As Welf said, we can skip the data generation step....

1.3 Load the (generated) data and get an overview

In [ ]:
```
import pandas as pd

feature_names = ['n_50', 'n_150', 'n_300', 'd_50', 'd_150', 'd_300', 't_p
df = pd.read_csv('../data/epidemic_process.csv', names=feature_names)
df.head()
```

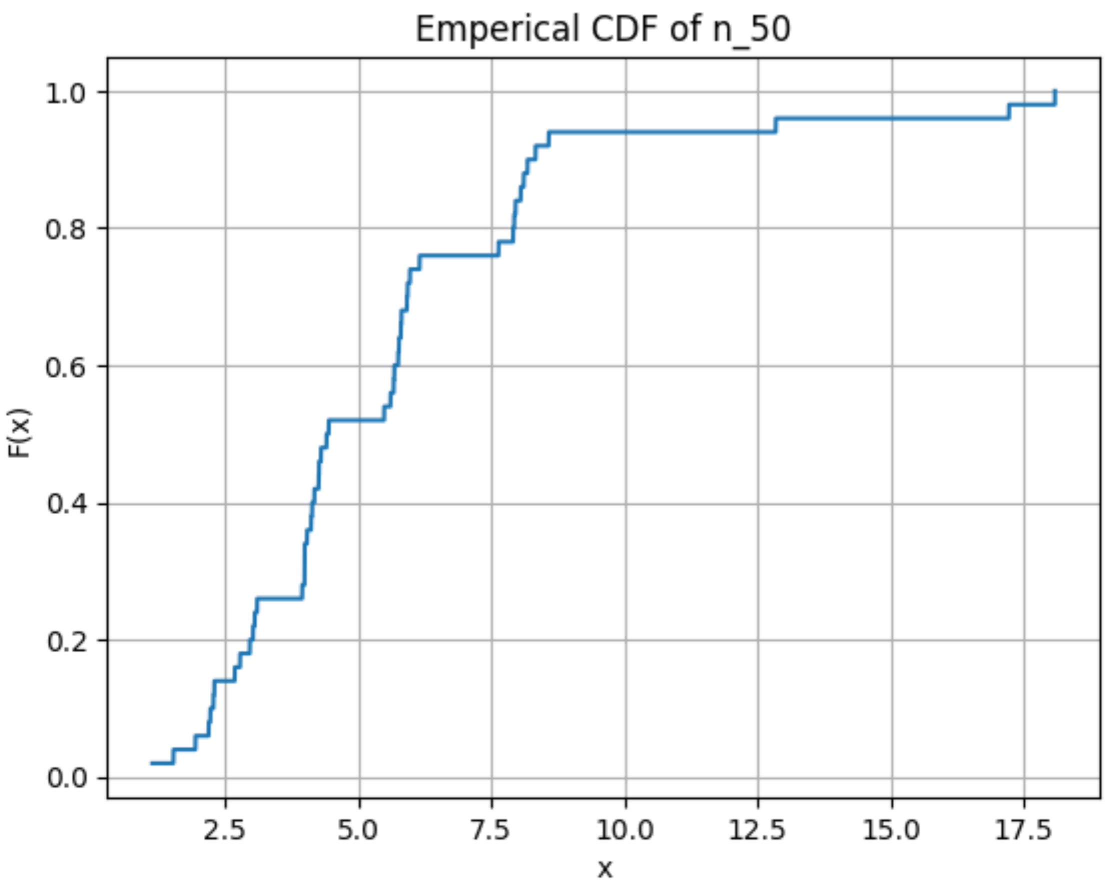
Out[ ]:

	n_50	n_150	n_300	d_50	d_150	d_300	t_peak	x_50
0	5.484789	31.727771	6.910956	1.086088	0.364691	-1.167716	155.625779	0.95663
1	8.578305	34.552430	3.908585	1.464196	-4.350747	-0.664125	120.744595	0.98218
2	1.525187	3.581051	7.528895	0.077954	0.445827	0.030962	357.805297	0.47234
3	6.151596	33.205968	6.199945	1.148558	-1.573964	-0.617079	133.964974	0.96100
4	4.443471	30.324971	8.335484	0.970687	2.765872	-1.672065	162.800388	0.88193

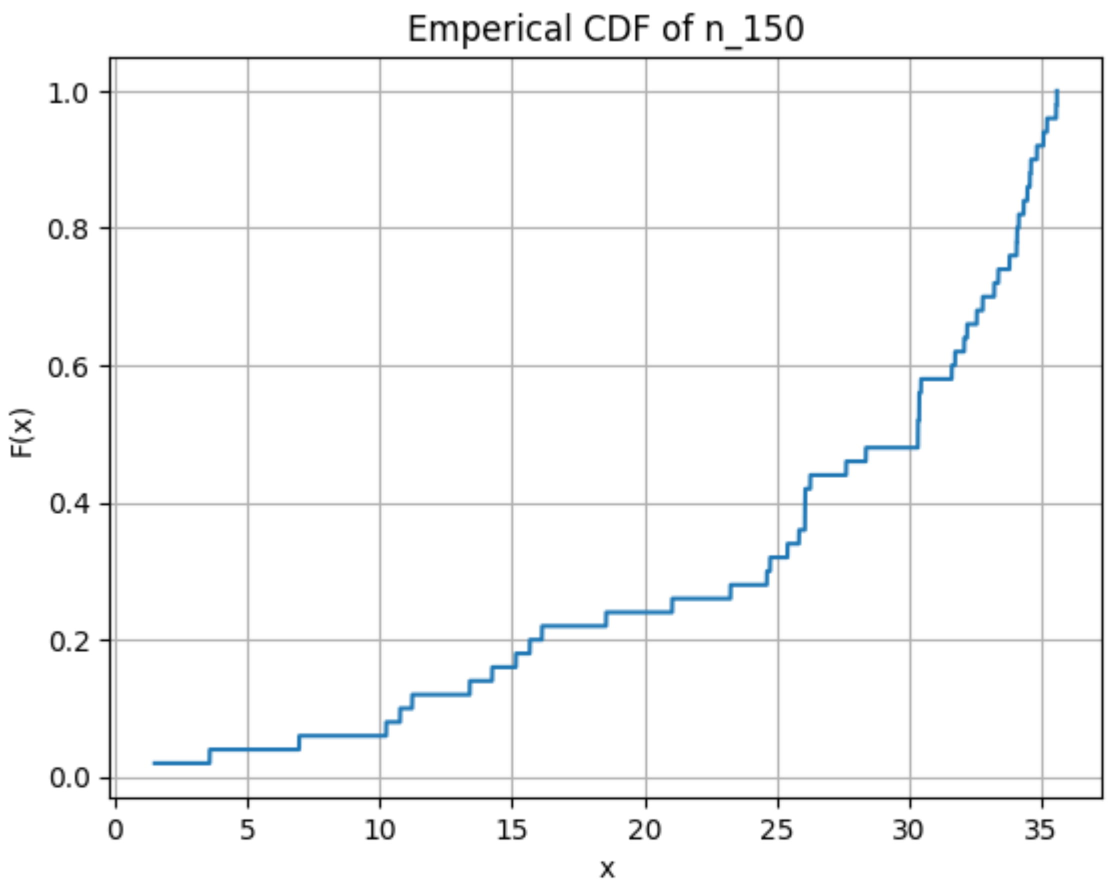
Plot the emperical cumulative probability distributions (CDFs) of the random variables (features).

In [ ]:
```
import matplotlib.pyplot as plt
from scipy.stats import cumfreq
import numpy as np

for f in feature_names:
    print(df[f].describe())

    cum_freq = cumfreq(df[f], numbins=100000)

    cum_prob = cum_freq.cumcount / len(df[f])

    # Plot the CDF
    plt.plot(cum_freq.lowerlimit + np.linspace(0, cum_freq.binsize*cum_fr
    plt.xlabel('x')
    plt.ylabel('F(x)')
    plt.title(f'Emperical CDF of {f}')
    plt.grid(True)
    plt.show()
```

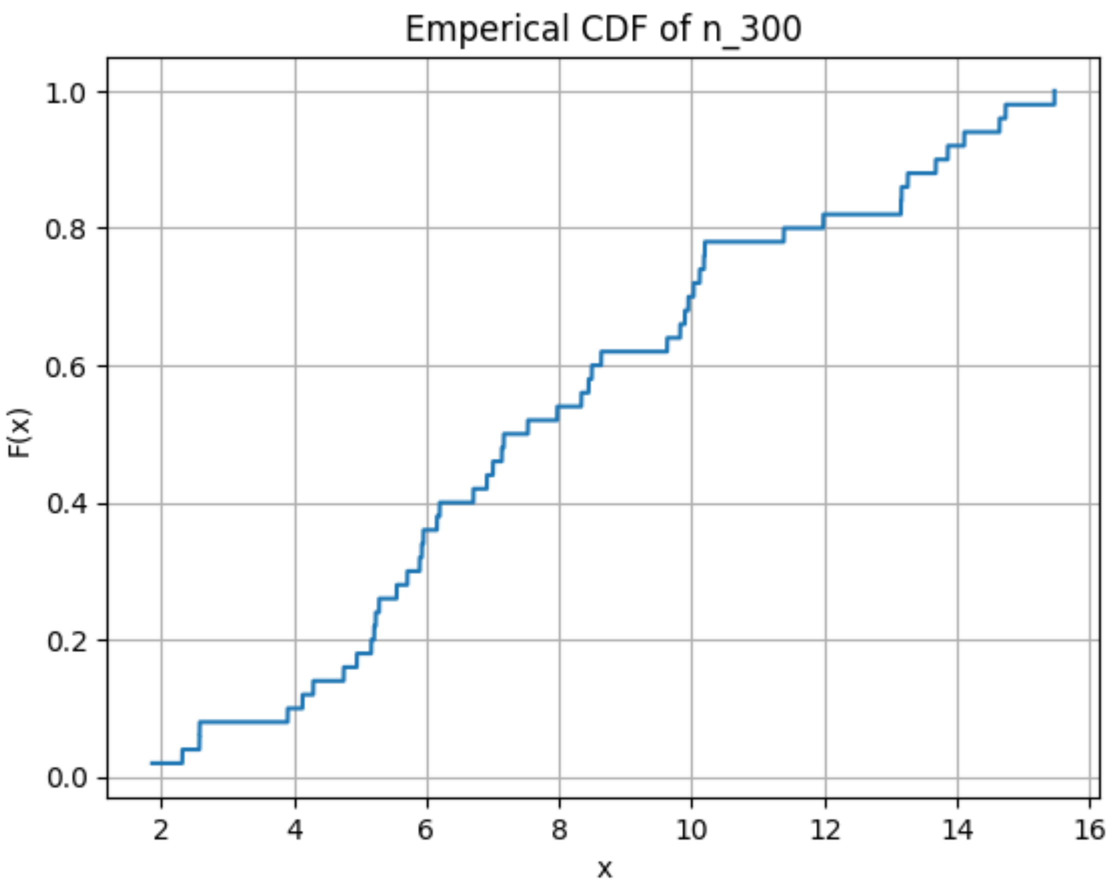
```
count    50.000000
mean      5.510800
std       3.396421
min       1.129245
25%       3.309000
50%       4.422730
75%       6.106346
max      18.092522
Name: n_50, dtype: float64
```



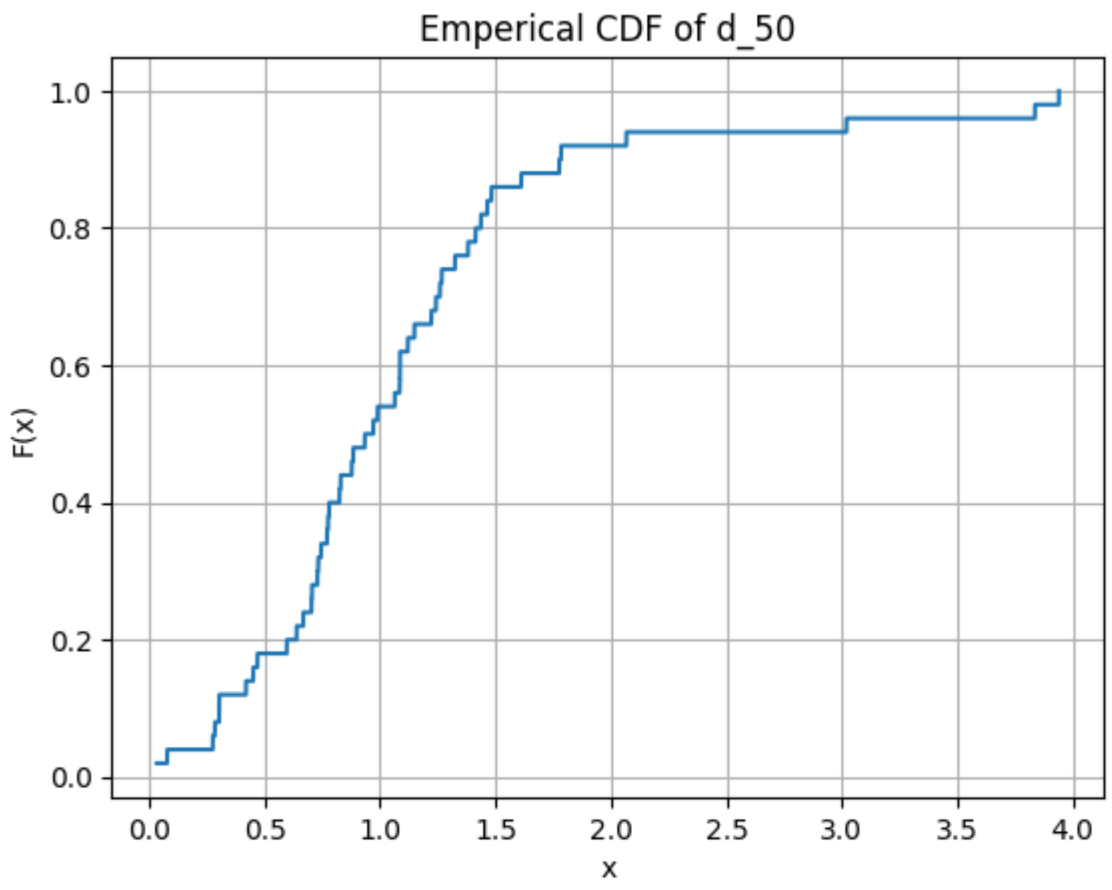
```
count    50.000000
mean     26.084033
std       9.348820
min       1.507993
25%      21.595062
50%      30.329100
75%      33.676859
max      35.575905
Name: n_150, dtype: float64
```



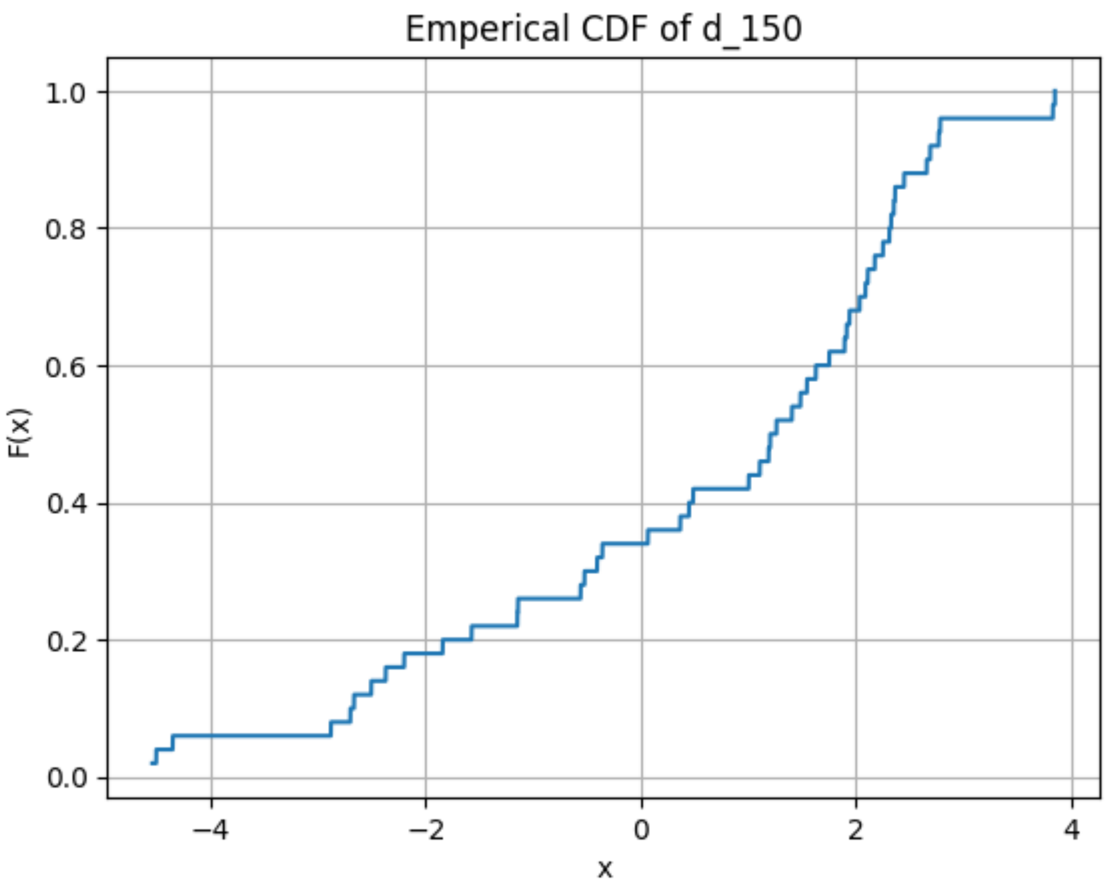
```
count    50.000000
mean      8.145338
std       3.640636
min       1.868088
25%       5.353104
50%       7.347345
75%      10.167518
max      15.466792
Name: n_300, dtype: float64
```



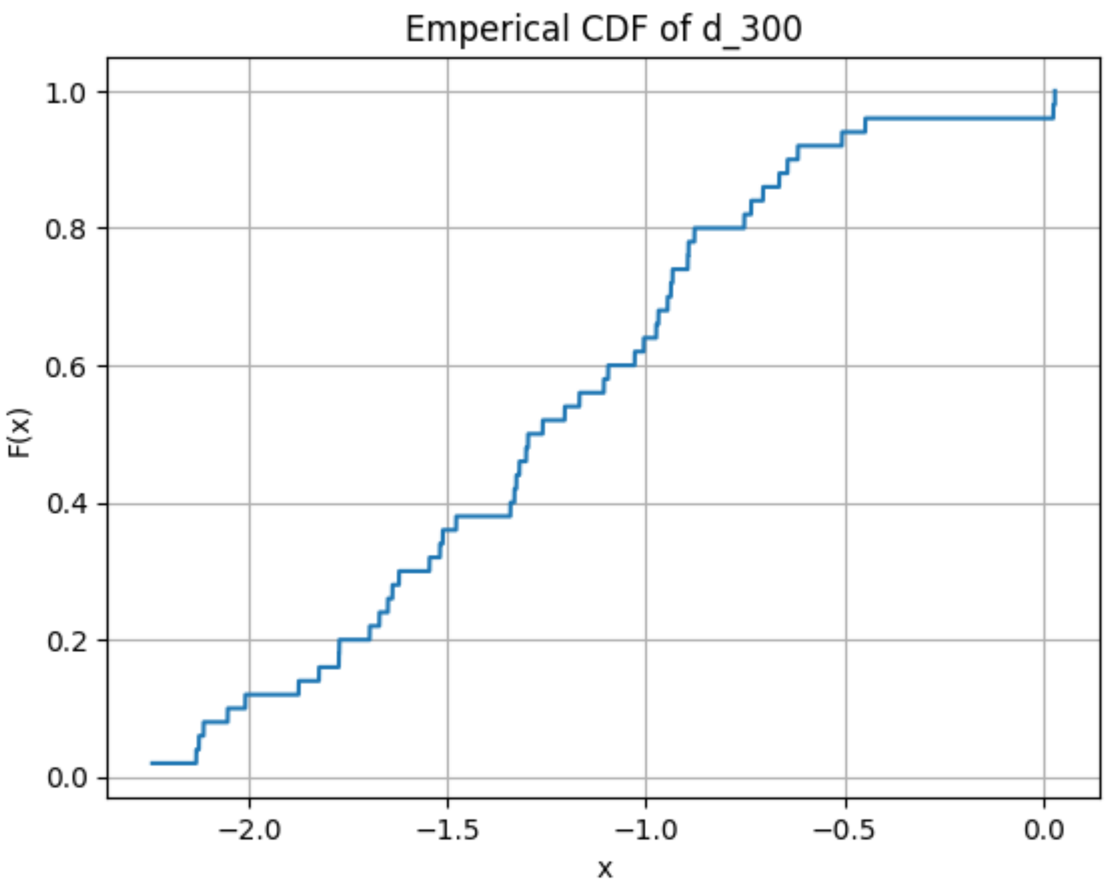
```
count    50.000000
mean      1.097608
std       0.784262
min       0.032972
25%       0.703376
50%       0.952191
75%       1.310096
max       3.940195
Name: d_50, dtype: float64
```



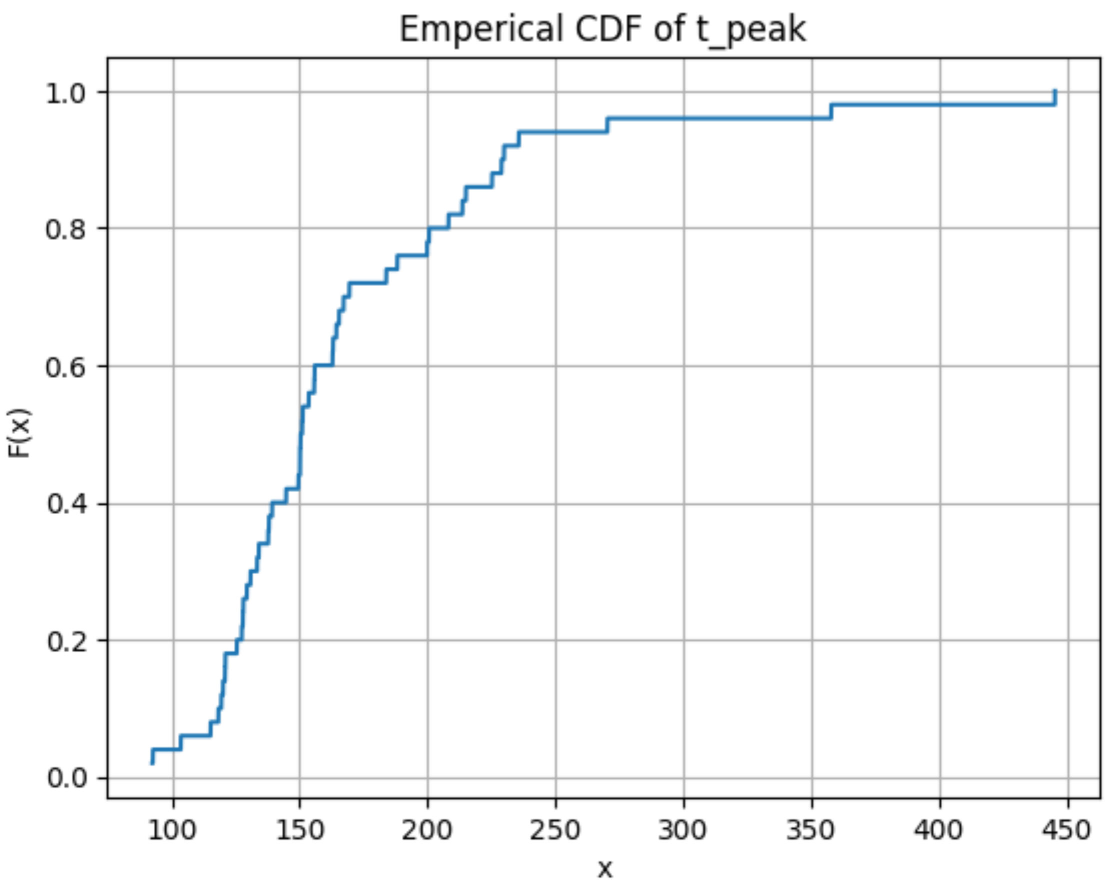
```
count    50.000000
mean      0.507043
std       2.193691
min      -4.539801
25%      -0.997498
50%       1.229447
75%       2.155732
max       3.846155
Name: d_150, dtype: float64
```



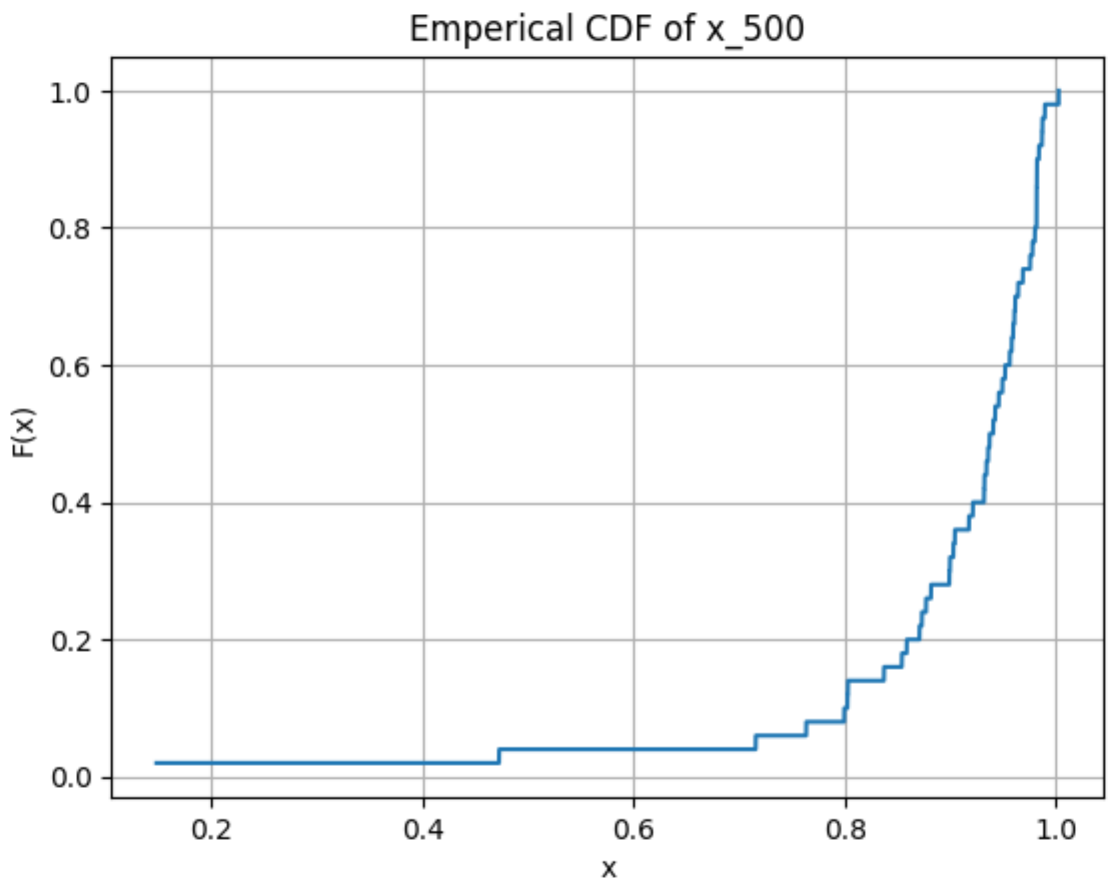
```
count    50.000000
mean     -1.249822
std       0.540493
min      -2.244317
25%      -1.647766
50%      -1.278831
75%      -0.904246
max       0.030962
Name: d_300, dtype: float64
```



```
count     50.000000
mean     167.165455
std       63.076660
min       92.341618
25%      128.262318
50%      150.599951
75%      187.041275
max      445.305297
Name: t_peak, dtype: float64
```



```
count    50.000000
mean      0.898774
std       0.141293
min       0.147541
25%       0.878408
50%       0.939200
75%       0.974210
max       1.003071
Name: x_500, dtype: float64
```



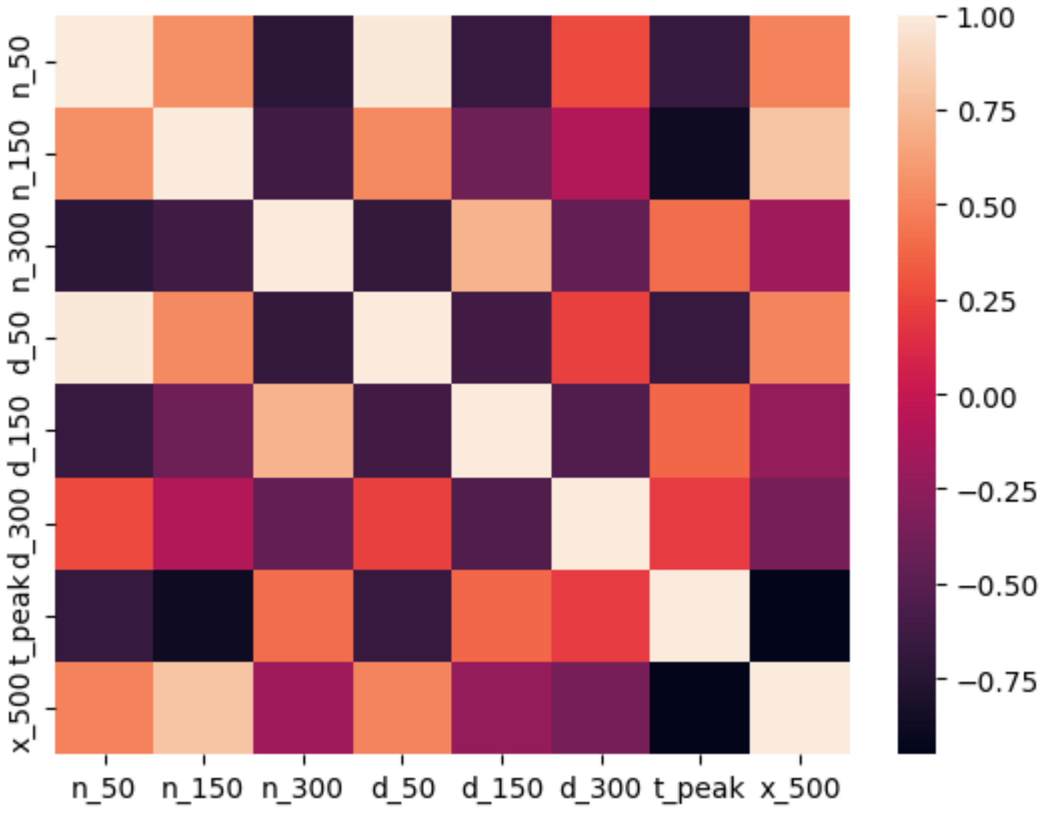
Recall, the sample mean value is an approximation of the expected value, or expectation of the random variable. The sample variance is the square of the sample standard deviation std.

Check the correlation between the features.

In [ ]:
```
import seaborn as sns
correlation = df.corr()
print(correlation)
sns.heatmap(correlation)
```

```
              n_50     n_150     n_300      d_50     d_150     d_300    t_pe
ak  \
n_50    1.000000  0.545743 -0.717694  0.984432 -0.663601  0.268068 -0.6727
63
n_150   0.545743  1.000000 -0.621597  0.523178 -0.405602 -0.094725 -0.8782
36
n_300  -0.717694 -0.621597  1.000000 -0.678025  0.710809 -0.449841  0.4028
68
d_50    0.984432  0.523178 -0.678025  1.000000 -0.609660  0.220863 -0.6646
39
d_150  -0.663601 -0.405602  0.710809 -0.609660  1.000000 -0.540961  0.3823
89
d_300   0.268068 -0.094725 -0.449841  0.220863 -0.540961  1.000000  0.2075
98
t_peak -0.672763 -0.878236  0.402868 -0.664639  0.382389  0.207598  1.0000
00
x_500   0.496107  0.797443 -0.176128  0.497659 -0.219834 -0.360582 -0.9501
76

             x_500
n_50    0.496107
n_150   0.797443
n_300  -0.176128
d_50    0.497659
d_150  -0.219834
d_300  -0.360582
t_peak -0.950176
x_500   1.000000
```

```
Out[ ]: <AxesSubplot:>
```



Recall, the (sample) correlation of two (samples of) random variables X and Y their (sample) covariance normalized (divided) by the product of their (sample) standard deviation.

Discuss your findings. Your answer goes here.

Answer: There is only one pair of variables that is very strong positive correlated, i.e. n_50 and d_50. Other very strong correlations are negative, i.e. t_peak and x_500; n_50 and d_150; and t_peak and n_150, respectively. In general, there are many correlated values (mostly negative correlated), which was to be expected, since the data was retrieved from a timeline of infection rates. So I would have assumed, that the numbers get smaller in the end the higher they were in the beginning, which is described by a negative correlation.

1.4 Try to fit parametric probability distributions

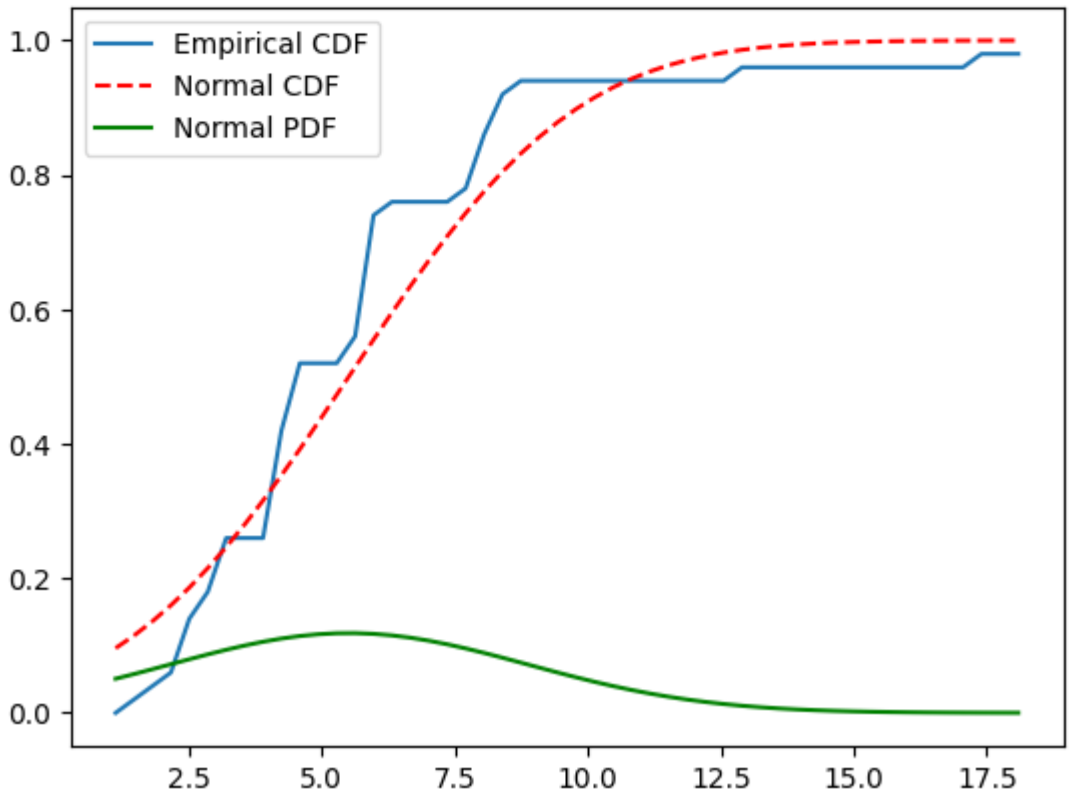
We go through a set of common probability distributions and try to fit any of them to the data. We use the Chi-square and the Kolmogorov-Smirnov tests to check the goodness of fit. *Note that fitting and testing using the same data is actually not quite correct. We should use cross-validation.*

Student: ... I neglected it, too.

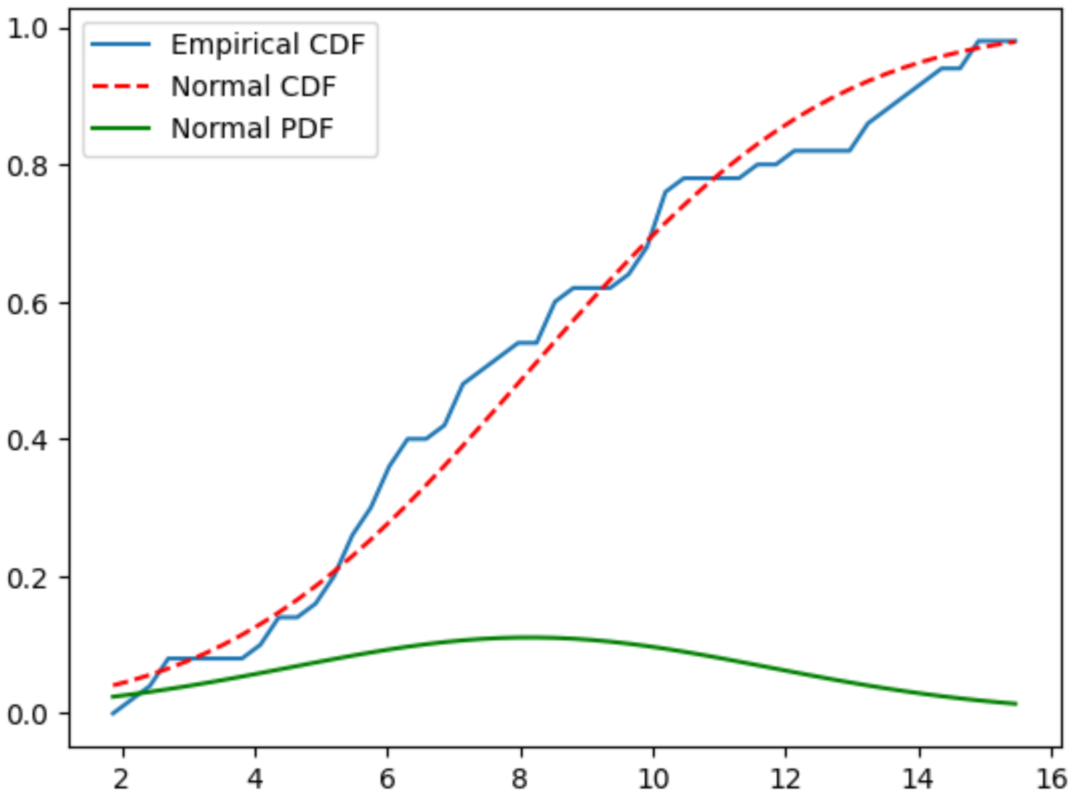
In [ ]:
```
from scipy.stats import norm, poisson, expon, gamma, genextreme, gaussian
from scipy.integrate import quad

def fit(data, func):
    if func == poisson:
        return [np.mean(data)] # using the mean of the data as parameter
    if func == gaussian_kde:
        return gaussian_kde(data)
    return func.fit(data)

def gaussian_cdf(x, kde):
    cdf_values = np.zeros_like(x)  # Initialize array for CDF values
    for i, xi in enumerate(x):
        cdf_values[i], _ = quad(kde.pdf, -np.inf, xi)  # Integrate KDE's
    return cdf_values

def cdf(data, pd, params):
    if pd == gaussian_kde:
        return gaussian_cdf(data, params)
    return pd.cdf(data, *params)

def pdf(data, pd, params):
    if pd == gaussian_kde:
        return params.pdf(data)
    return pd.pdf(data, *params)

class PDF():

    def __init__(self, func, params) -> None:
        self.func = func
        self.params = params

    def calc(self, x):
        return pdf(x, self.func, self.params)
```

```
distributions = {'Normal': norm,
                 'Poisson': poisson,
                 'Exponetial': expon,
                 'Gamma': gamma,
                 'ExtremeValue': genextreme,
                 'Kernel': gaussian_kde}

feature_pdfs = {"n_50":None,
                "n_150":None,
                "n_300":None,
                "d_50":None,
                "d_150":None,
                "d_300":None,
                "t_peak":None,
                "x_500":None,}

values_must_be_positive =["Poisson", "Exponential", "Gamma"]

for f in feature_names:
    print('')
    print(f'Check for feature: {f}')
    # Get x
    x_values = np.linspace(df[f].min(), df[f].max())

    # Get empirical CDF
    cum_prob = [len(df[df[f] < x])/len(df[f]) for x in x_values]

    for dist, func in distributions.items():
        if df[f].min() < 0 and dist in values_must_be_positive:
            continue

        params = fit(df[f], func)
        res = kstest(df[f], lambda x: cdf(x, func, params))

        # check KS-Test
        if res.pvalue < 0.05:
            print(f'Not {dist} with 5% significance level')
        else:
            expected = cdf(df[f], func, params) # need to do the followin
            total_expected = sum(expected)
            total_observed = sum(df[f])
            expected = [freq * total_observed / total_expected for freq i
            _, p_value = chisquare(df[f], f_exp=expected)

            # check Chi² Test
            if p_value < 0.05:
                print(f'Not {dist} with 5% significance level')
            else:
                print(f'{dist} with 5% significance level')
                print(f'Params: {params}')

                # Plot CDF
                plt.plot(x_values, cum_prob, label='Empirical CDF')

                # # Plot fitted CDF
                plt.plot(x_values, cdf(x_values, func, params), c='r', la

                # # Plot PDF
                plt.plot(x_values, pdf(x_values, func, params), c='g', la
                plt.legend()
                plt.show()

                feature_pdfs[f] = PDF(func, params)
                break
```

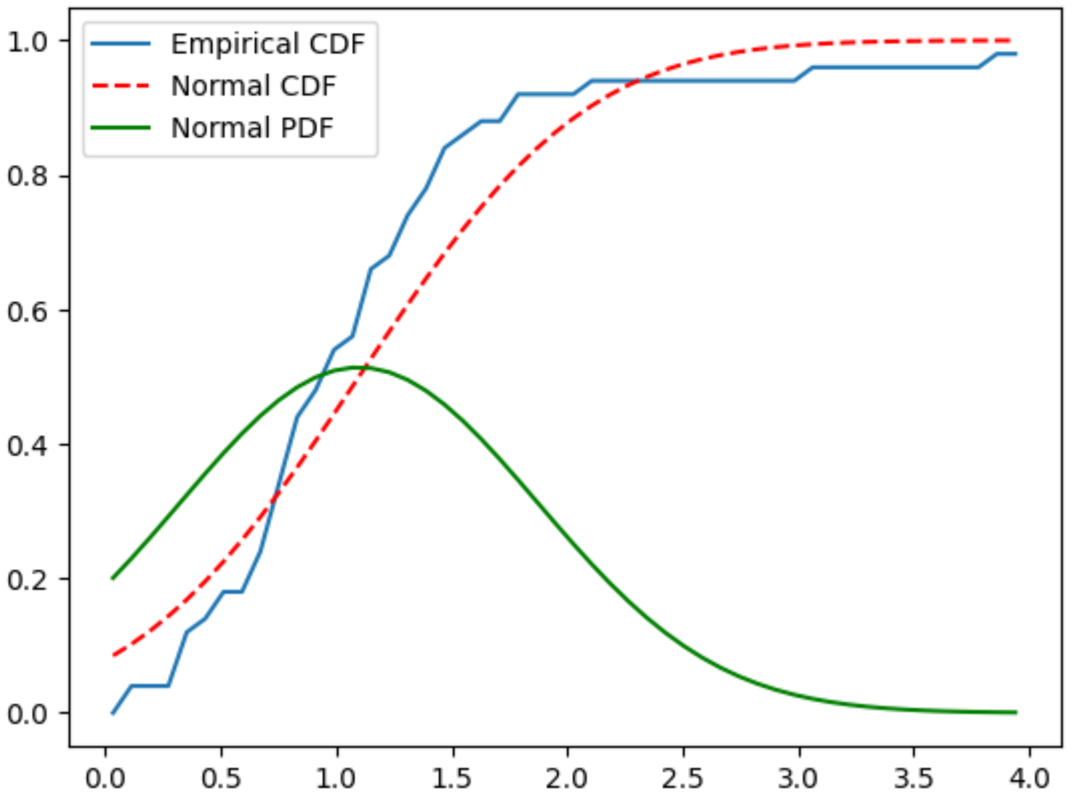
```
Check for feature: n_50
Normal with 5% significance level
Params: (5.510799932725158, 3.362285673435535)
```



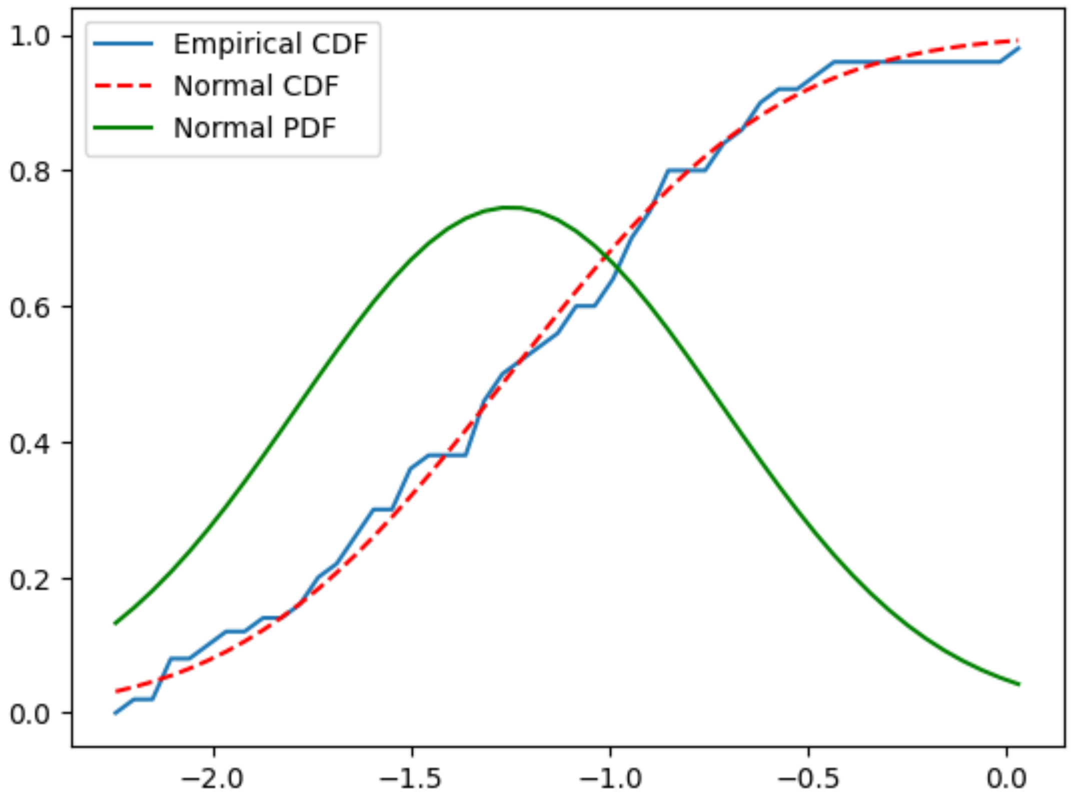
```
Check for feature: n_150
Not Normal with 5% significance level
Not Poisson with 5% significance level
Not Exponetial with 5% significance level
Not Gamma with 5% significance level
Not ExtremeValue with 5% significance level
Not Kernel with 5% significance level

Check for feature: n_300
Normal with 5% significance level
Params: (8.145337883057707, 3.6040461200663736)
```



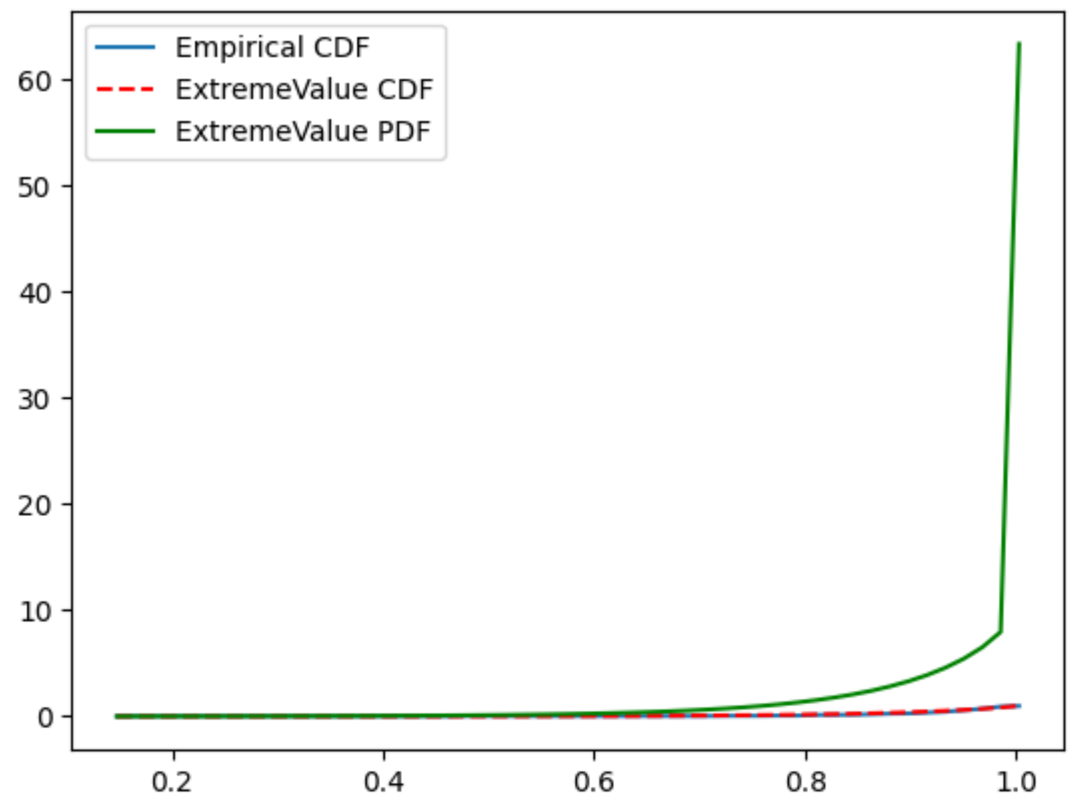
```
Check for feature: d_50
Normal with 5% significance level
Params: (1.0976084202155842, 0.7763794279146738)
```



```
Check for feature: d_150
Not Normal with 5% significance level
Not Exponetial with 5% significance level
Not ExtremeValue with 5% significance level
Not Kernel with 5% significance level

Check for feature: d_300
Normal with 5% significance level
Params: (-1.249822268966371, 0.5350603552002773)
```



```
Check for feature: t_peak
Not Normal with 5% significance level
Not Poisson with 5% significance level
Not Exponetial with 5% significance level
Not Gamma with 5% significance level
Not ExtremeValue with 5% significance level
Not Kernel with 5% significance level

Check for feature: x_500
Not Normal with 5% significance level
Not Poisson with 5% significance level
Not Exponetial with 5% significance level
Not Gamma with 5% significance level
ExtremeValue with 5% significance level
Params: (1.058815728423074, 0.8926803963611483, 0.11688284833632757)
```


Empirical CDF
ExtremeValue CDF
ExtremeValue PDF
60
50
40
30
20
10
0
0.2
0.4
0.6
0.8
1.0

Describe the fitted distributions. Your answer goes here.

Answer: For n_50 we could fitted a normal distribution with significance. However, the emperical CDF is still very wiggly compared to the fitted. Looking at the fitted PDF, the mean is aroud 5.5 and the standard deviation is about 3.36. Our data comes with much higher numbers, i.e. aroun 13 or even around 17. Thus the emperical CDF increased faster than the fitted normal distribution curve and platoed earlier in the end.

For n_300 we could fitted a normal distribution with significance around a mean of 8.15 and a standard deviation of about 3.6. Since there are no outliers like in n_50, the empirical CDF increases quite likely as the fitted CDF does.

For d_50 we could fitted a normal distribution with significance. However, the emperical CDF is still very wiggly compared to the fitted, like it was for n_50. Here, the sample data is more densed compared to n_50. Anyway, the emperical CDF increased faster than the fitted normal distribution curve and platoed earlier in the end. Looking at the fitted PDF, the mean is aroud 1.1 and the standard deviation is about 0.78.

For d_300 we could fitted a normal distribution with significance around a mean of -1.25 and a standard deviation of about 0.53. Since there are no outliers like in n_50, the empirical CDF increases quite likely as the fitted CDF does, like it did for n_300. However, here, the emperical CDF is very close to the fitted one.

For x_500 we could fitted a extreme value distribution with significance 53. According to the coverage of the fitted and the emperival CDF, the fit was quite good. There parameters of the resulting distribution are: ...

For n_150, d_150 and t_peak we could not fitted a distribution of the choosen ones with significance.

1.5 Joint and conditional probabilities, chain rule and Bayes' Theorem

Lets calculate the probability of having a mild start and a disastrous end of the epidemia. We translate that to the joint probability that no more than 4% are infected after 50 days, i.e., N50 ≤ 4% and more than 0.95% die in the end, i.e., X500 > 0.95%.

```
In [ ]: pos = len(df[(df['n_50'] <= 4) & (df['x_500'] > 0.95)])
        print(f'positive cases: {pos}')

        all = len(df)
        P = pos/all
        print(f'P: {P}')
```

```
positive cases: 1
P: 0.02
```

Student: So $P(N_{50} \leq 4\%, X_{500} > 0.95\%)$ *≈ 0.02 in my case, since I worked with only 50 countries instead of 125.*

We check the product of the two probabilities $P(N_{50} \leq 4\%)P(X_{500} > 0.95\%)$:

```
In [ ]: p_n50 = len(df[df['n_50'] <= 4])/len(df)
        p_x500 = len(df[df['x_500'] > 0.95])/len(df)

        P2 = p_n50 * p_x500
        print(f'P2: {P2}')
```

```
P2: 0.1428
```

We are not surprised that the result is different from the joint probability as the random variables N50 and X500 not independent (double-check the results from the correlation analysis).

Student: This holds in my case too

What is the conditional probability of more than 0.95% die in the end given that we know that no more 4% are infected after 50 days.

```
In [ ]: P_AB = pos/len(df[df['n_50'] <= 4])

        print(f'P_AB: {P_AB}')
```

```
P_AB: 0.058823529411764705
```

Student: So $P(X_{500} > 0.95\% | N_{50} \leq 4\%) \approx 0.0588.$

The product or chain rule of probability states that

$P(A, B) = P(A|B)P(B)(5)$

$P(X_{500} > 0.95\%, N_{50} \leq 4\%) = P(X_{500} > 0.95\% | N_{50} \leq 4\%)P(N_{50} \leq 4\%)(6)$

And we don't get disappointed:

```
In [ ]: P = P_AB * p_n50
        print(f'P: {P}')
```

```
P: 0.02
```

Let us numerically confirm Bayes' Theorem for this case. We'd expect that.

$$P(A|B) = \frac{P(B|A)P(A)}{P(B)}$$

$$P(X_{500} > 0.95\% | N_{50} \leq 4\%) = \frac{P(N_{50} \leq 4\% | X_{500} > 0.95\%)P(X_{500} > 0.95\%)}{P(N_{50} \leq 4\%)}$$

And we don't get disappointed:

In [ ]:
```
P_BA = pos/len(df[df['x_500'] > 0.95])
P_AB = P_BA * p_x500 / p_n50

print(f'P_AB: {P_AB}')
```

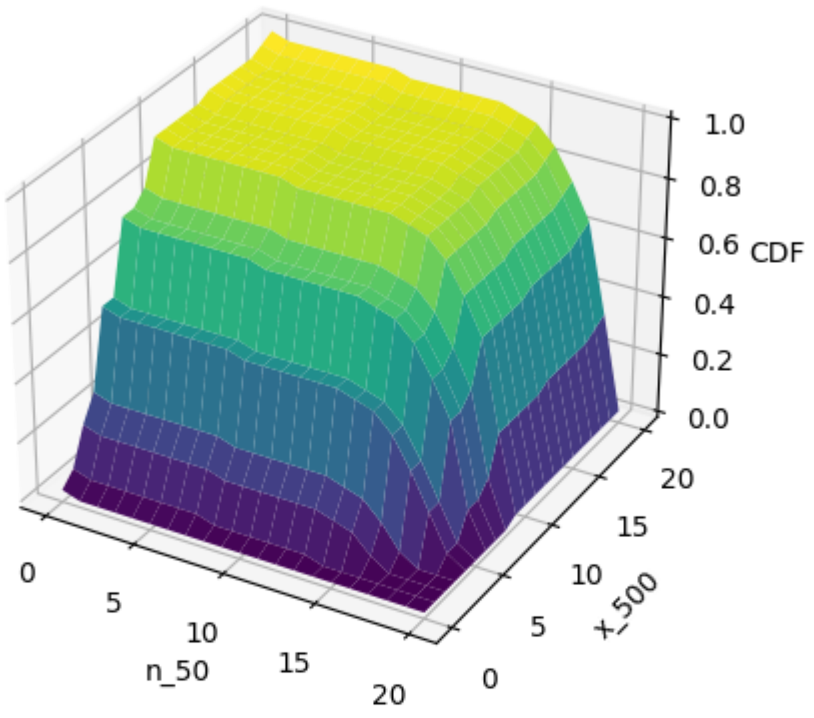
```
P_AB: 0.058823529411764 69
```

So far, we have looked at the joint (sample) probability of $P(N_{50} \leq n, X_{500} > x)$ for concrete bounds n = 4 and x = 0.95. Let us now understand the joint (sample) probability of $F(n, x) = P(N_{50} \leq n, X_{500} > x)$ as a function of these bounds n and x. Since, $0 \leq X_{500} \leq 100$ (*Student: In my case* $0 \leq X_{500} \leq 1$) this function is equal to joint (sample) cumulative distribution function:

$$F(n, x) = CDF_{N_{50}, 100-X_{500}}(n, 100 - x) \quad (3)$$
$$CDF_{N_{50}, 100-X_{500}}(n, y) = P(N_{50} \leq n, 100 - X_{500} \leq y) \quad (4)$$

In [ ]:
```
# define cdf and F function

def cdf_sample(df,n,y):
    pos_cases = len(df[(df['n_50'] <= n) & (df['x_500'].apply(lambda x: 1
    return pos_cases/len(df)

def F(df, n, x):
    cdf = cdf_sample(df,n,1-x)
    return cdf
```

In [ ]:
```
import numpy as np
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D


_, n_50_bin_edges = np.histogram(df['n_50'], bins=20)
_, x_500_bin_edges = np.histogram(df['x_500'], bins=20)


# Generate meshgrid for plotting
x_sequence = range(len(n_50_bin_edges))
y_sequence = range(len(x_500_bin_edges))

X, Y = np.meshgrid(x_sequence, y_sequence)

# Initialize an empty matrix to store computed values
Z = np.zeros((len(x_sequence), len(y_sequence)))

# Compute values for each pair of elements using a nested loop
for x in x_sequence:
    for y in y_sequence:
        Z[x, y] = F(df, n_50_bin_edges[x], x_500_bin_edges[y])

# Plot the surface
fig = plt.figure()
ax = fig.add_subplot(111, projection='3d')
ax.plot_surface(X, Y, Z, cmap='viridis')

# Set labels and title
ax.set_xlabel('n_50')
ax.set_ylabel('x_500')
ax.set_zlabel('CDF')

plt.show()
```



Interprete this CDF. Your answer goes here.

Answer: The plot shows the CDF of the joint probability of n_50 and x_500. It indecates, that the joint probability is likely to reach a platoe of 80-90%, whenever one of the probabilities (n_50 or x_500) comes with critical values. For n_50, these values are to be found in the first three quarters of the interval on that n_50 is given. For x_500, these values are reached since it is greater than the half of the interval on that x_500 is given (which is 0.5, since x_500 gives a percentage). So we can conclude, that as long x_500 is greater thatn 0.5 and n_50 is not in his last quarter, the joint probability is quite high. However, it will decrease very fast, if some of the features exceeds these critical values/boundaries.

That means, that it is very likely, that more than 50% of the people will not die in the end, as long as there was no overhaul in the beginning (i.e. very high infection rate). At a specific point, the more people get infected at the beginning, the more uncertain is it how many will not die.

Here, x_500 is in fact 1-x_500, i.e. th percentage of people not died from infection.

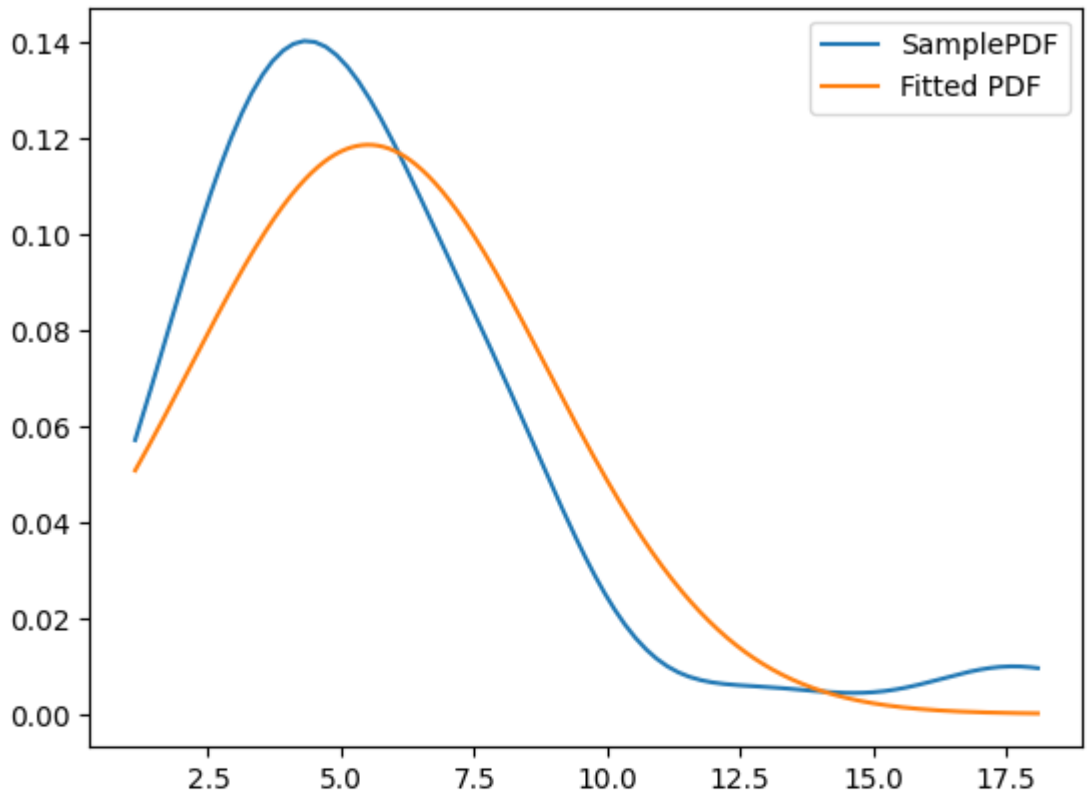
Finally, we compare a function interpolating a sample distribution with the fitted parameterized PDF of that distribution computed earlier, cf. distribution_fitting. We look at N50 and X500 as two examples.

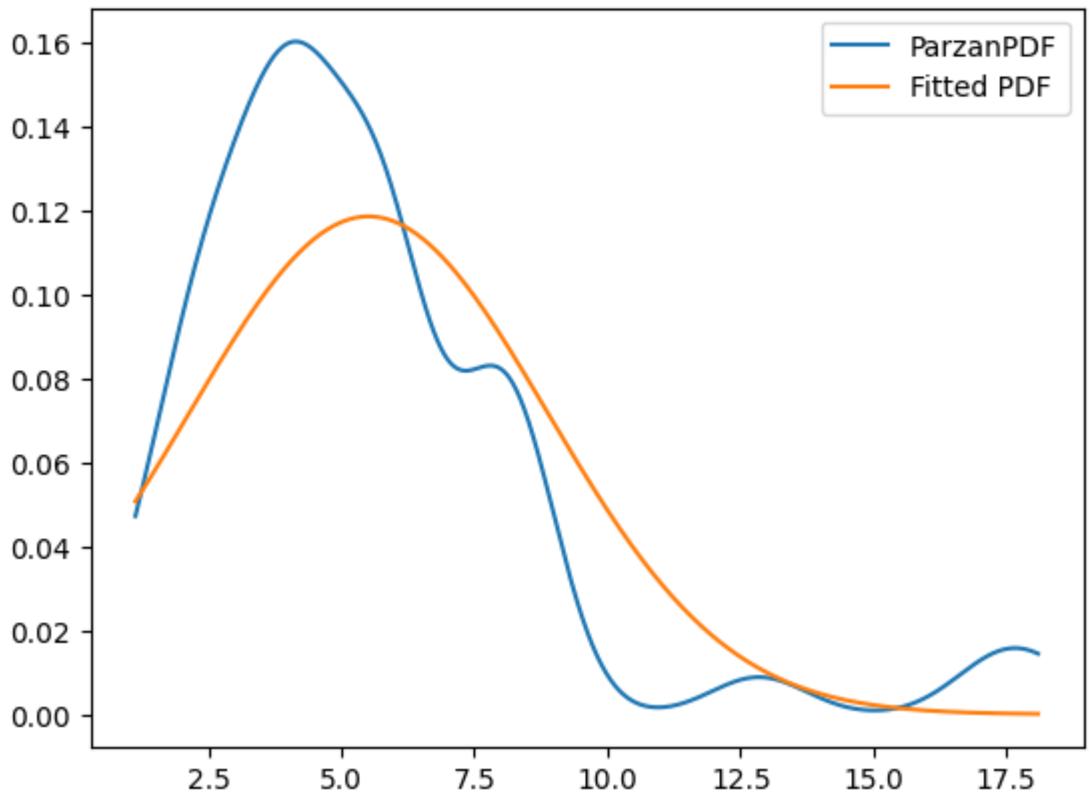
Therefore, we generate auxiliary functions plotPDF for plotting both functions, and two alternatives samplePDF and parzanPDF for interpolating the sample distribution. The former is simple to use and often good enough. The latter allows for fine tuning and is described in detail in the public notebook “Approximate PDFs with Parzen window density estimation”.

```
In [ ]: from scipy.interpolate import interp1d

        def samplePDF(sample, pd_fit):
            kde = gaussian_kde(sample)
            xi = np.linspace(-100, 100, 1000)
            f = kde.evaluate(xi)
            pdf = interp1d(xi, f, bounds_error=False, fill_value="extrapolate")

            x = np.linspace(min(sample), max(sample), 1000)

            plt.plot(x, pdf(x), label='SamplePDF')
            plt.plot(x, pd_fit.calc(x), label='Fitted PDF')
            plt.legend()
            plt.show()
            return pdf
```

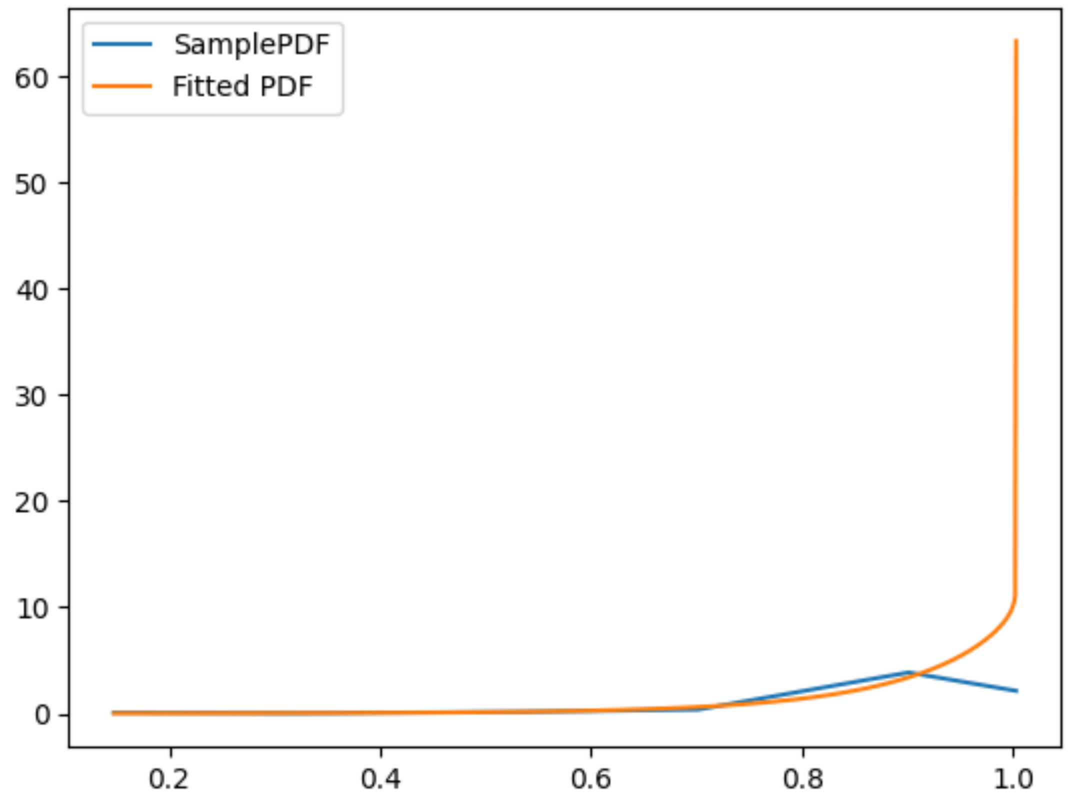
```
In [ ]: def parzanPDF(sample, a, b, h, pd_fit):
            x = np.linspace(a, b, 1000)
            mu = 0
            sigma = 1
            len_x = len(x)
            len_s = len(sample)
            f = np.zeros((len_x))
            for j in range(len_x):
                xi=x[j]
                for i in range(len_s):
                    f[j] = f[j] + norm.pdf((xi-sample[i])/h, mu, sigma)
                f[j] = f[j] / (len_s*h)

            pdf = interp1d(x, f, bounds_error=False, fill_value="extrapolate")

            x = np.linspace(min(sample), max(sample), 1000)

            plt.plot(x, pdf(x), label='ParzanPDF')
            plt.plot(x, pd_fit.calc(x), label='Fitted PDF')
            plt.legend()
            plt.show()
            return pdf
```

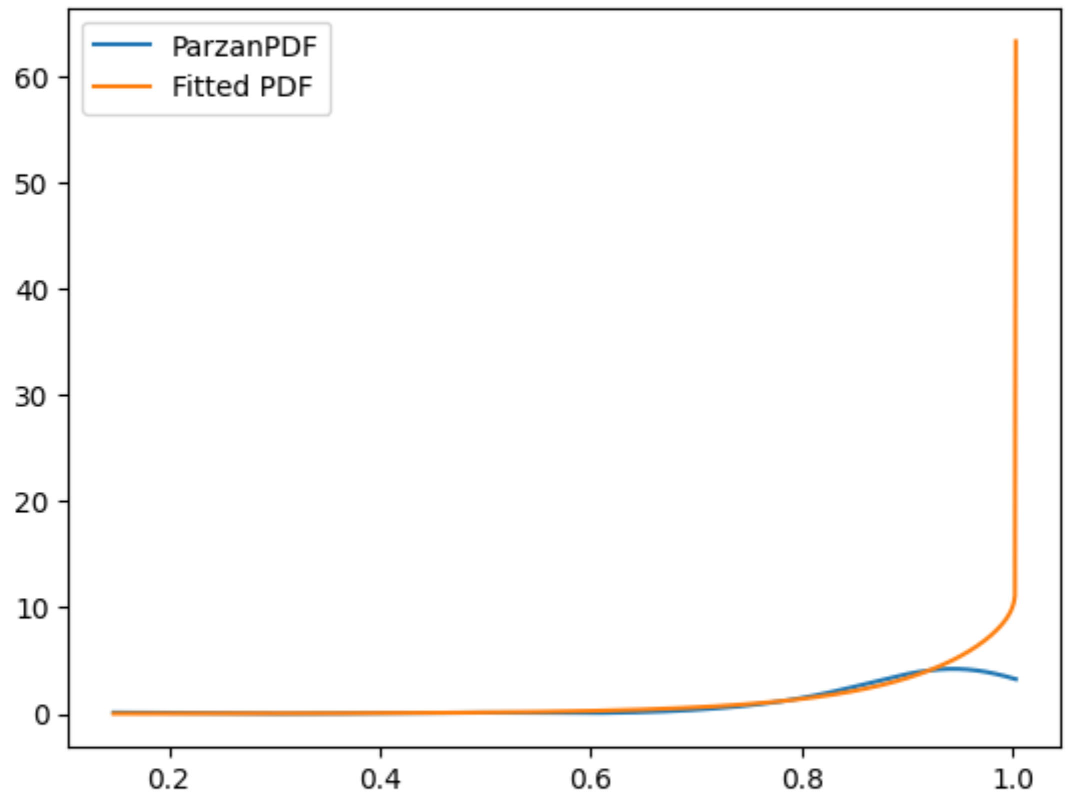
```
In [ ]: pd_n_50 = feature_pdfs['n_50']
        samplePDF_n_50 = samplePDF(df['n_50'], pd_n_50)
        PDF_n_50 = parzanPDF(df['n_50'], 0, 25, 0.9, pd_n_50)
```





```
In [ ]: pd_x_500 = feature_pdfs['x_500']
        PDF_x_500 = samplePDF(df['x_500'], pd_x_500)
        parzanPDF_n_50 = parzanPDF(df['x_500'], 0, 2, 0.07, pd_x_500)
```





1.6 Self-entropy of an event and entropy of a distribution

We define a function that calculates the entropy of a sample distribution, based on a interploated parameterless PDF approximation (calculated with samplePDF and parzanPDF, resp.) and the well-known parameterized distribition (calculated with distribution_fitting). We also compute the Kullback-Leibler (KL) divergence in both directions.

For demonstration purpose, we implement numeric integration manually as auxiliary function. It comes in two variants: trapezoid and simpson's 3/8 rule.

```
In [ ]: def trapez(f, a, b):
            N = int((b - a) * 100)
            x = np.linspace(a, b, N)
            dx = x[1] - x[0]
            y = np.zeros(N)
            for i in range(N):
                z = f(x[i])
                y[i] = z
            w = np.concatenate(([0.5], np.ones(N-2), [0.5]))
            I = np.sum(w * y) * dx
            return I
```

```
In [ ]: def simpson(f, a, b):
            N = 3 * (b - a) * 100 + 1
            x = np.linspace(a, b, N)
            dx = x[1] - x[0]
            I = 0
            for i in range(0, N - 3, 3):
                z0 = f(x[i])
                z1 = f(x[i + 1])
                z2 = f(x[i + 2])
                z3 = f(x[i + 3])
                I += z0 + 3 * z1 + 3 * z2 + z3
            I *= (3 * dx / 8)
            return I
```

```
In [ ]: def ite(b,t,f):
            if b:
                return t
            return f
```

```
In [ ]: import math

        a = -25
        b = 25
        f1  = lambda x : ite(PDF_n_50(x) <= 0, lambda x: 0, lambda x: PDF_n_50(x)
        entropy1 = lambda x : -1 * ite(PDF_n_50(x) <= 0, lambda x: 0, lambda x: P

        Integral1 = trapez(f1, a, b)
        Entropy1 = trapez(entropy1, a, b)

        print(f'Integral1 = {Integral1}')
        print(f'Entropy1 = {Entropy1}')
```

```
Integral1 = 0.9983712591471883
Entropy1 = 2.394884678336957
```

```
In [ ]: f2  = lambda x : ite(pd_n_50.calc(x) <= 0, lambda x:0, lambda x:pd_n_50.c
        entropy2 = lambda x : -1 * ite(pd_n_50.calc(x) <= 0, lambda x:0, lambda x

        Integral2 = trapez(f2, a, b)
        Entropy2 = trapez(entropy2, a, b)

        print(f'Integral2 = {Integral2}')
        print(f'Entropy2 = {Entropy2}')
```

```
Integral2 = 0.999999996612345
Entropy2 = 2.6315594684319747
```

In [ ]:
```
divergence_1_2 = lambda x : ite(PDF_n_50(x) <= 0, lambda x:0, lambda x:PD

Divergence_1_2_trapez = trapez(divergence_1_2, a, b)
Divergence_1_2_simposon = simpson(divergence_1_2, a, b)

print(f'Divergence_1_2_trapez = {Divergence_1_2_trapez}')
print(f'Divergence_1_2_simpson = {Divergence_1_2_simposon}')
```

```
Divergence_1_2_trapez = 0.2662580390084464
Divergence_1_2_simpson = 0.26625860780421157
```

In [ ]:
```
eps = 1e-32
divergence_2_1 = lambda x : ite(PDF_n_50(x) <= 0,
                                lambda x:pd_n_50.calc(x)*(math.log(pd_n_5
                                lambda x:pd_n_50.calc(x) * ( math.log(pd_

Divergence_2_1_trapez = trapez(divergence_2_1, a, b)
Divergence_2_1_simposon = simpson(divergence_2_1, a, b)

print(f'Divergence_2_1_trapez = {Divergence_2_1_trapez}')
print(f'Divergence_2_1_simpson = {Divergence_2_1_simposon}')
```

```
Divergence_2_1_trapez = 2.7032260335449165
Divergence_2_1_simpson = 2.705301474682776
```

Why is the entropy of N50 assuming is proportional to the interpolated PDF different from the one assuming it is proportional to the fitted PDF? Why are the KL divergences different? Your answers go here.

Answer: The fitted PDF comes with the assumption that there is a normal distribution, whereas the interpolated PDF was interpolated by finding any function that matches the datapoints best. So they have the potential to be different to each other. Hence the entropy is different.

Now that the entropy is different, we can say, that they are indeed different. The KL-divergence are assumed to be different, since the KL-divergence is an asymmertic function by definition.