Skin cancer CLASSIFICATION USING MULTIPROTOTYPE FUZZY LOGIC

Batch 3 Grp 13 EDI:

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About the Dataset:

Skin Cancer ISIC:

The skin cancer data. Contains 9 classes of skin cancer.

This set consists of 2357 images of malignant and benign oncological diseases, which were formed from The International Skin Imaging Collaboration (ISIC). All images were sorted according to the classification taken with ISIC, and all subsets were divided into the same number of images, with the exception of melanomas and moles, whose images are slightly dominant.

The data set contains the following diseases:

- · actinic keratosis
- · basal cell carcinoma
- dermatofibroma
- melanoma
- nevus
- pigmented benign keratosis
- -seborrheic keratosis
- squamous cell carcinoma
- vascular lesion

Dataset Link:

Skin Cancer ISIC

About the Project:

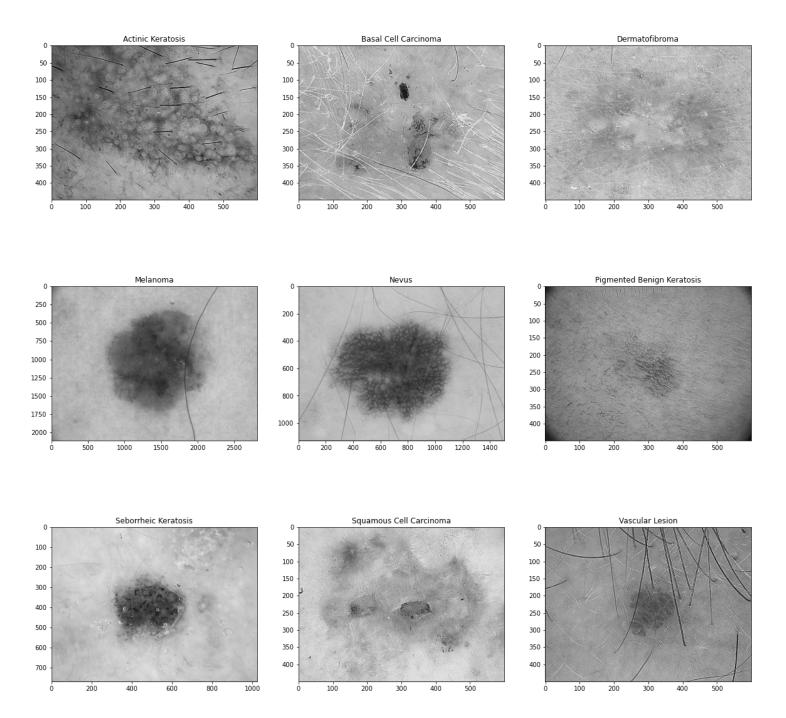
Problem Statement:

To classify the input image of skin cancer into the 9 available skin cancer classes using Multiprototype fuzzy logic

Dataset Statistics:

Number of images in each class:

Class	Total Images	Train Images	Test Images
Actinic Keratosis	130	114	16
Basal Cell Carcinoma	392	376	16
Dermatofibroma	111	95	16
Melanoma	454	438	16
Nevus	373	357	16
Pigmented Benign Keratosis	478	462	16
Seborrheic Keratosis	80	77	3
Squamous Cell Carcinoma	197	181	16
Vascular Lesion	142	139	3
Total	2357	2239	118



Flow chart:



Data Preprocessing:

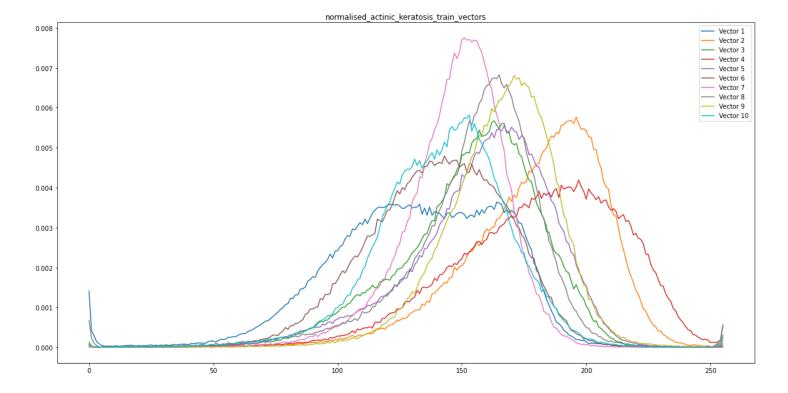
- The dataset is already divided into two parts: Train and Test each having nine classes as mentioned.
- The images are first converted to grayscaled images.
- For testing purpose there are two sets created in order to get better results.
- Set 1 => Grayscaled images
- Set 2 => Grayscaled and Sharpened images
- These images are stored in separate directory.

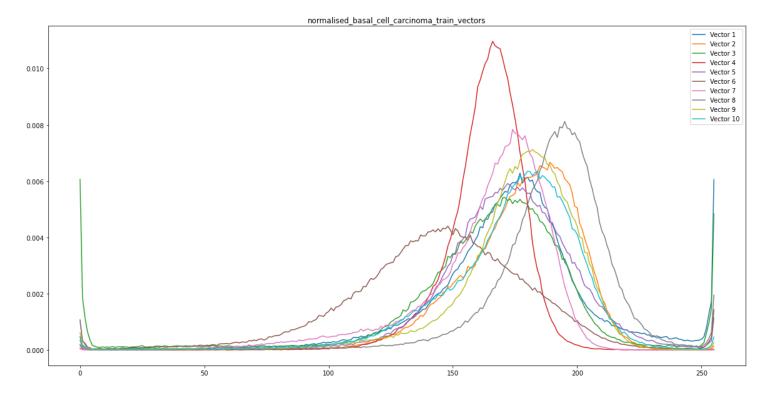
Feature Extraction:

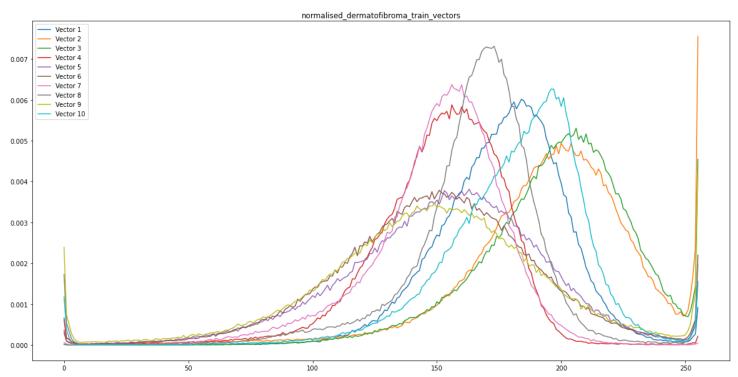
- The images from set 1 and set 2 are converted to vectors
- The dimension of this vector is 1 \times 256, where value at N'th index represents the frequency of pixel in
- These vectors are stored in separate file for further processing.

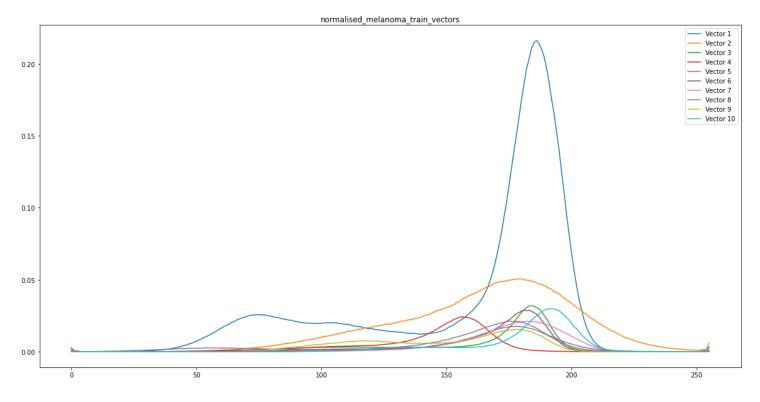
Normalization:

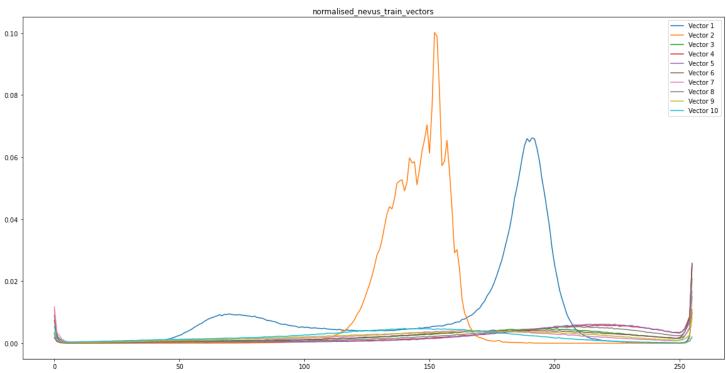
- These vectors have values between range [0 to 1038507 (set1 unsharpened)] and [0 to 808611 (set 2 s
- The values 1038507 and 808611 are the MAX_VALUE from test and train vectors in respective sets
- We divide MAX_VALUE with each element at every index in all vectors in train as well as train vectors i
- This reduces the time complexity of the further processing.
- These normalised vectors are saved in a separate file.
- Normalised vectors of all classes:

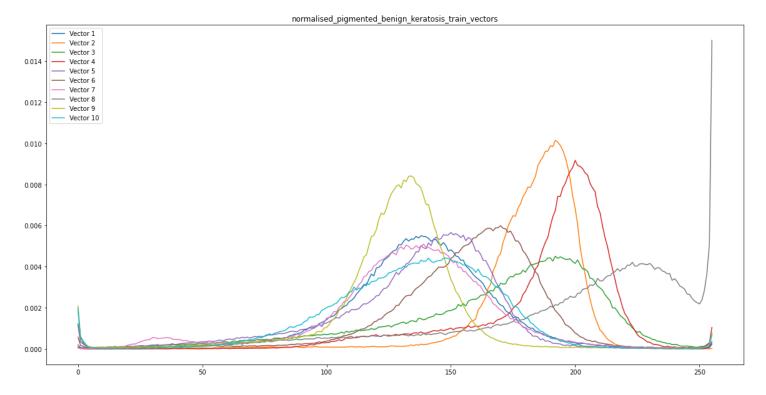


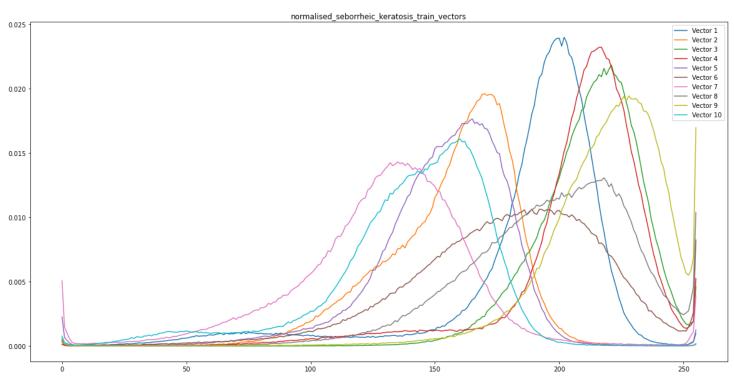


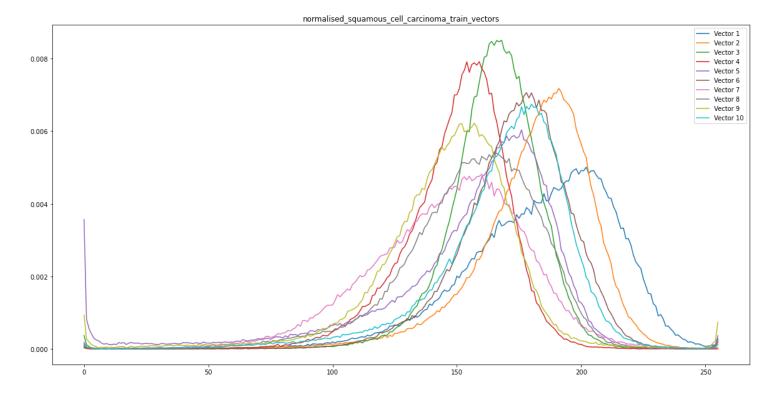


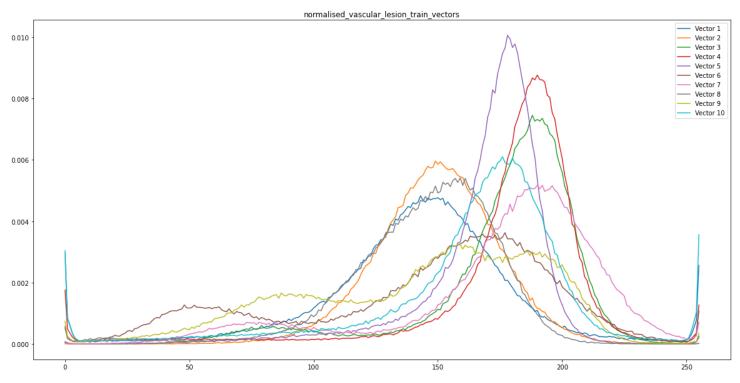




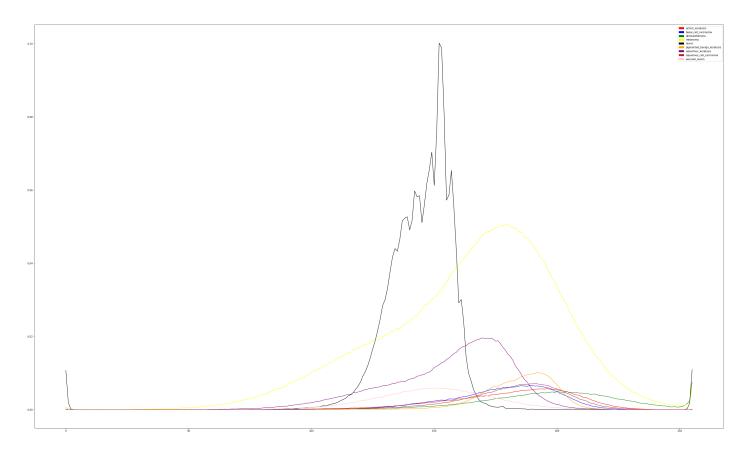








• All vectors in one graph:



Clustering:

- Clustering the vectors that are within the threshold distance(r) for each class.
- This process is done only for training vectors
- The distance between the vectors is calculated using the euclidean distance formula.



Threshold distance(r):

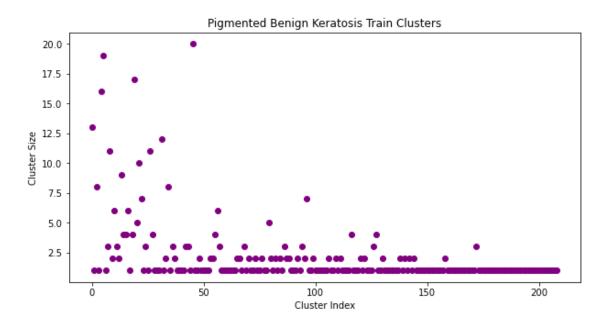
- The threshold distance is decided by trial and error method.

Clustering for set 1 (unsharpened images):

Class	Train Images	r values	No. of clusters
Actinic Keratosis	114	0.008	45
Basal Cell Carcinoma	376	0.008	162

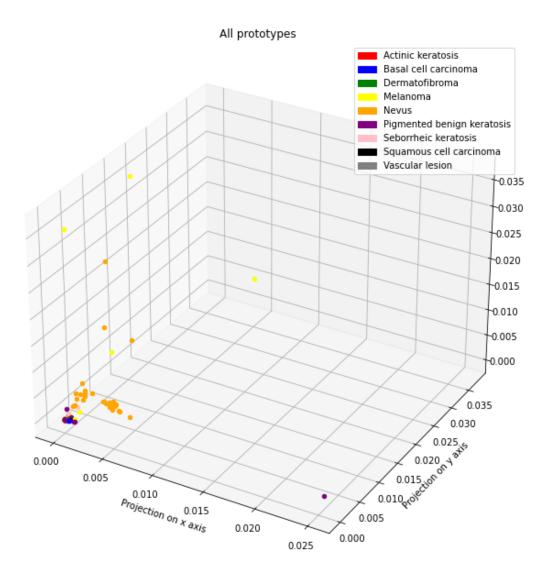
Class	Train Images	r values	No. of clusters	
Dermatofibroma	95	0.008	64	
Melanoma	438	0.05	123	
Nevus	357	0.05	148	
Pigmented Benign Keratosis	462	0.008	209	
Seborrheic Keratosis	77	0.05	18	
Squamous Cell Carcinoma	181	0.008	88	
Vascular Lesion	139	0.008	101	

e.g. Pigmented Benign Keratosis Clusters



Extracting prototypes:

- 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.
- Number of prototypes are equal to the number of clusters.
- Projection of all prototypes of all classes in 3-D

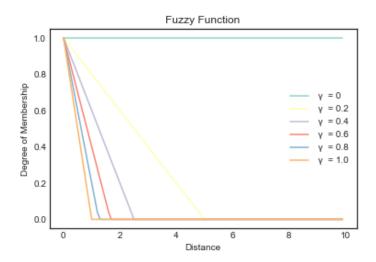


Classification:

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



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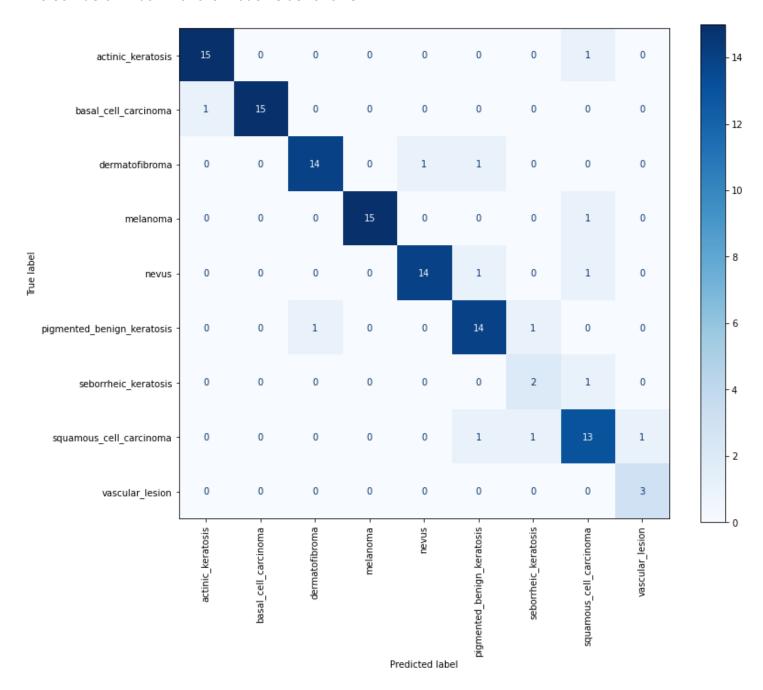


Results for set 1:

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

- 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 parame
- The optimal sensitivity parameter is used to classify the test vectors.
- The accuracy of the model is 88.98% for the optimal sensitivity parameter 0.0005

The confusion matrix for the model is as follows:



The classification report for the model is as follows:

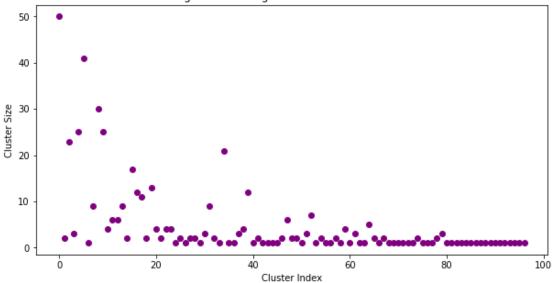
Class	Precision	Recall	F1-Score	Support
actinic_keratosis	0.94	0.94	0.94	16
basal_cell_carcinoma	1.00	0.94	0.97	16
dermatofibroma	0.93	0.88	0.90	16
melanoma	1.00	0.94	0.97	16
nevus	0.93	0.88	0.90	16

Class	Precision	Recall	F1-Score	Support
pigmented_benign_keratosis	0.82	0.88	0.85	16
seborrheic_keratosis	0.50	0.67	0.57	3
squamous_cell_carcinoma	0.76	0.81	0.79	16
vascular_lesion	0.75	1.00	0.86	3
accuracy			0.89	118
macro avg	0.85	0.88	0.86	118
weighted avg	0.90	0.89	0.89	118

Clustering for set 2 (sharpened images):

Class	Train Images	r values	No. of clusters
Actinic Keratosis	114	0.008	31
Basal Cell Carcinoma	376	0.008	84
Dermatofibroma	95	0.008	32
Melanoma	438	0.05	114
Nevus	357	0.05	128
Pigmented Benign Keratosis	462	0.008	97
Seborrheic Keratosis	77	0.05	15
Squamous Cell Carcinoma	181	0.008	46
Vascular Lesion	139	0.008	62

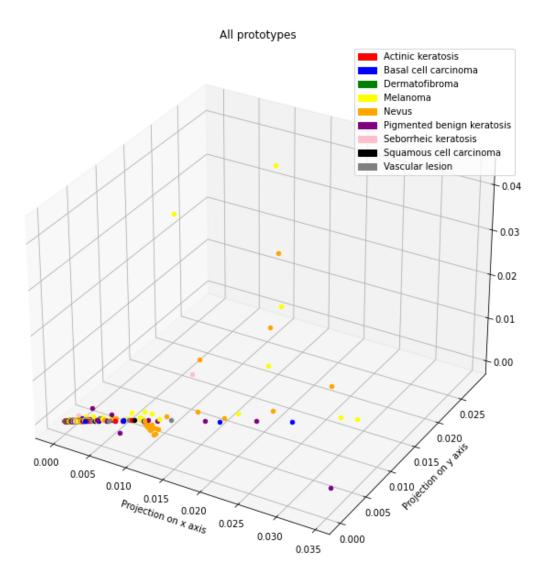
Pigmented Benign Keratosis Train Clusters



Extracting prototypes:

- 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.
- Number of prototypes are equal to the number of clusters.

- Projection of all prototypes of all classes in 3-D

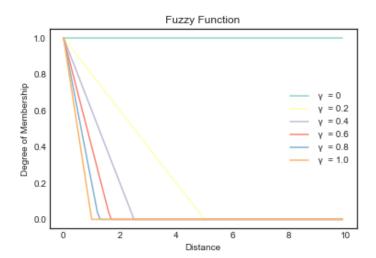


Classification:

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



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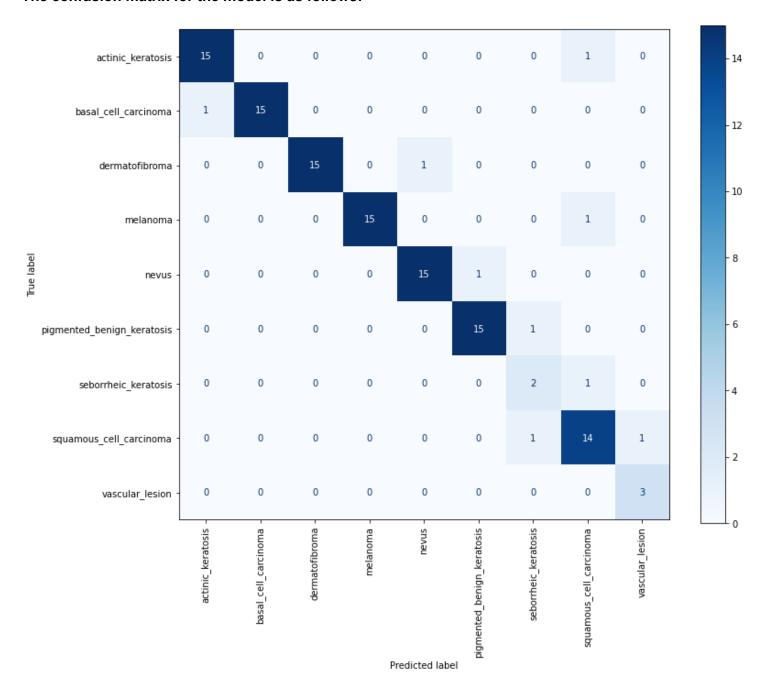


Results for set 2:

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

- 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 parame
- The optimal sensitivity parameter is used to classify the test vectors.
- The accuracy of the model is 92.37% for the optimal sensitivity parameter 0.0005

The confusion matrix for the model is as follows:



The classification report for the model is as follows:

Class	Precision	Recall	F1-Score	Support
actinic_keratosis	0.94	0.94	0.94	16
basal_cell_carcinoma	1.00	0.94	0.97	16
dermatofibroma	1.00	0.94	0.97	16
melanoma	1.00	0.94	0.97	16
nevus	0.94	0.94	0.94	16

Class	Precision	Recall	F1-Score	Support
pigmented_benign_keratosis	0.94	0.94	0.94	16
seborrheic_keratosis	0.50	0.67	0.57	3
squamous_cell_carcinoma	0.82	0.88	0.85	16
vascular_lesion	0.75	1.00	0.86	3
accuracy			0.92	118
macro avg	0.88	0.91	0.89	118
weighted avg	0.93	0.92	0.93	118

Inference:

• The accuracy of the model is 88.98% for set 1 & 92.37% for set 2 for the optimal sensitivity parameter (γ) 0.0005.

Unsharpened images

Class	Total Images	Train Images	Test Images	Threshold (r)	No. of Prototypes	Correctly classified images	Accuracy
Actinic Keratosis	130	114	16	0.008	45	15	93.75
Basal Cell Carcinoma	392	376	16	0.008	162	15	93.75
Dermatofibroma	111	95	16	0.008	64	14	87.5
Melanoma	454	438	16	0.05	123	15	93.75
Nevus	373	357	16	0.05	148	14	87.5
Pigmented Benign Keratosis	478	462	16	0.008	209	14	87.5

Class	Total Images	Train Images	Test Images	Threshold (r)	No. of Prototypes	Correctly classified images	Accuracy
Seborrheic Keratosis	80	77	3	0.05	18	2	66.66
Squamous Cell Carcinoma	197	181	16	0.008	88	13	81.25
Vascular Lesion	142	139	3	0.008	101	3	100
Total	2357	2239	118	0.008	958	105	88.98

Sharpened images

Class	Total Images	Train Images	Test Images	Threshold (r)	No. of Prototypes	Correctly classified images	Accuracy
Actinic Keratosis	130	114	16	0.008	31	15	93.75
Basal Cell Carcinoma	392	376	16	0.008	84	15	93.75
Dermatofibroma	111	95	16	0.008	32	15	87.5
Melanoma	454	438	16	0.05	114	15	93.75
Nevus	373	357	16	0.05	128	15	87.5
Pigmented Benign Keratosis	478	462	16	0.008	97	15	87.5
Seborrheic Keratosis	80	77	3	0.05	15	2	66.66
Squamous Cell Carcinoma	197	181	16	0.008	46	14	81.25
Vascular Lesion	142	139	3	0.008	62	3	100
Total	2357	2239	118	0.008	609	109	92.37

Future Work:

- The model can be improved by using a larger dataset.
- The model can be improved by reducing the threshold value of clustering.
- Images with 3 channels (coloured images) can be used.
- $\bullet\,$ Adjusting the value of $\gamma\,$