

2013

Feature extraction through median-split algorithm segmentation for melanoma detection

Venkata Sai Narasimha Kaushik Ghantasala

Follow this and additional works at: http://scholarsmine.mst.edu/masters_theses



Part of the [Electrical and Computer Engineering Commons](#)

Department:

Recommended Citation

Ghantasala, Venkata Sai Narasimha Kaushik, "Feature extraction through median-split algorithm segmentation for melanoma detection" (2013). *Masters Theses*. 7671.

http://scholarsmine.mst.edu/masters_theses/7671

This Thesis - Open Access is brought to you for free and open access by Scholars' Mine. It has been accepted for inclusion in Masters Theses by an authorized administrator of Scholars' Mine. This work is protected by U. S. Copyright Law. Unauthorized use including reproduction for redistribution requires the permission of the copyright holder. For more information, please contact scholarsmine@mst.edu.

**FEATURE EXTRACTION THROUGH MEDIAN-SPLIT ALGORITHM
SEGMENTATION FOR MELANOMA DETECTION**

by

VENKATA SAI NARASIMHA KAUSHIK GHANTASALA

A THESIS

**Presented to the Faculty of the Graduate School of the
MISSOURI UNIVERSITY OF SCIENCE AND TECHNOLOGY**

**In Partial Fulfillment of the Requirements for the Degree
MASTER OF SCIENCE IN ELECTRICAL ENGINEERING**

2013

Approved by

Randy H. Moss, Advisor

R. Joe Stanley

Bijaya Shrestha

©2013

Venkata Sai Narasimha Kaushik Ghantasala

All Rights Reserved

ABSTRACT

“Detection of melanoma remains an empirical clinical science. New tools for automatic discrimination of melanoma from benign lesions in digitized dermoscopy images may allow an improvement in early detection of melanoma. This research implements a fast version of the median split algorithm in an open source format and applied to four-color splitting of the lesion area to capture the architectural disorder apparent in melanoma colors. This version of the median split algorithm splits colors along the color axis with maximum range”. For a dermoscopy set of 888 images, K-means clustering algorithm is compared with a median split algorithm to find which model is performing better according to logistic regression analysis from SAS. For images with the median split algorithm, a full model of 208 features and a robust model of 45 features were developed for an 837 dermoscopy image set and a threshold was selected using logistic regression analysis that shows the most important features in both the models. Using this threshold, we checked the robustness and accuracy on a test model of 78 dermoscopy images with full and robust model. The median split algorithm is fast, requiring less than one second per image and only a four-color splitting, but it captures sufficient critical information regarding color disorder, with peripheral inter-color boundaries showing the highest significance for melanoma discrimination.

ACKNOWLEDGEMENTS

I would like to express deepest gratitude to my advisor, Dr. Randy H. Moss, for all his support, guidance, contributions and valuable suggestions during the course of research. I would also like to express my gratefulness to the committee members, Dr. Bijaya Shreshta and Dr. R. Joe Stanley, who gave me their valuable suggestions and have encouraged me throughout my research work. I feel privileged to have worked with all the three of them and this research study would not be possible without the support and help from the committee.

I would take this opportunity to express my gratefulness to my mentor Dr. William V. Stoecker who gave me his valuable inputs and suggestions for my research work. I would also like to thank my fellow members of the group, Jason Hagerty and Nabin Mishra who helped me with their valuable contributions towards my research work. I thank Raed chowdhary for the median split algorithm code. I also thank the whole research group who contributed in their own way for my research. A special thanks to all my professors who taught me various aspects of Electrical Engineering during the whole tenure of my Master's degree and supported me to move forward.

Last but never the least, I would like to express my special thanks to my parents, family, friends and the Almighty for all blessings and well wishes bestowed upon me.

TABLE OF CONTENTS

	Page
ABSTRACT	iii
ACKNOWLEDGEMENTS	iv
LIST OF ILLUSTRATIONS	x
LIST OF TABLES	xi
 SECTION	
1. INTRODUCTION.....	1
1.1 MEDIAN SPLIT ALGORITHM	1
1.2 EXAMPLE OF A MEDIAN SPLIT IMAGE.....	2
1.3 MEDIAN SPLIT PSEUDOCODE	4
1.4 MEDIAN SPLIT DECISION VARIABLE.....	4
1.5 MEDIAN SPLIT MODELS	5
2. MEDIAN SPLIT FEATURE EXTRACTION.....	6
2.1 INSTRUMENTATION AND IMAGES	6
2.2 IMAGES.....	6
3. DATA SEGMENTATION.....	8
4. FEATURE EXTRACTION FOR FULL MODEL.....	11
4.1 LESION FEATURES.....	11
4.2 SEGMENT FEATURES	12
5. ALGORITHM DESIGNED FOR FINDING THESE FEATURE.....	23
6. ROBUST MODEL	24

6.1	ADDITIONAL FEATURES FOR ROBUST MODEL	24
6.1.1	Newly Added Features.	24
6.2	FILTERING FULL MODEL INTO ROBUST MODEL.....	26
6.3	LESION FEATURES IN ROBUST MODEL.....	26
6.4	SEGMENT FEATURES IN ROBUST MODEL.....	26
6.4.1	1 st Segment Features in the Robust Model.	26
6.4.2	2 nd Segment Features in the Robust Model.	27
6.4.3	3 rd Segment Features in the Robust Model.....	28
6.4.4	4 th Segment Features in the Robust Model.	28
7.	SAS AND FEATURE SELECTION PROCESS	30
7.1	FEATURE SELECTION.....	30
7.2	LOGISTIC REGRESSION	31
7.3	ODDS RATIO ESTIMATES	32
8.	RESULTS.....	33
8.1	COMPARING K-MEANS SPLITTING ALGORITHM AND MEDIAN SPLIT ALGORITHM ON 888 IMAGES.....	34
8.1.1	Significant Features.....	34
8.1.1.1	K-means with SLENTY=SLSTAY=0.5.....	34
8.1.1.1.1	Significant lesion features.	34
8.1.1.1.2	Significant 1 st segment (darkest color) features.	34
8.1.1.1.3	Significant 2 nd segment features.....	35
8.1.1.1.4	Significant 3 rd segment features.	36
8.1.1.1.5	Significant 4 th segment (brightest color) features.....	37
8.1.1.2	Median split algorithm with SLENTY=SLSTAY=0.5.....	38

8.1.1.2.1	Significant lesion features.	38
8.1.1.2.2	Significant 1 st segment (darkest color) features.	38
8.1.1.2.3	Significant 2 nd segment features.	39
8.1.1.2.4	Significant 3 rd segment features.	41
8.1.1.2.5	Significant 4 th segment (brightest color) features.	42
8.1.1.3	K-means with SLENTY=SLSTAY=0.1.	43
8.1.1.3.1	Significant lesion features.	43
8.1.1.3.2	Significant 1 st segment (darkest color) features.	43
8.1.1.3.3	Significant 2 nd segment features.	44
8.1.1.3.4	Significant 3 rd segment features.	44
8.1.1.3.5	Significant 4 th segment (brightest color) features.	44
8.1.1.4	Median split algorithm with SLENTY=SLSTAY=0.1.	45
8.1.1.4.1	Significant lesion features.	45
8.1.1.4.2	Significant 1 st segment (darkest color) features.	45
8.1.1.4.3	Significant 2 nd segment features.	45
8.1.1.4.4	Significant 3 rd segment features.	45
8.1.1.4.5	Significant 4 th segment (brightest color) features.	45
8.1.2	Classification Results.	46
8.1.2.1	K-means with SLENTY=SLSTAY=0.5.	46
8.1.2.2	Median split algorithm with SLENTY=SLSTAY=0.5.	49
8.1.2.3	K-means with SLENTY=SLSTAY=0.1.	52
8.1.2.4	Median split algorithm with SLENTY=SLSTAY=0.1.	55
8.1.3	Receiver Operating Characteristic Curve.	57
8.1.3.1	Comparing ROC curve for median split and K-means algorithm for SLENTY=SLSTAY=0.5 for 888 set.	58

8.1.3.2 Comparing ROC curve for median split and K-means algorithm for SLENTY=SLSTAY=0.1 for 888 set.	58
8.2 COMPARING 837 IMAGES WITH THE FULL MODEL AND ROBUST MODEL.....	59
8.2.1 Significant Features.....	60
8.2.1.1 Full model.....	60
8.2.1.1.1 Significant lesion features.	60
8.2.1.1.2 Significant 1 st segment (darkest color) features.	60
8.2.1.1.3 Significant 2 nd segment features.	61
8.2.1.1.4 Significant 3 rd segment features.	62
8.2.1.1.5 Significant 4 th segment (brightest color) features.....	62
8.2.1.2 Robust model.....	64
8.2.1.2.1 Significant lesion features.	64
8.2.1.2.2 Significant 1 st segment (darkest color) features.	64
8.2.1.2.3 Significant 2 nd segment features.	64
8.2.1.2.4 Significant 3 rd segment features.	65
8.2.1.2.5 Significant 4 th segment (brightest color) features.....	65
8.2.2 Classification Results.	66
8.2.2.1 Full model.....	66
8.2.2.2 Robust model.....	69
8.2.3 Receiver Operating Characteristic Curve.....	71
8.2.3.1 Comparing ROC curve for full and robust model for median split with SLENTY=SLSTAY=0.5 for 837 set.	71
8.3 USING THE FULL MODEL ON TEST SET OF 78 IMAGES	72
8.3.1 Threshold Selection.....	73
8.3.2 Testing the Model and Threshold on the 78 Image Set.....	73

8.4	USING THE ROBUST MODEL ON TEST SET OF 78 IMAGES	74
8.4.1	Threshold Selection.....	74
8.4.2	Testing the Robust Model and Threshold on 78 Image Set	74
8.5	COMPARING ROC CURVE FOR 78 IMAGES WITH FULL MODEL AND ROBUST MODEL.....	75
8.5.1	Calculating Sensitivity and Specificity for each model.....	75
8.5.2	Plotting ROC curve for both the models.....	83
9.	CONCLUSION	85
10.	FUTURE WORK	86
APPENDICES		
A.	THRESHOLD SELECTION TABLE FOR FULL MODEL.....	87
B.	TABLE TO TEST THE OBTAINED THRESHOLD VALUE FOR FULL MODEL ON A TEST SET OF 78 IMAGES	127
C.	THRESHOLD SELECTION TABLE FOR ROBUST MODEL	132
D.	TABLE TO TEST THE OBTAINED THRESHOLD VALUE FOR ROBUST MODEL ON A TEST SET OF 78 IMAGES	172
REFERENCES		177
VITA		179

LIST OF ILLUSTRATIONS

	Page
Figure 1.1 Original Image—Dermoscopy Image	3
Figure 1.2 Median Split – 3 splits (RGB) and 4 regions	3
Figure 1.3 Median Split, 3 Splits create 4 colors in the lesion.	3
Figure 3.1 Original Image	8
Figure 3.2 Border Image that splits the lesion and skin part	9
Figure 3.3 Median Split Image using median split algorithm	9
Figure 3.4 Segment 1 (Darkest color segment)	9
Figure 3.5 Segment 2 (2 nd darkest color segment)	9
Figure 3.6 Segment 3 (3 rd darkest color segment).....	10
Figure 3.7 Segment 4 (brightest color segment)	10
Figure 4.1 a) Unfilled Segment ,b) Largest unfilled blob, c) Filled Segment, d) Largest filled blob.....	13
Figure 4.2 Perimeter of the Segment.....	14
Figure 4.3 External Perimeter of the Segment	14
Figure 8.1 Comparing ROC curve for Median Split and K-means algorithm for SLENTY=SLSTAY=0.5 for 888 set.....	58
Figure 8.2 Comparing ROC curve for Median Split and K-means algorithm for SLENTY=SLSTAY=0.1	59
Figure 8.3 Comparing ROC curve for Median Split Full model and robust model for SLENTY=SLSTAY=0.5 for 837 set	72
Figure 8.4 ROC curve comparison between full model and robust model for 78 image set...	84

LIST OF TABLES

	Page
Table 8.1 Classification results using K-means algorithm with SLENTY=SLSTAY=0.5 for 888 set.....	46
Table 8.2 Classification results using Median Split Algorithm with SLENTY=SLSTAY=0.5 for 888 set.....	49
Table 8.3 Classification Results using K-means Algorithm with SLENTY=SLSTAY=0.1 for 888 set.....	52
Table 8.4 Classification Results using Median Split Algorithm with SLENTY=SLSTAY=0.1 for 888 set.....	55
Table 8.5 Classification results for Full Model using median split algorithm with SLENTY=SLSTAY=0.5 for 837 set.....	66
Table 8.6 Classification results for Robust Model using median split algorithm with SLENTY=SLSTAY=0.5 for 837 set.....	69
Table 8.7 Sensitivity and Specificity values for robust model on 78 image set.....	75
Table 8.8 Sensitivity and Specificity values for full model on 78 image set.....	79

1. INTRODUCTION

Detection of malignant melanoma at early stages might be done by applying analytic methods to the dermoscopy melanoma images. This might increase the possibility of detecting potential melanoma which can decrease the chances of death. In 2012 in the United States, malignant melanoma has estimated to be found in 76,250 cases and there were 12,190 estimated deaths. Hence there are many methods being found for detection of melanoma at early stages. Of these, color methods splitting the entire lesion was investigated by Andreassi et al [1][2]. To discriminate melanoma images from benign images, one method is to segment the lesion image based on color and to identify features based on this segmentation. In this project, the architectural disorder of early in situ melanoma are captured using a technique to segment images termed as the median split technique (Umbaugh, 2011)[3]. This has advantages like speed, simplification of lesion architecture yet retention of critical features, and high discriminatory power for melanoma [3].

1.1 MEDIAN SPLIT ALGORITHM

Initially, the median split algorithm was applied to a set of 888 images using CVIP tools (<http://cviptools.ece.siu.edu>). This algorithm is designed based on the Heckbert color compression algorithm [4]. Median split algorithm is only applied to a particular region of interest (ROI) which is called the lesion part of the image. This ROI based on color so that the fewer colors are used in order describe the ROI. The resultant simplified image allows exact quantization of color areas, inter-color boundaries and color values. The color space is segmented by splitting the pixel histogram of a color segment. During each iteration, the color segment is split into two segments having equal number of pixels. In any color axis, the

segment which has the highest range is chosen for the subsequent split. In the chosen segment, the split is done along the color axis with the highest range. Division is done based on the median pixel M on the chosen axis. The chosen color axis and color bin satisfies the following condition.

1. chosen bin $= \operatorname{argmax}_{\text{bins}} \max_{\text{color axis in bins}} (\text{range of color axis})$
2. chosen color axis $= \operatorname{argmax}_{\text{color axis in chosen bin}} \text{range of color axis}$
3. $[\text{hist}(\text{bin}) < M]$ $=$ $[\text{hist}(\text{bin}) > M]$ along chosen axis

$[\] \Rightarrow$ denotes number of pixels that satisfies the condition within $[\]$.

$\text{hist}(\text{bin}) \Rightarrow$ histogram of pixels within the chosen bin.

For the list of color bins in the ROI, the old bins is replaced by the two new bins.

After the completion of a particular split, the segment (bin) list gets updated and the next segment for the split is chosen with highest range along any color axis. The algorithm continues until it reaches a specified number of colors. Empirically four colors appear to be sufficient to represent the colors within the lesion.

1.2 EXAMPLE OF A MEDIAN SPLIT IMAGE

Figures 1.1-1.3 show the splitting process for a melanoma image using range as the decision variable in red, green and blue (RGB) color space as performed on the ROI—the melanoma lesion only.



Figure 1.1 Original Image—Dermoscopy Image

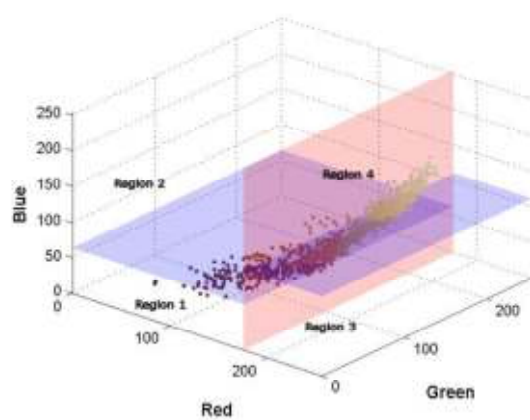


Figure 1.2 Median Split – 3 splits (RGB) and 4 regions

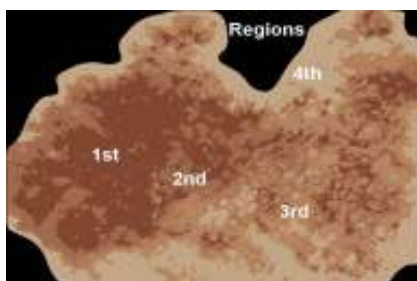


Figure 1.3 Median Split, 3 Splits create 4 colors in the lesion

1.3 MEDIAN SPLIT PSEUDOCODE

The algorithm of median split pseudocode is as follows.

```

for NumberofSplits(outer loop begins)
{
    for NumberofCurrentBins(inner loop)
    {
        find channel with largest range
    }
    find a bin with the largest range
    arrange pixels in bin with largest range in order of channel with largest range
    split bin into nearly equal bins ( as equal as possible after splitting)
    remap colors in bins to image (the pixels in bin are set to mean of bin )
}
}

```

Red, green, blue are the three channels used for each bin and the number of splits are set at three to produce four segments.

1.4 MEDIAN SPLIT DECISION VARIABLE

The main decision variable for the median split algorithm is range and the alternate decision variable for this would be variance and inter-quartile distances. There is a little random noise for contact dermoscopy images with evenly distributed LED lighting. To

eliminate most of the significant artifacts, pre-processing has to be done like removing the hairs that are protruding from the skin, removing bubbles from the gel interface and retaining the CVIP tools default decision variable (range). This helps to capture small variations in the image such as small networks which would not be captured efficiently using variance or inter-quartile distance.

1.5 MEDIAN SPLIT MODELS

The main aspects in this thesis work would be:

Here some results are compared to decide which model is better.

1. Comparing K-means splitting algorithm and median split algorithm on 888 images.
2. Comparing 837 images with the full model and the robust model.
3. Using the full model on test set of 78 images.
4. Using the robust model on test set of 78 images.
5. Comparing ROC curve for 78 images with full model and robust model.

2. MEDIAN SPLIT FEATURE EXTRACTION

2.1 INSTRUMENTATION AND IMAGES

A 3Gen DermLite Fluid attachment(3Gen LLC, San Juan Capistrano, CA) was used to obtain dermoscopy images for this study. Bright white LED lights, 10X magnification and a gel interface are used by this device.

2.2 IMAGES

For this study, three image sets are obtained. One image set of 888 images contains 195 melanoma and melanoma in situ images and 693 benign images. All of which were obtained in the study SBIR R44 CA-101639-02A2 of the National Institutes of Health (NIH). This image set is used in the thesis for comparing the median split technique with K-means algorithm. A set of 837 images (a subset of 888 images) was obtained by eliminating some poor images from the 888 set. Images were eliminated if they were out-of-focus or unzoomed. The 837 set contains 184 melanomas and 653 benign lesions. This set was used for developing a full model and a robust model. These full and robust models are tested on a disjoint test set of 78 images containing 39 melanomas and 39 benigns which are not a part of 888 image set. Lesion borders (ROIs) were manually drawn using second-order b-splines.

Some commonly used terms throughout the document are as follows.

1. **Original Image:** This is the original image obtained from contact dermoscopy.
2. **Median Split Image:** This is the image obtained after processing through the median split algorithm with the background skin is changed to black. The features are found from these images.

3. **Lesion part:** This represents the median split part of the image and this part is our main concentration. This is the non-black portion of the median split image.
4. **Lesion Border:** This is a hand-drawn border around the lesion part of the median split image.
5. **Skin part:** This part represents the skin part of the image which is nothing but the other side of the border of median split image. This part is not an essential part of our research.
6. **Color segments:** The lesion part is split into four segments depending on the color basis.
7. **Lesion features:** The features that are obtained for the whole lesion part are called the lesion features.
8. **Segment features:** The features that are obtained for each segment are called the segment features.
9. **Blob:** A connected group of segmented pixels on the basis of eight-connectivity is called a blob. While filling the blobs, some blobs with area less than 25 pixels are discarded.
10. **Unfilled segments:** The segments for which the holes are not filled and the blobs less than 25 pixels are not discarded are unfilled segments.
11. **Filled Segments:** The segments for which the holes are filled and the blobs less than 25 pixels are discarded are filled segments.
12. **Largest Blob:** The blob with largest area in a segment is known as largest blob.

3. DATA SEGMENTATION

There are three data sets one with 888 images, a subset of this set with 837 images and disjoint test set with 78 images.

The original Image is segmented to a median split image having 4 segments based on the median split algorithm. The code is written in such a way that the darkest color measured using intensity is segmented as first segment and then the brighter ones, in order of intensity. The brightest color is segmented as the last segment. As described later, 12 features called the lesion features are extracted from lesion as a whole and 49 features called the segment features are extracted from each of the four segments, for a total of 208 features. The following are the four segments for a median split Image.

Figure 3.1 describes the original image, Figure 3.2 describes the border image that splits lesion and skin part. Figure 3.3 describes the median split image. Figure 3.4 to 3.7 describes about each segment from darkest color to brightest color.



Figure 3.1 Original Image



Figure 3.2 Border Image that splits the lesion and skin part



Figure 3.3 Median Split Image using median split algorithm



Figure 3.4 Segment 1 (Darkest color segment)



Figure 3.5 Segment 2 (2nd darkest color segment)



Figure 3.6 Segment 3 (3rd darkest color segment)



Figure 3.7 Segment 4 (brightest color segment)

4. FEATURE EXTRACTION FOR FULL MODEL

4.1 LESION FEATURES

The features that are obtained for the whole lesion are lesion features. There are a total of 12 lesion features. Listed below are the lesion features.

1. Ring Value.

Ring Value

$$= \frac{\text{highest number pixels of the segment present within the border of the lesion}}{\text{Total Number of Pixels in the border of the lesion}}$$

The ratio of number of pixels of each segment that are present in the peripheral ring/lesion border to the total number of pixels in the peripheral ring/lesion border is calculated. This value is measured for all the four segments and the highest of them is considered as the Ring Value.

2. Maximum Color Segment in the Ring.

The segment which has the highest ring value is considered as the Maximum Color Segment in the Ring. This is represented by the segment number 1, 2, 3, or 4.

3. Is Last Color Maximum in the Peripheral Ring.

This gives us the data whether or not the last or the brightest color has the maximum ring value. If the last or the brightest color has the maximum ring value, then it is represented as 1 or else it is represented as 0.

4. Total Area. Total number of pixels that are present in the whole lesion

5. **Centroid(X-axis).** X-coordinate of the centroid of whole lesion.
6. **Centroid(Y-axis).** Y-coordinate of the centroid of whole lesion.
7. **Standard deviation of centroid (X-axis).** Standard deviation of the X-coordinate of the centroid. **Standard deviation** is obtained by square-root of sum of squared differences between lesion pixel and its centroid divided by number of pixels in the segment.
8. **Standard deviation of centroid (Y-axis).** Standard deviation of the Y-coordinate of the centroid. **Standard deviation** is obtained by square-root of sum of squared differences between lesion pixel and its centroid divided by number of pixels in the segment.
9. **Average R Value of Skin.** Average Red color value of skin is calculated.
10. **Average G Value of Skin.** Average Green color value of skin is calculated.
11. **Average B Value of Skin.** Average Blue color value of skin is calculated.
12. **Background Skin Luminance.** Average luminance of the skin is calculated.

$$\text{Luminance} = 0.3 *(\text{R value}) + (0.59* \text{G value}) + (0.11*\text{B value}) [1]$$

4.2 SEGMENT FEATURES

The features that are obtained for each segment in the median split image are segment features. There are a total of four segments. The first segment obtained is always the darkest segment by intensity and the last segment is the brightest segment. Intensity gives measure of strength of the color.

There is concept here called filling of blobs. A segment is considered and the small holes are filled for the blob. After filling the blobs, small blobs that are less than 25 pixels in area are removed. This segment is called a **filled segment**. The segment that was obtained as it was in the Median split image is considered as an **unfilled segment**. Figure 4.1a and 4.1c shows the difference between unfilled and filled segment. The blob which has largest area is considered as the **Largest Blob**. Figure 4.1b and 4.1d shows the largest blob of an image.

This is clearly shown in the figure below [1]:

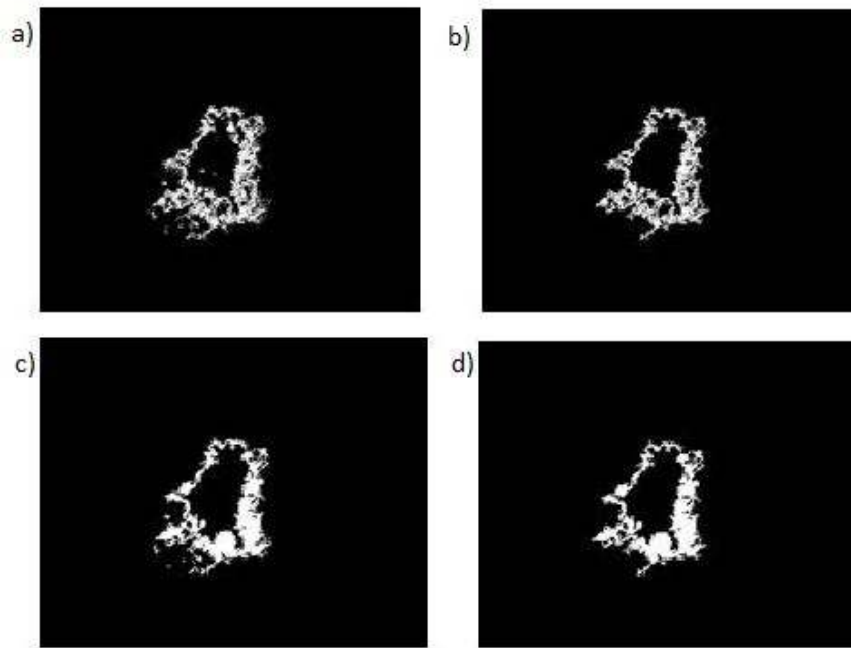


Figure 4.1 a) Unfilled Segment ,b) Largest unfilled blob, c) Filled Segment, d) Largest filled blob.

The other concept is Intensity Drop. The perimeter of a segment is considered and another perimeter is drawn exactly one pixel wide just outside the original perimeter. The difference in average intensity in the one-pixel wide perimeter to the original perimeter of the image is considered as the **Intensity Drop**.

There is a difference in the terms perimeter and external perimeter. Perimeter means the internal and external perimeter of an image, whereas external perimeter gives perimeter of only outer part of the image. This is explained in the figures below.

Figure 4.2 is the perimeter of the segment and Figure 4.3 is the external perimeter of the segment.

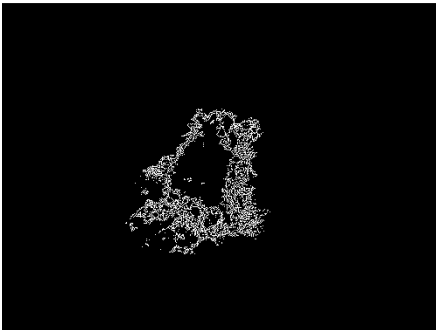


Figure 4.2 Perimeter of the Segment

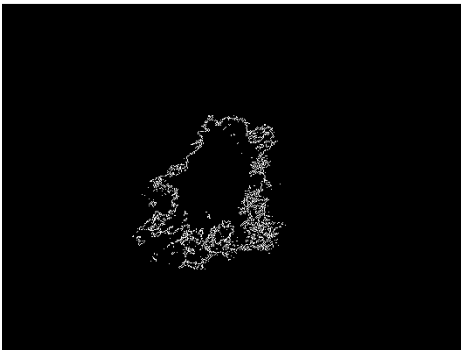


Figure 4.3 External Perimeter of the Segment

Each segment has 49 features. Listed below are the segment features and their definitions.

1. Segment Value in the Ring.

Segment Value in Ring

$$= \frac{\text{common area of the particular segment present within the border of the lesion}}{\text{Total Number of Pixels in the border of the lesion}}$$

The ratio of number of pixels of the particular segment that are present in the peripheral ring/lesion border to the total number of pixels in the peripheral ring/lesion border is calculated as the Segment Value in the Ring.

2. **Average Red Value.** Average red value of the segment is calculated in the segment.
3. **Average Green Value.** Average green value of the segment is calculated in the segment.
4. **Average Blue Value.** Average blue value of the segment is calculated in the segment.
5. **Number of Blobs before Filling.** This feature gives the number of blobs present in the unfilled segment.
6. **Number of Blobs after Filling.** This feature gives the number of blobs present in the filled segment.
7. **Area of the Segment before Filling.** The total number of pixels in an unfilled segment is the Area of Segment before Filling.
8. **Area of Largest Blob before Filling.** The total number of pixels in the largest blob of an unfilled segment is the Area of Largest Blob before Filling
9. **Area of the Segment after Filling.** The total number of pixels in a filled segment is the Area of Segment before Filling.

- 10. Area of Largest Blob after Filling.** The total number of pixels in the largest blob of an filled segment is the Area of Largest Blob after Filling
- 11. Perimeter of Segment before Filling.** The internal and external perimeter of the unfilled segment is calculated. This is nothing but the number of pixels on the border of the unfilled segment.
- 12. Perimeter of Largest Blob before Filling.** The internal and external perimeter of the largest blob of an unfilled segment is calculated. This is nothing but the number of pixels on the border of the largest blob of an unfilled segment.
- 13. Perimeter of Segment after Filling.** The internal and external perimeter of the filled segment is calculated. This is nothing but the number of pixels on the border of the filled segment.
- 14. Perimeter of Largest Blob after Filling.** The internal and external perimeter of the largest blob of a filled segment is calculated. This is nothing but the number of pixels on the border of the largest blob of a filled segment.
- 15. Normalized Perimeter of Segment before Filling.** The perimeter of segment before filling is normalized by dividing it by the square root of the whole lesion area.
- 16. Normalized Perimeter of Largest Blob before Filling.** The perimeter of largest blob before filling is normalized by dividing it by the square root of the whole lesion area.
- 17. Normalized Perimeter of Segment after Filling.** The perimeter of segment after filling is normalized by dividing it with the square root of the whole lesion area.

- 18. Normalized Perimeter of Largest Blob after Filling.** The perimeter of largest blob after filling is normalized by dividing it with the square root of the whole lesion area.
- 19. Intensity Drop of Segment Perimeter before Filling.** The perimeter of a segment before filling is considered and another perimeter is drawn exactly one pixel wide outside. The difference of average intensity in the one-pixel wide perimeter to that of the perimeter of the segment is the **Intensity Drop of Segment Perimeter before Filling.**
- 20. Intensity Drop of Largest Blob Perimeter before Filling.** The perimeter of a largest blob before filling is considered and another perimeter is drawn exactly one pixel wide outside. The difference of average intensity in the one-pixel wide perimeter to that of the perimeter of the largest blob is the **Intensity drop of largest blob Perimeter before filling.**
- 21. Intensity Drop of Segment Perimeter after Filling.** The perimeter of a segment after filling is considered and another perimeter is drawn exactly one pixel wide outside. The difference of average intensity in the one-pixel wide perimeter to that of the perimeter of the segment is the **Intensity Drop of Segment Perimeter after Filling.**
- 22. Intensity Drop of Largest Blob Perimeter after Filling.** The perimeter of a largest blob after filling is considered and another perimeter is drawn exactly one pixel wide outside. The difference of average intensity in the one-pixel wide perimeter to that of the perimeter of the segment is considered as the **Intensity Drop of Largest Blob Perimeter after Filling.**

- 23. External Perimeter of Segment before Filling.** The external perimeter of the unfilled segment is calculated. This is nothing but the number of pixels on the external border of the unfilled segment.
- 24. External Perimeter of Largest Blob before Filling.** The external perimeter of the largest blob of an unfilled segment is calculated. This is nothing but the number of pixels on the external border of the largest blob of an unfilled segment.
- 25. External Perimeter of Segment after Filling.** The external perimeter of the filled segment is calculated. This is nothing but the number of pixels on the external border of the filled segment.
- 26. External Perimeter of Largest Blob after Filling.** The external perimeter of the largest blob of a filled segment is calculated. This is nothing but the number of pixels on the external border of the largest blob of a filled segment.
- 27. Normalized External Perimeter of Segment before Filling.** The external perimeter of segment before filling is normalized by dividing it with the square root of the whole lesion area.
- 28. Normalized External Perimeter of Largest Blob before Filling.** The external perimeter of largest blob before filling is normalized by dividing it with the square root of the whole lesion area.
- 29. Normalized External Perimeter of Segment after Filling.** The external perimeter of segment after filling is normalized by dividing it by the square root of the whole lesion area.

- 30. Normalized External Perimeter of Largest Blob after Filling.** The external perimeter of largest blob after filling is normalized by dividing it by the square root of the whole lesion area.
- 31. Intensity Drop of Segment External Perimeter before Filling.** The external perimeter of a segment before filling is considered and another perimeter is drawn exactly one pixel wide outside. The difference of average intensity in the one-pixel wide perimeter to the perimeter of the segment is considered as the **Intensity Drop of Segment External Perimeter before Filling.**
- 32. Intensity Drop of Largest Blob External Perimeter before Filling.** The external perimeter of a largest blob before filling is considered and another perimeter is drawn exactly one pixel wide outside. The difference of average intensity in the one-pixel wide perimeter to the perimeter of the segment is the **Intensity Drop of Largest Blob External Perimeter before Filling.**
- 33. Intensity Drop of Segment External Perimeter after Filling.** The external perimeter of a segment after filling is considered and another perimeter is drawn exactly one pixel wide outside. The difference of average intensity in the one-pixel wide perimeter to the perimeter of the segment is the **Intensity Drop of Segment External Perimeter after Filling.**
- 34. Intensity Drop of Largest Blob External Perimeter after Filling.** The external perimeter of a largest blob after filling is considered and another perimeter is drawn exactly one pixel wide outside. The difference of average intensity in the one-pixel wide perimeter to the perimeter of the segment is the **Intensity Drop of Largest Blob External Perimeter after Filling.**

- 35. Centroid X-axis of Segment.** X-coordinate of the centroid of segment.
- 36. Centroid Y-axis of Segment.** Y-coordinate of the centroid of segment.
- 37. Standard Deviation of Centroid X-axis of Segment.** Standard deviation of x-coordinate of the centroid of the segment. **Standard deviation** is obtained by square-root of sum of squared differences between lesion pixel and its centroid divided by number of pixels in the segment.
- 38. Standard Deviation of Centroid Y-axis of Segment.** Standard deviation of y-coordinate of the centroid of the segment. **Standard deviation** is obtained by square-root of sum of squared differences between lesion pixel and its centroid divided by number of pixels in the segment.
- 39. Euclidean Distance of the Segment Centroid from Lesion Centroid.** This is the distance between the centroid of the lesion and the centroid of the segment. If (x_1, y_1) is the segment centroid and (x, y) is the lesion centroid, then

$$\text{Euclidean distance} = \sqrt{(x - x_1)^2 + (y - y_1)^2}$$

- 40. Normalized Euclidean Distance of the Segment Centroid from Lesion Centroid.** Euclidean distance of the segment is normalized by dividing it by square root of total lesion area.
- 41. Absolute Luminance of the Segment.** The average Absolute Luminance of the Segment is calculated using R, G, B color values.

$$\text{Absolute Luminance of the segment} = (0.3 * R) + (0.59 * G) + (0.11 * B).$$

42. Relative Luminance of the Segment. The Relative Luminance of the Segment is calculated which is the difference between average absolute luminance of the segment and average background luminance of the skin.

$$\text{Relative Luminance} = \text{Absolute Luminance} - \text{Skin Luminance.}$$

43. Relative R Value of the Segment. The relative R value of the segment is calculated which is the difference between average segment R value and the average skin R value.

$$\text{Relative R color} = \text{Average R of the segment} - \text{Average R of the skin.}$$

44. Relative G Value of the Segment. The relative G value of the segment is calculated which is the difference between average segment G value and average skin G value.

$$\text{Relative G color} = \text{Average G of the segment} - \text{Average G of the skin.}$$

45. Relative B Value of the Segment. The relative B value of the segment is calculated which is the difference between average segment B value and average skin B value.

$$\text{Relative B color} = \text{Average B of the segment} - \text{Average B of the skin.}$$

46. Average Distance of All Pixels of the Segment from Lesion Centroid. The distance of all pixels from the segment to the lesion centroid is calculated and averaged to determine the Average distance of all pixels of the segment from Lesion Centroid.

47. Red Chromaticity of the Segment. This calculates the average Red chromaticity of a given segment using the original image R value using the formula $R_{ch} = \frac{R}{R+G+B}$

48. Variance of Red Chromaticity of the Segment. The average of squared difference from the mean of red chromaticity is Variance of Red Chromaticity. The var function can be used in Matlab to find this value.

49. Standard Deviation of Red Chromaticity of the Segment. The square root of the variance of red chromaticity gives us the standard deviation of red chromaticity [1].

5. ALGORITHM DESIGNED FOR FINDING THESE FEATURE

The program for finding the features is written in Matlab. First, the original image, the median split image and the border image are selected as the inputs. Then the Lesion features for the whole lesion are found. The image is reshaped into a single column and the number of colors in the median split image are found. There is a loop which runs four times, once for each color. These colors are sorted based on their intensity in ascending order, which means the darkest color comes out first.

The median split image is segmented into four images each with one color and finds all the segment features of that median split image. All these features are consolidated and loaded into a spreadsheet. Forward step-wise logistic regression implemented in SAS is used to find the important features and efficiency of the data obtained.

6. ROBUST MODEL

The more robust model is one in which the features of the image are scale and rotation invariant. It means the features should not change depending on how the image is captured by the camera.

For this, there were some features that were eliminated. Eliminating the features might decrease the c value of this model but it is the best model that can be suggested.

6.1 ADDITIONAL FEATURES FOR ROBUST MODEL

Area of the segment is replaced by **Normalized area of the segment**. Area of the segment is normalized by dividing it by total lesion area which gives **Normalized area of the segment**.

Average distance of all pixels in a segment from lesion centroid is replaced by **Normalized average distance of all pixels in a segment from lesion centroid**. This is done by dividing **Average distance of all pixels in a segment from lesion centroid** by square root of total lesion area to obtain **Normalized average distance of all pixels in a segment from lesion centroid**.

6.1.1 Newly Added Features.

1. **Green Chromaticity of the Segment.** This calculates the average green chromaticity

of a given segment using the original image G value using the formula $G_{ch} = \frac{G}{R+G+B}$

2. **Variance of Green Chromaticity of the Segment.** The average of the squared difference from the mean of green chromaticity is Variance of Green Chromaticity. The var function can be used in Matlab to find this value.
3. **Standard Deviation of Green Chromaticity of the Segment.** The square root of variance gives us the standard deviation of green chromaticity.
4. **Blue Chromaticity of the Segment.** This calculates the average blue chromaticity of a given segment using the original image B value using the formula $B_{ch} = \frac{B}{R+G+B}$
5. **Variance of Blue Chromaticity of the Segment.** The average of the squared difference from the mean of blue chromaticity is Variance of Blue Chromaticity. The var function can be used in Matlab to find this value.
6. **Standard Deviation of Blue chromaticity of the Segment.** The square root of variance gives us the standard deviation of blue chromaticity.
7. **Major Axis Length.** The major axis length of the segment is calculated. This can be done using regionprops in Matlab
8. **Minor Axis Length.** The minor axis length of the segment is calculated. This can be done using regionprops in Matlab
9. **Elongation.** Elongation for each segment is calculated using the below formulae.

$$\text{Elongation} = \frac{\text{Minor Axis Length}}{\text{Major Axis Length}}$$

6.2 FILTERING FULL MODEL INTO ROBUST MODEL

Firstly, the model with all the features except the scale and rotation variant features and adding the above new features is found for the 837 image data set. This decreases the number of features from 208 to 156.

This data is run into forward step-wise logistic regression in SAS.

The SAS returns the list file which has odd ratio estimates that gives the information about the important features and the value of each feature determines its importance.

Depending on these values, the number of features from 156 to 45 are filtered.

Of the above discussed features, here are the features of that include the robust model.

6.3 LESION FEATURES IN ROBUST MODEL

These are the remaining Lesion features in our Robust Model

1. Ring Value.
2. Average B Value of the Skin.

6.4 SEGMENT FEATURES IN ROBUST MODEL

There are some features that are deleted, some features that are replaced by other features and some added features to get the robust model.

6.4.1 1st Segment Features in the Robust Model.

1. Segment value in the ring.

2. Normalized Area of the segment before filling.
3. Intensity drop of segment perimeter after filling.
4. Intensity drop of largest blob perimeter after filling.
5. Relative Luminance of the segment.

6.4.2 2nd Segment Features in the Robust Model.

1. Average Red Value.
2. Number of blobs after filling.
3. Normalized Perimeter of segment before filling.
4. Normalized Perimeter of segment after filling.
5. Intensity drop of segment perimeter before filling.
6. Intensity drop of largest blob perimeter before filling.
7. Intensity drop of segment perimeter after filling.
8. Intensity drop of largest blob perimeter after filling.
9. Normalized Euclidean distance of the segment.
10. Normalized average distance of all pixels of the segment from the lesion centroid.
11. Variance of red chromaticity of the segment.
12. Minor Axis Length.
13. Elongation.

6.4.3 3rd Segment Features in the Robust Model.

1. Normalized Area of the segment before filling.
2. Normalized Area of largest blob before filling.
3. Normalized Perimeter of segment before filling.
4. Normalized Perimeter of largest blob before filling.
5. Intensity drop of segment perimeter before filling.
6. Normalized Euclidean distance of the segment.
7. Normalized average distance of all pixels in a segment from the lesion centroid.
8. Standard deviation of red chromaticity of the segment.
9. Variance of green chromaticity of the segment.
10. Standard deviation of green chromaticity of the segment.

6.4.4 4th Segment Features in the Robust Model.

1. Segment value in the ring.
2. Average Blue Value.
3. Number of blobs after filling.
4. Normalized area of largest blob after filling.
5. Normalized Perimeter of the segment before filling.
6. Normalized Perimeter of largest blob before filling.

7. Normalized Perimeter of the segment after filling.
8. Intensity drop of the segment perimeter before filling.
9. Intensity drop of the segment perimeter after filling.
10. Normalized Euclidean distance of the segment.
11. Normalized average distance of all pixels of the segment from lesion centroid.
12. Variance of red chromaticity of the segment.
13. Standard deviation of red chromaticity of the segment.
14. Variance of blue chromaticity of the segment.
15. Elongation.

These features are found for both the 837 image data set and 78 images data set.

7. SAS AND FEATURE SELECTION PROCESS

The features of the Full and Robust models are consolidated in separate spread sheets. These spreadsheets are run through forward stepwise logistic regression as implemented in SAS to find the significant features and to build our models.

7.1 FEATURE SELECTION

SAS means Statistical Analysis System, software from SAS institute to perform data warehousing, statistical analysis and data mining, applications development many other operations [4]. SAS is used especially to find statistical analyses of large amounts of data. For our project, SAS implements forward stepwise logistic regression which helps us in finding the significant features and model building.

There are two main variables that determine significance level in SAS which can be modified on our requirement before running it. They are.

1. SLENTY.
2. SLSTAY.

SLENTY determines the minimum value of p-value required for a feature to be included in the model. It can have values like 0.05, 0.1, 0.2, 0.3, 0.4, and 0.5.

SLSTAY determines the consistent level of p-value that the feature must have to stay in the model. It can have values like 0.05, 0.1, 0.2, 0.3, 0.4, and 0.5.

SLENTY=SLSTAY=0.5 produces the model with best diagnostic accuracy when there is a model with large number of features. In this project, the results between SLENTY=SLSTAY=0.1 and SLENTY=SLSTAY=0.5 are compared to get information on the behavior of our model.

After setting these variables, spreadsheet is run through SAS to implement forward stepwise logistic regression and it gives us a list file which contains all significant features for classifying melanoma v/s non-melanoma, sensitivity and specificity of each image, etc using which the model can be built.

Significant features are those that help significantly in the differentiation process which is used to analyze the data [4].

7.2 LOGISTIC REGRESSION

This stepwise logistic regression model allows us to determine if a specific feature is significant. This resulting model can be used to predict the probability of occurrence of an event by fitting data to a logistic function $[f(z)]$.

The logistic function, $f(z) = \frac{e^z}{e^z+1} = \frac{1}{1+e^{-z}}$, where $z = \beta_0 + \beta_1x_1 + \beta_2x_2 + \dots + \beta_kx_k$

β_0 is called as intercept and $\beta_1, \beta_2, \beta_3, \dots, \beta_k$ are the regression coefficients for the features $x_1, x_2, x_3, x_4, \dots, x_k$ respectively. $f(z)$ gives the probability of outcome of any event. z is the measure of total contribution of all independent variables used in the model.

The SAS output list file has a section named “Analysis of Maximum Likelihood estimates” which gives us the values for β and x . The above coefficients $\beta_0, \beta_1, \beta_2, \beta_3, \dots, \beta_k$ represents the size of contribution of each particular feature. On the basis of significance

levels in the estimate (current model), logistic regression gets applied with significant columns (features). Depending on the above information, the lesions are classified into benign and melanoma as follows.

Let us suppose some threshold value as 'a'. So the lesions with $f(z) < a$ are classified as benign and the lesions with $f(z) > a$ are classified as melanomas. These classifications are compared with clinical diagnoses for benign lesions and a dermatopathologist's diagnoses for melanoma lesions [5].

7.3 ODDS RATIO ESTIMATES

The odds ratio takes on values in between zero ('0') and infinity. The neutral value is one ('1') which means that there is no difference between groups compared. If a group is close to zero or infinity, it means that there is a very large difference. If a group one has a larger proportion than group two, it means that odds ratio is larger than one. The odds ratio will take its inverse if the two proportions are swapped.

These odd ratios can be compared with Risk ratio that are easier to interpret compared to odds ratio. Generally, odd ratios are used more often. The odds ratio is more closely related to statistical technique such as logistic regression. The attractive property with odds ratio is that however the table is rotated, it always takes either same or inverse (1/odds) of that value.

In our research project, the list file gives odd ratio information of the important features that are found. If the value of the odds ratio is near to one ('1'), it means the feature is not so important. If the value of odd ratio is far smaller or larger than one ('1'), then that feature is considered to be important.

8. RESULTS

There are three data sets in the project. The 888 set will be used to compare K-means segmentation [5] with median-split segmentation. Two models, a full model and a smaller robust model will be developed using the 837 set. Classification results on the 837 set will be reported to both models. These same two models will be then applied to the test set of 78 images and results will be reported.

Thus, the following things will be done

1. Comparing K-means splitting algorithm and Median Split Algorithm on 888 images.
2. Comparing 837 images with the full model and Robust model.
3. Using the full model on test set of 78 images.
4. Using the robust model on test set of 78 images.
5. Comparing ROC curve for 78 images with full model and robust model.

The consolidated data for a given set is input into SAS which returns a list file containing a table with estimate of correct melanomas and non-melanomas. The stepwise logistic regression gives us the significant features list, sensitivity and specificity information, and c value. These significant features also include some of the lesion and segment features. Segment features are listed from darkest color to the brightest. The value returned for these features determines their significance.

8.1 COMPARING K-MEANS SPLITTING ALGORITHM AND MEDIAN SPLIT ALGORITHM ON 888 IMAGES

8.1.1 Significant Features. Stepwise logistic regression returns 90 significant features with SLENTY=SLSTAY=0.5 for splitting the lesion using the K means algorithm whereas it returns 122 significant features using the median split algorithm. Stepwise logistic regression returns 21 significant features with SLENTY=SLSTAY=0.1 using the K means algorithm and 19 significant features using median split algorithm.

These are listed below.

8.1.1.1 K-means with SLENTY=SLSTAY=0.5.

8.1.1.1.1 Significant lesion features.

1. Ring value
2. Maximum segment in peripheral ring
3. Last segment in peripheral ring

8.1.1.1.2 Significant 1st segment (darkest color) features.

1. Segment value in the ring
2. Number of blobs in the segment before filling
3. Area of the segment before filling
4. Area of the segment after filling
5. Area of the largest blob before filling
6. Area of the largest blob after filling
7. Normalized perimeter of segment before filling
8. Normalized perimeter of largest blob after filling
9. Intensity drop of the perimeter of segment before filling

10. Intensity drop of the perimeter of segment after filling
11. Intensity drop of the perimeter of largest blob after filling
12. Normalized Intensity drop of the perimeter of segment before filling
13. Normalized Intensity drop of the perimeter of segment after filling
14. Normalized Intensity drop of the perimeter of largest blob after filling
15. Average skin R value
16. Average skin G value
17. Average distance of the pixels
18. Average red chromaticity of the segment
19. Variance of average red chromaticity of the segment
20. Standard deviation of red chromaticity of the segment.

8.1.1.1.3 Significant 2nd segment features.

1. Segment value in the ring
2. Average Red value of the segment
3. Number of blobs before filling
4. Number of blobs after filling
5. Perimeter of largest blob in the segment before filling
6. Normalized perimeter of the segment before filling
7. Normalized perimeter of largest blob in the segment before filling
8. Intensity drop of perimeter of the segment before filling
9. Intensity drop of perimeter of the segment after filling
10. Intensity drop of perimeter of the largest blob before filling
11. Normalized intensity drop of perimeter of the segment before filling
12. External perimeter of the segment after filling

13. External perimeter of the largest blob of the segment after filling.
14. Normalized external perimeter of the segment after filling.
15. Normalized external perimeter of largest blob in segment before filling
16. Normalized external perimeter of largest blob in segment after filling
17. Intensity drop of perimeter of the segment before filling
18. Intensity drop of external perimeter of the largest blob before filling
19. Normalized Intensity drop of perimeter of the segment after filling
20. Euclidean distance of the segment centroid from the lesion centroid
21. Average distance of the segment for all pixels from lesion centroid
22. Average red chromaticity of the segment

8.1.1.1.4 Significant 3rd segment features.

1. Segment value in the ring
2. Number of blobs in the segment before filling
3. Area of segment before filling
4. Area of largest blob in segment before filling
5. Perimeter of segment before filling
6. Perimeter of segment after filling
7. Perimeter of largest blob in segment before filling
8. Perimeter of largest blob in segment after filling
9. Normalized perimeter of largest blob in segment after filling
10. Intensity drop of the perimeter of the segment before filling
11. Intensity drop of the perimeter of the largest blob in the segment before filling
12. External perimeter of the segment before filling
13. External perimeter of the largest blob in segment before filling

14. External perimeter of the largest blob in segment after filling
15. Intensity drop of the external perimeter of the segment after filling
16. Intensity drop of the external perimeter of the largest blob of segment after filling
17. Euclidean distance of the segment centroid from the lesion centroid
18. Normalized Euclidean distance of the segment centroid from the lesion centroid
19. Absolute Luminance of the segment
20. Standard deviation of red chromaticity of segment

8.1.1.1.5 Significant 4th segment (brightest color) features.

1. Percentage of segment in the peripheral ring
2. Average green value of the segment
3. Number of blobs in the segment before filling
4. Number of blobs in the segment after filling
5. Area of the segment after filling
6. Area of the largest blob in the segment after filling
7. Perimeter of the segment before filling
8. Normalized perimeter of the largest blob in the segment before filling
9. Intensity drop of the perimeter of largest blob in segment before filling
10. Intensity drop of the perimeter of largest blob in segment after filling
11. Normalized intensity drop of the perimeter of segment before filling
12. Normalized intensity drop of the perimeter of segment after filling
13. External perimeter of the segment before filling
14. External perimeter of the segment after filling
15. Normalized external perimeter of the segment before filling
16. Normalized external perimeter of the segment after filling

17. Normalized external perimeter of the largest blob in the segment before filling
18. Normalized external perimeter of the largest blob in the segment after filling
19. Intensity drop of external perimeter of the segment before filling
20. Intensity drop of external perimeter of largest blob in the segment before filling
21. Normalized intensity drop of external perimeter of the segment before filling
22. X- axis Centroid of the segment
23. Y- axis Centroid of the segment
24. Average distance of all pixels in the segment from lesion centroid
25. Average red chromaticity of the segment [5].

8.1.1.2 Median split algorithm with SLENTRY=SLSTAY=0.5.

8.1.1.2.1 Significant lesion features.

1. Total Area
2. Centroid (X axis)
3. Centroid (Y axis)

8.1.1.2.2 Significant 1st segment (darkest color) features.

1. Standard deviation of red chromaticity of the segment
2. Variance of Red chromaticity of the segment
3. Average G value of the skin
4. Normalized perimeter of the segment after filling
5. Average distance of all the Pixels of the segment from lesion centroid
6. Centroid Y-axis of segment
7. Normalized intensity drop of largest blob perimeter after filling
8. Normalized intensity drop of largest blob perimeter before filling

9. Normalized perimeter of the segment before filling
10. Centroid X-axis of segment
11. Intensity drop of largest blob perimeter after filling
12. Normalized perimeter of largest blob before filling
13. Normalized Intensity drop of segment perimeter after filling
14. Perimeter of largest blob after filling
15. Area of largest blob of the segment after filling
16. Perimeter of the segment before filling
17. Area of largest blob before filling
18. Average R value of skin
19. Normalized perimeter of largest blob after filling
20. Perimeter of largest blob after filling
21. Number of blobs before filling
22. Area of the segment before filling
23. Number of blobs after filling
24. Segment value in the ring
25. Normalized Euclidean distance from segment centroid to lesion centroid
26. Euclidean distance from segment centroid to lesion centroid
27. Perimeter of the segment after filling

8.1.1.2.3 Significant 2nd segment features.

1. Variance of Red chromaticity of the segment
2. Standard deviation of red chromaticity of the segment
3. Intensity drop of largest blob perimeter before filling
4. Intensity drop of external segment perimeter before filling

5. Normalized Euclidean distance from segment centroid to lesion centroid
6. Normalized intensity drop of largest blob perimeter after filling
7. Normalized Intensity drop of largest blob perimeter after filling
8. Intensity drop of largest blob perimeter before filling
9. Average Green Value
10. Intensity drop of largest blob perimeter before filling
11. Normalized intensity drop of largest blob perimeter before filling
12. Normalized intensity drop of segment perimeter before filling
13. Perimeter of largest blob after filling
14. Area of Largest blob after filling
15. Normalized intensity drop of largest blob perimeter before filling
16. Area of segment before filling
17. Area of segment after filling
18. Normalized intensity drop of external perimeter of segment after filling
19. Perimeter of largest blob before filling
20. Area of largest blob before filling
21. Normalized external perimeter of segment after filling
22. Average Red value
23. Number of blobs after filling
24. Normalized perimeter of segment before filling
25. Perimeter of the segment before filling
26. Normalized external perimeter of segment before filling
27. Normalized intensity drop of external perimeter of largest blob after filling
28. External perimeter of segment before filling
29. Centroid X axis of the segment

30. Area of largest blob of segment before filling
31. Normalized intensity drop of external perimeter of largest blob after filling
32. Intensity drop of external perimeter of largest blob after filling
33. Normalized perimeter of largest blob before filling
34. Euclidean distance from segment centroid to lesion centroid
35. External perimeter of largest blob before filling

8.1.1.2.4 Significant 3rd segment features.

1. Segment value in the ring
2. Average Distance of all the Pixels of the segment from Lesion Centroid
3. Area of largest blob before filling
4. Intensity drop of external segment perimeter after filling
5. Intensity drop of largest blob before filling
6. Normalized external perimeter of the segment before filling
7. Red Chromaticity of the segment
8. Centroid Y axis of the segment
9. Intensity drop of segment perimeter after filling
10. Intensity drop of largest blob perimeter before filling
11. Absolute Luminance of the segment
12. Normalized intensity drop of largest blob perimeter before filling
13. Intensity drop of largest blob external perimeter after filling
14. Normalized perimeter of largest blob after filling
15. Perimeter of segment before filling
16. Normalized intensity drop of segment external perimeter before filling
17. Centroid x axis of segment

18. Normalized Euclidean distance from segment centroid to lesion centroid
19. Euclidean distance from segment centroid to lesion centroid
20. Average Blue value
21. Area of the segment after filling
22. External perimeter of segment before filling
23. Perimeter of largest blob before filling
24. Normalized intensity drop of segment external perimeter before filling
25. Normalized intensity drop of largest blob external perimeter after filling

8.1.1.2.5 Significant 4th segment (brightest color) features.

1. Average Distance of all the Pixels of the segment from lesion centroid
2. Intensity drop of segment perimeter before filling
3. Number of blobs after filling
4. Normalized intensity drop of the segment perimeter before filling
5. External perimeter of segment before filling
6. External perimeter of largest blob after filling
7. Normalized perimeter of largest blob before filling
8. Normalized external perimeter of largest blob after filling
9. Normalized external perimeter of largest blob before filling
10. Standard deviation of red chromaticity
11. Normalized Intensity drop of largest blob perimeter before filling
12. Intensity drop of segment perimeter after filling
13. Normalized Intensity drop of segment perimeter after filling
14. Normalized intensity drop of largest blob perimeter before filling
15. Normalized intensity drop of external perimeter of largest blob after filling

16. Intensity drop of largest blob perimeter before filling
17. Area of largest blob before filling
18. Perimeter of segment before filling
19. Segment value in the ring
20. Area of segment after filling
21. Normalized intensity drop of largest blob perimeter after filling
22. Normalized Euclidean distance from segment centroid to lesion centroid
23. Intensity drop of external perimeter of largest blob after filling
24. Intensity drop of external perimeter of largest blob before filling
25. Intensity drop of external perimeter of segment after filling
26. Perimeter of largest blob after filling
27. Average Blue color value of the segment
28. Euclidean distance from segment centroid to lesion centroid
29. Number of blobs before filling
30. Perimeter of the segment after filling
31. External perimeter of segment after filling
32. Normalized external perimeter of segment after filling

8.1.1.3 K-means with SLENTRY=SLSTAY=0.1.

8.1.1.3.1 Significant lesion features.

1. Total Area
2. X-axis centroid of the lesion

8.1.1.3.2 Significant 1st segment (darkest color) features.

1. Average blue color value for the segment

2. Area of the segment before filling
3. Variance of red chromaticity of the segment
4. Standard deviation of red chromaticity of the segment

8.1.1.3.3 Significant 2nd segment features.

1. Percentage of the segment in the peripheral ring
2. Average red color value for the segment.
3. Euclidean distance of the segment centroid from lesion centroid

8.1.1.3.4 Significant 3rd segment features.

1. Segment value in the ring
2. External perimeter of the segment after filling
3. Standard deviation of red chromaticity of the segment

8.1.1.3.5 Significant 4th segment (brightest color) features.

1. Average green color value of the segment
2. Normalized perimeter of the segment after filling
3. Normalized perimeter of largest blob in the segment after filling
4. External perimeter of the segment before filling
5. External perimeter of the segment after filling
6. Normalized intensity drop of external perimeter of the segment before filling
7. Y-axis centroid of the segment
8. Euclidean distance of the segment centroid from lesion centroid
9. Average distance of all pixels of the segment from lesion centroid [5]

8.1.1.4 Median split algorithm with SLENTY=SLSTAY=0.1.**8.1.1.4.1 Significant lesion features.**

1. Ring Value
2. Total Area
3. Centroid (X-axis)

8.1.1.4.2 Significant 1st segment (darkest color) features.

1. Average G value of the skin
2. Normalized perimeter of the segment after filling

8.1.1.4.3 Significant 2nd segment features.

1. Variance of red chromaticity of the segment
2. External perimeter of largest blob after filling
3. Intensity drop of largest blob external perimeter before filling
4. Background luminance of the skin

8.1.1.4.4 Significant 3rd segment features.

1. Segment value in the ring
2. Normalized perimeter of largest blob after filling
3. Centroid X axis of the segment

8.1.1.4.5 Significant 4th segment (brightest color) features.

1. Normalized external perimeter of the segment before filling
2. Average distance of all pixels of the segment from lesion centroid
3. Red chromaticity of the segment
4. Centroid Y axis of the segment
5. Intensity drop of the segment perimeter before filling

6. Number of blobs after filling
7. Normalized Intensity drop of the segment perimeter before filling

8.1.2 Classification Results. The melanoma and benign lesions that are found in the model can be found by sensitivity and specificity percentages. Sensitivity is defined as the number of true positives divided by the number of melanoma lesions. Specificity is defined as the number of true negatives divided by the number of benign lesions. The probability levels along with the specificity and sensitivity for K-means and Median split algorithm with SLENTY=SLSTAY=0.5 and 0.1 are as shown below in the Tables 8.1 to 8.4. Table 8.1 and 8.3 gives the classification results for K-means algorithm and Table 8.2 and 8.4 gives the classification results for median split algorithm.

8.1.2.1 K-means with SLENTY=SLSTAY=0.5.

Table 8.1 Classification results using K-means algorithm with SLENTY=SLSTAY=0.5 for 888 set. [5]

Prob Level	Sensitivity %	Specificity %
0	100	0
0.02	94.9	26.4
0.04	91.8	39.5
0.06	86.2	49.5
0.08	82.6	58
0.1	80	63.8
0.12	76.4	68.5

Table 8.1 Classification results using K-means algorithm with
 SLENTY=SLSTAY=0.5 for 888 set (cont.)

Prob Level	Sensitivity %	Specificity %
0.14	75.4	72
0.16	72.3	75.5
0.18	71.8	77.6
0.2	70.3	79.2
0.22	69.7	81.2
0.24	67.2	82.3
0.26	64.6	83.4
0.28	61.5	84.3
0.3	57.4	85.4
0.32	57.4	86.1
0.34	55.9	86.9
0.36	55.9	87.2
0.38	54.9	87.7
0.4	52.8	88.7
0.42	51.3	89.2
0.44	50.3	89.5
0.46	49.7	89.6
0.48	49.2	89.8
0.5	48.2	90.5
0.52	47.7	91.2

Table 8.1 Classification results using K-means algorithm with
 SLENTY=SLSTAY=0.5 for 888 set (cont.)

Prob Level	Sensitivity %	Specificity %
0.54	46.2	92.1
0.56	45.1	92.2
0.58	45.1	92.9
0.6	43.1	93.7
0.62	41.5	94.1
0.64	41	94.4
0.66	38.5	94.9
0.68	37.4	95.8
0.7	36.4	95.8
0.72	35.9	96.5
0.74	35.4	96.7
0.76	33.3	97
0.78	32.3	97.3
0.8	31.8	97.4
0.82	31.8	97.4
0.84	29.7	97.5
0.86	28.7	98.4
0.88	27.7	99
0.9	26.7	99
0.92	23.6	99

Table 8.1 Classification results using K-means algorithm with SLENTY=SLSTAY=0.5 for 888 set (cont.)

Prob Level	Sensitivity %	Specificity %
0.94	21	99.4
0.96	17.9	99.6
0.98	12.3	99.7
1	0	100

8.1.2.2 Median split algorithm with SLENTY=SLSTAY=0.5.

Table 8.2 Classification results using Median Split Algorithm with SLENTY=SLSTAY=0.5 for 888 set

Prob Level	Sensitivity %	Specificity %
0	100	0
0.02	94.3	43.4
0.04	90.2	53.7
0.06	85.6	61.4
0.08	80.4	66.1
0.1	76.8	69
0.12	75.3	72.3
0.14	74.2	74.5
0.16	71.6	76.2

Table 8.2 Classification results using Median Split Algorithm with
 SLENTY=SLSTAY=0.5 for 888 set(cont.)

Prob Level	Sensitivity %	Specificity %
0.18	69.6	78.4
0.2	68	79.5
0.22	65.5	80.8
0.24	64.4	81.7
0.26	63.4	82.9
0.28	62.9	83.7
0.3	61.3	84.4
0.32	61.3	85
0.34	60.3	85.4
0.36	59.8	85.9
0.38	58.2	86.3
0.4	56.2	86.7
0.42	55.7	87
0.44	54.6	87.8
0.46	52.6	88
0.48	52.6	88.8
0.5	52.1	89.3
0.52	50.5	89.5
0.54	49.5	89.9
0.56	49.5	90.3

Table 8.2 Classification results using Median Split Algorithm with
 SLENTY=SLSTAY=0.5 for 888 set(cont.)

Prob Level	Sensitivity %	Specificity %
0.58	48.5	90.6
0.6	47.4	91.2
0.62	47.4	91.5
0.64	46.9	91.5
0.66	45.4	92.2
0.68	42.8	92.8
0.7	41.2	93.4
0.72	39.7	94.1
0.74	39.2	94.5
0.76	38.7	95.2
0.78	37.6	95.7
0.8	36.6	96
0.82	33.5	96.5
0.84	33	96.5
0.86	33	96.7
0.88	32.5	97
0.9	29.9	97.3
0.92	27.3	97.8
0.94	26.3	98.1
0.96	23.7	98.4

Table 8.2 Classification results using Median Split Algorithm with SLENTY=SLSTAY=0.5 for 888 set(cont.)

Prob Level	Sensitivity %	Specificity %
0.98	19.1	99
1	0	100

8.1.2.3 K-means with SLENTY=SLSTAY=0.1.

Table 8.3 Classification Results using K-means Algorithm with SLENTY=SLSTAY=0.1 for 888 set [5]

Prob Level	Sensitivity %	Specificity %
0	100	0
0.02	99.5	5.6
0.04	96.4	21.9
0.06	93.3	36.4
0.08	91.3	47.6
0.1	87.2	56.9
0.12	83.1	63.9
0.14	80.5	68.3
0.16	77.9	71
0.18	75.9	73.4
0.2	73.3	76.6
0.22	71.8	77.6

Table 8.3 Classification Results using K-means Algorithm with
 SLENTY=SLSTAY=0.1 for 888 set (cont.)

Prob Level	Sensitivity %	Specificity %
0.24	71.3	79.4
0.26	69.2	81.7
0.28	67.7	83.3
0.3	65.6	84.1
0.32	63.6	86.3
0.34	61	88
0.36	58.5	88.2
0.38	56.4	89.6
0.4	53.8	90.5
0.42	52.3	91.5
0.44	50.3	92.2
0.46	48.2	92.8
0.48	47.2	93.4
0.5	45.6	93.5
0.52	44.1	94.4
0.54	41	94.8
0.56	38.5	95.4
0.58	36.4	95.5
0.6	32.8	96.1
0.62	32.3	96.7

Table 8.3 Classification Results using K-means Algorithm with
SLENTY=SLSTAY=0.1 for 888 set (cont.)

Prob Level	Sensitivity %	Specificity %
0.64	29.7	97
0.66	28.7	97.5
0.68	28.7	97.5
0.7	25.6	97.8
0.72	24.6	98.1
0.74	22.1	98.4
0.76	20.5	98.6
0.78	17.4	98.8
0.8	15.9	99
0.82	14.9	99
0.84	13.8	99.1
0.86	10.3	99.4
0.88	8.7	99.4
0.9	6.7	99.9
0.92	5.1	100
0.94	3.1	100
0.96	2.1	100
0.98	1	100
1	0	100

8.1.2.4 Median split algorithm with SLENTY=SLSTAY=0.1.

Table 8.4 Classification Results using Median Split Algorithm with SLENTY=SLSTAY=0.1 for 888 set

Prob Level	Sensitivity %	Specificity %
0	100	0
0.02	100	4.9
0.04	96.4	20.3
0.06	93.8	34.7
0.08	91.2	47.6
0.1	89.6	56.5
0.12	87	63.3
0.14	84.5	69.7
0.16	81.9	73.3
0.18	77.7	76.7
0.2	75.1	79.5
0.22	72	82.9
0.24	70.5	84.1
0.26	69.4	85.4
0.28	66.8	86.3
0.3	64.8	87.3
0.32	63.7	88.5

Table 8.4 Classification Results using Median Split Algorithm with
 SLENTY=SLSTAY=0.1 for 888 set (cont.)

Prob Level	Sensitivity %	Specificity %
0.34	61.1	89.5
0.36	57.5	90.2
0.38	56	90.9
0.4	54.9	91.4
0.42	51.3	92.2
0.44	49.2	93.1
0.46	47.2	93.4
0.48	44.6	93.8
0.5	43.5	94.5
0.52	42.5	94.7
0.54	42	95.4
0.56	39.9	95.7
0.58	38.9	95.8
0.6	37.8	96.3
0.62	35.8	96.7
0.64	35.2	96.8
0.66	33.7	97.1
0.68	32.6	97.3
0.7	30.6	97.8
0.72	28.5	98

Table 8.4 Classification Results using Median Split Algorithm with SLENTY=SLSTAY=0.1 for 888 set (cont.)

Prob Level	Sensitivity %	Specificity %
0.74	26.4	98.3
0.76	24.4	98.6
0.78	22.3	99
0.8	20.2	99
0.82	17.6	99.1
0.84	17.6	99.1
0.86	15.5	99.6
0.88	13	99.6
0.9	11.4	99.6
0.92	9.8	99.6
0.94	5.7	99.6
0.96	4.7	99.6
0.98	2.6	99.9
1	0	100

8.1.3 Receiver Operating Characteristic Curve. The accuracy of the model can be tested by plotting the ROC (receiver operating characteristics) curve. This is a plot of sensitivity v/s 1-specificity. For different SLENTY=SLSTAY, different significant columns are obtained.

The accuracy of the model is calculated by the area under ROC curve. The area under the curve for $SLENTY=SLSTAY=0.5$ and 0.1 are calculated and compared for the K-means and Median split algorithm for 888 set.

8.1.3.1 Comparing ROC curve for median split and K-means algorithm for $SLENTY=SLSTAY=0.5$ for 888 set. The ROC curve for median split algorithm is 0.936 and ROC curve for K-means algorithm is 0.902 with $SLENTY=SLSTAY=0.5$. There are 122 significant features found for median split algorithm and 90 features for k-means algorithm. Figure 8.1 is the ROC curve between sensitivity and 1-specificity comparing median split algorithm and K-means algorithm for 888 set with $SLENTY=SLSTAY=0.5$.

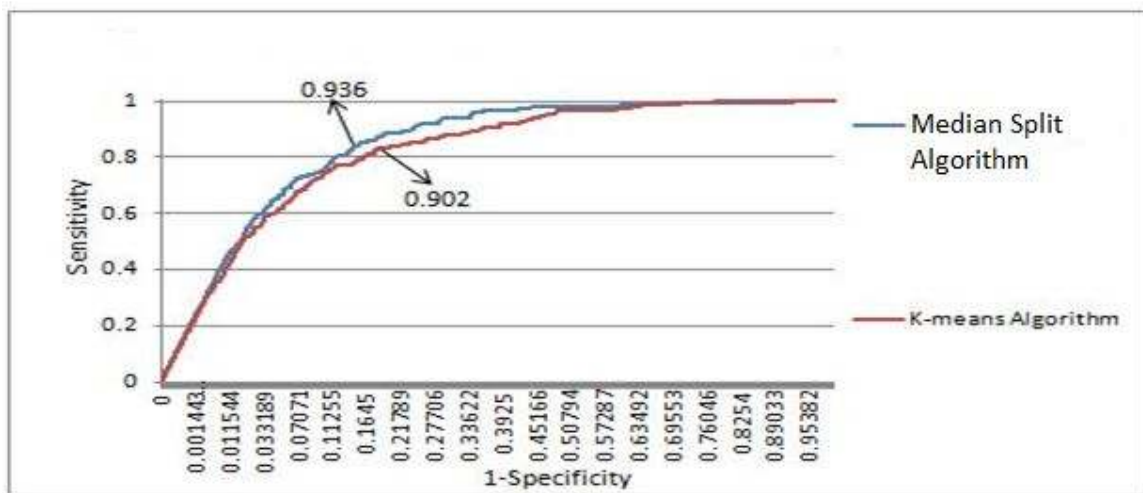


Figure 8.1 Comparing ROC curve for Median Split and K-means algorithm for $SLENTY=SLSTAY=0.5$ for 888 set [5].

8.1.3.2 Comparing ROC curve for median split and K-means algorithm for $SLENTY=SLSTAY=0.1$ for 888 set. The ROC curve for median split algorithm is 0.859 and ROC curve for K-means algorithm is 0.849. There are 19 significant features found for median split algorithm and 21 features for k-means algorithm.

Figure 8.2 is the ROC curve between sensitivity and 1-specificity comparing median split algorithm and K-means algorithm for 888 set with SLENTY=SLSTAY=0.1.

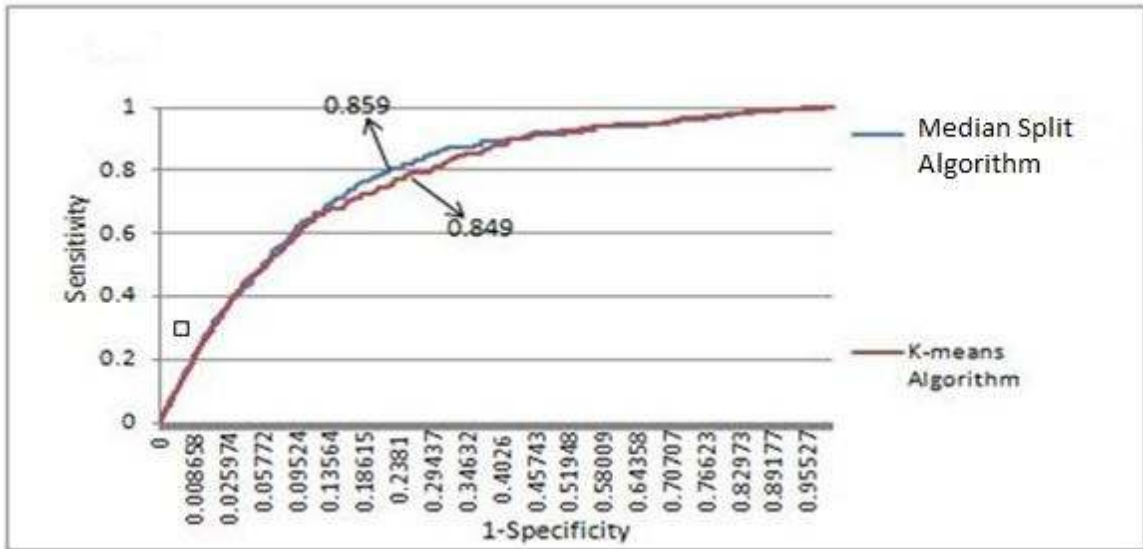


Figure 8.2 Comparing ROC curve for Median Split and K-means algorithm for SLENTY=SLSTAY=0.1 [5]

8.2 COMPARING 837 IMAGES WITH THE FULL MODEL AND ROBUST MODEL

There are some images in the 888 set which are not of high quality; hence those images are eliminated from the 888 set. The resulting 837 image set is considered from this part of our research.

The full model set has 208 features, of which some features are not scale invariant and rotation invariant which means the feature value depends on how the photo was taken.

The robust model is obtained after eliminating the features that are not scale invariant, rotation invariant and the non-significant features according to odds ratio estimates has 45 features.

8.2.1 Significant Features. For the full model, step-wise logistic regression returns 87 significant features out of 208 features with SLENTY=SLSTAY=0.5 for splitting the lesion using median split Algorithm. For Robust model, stepwise logistic regression returns 36 significant features out of 45 features with SLENTY=SLSTAY=0.5 for splitting the lesion using median split algorithm.

The important features for both are as listed below.

8.2.1.1 Full model.

8.2.1.1.1 Significant lesion features.

1. Total Area
2. Average G value of the skin.
3. Ring Value
4. Average R value of the skin.

8.2.1.1.2 Significant 1st segment (darkest color) features.

1. Standard deviation of red chromaticity of the segment
2. Variance of red chromaticity of the segment
3. Relative R value of the segment.
4. Segment value in the ring
5. Standard deviation of centroid X-axis of segment
6. Intensity drop of the largest blob perimeter after filling
7. Normalized perimeter of the segment after filling
8. Intensity drop of the segment perimeter before filling
9. Intensity drop of the segment perimeter after filling
10. Segment value in the ring

11. Centroid Y axis of the segment
12. Normalized Euclidean distance of the segment centroid to lesion centroid
13. Euclidean distance of the segment centroid to lesion centroid

8.2.1.1.3 Significant 2nd segment features.

1. Variance of red chromaticity of the segment
2. Number of blobs after filling
3. Euclidean distance of the segment centroid to lesion centroid
4. Intensity drop of segment perimeter before filling
5. Intensity drop of segment perimeter after filling
6. Number of blobs after filling
7. Normalized Euclidean distance of the segment centroid to lesion centroid
8. Centroid Y-axis of the segment
9. External perimeter of the segment before filling
10. Average Red value
11. Number of blobs before filling
12. Standard deviation of centroid X axis of segment
13. Average distance of all the pixels of the segment from lesion centroid
14. Standard deviation of centroid Y axis of segment
15. Intensity drop of segment external perimeter before filling
16. External perimeter of largest blob after filling
17. Perimeter of largest blob after filling
18. Segment value in the ring
19. Intensity drop of segment external perimeter after filling

8.2.1.1.4 Significant 3rd segment features.

1. Relative R value of the segment.
2. Perimeter of segment after filling
3. Standard deviation of centroid X-axis of segment
4. Standard deviation of red chromaticity of the segment
5. Normalized perimeter of largest blob before filling
6. Normalized external perimeter of the largest blob after filling
7. Relative Luminance of the segment
8. Centroid Y-axis of the segment
9. Standard deviation of red chromaticity of the segment
10. Standard deviation of centroid Y axis of the segment
11. Intensity drop of the segment external perimeter after filling
12. Area of largest blob before filling
13. Intensity drop of the segment external perimeter after filling
14. Number of blobs before filling
15. Perimeter of the segment before filling
16. External perimeter of the segment before filling
17. Normalized external perimeter of the segment after filling
18. Perimeter of largest blob before filling
19. Normalized perimeter of the segment after filling

8.2.1.1.5 Significant 4th segment (brightest color) features.

1. Normalized perimeter of the segment before filling
2. Segment value in the ring
3. External perimeter of largest blob after filling

4. Red Chromaticity of the segment
5. Normalized perimeter of the segment after filling
6. Perimeter of the segment before filling
7. Average distance of all the pixels of the segment from Lesion centroid
8. Number of blobs after filling
9. Intensity drop of the segment perimeter before filling
10. External perimeter of the segment before filling
11. Normalized external perimeter of the largest blob before filling
12. Standard deviation of red chromaticity of the segment
13. Area of the largest blob before filling
14. Perimeter of the largest blob after filling
15. Intensity drop of the segment perimeter after filling
16. Normalized external perimeter of the largest blob after filling
17. Standard deviation of centroid X axis of the segment
18. Variance of red chromaticity of the segment
19. Normalized perimeter of the largest blob after filling
20. Normalized perimeter of the largest blob before filling
21. Average distance of all the pixels of the segment from Lesion centroid
22. Normalized Intensity drop of the segment perimeter before filling
23. Intensity drop of the segment external perimeter before filling
24. Intensity drop of the largest blob external perimeter before filling
25. Number of blobs before filling
26. Standard deviation of red chromaticity of segment
27. Intensity Drop of largest blob perimeter before filling
28. Intensity drop of the segment perimeter after filling

29. Intensity drop of the largest blob external perimeter after filling
30. Standard deviation of centroid X axis of the segment
31. Standard deviation of centroid Y axis of the segment
32. Area of the segment before filling

8.2.1.2 Robust model.

8.2.1.2.1 Significant lesion features.

1. Ring Value

8.2.1.2.2 Significant 1st segment (darkest color) features.

1. Relative Luminance of the segment
2. Segment value in the ring
3. Area of the segment before filling

8.2.1.2.3 Significant 2nd segment features.

1. Variance of red chromaticity of the segment
2. Normalized perimeter of the segment after filling
3. Normalized perimeter of the segment before filling
4. Minor Axis Length
5. Intensity drop of the segment perimeter after filling
6. Intensity drop of the segment perimeter before filling
7. Normalized Average distance of all the pixels of the segment from Lesion centroid.
8. Number of blobs after filling
9. Normalized Euclidean distance from segment centroid to lesion centroid
10. Intensity drop of the segment perimeter after filling

11. Elongation
12. Intensity drop of the largest blob perimeter before filling

8.2.1.2.4 Significant 3rd segment features.

1. Standard deviation of green chromaticity of the segment
2. Variance of green chromaticity of the segment
3. Intensity drop of the segment perimeter before filling
4. Normalized perimeter of largest blob before filling
5. Normalized Area of segment before filling
6. Normalized Area of largest blob before filling
7. Normalized perimeter of the segment before filling
8. Standard deviation of red chromaticity of the segment

8.2.1.2.5 Significant 4th segment (brightest color) features.

1. Normalized Average distance of all the pixels of segment from Lesion centroid
2. Number of blobs after filling
3. Intensity drop of the segment perimeter before filling
4. Variance of blue chromaticity of the segment
5. Elongation
6. Normalized area of largest blob of the segment after filling
7. Variance of red chromaticity of the segment
8. Normalized perimeter of the segment after filling
9. Intensity drop of the segment perimeter after filling
10. Normalized perimeter of the segment before filling
11. Normalized perimeter of the largest blob before filling
12. Standard deviation of red chromaticity of the segment

8.2.2 Classification Results. The probability levels along with the specificity and sensitivity for the median split algorithm for the full model and the robust model with $SLENTY=SLSTAY=0.5$ are as shown below in the Tables 8.5 and 8.6 respectively.

8.2.2.1 Full model.

Table 8.5 Classification results for Full Model using median split algorithm with $SLENTY=SLSTAY=0.5$ for 837 set

Prob level	Sensitivity %	Specificity %
0	100	0
0.02	94	43.5
0.04	91.3	53.9
0.06	87	61.1
0.08	84.2	65.5
0.1	83.2	68.3
0.12	79.3	70.3
0.14	77.2	71.8
0.16	76.1	74.1
0.18	73.9	75.5
0.2	71.7	77.2
0.22	69	78.4
0.24	66.3	79.6

Table 8.5 Classification results for Full Model using median split algorithm with SLENTY=SLSTAY=0.5 for 837 set (cont.)

Prob level	Sensitivity %	Specificity %
0.26	63	81.2
0.28	61.4	81.8
0.3	59.2	82.8
0.32	59.2	84.4
0.34	58.2	85.9
0.36	57.6	87
0.38	56.5	87.7
0.4	54.9	88.2
0.42	54.9	88.5
0.44	54.3	88.7
0.46	52.7	89
0.48	52.2	89.4
0.5	50	90
0.52	49.5	90.7
0.54	48.9	91.9
0.56	47.8	92.2
0.58	46.7	92.8
0.6	45.1	93.4
0.62	44	93.9
0.64	44	94.5

Table 8.5 Classification results for Full Model using median split algorithm with SLENTY=SLSTAY=0.5 for 837 set (cont.)

Prob level	Sensitivity %	Specificity %
0.66	41.3	94.9
0.68	38	95.1
0.7	36.4	95.3
0.72	34.8	95.7
0.74	34.8	95.7
0.76	34.2	95.9
0.78	33.7	96.3
0.8	33.2	96.9
0.82	32.1	97.4
0.84	31.5	97.7
0.86	30.4	97.9
0.88	29.9	98
0.9	29.3	98.5
0.92	27.7	98.5
0.94	27.2	98.9
0.96	26.1	99.4
0.98	22.3	99.5
1	0	100

8.2.2.2 Robust model

Table 8.6 Classification results for Robust Model using median split algorithm with SLENTY=SLSTAY=0.5 for 837 set

Prob level	Sensitivity %	Specificity %
0	100	0
0.02	99.5	10.6
0.04	96.2	25.7
0.06	94	36.3
0.08	89.7	46.1
0.1	88.6	54.4
0.12	84.2	60.6
0.14	81.5	64.2
0.16	77.7	68
0.18	73.9	71.2
0.2	71.2	73.8
0.22	69	77.2
0.24	65.2	78.6
0.26	62.5	80.7
0.28	59.8	82.4
0.3	57.6	83.8
0.32	57.1	85.3
0.34	55.4	86.5

Table 8.6 Classification results for Robust Model using median split algorithm with SLENTY=SLSTAY=0.5 for 837 set (cont.)

Prob level	Sensitivity %	Specificity %
0.36	53.3	88.1
0.38	51.6	89.3
0.4	49.5	90.4
0.42	46.7	91
0.44	42.9	92
0.46	41.8	92.6
0.48	40.8	93.1
0.5	39.7	94
0.52	38	94.3
0.54	37	94.8
0.56	35.3	95.4
0.58	34.2	95.7
0.6	33.2	95.7
0.62	32.1	96.2
0.64	30.4	96.8
0.66	29.9	97.2
0.68	28.8	97.5
0.7	27.7	97.5
0.72	26.6	97.9
0.74	24.5	98.3

Table 8.6 Classification results for Robust Model using median split algorithm with SLENTY=SLSTAY=0.5 for 837 set (cont.)

Prob level	Sensitivity %	Specificity %
0.76	22.8	98.5
0.78	21.7	98.6
0.8	19	98.6
0.82	16.3	98.9
0.84	14.7	99.1
0.86	14.7	99.2
0.88	12.5	99.5
0.9	12	99.5
0.92	10.3	99.7
0.94	6.5	99.8
0.96	3.8	99.8
0.98	1.1	100
1	0	100

8.2.3 Receiver Operating Characteristic Curve. The ROC curve is compared between Full model and robust model of Median split Algorithm for SLENTY=SLSTAY=0.5.

8.2.3.1 Comparing ROC curve for full and robust model for median split with SLENTY=SLSTAY=0.5 for 837 set. The ROC curve for median split algorithm using full model is 0.930 and using robust model is 0.850. There are 87 significant features found for median split algorithm with full model and 36 features for robust model.

Figure 8.3 is the ROC curve between sensitivity and 1-specificity comparing full model and robust model for median split algorithm for 837 set with $SLENTY=SLSTAY=0.5$.

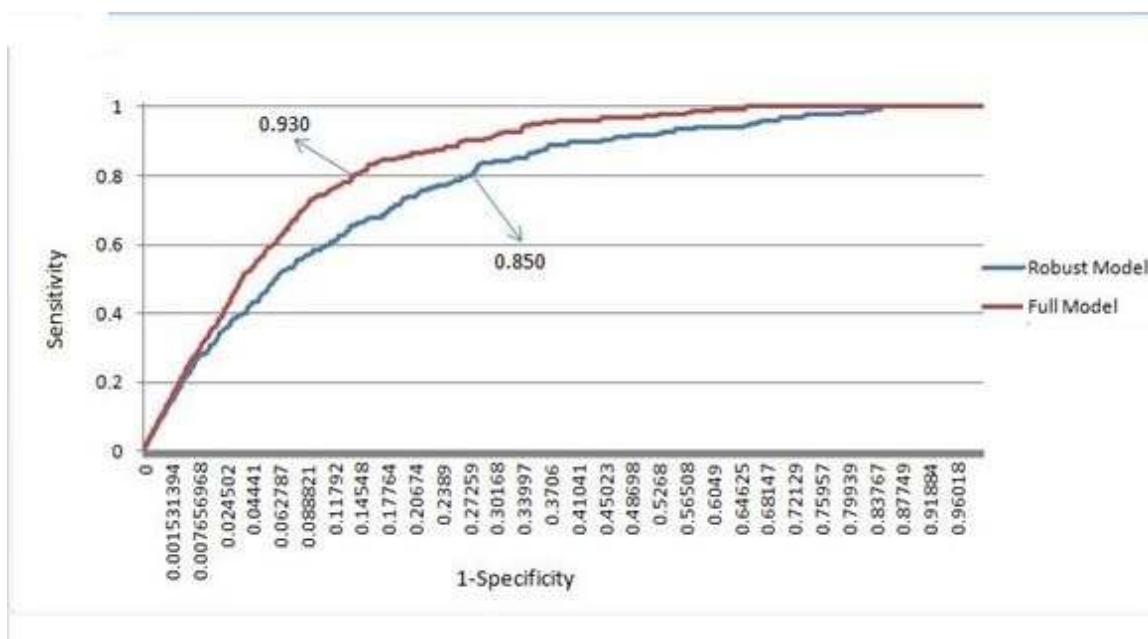


Figure 8.3 Comparing ROC curve for Median Split Full model and robust model for $SLENTY=SLSTAY=0.5$ for 837 set

8.3 USING THE FULL MODEL ON TEST SET OF 78 IMAGES

There is a disjoint test set selected to check the correctness of our model which was found using the 837 set. For this, a test set of 78 images is selected which are not the part of 837 images. These 78 images consists of 39 melanomas and 39 benigns.

8.3.1 Threshold Selection. All the 208 features are found on these images and $f(z)$ is calculated for these images using the formula from the 837 full model set. The threshold is set in the 837 full model set by sorting them on the basis of the $f(z)$ value. After sorting, a threshold value is selected to get 99% correct melanoma separation above the threshold value. This threshold value should also divide the test set in the same way which means our model is good with any image set. APPENDIX A gives you the information on how $f(z)$ is sorted and how the threshold value is selected for 837 set. The threshold in the appendix A is marked in yellow. The threshold found for 837 image set with full model is 0.0196. There are just 2 wrongly detected melanomas below this threshold which means that 99% correct melanoma separation is done using this threshold. This resulted in 366 wrongly detected benigns above this threshold and 44% correct benign separation using this threshold.

8.3.2 Testing the Model and Threshold on the 78 Image Set. The same 0.01965 value is used to verify on a test set to check the correctness of our model. APPENDIX B gives you the information on how many melanomas are found below the threshold for 78 image set. The melanoma or benign columns till the threshold are marked in red in appendix B because the melanomas are wrongly detected. This model gives 8 wrongly detected melanomas below the threshold and 27 wrongly detected benign above the threshold for 78 image set. This means that there was around 79% of correct separation of melanomas and 30% of correct separation of benigns. Hence, this model failed for a test set and this model cannot be used for other set of images.

8.4 USING THE ROBUST MODEL ON TEST SET OF 78 IMAGES

There is a test set selected to check the correctness of our robust model which was found using 837 set. For this, a test set of 78 images are selected which are not the part of 837 images. These 78 images have 39 melanomas and 39 benigns.

8.4.1 Threshold Selection. Robust 45 features are found on these images and $f(z)$ is calculated for these images using the formula from the 837 robust model set. APPENDIX C gives you the information on how $f(z)$ is sorted and how the threshold value is selected for 837 set using robust mode. The threshold value in the appendix C is marked in yellow.

The threshold found for 837 image set with robust model is **0.02884**. There are just 2 wrongly detected melanomas below this threshold which means that 99% correct melanoma separation is done above this threshold. This resulted in 538 wrongly detected benign above this threshold and 17.6% correct benign separation below the threshold.

8.4.2 Testing the Robust Model and Threshold on 78 Image Set. The same 0.02884 value is used to verify on a test set to check the correctness of our model. APPENDIX D gives the information about the number of melanomas that are found below the threshold for 78 image set using robust model. The threshold value in appendix D is marked in green to identify the better separation of melanomas for robust model when compared to full model. This model gives only 1 wrongly detected melanoma below the threshold and 32 wrongly detected benign above the threshold for the 78 image set. This means that there was 97.4% of correct separation of melanomas and 18% of correct benign separation even for the test set. Hence, this model is more robust than the model with more features. Hence though the c value is less for a robust model, it gives better results even with other set of images whereas full model fails to do so.

8.5 COMPARING ROC CURVE FOR 78 IMAGES WITH FULL MODEL AND ROBUST MODEL

The ROC curve is plotted for full and robust model and compared in this section. The ROC curve is plotted between sensitivity and 1-specificity.

8.5.1 Calculating Sensitivity and Specificity for each model. With the $f(z)$ values obtained from 837 set, the true positives and true negatives are calculated and based on which sensitivity, specificity information is calculated to plot the ROC curve. True positives are the melanomas that are correctly detected above a threshold and true negatives are the benign that are correctly detected below the threshold. Each $f(z)$ value for 78 image set is taken as a threshold and at each threshold, each image is classified as true positive or true negative. After this classification, the number of true positives and true negatives obtained at that threshold are calculated, sensitivity and specificity is obtained at each threshold. Sensitivity is true positives divided by number of melanomas and specificity is true negatives divided by number of benigns in the set. In this way, sensitivity and specificity is calculated at each threshold and the graph is plotted between sensitivity and 1-specificity. This is done for both full and robust model. Below table 8.7 shows the sensitivity and 1-specificity values for robust model and table 8.8 shows the sensitivity and 1-specificity values for full model.

Table 8.7 Sensitivity and Specificity values for robust model on 78 image set.

Sensitivity	1-Specificity
0	0.025641
0	0.051282
0.025641	0.051282
0.025641	0.076923

Table 8.7 Sensitivity and Specificity values for robust model on 78 image set. (cont.)

Sensitivity	1-Specificity
0.025641	0.102564
0.025641	0.128205
0.051282	0.128205
0.076923	0.128205
0.102564	0.128205
0.128205	0.128205
0.128205	0.153846
0.153846	0.153846
0.179487	0.153846
0.205128	0.153846
0.205128	0.179487
0.230769	0.179487
0.25641	0.179487
0.282051	0.179487
0.307692	0.179487
0.307692	0.205128
0.333333	0.205128
0.358974	0.205128
0.358974	0.230769
0.358974	0.25641
0.358974	0.282051

Table 8.7 Sensitivity and Specificity values for robust model on 78 image set. (cont.)

Sensitivity	1-Specificity
0.384615	0.282051
0.410256	0.282051
0.410256	0.307692
0.435897	0.307692
0.461538	0.307692
0.487179	0.307692
0.487179	0.333333
0.512821	0.333333
0.538462	0.333333
0.564103	0.333333
0.589744	0.333333
0.589744	0.358974
0.589744	0.384615
0.589744	0.410256
0.589744	0.435897
0.615385	0.435897
0.615385	0.461538
0.641026	0.461538
0.641026	0.487179
0.666667	0.487179
0.666667	0.512821

Table 8.7 Sensitivity and Specificity values for robust model on 78 image set. (cont.)

Sensitivity	1-Specificity
0.692308	0.512821
0.717949	0.512821
0.717949	0.538462
0.717949	0.564103
0.717949	0.589744
0.74359	0.589744
0.769231	0.589744
0.794872	0.589744
0.820513	0.589744
0.820513	0.615385
0.846154	0.615385
0.846154	0.641026
0.871795	0.641026
0.897436	0.641026
0.897436	0.666667
0.897436	0.692308
0.897436	0.717949
0.897436	0.74359
0.897436	0.769231
0.923077	0.769231
0.948718	0.769231

Table 8.7 Sensitivity and Specificity values for robust model on 78 image set. (cont.)

Sensitivity	1- Specificity
0.974359	0.769231
0.974359	0.794872
0.974359	0.820513
0.974359	0.846154
0.974359	0.871795
0.974359	0.897436
1	0.897436
1	0.923077
1	0.948718
1	0.974359
1	1

Table 8.8 Sensitivity and Specificity values for full model on 78 image set.

Sensitivity	1- Specificity
0.025641	0
0.025641	0.025641
0.025641	0.051282
0.051282	0.051282
0.051282	0.076923
0.051282	0.102564

Table 8.8 Sensitivity and Specificity values for full model on 78 image set. (cont.)

Sensitivity	1-Specificity
0.076923	0.102564
0.102564	0.102564
0.128205	0.102564
0.128205	0.128205
0.153846	0.128205
0.153846	0.153846
0.153846	0.179487
0.179487	0.179487
0.205128	0.179487
0.205128	0.205128
0.205128	0.230769
0.230769	0.230769
0.25641	0.230769
0.25641	0.25641
0.282051	0.25641
0.282051	0.282051
0.307692	0.282051
0.307692	0.307692
0.333333	0.307692
0.358974	0.307692
0.384615	0.307692

Table 8.8 Sensitivity and Specificity values for full model on 78 image set. (cont.)

Sensitivity	1-Specificity
0.384615	0.333333
0.384615	0.358974
0.384615	0.384615
0.410256	0.384615
0.410256	0.410256
0.435897	0.410256
0.435897	0.435897
0.435897	0.461538
0.461538	0.461538
0.487179	0.461538
0.512821	0.461538
0.512821	0.487179
0.538462	0.487179
0.538462	0.512821
0.538462	0.538462
0.564103	0.538462
0.564103	0.564103
0.589744	0.564103
0.615385	0.564103
0.615385	0.589744
0.615385	0.615385

Table 8.8 Sensitivity and Specificity values for full model on 78 image set. (cont.)

Sensitivity	1-Specificity
0.641026	0.615385
0.666667	0.615385
0.666667	0.641026
0.692308	0.641026
0.717949	0.641026
0.74359	0.641026
0.769231	0.641026
0.794872	0.641026
0.794872	0.666667
0.794872	0.692308
0.794872	0.717949
0.794872	0.74359
0.794872	0.769231
0.794872	0.794872
0.820513	0.794872
0.820513	0.820513
0.820513	0.846154
0.820513	0.871795
0.820513	0.897436
0.820513	0.923077
0.820513	0.948718

Table 8.8 Sensitivity and Specificity values for full model on 78 image set. (cont.)

Sensitivity	1-Specificity
0.820513	0.974359
0.846154	0.974359
0.871795	0.974359
0.871795	1
0.897436	1
0.923077	1
0.948718	1
0.974359	1
1	1

8.5.2 Plotting ROC curve for both the models. The ROC curve is plotted for full model and robust model using the above sensitivity and specificity values. Figure 8.4 shows the ROC curve comparison between full and robust model.

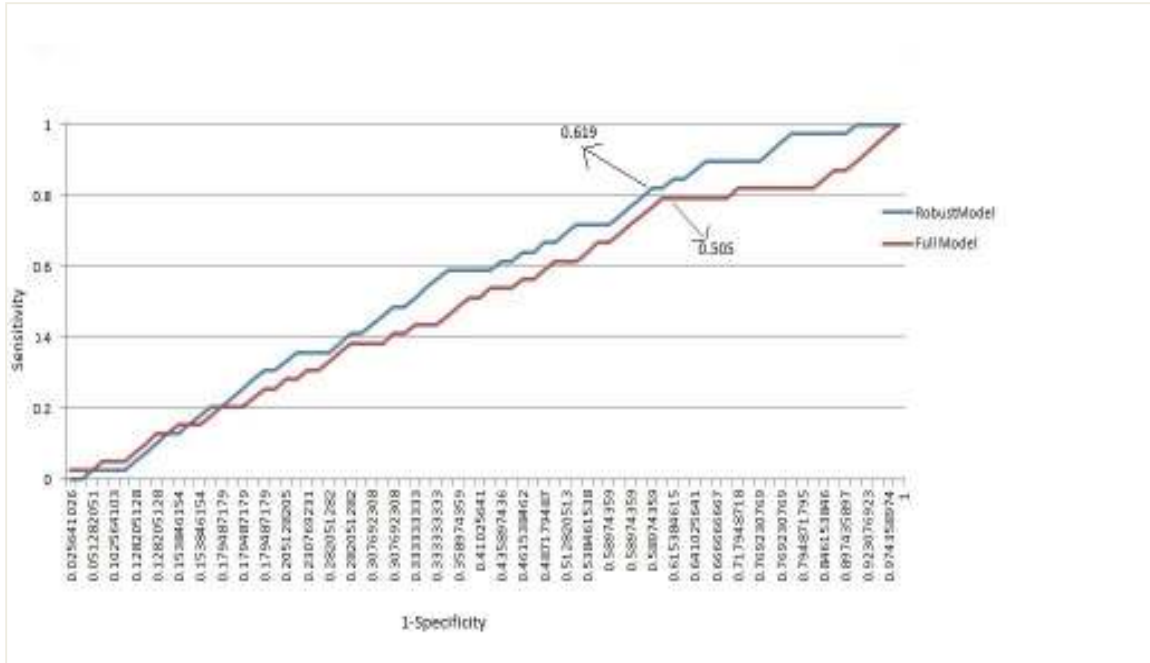


Figure 8.4 ROC curve comparison between full model and robust model for 78 image set.

The ROC curve is plotted for both the models and the ROC value can be found using the below steps.

1. All the sensitivity values are considered as $y_1, y_2, y_3, \dots, y_n$ and all the 1-specificity values are considered as $x_1, x_2, x_3, x_4, \dots, x_n$.
2. $\Delta x_2 = x_2 - x_1$, $\Delta x_3 = x_3 - x_2, \dots, \Delta x_n = x_n - x_{n-1}$ are considered.
3. ROC value = $y_2 * \Delta x_2 + y_3 * \Delta x_3 + \dots + y_n * \Delta x_n$.

The above calculation gives us the ROC value. The ROC for a robust model is 0.0619 and the ROC for a full model is 0.505.

9. CONCLUSION

The current study compares the K-means clustering algorithm with the median split algorithm to segment the dermoscopy images. These segment and lesion features help us in distinguishing the image between melanoma and benign tumors. For this, a data set of 888 images with 195 melanomas and 693 benigns is used. A total of 226 features that are found are analyzed using forward step-wise logistic regression. This gave 90 significant features with the K-means algorithm and 122 significant features for the median split algorithm. The area under the ROC (Receiver Operating Characteristic) curve for K-means is 0.902 whereas for median split algorithm is 0.932. Hence, the median split algorithm gave better results compared to the K-means algorithm.

There is another set which is a subset of the 888 images known as the 837 set which has 184 melanomas and 653 benign lesions. This set is used to build our full and robust model. A full model is built with 208 features that are run into stepwise logistic regression in SAS. Using the odds ratio estimates in SAS results and eliminating the scale and rotation invariant images, a robust model with 45 features is developed. Threshold values are found for full and robust models and tested on a test set of 78 images which are not part of 837 image set. These 78 images have 39 melanoma and 39 benign lesions. The full model and robust model developed from 837 set with threshold that provides 99% correct melanoma separation. The full model gives 11% wrongly detected melanomas whereas the robust model gives only 2.6% wrongly detected melanomas for 78 image set. The area under the ROC curve for full model is 0.930 and area under the ROC curve for robust model is 0.850 for 837 set. Hence, this concludes that though full model has better area under ROC curve, the robust model is more accurate and robust with any image set.

10. FUTURE WORK

The accuracy of Median split robust model can be further developed using different features, cutting down some of the less important features making our model more robust. This has to be tested on a large scale and various types of images to check if there are any errors. These errors have to be corrected and model has to be made more efficient increasing the area under ROC curve.

APPENDIX A

THRESHOLD SELECTION TABLE FOR FULL MODEL

Image Name	Melanoma or Benign	f(z)
ag100108rab825_CNP	0	0
BS100108per137_CNP	0	0
bw081508rol460_CNP	0	0
je052507dru7_CNP	0	0
js020108rol283_CNP	0	0
LW102108per159_CNP	0	0
me012908rab547_CNP	0	0
mk051007_CNP	0	0
ms062907dru40_CNP	0	0
ao061407rol126_CNP	0	0.00001
re042408rol373_CNP	0	0.00001
jf050208rab694_CNP	0	0.00003
cw011909rol560_CNP	0	0.00004
EH112607per47_CP	0	0.00004
or100608rol498_CNP	0	0.00004
kr123107rol264_CNP	0	0.00005
LP111808per187_CNP	0	0.00005
GH010609per201_CNP	0	0.00006
ds042307rab111_CNP	0	0.00008
eb053107rolla105_CNP	0	0.00008
js091807rol215_CNP	0	0.00008
re042408rol374_CNP	0	0.00008

Image Name	Melanoma or Benign	f(z)
sf031309rab1001_CNP	0	0.0001
sw120308rab897_CNP_whole	0	0.00011
de122106rol34_NCP	0	0.00014
ee122508dru145_CNP	0	0.00017
bz080807dru74_CNP	0	0.00019
tw052507dru6_CNP	0	0.00019
ca032508rol345_CNP	0	0.0002
nw030707tre13_CNP	0	0.00022
jf051007rab133_CNP	0	0.00025
DH062308PER92_CNP	0	0.00026
JH101408per145_CNP	0	0.00026
ls012607rab7_CNP	0	0.00027
lt111407dru113_CNP	0	0.00027
DH062308PER91_CNP	0	0.00031
ml033108rol347_CNP	0	0.00033
nd112007dru123_CNP	0	0.00033
dl121807rab484_CNP	0	0.00036
js052907dru11_CNP	0	0.00037
cd112107dru126_CNP	0	0.0004
SC050808per79_CNP	0	0.0004
di062607dru34_CNP	0	0.00041
dd081307rolla188_CNP	0	0.00044

Image Name	Melanoma or Benign	f(z)
de010609dru217_CNP	0	0.00044
rc062509rab1118_CNP	0	0.00046
pb050708dru160_CNP	0	0.00047
jp030907rab56_CNP	0	0.00049
cv022908dru146_CNP	0	0.00051
es090507rab296_CNP	0	0.00051
jb112108rol523_CNP	0	0.00054
es091107dru88_CNP	0	0.00055
eo073007dru61_CNP	0	0.00064
tb041207rab103_CNP	0	0.00064
cb071607rol159_CNP	0	0.00066
js091807rol216_CNP	0	0.00069
ek060309dru256_CNP	0	0.00072
ar031607rab68_CNP	0	0.00073
sk101807rab370_CNP	0	0.00074
RD092608per128_CNP	0	0.00075
kb073107rol173_CNP	0	0.00076
mo112008rol552_CNP	0	0.00077
ak051007rab132_CNP	0	0.00078
cf053107tre29_CNP	0	0.00079
eb040308rab632_CNP	0	0.00079
lc052407dru5_CNP	0	0.0008

Image Name	Melanoma or Benign	f(z)
sz110607dru109_CNP	0	0.00082
jh082007rol195_CNP	0	0.00083
as101807rab369_CNP	0	0.00088
kb022707rol53_NCP	0	0.00088
DT111507per46_CNP	0	0.00089
vf032409rab1013_CNP	0	0.00089
kr020408rol287_CNP	0	0.00094
mp020509rab958_CNP	0	0.00105
ja061807rol130_CNP	0	0.00106
LB110907per42_CNP	0	0.00106
ap033108rab625_CNP	0	0.00114
ks112107rab440_CNP	0	0.00118
gv073107dru67_CNP	0	0.0012
bf121207rab466_CNP	0	0.00125
pb061107dru17_CNP	0	0.00126
se022307rab40_CNP	0	0.00132
db010307rol268_CNP	0	0.00142
sl072307dru55_CNP	0	0.00142
JF100208per141_CNP	0	0.00144
mr021109rab973_CNP	0	0.00144
lv041708rab662_CNP	0	0.00147
ll052407tre25_CP	0	0.00151

Image Name	Melanoma or Benign	f(z)
gt071207rab228_CNP	0	0.00152
dl111407dru111_CNP	0	0.00154
as090507dru85_CNP	0	0.00157
TP021009per204_CNP	0	0.00159
dm082608rol468_CNP	0	0.00171
mt033108rab627_CNP	0	0.00174
if040208rab629_CNP	0	0.0018
kd052008rol392_CNP	0	0.00182
jt051408rab712_CNP	0	0.00185
rh091907rab315_CNP	0	0.00185
EF061608PER89_CNP	0	0.00189
ra040308rol349_CNP	0	0.00192
sg052407dru2_CNP	0	0.00192
av072607_CNP	0	0.00194
cm102907_CNP	0	0.00196
sw120308rab898_CNP	0	0.00197
ar111907rab432_CNP	0	0.00198
re042408rol372_CNP	0	0.00212
tr040408rab637_CNP	0	0.00213
wbeb080707dru72_NCP	0	0.00215
lr112608rab889_CNP	0	0.00223
ca022807rab46_CNP	0	0.00224

Image Name	Melanoma or Benign	f(z)
GB021709per207_CNP	0	0.00237
jp030907rab57_CNP	0	0.00237
nn092607kolm24_CNP	0	0.00237
jj061307dru21_CNP	0	0.00241
RD092608per129_CNP	0	0.00243
oj070609rab1139_CNP	0	0.00258
sm010209rol547_CNP	0	0.00267
rl103107rab379_CNP	0	0.0027
bj041207tre16_CNP	0	0.00271
as040408rab635_CNP	0	0.00272
mr022709rab995_CNP	0	0.0028
kf031209rab996_CNP	0	0.00288
dl052609rab1064_CNP	0	0.0029
ac031008rol336_CNP	0	0.00292
dz101107rab359_CNP	0	0.00292
gp020609rab963_CNP	0	0.00292
jm041808rab665_CNP	0	0.00293
jw072707rol169_CNP	0	0.00293
ad021607rab35_CNP	0	0.00294
cp040108rab628_CNP	0	0.00299
tm032808rab620_CNP	0	0.003
AW122807per54_CNP	0	0.00308

Image Name	Melanoma or Benign	f(z)
dd070207rab205_CNP	0	0.00309
tr022908rol326_CNPb	0	0.0031
sr110807dru110_CNP	0	0.00321
as070307rab211_CNP	0	0.00327
wa051608dru176_CNP	0	0.00329
jc091608rab811_CNP	0	0.0033
gm110507dru106_CNP	0	0.00337
jc091608rab810_CNP	0	0.00339
cm121707_CNP	0	0.00342
rc082707rab275_CNP	0	0.00347
wb080707dru73_CNP	0	0.00347
jv033009rab1016_CNP	0	0.00348
nm081407rab263_CNP	0	0.00352
bg121107rab465_CNP	0	0.00365
kf070507_CP	0	0.0037
me110608rab863_CNP	0	0.00379
jp070207rab204_CNP	0	0.00382
ar092408rab816_CNP	0	0.00386
cs071807rolla163_CNP	0	0.00388
mf061907dru29_CNP	0	0.00392
st032107rab73_CNP	0	0.00402
gp020609rab962_CNP	0	0.00403

Image Name	Melanoma or Benign	f(z)
mp080107dru69_CNP	0	0.00405
re042408rol370_CNP	0	0.00413
tz020708dru143_CNP	0	0.00418
RV122007per51_CNP	0	0.00419
cp060107rolla110_CNP	0	0.00434
ef042408rab683_CNP	0	0.00434
ab021709rol577_CNP	0	0.00435
jp062507rab197_CNP	0	0.00445
sb032207tre15_CNP	0	0.00446
GA052308per84_CNP	0	0.00452
kb012908rol281_CNP	0	0.00457
sl011309dru219_CNP	0	0.00462
dk071408rab760_CNP	0	0.00465
rl103107rab378_CNP	0	0.00467
MG100507per31_CNP	0	0.00483
LM103108per167_CNP	0	0.00485
ck122308rab910_CNP	0	0.00486
JK091108per106_CNP	0	0.00504
CR082508per98_CNP	0	0.00507
jt082807rab280_CNP	0	0.00507
js070907rab223_CNP	0	0.00519
mr111207rab412_CNP	0	0.00523

Image Name	Melanoma or Benign	f(z)
er062909dru260_CNP	0	0.00525
dp070907rab222_CNP	0	0.00527
gn032508rol344_CNP	0	0.0053
jc041009rab1033_CNP	0	0.00535
br121007rab461_CNP	0	0.00545
sm092507dru94_CNP	0	0.00548
mr110807rab403_CNP	0	0.00549
fa060107dru15_CNP	0	0.00558
jv053008rab734_CNP	0	0.00573
mp011909rab938_CNP	0	0.00573
kh112807dru127_CNP	0	0.00576
lg091107dru89_CNP	0	0.00578
rc100207kolm27_CNP	0	0.0058
tc041409rab1036_CNP	0	0.0059
cj082207rab272_CNP	0	0.00604
sl072307dru56_CNP	0	0.00609
pl050608dru158_CNP	0	0.00612
rc021208rab556_CNP	0	0.00641
rb050108rab692_CNP	0	0.00645
as042808dru149_CNP	0	0.00647
jh050207rab122_CNP	0	0.00667
me012908rab548_CNP	0	0.00675

Image Name	Melanoma or Benign	f(z)
JS121907per50_CNP	0	0.0068
pk082907rab281_CNP	0	0.00692
ds040109rab1023_CNP	0	0.00694
rk020909rab964_CNP	0	0.00707
am021408rol294_CNP	0	0.00729
td071708rab766_CNP	0	0.00747
ny012208rab535_CNP	0	0.00748
SH092908per135_CNP	0	0.00748
kj082807kolm12_CNP	0	0.00754
lm011608rab518_CNP	0	0.00761
mc111507dru117_CNP	0	0.00788
kl090407dru81_CNP	0	0.00789
db073008rab779_CNP	0	0.00801
lc052207rol89_CNP	0	0.0081
MC041408per74_CNP	0	0.00822
wt022007tre8_CNP	0	0.00842
td071708rab767_CNP	0	0.00852
bl081808rol462_CNP	0	0.00872
me012908rab546_CNP	0	0.00883
dw092608rab823_CNP	0	0.00884
sp011409dru221_CNP	0	0.00898
jj051408dru172_CNP	0	0.00908

Image Name	Melanoma or Benign	f(z)
rs010308rab503_CNP	0	0.00915
rs121207rab468_CNP	0	0.00948
js091208rol485_CNPwhole	0	0.00954
cw051208rab703_CNP	0	0.00963
PG091108per109_CNP	0	0.00968
jm020909rol569_CNP	0	0.00969
ss021207rab30_CNP	0	0.0097
rc052308rab728_CNP	0	0.00973
dt052008dru181_CNP	0	0.0098
CT110907per40_CNP	0	0.00993
MT060807per2_CP	0	0.01002
rb091007rol202_CNP	0	0.01016
ll040307rol5_CNP	0	0.01033
hw021508rol301_CNP	0	0.01038
js071508rol436_CNP	0	0.01056
as051408rab707_CNP	1	0.01078
bk061208rab740_CNP	0	0.01083
jh022307rab41_CNP	0	0.01097
ts052407rab158_CNP	0	0.01098
jw021709rab978_CNP	0	0.01142
wr052407dru3_CNP	0	0.01216
se062607dru36_CNP	0	0.01229

Image Name	Melanoma or Benign	f(z)
jp051707rab144_CNP	0	0.01232
oa073107dru65_CNP	0	0.01238
as070307rab212_CNP	0	0.01241
as080207rab249_CNP	0	0.01259
RT082908per101_CNP	0	0.0127
cc080307rol177_CNP	0	0.01273
mc111507dru115_CNP	0	0.01279
ha092407kolm20_CNP	0	0.01281
hl101708rab844_CNP	0	0.01284
ma051507_CNP	0	0.01286
am021508rol297_CNP	0	0.01293
dp032508rab614_CNP	0	0.01329
ld011508dru138_CNP	0	0.01332
rb070109rab1127_CNP	0	0.01341
tt012609rab945_CNP	0	0.01345
ew022807rol21_CNP	0	0.01426
dp041808rab664_CNP	0	0.01434
bj011509rab935_CNP	0	0.01469
sw053007rab161_CNP	0	0.01474
cm052507rol98_CNP	0	0.01487
kf031708rab604_CNP	0	0.01496
wb070209rab1136_CNP	0	0.01541

Image Name	Melanoma or Benign	f(z)
rk020909rab965_CNP	0	0.01549
tc101907rolla242_CNP	0	0.01555
ra040308rol350_CNP	0	0.01574
ks040209rab1021_CNP	0	0.016
md110807rab400_CNP	1	0.016
jh051007rol73_CNP	0	0.01613
DT111507per45_CNP	0	0.01629
SS110708per174_CNP	0	0.01647
jg092408rab818_CNP	0	0.01649
fr050808dru162_CNP	0	0.01653
rd062107rab201_CNP	0	0.01658
mg080607rab251_CNP	0	0.01709
RT092107per25_CNP	0	0.01742
sm071607dru50_CNP	0	0.01746
es010708dru136_CNP	0	0.01754
dt010908rab508_CNP	0	0.01797
jp051707rab143_CNP	0	0.01811
lc032608rab616_CNP	0	0.01829
kb012908rol282_CNP	0	0.01837
EQ071607per10_CNP	0	0.01869
kp042607rab118_CNP	0	0.01878
jb042308rab677_CNP	0	0.01893

Image Name	Melanoma or Benign	f(z)
dc110607rab395_CNP	0	0.01929
jg012108rab529_CNP	0	0.01958
jd070607rol148_CNP	0	0.01965
ma071408rab759_CNP	1	0.02009
ss040308rol352_CNP	0	0.0201
ev112408rol527_CNP	0	0.02022
jl110408rol518_CNP	0	0.02035
oa073107dru66_CNP	0	0.02065
JD061808PER90_CNP	0	0.02129
hl062609rab1124_CNP	1	0.0214
is070607dru45_CNP	0	0.02167
lc060807rol119_CNP	0	0.02194
ri012109rab942_CNP	0	0.02203
ab061507_CNP	0	0.02236
pb091908rol492_CNP	0	0.02272
lg081707rolla194_CNP	0	0.02308
pg080707rab254_CNP	0	0.02331
BB062508PER94_CNP	0	0.02333
rw010709rab921_CNP	0	0.02406
ck020508rol291_CNP	0	0.0241
ss080307rol174_CNP	0	0.02427
jh121307rab471_CNP	0	0.02441

Image Name	Melanoma or Benign	f(z)
de111808dru254_CP	0	0.02444
lb121807rab483_CNP	0	0.02461
ah042009rab1046_CNP	0	0.02465
bg121107rab464_CNP	0	0.02551
rr073007dru62_CNP	0	0.02565
sm010308rab502_CNP	0	0.02597
ng040908rab646_CNP	0	0.02661
lp020907rol43_CP	0	0.02703
nz052307rab153_CNP	0	0.02735
ak041009rab1034_CP	0	0.02763
jj030207tre11_CNP	0	0.02781
rh032808rol346_CNP	0	0.02791
gm012208rab532_CNP	0	0.02793
jm033109rab1020_CNP	0	0.02836
ab081307rab260_CNP	0	0.0285
rr042009rol613_CNP	1	0.02864
cb041509rab1039_CNP	0	0.02897
as073107rab244_CNP	0	0.02914
cc091608rab807_CNP	0	0.02922
jb080607rolla181_CNP	0	0.02939
cb112107rab439_CNP	0	0.02946
gp020609rab961_CNP	0	0.02955

Image Name	Melanoma or Benign	f(z)
tm033009rab1018_CNP	0	0.02968
mc070808rab756_CNP	0	0.02974
ds041808rol362_CNP	0	0.03006
jv060508rol403_CNP	0	0.03051
jd020707rab19_CNP	0	0.03061
ks020408rol286_CNP	0	0.03067
ef042408rab684_CNP	0	0.03081
ag080907rab259_CNP	1	0.03091
ob092407rab329_CNP	0	0.03143
bh113007rab373_CNP	0	0.03192
md110608rab866_CNP	0	0.03192
sr020209rab960_CNP	0	0.03207
mv052107rab150_CNP	0	0.03211
ce061908rol417_CNP	0	0.03242
lg081707rolla193_CNP	0	0.03249
as110408rab860_CNP	0	0.03289
JF100208per140_CNP	0	0.03308
bh113007rab451_CNP	0	0.03315
yd040407rab97_CNP	0	0.03434
mr051707_CNP	0	0.03482
md110608rab865_CNP	0	0.0352
dl072108rab771_CNP	0	0.03659

Image Name	Melanoma or Benign	f(z)
ka052307_CNP	0	0.03687
NS091108per107_CNP	0	0.0369
lv061908rab747_CNP	0	0.03723
kr120307rab455_CNP	0	0.03728
rb053007dru13_CNP	0	0.03742
cc061207dru20_CNP	0	0.03769
mj071807dru52_CNP	0	0.03835
jc050307rab125_CNP	0	0.03853
rm052907dru9_CNP	0	0.0386
em011808rab525_CNP	0	0.03866
ah042009rab1047_CNP	0	0.03877
JT111208per183_CNP	0	0.03935
RT082908per100_CNP	0	0.03993
dm121007dru131_CNP	0	0.04029
AV110408rab858_CNP	0	0.04035
DB052108per82_CNP	0	0.04109
sb020408rol289_CNP	0	0.04151
as030308rab586_CNP	0	0.04189
bc091807kolm19_CNP	0	0.04275
JG102907per38_CNP	0	0.04278
CK122308rab911_CNP	0	0.04307
ky092507kolm22_CNP	0	0.04377

Image Name	Melanoma or Benign	f(z)
kv071808rab770_CNP	0	0.0444
mp062309rab1113_CNP	0	0.04463
jw021709rab979_CNP	0	0.04502
gm110507dru108_CNP	0	0.04534
AV110408rab857_CNP	0	0.04553
ac031008rol337_CNP	0	0.046
rc082707rab274_CNP	1	0.04646
cb072508rab776_CNP	0	0.04692
st032107rab72_CNP	0	0.04731
gm012208rab534_CNP	0	0.04805
tr121907rab489_CNP	0	0.04815
dt052008dru182_CNP	0	0.04857
pw111907rab433_CNP	0	0.04901
mc111507dru116_CNP	0	0.04911
mj071807dru53_CNP	0	0.04926
jd020209rab953_CNP	0	0.0494
VG082707per17_CNP	0	0.04952
jb051208dru169_CP	0	0.04999
ad040609rab1028_CNP	0	0.05003
bw070307rab209_CNP	0	0.05008
nd021109rab972_CNP	0	0.05008
cp050707rab127_CNP	0	0.05132

Image Name	Melanoma or Benign	f(z)
cg032009rab1010_CNP	0	0.05133
wv072607dru59_CNP	0	0.05179
dt062507rol138_CNP	0	0.05235
LB110907per41_CNP	0	0.05261
ck122308rab909_CNP	0	0.0527
as073008rab781_CNP	0	0.05275
dc020108rol284_CNP	0	0.05434
mo082207rab271_CNP	0	0.05553
rb050207_NCP	0	0.05626
sa082107kolm9_CNP	0	0.05687
jc041009rab1032_CNP	0	0.05696
mk021009rab970_CNP	0	0.05715
sa060109rab1073_CNP	0	0.05718
MJ120507per49_CNP	0	0.05732
jb061108rab737_CNP	0	0.05831
ad040507rab98_CNP	0	0.05836
da102607dru100_CNP	0	0.05858
rm062107dru30_CNP	0	0.05876
mc111507dru118_CNP	0	0.05943
ps070607dru44_CNP	0	0.05958
rb120407rab457_CNP	0	0.05961
th040609rab1029_CNP	0	0.06044

Image Name	Melanoma or Benign	f(z)
KS020209per203_CNP	0	0.06105
pa032808rab624_CNP	0	0.06122
rr031207rol14_CNP	0	0.06186
jp030608rol332_CNP	0	0.06212
DZ091508per116_CNP	0	0.06284
gr110408rab859_CNP	0	0.06459
eb032607rab81_CNP	0	0.06558
wc050208rab696_CNP	1	0.06599
de011209rab929_CNP	0	0.06665
ew101907rol239_CNP	0	0.06764
jw021709rab977_CNP	0	0.06809
jn091707rol212_CNP	0	0.06867
sp070207rab203_CNP	0	0.06948
as101807rab368_CNP	0	0.06966
rb051908rab722_CNP	0	0.07018
om070209rab1132_CNP	0	0.07048
wr052407dru4_CNP	0	0.07199
dr052209rab1062_CNP	0	0.07223
JG071807per11_CNP	0	0.07224
MS102507per33_CNP	0	0.07231
sl052609rab1063_CNP	1	0.07328
lt030207rol20_CNP	0	0.07338

Image Name	Melanoma or	
	Benign	f(z)
dl012408dru139_CNP	0	0.07501
lr061108rab738_CNP	0	0.07519
ks070907rolla151_CNP	0	0.07653
jb072007rol165_CNP	0	0.07729
pf072407dru57_CNP	0	0.07833
bf062509rab1116_CNP	0	0.07953
rc041608rab660_CNP	0	0.07992
ew061507rol127_CNP	0	0.08001
lm062909rab1125_CNP	0	0.08384
tl073107dru68_CNP	0	0.08542
bb082107rol196_CNP	1	0.08585
jb031809rab1005_CNP	0	0.08697
TT010308per55_CNP	0	0.08711
ja060407dru16_CNP	0	0.08753
mg061807_CNP	0	0.08764
pa032808rab623_CNP	0	0.08833
cp051408dru171_CNP	0	0.08905
vn080309rol653_CNP	1	0.09006
ve121907rab485_CNP	1	0.09042
dl011409rab934_CNP	1	0.09117
mr051608rab721_CNP	0	0.09119
rp100907rab348_CNP	0	0.09128

Image Name	Melanoma or Benign	f(z)
lp071107dru47_CNP	0	0.09129
mb032609rab1015_CNP	0	0.09245
lz032907rab84_CNP	0	0.09418
dl111407dru112_CNP	0	0.09463
ld061507dru25_CNP	0	0.09513
dm042307rol59_CNP	0	0.09621
es010408rab505_CNP	0	0.09745
ct042909rab1054_CNP	0	0.09826
dh031309rab1000_CNP	0	0.09916
jm033109rab1019_CNP	0	0.10095
ag061307rab186_CNP	0	0.10113
pm030107tre10_CNP	0	0.10121
jd032207rol57_CP	0	0.10443
br112107dru125_CNP	0	0.10504
as090507dru86_CNP	0	0.10508
rm052907dru10_CNP	0	0.10524
pc042009rab1044_CNP	1	0.10821
gm110507dru107_CNP	0	0.10882
mc062107_CNP	0	0.10897
md072308rab773_CNP	0	0.10914
kv090707rol200_CNP	0	0.10956
lp062007rab200_CNP	1	0.11071

Image Name	Melanoma or Benign	f(z)
pb050808rol381_CNP	0	0.11142
mm053007tre26_CP	0	0.11375
pr070109rab1130_CNP	1	0.11503
KB060807per1_CNP	0	0.11507
GA052308per83_CNP	0	0.11528
lw022708rab580_CNP	1	0.11624
db021207rol24_CNP	0	0.11695
rk11108rab874_CNP	0	0.11748
mr062408rol418_CNP	0	0.11755
pl062309rab1111_CNP	0	0.11809
no051908rol390_CNP	0	0.12051
sk082007rab268_CNP	0	0.12067
ar121407rab476_CNP	1	0.12311
ar092408rab815_CNP	0	0.12511
oa073107dru64_CNP	0	0.12546
ve112108rab886_CNP	0	0.12831
ng040908rab645_CNP	0	0.13001
LS021108per64_CNP	0	0.13154
br121007rab462_CNP	0	0.13161
DY012808per61_CNP	0	0.13228
ap121608Rab900_CNP	0	0.13364
ss032007rol9_CNP	0	0.13407

Image Name	Melanoma or Benign	f(z)
mg050508rab698_CNP	0	0.13534
PH2100407per30_CNP	0	0.14236
ar100208rab827_CNP	0	0.14285
cn101807rol238_CNP	0	0.1429
jl111407dru114_CNP	0	0.14295
tb091007dru87_CNP	0	0.1441
pw062907rol141_CNP	0	0.14562
md032607rab79_CNP	0	0.14571
jb041708rab661_CNP	0	0.1462
SRT123107rab501_CNP	0	0.1463
kr050508dru155_CNP	0	0.15044
hk030508rab589_CNP	1	0.1536
kf052908rab731_CNP	0	0.15422
em051608rol386_CNP	0	0.15475
hc051407rol78_CNP	0	0.15675
mm062207dru33_CNP	1	0.15716
HB122208per200_CNP	1	0.15741
as112707rab444_CNP	0	0.15751
ar091407rab309_CNP	0	0.16041
LM103108per168_CNP	0	0.16151
BA070907per7_CNP	0	0.16223
ro031909rab1007_CNP	0	0.16281

Image Name	Melanoma or Benign	f(z)
mf072308rab772_CNP	0	0.1634
ca050907rab128_CNP	0	0.16413
RW091708per121_CNP	0	0.16436
cm072508rab777_CNP	0	0.16548
fh080607rolla183_CNP	0	0.16684
pw050707tre17_CNP	0	0.16896
ls111108rab872_CNP	0	0.16927
ed052109rab1060_CP	1	0.17069
as090707rab300_CNP	1	0.17261
jk032807rab83_CNP	0	0.17268
st012108rol277_CP	0	0.17377
kj112508rab888_CNP	0	0.17572
cw081507dru77_CNP	0	0.17851
pm060407rab169_CNP	0	0.18135
md120908rol539_CNP	0	0.18274
kr123107rol263_CNP	0	0.18294
JT111208per182_CNP	0	0.18395
mr110807rab404_CNP	0	0.18453
mv021607rab34_CNP	1	0.1878
kp012907rab9_CNP	0	0.18812
im102008rab845_CNP	0	0.19276
jn091707rol211_CNP	0	0.19305

Image Name	Melanoma or Benign	f(z)
lf032808rab621_CNP	0	0.19314
md033007rol6_CNP	0	0.19515
gv041509rab1041_CNP	0	0.19914
DY012808per60_CNP	0	0.20068
cs050808dru164_CNP	0	0.20133
sa031308rab601_CNP	1	0.20382
ef120407dru128_CNP	0	0.20434
mc041307rab105_CNP	0	0.20466
sm0417409rab1042_CNP	0	0.20533
sp071807dru54_CNP	0	0.20547
tc101907rolla241_CNP	0	0.20621
rm021309rab952_CNP	0	0.20698
rb121707rab480_CNP	0	0.20709
ck062209rol641_CNP	0	0.20919
db070307dru43_CNP	0	0.20985
ra091207rab305_CNP	0	0.21279
la090408rol477_CNP	0	0.21416
av042908rab686_CNP	0	0.21459
cp060509rab1078_CNP	0	0.21465
sa082207rab273_CNP	1	0.21591
rm022707rol54_NCP	0	0.21821
tw010307rol266_CNP	0	0.21825

Image Name	Melanoma or Benign	f(z)
HC102607per35_CNP	0	0.22055
MC041408per73_CNP	0	0.22135
rr121107dru133_CNP	0	0.22961
HC102607per34_CNP	0	0.22989
rw111308rol519_CNP	0	0.23049
pk082907rab282_CNP	1	0.23063
nz010807rol36_NCP	0	0.23089
re042408rol375_CNP	0	0.23099
jb110907rab407_CNP	0	0.23248
sc100208rab826_CNP	0	0.23261
wg082008rab748_CNP	0	0.2336
kd100807rol229_CNP	0	0.23586
sc042308rab678_CNP	1	0.23815
pt052609rab1065_CNP	0	0.24329
md032607rab80_CNP	0	0.24347
mg101608rol507_CNP_whole	0	0.2435
yc070209rab1135_CNP	0	0.24366
mc071707_CNP	0	0.24546
HS050508per76_CNP	0	0.24735
CL072108PER96_CNP	0	0.24869
gs071508rab761_CNP	0	0.24949
gc061307_CP	0	0.24997

Image Name	Melanoma or Benign	f(z)
dn081707rab266_CNP	0	0.25032
mr022007rolla47_NCP	0	0.251
re042408rol376_CNP	0	0.25193
mk042709rab1053_CNP	0	0.25291
jp062507rab198_CNP	0	0.25473
ms041808rab666_CNP	1	0.25595
fh080607rolla182_CNP	0	0.25759
al111907rab434_CNP	0	0.25928
jd022009rab985_CNP	1	0.25964
rp100907rab349_CNP	0	0.26008
wh052907rol102_CNP	1	0.26243
cl050307rab124_CNP	0	0.26508
dp111308rab875_CNP	0	0.26848
lb060608rol407_CNP	0	0.26893
kr110408rab856_CNP	0	0.26989
ri012109rab943_CNP	0	0.27058
HG031408per68_CNP	0	0.27123
bk041008rab649_CNP	1	0.27288
jy011609rol557_CNP	1	0.27318
ja012808rol278_CNP	0	0.27386
pb032207tre14_CNP	1	0.27864
al050708rab700_CNP	0	0.28004

Image Name	Melanoma or Benign	f(z)
rm100107kolm26_CNP	0	0.28372
mp011909rab937_CNP	0	0.28858
ph113007rab452_CNP	1	0.29214
bf032309rab1012_CNP	0	0.29241
bc061807rol129_CNP	0	0.29255
as051408rab709_CNP	1	0.29261
dr031207rab60_CNP	0	0.29626
rf071808rol438_CNP	0	0.30062
rm013008rab549_CNP	0	0.30485
vk052208rab725_CNP	1	0.30594
ml061708rol412_CNP	1	0.30687
es102708rab848_CNP	0	0.30727
hm031708rab605_CNP	1	0.30843
jg092408rab819_CNP	0	0.30943
aa021907rab38_CNP	1	0.30976
gw100807rol227_CNP	0	0.30978
jn091707rol208_CNP	0	0.31443
rv012408dru140_CNP	0	0.32017
fh080607rolla184_CNP	0	0.32729
ra080608rab789_CNP	0	0.33082
ke091907rab316_CNP	0	0.3354
lr013007rab15_NCP	1	0.33786

Image Name	Melanoma or Benign	f(z)
cw021907rab37_CNP	0	0.34584
rr051107_CNP	1	0.3475
jh021808rol303_CNP	0	0.34788
dh081007rol187_CNP	0	0.35348
ev060507rol117_CNP	1	0.35584
SR020209per202_CNP	0	0.35616
da102607dru99_CNP	0	0.3643
wt022007tre6_CNP	1	0.36551
gm012208rab531_CNP	0	0.36625
as062807dru37_CNP	0	0.37178
es072408rab775_CNP	1	0.37207
cv052308rol394_CNP	0	0.37352
ag061307rab185_CNP	0	0.37658
sp051007rol74_CNP	0	0.38659
jk051508rab716_CNP	1	0.38872
dn081407kolm4_CNP	0	0.39109
JG071807per12_CNP	0	0.39144
tf051809rab1057_CNP	1	0.39522
cm051607tre18_CP	0	0.39569
dk041307rab106_CNP	0	0.39692
jk053007rab166_CNP	0	0.39892
mh011608rab517_CNP	0	0.39901

Image Name	Melanoma or Benign	f(z)
ri012109rab941_CNP	0	0.40898
jh121307rab472_CNP	0	0.40909
jy073107rol171_CNP	1	0.40981
RV122007per52_CNP	0	0.41178
rm013009rab955_CNP	1	0.41528
jb070708rol424_CNP	0	0.41879
ss080307rol175_CNP	0	0.41897
dh081207rab258_CNP	1	0.41914
hw021508rol300_CNP	0	0.425
sm102407rab372_CNP	0	0.42992
cb052407rab159_CNP	1	0.44534
wg030107rab49_CNP	1	0.44829
HW011108per58_CNP	1	0.45064
bn042108rab669_CNP	0	0.45153
dm040308rab631_CNP	1	0.45234
pm060407rab168_CNP	0	0.45424
ch021308rab558_CNP	1	0.45902
ms121708rab903_CNP	1	0.46071
lp092407rol217_CNP	0	0.46318
jg092408rab817_CNP	0	0.46694
hb021909rab982_CNP	1	0.47151
sw061807rab190_CNP	1	0.47369

Image Name	Melanoma or Benign	f(z)
HG061807per3_CNP	1	0.47442
tg071808rab768_CNP	1	0.4749
ck111907dru120_CNP	0	0.47815
jr073007dru63_CNP	0	0.48592
ss123108rab915_CNP	1	0.48601
ts052407rab157_CNP	0	0.48721
ss120208rab894_CNP	1	0.49024
rb021207rab24_CNP	1	0.49467
im011707rab4_CNP	1	0.49934
rb021207rab25_CNP	1	0.49973
as042108rab670_CNP	0	0.50248
me110608rab864_CNP	0	0.51875
mo121307rab470_CNP	1	0.51939
sw080907rab257_CNP	1	0.5212
pc042009rab1045_CNP	1	0.52285
dd090407rol198_CNP	0	0.52461
aj020907rol44_NCP	1	0.52956
fw083007rab287_CNP	1	0.53119
lh121608rab902_CNP	0	0.5359
HM092408per124_CNP	1	0.53733
ll040207rab90_CNP	1	0.53815
jg100807rab346_CNP	1	0.54075

Image Name	Melanoma or Benign	f(z)
cp060107rolla112_CNP	0	0.54307
bc041108rol358_CNP	0	0.54982
kg012607rab1_CNP	1	0.55402
hs061407rolla123_CNP	0	0.55454
bb040407rab96_CNP	1	0.55881
HS050508per77_CNP	0	0.56108
ra091207rab306_CNP	0	0.56132
cl060109rab1076_CNP	1	0.56212
jp062507rab199_CNP	0	0.56319
dm040907rab100_CNP	1	0.56755
ak051007rab131_CNP	1	0.58588
lm040407rab93_CNP	1	0.58994
rw113007rab371_CNP	1	0.59827
sw021507rol23_CNP	0	0.60741
am032608rab615_CNP	0	0.61439
ad040609rab1027_CNP	1	0.61666
mm011708rab523_CNP	1	0.61833
bb061107rol121_CNP	0	0.62423
cb022508rol310_CNP	1	0.62668
bm022108rab572_CNP	0	0.63771
bm021108rab555_CNP	1	0.64503
nc061107rab180_CNP	1	0.64503

Image Name	Melanoma or Benign	f(z)
CI030608rab590_CNP	0	0.64642
iq012709rab948_CNP	1	0.6472
cg031108rol339_CNP	1	0.66425
lr022908rab584_CNP	1	0.67015
CR082508per99_CNP	0	0.67571
dl022307rab42_CNP	0	0.68332
dm041309rab1034_CNP	1	0.68899
jv013007rab16_CNPa	0	0.69531
rk11108rab873_CNP	0	0.69878
sw011309rab930_CNP	1	0.70036
ag061307rab184_CNP	1	0.70444
sb012607rol40_NCP	1	0.70935
gc020807rol42_NCP	1	0.70952
WM083007per19_CNP	1	0.71214
lr013007rab14_CNP	1	0.71284
as033007rab88_CNP	1	0.72979
tb092807rab341_CNP	1	0.73119
ll090508rab799_CNP	1	0.73261
br070109rab1126_CNP	1	0.74064
es090507rab295_CNP	1	0.74133
lr013007rab13_NCP	1	0.74214
dk042408rab681_CNP	1	0.74241

Image Name	Melanoma or Benign	f(z)
aw060908rol408_CNP	1	0.74301
he022008rab568_CNP	1	0.74755
bw072307rol166_CNP	1	0.75767
ap081607rol190_CNP	1	0.76907
JD100407per28_CNP	1	0.77386
ad081507rab264_CP	1	0.77553
lm040407rab94_CNP	1	0.77581
ag070808rol430_CNP	1	0.78001
pk080708rab793_CNP	1	0.78249
sw011309rab932_CNP	1	0.78681
rs031308rab602_CNP	1	0.78789
hb011008rol272_CNP	0	0.78894
ch121907rab487_CNP	1	0.79142
wc031407rab63_CNP	1	0.79402
bt011108rab512_CNP	1	0.80096
jg030308rol327_CNP	1	0.80259
jc081508rol453_CNP	1	0.80339
db040309rab1026_CNP	0	0.80639
tb110508rab864_CNP	0	0.81656
rp041307rol1_CNP	1	0.82596
dd080107dru70_CNP	1	0.82675
sh091407dru90_CNP	1	0.82899

Image Name	Melanoma or Benign	f(z)
ll061107_NCP	1	0.82947
jj121407rol250_CNP	1	0.83874
re042408rol371_CNP	0	0.84367
df101207rab364_CNP	1	0.84666
dw092608rab822_CNP	1	0.85325
lb022608rol319_CNPc	1	0.86621
dc061907dru28_CNP	0	0.8855
sw042808rab689_CNP	1	0.88813
ak030608rab591_CNP	1	0.88897
mb091407dru91_CNP	1	0.90855
ma022609rab994_CNPa	1	0.92532
hs061407rolla124_CNP	1	0.92568
tb013107rab18_CNPa	1	0.92709
cs042607rab116_CNP	1	0.93007
es021009rab967_CNP	0	0.94214
rr041508rol360_CNP	1	0.94418
cd030907rab58_CNP	1	0.95059
jb012709rab946_CNP	0	0.95202
jb080607rolla180_CNP	1	0.95789
rw082608rol470_CNPwhole_	1	0.96522
sz121107dru132_CNP	1	0.96641
lg103107rab374_CNP	1	0.96916

Image Name	Melanoma or Benign	f(z)
ty032107rab74_CNP	1	0.97224
kf102408rol514_CNP	1	0.97312
wt061507rab188_CNP	1	0.97705
es101207rab362_CNP	1	0.9814
ch121907rab488_CNP	1	0.98295
po052507rol97_CNP	1	0.98465
hf020708rab552_CNP	1	0.9847
dr051509rol623_CNP	1	0.98557
wc112807_CNP	1	0.98872
sf030509rol591_CNP	1	0.99015
sw011309rab931_CNP	1	0.99035
yr042308dru148_CNP	1	0.99198
hs061507rab189_CNP	1	0.9923
dw092608rab821_CNP	1	0.99345
hh031207rol15_CNP	1	0.99437
hl101708rab843_CNP	1	0.99578
al102708rab846_CNP	1	0.99588
st052809rab1070_CNP	1	0.9959
jr021808rab566_CNP	1	0.99596
hv062207dru31_CNP	1	0.99642
sm091008rab801_CNP	1	0.9967
ng021207rab27_CNP	1	0.99699

Image Name	Melanoma or Benign	f(z)
jf022108rab570_CNP	1	0.99798
LF071307per8_CNP	1	0.9982
hv071307rol156_CNP	1	0.99869
mr111207rab411_CNP	1	0.99896
ww053008rol398_CNP	1	0.99916
ak061908rab746_CNP	1	0.99946
rr070507rab216_CNP	1	0.99946
dp070507rab218_CNP	1	0.99955
jf022108rab571_CNP	1	0.99963
jk051508rab715_CNP	1	0.99968
ts101707rab367_CNP	1	0.9997
jk061107rol120_CNP	1	0.99978
ea012108rab530_CNP	1	0.99982
gt030907rab54_CNP	1	0.99987
GW052108per80_CNP	1	0.99987
rb031207rab59_CNP	1	0.9999
jt092508rol497_CNP_whole	1	0.99996
pr100907a_rol232_CNP	1	0.99997
JW092807per27_CNP	1	1
mb092208rol493_CNP	1	1
mh110507dru105_CNP	1	1
rl030409rab998_CNP	1	1

Image Name	Melanoma or Benign	f(z)
tr062509rol643_CNP	1	1

APPENDIX B

**TABLE TO TEST THE OBTAINED THRESHOLD VALUE FOR FULL MODEL
ON A TEST SET OF 78 IMAGES**

Image Name	Melanoma or Benign	f(z)
wb090808rol482_CNP	1	7.28E-05
gt021309rab975_CNP	1	0.00073
sb020408rol288_CNP	1	0.000908
jk070808rol428_CNP	1	0.000939
jl072709dru275_CNP	1	0.001301
aw122807per53_CNP	0	0.003041
db060208rol399_CNP	1	0.003302
rs071609rab1149_CNP	1	0.004592
ah013009rab951_CNP	0	0.005765
ar061709rab1105_CNP	0	0.006577
an111507dru119_CNP	0	0.007139
as051707rab145_CNP	0	0.007206
am071509dru270_CNP	0	0.007492
ar061709rab1104_CNP	0	0.008767
bb042108rab667_CNP	0	0.009849
jp100907rol231_CNP	1	0.010834
as051408rab710_CNP	0	0.012521
ar091407rab310_CNP	0	0.015473
ac011108dru137_CNP	0	0.017813
ab063008per95_CNP	0	0.019679
as051408rab706_CNP	0	0.01984

Image Name	Melanoma or Benign	f(z)
at102907dru101_CNP	0	0.024512
eo072209rab1152_CNP	1	0.026753
pt072109dru271_CNP	1	0.030547
rt011408rol273_CNP	1	0.032038
bh070207dru41_CNP	1	0.033884
kh052609rol626_CNP	1	0.035082
ac060909rab1087_CNP	0	0.03702
bh011309dru220_CNP	1	0.038365
et121807dru134_CNP	1	0.048554
ap042507_CNP	0	0.052765
ak012909rab949_CNP	0	0.056004
sc061307dru22_CNP	1	0.062309
jl072709dru273_CNP	1	0.063475
ah072009rab1151_CNP	0	0.071887
dh060308rol401_CNP	1	0.077564
as051408rab711_CNP	0	0.097408
as051408rab708_CNP	0	0.099573
eh071607rolla158_CNP	1	0.128847
an062209rol640_CNP	0	0.157452
nm011508rol275_CNP	1	0.165095
ck081007rolla186_CNP	1	0.169965
da123107rol261_CNP	1	0.191022

Image Name	Melanoma or Benign	f(z)
as033007rab87_CNP	0	0.206606
af083007_CNP	0	0.219347
tb072409rol650_CNP	1	0.237317
al102708rab847_CNP	0	0.295314
ed061907rol131_CNP	1	0.314994
aw031408per70_CNP	0	0.346435
am010809rab925_CNP	0	0.35185
ah091208per115_CNP	0	0.358748
co082107dru78_CNP	1	0.362685
db061008rol409_CNP	1	0.395443
hs061109rab1092_CNP	1	0.414456
ar031607rab67_CNP	0	0.466889
cd030907_CNP	1	0.534184
aj021808rab562_CNP	0	0.554069
nm073107rol172_CNP	1	0.564642
ah011909rab940_CNP	0	0.630997
jw071007rol152_CNP	1	0.64601
mb052308rol396_CNP	1	0.689943
ab030209rol586_CNP	0	0.810008
ap060509rab1080_CNP	0	0.825089
rl061109rab1093_CNP	1	0.830532
rs061708rol414_CNP	1	0.846735

Image Name	Melanoma or Benign	f(z)
aa051308rol383_CNP	0	0.866346
ah112608rab890_CNP	0	0.882649
js070109rab1131_CNP	1	0.882769
as021609rab976_CNP	0	0.928125
wf042407rol61_CNP	1	0.931415
ld102108rol510_CNP	1	0.945446
lr091908rol491_CNP	1	0.960376
ag032009rol598_CNP	0	0.994384
ab090407dru83_CNP	0	0.999276
dc013009rol562_CNP	1	0.999665
ah122107rol256_CNP	0	0.999851
as071309rab1147_CNP	0	0.999985
cp040209rol610_CNP	1	1

APPENDIX C

THRESHOLD SELECTION TABLE FOR ROBUST MODEL

Image Name	Melanoma or benign	f(z)
me012908rab547_CNP	0	0.00005
LW102108per159_CNP	0	0.00165
bw081508rol460_CNP	0	0.0018
ak051007rab132_CNP	0	0.00242
NS091108per107_CNP	0	0.00376
sz110607dru109_CNP	0	0.00461
jh082007rol195_CNP	0	0.00467
mp080107dru69_CNP	0	0.00557
lc052407dru5_CNP	0	0.00562
jp030907rab56_CNP	0	0.00586
DT111507per45_CNP	0	0.006
nd112007dru123_CNP	0	0.00771
BS100108per137_CNP	0	0.00778
lb121807rab483_CNP	0	0.00778
pw111907rab433_CNP	0	0.00781
gm110507dru106_CNP	0	0.00796
lt111407dru113_CNP	0	0.00813
jc091608rab810_CNP	0	0.00825
sg052407dru2_CNP	0	0.00842
kb012908rol281_CNP	0	0.00904
ks112107rab440_CNP	0	0.00919
se062607dru36_CNP	0	0.00938

Image Name	Melanoma or benign	f(z)
ap033108rab625_CNP	0	0.00941
DT111507per46_CNP	0	0.01011
ac031008rol336_CNP	0	0.01038
as042808dru149_CNP	0	0.01047
ek060309dru256_CNP	0	0.01084
fa060107dru15_CNP	0	0.01094
jp051707rab144_CNP	0	0.01097
es091107dru88_CNP	0	0.01099
rr073007dru62_CNP	0	0.01111
dz101107rab359_CNP	0	0.01126
gp020609rab962_CNP	0	0.01142
LP111808per187_CNP	0	0.01146
ls012607rab7_CNP	0	0.01166
mr022709rab995_CNP	0	0.01182
ag100108rab825_CNP	0	0.01195
nw030707tre13_CNP	0	0.01232
ky092507kolm22_CNP	0	0.01245
bz080807dru74_CNP	0	0.01257
jt051408rab712_CNP	0	0.01263
de010609dru217_CNP	0	0.01268
ro031909rab1007_CNP	0	0.01308
sw120308rab897_CNP_whole	0	0.01337

Image Name	Melanoma or benign	f(z)
JF100208per141_CNP	0	0.01377
kb073107rol173_CNP	0	0.01383
dl052609rab1064_CNP	0	0.01389
RD092608per129_CNP	0	0.01411
as070307rab212_CNP	0	0.01425
DH062308PER91_CNP	0	0.01437
se022307rab40_CNP	0	0.0144
mt033108rab627_CNP	0	0.01522
ks040209rab1021_CNP	0	0.01562
cm102907_CNP	0	0.01588
tw052507dru6_CNP	0	0.01593
lb060608rol407_CNP	0	0.0163
jf050208rab694_CNP	0	0.01675
mg080607rab251_CNP	0	0.01697
lv061908rab747_CNP	0	0.01704
sk101807rab370_CNP	0	0.01721
kr120307rab455_CNP	0	0.01835
js070907rab223_CNP	0	0.01838
GA052308per84_CNP	0	0.01882
bg121107rab465_CNP	0	0.01888
AV110408rab857_CNP	0	0.01909
av072607_CNP	0	0.01936

Image Name	Melanoma or benign	f(z)
SC050808per79_CNP	0	0.01946
sf031309rab1001_CNP	0	0.01954
jp070207rab204_CNP	0	0.0196
ms062907dru40_CNP	0	0.01993
rh091907rab315_CNP	0	0.01999
oa073107dru65_CNP	0	0.02004
jh121307rab471_CNP	0	0.02019
jb051208dru169_CP	0	0.02043
mp020509rab958_CNP	0	0.02102
sp011409dru221_CNP	0	0.02123
bl081808rol462_CNP	0	0.02137
sr110807dru110_CNP	0	0.02144
pb050708dru160_CNP	0	0.02187
ds041808rol362_CNP	0	0.02188
tb041207rab103_CNP	0	0.02246
mc111507dru115_CNP	0	0.02248
lv041708rab662_CNP	0	0.02251
ps070607dru44_CNP	0	0.02267
rv012408dru140_CNP	0	0.02277
ah042009rab1046_CNP	0	0.02308
tz020708dru143_CNP	0	0.02323
sw120308rab898_CNP	0	0.02349

Image Name	Melanoma or benign	f(z)
me110608rab863_CNP	0	0.02376
cd112107dru126_CNP	0	0.0238
vf032409rab1013_CNP	0	0.02382
om070209rab1132_CNP	0	0.02397
RT092107per25_CNP	0	0.0246
pb091908rol492_CNP	0	0.02462
ah042009rab1047_CNP	0	0.02556
CT110907per40_CNP	0	0.02593
nz052307rab153_CNP	0	0.02608
as070307rab211_CNP	0	0.02621
mk051007_CNP	0	0.02625
db010307rol268_CNP	0	0.02633
jm041808rab665_CNP	0	0.02641
sl052609rab1063_CNP	1	0.02651
am021408rol294_CNP	0	0.02655
ll052407tre25_CP	0	0.02686
kf031708rab604_CNP	0	0.02717
pw062907rol141_CNP	0	0.02727
cf053107tre29_CNP	0	0.0273
MS102507per33_CNP	0	0.0275
dp041808rab664_CNP	0	0.02768
dt010908rab508_CNP	0	0.02787

Image Name	Melanoma or benign	f(z)
as033007rab88_CNP	1	0.02792
MG100507per31_CNP	0	0.02796
nn092607kolm24_CNP	0	0.02811
oa073107dru66_CNP	0	0.02814
sm071607dru50_CNP	0	0.02842
jb112108rol523_CNP	0	0.02869
ad040609rab1028_CNP	0	0.02884
rc082707rab274_CNP	1	0.0289
ny012208rab535_CNP	0	0.02901
mf061907dru29_CNP	0	0.02924
mg050508rab698_CNP	0	0.02935
ts052407rab158_CNP	0	0.02943
dw092608rab823_CNP	0	0.02961
DY012808per60_CNP	0	0.02963
tc041409rab1036_CNP	0	0.02975
dl121807rab484_CNP	0	0.02982
AW122807per54_CNP	0	0.02998
JK091108per106_CNP	0	0.03082
jh051007rol73_CNP	0	0.03089
db073008rab779_CNP	0	0.03099
kf052908rab731_CNP	0	0.03143
RT082908per101_CNP	0	0.03169

Image Name	Melanoma or benign	f(z)
sl072307dru56_CNP	0	0.03173
pg080707rab254_CNP	0	0.03192
db021207rol24_CNP	0	0.03218
bk061208rab740_CNP	0	0.03251
ld011508dru138_CNP	0	0.03311
jj051408dru172_CNP	0	0.0335
as051408rab709_CNP	1	0.03354
GH010609per201_CNP	0	0.03364
MC041408per74_CNP	0	0.03371
gp020609rab963_CNP	0	0.03385
jw021709rab978_CNP	0	0.03386
dd070207rab205_CNP	0	0.0346
JT111208per183_CNP	0	0.03481
md110608rab866_CNP	0	0.03508
ab061507_CNP	0	0.0352
pl062309rab1111_CNP	0	0.03542
st032107rab73_CNP	0	0.03552
kf070507_CP	0	0.03604
gm012208rab532_CNP	0	0.03619
rc041608rab660_CNP	0	0.03623
mb032609rab1015_CNP	0	0.03626
pl050608dru158_CNP	0	0.03639

Image Name	Melanoma or benign	f(z)
JH101408per145_CNP	0	0.03641
mr110807rab403_CNP	0	0.03687
js052907dru11_CNP	0	0.03699
br112107dru125_CNP	0	0.03732
RT082908per100_CNP	0	0.03732
ab021709rol577_CNP	0	0.03762
gm110507dru107_CNP	0	0.03778
BB062508PER94_CNP	0	0.03782
cc091608rab807_CNP	0	0.03817
dp070907rab222_CNP	0	0.03845
sm010308rab502_CNP	0	0.03851
sb032207tre15_CNP	0	0.03875
jw072707rol169_CNP	0	0.03886
mc111507dru117_CNP	0	0.03913
cb112107rab439_CNP	0	0.03915
rb120407rab457_CNP	0	0.03919
gs071508rab761_CNP	0	0.03927
jb061108rab737_CNP	0	0.03955
ll040307rol5_CNP	0	0.0401
ef120407dru128_CNP	0	0.04031
sw053007rab161_CNP	0	0.04035
as101807rab369_CNP	0	0.04083

Image Name	Melanoma or benign	f(z)
as090707rab300_CNP	1	0.04132
DB052108per82_CNP	0	0.04165
me012908rab548_CNP	0	0.04172
jc041009rab1033_CNP	0	0.04174
rb021207rab24_CNP	1	0.04184
mo082207rab271_CNP	0	0.04212
sb020408rol289_CNP	0	0.04217
cw011909rol560_CNP	0	0.04281
jw021709rab979_CNP	0	0.04323
rb121707rab480_CNP	0	0.04325
es090507rab296_CNP	0	0.04338
kv071808rab770_CNP	0	0.04377
if040208rab629_CNP	0	0.04426
rb091007rol202_CNP	0	0.04459
ck020508rol291_CNP	0	0.04461
dm082608rol468_CNP	0	0.04464
kr050508dru155_CNP	0	0.04489
ck111907dru120_CNP	0	0.0451
jc050307rab125_CNP	0	0.04511
DH062308PER92_CNP	0	0.0452
jt082807rab280_CNP	0	0.04542
ar111907rab432_CNP	0	0.04585

Image Name	Melanoma or benign	f(z)
dk071408rab760_CNP	0	0.04597
kf031209rab996_CNP	0	0.04629
me012908rab546_CNP	0	0.04651
sm0417409rab1042_CNP	0	0.04662
im011707rab4_CNP	1	0.04697
ds040109rab1023_CNP	0	0.04712
rc062509rab1118_CNP	0	0.04737
cg032009rab1010_CNP	0	0.04744
mm053007tre26_CP	0	0.04749
jp030907rab57_CNP	0	0.04764
wa051608dru176_CNP	0	0.04768
ve112108rab886_CNP	0	0.04867
td071708rab766_CNP	0	0.04925
la090408rol477_CNP	0	0.04942
kj082807kolm12_CNP	0	0.0496
jb042308rab677_CNP	0	0.05008
wv072607dru59_CNP	0	0.05052
eb040308rab632_CNP	0	0.05056
ss021207rab30_CNP	0	0.05077
jr073007dru63_CNP	0	0.05112
sr020209rab960_CNP	0	0.05149
as073107rab244_CNP	0	0.05166

Image Name	Melanoma or benign	f(z)
js091807rol215_CNP	0	0.05244
as051408rab707_CNP	1	0.05251
ss040308rol352_CNP	0	0.05281
lc032608rab616_CNP	0	0.05347
RD092608per128_CNP	0	0.05374
lg091107dru89_CNP	0	0.05401
ed052109rab1060_CP	1	0.05414
sm092507dru94_CNP	0	0.05509
lr061108rab738_CNP	0	0.05514
ra091207rab305_CNP	0	0.05582
LB110907per42_CNP	0	0.05599
gt071207rab228_CNP	0	0.05605
md110807rab400_CNP	1	0.05608
jd020707rab19_CNP	0	0.05611
dl111407dru111_CNP	0	0.05628
mf072308rab772_CNP	0	0.05655
jj030207tre11_CNP	0	0.05657
nd021109rab972_CNP	0	0.05686
hl062609rab1124_CNP	1	0.0572
as062807dru37_CNP	0	0.05724
st032107rab72_CNP	0	0.0577
mr021109rab973_CNP	0	0.05786

Image Name	Melanoma or benign	f(z)
ef042408rab684_CNP	0	0.05788
bg121107rab464_CNP	0	0.05802
sl011309dru219_CNP	0	0.05806
ef042408rab683_CNP	0	0.05812
rk020909rab965_CNP	0	0.05819
gn032508rol344_CNP	0	0.05865
EH112607per47_CP	0	0.05894
td071708rab767_CNP	0	0.05962
fh080607rolla184_CNP	0	0.06005
bh113007rab451_CNP	0	0.06024
hl101708rab844_CNP	0	0.06024
ja061807rol130_CNP	0	0.06034
as040408rab635_CNP	0	0.06088
as030308rab586_CNP	0	0.06102
jp051707rab143_CNP	0	0.06111
db070307dru43_CNP	0	0.0612
mk042709rab1053_CNP	0	0.06137
th040609rab1029_CNP	0	0.06147
jf051007rab133_CNP	0	0.0621
ad040507rab98_CNP	0	0.06223
ld061507dru25_CNP	0	0.06247
rc082707rab275_CNP	0	0.06252

Image Name	Melanoma or benign	f(z)
ri012109rab942_CNP	0	0.06326
lz032907rab84_CNP	0	0.06349
ce061908rol417_CNP	0	0.06388
da102607dru99_CNP	0	0.06396
jh050207rab122_CNP	0	0.06405
tm032808rab620_CNP	0	0.06526
sp051007rol74_CNP	0	0.06541
SRT123107rab501_CNP	0	0.06627
pa032808rab624_CNP	0	0.0664
da102607dru100_CNP	0	0.06652
kj112508rab888_CNP	0	0.06659
jv033009rab1016_CNP	0	0.06722
bj011509rab935_CNP	0	0.06749
de011209rab929_CNP	0	0.06786
dd081307rolla188_CNP	0	0.0679
sp070207rab203_CNP	0	0.06796
jp062507rab197_CNP	0	0.06801
mj071807dru53_CNP	0	0.0681
gm012208rab531_CNP	0	0.06837
ar100208rab827_CNP	0	0.0685
gm012208rab534_CNP	0	0.06863
is070607dru45_CNP	0	0.06875

Image Name	Melanoma or benign	f(z)
GB021709per207_CNP	0	0.06883
bb082107rol196_CNP	1	0.06904
CK122308rab911_CNP	0	0.06915
ap121608Rab900_CNP	0	0.06941
wt022007tre8_CNP	0	0.07108
ng040908rab646_CNP	0	0.07133
cv022908dru146_CNP	0	0.07196
kb012908rol282_CNP	0	0.07197
bw070307rab209_CNP	0	0.07256
tb091007dru87_CNP	0	0.07316
lr112608rab889_CNP	0	0.07323
em011808rab525_CNP	0	0.07326
mc070808rab756_CNP	0	0.07341
js020108rol283_CNP	0	0.07403
nm081407rab263_CNP	0	0.0741
ha092407kolm20_CNP	0	0.0747
dm121007dru131_CNP	0	0.07484
DZ091508per116_CNP	0	0.07508
eb032607rab81_CNP	0	0.07542
rb051908rab722_CNP	0	0.07544
cw051208rab703_CNP	0	0.07567
bk041008rab649_CNP	1	0.07576

Image Name	Melanoma or benign	f(z)
MJ120507per49_CNP	0	0.07675
mk021009rab970_CNP	0	0.07677
eb053107rolla105_CNP	0	0.07755
JF100208per140_CNP	0	0.07773
mp011909rab938_CNP	0	0.0782
kr020408rol287_CNP	0	0.07833
sa060109rab1073_CNP	0	0.07883
kp012907rab9_CNP	0	0.07928
cc061207dru20_CNP	0	0.07963
mc111507dru118_CNP	0	0.08007
as080207rab249_CNP	0	0.08027
ma071408rab759_CNP	1	0.08043
cp060107rolla110_CNP	0	0.0806
kr123107rol264_CNP	0	0.08078
am021508rol297_CNP	0	0.08158
di062607dru34_CNP	0	0.08185
jd070607rol148_CNP	0	0.08243
sa031308rab601_CNP	1	0.08244
mg101608rol507_CNP_whole	0	0.08261
as090507dru85_CNP	0	0.08262
er062909dru260_CNP	0	0.08345
rc021208rab556_CNP	0	0.08415

Image Name	Melanoma or benign	f(z)
kp042607rab118_CNP	0	0.08452
LM103108per167_CNP	0	0.08466
cw021907rab37_CNP	0	0.08473
TP021009per204_CNP	0	0.08497
cv052308rol394_CNP	0	0.08519
lt030207rol20_CNP	0	0.0854
ak041009rab1034_CP	0	0.08544
rr121107dru133_CNP	0	0.08552
ag061307rab186_CNP	0	0.08563
gp020609rab961_CNP	0	0.08598
cm121707_CNP	0	0.08609
tc101907rolla242_CNP	0	0.08614
ja012808rol278_CNP	0	0.08715
jv053008rab734_CNP	0	0.08735
dc110607rab395_CNP	0	0.08877
ck122308rab909_CNP	0	0.0888
or100608rol498_CNP	0	0.08939
mr051608rab721_CNP	0	0.08962
GA052308per83_CNP	0	0.08966
kl090407dru81_CNP	0	0.08977
br121007rab461_CNP	0	0.09063
ar121407rab476_CNP	1	0.09064

Image Name	Melanoma or benign	f(z)
bh113007rab373_CNP	0	0.0911
am032608rab615_CNP	0	0.09129
rh032808rol346_CNP	0	0.09187
jv060508rol403_CNP	0	0.09253
im102008rab845_CNP	0	0.09306
cw081507dru77_CNP	0	0.09308
rc100207kolm27_CNP	0	0.09338
jb110907rab407_CNP	0	0.09352
mo112008rol552_CNP	0	0.09397
as112707rab444_CNP	0	0.09412
fr050808dru162_CNP	0	0.0945
jn091707rol212_CNP	0	0.09461
wb070209rab1136_CNP	0	0.09481
mg061807_CNP	0	0.09484
dd080107dru70_CNP	1	0.09524
ar091407rab309_CNP	0	0.09605
dc020108rol284_CNP	0	0.09611
yd040407rab97_CNP	0	0.09658
jd022009rab985_CNP	1	0.0971
md110608rab865_CNP	0	0.09728
rm062107dru30_CNP	0	0.09785
gr110408rab859_CNP	0	0.0983

Image Name	Melanoma or benign	f(z)
jw021709rab977_CNP	0	0.09841
SS110708per174_CNP	0	0.09853
cn101807rol238_CNP	0	0.09869
ri012109rab941_CNP	0	0.09915
HG031408per68_CNP	0	0.09959
RV122007per51_CNP	0	0.09963
lp062007rab200_CNP	1	0.0998
cb071607rol159_CNP	0	0.10053
md120908rol539_CNP	0	0.10157
hw021508rol301_CNP	0	0.10161
pk082907rab281_CNP	0	0.10161
pf072407dru57_CNP	0	0.10181
MT060807per2_CP	0	0.10259
lg081707rolla194_CNP	0	0.1027
dm042307rol59_CNP	0	0.10289
wr052407dru4_CNP	0	0.10577
dl111407dru112_CNP	0	0.10581
pb061107dru17_CNP	0	0.10596
cs071807rolla163_CNP	0	0.10612
ra040308rol349_CNP	0	0.10629
dl012408dru139_CNP	0	0.10722
rm052907dru9_CNP	0	0.10726

Image Name	Melanoma or benign	f(z)
ca022807rab46_CNP	0	0.10771
cb072508rab776_CNP	0	0.10777
rk11108rab874_CNP	0	0.10792
dp111308rab875_CNP	0	0.10803
JG071807per11_CNP	0	0.1084
al111907rab434_CNP	0	0.10898
ar031607rab68_CNP	0	0.10928
ml033108rol347_CNP	0	0.10942
rw111308rol519_CNP	0	0.1101
rk020909rab964_CNP	0	0.11067
sm010209rol547_CNP	0	0.1108
AV110408rab858_CNP	0	0.11145
de122106rol34_NCP	0	0.1115
jg092408rab818_CNP	0	0.11177
tr022908rol326_CNPb	0	0.11237
cp060509rab1078_CNP	0	0.11432
bc091807kolm19_CNP	0	0.11444
pc042009rab1044_CNP	1	0.11474
mr110807rab404_CNP	0	0.1149
ag061307rab185_CNP	0	0.11528
cp040108rab628_CNP	0	0.11773
lm011608rab518_CNP	0	0.11783

Image Name	Melanoma or benign	f(z)
js091208rol485_CNPwhole	0	0.11851
ee122508dru145_CNP	0	0.11884
jp030608rol332_CNP	0	0.11913
JT111208per182_CNP	0	0.11938
rd062107rab201_CNP	0	0.12051
tb110508rab864_CNP	0	0.12071
jm033109rab1019_CNP	0	0.12101
es010708dru136_CNP	0	0.12192
br121007rab462_CNP	0	0.12228
ca050907rab128_CNP	0	0.12267
rm052907dru10_CNP	0	0.12285
tt012609rab945_CNP	0	0.12369
rm021309rab952_CNP	0	0.12401
ks020408rol286_CNP	0	0.12539
ks070907rolla151_CNP	0	0.12696
ag080907rab259_CNP	1	0.12738
ss123108rab915_CNP	1	0.12973
es072408rab775_CNP	1	0.13072
rl103107rab379_CNP	0	0.13107
ri012109rab943_CNP	0	0.1312
tw010307rol266_CNP	0	0.13249
ls111108rab872_CNP	0	0.13258

Image Name	Melanoma or benign	f(z)
pr070109rab1130_CNP	1	0.13341
bj041207tre16_CNP	0	0.13528
ss032007rol9_CNP	0	0.13585
ke091907rab316_CNP	0	0.13604
wg082008rab748_CNP	0	0.13641
ra091207rab306_CNP	0	0.13751
rr042009rol613_CNP	1	0.13788
nz010807rol36_NCP	0	0.13791
CI030608rab590_CNP	0	0.1381
av042908rab686_CNP	0	0.13865
es010408rab505_CNP	0	0.13972
jh022307rab41_CNP	0	0.14019
jd020209rab953_CNP	0	0.14052
cb022508rol310_CNP	1	0.14236
aa021907rab38_CNP	1	0.14252
tm033009rab1018_CNP	0	0.1428
lc052207rol89_CNP	0	0.14347
cj082207rab272_CNP	0	0.14398
rb053007dru13_CNP	0	0.14412
wr052407dru3_CNP	0	0.14503
ad021607rab35_CNP	0	0.14544
fh080607rolla182_CNP	0	0.14547

Image Name	Melanoma or benign	f(z)
me110608rab864_CNP	0	0.14579
dp032508rab614_CNP	0	0.14626
DY012808per61_CNP	0	0.1464
rb050108rab692_CNP	0	0.14672
jl111407dru114_CNP	0	0.14673
LB110907per41_CNP	0	0.14749
hm031708rab605_CNP	1	0.14952
sl072307dru55_CNP	0	0.15094
tr040408rab637_CNP	0	0.15173
sc042308rab678_CNP	1	0.15195
cs050808dru164_CNP	0	0.15355
ja060407dru16_CNP	0	0.15422
ev112408rol527_CNP	0	0.15432
jc091608rab811_CNP	0	0.15587
cm052507rol98_CNP	0	0.15598
hc051407rol78_CNP	0	0.15919
as073008rab781_CNP	0	0.15925
rs010308rab503_CNP	0	0.16112
cm051607tre18_CP	0	0.16202
tr121907rab489_CNP	0	0.16225
rs121207rab468_CNP	0	0.16386
re042408rol376_CNP	0	0.16422

Image Name	Melanoma or benign	f(z)
dr052209rab1062_CNP	0	0.16442
ck122308rab910_CNP	0	0.16459
kh112807dru127_CNP	0	0.16606
bf062509rab1116_CNP	0	0.16713
ev060507rol117_CNP	1	0.16721
jb031809rab1005_CNP	0	0.16729
kb022707rol53_NCP	0	0.16803
as090507dru86_CNP	0	0.16838
CL072108PER96_CNP	0	0.16926
mc062107_CNP	0	0.17004
oa073107dru64_CNP	0	0.17017
re042408rol375_CNP	0	0.17048
mr022007rolla47_NCP	0	0.17074
cb041509rab1039_CNP	0	0.17107
mc111507dru116_CNP	0	0.17144
ac031008rol337_CNP	0	0.1721
dl011409rab934_CNP	1	0.17246
kv090707rol200_CNP	0	0.17481
br070109rab1126_CNP	1	0.17592
jn091707rol211_CNP	0	0.17641
rm013009rab955_CNP	1	0.17679
mm062207dru33_CNP	1	0.17787

Image Name	Melanoma or benign	f(z)
al050708rab700_CNP	0	0.1788
aw060908rol408_CNP	1	0.17907
ak051007rab131_CNP	1	0.1795
tl073107dru68_CNP	0	0.18014
jb080607rolla180_CNP	1	0.18074
ma051507_CNP	0	0.18092
kd052008rol392_CNP	0	0.18425
lp020907rol43_CP	0	0.18443
wc050208rab696_CNP	1	0.18482
gw100807rol227_CNP	0	0.18597
SH092908per135_CNP	0	0.1864
pb050808rol381_CNP	0	0.18824
HS050508per76_CNP	0	0.1886
wbeb080707dru72_NCP	0	0.1889
jj121407rol250_CNP	1	0.18906
rp100907rab349_CNP	0	0.18919
eo073007dru61_CNP	0	0.18926
de111808dru254_CP	0	0.1893
jg092408rab819_CNP	0	0.18943
mr062408rol418_CNP	0	0.18988
rc052308rab728_CNP	0	0.19115
ms041808rab666_CNP	1	0.19138

Image Name	Melanoma or benign	f(z)
ar092408rab816_CNP	0	0.19161
mc071707_CNP	0	0.19244
pc042009rab1045_CNP	1	0.19245
pa032808rab623_CNP	0	0.19248
bf121207rab466_CNP	0	0.1927
ew061507rol127_CNP	0	0.19305
ph113007rab452_CNP	1	0.19324
js071508rol436_CNP	0	0.19546
ew022807rol21_CNP	0	0.19642
HC102607per35_CNP	0	0.19682
pm060407rab169_CNP	0	0.19908
ew101907rol239_CNP	0	0.19969
ao061407rol126_CNP	0	0.2003
gv041509rab1041_CNP	0	0.20082
jj061307dru21_CNP	0	0.20083
jh121307rab472_CNP	0	0.20116
HB122208per200_CNP	1	0.20141
dt052008dru181_CNP	0	0.21073
TT010308per55_CNP	0	0.21084
jb080607rolla181_CNP	0	0.21097
oj070609rab1139_CNP	0	0.21323
HG061807per3_CNP	1	0.2133

Image Name	Melanoma or benign	f(z)
bm022108rab572_CNP	0	0.21398
CR082508per99_CNP	0	0.21636
jn091707rol208_CNP	0	0.21668
kr123107rol263_CNP	0	0.21788
vn080309rol653_CNP	1	0.22022
CR082508per98_CNP	0	0.22141
cm072508rab777_CNP	0	0.22336
VG082707per17_CNP	0	0.22343
re042408rol370_CNP	0	0.22352
hs061407rolla123_CNP	0	0.22363
mv052107rab150_CNP	0	0.22449
bm021108rab555_CNP	1	0.2261
cl050307rab124_CNP	0	0.22663
cp051408dru171_CNP	0	0.22766
ll061107_NCP	1	0.22777
ml061708rol412_CNP	1	0.23098
JS121907per50_CNP	0	0.2331
hw021508rol300_CNP	0	0.23316
rb050207_NCP	0	0.23364
ca032508rol345_CNP	0	0.2347
as042108rab670_CNP	0	0.23782
rm100107kolm26_CNP	0	0.23876

Image Name	Melanoma or benign	f(z)
gv073107dru67_CNP	0	0.23964
KS020209per203_CNP	0	0.24099
wt022007tre6_CNP	1	0.24117
st012108rol277_CP	0	0.24129
LM103108per168_CNP	0	0.24227
KB060807per1_CNP	0	0.24298
hk030508rab589_CNP	1	0.24666
JD100407per28_CNP	1	0.25013
lm040407rab93_CNP	1	0.25157
dl022307rab42_CNP	0	0.25159
lh121608rab902_CNP	0	0.25161
em051608rol386_CNP	0	0.25257
sp071807dru54_CNP	0	0.25359
sm102407rab372_CNP	0	0.25403
fw083007rab287_CNP	1	0.25417
tf051809rab1057_CNP	1	0.2545
EF061608PER89_CNP	0	0.25468
yc070209rab1135_CNP	0	0.25487
md032607rab80_CNP	0	0.25495
ss120208rab894_CNP	1	0.25566
sh091407dru90_CNP	1	0.25903
gm110507dru108_CNP	0	0.26

Image Name	Melanoma or benign	f(z)
HW011108per58_CNP	1	0.26049
pk082907rab282_CNP	1	0.263
jm033109rab1020_CNP	0	0.26699
jb070708rol424_CNP	0	0.26788
dn081407kolm4_CNP	0	0.27176
wt061507rab188_CNP	1	0.27216
js091807rol216_CNP	0	0.27366
mc041307rab105_CNP	0	0.27674
sa082107kolm9_CNP	0	0.2799
mr051707_CNP	0	0.28067
jb041708rab661_CNP	0	0.2809
bf032309rab1012_CNP	0	0.28126
JG071807per12_CNP	0	0.28126
mr111207rab412_CNP	0	0.28218
rm022707rol54_NCP	0	0.28318
dn081707rab266_CNP	0	0.28322
jp062507rab199_CNP	0	0.28333
sc100208rab826_CNP	0	0.28364
dm041309rab1034_CNP	1	0.28385
mj071807dru52_CNP	0	0.28431
md032607rab79_CNP	0	0.28509
rb021207rab25_CNP	1	0.28876

Image Name	Melanoma or benign	f(z)
bb061107rol121_CNP	0	0.28906
lw022708rab580_CNP	1	0.28936
je052507dru7_CNP	0	0.29106
dk041307rab106_CNP	0	0.29466
mp062309rab1113_CNP	0	0.29748
jm020909rol569_CNP	0	0.29815
dd090407rol198_CNP	0	0.29839
lr022908rab584_CNP	1	0.29931
ab081307rab260_CNP	0	0.29977
md072308rab773_CNP	0	0.30057
es101207rab362_CNP	1	0.30324
jl110408rol518_CNP	0	0.30486
rp100907rab348_CNP	0	0.30514
md033007rol6_CNP	0	0.30776
lm062909rab1125_CNP	0	0.30976
tb092807rab341_CNP	1	0.31027
rp041307rol1_CNP	1	0.31049
cc080307rol177_CNP	0	0.31131
ll090508rab799_CNP	1	0.31528
sw080907rab257_CNP	1	0.31747
ob092407rab329_CNP	0	0.31999
ch021308rab558_CNP	1	0.3212

Image Name	Melanoma or benign	f(z)
ra040308rol350_CNP	0	0.32134
db040309rab1026_CNP	0	0.32194
ck062209rol641_CNP	0	0.32334
lc060807rol119_CNP	0	0.32454
sa082207rab273_CNP	1	0.32497
LF071307per8_CNP	1	0.32551
dc061907dru28_CNP	0	0.32777
sw021507rol23_CNP	0	0.32807
ds042307rab111_CNP	0	0.32839
dm040907rab100_CNP	1	0.3299
as101807rab368_CNP	0	0.33063
LS021108per64_CNP	0	0.33221
es090507rab295_CNP	1	0.33334
aj020907rol44_NCP	1	0.33338
re042408rol374_CNP	0	0.33466
kr110408rab856_CNP	0	0.33475
jk053007rab166_CNP	0	0.33556
jg030308rol327_CNP	1	0.33607
sk082007rab268_CNP	0	0.33664
jp062507rab198_CNP	0	0.33794
jc041009rab1032_CNP	0	0.34
ve121907rab485_CNP	1	0.34041

Image Name	Melanoma or benign	f(z)
mv021607rab34_CNP	1	0.34189
jg092408rab817_CNP	0	0.34192
fh080607rolla183_CNP	0	0.34265
rf071808rol438_CNP	0	0.34592
dh031309rab1000_CNP	0	0.34633
lg081707rolla193_CNP	0	0.34804
dl072108rab771_CNP	0	0.35463
lf032808rab621_CNP	0	0.35994
lr013007rab15_NCP	1	0.36135
pt052609rab1065_CNP	0	0.36886
dh081207rab258_CNP	1	0.37008
JG102907per38_CNP	0	0.37565
BA070907per7_CNP	0	0.38462
kd100807rol229_CNP	0	0.38505
jb072007rol165_CNP	0	0.38656
kg012607rab1_CNP	1	0.38682
pw050707tre17_CNP	0	0.38791
vk052208rab725_CNP	1	0.38835
jb012709rab946_CNP	0	0.39251
jy073107rol171_CNP	1	0.39503
rm013008rab549_CNP	0	0.39552
PG091108per109_CNP	0	0.39649

Image Name	Melanoma or benign	f(z)
bn042108rab669_CNP	0	0.39667
rk11108rab873_CNP	0	0.39695
ty032107rab74_CNP	1	0.39707
sw061807rab190_CNP	1	0.40354
po052507rol97_CNP	1	0.40699
nc061107rab180_CNP	1	0.40737
wb080707dru73_CNP	0	0.40768
re042408rol373_CNP	0	0.40827
dt052008dru182_CNP	0	0.40833
jk032807rab83_CNP	0	0.41069
dt062507rol138_CNP	0	0.41595
lb022608rol319_CNPc	1	0.41692
lp092407rol217_CNP	0	0.41961
rw010709rab921_CNP	0	0.42122
hb021909rab982_CNP	1	0.42987
rb070109rab1127_CNP	0	0.43101
SR020209per202_CNP	0	0.43714
gt030907rab54_CNP	1	0.44173
rr031207rol14_CNP	0	0.4427
cl060109rab1076_CNP	1	0.4434
ll040207rab90_CNP	1	0.44456
pm060407rab168_CNP	0	0.44503

Image Name	Melanoma or benign	f(z)
ts052407rab157_CNP	0	0.44576
bt011108rab512_CNP	1	0.4496
jy011609rol557_CNP	1	0.45115
dm040308rab631_CNP	1	0.45258
lg103107rab374_CNP	1	0.45276
rl103107rab378_CNP	0	0.45417
jk051508rab716_CNP	1	0.45517
hb011008rol272_CNP	0	0.45797
ak030608rab591_CNP	1	0.46093
dk042408rab681_CNP	1	0.4624
tg071808rab768_CNP	1	0.46486
no051908rol390_CNP	0	0.46767
ss080307rol174_CNP	0	0.46877
sb012607rol40_NCP	1	0.47326
ra080608rab789_CNP	0	0.48037
ad040609rab1027_CNP	1	0.48156
hh031207rol15_CNP	1	0.48633
pk080708rab793_CNP	1	0.48653
hl101708rab843_CNP	1	0.49407
MC041408per73_CNP	0	0.49496
ss080307rol175_CNP	0	0.49625
pm030107tre10_CNP	0	0.50201

Image Name	Melanoma or benign	f(z)
as110408rab860_CNP	0	0.50489
mh011608rab517_CNP	0	0.50607
gc020807rol42_NCP	1	0.50737
ma022609rab994_CNPa	1	0.5101
cp060107rolla112_CNP	0	0.51025
sw011309rab932_CNP	1	0.5105
wg030107rab49_CNP	1	0.51289
lr013007rab14_CNP	1	0.52085
cg031108rol339_CNP	1	0.52324
es021009rab967_CNP	0	0.5237
ka052307_CNP	0	0.53023
ar092408rab815_CNP	0	0.54165
mb091407dru91_CNP	1	0.55082
es102708rab848_CNP	0	0.56511
cp050707rab127_CNP	0	0.56524
RV122007per52_CNP	0	0.56623
mm011708rab523_CNP	1	0.5694
sz121107dru132_CNP	1	0.57278
bc061807rol129_CNP	0	0.57306
bc041108rol358_CNP	0	0.57575
re042408rol372_CNP	0	0.58043
al102708rab846_CNP	1	0.58161

Image Name	Melanoma or benign	f(z)
rr041508rol360_CNP	1	0.58178
jh021808rol303_CNP	0	0.58836
ap081607rol190_CNP	1	0.59218
WM083007per19_CNP	1	0.59388
ng021207rab27_CNP	1	0.59549
jd032207rol57_CP	0	0.59793
re042408rol371_CNP	0	0.60007
mo121307rab470_CNP	1	0.60888
lp071107dru47_CNP	0	0.61611
dw092608rab822_CNP	1	0.62024
HC102607per34_CNP	0	0.62516
wh052907rol102_CNP	1	0.62569
ng040908rab645_CNP	0	0.63475
lr013007rab13_NCP	1	0.63771
ag070808rol430_CNP	1	0.64054
he022008rab568_CNP	1	0.65853
ms121708rab903_CNP	1	0.65877
sw042808rab689_CNP	1	0.65931
ea012108rab530_CNP	1	0.66052
mp011909rab937_CNP	0	0.6627
ch121907rab487_CNP	1	0.66573
PH2100407per30_CNP	0	0.66661

Image Name	Melanoma or benign	f(z)
JD061808PER90_CNP	0	0.66817
rw113007rab371_CNP	1	0.67518
dr051509rol623_CNP	1	0.69552
iq012709rab948_CNP	1	0.6956
jf022108rab570_CNP	1	0.69599
EQ071607per10_CNP	0	0.69658
RW091708per121_CNP	0	0.69983
dr031207rab60_CNP	0	0.7103
jg012108rab529_CNP	0	0.73252
rr051107_CNP	1	0.73421
ct042909rab1054_CNP	0	0.75005
tb013107rab18_CNPb	1	0.75292
wc112807_CNP	1	0.75306
HS050508per77_CNP	0	0.75434
df101207rab364_CNP	1	0.75748
mb092208rol493_CNP	1	0.75827
jc081508rol453_CNP	1	0.75942
hs061407rolla124_CNP	1	0.76883
pb032207tre14_CNP	1	0.77002
sf030509rol591_CNP	1	0.77008
cd030907rab58_CNP	1	0.77767
dh081007rol187_CNP	0	0.79223

Image Name	Melanoma or benign	f(z)
JW092807per27_CNP	1	0.79399
hs061507rab189_CNP	1	0.79821
gc061307_CP	0	0.79919
ww053008rol398_CNP	1	0.80536
jk061107rol120_CNP	1	0.80956
hv071307rol156_CNP	1	0.80989
sm091008rab801_CNP	1	0.81195
ad081507rab264_CP	1	0.81971
rw082608rol470_CNPwhole_	1	0.81983
bw072307rol166_CNP	1	0.82199
wc031407rab63_CNP	1	0.83112
cs042607rab116_CNP	1	0.83265
rs031308rab602_CNP	1	0.83381
ak061908rab746_CNP	1	0.84075
cb052407rab159_CNP	1	0.84146
GW052108per80_CNP	1	0.8445
jv013007rab16_CNPa	0	0.866
HM092408per124_CNP	1	0.87203
bb040407rab96_CNP	1	0.88106
sw011309rab930_CNP	1	0.88324
lm040407rab94_CNP	1	0.88325
jf022108rab571_CNP	1	0.88949

Image Name	Melanoma or benign	f(z)
rl030409rab998_CNP	1	0.91905
rr070507rab216_CNP	1	0.92525
hv062207dru31_CNP	1	0.92547
yr042308dru148_CNP	1	0.92577
jr021808rab566_CNP	1	0.92723
tc101907rolla241_CNP	0	0.92723
hf020708rab552_CNP	1	0.92797
ch121907rab488_CNP	1	0.93018
st052809rab1070_CNP	1	0.93264
sw011309rab931_CNP	1	0.93294
jg100807rab346_CNP	1	0.93981
rb031207rab59_CNP	1	0.94942
mr111207rab411_CNP	1	0.94974
dp070507rab218_CNP	1	0.95513
ag061307rab184_CNP	1	0.95617
kf102408rol514_CNP	1	0.95824
pr100907a_rol232_CNP	1	0.97057
jk051508rab715_CNP	1	0.97375
dw092608rab821_CNP	1	0.97463
mh110507dru105_CNP	1	0.9781
ts101707rab367_CNP	1	0.97828
jt092508rol497_CNP_whole	1	0.98585

Image Name	Melanoma or benign	f(z)
tr062509rol643_CNP	1	0.99822

APPENDIX D

**TABLE TO TEST THE OBTAINED THRESHOLD VALUE FOR ROBUST
MODEL ON A TEST SET OF 78 IMAGES**

Image Name	Melanoma or benign	f(z)
at102907dru101_CNP	0	0.005802858
aw122807per53_CNP	0	0.00602317
as033007rab87_CNP	0	0.013120979
an111507dru119_CNP	0	0.015992481
wb090808rol482_CNP	1	0.020701551
ac011108dru137_CNP	0	0.025393849
am071509dru270_CNP	0	0.025557012
ak012909rab949_CNP	0	0.025768761
ar061709rab1104_CNP	0	0.032940079
ac060909rab1087_CNP	0	0.03319215
et121807dru134_CNP	1	0.033224172
sb020408rol288_CNP	1	0.03823963
db060208rol399_CNP	1	0.040991281
ar091407rab310_CNP	0	0.042287791
ah011909rab940_CNP	0	0.044994236
ap042507_CNP	0	0.045923118
ah091208per115_CNP	0	0.049155937
as051408rab711_CNP	0	0.05400771
eo072209rab1152_CNP	1	0.055560862
gt021309rab975_CNP	1	0.056664669
as051408rab708_CNP	0	0.057652304
mb052308rol396_CNP	1	0.061714618

Image Name	Melanoma or benign	f(z)
ar061709rab1105_CNP	0	0.065149285
rt011408rol273_CNP	1	0.071183933
wf042407rol61_CNP	1	0.074134603
jl072709dru275_CNP	1	0.082221745
rs071609rab1149_CNP	1	0.087253765
as051408rab710_CNP	0	0.090753263
ab063008per95_CNP	0	0.101315204
ah013009rab951_CNP	0	0.103710888
kh052609rol626_CNP	1	0.104180503
pt072109dru271_CNP	1	0.104583842
as051408rab706_CNP	0	0.117708425
tb072409rol650_CNP	1	0.118386979
aj021808rab562_CNP	0	0.126036364
jk070808rol428_CNP	1	0.130906574
an062209rol640_CNP	0	0.131265422
bh070207dru41_CNP	1	0.132141203
aw031408per70_CNP	0	0.137935759
ab030209rol586_CNP	0	0.166755513
as051707rab145_CNP	0	0.171286696
ah072009rab1151_CNP	0	0.176991733
sc061307dru22_CNP	1	0.185082803
dh060308rol401_CNP	1	0.190361335

Image Name	Melanoma or benign	f(z)
jp100907rol231_CNP	1	0.192384862
hs061109rab1092_CNP	1	0.211414697
bb042108rab667_CNP	0	0.21681553
jl072709dru273_CNP	1	0.268884102
ed061907rol131_CNP	1	0.273394297
cp040209rol610_CNP	1	0.280298184
as021609rab976_CNP	0	0.283821022
da123107rol261_CNP	1	0.300648192
eh071607rolla158_CNP	1	0.307297047
al102708rab847_CNP	0	0.349629925
af083007_CNP	0	0.350201132
ag032009rol598_CNP	0	0.41567431
dc013009rol562_CNP	1	0.417682586
nm011508rol275_CNP	1	0.43552547
aa051308rol383_CNP	0	0.439754358
rs061708rol414_CNP	1	0.453269823
nm073107rol172_CNP	1	0.482946675
db061008rol409_CNP	1	0.483113677
ck081007rolla186_CNP	1	0.53313208
ar031607rab67_CNP	0	0.543556532
jw071007rol152_CNP	1	0.561524274
cd030907_CNP	1	0.599738348

Image Name	Melanoma or benign	f(z)
ld102108rol510_CNP	1	0.600773377
ap060509rab1080_CNP	0	0.619249621
js070109rab1131_CNP	1	0.632467799
co082107dru78_CNP	1	0.652837384
bh011309dru220_CNP	1	0.662607089
lr091908rol491_CNP	1	0.702727916
am010809rab925_CNP	0	0.706904028
ah122107rol256_CNP	0	0.829749929
ah112608rab890_CNP	0	0.873357794
rl061109rab1093_CNP	1	0.877859386
as071309rab1147_CNP	0	0.935336602
ab090407dru83_CNP	0	0.968454824

REFERENCES

1. Kaushik. V.S.N Ghantasala, Raed H. Chowdhary, Uday Guntupalli, Jason Hagerty, Randy H. Moss, Ryan K. Rader and William V. Stoecker “THE MEDIAN SPLIT ALGORITHM FOR DETECTION OF CRITICAL MELANOMA COLOR FEATURES”, 8th International Conference on Computer Vision Theory and Applications, Poster Paper 284, Barcelona, Spain,2013.
2. Andreassi, L., Perotti, R., Rubegni, P., Burrioni, M., Cevenini, G., Biagioli, M., Taddeucci, P., Barbini, P. (1999). Digital dermoscopy analysis for the differentiation of atypical nevi and early melanoma: a new quantitative semiology. *Archives of Dermatology*, 135(12), 1459-65.
3. Umbaugh, S.E. (2011). *Digital Image Processing and Analysis: Human and Computer Vision Applications with CVIptools* (2nd ed.). Boca Raton: CRC Press.
4. Introduction to SAS. UCLA: Academic Technology Services, Statistical Consulting Group <http://www.ats.ucla.edu/stat/sas/>. Last referred 03/12/2012.
5. Snigdha Bommadevara(2013), FEATURE EXTRACTION THROUGH K-MEANS SEGMENTATION FOR MELANOMA DETECTION, M.S. Thesis, Electrical and Computer Engineering, Missouri University of Science and Technology, Rolla MO 65401.
6. Faziloglu Y, Stanley RJ, Moss RH, Van Stoecker W, McLean RP. (2003). Colour histogram analysis for melanoma discrimination in clinical images. *Skin Research and Technology*. 9(2), 147-156.
7. Heckbert, P. (1982). Color image quantization for frame buffer display. In *Proceedings of SIGGRAPH '82*, 297.
8. Henning, J.S., Dusza, S.W., Wang, S.Q., Marghoob, A.A., Rabinovitz, H.S., Polsky, D., & Kopf, A.W. (2007). The CASH (color, architecture, symmetry, and homogeneity) algorithm for dermoscopy. *Journal of the American Academy of Dermatology*, 56(1), 45-52.
9. Khan, A., Gupta, K., Stanley, R.J., Stoecker, W.V., Moss, R.H., Argenziano, G., ... Cognetta, A.B. (2009). Fuzzy logic techniques for blotch features evaluation in dermoscopy images. *Computerized Medical Imaging and Graphics*, 33(1), 50-57.
10. Rogers, H.W., Weinstock, M.A., Harris, A.R., et al. Incidence estimate of non-melanoma skin cancer in the United States, 2006. *Arch Dermatol* 2010; 146(3):283-287.

11. Siegel, R., Naishadham, D., and Jemal, A. (2012). Cancer Statistics, 2012. CA: A Cancer Journal for Clinicians, 62(1), 10-29.
12. Mocellin, S., and Nitti, D. (2011). Cutaneous melanoma in situ: translational evidence from a large population-based study. *Oncologist*, 16(6), 896-903.
13. Hamerly, G. and Elkan, C. (2002). "Alternatives to the k-means algorithm that find better clusterings". Proceedings of the eleventh international conference on Information and knowledge management (CIKM), H.3.3, I.5.3, 600-607.
14. Menzies, S.W. and Zalaudek, I. (2006). Why perform dermoscopy? The evidence for its role in the routine management of pigmented skin lesions. *Archives of Dermatology*, 142, 1211-1222.
15. Liang Wang, Christopher Leckie, Kotagiri Ramamohanarao, James Bezdek (2009), Automatically Determining the Number of Clusters in Unlabeled Data Sets, *IEEE Transactions on Knowledge and Data Engineering*, 21,(3),335-350.
16. Srinivasulu Aside, Subba Rao Ch D.V, Saikrishna V. (2010). Finding the Number of Clusters in Unlabeled Datasets using Extended Dark Block Extraction, *International Journal of Computer applications*, 7(3), 0975 -8887.
17. Agresti, A. (2007), Building and applying, logistic regression models, *An Introduction to Categorical Data Analysis*, Hoboken: Wiley, p. 138.

VITA

Venkata Sai Narasimha Kaushik Ghantasala was born in the city of Hyderabad located at Andhra Pradesh, India. He received his Bachelor's degree in May 2011 from CVR college of Engineering, Hyderabad which was then affiliated to Jawaharlal Nehru Technological University, Hyderabad, Andhra Pradesh, INDIA. He got admitted into Missouri University of Science and Technology in August 2011 where he worked as a research assistant under Dr. Randy H. Moss on the project 'Feature Extraction through Median Split algorithm for Segmentation for Melanoma Detection'. He worked as LTE QA intern in Broadcom Corporation, Sunnyvale, CA, USA for 7 months. Later in December 2013, he received his Master's degree in Electrical Engineering from the Missouri University of Science and Technology, Rolla, Missouri, USA.