COVID-19 RADIOGRAPHY BASED CLASSIFICATION USING MULTIPROTOTYPE FUZZY LOGIC

Batch 1 Grp 2 EDI :

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About the Dataset:

COVID-19 CHEST X-RAY DATABASE:

A team of researchers from Qatar University, Doha, Qatar, and the University of Dhaka, Bangladesh along with their collaborators from Pakistan and Malaysia in collaboration with medical doctors have created a database of chest X-ray images for COVID-19 positive cases along with Normal and Viral Pneumonia images. This COVID-19, normal and other lung infection dataset is released in stages. In the first release we have released 219 COVID-19, 1341 normal and 1345 viral pneumonia chest X-ray (CXR) images. In the first update, we have increased the COVID-19 class to 1200 CXR images. In the 2nd update, we have increased the database to 3616 COVID-19 positive cases along with 10,192 Normal, 6012 Lung Opacity (Non-COVID lung infection) and 1345 Viral Pneumonia images and corresponding lung masks. We will continue to update this database as soon as we have new x-ray images for COVID-19 pneumonia patients.

Formats

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- All the images are in Portable Network Graphics (PNG) file format and resolution are 299*299 pixels.
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Objective

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-  Researchers can use this database to produce useful and impactful scholarly work on COVID-19, which can help ir
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COVID-19 data:

> COVID data are collected from different publicly accessible dataset, online sources and published papers.
>
> - 2473 CXR images are collected from padchest dataset[1].
> - 183 CXR images from a Germany medical school[2].
> - 559 CXR image from SIRM, Github, Kaggle & Tweeter[3,4,5,6]
> - 400 CXR images from another Github source[7].

Normal images:

> 10192 Normal data are collected from from three different dataset.

> - 8851 RSNA [8]
> - 1341 Kaggle [9]

Lung opacity images:

> 6012 Lung opacity CXR images are collected from Radiological Society of North America (RSNA) CXR dataset [8]

Viral Pneumonia images:bo

> 1345 Viral Pneumonia data are collected from the Chest X-Ray Images (pneumonia) database [9]

Dataset Link:

COVID-19 Chest X-Ray Database

Dataset Reference:

[1]https://bimcv.cipf.es/bimcv-projects/bimcv-covid19/#1590858128006-9e640421-6711

[2]https://github.com/ml-workgroup/covid-19-image-repository/tree/master/png

[3]https://sirm.org/category/senza-categoria/covid-19/

[4]https://eurorad.org

[5]https://github.com/ieee8023/covid-chestxray-dataset

[6]https://figshare.com/articles/COVID-19_Chest_X-Ray_Image_Repository/12580328

[7]https://github.com/armiro/COVID-CXNet

[8]https://www.kaggle.com/c/rsna-pneumonia-detection-challenge/data

[9] https://www.kaggle.com/paultimothymooney/chest-xray-pneumonia

About the Project:

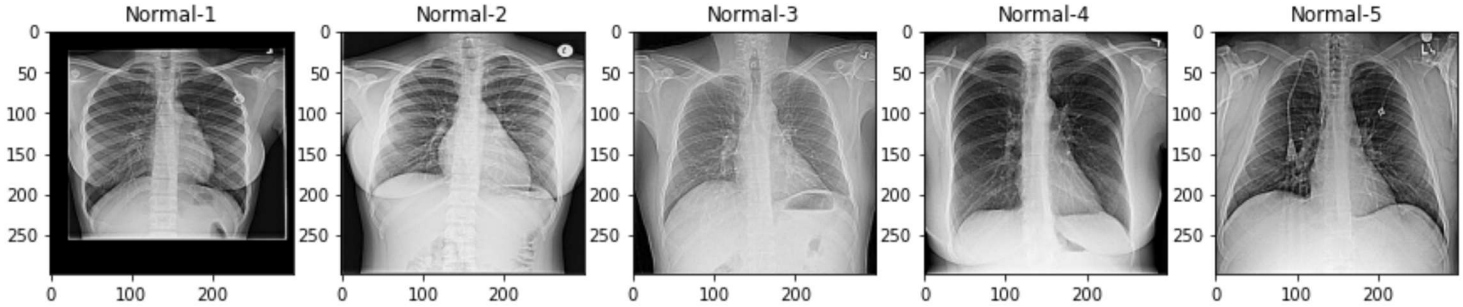
Problem Statement:

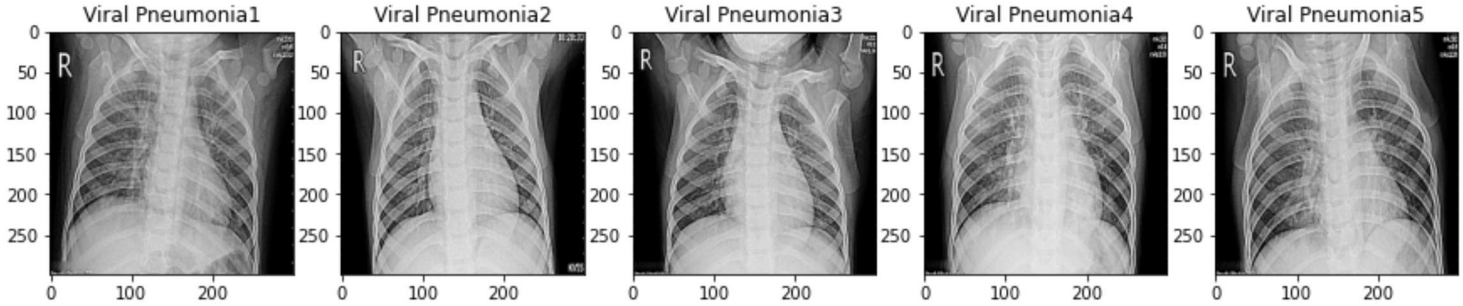
> To classify the chest X-ray images of COVID-19 patients into COVID-19 , Viral Pneumonia and Normal classes using the Multi-Prototype Fuzzy Logic algorithm.

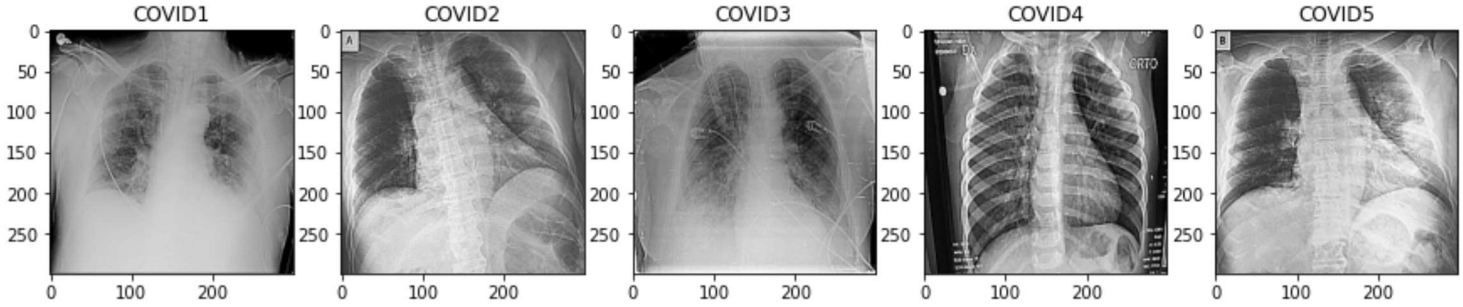
Dataset Statistics:

Number of images in each class:

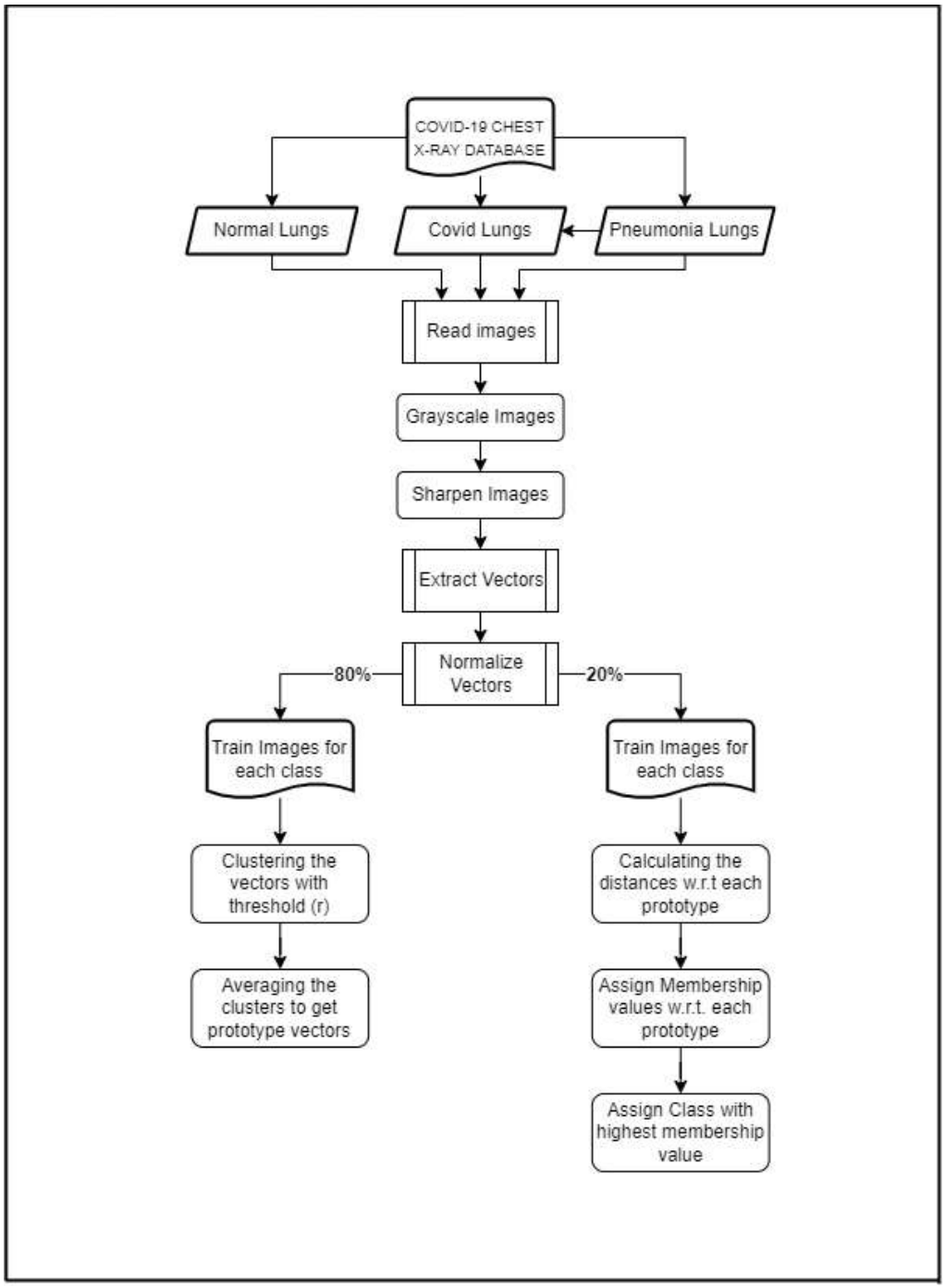
Class	Total Images	Train Images	Test Images
Normal	10192	8153	2039
COVID-19	3616	2892	724
Viral Pneumonia	1345	1076	269


Normal-1
Normal-2
Normal-3
Normal-4
Normal-5


Viral Pneumonia1
Viral Pneumonia2
Viral Pneumonia3
Viral Pneumonia4
Viral Pneumonia5

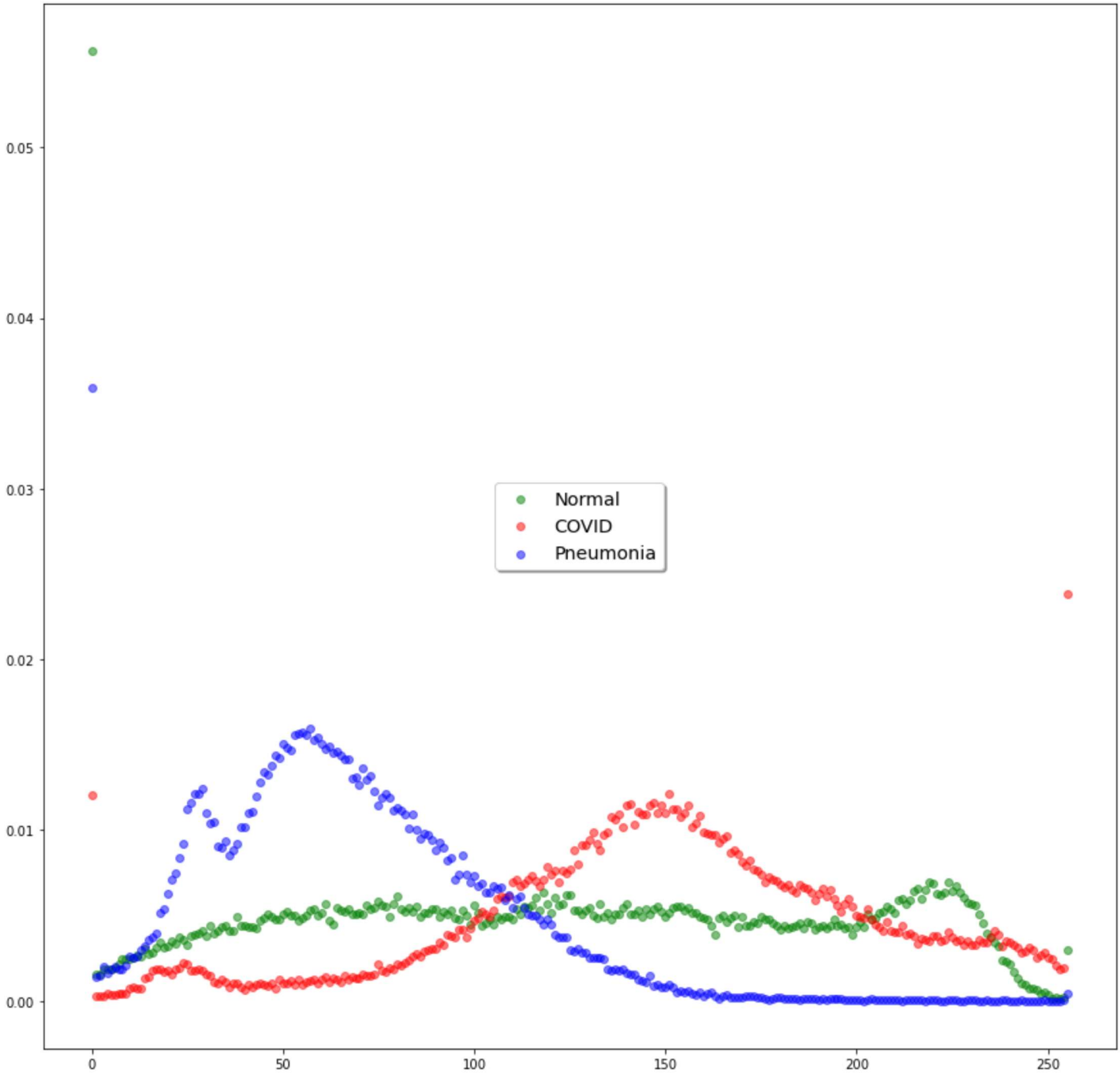

COVID1
COVID2
COVID3
COVID4
COVID5

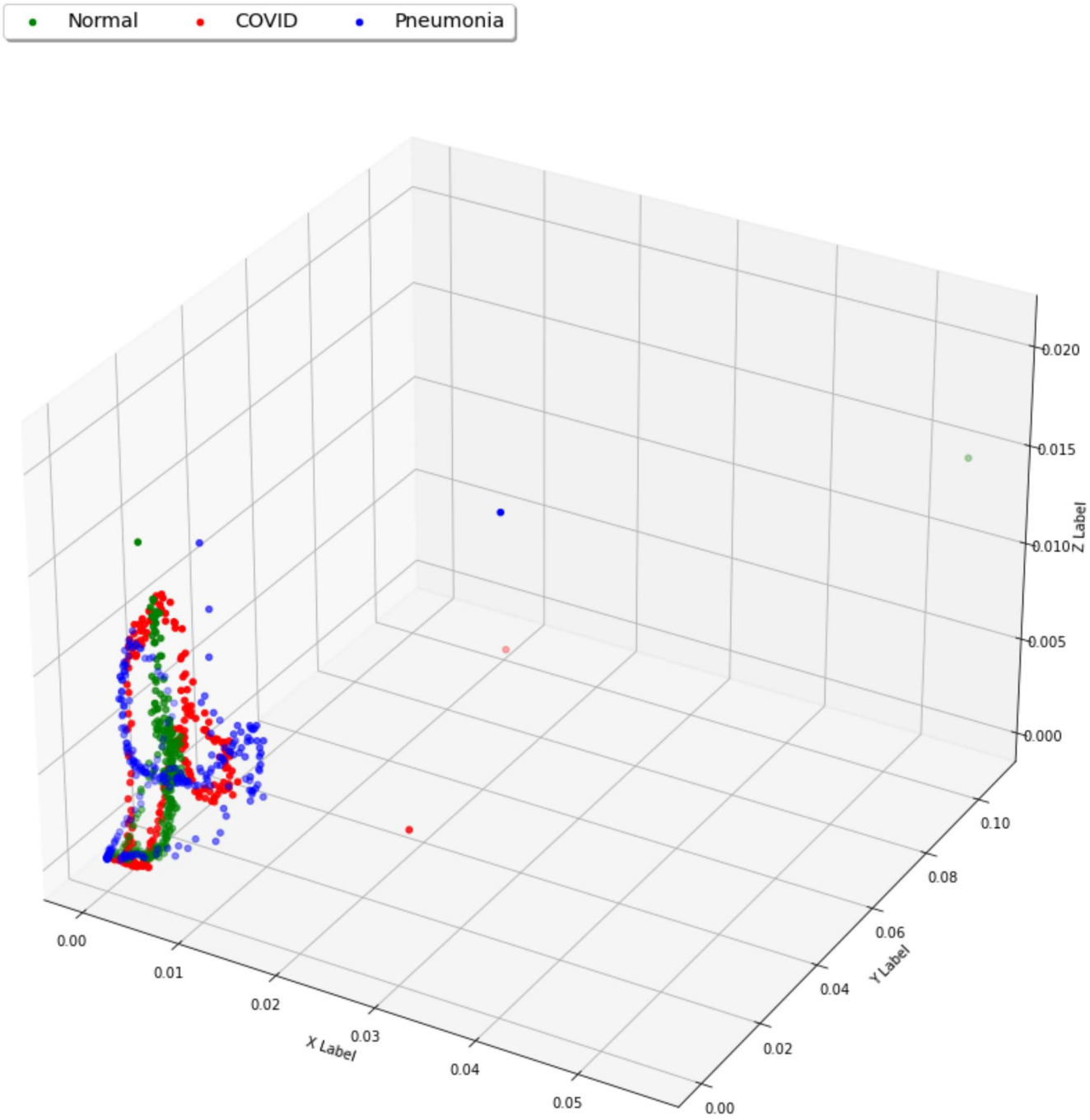
Flow chart:



Data Preprocessing:

- The dataset is divided into train and test sets in the ratio 80:20.
- The images are converted to grayscale.
- The images are sharpened using the standard composite laplacian mask filter with a kernel size of 3.
- Vectors are extracted from the images.
- Vectors are 256 dimensional where each dimension represents the intensity of the pixel in the image.
- The value of each dimension is the frequency of that intensity of the pixel in the image.
- The vectors are then normalized to unit length.


Normal
COVID
Pneumonia
0.05
0.04
0.03
0.02
0.01
0.00
0
50
100
150
200
250



Clustering:

- Clustering the vectors that are within the threshold distance(r) for each class.
- The distance between the vectors is calculated using the euclidean distance formula.
- Each cluster represents a prototype vector of the respective class.
- The prototype vectors are used to classify the test images.

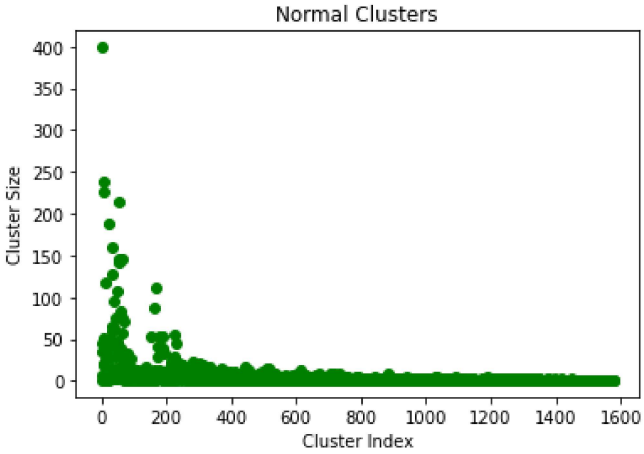
Threshold distance(r):

- The threshold distance is decided by trial and error method.
- Experimentally, two sets of threshold distances are found to give better results.
- r values for classes normal, covid-19 and viral pneumonia respectively are:
    - set 1: r = 0.025, 0.019, 0.015
    - set 2: r = 0.018, 0.012, 0.012

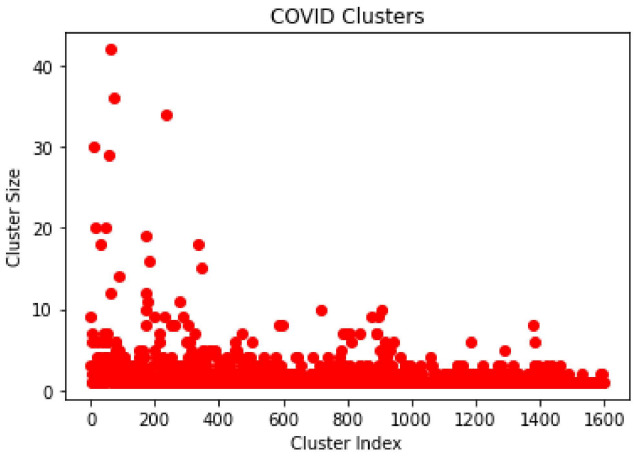
Class	Set 1	Set 2
Normal	0.025	0.018
COVID-19	0.019	0.012
Pneumonia	0.015	0.012

Clustering for set 1:

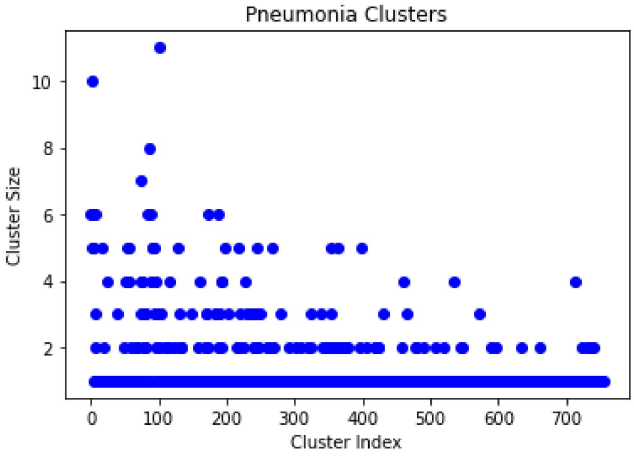
- Class Normal:
    - Number of training vectors => 8153
    - For r = 0.025, no. of clusters => 1579



- Class COVID-19:
    - Number of vectors => 2893
    - For r = 0.019, no. of clusters => 1597



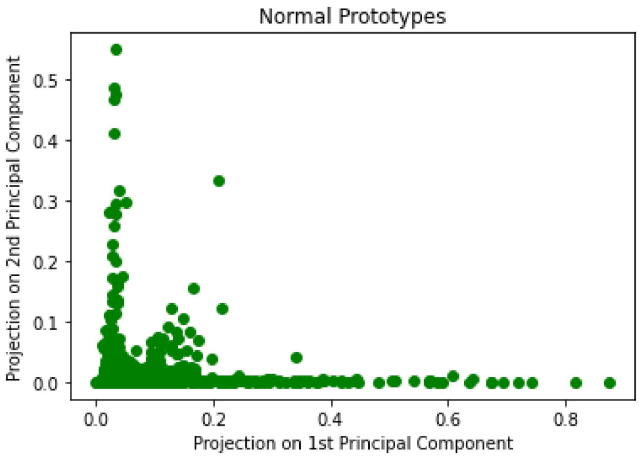
- Class Viral Pneumonia:
  - Number of vectors => 1068
  - For r = 0.015, no. of clusters => 755

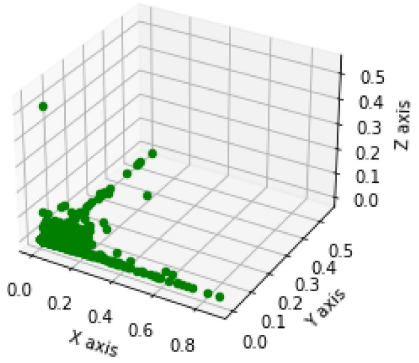


Averaging the clusters:

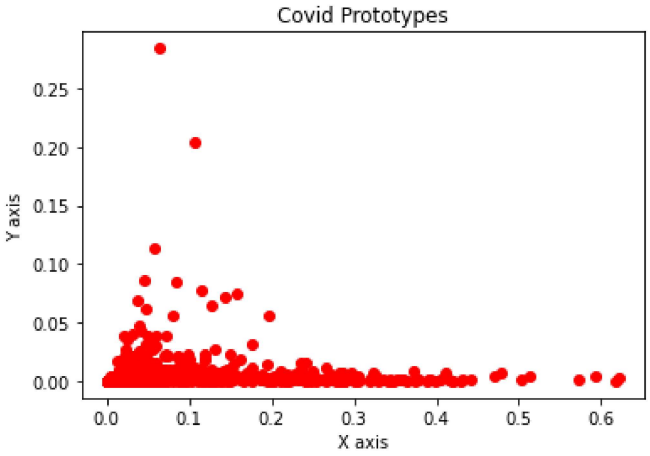
- Averaging the clusters to get the prototype vectors for each class.
- Each average vector represents the prototype vector of the respective class.
- The prototype vectors are used to classify the test images.

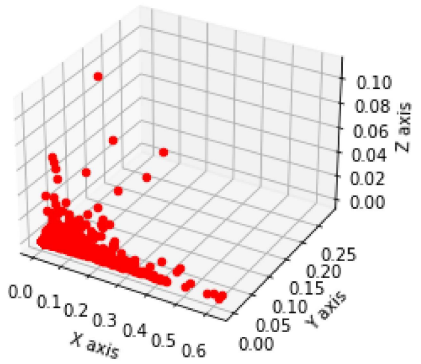
- Class Normal:
  - Number of prototypes => 1579



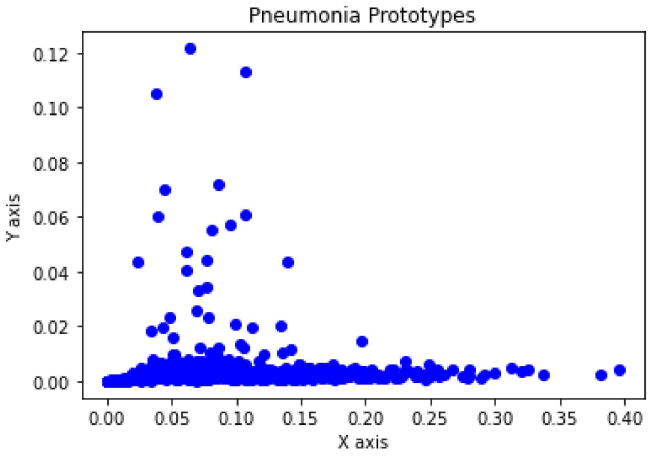


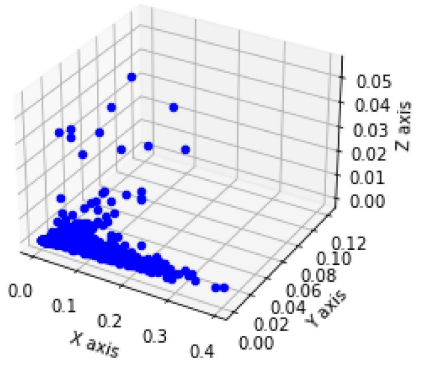
- Class COVID-19:
    - Number of prototypes => 1597



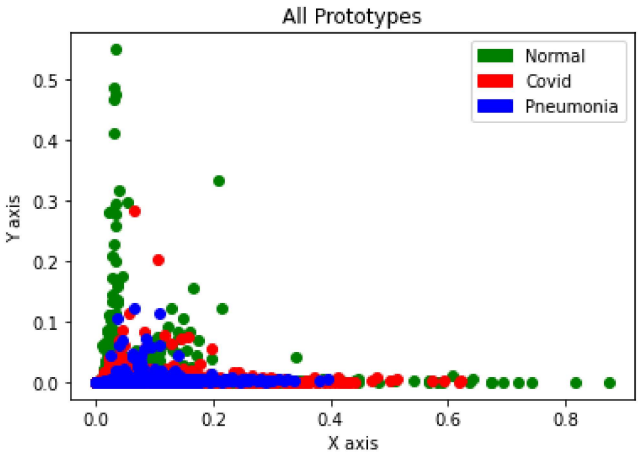


- Class COVID-19:
    - Number of prototypes => 755

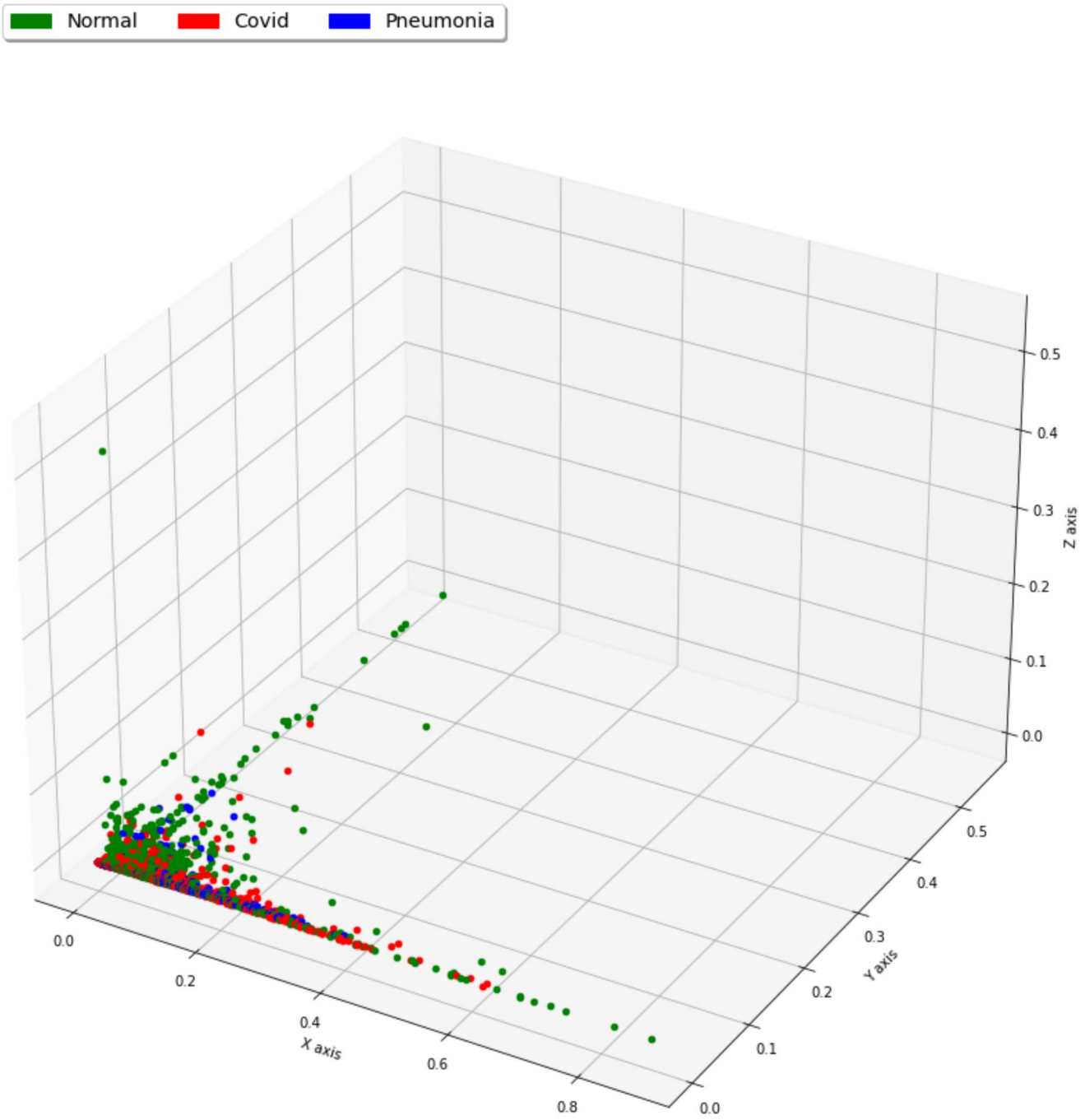




- All class prototypes in 2D:



- All class prototypes in 3D:



Classification:

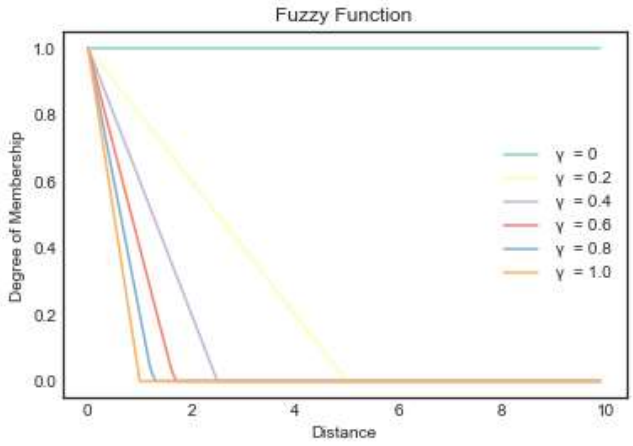
- The test vectors are classified into the respective classes using the prototype vectors.
- The distance between the test image vector and the prototype vectors is calculated using the euclidean distance for
- Each test vector is assigned a degree of membership with respect to each prototype vector.
- The degree of membership of the test vector with the prototype vector of the respective class is calculated using t

- let x be a 256 dimensional test vector
- let y be a 256 dimensional prototype vector

$$\text{Euclidean Distance} = d_x = \sqrt{\sum_{i=1}^{n}(x_i - y_i)^2}$$

$$\mu_x = \begin{cases} 0 & \text{if } \gamma * d > 1 \\ 1 & \text{if } \gamma * d = 0 \\ 1 - \gamma * d & \text{if } 0 < \gamma * d < 1 \end{cases}$$

$$\text{where, } \gamma = \text{ sensitivity parameter}$$
$$\text{d} = \text{distance between the test vector and the prototype vector}$$



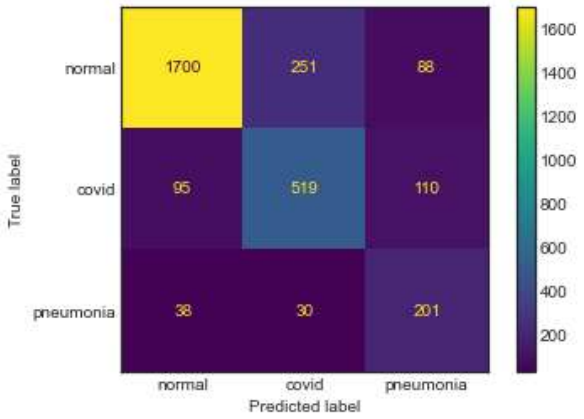
Results for set 1:

- The accuracy of the model is calculated using the following formula:

$$\text{Accuracy} = \frac{\text{Number of correctly classified test vectors}}{\text{Total number of test vectors}} * 100$$

- The accuracy of the model is calculated for each sensitivity parameter.
- The sensitivity parameter that gives the highest accuracy is selected as the optimal sensitivity parameter.
- The optimal sensitivity parameter is used to classify the test vectors.
- The accuracy of the model is 79.81% for the optimal sensitivity parameter 0.1.

The confusion matrix for the model is as follows:



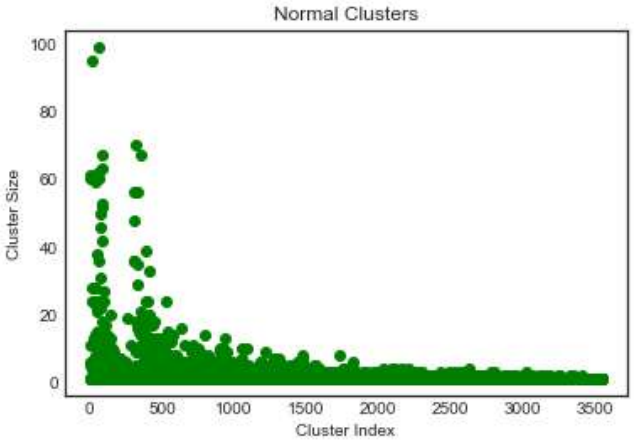
The classification report for the model is as follows:

Class	Precision	Recall	F1-Score	Support
covid	0.65	0.72	0.68	724
normal	0.93	0.83	0.88	2039
pneumonia	0.50	0.75	0.60	269
Accuracy			0.80	3032
Macro Avg	0.69	0.77	0.72	3032
Weighted Avg	0.82	0.80	0.81	3032

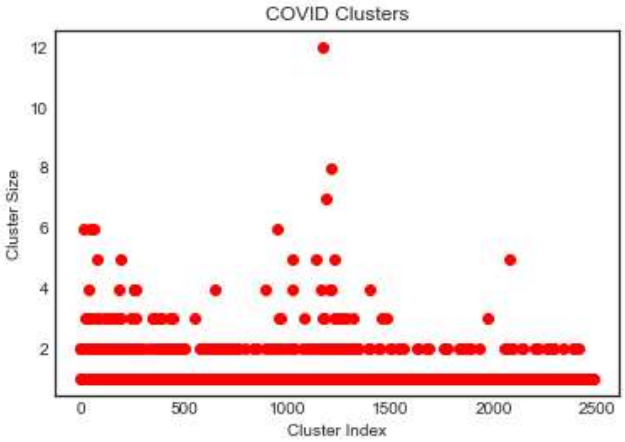
Clustering for set 2:

- Repeating the above steps for this set values, we get,

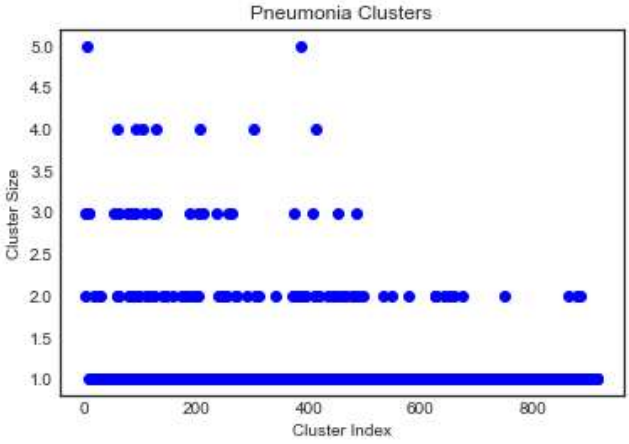
- Class Normal:
    - Number of training vectors => 8153
    - For r = 0.018, no. of clusters => 3555



- Class COVID-19:
    - Number of vectors => 2893
    - For r = 0.012, no. of clusters => 2481



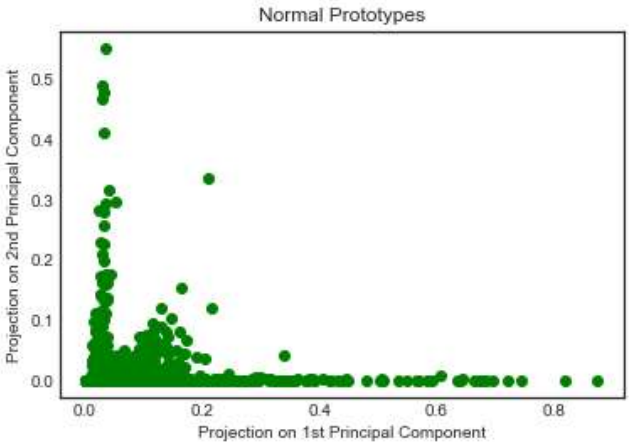
- Class Viral Pneumonia:
    - Number of vectors => 1068
    - For r = 0.012, no. of clusters => 917

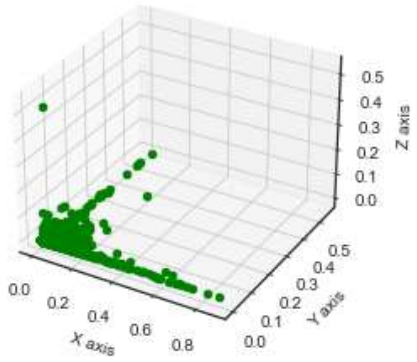


Averaging the clusters:

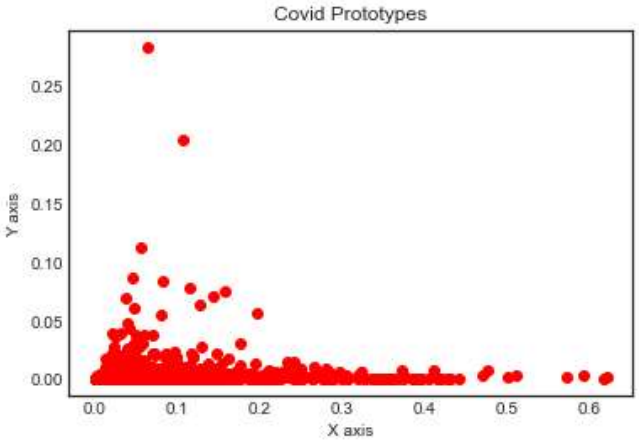
- Averaging the clusters to get the prototype vectors for each class.
- Each average vector represents the prototype vector of the respective class.
- The prototype vectors are used to classify the test images.

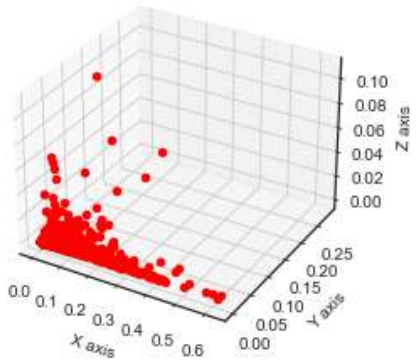
- Class Normal:
    - Number of prototypes => 3555



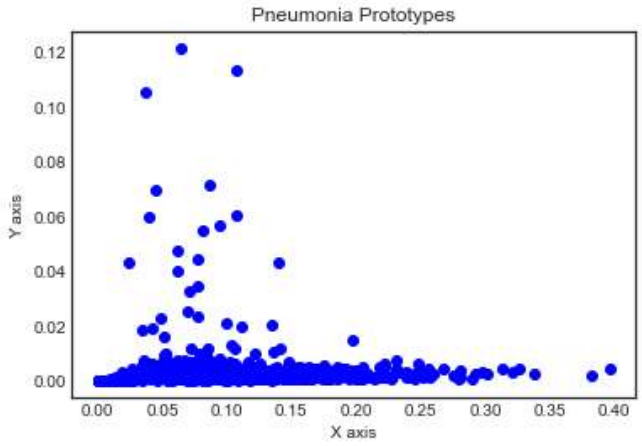


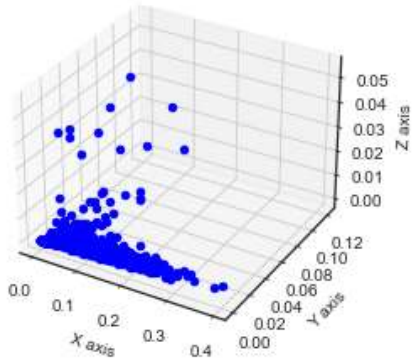
- Class COVID-19:
    - Number of prototypes => 2481



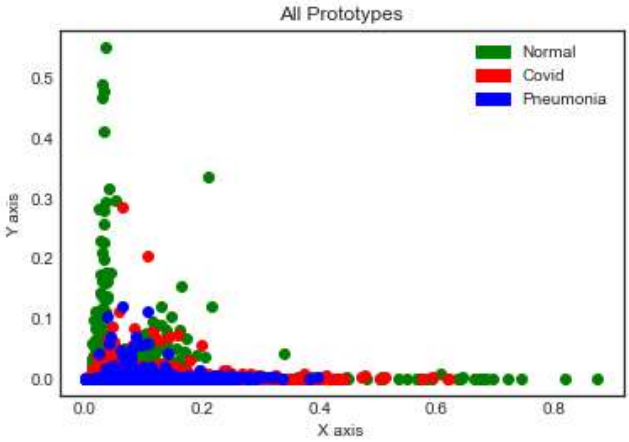


- Class COVID-19:
    - Number of prototypes => 917

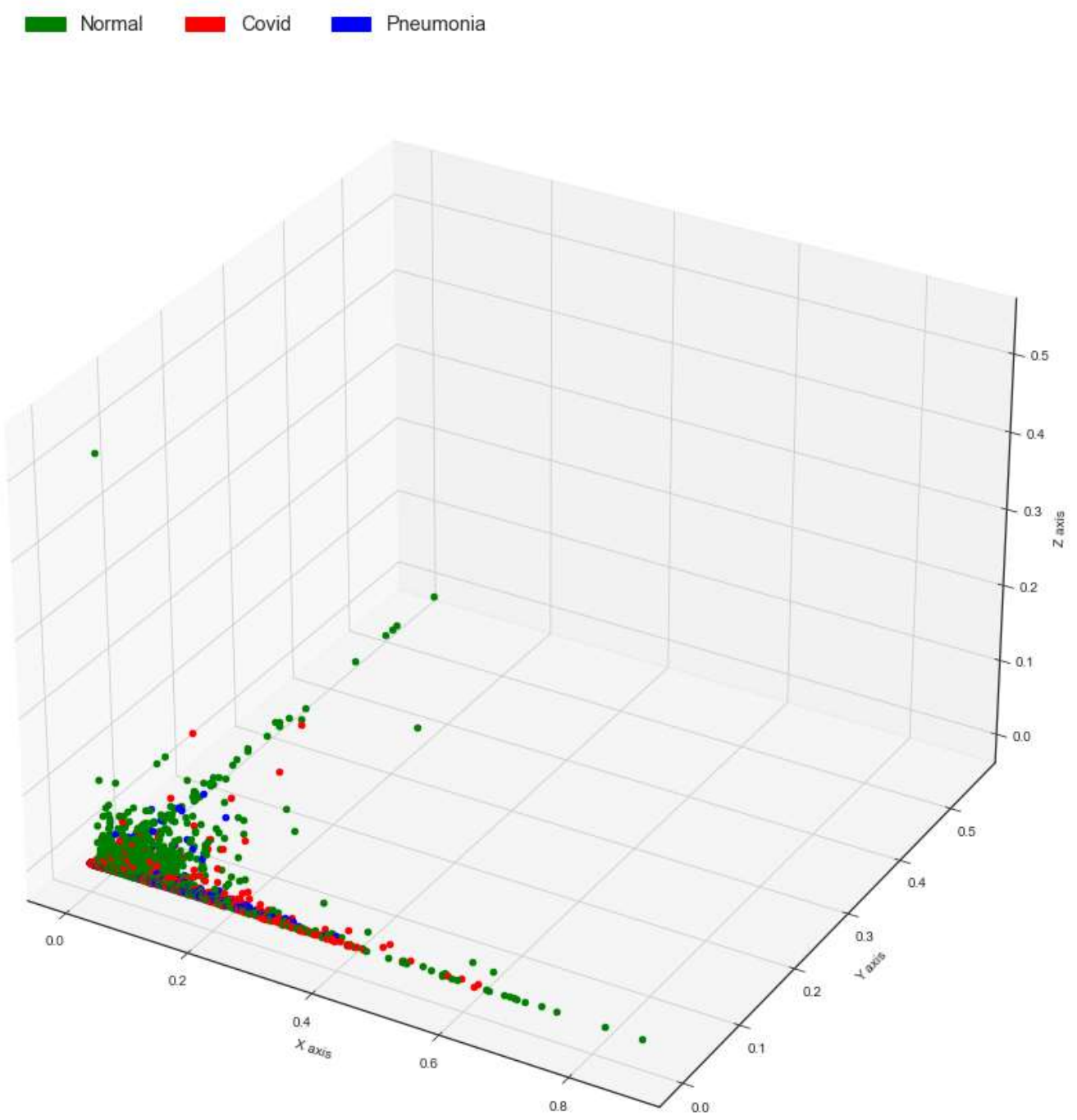




- All class prototypes in 2D:



- All class prototypes in 3D:



Classification:

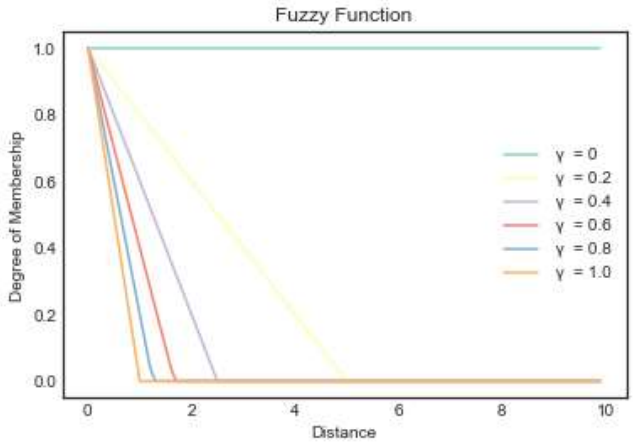
- The test vectors are classified into the respective classes using the prototype vectors.
- The distance between the test image vector and the prototype vectors is calculated using the euclidean distance for
- Each test vector is assigned a degree of membership with respect to each prototype vector.
- The degree of membership of the test vector with the prototype vector of the respective class is calculated using t

- let x be a 256 dimensional test vector
- let y be a 256 dimensional prototype vector

$$\text{Euclidean Distance} = d_x = \sqrt{\sum_{i=1}^{n}(x_i - y_i)^2}$$

$$\mu_x = \begin{cases} 0 & \text{if } \gamma * d > 1 \\ 1 & \text{if } \gamma * d = 0 \\ 1 - \gamma * d & \text{if } 0 < \gamma * d < 1 \end{cases}$$

$$\text{where, } \gamma = \text{ sensitivity parameter}$$
$$\text{d} = \text{distance between the test vector and the prototype vector}$$



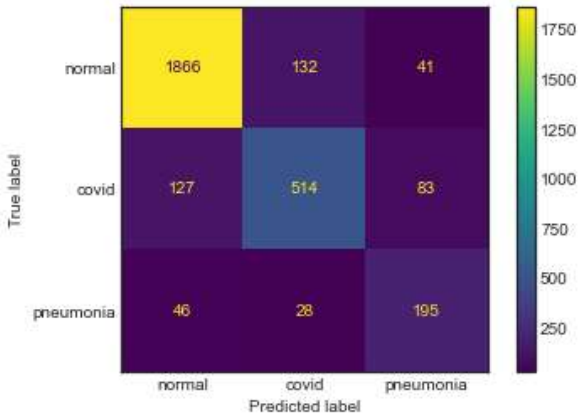
Results for set 2:

- The accuracy of the model is calculated using the following formula:

$$\text{Accuracy} = \frac{\text{Number of correctly classified test vectors}}{\text{Total number of test vectors}} * 100$$

- The accuracy of the model is calculated for each sensitivity parameter.
- The sensitivity parameter that gives the highest accuracy is selected as the optimal sensitivity parameter.
- The optimal sensitivity parameter is used to classify the test vectors.
- The accuracy of the model is 84.92% for the optimal sensitivity parameter 0.1.

The confusion matrix for the model is as follows:



The classification report for the model is as follows:

Class	Precision	Recall	F1-Score	Support
covid	0.76	0.71	0.74	724
normal	0.92	0.92	0.92	2039
pneumonia	0.61	0.72	0.66	269
Accuracy			0.85	3032
Macro Avg	0.76	0.78	0.77	3032
Weighted Avg	0.85	0.85	0.85	3032

Inference:

- The accuracy of the model is **79.81%** for **set 1** & **84.92** for **set 2** for the optimal sensitivity parameter (**γ**) **0.1**.
- The average test time for an image is **1.246 seconds.** for **set 1**
- The average test time for an image is **4.09 seconds.** for **set 2**

$$\text{SET - 1 : for } \gamma = 0.1$$

Class	Total Images	Train Images	Test Images	Threshold (r)	No. of prototypes	Correctly Classified Images	Accuracy
All Classes	15153	12121	3032	0.0196(avg)	3931	2420	79.81%
Normal	10192	8153	2039	0.025	1579	1700	83.37%
Covid	3616	2892	724	0.019	1597	519	71.68%
Viral Pneumonia	1345	1076	269	0.015	755	201	74.72%

$$\text{SET - 2 : for } \gamma = 0.1$$

Class	Total Images	Train Images	Test Images	Threshold (r)	No. of prototypes	Correctly Classified Images	Accuracy
All Classes	15153	12121	3032	0.014 (avg)	3931	2588	84.92%
Normal	10192	8153	2039	0.018	2481	1869	91.53%
Covid	3616	2892	724	0.012	917	526	72.85%
Viral Pneumonia	1345	1076	269	0.012	1333	193	71.68%

Future Work:

- The model can be improved by using a larger dataset.
- The model can be improved by reducing the threshold value of clustering
- The time complexity of the model can be reduced.