Sec 3.

1. a. $\left(\frac{1-q}{n}\right)^{c} \cdot q$

$\sum_{c=0}^{n} 10^{c} = r$ = upper

$\sum_{c=0}^{n-1} 10^{c} + 1 = r$ = lower band

b. $\lim_{r \to \infty} \frac{\log\left(\left(\frac{1-q}{n}\right)^{\log_n(r)} \cdot q\right)}{\log(r)}$ ↙ straight into wolfram

$\log_n(r) = c$

$\rightarrow \frac{\log\left(\frac{1-q}{n}\right)}{\log(n)}$ change of base $= \log_n\left(\frac{1-q}{n}\right)$

c. we have a non-zero asymptote, so it is heavy tailed. i.e. the ratio is non-zero for $\frac{p_r}{r}$ b/c the ratio at logs is non-zero. on one end of the scale, it is a very steep curve as well. This means heavy tail.

The difference is this eq. is prob of a specific word of rank r being chosen, instead of any of length c.

3. a. $E[fd]$ $\quad f_d = c \cdot d^{-\alpha}$,

n is on order of c.

$$\frac{1}{c}\sum_{d=1}^{\delta} d \cdot c d^{-\alpha} = \frac{1}{c} \cdot c \sum_{d=1}^{\delta} d^{1-\alpha}$$
$$= \frac{1}{c} \cdot c \cdot \sum_{d=1}^{c^{\frac{1}{\alpha}}} d^{1-\alpha}$$
$$= \frac{1}{c} \cdot \Theta(c^{\frac{2}{\alpha}})$$
$$= \Theta(c^{\frac{2}{\alpha}-1})$$

ii) $p(D \geq cu) \leq \frac{E[D]}{cu}$

$$1 - p(D \geq cu) \geq 1 - \frac{E[D]}{cu}$$

$p(D < cu) \geq 1 - \frac{E[D]}{cu}$ we have terms on similar $\theta$, for $\theta$, we need $d$

$\geq 1 - \frac{k_1}{k_2}$, Setting $k_2 = 2k_1$ gives us the desired result.

iii) $$\frac{1}{2}\sum_{d=c^{\frac{1}{\alpha}-\epsilon}}^{c^{\frac{1}{\alpha}}} d \cdot c \cdot d^{-\alpha} = \frac{1}{2} c \sum_{d=c^{\frac{1}{\alpha}-\epsilon}}^{c^{\frac{1}{\alpha}}} d^{1-\alpha} = \underbrace{c \sum_{d=1}^{c^{\frac{1}{\alpha}}} d^{1-\alpha}}_{\Theta(c^{\frac{2}{\alpha}})} - c \sum_{d=1}^{c^{\frac{1}{\alpha}-\epsilon}} d^{1-\alpha}$$

$$\sum_{d=1}^{t} d^{-\beta} = \Theta(t^{1-\beta})$$
$t = c^{\frac{1}{\alpha}-\epsilon}$
$\beta = \alpha - 1$
$\Theta(c \cdot c^{(\frac{1}{\alpha}-\epsilon)(2-\alpha)})$
$\Theta(c \cdot c^{\frac{2}{\alpha}-1-2\epsilon+\alpha\epsilon})$
$\Theta(c^{\frac{2}{\alpha}-\epsilon(2-\alpha)})$

$$= \Theta(c^{\frac{2}{\alpha}} - c^{\frac{2}{\alpha}-\epsilon(2-\alpha)})$$

smaller order term goes away in $\theta$ notation.

$$= \Theta(c^{\frac{2}{\alpha}}) \in \Theta(m) \checkmark$$

iv) $$p(L) = \frac{c\sum_{d=c^{\frac{1}{\alpha}-\epsilon}}^{\delta} d^{1-\alpha}}{c\sum_{d=1}^{\delta} d^{1-\alpha}} \quad \text{so} = \Theta(1)$$

$\Theta(m)$

$m = \Theta(m)$

$p(S) = 1 - p(L)$

$p(\ell) = 1 - p(S)^d$

So: $\frac{1}{n}\sum_{d=1}^{\delta} c d^{-\alpha} p(\ell)$ $\quad \Theta(1)$

$$\frac{1}{n}\underbrace{\sum_{d=1}^{\delta} c d^{-\alpha}}_{\Theta(n)} \underbrace{(1 - \underbrace{(\underbrace{1 - p(L)}_{\Theta(1)})^d}_{\text{smaller than } 1})}_{\text{smaller than } 1}$$

order of $\Theta(1)$

$$\frac{\Theta(n)}{n}\Theta(1) \Rightarrow \Theta(1) \checkmark$$

v) by ii) and iv), we have

$$\frac{c^{\frac{1}{\alpha}-\epsilon}}{c^{\frac{2}{\alpha}-1}} \rightarrow c^{1-\frac{1}{\alpha}-\epsilon} \text{ as desired.}$$

c is order of n.

So we have

$\Omega(n^{1-\frac{1}{\alpha}-\epsilon})$ as desired!

5. a. $\ell < k$

$$Pr = \sum_{i=0}^{\ell-1} p^2 \cdot (1-p)^{\ell-1}$$

$\ell = k$

$$Pr = \left(\sum_{i=0}^{\ell-1} p^2 (1-p)^{\ell-1}\right) + (1-p)^{k+1} + (k+1)(1-p)^k p$$

Plugging into mathematica, mult by $\ell$ for Ev, we get

$$\frac{2-p+(1-p)^k(-2+p-kp)}{p}$$

b. Expected Avg Shortest path length:

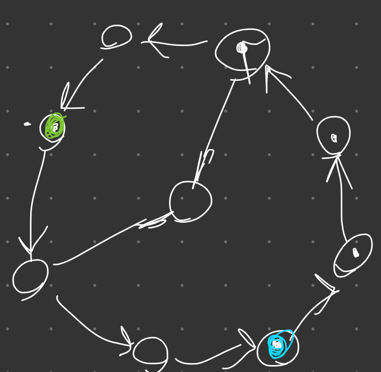
$$\frac{-3+2p+2np-np^2+(1-p)^n(3+(-2+n)p)}{(-1+n)p^2}$$

Scales exponentially w/n.

for no central node, $\dfrac{\frac{1}{n} \cdot n\sum^{n-1} k}{n-1} = \dfrac{\frac{(n-1)(n-2)}{2}}{n-1} = \dfrac{n-2}{2}$

Scales linearly

c.



works in all but this case, in which case it will add 1 to the Shortest path

The algo would work in all but 1 class of cases. if B always routes to the closest node, we always want to take B, since in most cases, we skip at least 1 hop of length 1 if we take B. Thus, given a path through B or not through B, we would want to take B in most cases. The case we wouldn't want to is the one where if we take B, but the closest exit from B is the one we took, as above going from Blue to green. In cases like this, the algo takes B, but comes back where it entered and moves on, rather than skip B. in this case, we add 1 to the shortest path, which is pretty close to the real shortest path. An "accidental" traversal of B would only happen once, since if it happened twice, the first traversal would have come out at the second traversal's point, a contradiction. Thus, this algo admits the shortest path in all but 1 case, when we have to take B, but the edge closest to the destination is the one we took, adding 1 to the resulting path, which is very close to the real shortest path.

6. a. $m_i(t+1) - m_i(t)$

| | | |
|---|---|---|
| $i = t+1$ <br> indiv only, inc $= 1$ | $i \leq t$ <br> $\frac{m_i(t)}{2t-1} =$ inc. | $i > t$ <br> inc $= 0$. |

$$m_i(t+1) = \frac{m_i(t)}{2t-1} + m_i(t)$$

B. Using MV approx and cont. approx, we can see how the eqn follows from newton's method w/ $h=1$.

C. DSolve:

$$m_i(t) = 0 \text{ if } t < 1$$
$$= \sqrt{-1+2t}\, C_1 \text{ if } t > i$$
$$= 1 \text{ if } t = i$$

$$1 = m_i(i) = \sqrt{-1+2t} \cdot C_1$$

$$\log c = \frac{1}{\frac{1}{2}\log 2i}$$

$$C_1 = \frac{1}{\sqrt{2i}}$$

D. $\frac{m_p(t)}{\sum_{i=1}^{t} m_i(t)}$

Subbing in c and solving we get

$\frac{1}{\text{Harmonic\#}(t, \frac{1}{2})}$ which goes to 0 as time moves on.

Thus, popular product share less market share.

# Problem2

February 1, 2023

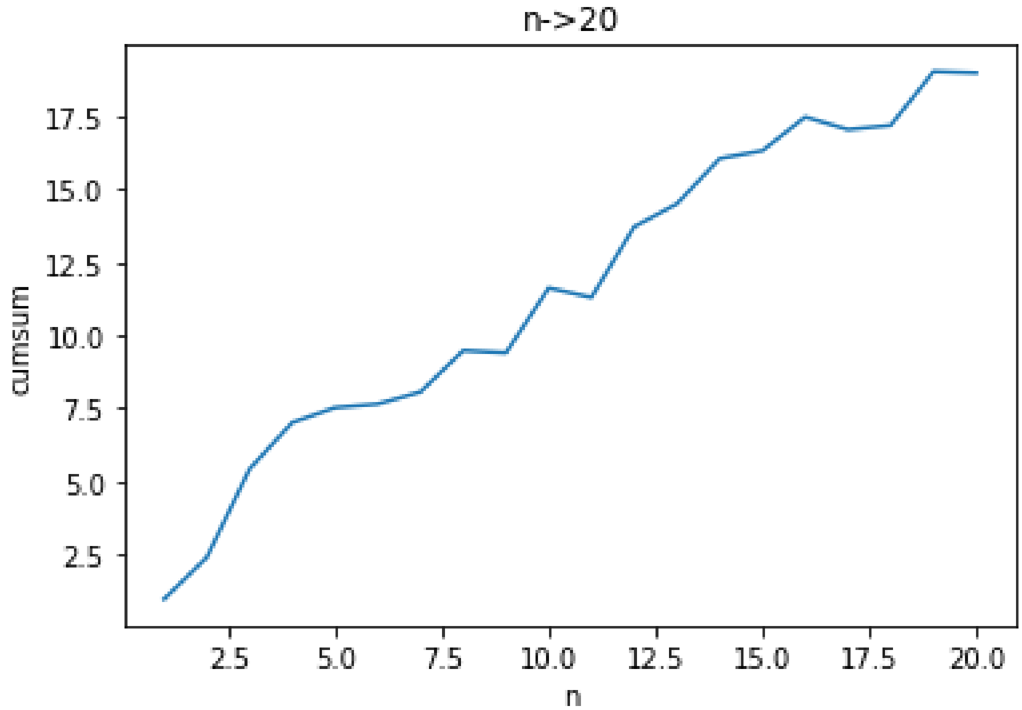
```
In [307]: import numpy as np
          import matplotlib.pyplot as plt
```

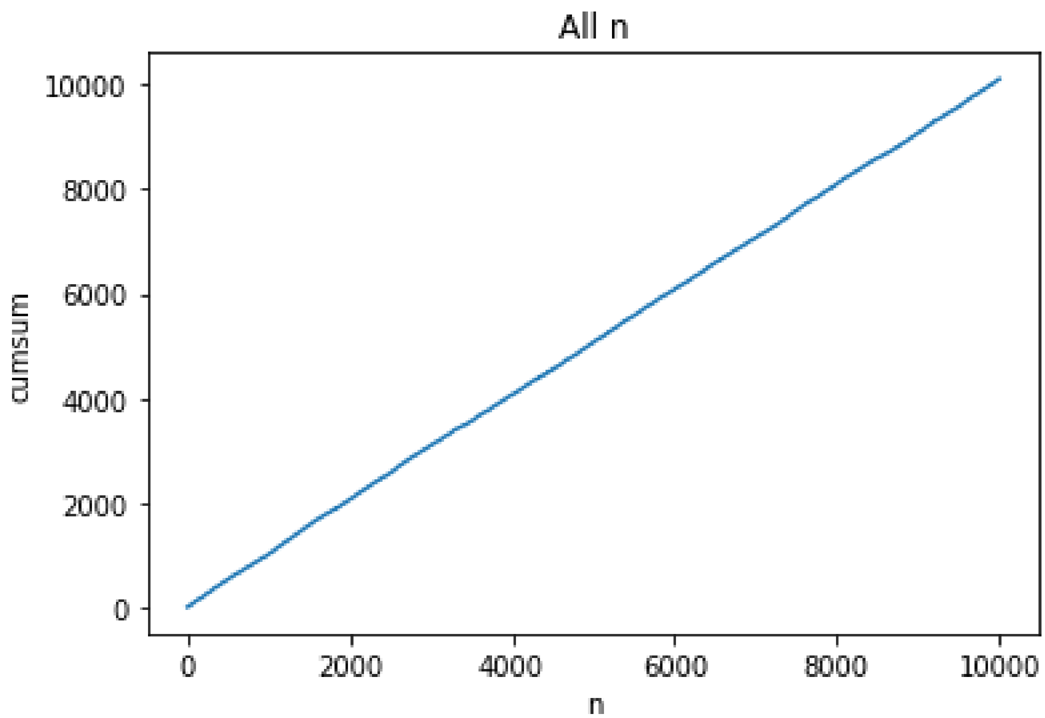
## 1 Part A

```
In [308]: N = 10000
          norm_dist = np.random.normal(1, 1, (N,))
          weib = np.random.weibull(0.3, (N,))
          pareto = (np.random.pareto(0.5, (N,)) + 1) * (1/3)
```

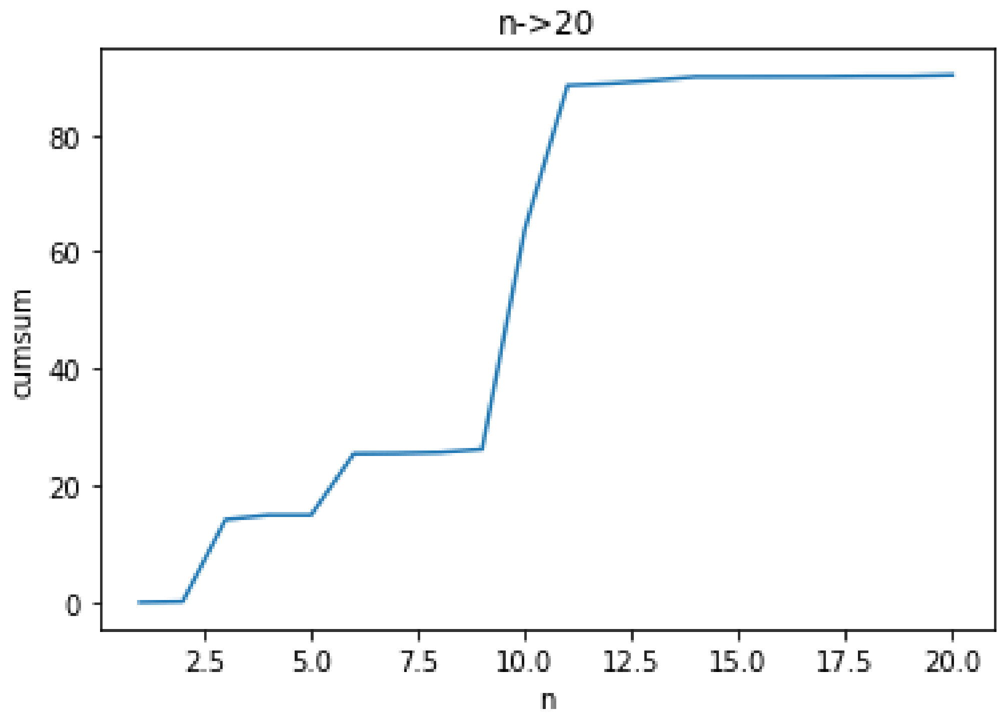
```
In [309]: def make_plots_A(dist):
              plt.plot(np.arange(1, 21, 1), np.cumsum(dist)[:20])
              plt.title("n->20")
              plt.xlabel("n")
              plt.ylabel("cumsum")
              plt.show()
              plt.plot(np.arange(N), np.cumsum(dist))
              plt.title("All n")
              plt.xlabel("n")
              plt.ylabel("cumsum")
              plt.show()
```

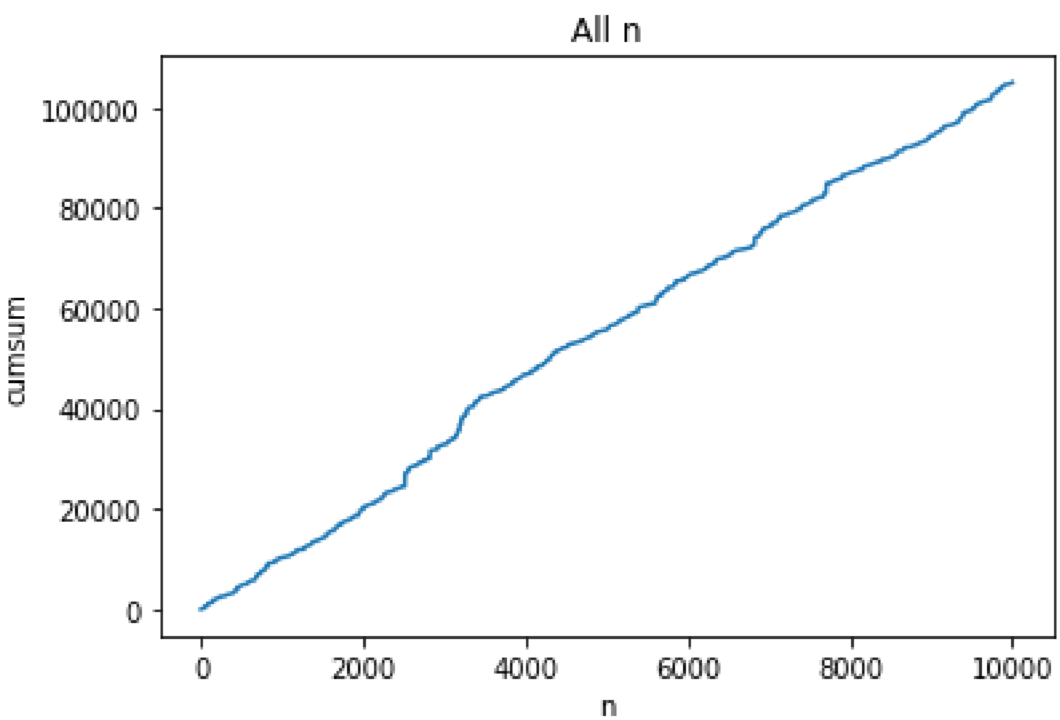
```
In [310]: make_plots_A(norm_dist)
```


n->20
cumsum
n
17.5
15.0
12.5
10.0
7.5
5.0
2.5
2.5
5.0
7.5
10.0
12.5
15.0
17.5
20.0

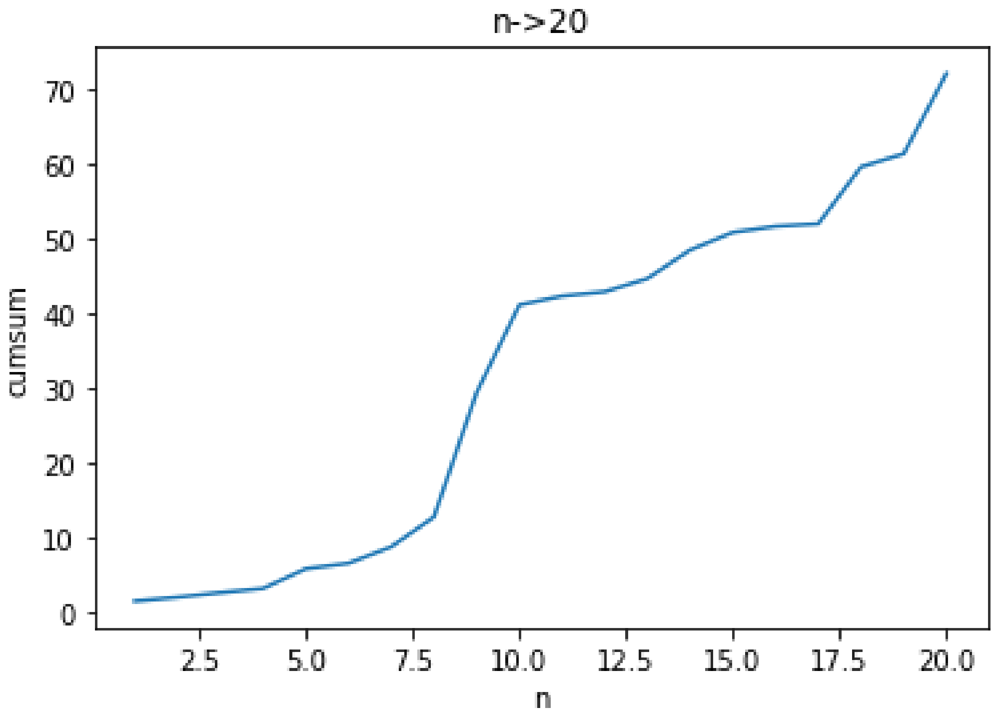

All n
cumsum
n
10000
8000
6000
4000
2000
0
0
2000
4000
6000
8000
10000

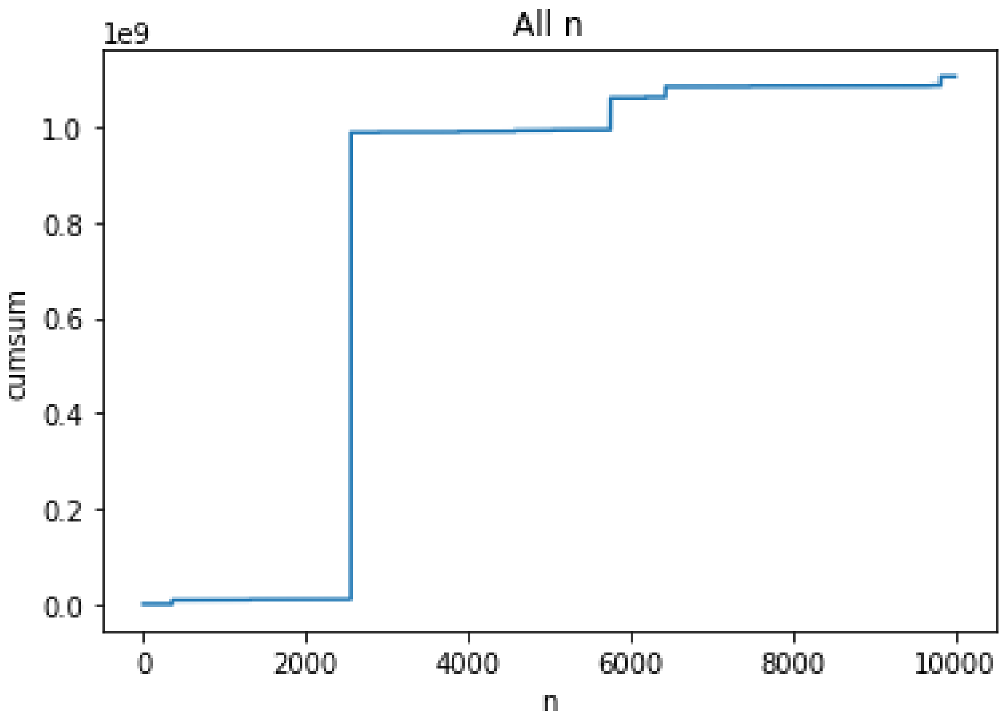
```
In [311]: make_plots_A(weib)
```



```
In [312]: make_plots_A(pareto)
```

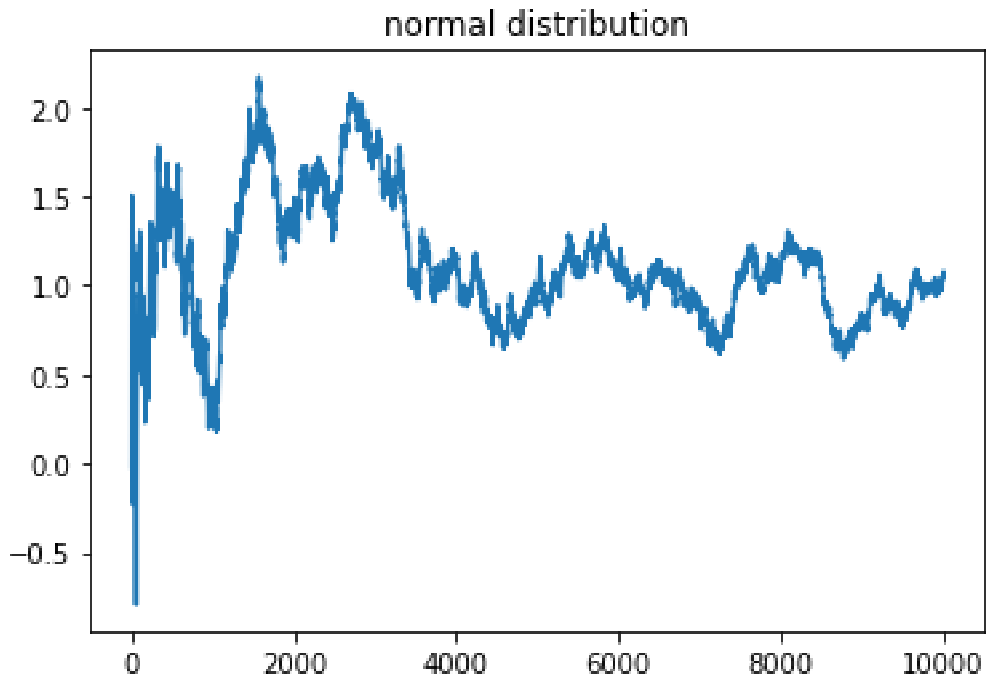


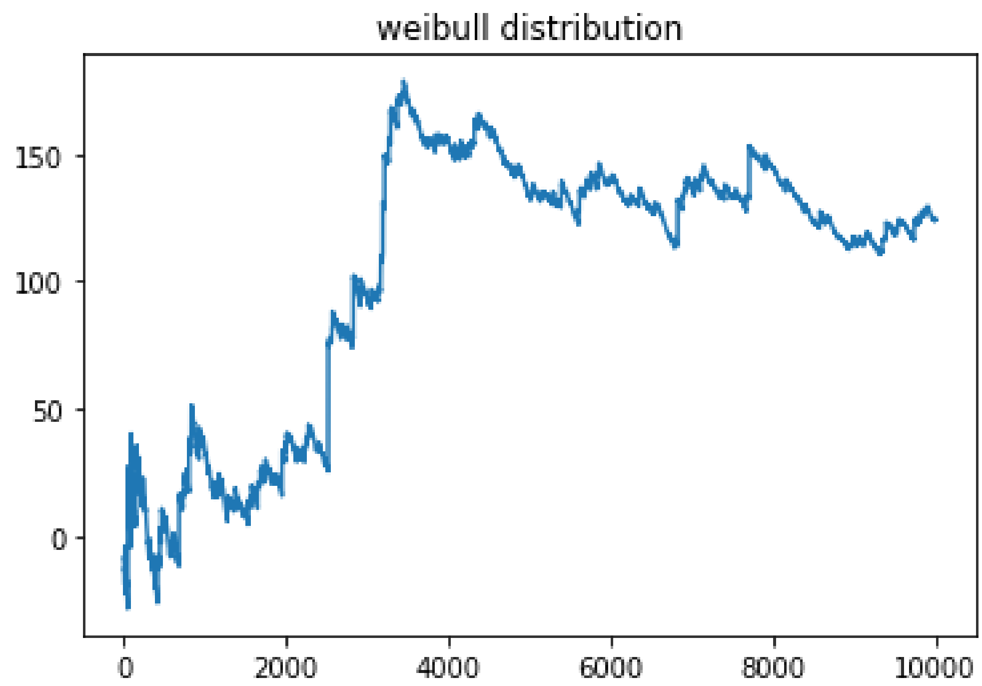



## 2 Part B

In [322]:
```
def make_plots_B(dist, mean, distribution):
    cumsum = np.cumsum(dist)
    deviations = (cumsum - np.arange(1, N+1, 1) * mean) / np.sqrt(np.arange(1, N+1, 1
    plt.plot(np.arange(1, N+1, 1), deviations)
    plt.title(distribution)
    plt.show()
```

In [323]:
```
make_plots_B(norm_dist, 1, "normal distribution")
make_plots_B(weib, 9.26053, "weibull distribution")
```


normal distribution
2.0
1.5
1.0
0.5
0.0
−0.5
0
2000
4000
6000
8000
10000

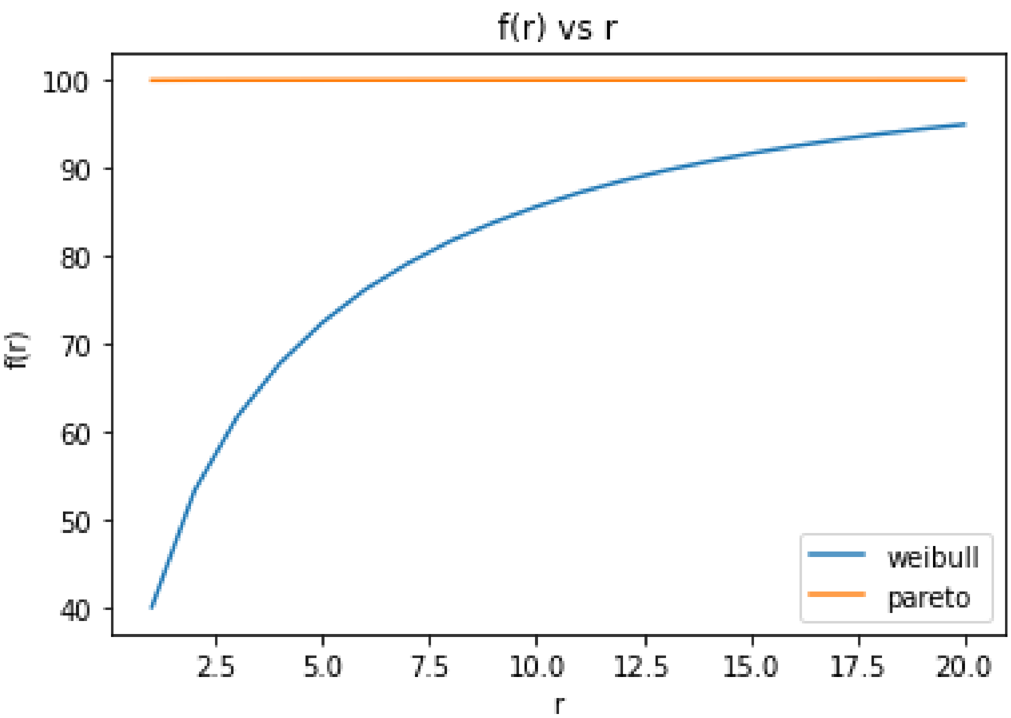

weibull distribution
150
100
50
0
0
2000
4000
6000
8000
10000

## 3 Part C

```
In [316]: def frac(dist):
              rs = (np.arange(0.01, 0.21, 0.01) * N).astype(int)
              sorted_dist = sorted(dist, reverse=True)
              cumsum = np.cumsum(sorted_dist)
              fracs = np.array([cumsum[r] for r in rs])
              fracs = fracs / np.sum(dist) * 100
              return fracs
```

```
In [317]: fracs_weib = frac(weib)
          fracs_pareto = frac(pareto)
          plt.plot(np.arange(1, 21, 1), fracs_weib, label="weibull")
          plt.plot(np.arange(1, 21, 1), fracs_pareto, label="pareto")
          plt.title("f(r) vs r")
          plt.xlabel("r")
          plt.ylabel("f(r)")
          plt.legend()
```

```
Out[317]: <matplotlib.legend.Legend at 0x7f3836ceb670>
```



# 4 Part D

In [318]:
```
from statsmodels.distributions.empirical_distribution import ECDF
from sklearn.linear_model import LinearRegression
from sklearn.metrics import r2_score
```

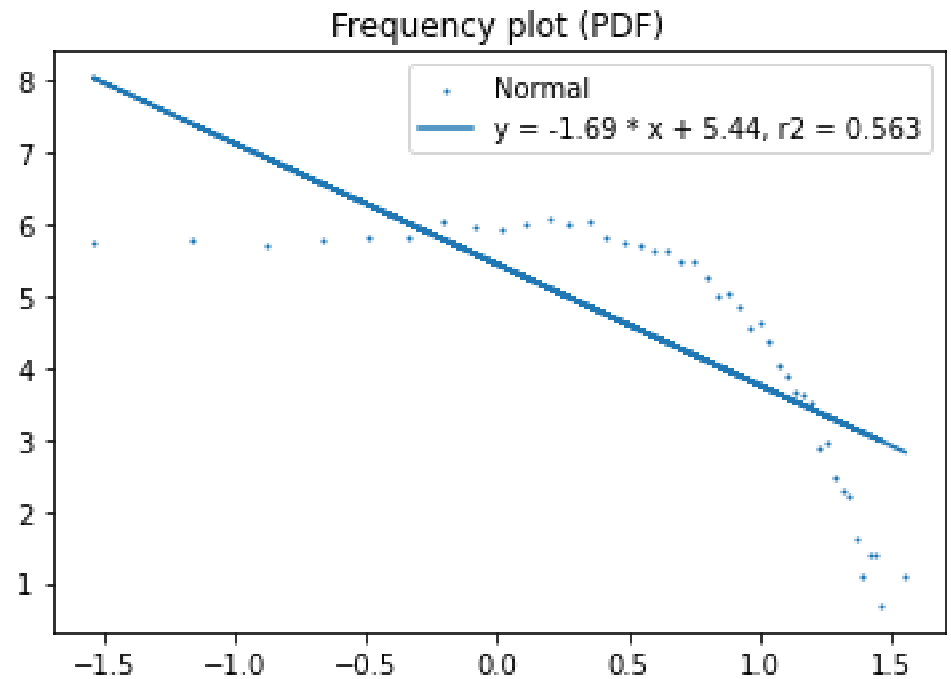
In [319]:
```
# Note: Feel free to modify this template as you wish or build your own from scratch
# This is a tricky problem to implement so we hope we are helping by providing a tem

def pdf(data, dx=1):
    '''Takes an array with random samples from a distribution,
    and creates an approximate PDF of points, to use when frequency
    Returns a tuple of two vectors x, y where
    y_i = P(x_i - dx/2 <= data < x_i + dx/2)'''

    low, high = np.min(data), np.max(data)
    x, y = [], []

    for d in data:
        i = int((d + dx / 2 - low) / dx)
        xi = low + i * dx
        if xi in x:
            y[x.index(xi)] += 1
        else:
            x.append(xi)
            y.append(1)

    return np.array(x), np.array(y)

def ccdf(data):
    '''Takes an array with random samples from a
    distribution, and creates an approximate CCDF
    (complementary CDF) of points. Returns a tuple of
    two vectors x, y where y_i = P(data > x_i)'''
    # TODO: Complete this function

    # Use this when creating the rank plot
    # HINT: To generate an approximate CDF (not CCDF), one would sort the random sam
    # return those as the x values, and then create a range from 1 to n
    # (scaled by 1/n) for the y values. How does this change when creating a CCDF?
    x = 1-np.sort(data)
    y = [i / N for i in range(1, N+1, 1)]
    return x, y

def keep_positive(data):
    '''Takes an array with random samples from
    a distribution, and filters our negative and
    zero entries (in both x and y) in data'''
```

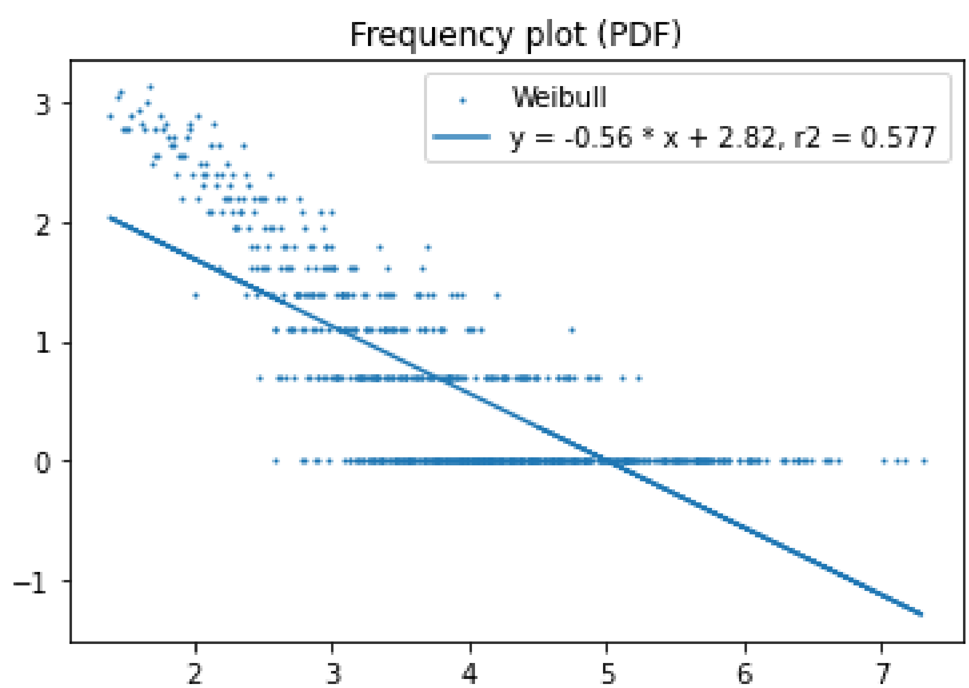
```python
    # TODO: Complete this function
    for dist in range(len(data)):
        x, y = data[dist]
        x = np.array(x)
        y = np.array(y)
        x_pos = x > 0
        y_pos = y > 0
        x = x[x_pos & y_pos]
        y = y[y_pos & x_pos]
        data[dist] = (x, y)
    return data

def non_outliers(x, m):
    '''Takes an array x of data and an integer m,
    and returns a list z of boolean values such
    that z_i indicates whether the mean-centered
    value x_i is within m std devs of the values in x'''
    # TODO: Complete this function
    x_mean = np.mean(x)
    x_std = np.std(x)
    x_centered = x - x_mean
    z = np.abs(x_centered) <= m * x_std
    return z

def reject_outliers(data, m):
    '''Takes an array of data (data here is a
    tuple (x,y), where x and y are arrays:
    in the form resulting from pdf() or ccdf(), for example)
    and an integer m, and removes outliers from the data'''
    # TODO: Complete this function

    # Note that since we are plotting on log-log scale
    # Removing outliers should happen AFTER we move to log-log scale

    # HINT: This function returns the (x, y) tuples in data that
    # are not outliers (non_outliers() is helpful here)

    # HINT: You must set m to a default value that defines how many
    # standard deviations away an outlier is. We are testing that
    # these distributions are heavy-tailed, so too tight of a range
    # won't be helpful.
    x, y = data
    m = 2
    x_non = non_outliers(x, m)
    y_non = non_outliers(y, m)
    x = x[x_non & y_non]
    y = y[x_non & y_non]
    return (x, y)
```

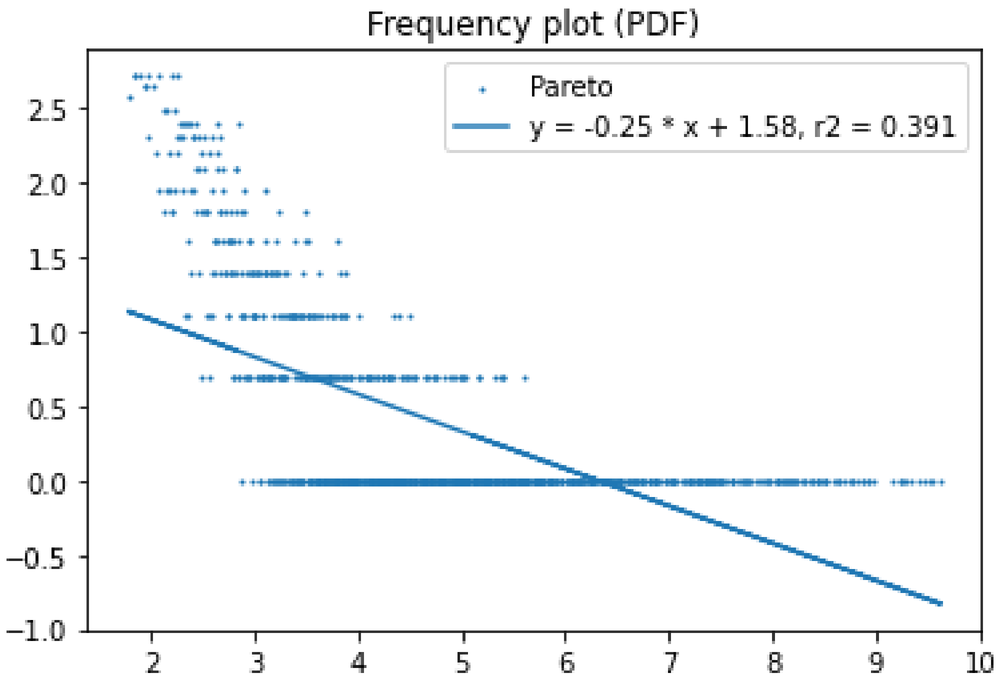
```
def linear_regression(X, y):
    '''Takes (one-dimensional) training data X
    and labels y and fits the simple linear regression
    model y = mX + b, and computes the coefficient
    of determination (r^2). Returns a tuple (m, b, r^2)'''
    # TODO: Complete this function
    reg = LinearRegression()
    reg.fit(X.reshape(-1, 1), y)
    ypred = reg.predict(X.reshape(-1, 1))
    return (reg.coef_, reg.intercept_, r2_score(y, ypred))

def make_graphs_d(data, title, labels, ylabel='', xlabel=''):
    """
    Build respective PDF/CCDF for all three distributions
    Attempts to create a best-fit line
    And plots this line alongside the points
    data: List of pdf() outputs from all 3 distributions
    title: Either
        Frequency plot (PDF)
        Rank plot (CCDF)
    labels: List of distribution names
        i.e. ["Normal, Weibull, Pareto"]
    """
    # General plotting function for points, as well as best-fit line

    for (X, y), label in zip(data, labels):
        m, b, r2 = linear_regression(X, y)
        plt.scatter(X, y, label=label, s=1)
        plt.plot(X, b + m * X, label='y = %.2f * x + %.2f, r2 = %.3f' % (m, b, r2))
        plt.title(title)
        plt.xlabel(xlabel)
        plt.ylabel(ylabel)
        plt.legend()
        plt.show()
```

In [320]:
```
# Concatenate data into one list to reduce code repetition
Xi = [norm_dist, weib, pareto]
names = ["Normal", "Weibull", "Pareto"]

# Build the PDF and turn it into a log-log scale,
# first removing all negative values and corresponding indices
# TODO: When (if at all) do we remove outliers here?
# Before or after we convert to log-scale?
data = [pdf(Xi[i], dx=0.1) for i in range(3)]
data = keep_positive(data)
data = [(np.log(X), np.log(y)) for (X, y) in data]
data = [reject_outliers(data[i], 4) for i in range(len(data))]
```

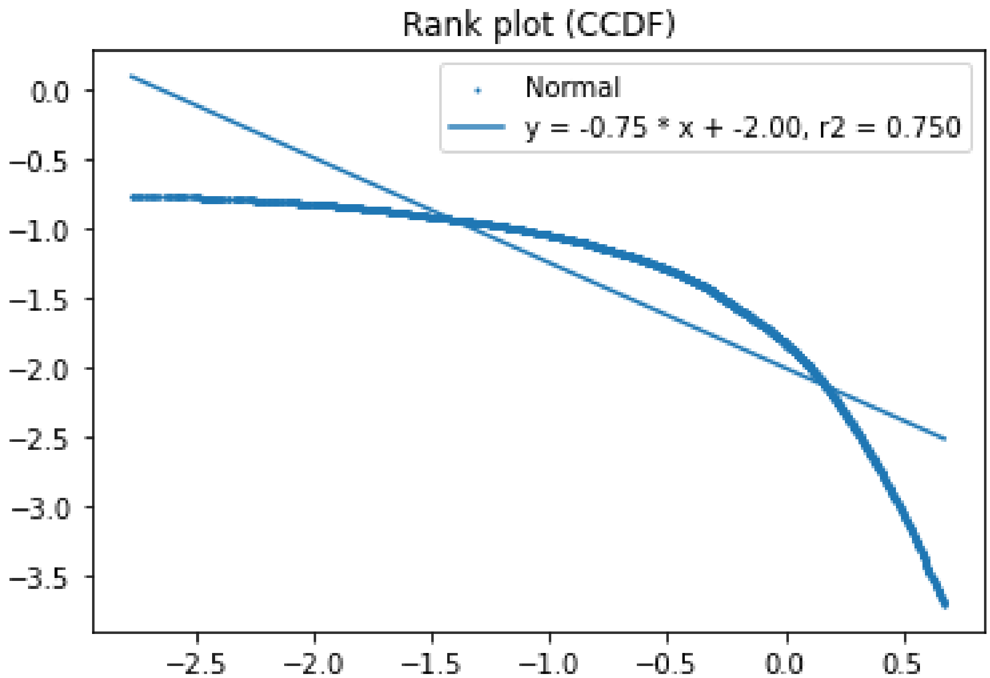
```
# Plot the frequencies
make_graphs_d(data, 'Frequency plot (PDF)', names)
```

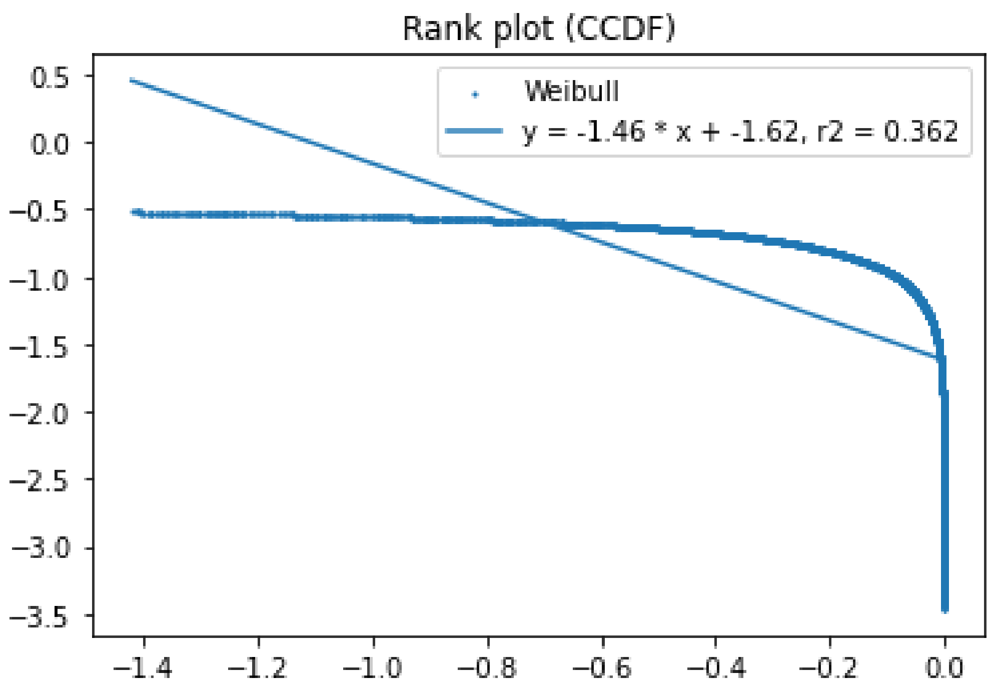


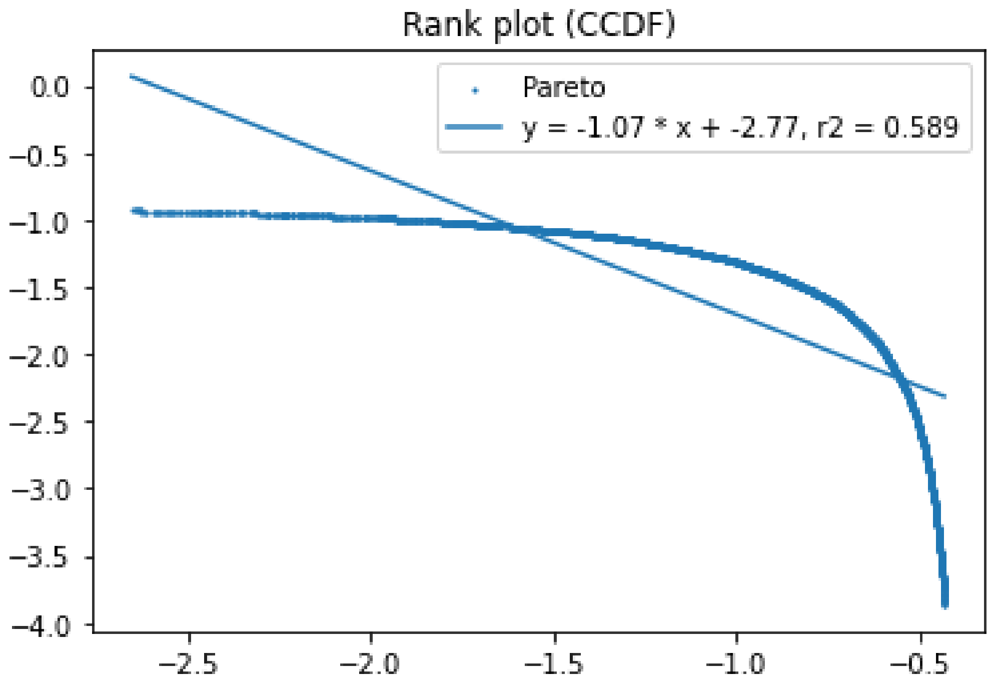






In [321]:
```
data = [ccdf(Xi[i]) for i in range(3)]

# Build the CCDF and turn it into a log-log scale,
# first removing all negative values and corresponding indices
# TODO: Do we remove outliers here?
data = keep_positive(data)
data = [(np.log(X), np.log(y)) for (X, y) in data]
data = [reject_outliers(data[i], 4) for i in range(len(data))]
# Plot the ranks
make_graphs_d(data, 'Rank plot (CCDF)', names)
```


Rank plot (CCDF)
Normal
y = -0.75 * x + -2.00, r2 = 0.750


Rank plot (CCDF)
Weibull
y = -1.46 * x + -1.62, r2 = 0.362




For the plots,

Filtering out outliers makes sense because on a log scale, big outliers can mess with the graph ranges. Small outliers become big outliers in log, while big outliers become even bigger.

We see that the normal distribution is not heavy-tailed, but the other 2 are. It's easier to see this because best fits have better linearity for normal, but they are worse for weibull and pareto, and we see a sharp drop off in the points in the emperical ccdf.

# Problem4

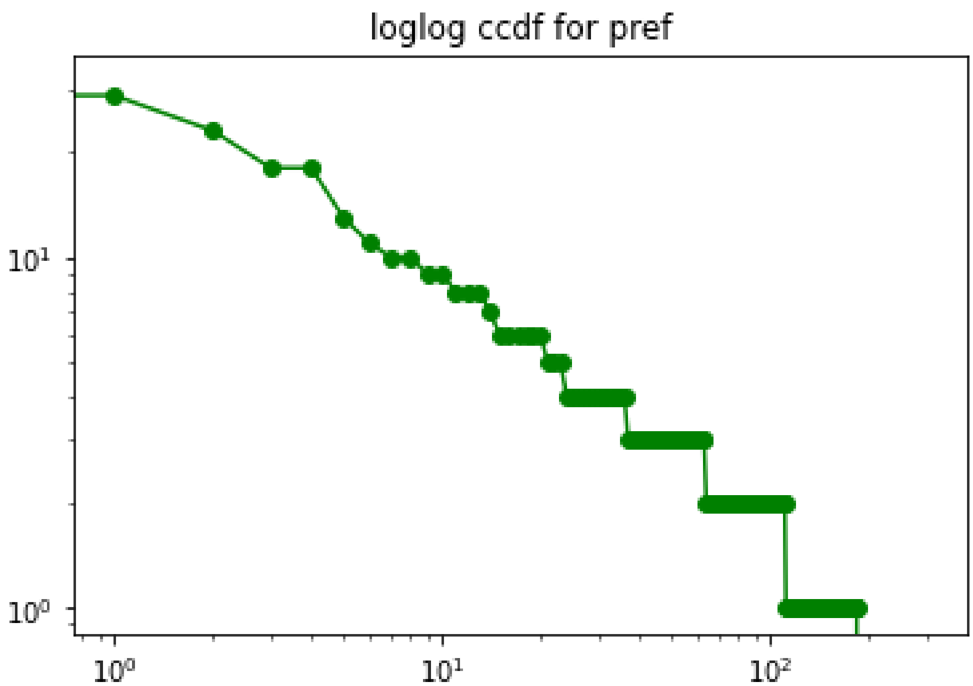
February 1, 2023

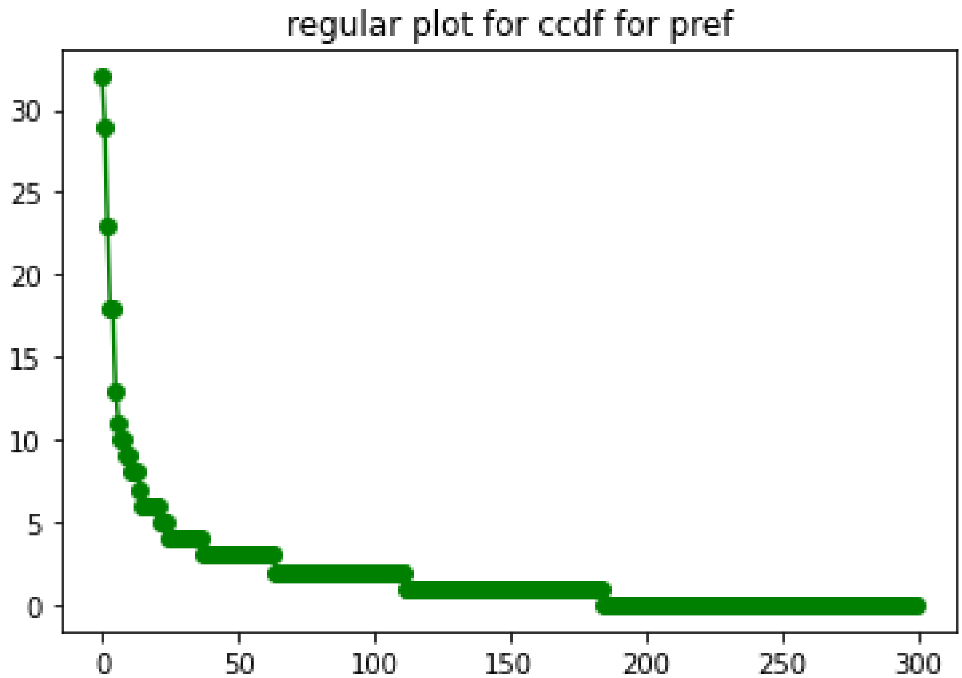
```
In [57]: import numpy as np
         import networkx as nx
         import matplotlib.pyplot as plt

In [66]: def get_deg_sum(G):
             nodes = list(G.nodes())
             tot = 0
             for node in nodes:
                 tot += G.degree(node)
             return tot

         # A
         def gen_pref(T):
             G = nx.Graph()
             G.add_edge(0, 1)
             for newcomer in range(2, T, 1):
                 G.add_node(newcomer)
                 deg_sum = get_deg_sum(G)
                 for existing in range(newcomer):
                     p = G.degree(existing) / deg_sum
                     if np.random.random() < p:
                         G.add_edge(newcomer, existing)

             degrees = [d for n, d in G.degree()]
             return G, degrees

         # B
         def configuration_graph(degrees):
             v = []
             G = nx.Graph()
             for i, k in enumerate(degrees):
                 v.extend([i for x in range(k)])
             v = np.random.permutation(v)
             for i in range(0, len(v), 2):
                 G.add_edge(v[i], v[i+1])
             return G
```

# 1 A

```
In [67]: T = 300
         G_pref, degrees = gen_pref(300)
```

```
In [75]: degree_sequence = sorted(degrees, reverse=True)
         plt.loglog(degree_sequence, "g-", marker="o")
         plt.title("loglog ccdf for pref")
         plt.show()
         plt.plot(degree_sequence, "g-", marker="o")
         plt.title("regular plot for ccdf for pref")
         plt.show()
```



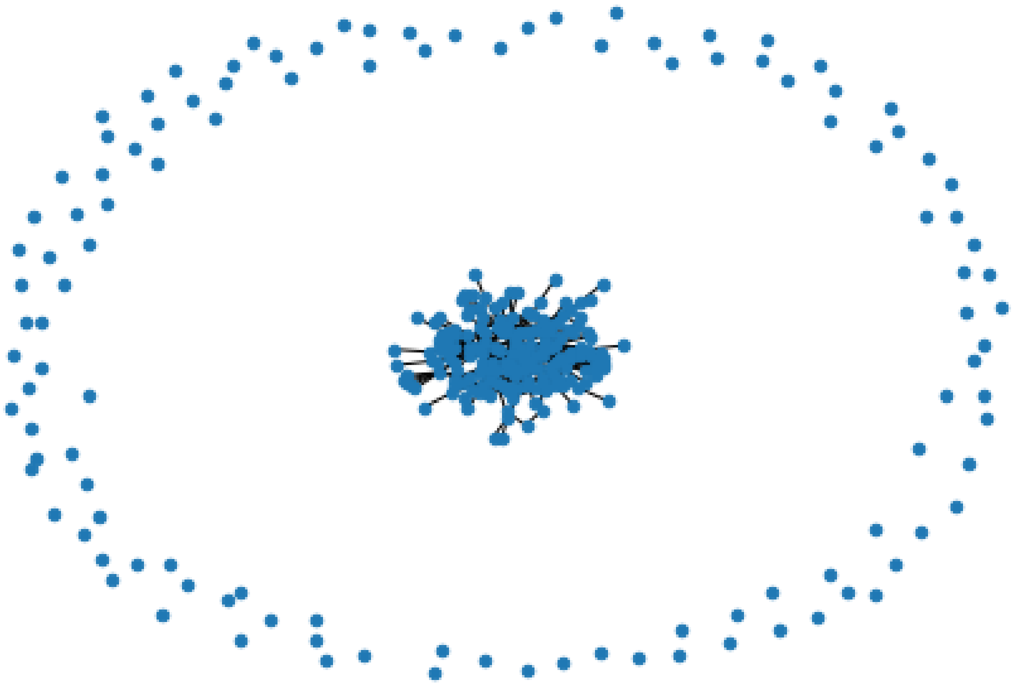



We definitely see a heavy-tail here given these plots.

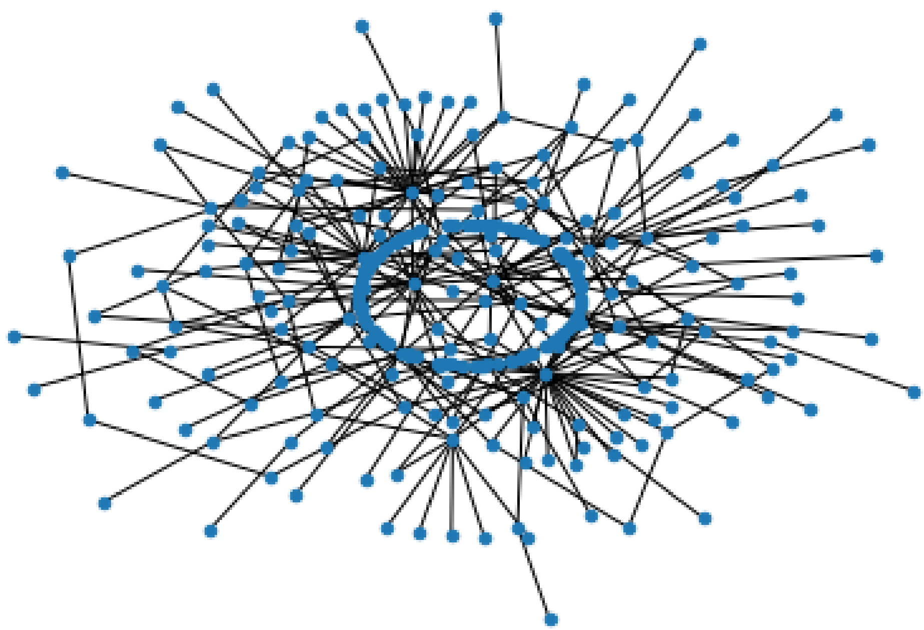
## 2 B

In [69]:
```
T = 300
G_pref, degrees = gen_pref(300)
G_config = configuration_graph(degrees)
```

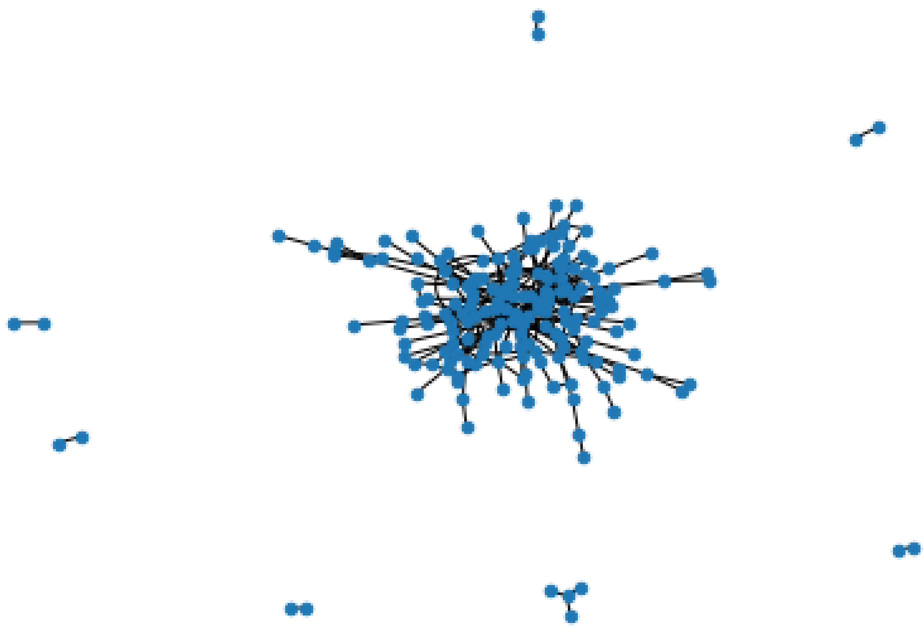
In [77]:
```
nx.draw(G_pref, node_size=20)
```



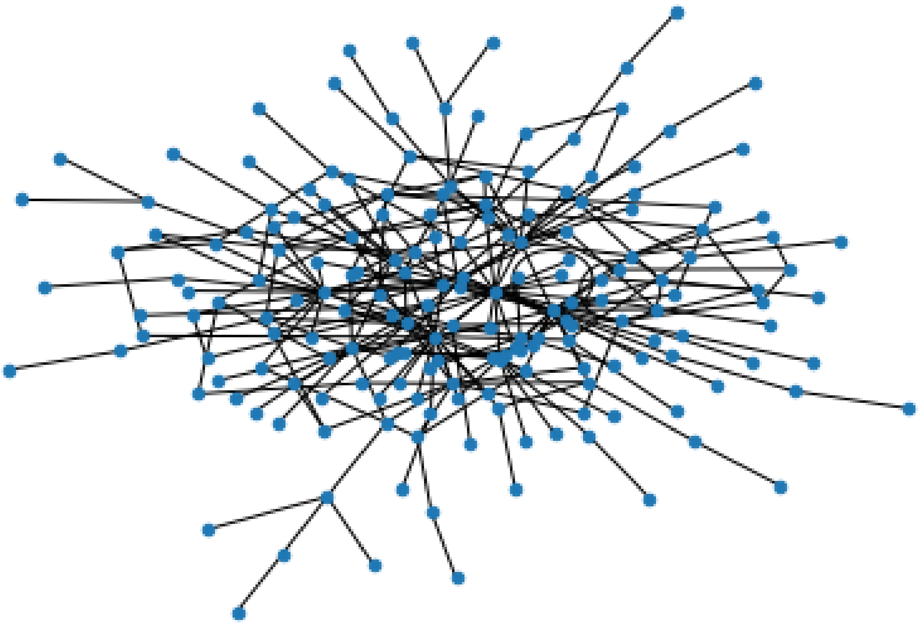
```
In [79]: nx.draw_kamada_kawai(G_pref, node_size=20)
```



```
In [81]: nx.draw(G_config, node_size=20)
```



```
In [80]: nx.draw_kamada_kawai(G_config, node_size=20)
```



## 3 C

The differences I see are that the pref generated graph has a more uniform structure of disconnected components, while the config graph has smaller, disconnected clusters all around a main cluster in the middle. The pref graph has a bit more structure to it as well, forming a "social circle" of sorts with the highly connected nodes.

In[10]:= $P(\mathrm{l\_}, \mathrm{k\_}) := \sum_{i=0}^{l-1} \left(p^2 (1-p)^{l-1}\right);$

In[11]:= $\mathrm{Pe}(\mathrm{l\_}, \mathrm{k\_}) := P(l, k) + \left((1-p)^{k+1} + (k+1)\, p\, (1-p)^k\right);$

```
In[12]:= FullSimplify[Sum[P[l, k] * l, {l, 1, k - 1}] + Pe[k, k] * k]
```

Out[12]= $\dfrac{2 - p + (1-p)^k (-2 + p - k\, p)}{p}$

```
In[13]:= Es[k_] := FullSimplify[Sum[P[l, k] * l, {l, 1, k - 1}] + Pe[k, k] * k]

In[14]:= FullSimplify[Sum[Es[k], {k, 1, n - 1}] / (n - 1)]
```

Out[14]= $\dfrac{-3 + 2\, p + 2\, n\, p - n\, p^2 + (1-p)^n\, (3 + (-2+n)\, p)}{(-1+n)\, p^2}$

large output | show less | show more | show all | set size limit...