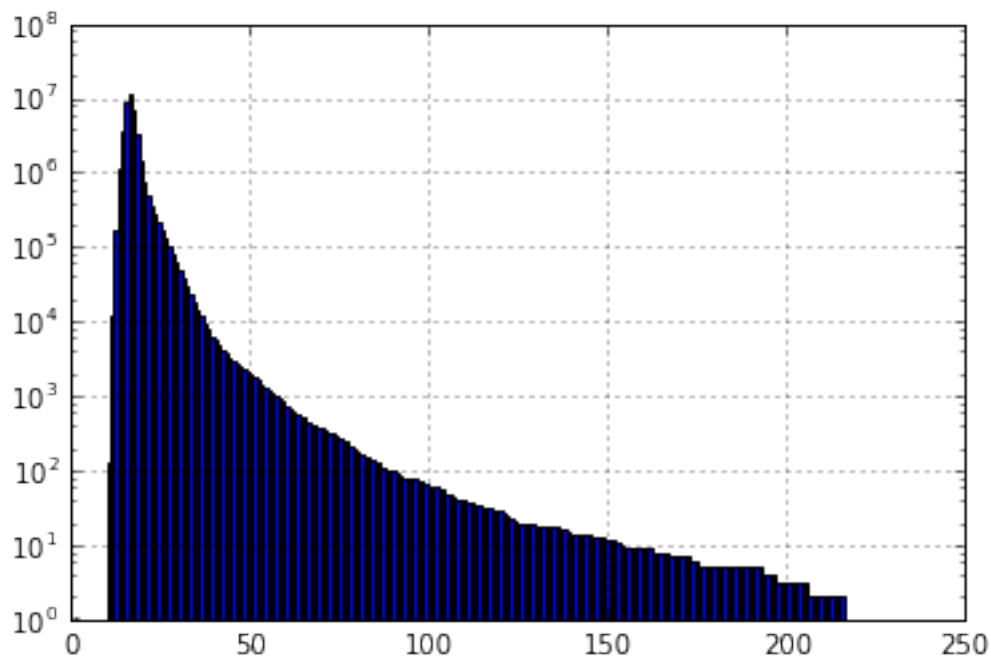
```
In [32]: %matplotlib inline
import numpy as np
import pandas as pd
from matplotlib import pyplot as plt
```

```
In [33]: ## Human chromosome 22 versus the Mouse genome
```

```
X = pd.Series(np.loadtxt('genome_data/Homo_sapiens.GRCh38.dna.chromosome.22_Mus_musculus', dtype=float))
X.describe()
```

```
Out[33]: count    3.915978e+07
mean        1.653234e+01
std         2.970284e+00
min         1.000000e+00
25%         1.500000e+01
50%         1.600000e+01
75%         1.700000e+01
max         2.200000e+02
dtype: float64
```

```
In [34]: X.hist(bins=220)
plt.yscale('log')
```

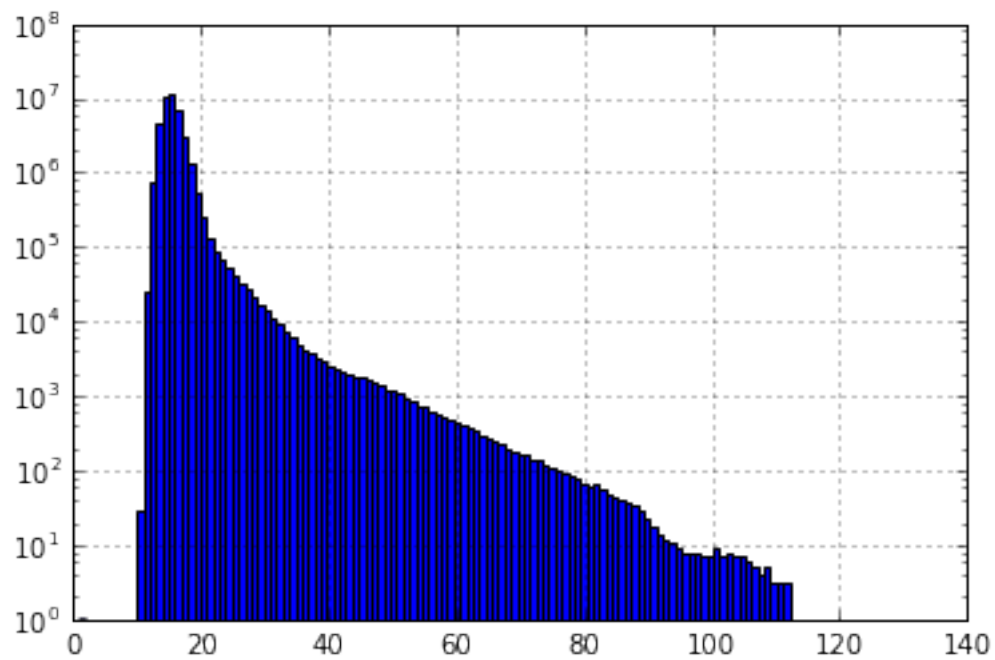


```
In [35]: ## Human chromosome 22 versus the Danio rerio genome
```

```
X = pd.Series(np.loadtxt('genome_data/Homo_sapiens.GRCh38.dna.chromosome.22__Danio_rerio', dtype=float64))
X.describe()
```

```
Out[35]: count    3.915978e+07
mean      1.511217e+01
std       2.150187e+00
min       1.000000e+00
25%      1.400000e+01
50%      1.500000e+01
75%      1.600000e+01
max       1.220000e+02
dtype: float64
```

```
In [36]: X.hist(bins=122)
plt.yscale('log')
```



```
In [ ]:
```