Q1. Assume there are 120 students in our B565 class, and each person has a 2% of chance of carrying coronavirus. We also know that the Omicron variant dominates and let's assume that it accounts for 90% of the new Covid cases. What's the probability that the entire class is free of coronavirus and Omicron, respectively? Show your work. [10 pts]

i. The probability that the entire class is free of coronavirus:
If each student has a 2% chance of carrying coronavirus, then each student has a 98% chance of not carrying coronavirus.
1-0.02=0.98 is the probability that a student doesn't have the coronavirus.
Hence, if a class of 120 students doesn't have coronavirus, the probability of that happening is **0.98^120=0.08853787272** which is 8.8% approximately. (We multiply the probability of each student not having coronavirus).

ii. The probability that the entire class is free of Omicron:
If each student has a 2% chance of carrying coronavirus, then each student has a 0.02*0.9=0.018 probability of carrying Omicron variant. The probability of a student not having Omicron is 1-0.018=0.982.
Hence, if a class of 120 students doesn't have coronavirus, the probability of that happening is **0.982^120=0.0.11307810828** which is 11.3% approximately. (We multiply the probability of each student not having Omicron).

Q2. Let Ω be the space of possible outcomes of a fair die (with six sides) thrown twice. What is Ω? Let A be the event that a 4 is observed on either individual throw or the sum of both throws is at least 5. Let B be the event that the difference between the two throws is exactly two. Are A and B independent? What is the probability of B given A? What is the probability of A given B? Show your work. [15 pts]

i. Ω={(1, 1),(1, 2),(1, 3),(1, 4),(1, 5),(1, 6),(2, 1),(2, 2),(2, 3),(2, 4),(2, 5),(2, 6),(3, 1),(3, 2),(3, 3),(3, 4),(3, 5),(3, 6),(4, 1),(4, 2),(4, 3),(4, 4),(4, 5),(4, 6),(5, 1),(5, 2),(5, 3),(5, 4),(5, 5),(5, 6),(6, 1),(6, 2),(6, 3),(6, 4),(6, 5),(6, 6)}. Size of Ω is 36.
n(Ω)=36

ii. A=Event when a 4 is observed on either individual throw or the sum of both throws is at least 5
A={(1, 4),(1, 5),(1, 6),(2, 3),(2, 4),(2, 5),(2, 6),(3, 2),(3, 3),(3, 4),(3, 5),(3, 6),(4, 1),(4, 2), (4, 3),(4, 4),(4, 5),(4, 6),(5, 1),(5, 2),(5, 3),(5, 4),(5, 5),(5, 6),(6, 1),(6, 2),(6, 3),(6, 4),(6, 5),(6, 6)}
n(A)=36.

B=The event that the difference between the two throws is exactly two.
B={(1,3),(2,4),(3,5),(4,6),(3,1),(4,2),(5,3),(6,4)}.
n(B)=8

Set A∩B={(2,4),(3,5),(4,6),(4,2),(5,3),(6,4)}. n(A∩B)=6.
A and B are not independent as A∩B is not empty. .

$P(A)=n(A)/n(\Omega)=30/36=5/6$

$P(B)=n(B)/n(\Omega)=30/36=8/36=2/9$

$P(A\cap B)= n(A\cap B)/n(\Omega)=6/36=1/6$

iii. **$P(B|A)=(P(A|B)P(B))/P(A)=P(A\cap B)/P(A)=(1/6)/(5/6)=1/5$**

iv. **$P(A|B)=(P(B|A)P(A))/P(B)=P(A\cap B)/P(B)=(1/6)/(2/9)=3/4$**

Q3. Recall that given two vectors x and y of n dimensions, their cosine similarity, Euclidean distance, and correlation can be computed as follows. [15 pts]
Cosine similarity, cos(x, y) = (x · y)/||x||.||y||
Euclidean distance, d(x, y) = (∑ n i=1(xi − yi)^2)^1/2
Correlation, corr(x, y) = Sxy/(SxSy)
=(∑ n i=1 (xi − x¯)(yi − y¯))/ (∑ n i=1 (xi − x¯)^2)^1/2 .(∑ n i=1 (yi − y¯) ^2)^1/2

Sets can also be represented as vectors of zeros and ones, so for those vectors, Jaccard similarity (intersection over union) can be used. For the following vectors x and y, calculate the indicated similarity or distance measures. Show the steps.
• x = (1, 1, 1, 1), y = (2, 2, 2, 2) cosine, correlation and Euclidean.
• x = (0, 1, 0, 1), y = (1, 0, 1, 0), cosine, correlation, Euclidean, Jaccard
• x = (0, −1, 0, 1), y = (1, 0, −1, 0), cosine, correlation, Euclidean
• x = (1, 1, 0, 1, 0, 1), y = (1, 1, 1, 0, 0, 1) cosine, correlation, Jaccard
• x = (2, −1, 0, 2, 0, −3), y = (−1, 1, −1, 0, 0, −1) cosine, correlation

i. x = (1, 1, 1, 1), y = (2, 2, 2, 2)

a. Cosine Similarity:
   x.y=1.2+1.2+1.2+1.2=8
   ||x||=(1^2+1^2+1^2+1^2)^(1/2)=2
   ||y||=(2^2+2^2+2^2+2^2)^(1/2)=4
   cos(x, y) = (x · y)/||x||.||y||=8/(2*4)=1

b. Correlation:
   x¯=(∑ n i=1(xi))/n=(1+1+1+1)/4=1
   y¯=(∑ n i=1(yi))/n=(2+2+2+2)/4=2
   (∑ n i=1 (xi − x¯)(yi − y¯))=(1-1)*(2-2)+(1-1)*(2-2)+(1-1)*(2-2)+(1-1)*(2-2)=0
   (∑ n i=1 (xi − x¯)^2)=(1-1)^2+(1-1)^2+(1-1)^2+(1-1)^2=0
   (∑ n i=1 (xi − x¯)^2)^1/2=0
   (∑ n i=1 (yi − y¯)^2)=(2-2)^2+(2-2)^2+(2-2)^2+(2-2)^2=0
   (∑ n i=1 (yi − y¯)^2)^1/2=0

Since, both the numerator and the denominator are 0, the correlation for vectors x and y are not defined.

c. Euclidean distance:
$\sum n\ i=1(xi - yi)^2=(1-2)^2+(1-2)^2+(1-2)^2+(1-2)^2=4*(-1)^2=4$
$(\sum n\ i=1(xi - yi)^2)^{1/2} =4^{(1/2)}=2$

ii. x = (0, 1, 0, 1), y = (1, 0, 1, 0)

a. Cosine Similarity:
$x.y=0.1+1.0+0.1+1.0=0$
$||x||=(0^2+1^2+0^2+1^2)^{(1/2)}=2^{(1/2)}$
$||y||=(1^2+0^2+1^2+0^2)^{(1/2)}=2^{(1/2)}$
$\cos(x, y) = (x \cdot y)/||x||.||y||=0$

b. Correlation:
$\bar{x}=(\sum n\ i=1(xi))/n=(0+1+0+1)/4=1/2$
$\bar{y}=(\sum n\ i=1(yi))/n=(1+0+1+0)/4=½$

$(\sum n\ i=1\ (xi - \bar{x})(yi - \bar{y}))$
$=(0-1/2)(1-1/2)+(1-1/2)(0-1/2)+(0-1/2)(1-1/2)+(1-1/2)(0-1/2)=(-1/4)*4=-1$

$(\sum n\ i=1\ (xi - \bar{x})^2)=(0-1/2)^2+(1-1/2)^2+(0-1/2)^2+(1-1/2)^2=4*1/4=1$
$(\sum n\ i=1\ (xi - \bar{x})^2)^{1/2}=1$
$(\sum n\ i=1\ (yi - \bar{y})^2)=(1-1/2)^2+(0-1/2)^2+(1-1/2)^2+(0-1/2)^2=4*1/4=1$
$(\sum n\ i=1\ (yi - \bar{y})^2)^{1/2}=1$
Hence,
$corr(x, y) = Sxy/(SxSy)= -1/1*1=-1$

c. Euclidean distance:
$\sum n\ i=1(xi - yi)^2=(0-1)^2+(1-0)^2+(0-1)^2+(1-0)^2=4$
$(\sum n\ i=1(xi - yi)^2)^{1/2} =4^{(1/2)}=2$

d. Jaccard Coefficient:
$JC= (f11)/(f01+f10+f11)=0/(2+2+0)=0$

iii. x = (0, −1, 0, 1), y = (1, 0, −1, 0)

a. Cosine Similarity:
$x.y=0.1+-1.0+0.-1+1.0=0$
$||x||=(0^2+(-1)^2+0^2+1^2)^{(1/2)}=2^{(1/2)}$
$||y||=(1^2+0^2+(-1)^2+0^2)^{(1/2)}=2^{(1/2)}$
$\cos(x, y) = (x \cdot y)/||x||.||y||=0$

b. Correlation:
x¯=(∑ n i=1(xi))/n=(0+-1+0+1)/4=0
y¯=(∑ n i=1(yi))/n=(1+0+-1+0)/4=0

(∑ n i=1 (xi − x¯)(yi − y¯))
=(0)(1)+(-1)(0)+(0)(-1)+(1)(0)=0
(∑ n i=1 (xi − x¯)^2)=(0)^2+(-1)^2+(0)^2+(1)^2=2
(∑ n i=1 (xi − x¯)^2)^1/2=2^1/2
(∑ n i=1 (yi − y¯)^2)=(1)^2+(0)^2+(-1)^2+(0)^2=2
(∑ n i=1 (yi − y¯)^2)^1/2=2^½

Hence,
corr(x, y) = Sxy/(SxSy)= 0

c. Euclidean distance:
∑ n i=1(xi − yi)^2=(0-1)^2+(-1-0)^2+(0-(-1))^2+(1-0)^2=4
(∑ n i=1(xi − yi)^2)^1/2 =4^(1/2)=2

iv. x = (1, 1, 0, 1, 0, 1), y = (1, 1, 1, 0, 0, 1)

a. Cosine Similarity:
x.y=1.1+1.1+0.1+1.0+0.0+1.1=3
||x||=(1^2+1^2+0^2+1^2+0^2+1^2)^(1/2)=4^(1/2)=2
||y||=(1^2+1^2+1^2+0^2+0^2+1^2)^(1/2)=4^(1/2)=2
cos(x, y) = (x · y)/||x||.||y||=3/(2*2)=0.75

b. Correlation:
x¯=(∑ n i=1(xi))/n=(1+1+0+1+0+1)/6=4/6=2/3
y¯=(∑ n i=1(yi))/n=(1+1+1+0+0+1)/6=4/6=2/3

(∑ n i=1 (xi − x¯)(yi − y¯))
=(1-2/3)(1-2/3)+(1-2/3)(1-2/3)+(0-2/3)(1-2/3)+(1-2/3)(0-2/3)+(0-2/3)(0-2/3)+(1-2/3)(1-2/3)
=1/9+1/9-2/9-2/9+4/9+1/9=3/9=1/3

(∑ n i=1 (xi− x¯)^2)=(1-2/3)^2+(1-2/3)^2+(0-2/3)^2+(1-2/3)^2+(0-2/3)^2+(1-2/3)^2=1/9+1/9+4/9+1/9+4/9+1/9
=4/3
(∑ n i=1 (xi − x¯)^2)^1/2=(4/3)^1/2
(∑ n i=1 (yi − y¯)^2)=(1-2/3)^2+(1-2/3)^2+(1-2/3)^2+(0-1/2)^2+(0-1/2)^2+(1-2/3)^2=1/9+1/9+1/9+4/9+4/9+1/9
=4/3
(∑ n i=1 (yi − y¯)^2)^1/2=(4/3)^1/2
Hence,

corr(x, y) = Sxy/(SxSy)= 1/3/(4/3)^1/2*(4/3)^1/2=0.25

c. Jaccard Coefficient:
JC= (f11)/(f01+f10+f11)=3/(1+1+3)=0.6

v. x = (2, −1, 0, 2, 0, −3), y = (−1, 1, −1, 0, 0, −1)

a. Cosine Similarity:

x.y=2.-1+-1.1+0.-1+2.0+0.0+-3.-1=-2-1+3=0
||x||=(2^2+-1^2+0^2+2^2+0^2+-3^2)^(1/2)=18^(1/2)
||y||=(-1^2+1^2+-1^2+0^2+0^2+-1^2)^(1/2)=4^(1/2)=2
cos(x, y) = (x · y)/||x||.||y||=0/(2*(18)^1/2)=0.0

b. Correlation:

x¯=(∑ n i=1(xi))/n=(2-1+0+2+0-3)/6=0
y¯=(∑ n i=1(yi))/n=(-1+1-1+0+0-1)/6=-2/6

(∑ n i=1 (xi − x¯)(yi − y¯))
=(2)(-1+2/6)+(-1)(1+2/6)+(0)(1+2/6)+(2)(-2/6)+(0)(+2/6)+(-3)(-1+2/6)=0

(∑ n i=1 (xi − x¯)^2)=(2)^2+(-1)^2+(0)^2+(2)^2+0^2+(-3)^2=18
(∑ n i=1 (xi − x¯)^2)^1/2=18^1/2
(∑ n i=1 (yi − y¯)^2)=(-1+2/6)^2+(1+2/6)^2+(1+2/6)^2+(-2/6)^2+(+2/6)^2+(-1+2/6)^2
=10/3
(∑ n i=1 (yi − y¯)^2)^1/2=(10/3)^1/2
Hence,
corr(x, y) = Sxy/(SxSy)= 0/((18^½)*((10/3)^1/2))=0

```python
In [3]: microbiome.describe()
```

Out[3]:

	k__Archaea|p__Euryarchaeota|c__Methanobacteria|o__Methanobacteriales|f__Methanobacteriacea
count	
mean	
std	
min	
25%	
50%	
75%	
max	

8 rows × 572 columns

```python
In [4]: class_column = microbiome['Class'].tolist()
```

```python
In [5]: microbiome = microbiome.drop('Class', 1)
```

```python
In [6]: from sklearn.decomposition import PCA
pca = PCA(n_components=2)
pca.fit(microbiome)
#the results will show that PC1 dominates for the original data
print("variance explained", pca.explained_variance_ratio_, "singular_values", pca.singular_values_)
print(pca.explained_variance_ratio_.sum())
#transform the data according to the PCA results
microbiome_transformed = pca.transform(microbiome)
```

```
variance explained [0.29922075 0.06936047] singular_values [337.41686876
162.45270424]
0.3685812134598305
```

Using PCA, the data matrix is projected to its first two principal components. The projected values of the original data are stored in a pandas DataFrame object named projected. 0.3685812134598305 is the variability captured by 2 dimensions using PCA.

```python
In [8]: projected = pd.DataFrame(microbiome_transformed,columns=['pc1','pc2'],index=range(1,345))
projected['Class'] =class_column

projected
```

Out[8]:

	pc1	pc2	Class
1	-2.943049	-2.248375	n
2	-7.215752	1.835718	n
3	24.051681	-4.850785	n
4	-8.684207	6.431731	n
5	2.565706	-3.969398	n
...	...	...	...
340	-7.294597	1.556875	n
341	-2.864927	18.011306	n
342	-8.629940	-7.938661	n
343	-6.603719	-2.611676	n
344	-8.060710	-9.187330	n

344 rows × 3 columns

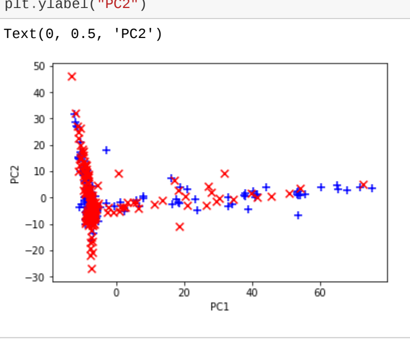
```python
In [9]: import matplotlib.pyplot as plt

colors = {'n':'b', 't2d':'r'}
markerTypes = {'n':'+', 't2d':'x'}

for classType in markerTypes:
    d = projected[projected['Class']==classType]
    plt.scatter(d['pc1'],d['pc2'],c=colors[classType],s=60,marker=markerTypes[classType])

plt.xlabel("PC1")
plt.ylabel("PC2")
```

Out[9]: Text(0, 0.5, 'PC2')



```python
In [10]: # #apply standardscaler to scale the data
from sklearn.preprocessing import StandardScaler
microbiome_scaled = StandardScaler().fit_transform(microbiome)
first_column = np.array(microbiome_scaled[:, 0])
print(first_column[:10], "...")
print("mean %.2f" % first_column.mean())
print("var %.2f" % first_column.var())
```

```
[ 0.35190848  0.60963684 -0.17202823 -0.17202823  0.60445464 -0.17202823
 -0.17202823 -0.17202823 -0.17202823 -0.17202823] ...
mean -0.00
var 1.00
```

```python
In [11]: pca_scaled = PCA(n_components=2)
pca_scaled.fit(microbiome_scaled)
print("variance explained", pca_scaled.explained_variance_ratio_, "singular_values", pca_scaled.singular_values_)
#print(microbiome_scaled)
microbiome_scaled_transformed = pca_scaled.transform(microbiome_scaled)
```

```
variance explained [0.05774328 0.0388078 ] singular_values [106.59282118
87.38497417]
```

```python
In [12]: projected_scaled = pd.DataFrame(microbiome_scaled_transformed,columns=['pc1','pc2'],index=range(1,345))
projected_scaled['Class'] =class_column

projected_scaled
```

Out[12]:

	pc1	pc2	Class
1	-1.141012	-0.439461	n
2	-0.968041	-0.449722	n
3	3.600214	-0.127970	n
4	-0.564952	-0.295627	n
5	-0.814761	-0.414652	n
...	...	...	...
340	1.395982	0.923275	n
341	-0.391177	-0.200669	n
342	-0.622712	-0.350434	n
343	4.654344	0.850055	n
344	2.848240	0.739558	n

344 rows × 3 columns

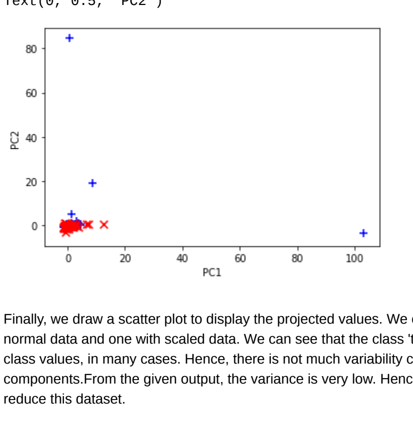
```python
In [13]: import matplotlib.pyplot as plt

colors = {'n':'b', 't2d':'r'}
markerTypes = {'n':'+', 't2d':'x'}

for classType in markerTypes:
    d = projected_scaled[projected_scaled['Class']==classType]
    plt.scatter(d['pc1'],d['pc2'],c=colors[classType],s=60,marker=markerTypes[classType])

plt.xlabel("PC1")
plt.ylabel("PC2")
```

Out[13]: Text(0, 0.5, 'PC2')



```
 't2d',
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```

```python
In [16]: microbiome1 = microbiome1.drop('Class', 1)
```

```python
In [17]: x = microbiome1
y = class_column1
```

Then, we'll define the model by using the TSNE class, here the n_components parameter defines the number of target dimensions.

```python
In [18]: tsne = TSNE(n_components=2, verbose=1, random_state=123)
z = tsne.fit_transform(x)
```

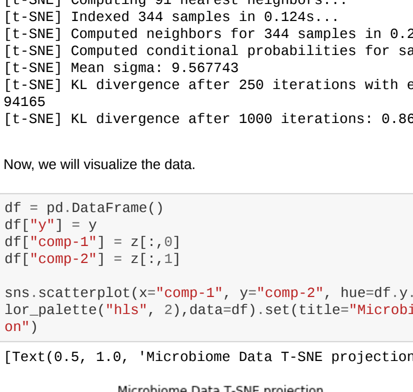
```
[t-SNE] Computing 91 nearest neighbors...
[t-SNE] Indexed 344 samples in 0.124s...
[t-SNE] Computed neighbors for 344 samples in 0.291s...
[t-SNE] Computed conditional probabilities for sample 344 / 344
[t-SNE] Mean sigma: 9.567743
[t-SNE] KL divergence after 250 iterations with early exaggeration: 67.894165
[t-SNE] KL divergence after 1000 iterations: 0.865274
```

Now, we will visualize the data.

```python
In [19]: df = pd.DataFrame()
df["y"] = y
df["comp-1"] = z[:,0]
df["comp-2"] = z[:,1]

sns.scatterplot(x="comp-1", y="comp-2", hue=df.y.tolist(),palette=sns.color_palette("hls", 2),data=df).set(title="Microbiome Data T-SNE projection")
```

Out[19]: [Text(0.5, 1.0, 'Microbiome Data T-SNE projection')]



t-SNE offers slightly better separation of the classes and there is not much overlap between the data points. It offers good dimensionality reduction too.

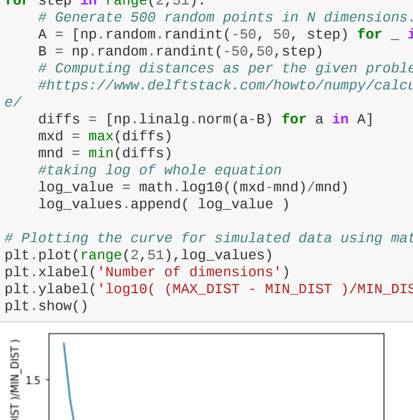
Q5. The plot below was used to demonstrate the Curse of Dimensionality. Implement a code to simulate your own data, and generate your special plot of curse of dimensionality. Try dimensions from 2 to 50 with a step size of 1. And for each dimension, randomly generate 500 data points. Use Euclidean distance. [30 pts]

We are assuming A is the set of points given and B is the reference point, if you compute the distance from B to each of the points in B, the difference between the maximum distance and the minimum distance goes to 0.

```python
In [23]: import numpy as np
import matplotlib.pyplot as plt
import math

log_values = []
for step in range(2,51):
    # Generate 500 random points in N dimensions.
    A = [np.random.randint(-50, 50, step) for _ in range(500)]
    B = np.random.randint(-50,50,step)
    # Computing distances as per the given problem
    #https://www.delftstack.com/howto/numpy/calculate-euclidean-distance/
    diffs = [np.linalg.norm(a-B) for a in A]
    mxd = max(diffs)
    mnd = min(diffs)
    #taking log of whole equation
    log_value = math.log10((mxd-mnd)/mnd)
    log_values.append( log_value )

# Plotting the curve for simulated data using matplotlib
plt.plot(range(2,51),log_values)
plt.xlabel('Number of dimensions')
plt.ylabel('log10( (MAX_DIST - MIN_DIST )/MIN_DIST )')
plt.show()
```

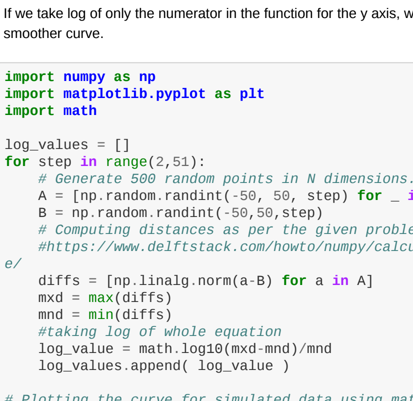


If we take log of only the numerator in the function for the y axis, we get a better and much smoother curve.

```python
In [24]: import numpy as np
import matplotlib.pyplot as plt
import math

log_values = []
for step in range(2,51):
    # Generate 500 random points in N dimensions.
    A = [np.random.randint(-50, 50, step) for _ in range(500)]
    B = np.random.randint(-50,50,step)
    # Computing distances as per the given problem
    #https://www.delftstack.com/howto/numpy/calculate-euclidean-distance/
    diffs = [np.linalg.norm(a-B) for a in A]
    mxd = max(diffs)
    mnd = min(diffs)
    #taking log of whole equation
    log_value = math.log10(mxd-mnd)/mnd
    log_values.append( log_value )

# Plotting the curve for simulated data using matplotlib
plt.plot(range(2,51),log_values)
plt.xlabel('Number of dimensions')
plt.ylabel('log10( (MAX_DIST - MIN_DIST )/MIN_DIST )')
plt.show()
```



References:

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[3]. https://www.kaggle.com/morecoding/scalingpca-demo/

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