recurrence-distribution

August 26, 2018

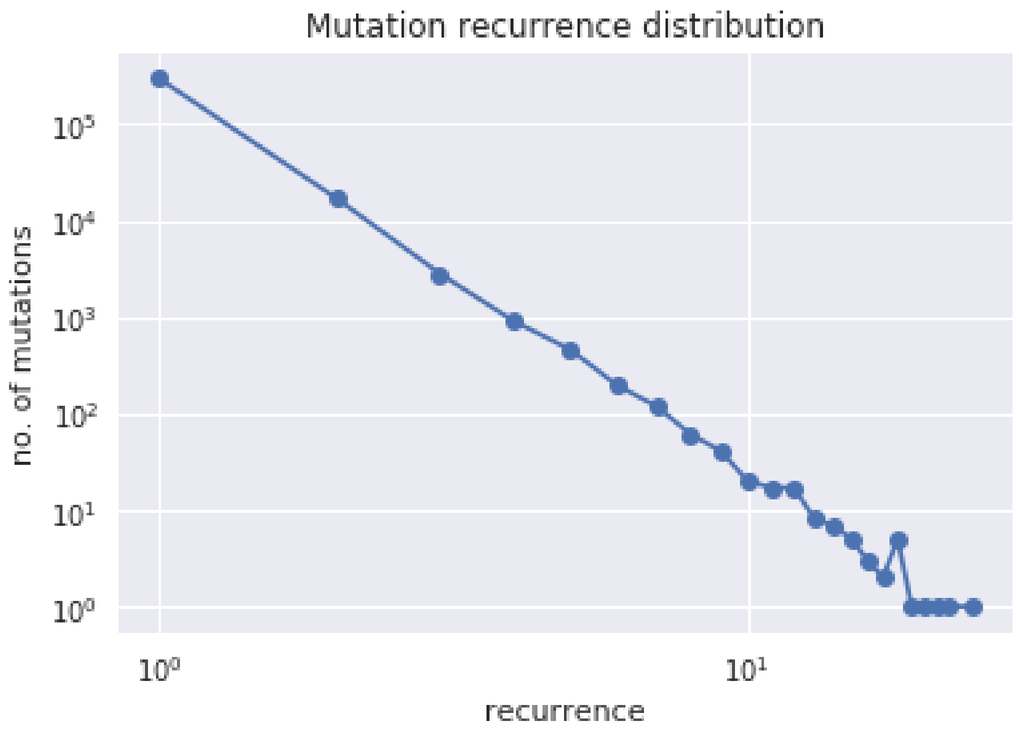
```
In [1]: %matplotlib inline

        import matplotlib.pyplot as plt
        import seaborn as sns
        import numpy as np
        from scipy import optimize

        sns.set()

In [2]: from ICGC_data_parser import SSM_Reader

In [3]: from collections import Counter

        def recurrence_data(mutation, parser):
            "Fetch the recurrence data for a given mutation."
            recurrence_by_project = {occ.project_code:{'affected_donors': occ.affected_donors,
                                                       'tested_donors': occ.tested_donors}
                                     for occ in parser(mutation)}
            return {'mutation_id' : mutation.ID,
                    'proj_recurrence' : recurrence_by_project,
                    'total_affected_donors': mutation.INFO['affected_donors'],
                    'total_tested_donors': mutation.INFO['tested_donors']}
        # ---


        def recurrence_distribution(filename, project=None, filters=None):
            """Searches through input file for mutations related to
            the given cancer project.

            Gets the mutation recurrence distribution for the data
            (i.e. how many mutations are repeated in `n` different
            patients?)
            """
            if filters is None:
                filters = []

            # Open mutations file
            reader = SSM_Reader(filename=filename)
            OCCURRENCES = reader.subfield_parser('OCCURRENCE')

            # Initialize distribution
            tested_donors = None
            distribution = Counter()

            for record in reader.parse(filters=[project]+filters):
                recurrence = recurrence_data(record, OCCURRENCES)

                if project: # When a project is specified
                    proj_recurrence = recurrence['proj_recurrence'][project]
                    proj_affected = proj_recurrence['affected_donors']
                    distribution[int(proj_affected)] += 1

                    if tested_donors is None:
                        tested_donors = proj_recurrence['tested_donors']

                else: # When all projects are parsed
                    total_affected = recurrence['total_affected_donors']
                    distribution[int(total_affected)] += 1

                    if tested_donors is None:
                        tested_donors = recurrence['total_tested_donors']

            return distribution, tested_donors
        # ---

        distribution, tested_donors = recurrence_distribution('data/data-release-25/ssm_sample
```

```
In [4]: for i in sorted(distribution.keys()):
            print(i, distribution[i])
        print(tested_donors)
```

```
1 295368
2 17083
3 2809
4 910
5 458
6 197
7 119
8 61
9 41
10 20
11 17
12 17
13 8
14 7
15 5
```

```
16 3
17 2
18 5
19 1
20 1
21 1
22 1
24 1
12198
```

```
In [6]: x = sorted(distribution.keys())
        y = [distribution[i] for i in x]

        plt.plot(x, y, marker='o')
        plt.yscale('log')
        plt.xscale('log')
        plt.title('Mutation recurrence distribution')
        plt.xlabel('recurrence')
        plt.ylabel('no. of mutations')
        plt.show()
```



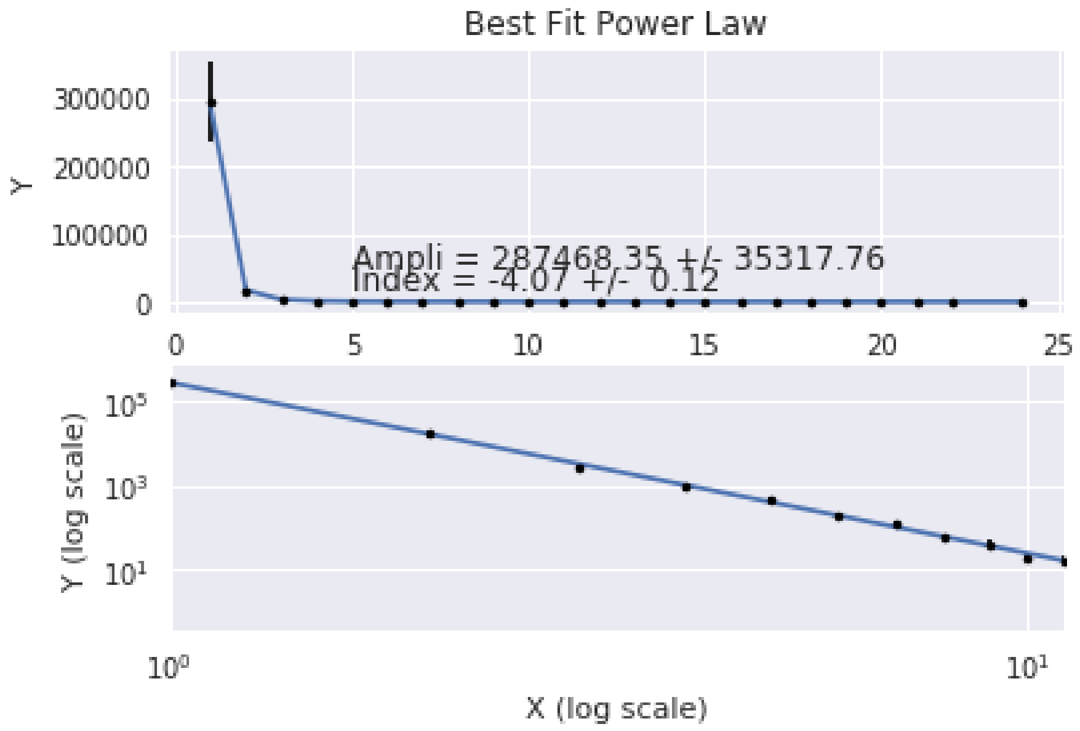
```
In [18]: xdata = np.array(x)
         ydata = np.array(y)
         yerr = 0.2 * ydata
```

```
In [19]: ##########
         # Fitting the data -- Least Squares Method
         ##########

         # Power-law fitting is best done by first converting
         # to a linear equation and then fitting to a straight line.
         # Note that the `logyerr` term here is ignoring a constant prefactor.
         #
         #  y = a * x^b
         #  log(y) = log(a) + b*log(x)
         #
         # Define function for calculating a power law
         powerlaw = lambda x, amp, index: amp * (x**index)

         logx = np.log10(xdata)
         logy = np.log10(ydata)
         logyerr = yerr / ydata

         # define our (line) fitting function
         fitfunc = lambda p, x: p[0] + p[1] * x
         errfunc = lambda p, x, y, err: (y - fitfunc(p, x)) / err

         pinit = [1.0, -1.0]
         out = optimize.leastsq(errfunc, pinit,
                                args=(logx, logy, logyerr), full_output=1)

         pfinal = out[0]
         covar = out[1]
         print(pfinal)
         print(covar)

         index = pfinal[1]
         amp = 10.0**pfinal[0]

         indexErr = np.sqrt( covar[1][1] )
         ampErr = np.sqrt( covar[0][0] ) * amp

         ##########
         # Plotting data
         ##########

         plt.clf()
         plt.subplot(2, 1, 1)
         plt.plot(xdata, powerlaw(xdata, amp, index))     # Fit
         plt.errorbar(xdata, ydata, yerr=yerr, fmt='k.')  # Data
         plt.text(5, 50000, 'Ampli = %5.2f +/- %5.2f' % (amp, ampErr))
         plt.text(5, 20000, 'Index = %5.2f +/- %5.2f' % (index, indexErr))
         plt.title('Best Fit Power Law')
```

```
        plt.xlabel('X')
        plt.ylabel('Y')

        plt.subplot(2, 1, 2)
        plt.loglog(xdata, powerlaw(xdata, amp, index))
        plt.errorbar(xdata, ydata, yerr=yerr, fmt='k.')  # Data
        plt.xlabel('X (log scale)')
        plt.ylabel('Y (log scale)')
        plt.xlim(1.0, 11)
```

```
[ 5.45859004 -4.07123806]
[[ 0.01509406 -0.01369372]
 [-0.01369372  0.01404109]]
```

```
Out[19]: (1.0, 11)
```


Best Fit Power Law
Y
Ampli = 287468.35 +/- 35317.76
Index = -4.07 +/- 0.12
Y (log scale)
10^5
10^3
10^1
10^0
10^1
X (log scale)