IMAGE PROCESSING AND MACHINE LEARNING FOR THE DIAGNOSIS OF MELANOMA CANCER

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Abstract: Melanoma cancer is one of the most dangerous and potentially deadly types of skin cancer; however, if diagnosed early, it is nearly one-hundred percent curable (UnderstMel09). Here we propose an efficient system which helps with the early diagnosis of melanoma cancer. Different image processing techniques and machine learning algorithms are evaluated to distinguish between cancerous and non-cancerous moles. Two image feature databases were created: one compiled from a dermatologist-training tool for melanoma from Hosei University and the other created by extracting features from digital pictures of lesions using a software called Skinseg. We then applied various machine learning techniques on the image feature database using a Python-based tool called Orange. The experiments suggest that among the methods tested, the combination of Bayes machine learning with Hosei image feature extraction is the best method for detecting cancerous moles. Then, using this method, a computer tool was developed to return the probability that an image is cancerous. This is a very practical application as it allows for at-home findings of the probability that a mole is cancerous. This does not replace visits to a doctor, but provides early information that allows people to be proactive in the diagnosis of melanoma cancer.

1 INTRODUCTION

The warning signs of melanoma cancer can be summarized by the ABCDE method as described by the Skin Cancer Foundation (UnderstMel09). Each letter in ABCDE stands for a feature of a mole that indicates that it might be malignant: Asymmetry, Boarder irregularity, Colour, Diameter, and Evolving (Fig. 1). A mole that evolves, or changes at all in color, shape, or size, is another warning sign of melanoma. (UnderstMel09). The diagnosis of melanoma is not based on just one of these factors but a combination of all of them.

Many dermatologists use a surgical method, called an excisional biopsy, to further test for melanoma at the microscopic level. Ideally, the mole would be noticed early on, so the cancer would still be isolated in the mole and not have spread to the lymph nodes. If it is noticed at this stage, only one surgery is needed to cure the body of cancer. The problem is, however, that often moles are not diagnosed until the cancer has developed past this stage. A device that would give simple feedback on moles, therefore, would be beneficial in helping patients check their moles at home and therefore encouraging early diagnosis.

A new technology that is beginning to be developed is using imaging techniques to diagnose melanoma (Stevens09). Although a good concept, current imaging technologies are not for individual home use. By making the system more accessible to individual users, the process can help in the early diagnosis of melanoma.

Overall, the process involves image capturing, image processing, feature extraction, and machine learning for the diagnosis of melanoma. Although these techniques cannot replace surgical diagnosis by doctors, they provide a foundation for the early diagnosis of melanoma. Because early diagnosis is so important, this process has very practical applications in the real world and could potentially be used to save lives.

The first step in the imaging process is image capturing or image acquisition. One method of image acquisition some dermatologists use is a method called dermoscopy, which allows them to obtain an image which displays colors of the epidermis, the dermoepidermal junction, and the

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papillary dermis not visible to the naked eye. (Stanganelli08).

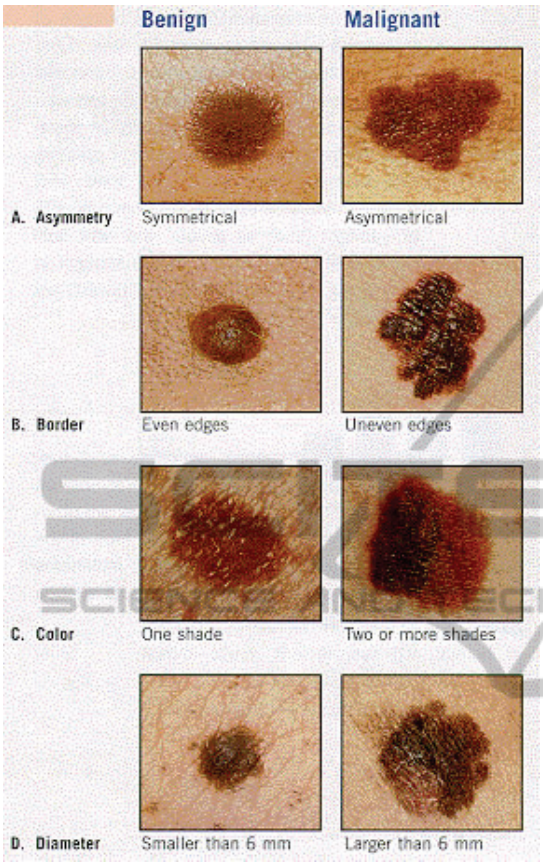

Figure 1: Distinguishing using ABCD method, *Source: The Ear, Nose, and Throat Alliance: http://www.allianceent.net/index.php?section=3&pid=198.*

Before extracting features, it is important to perform some pre-processing and noise reduction to enhance the images. One technique for noise reduction is combining many images by frame averaging (Bosdogianni99). Another technique, called neighborhood averaging, involves adding together the color or brightness values for pixels in a certain area and then dividing by the number of pixels in that area. This average value is then used to construct a new image with less noise. Another type of neighborhood averaging, involves replacing each pixel with the average of its neighbors (Bosdogianni99). Neighborhood averaging reduces noise; however, it also blurs edges, displaces boundaries, and reduces contrast. Other image processing techniques can be used to correct non-uniform illumination (Russ95). One currently available software uses image processing and noise-reduction to digitally remove hair from images of moles. To do this it identifies the dark hair locations by a generalized grayscale closing operation and makes sure the shape of the hair pixels are thin and long structures. It then replaces the hair pixels by a bilinear interpolation and levels the replaced pixels with an adaptive median filter. (DermWeb07)

The next step is feature extraction. For the purposes of our project, the features we would need are the ones described by the ABCDE method. Two important first steps in feature extraction are edge detection and image segmentation (Bosdogianni99). In image segmentation, we must divide up the image into uniform regions. In order to do so, there are many methods available, the simplest of which are histogramming and thresholding (Bosdogianni99). For an image of a mole, the histogram will usually have two peaks. However, if the mole has multiple colors, and therefore is possibly malignant, the histogram would have three peaks, or one of the peaks would not be well defined. Therefore, by looking at the histogram, we can determine a variation in color of the mole. Once the image is thresholded, we know the points of the outer edge of the image (Bosdogianni99). Using these points, we can determine the perimeter of the mole and use an integral function to find the area. By comparing the perimeter to the area using some predefined algorithm we can extract the asymmetry, border irregularity, and diameter of a mole. Finally, given multiple images over time and comparing their features, we can determine if a mole is evolving. For this project, however, we will focus on features in one given point of time.

There are many available tools for feature extraction. One tool is CVIPtools (CVIP06). We can use this software for image processing and feature extraction. This tool can do the segmentation of an image using Fuzzy C Mean, Grey Level Quantization, Histogram Thresholding, and many more techniques. It can also preform edge detection, and various transforms including Fast-Fourier Transform, Hadamard, and Walsh. Finally, we can use this tool to extract texture features, spectral features, and for pattern classification and image segmentation. (CVIP06) Other similar tools that can be used for feature extraction or preprocessing of images of moles are Dull Razor, Hosei tool, and Skinseg (DermWeb07) (Hosei09) (Skinseg98).

After extracting the features, the next step is to create a machine learning database. In this database, we store the images, their features, and whether or not they were cancerous as evaluated by trained dermatologists using microscopic evaluation. Then,

using the database, we perform machine learning algorithms to determine patterns of cancerous moles. In order to do this, we can use various methods one of which is decision trees. Using this approach, based on the features in the database we create a decision tree. This can be done by ID3 top-down method, which is a greedy algorithm. In this method, construction of a decision tree starts by picking a key variable (feature) to segment the database and then applying other features one by one until all the elements have been mapped to the outcome/decision. In order to choose variables that optimize the decision tree, we can look at the entropy of each variable. The entropy can be found by the following equation, and we always choose the variable with the highest entropy gain: H(S) = -p+ log2(p+) – p-log2(p-) where p+ is the probability that the variable is positive and p- is the probability that the variable is negative. Then, using this decision tree, we can predict whether an image not in the current database will be cancerous. (DeLaCruz09). Other methods of machine learning are neural networks, constructive induction, and support vector machines.

2 IMAGE ACQUISITION

The first step in this process was to acquire a set of preliminary images for the machine learning process. Some of these images needed to be of cancerous moles while others of benign moles. The images we used are standard images taken from a normal commercial household camera. We chose to use images from a normal camera because it fits with our low-cost application criteria and is accessible to the common person. We contacted local dermatologists and collected some images, and then collected more from dermatologists' training sites on the web (Stevens09). Our overall database included 150 images with 30% of those for benign moles, and 70% as cancerous moles.

3 FEATURE EXTRACTION

The next step in the process was feature extraction. We explored a variety of different tools for feature extraction. The first tool we experimented with was **Skinseg**, a tool developed by Wright State University. This tool segments a given image to isolate the portion of interest (i.e. the mole) and extracts a set of features from this segment.

From the images collected, we opened each image individually within the Skinseg program and used it to identify the region of interest (mole) using available methods of segmentation. Fig. 2 shows a segmented picture of the mole after automatic segmentation.

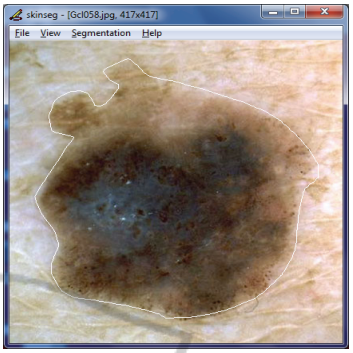

Figure 2: Segmented Image using Skinseg tool.

Once the image was segmented, the tool allowed us to view the features and save them to a text file, as illustrated in Fig. 3.

Once all of the feature files were saved, we used a Python script to read all the files and create a single database (skinsegdb.tab) of the selected extracted features. The database contained one row for each image with all the feature values separated by tabs (Fig 4). This was the format required by the machine learning tools in the next part of the project.

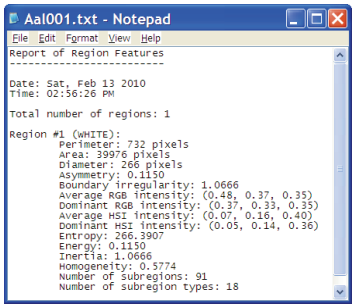

Figure 3: Extracted Image Features using Skinseg tool.

Once all of the feature files were saved, we used a Python script to read all the files and create a single database (skinsegdb.tab) of the selected extracted features. The database contained one row for each image with all the feature values separated by tabs (a partial snapshot of the database is shown in Fig. 4). This was the format required by the machine learning tools in the next part of the project.

The second tool we used was the Hosei Tool, created by Hosei University in Japan. This is a learning tool for dermatologists, and it has predetermined features for given images. Most

	A	B	C	D	E	F	G	H
1	Melanoma?	Asymmetry	BoundaryIrregularity	Average(R)GB	AverageR(G)B	AverageR(B)	Dominant(R)GB	Domir(G)B
2	Yes No	c	c	c	c	c	c	c
3	class							
4	Yes	0.115	1.0666	0.48	0.37	0.35	0.37	
5	No	0.2125	1.1127	0.61	0.41	0.29	0.73	
6								
7								
8	No	0.0949	0.8356	0.36	0.32	0.3	0.11	
9	No	0.1792	1.1276	0.33	0.22	0.16	0.71	
10	No	0.0796	0.921	0.39	0.27	0.19	0.73	
11	No	0.0946	1.0714	0.37	0.27	0.21	0.64	
12	No	0.1272	0.9797	0.46	0.37	0.28	0.95	

Figure 4: Partial snapshot of database of features extracted from images using Skinseg tool.

likely, these features were determined by doctor inspection. Using this tool website, we retrieved a set of pictures along with their image features. These features included Symmetry, Borders, Color, Pigment Network, Branched Steaks, Homogenous, Dots & Globules, Atypical Pigment, Blue Whitesh Veil, Atypical Vascular Pattern, Irregular Streaks, Irregular Pigmentation and Regression Structures. We then created the second database (hoesidb.tab) using the similar process as for Skinseg feature database. The partial snapshot of hoseidb.tab is shown in Fig. 5. The database contained one row for each image with all the feature values separated by tabs. This was the format required by the machine learning tools in the next part of the project.

	Name	Melanoma?	Symmetry	Borders	Color	Pigment Network	Branched Steaks	Homogenous	Dots	Globul
1	d	Yes No	d	d	d	d	d	d	d	d
2		class								
3	Aal001	Yes	0	8	3	No	No	Yes	Yes	Yes
4	Aal006	No	0	0	3	Yes	No	No	Yes	Yes
5	Abl145	No	2	8	2	No	No	No	Yes	Yes
6	Abl165	No	1	2	3	Yes	No	Yes	Yes	Yes
7	Acl207	No	1	8	2	No	Yes	Yes	No	No
8	Acl215	No	0	0	3	Yes	No	No	No	No
9	Acl263	No	0	8	4	No	No	Yes	Yes	Yes

Figure 5: Partial snapshot of the database of features extracted from images using Hosei tool.

We also explored a few other tools, but did not use them for the data gathering and comparison part.

CVIP tool, developed by Southern Illinois University at Edwardsville, is very powerful, but mostly interactive, so we did not use it for this project. We realized that it is possible to create a code which does the feature extraction in a more automatic way, but we chose to use Skinseg and the Hosei tool instead (Skinseg98) (Hosei09). This can be used in future research work. Mole Expert Micro is a commercial software for the feature extraction of melanoma images. We were able to receive an evaluation version of this software. Unfortunately, this software required a value for the number of pixels per millimeter of the image. Since this data was not available for our images, we could not use this tool.

Open CV tool from Intel would be very powerful in completely automating the process of feature extraction; however, it is not specifically designed for melanoma images. This would require adapting it and customizing it to this project. In the future, we plan to use Open CV or get the source code for Skinseg in order to completely automate the feature extraction process for deployment in a website.

4 MACHINE LEARNING

Once we compiled the data of the extracted features into the database, we used this database for application of machine learning algorithms. There are a variety of methods for machine learning that we tested:

1. Majority Learning: This is a basic technique which gives a probability of a given mole being cancerous based on the probability that any given mole in the training set is cancerous.
2. Bayes Learning: In Bayes learning, Bayesian networks are created which represent the relationship between a given feature and the probability that the mole is cancerous. Combined, these networks can give a probability for whether or not the mole is cancerous.
3. Decision Trees: This machine learning method creates a tree based on the training data. There are a variety of different techniques for how to create the best tree and to distinguish which features are important and which are not. In this method the leaves of the tree describe positive or negative decisions.
4. kNN (Neural Nets): Neural Networks are made of interconnecting neurons and operate based on the model of biological neural networks.

In order to test these methods we used a toolkit called Orange which is Python based (Orange09). We wrote code in this program to test the percent accuracies of different sets of data for a given machine learning method and feature extraction method.

5 RESULTS

We ran four different machine learning methods (Majority, Bayes, Decision Tree & kNN) on the two set of the databases created using Skinseg and Hosei

tools and measured the accuracy of the diagnosis. For the purposes of the experiment, the Orange tool was used to segment the database into the 'learning set' and 'test set'. The 'learning set' allows the algorithm to learn while 'test set' is used to test the accuracy of the learning method. For example, if the database had 150 entries, then 2 entries could be the test set while 148 entries are used for learning. This could also be specified as a percentage. In the practical implementation of the melanoma detection tool using this method, the entire dataset becomes the learning set. A new image submitted by the patient is the test set for which the algorithm would provide the probability of it being cancerous or benign.

We ran the tests with multiple runs for each of the two feature extraction tools (Hosei and Skinseg) and the four machine learning methods (Majority Learning, Naïve Bayes, Decision Tree, k-nearest-neighbour) combination. Number of entries in the 'test set' ranged from 1 to 10, and then a final run was made where 'test set' was kept at 10% of the entries in the set. So for 150 entries, this was 15. Then, for each set, we determined an average accuracy from these 11 runs.

For Majority Learning method used on the Skinseg and Hosei feature extraction databases, the percentage accuracy was best when 2 entries were taken out in 'test set'. We noted that the method performed the same for either of the two databases. With Naïve Bayes learning method for the two databases, the average accuracy was low for Skinseg database, but is pretty good for the Hosei database. It was interesting to note that with two entries in the test set, the accuracy was good for this method as well. Decision Tree learning method did not perform well for either of the database as compared to other methods. The k-Nearest-Neighbor learning method showed better results for the Hosei database.

Fig 6 shows the summarized results from comparison of the different learning methods over the two databases (Hosei and Skinseg). Clearly, the Naïve Bayes learning method used with the Hosei database produced the best results.

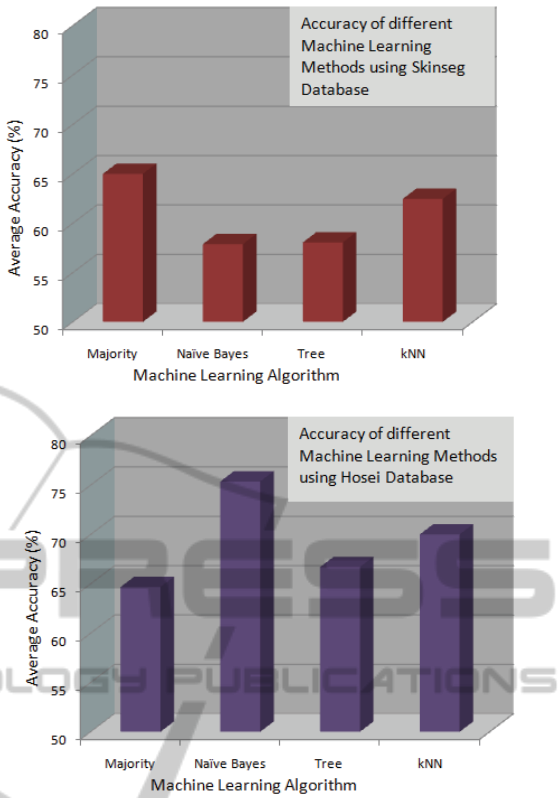

Figure 6: Results of different Machine Learning methods using each of the two databases.

6 CONCLUSIONS

Overall, we found that the Hosei tool for feature extraction and the Bayes machine learning method was the most effective combination for this application. The Hosei tool gave better results than Skinseg . This result was as expected, as errors in the segmentations of moles were a factor in the feature extraction from Skinseg but not from the extraction using Hosei tool. the set of Hosei methods, most of the machine learning methods showed close results, but Bayes performed slightly better with the Hosei tool. Overall we had expected the accuracy to be more than what we found. The average accuracy for the best methods was about 75% (Bayes/Hosei). It can be noted that our learning database was not very big, and the accuracy improves with a larger database. In order to improve the results, we plan on repeating the experiment with a different data set of additional images. Furthermore, these results are good given that the quality of the entrance data is low, because none of the pictures were taken with a standard camera or lighting.

In our experiment, we eliminated some variables from the machine learning database such as the number of pixels, the perimeter and area of a mole, and the filename. We eliminated the pixels and perimeter and area because the pictures were scaled differently so including these variables would have skewed the results. Of course we also eliminated the file name. Along the same lines, one limitation of my project was that we could not use size of the mole, because every picture is taken with a different scale. In the future, we can either set a standard size

or use a field size ring such as a quarter to distinguish relative sizes. Also, we did not use the 'evolution' feature of the moles because we did not have such images (evolving moles) available.

In discussing our results with the dermatologists we got positive feedback for the use of the method with some improvements in real world (Stevens09) (Koppula09). We discussed the lack of using the mole size in my experiment and Dr Koppula felt that not using the size itself is not a big limitation, since the size is often very misleading just by itself. It has to be compared to other moles on the skin. Evolution of the mole and changing size overtime is important, and if this is captured in the machine learning algorithm, this would be good. (Koppula09)

We are now using the information that we gathered from this experiment to create a website which will allow users at home to upload an image of a mole and the website would return a probability of how likely it is that this mole is cancerous. The only limitation in this so far is that Skinseg, or the feature extraction step, is not automated. We continue to work on this project and automate this step by either writing code in Open CV or finding the source code for Skinseg. We are also planning to create a smartphone application. This application would allow a user to take an image of a mole with the phone camera, upload it to the website, and get immediate result from the website. If the resulting probability is very high, the application could even call the doctor. This would also allow us to collect more images. If the user confirms the prognosis, we can add the image to our learning database. This would then improve the accuracy of the results. With a larger set of database, we plan on using a parallel computing architecture, such as CUDA, for faster computation on the backend server. This would be beneficial in providing real-time instant response to the user.

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