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RESEARCH ARTICLE

IMAGE PROCESSING AND NEURAL NETWORK TECHNIQUES IN ASSISTING OF EARLY DETECTION OF ORAL CANCER- A NOVEL METHOD

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ABSTRACT

Oral cancer is the sixth most common cancer globally and most reported cancer in India with fourteen deaths in an hour on a yearly basis. Oral cancers can be cured with early detection but the biggest hindrances are lack of awareness, cost of tests and the immense workload of the cyto-pathologist leading to delay and errors in the detection process. An effective, semi-automated system described in this paper has made an attempt towards mitigating the above mentioned issues by combining techniques like Papanicolaou (Pap) smear, image processing and neural networks. The primary concern and objective of the system developers is to help cure the menace of oral cancer that is plaguing India and the world. This system is perhaps one of the first successful attempts at semi-automating the process.

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INTRODUCTION

Oral cancer is a class of cancers that occur in different parts of the oral cavity i.e., mouth, throat, tongue. It is the sixth most reported cancer globally out of which 62% of the reported cases are from developing countries. Oral cancers accounts for 30% of all cancers reported in India and annually 1.3 lakh of Indians succumb to oral cancer, which implies 14 deaths per hour. (Ken Russell Coelho, 2012) Most cases of oral cancer can be cured with early detection. (Maraki *et al.*, 2004; Kaugars *et al.*, 1998) Most deaths due to cancer are reported from rural areas. The reason to this being; high illiteracy rate, lack of awareness, the lack of access to medical care and the high cost of treatment. Compounding to the higher rates of incidence of oral cancer is the widespread use of tobacco in smoke (beedi, hookah and cigarettes) and smokeless (gutka, paan, khainni etc.) mediums which is very popular in rural areas. (Ken Russell Coelho, 2012) Other major burden in India is regarding the scarce diagnostic infrastructure, crucial investigatory centres and services to the needy, is at paucity. Facilities are significantly higher in the urban areas when compared with the rural inhabitants.

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Most of the patients even if diagnosed with cancer are unable to obtain better treatment, as there is dearth in the knowledge about the etiology and risk factors. There are no uniform protocols for management, minimal access to newer therapies and drug regimes. (Prasad, 2014) The Pap smear test (Papanicolaou stain) though initially used for screening cervical cancer has now been proven to be effective in screening for oral cancer too. (Rickles, 1972; Mehrotra *et al.*, 2011) Sensitivity of PAP analysis in oral smears for the detection of oral cancer is 91.176%, while specificity for the detection of non-neoplastic cells was 100%. The positive and negative predictive values were 100% and 76.92%, respectively. (Rajput *et al.*, 2010) Previously attempts have been made to automate the process of Pap staining in order to analyse cancer smears, and during the nineties there was strong competition between the American companies developing screening technology as well as struggles to get the various solutions approved by the powerful Food and Drug Administration, FDA. (EwertBengtsson and PatrikMalm, 2014; Cowpe *et al.*, 1993; Sciubba, 1999) When samples are scrutinized manually, it takes around 5-10 minutes. There are recommendations saying that, due to the hazards of fatigue, a pathologist should not work more than 7 hours a day and analyse no more than 70 samples. Even when following this recommendation, the pathologist has to inspect three image

fields per second on the average. Furthermore, since the visible changes may be quite local, the pathologist needs to maintain full concentration all the time in order not to risk missing some diagnostic cells. (Elsheikh *et al.*, 2013) Though no proof can be stated here but very often the pathologists are overworked well beyond the stated guideline. All the above mentioned reasons accumulate and the pathologist may pass a positive sample as a negative sample. The cost of such an error could be paid by the patient's life. There have been attempts at an automated system since 1970's by several companies. Each of them have failed at it owing to technological restrictions of that era, namely; reliance on purely analog electronics, lack of computing power, memory restrictions that prohibited high resolutions images of samples and lack of microscopes providing such a resolution. (EwertBengtsson and PatrikMalm, 2014; Tanaka *et al.*, 1987) The system described uses signal processing and image processing techniques to extract data from the Pap stained sample's images. Neural networks techniques, namely Linear Vector Quantisation (LVQ) is used to classify the positive and negative samples. The system proposed in this study has made a successful attempt at screening and analysing pap smears from the oral cavity and be able to classify them as "potentially cancerous" or "positive" and "definitely healthy" or "negative". The positive samples are then forwarded to the cyto-pathologist for another review where he can further spot abnormalities in the sample that the machine had missed or re-confirm what the machine had already spotted. This helps reduce the work load of a cyto-pathologist by an appreciable amount since he now needs to examine only a fraction of the total samples sent to him for analysis.

MATERIALS AND METHODS

There are three major phases to processing samples in the proposed system which will be described below. These steps have been performed for 10 healthy samples (negative) and 8 diseased samples (positive). The staining procedure is to be performed by the pathologist while the other two are performed by the system proposed.

A. Staining Procedure

Pap smear is categorized as exfoliative cytology. Though the Pap smear test doesn't render useless the need for a biopsy, it is a useful tool in adjunction to biopsy because of its affordability. Pap smear is a painless, atraumatic and simple procedure for collecting a sample of superficial cells. The Pap smear test has also proven its merit in detecting malignant and pre-cancerous lesions. The above mentioned qualities of Pap make it a preferred method for initial and preventative screening. (Rickles, 1972; Mehrotra *et al.*, 2006; Mehrotra *et al.*, 2011)

- i) The first step is gathering the sample from a patient's oral cavity, wherever the lesion is present. A tongue blade/swab is used to scrape the lesion. (Rickles, 1972)
- ii) The lesion acquired on the tongue blade/swab is then smeared on a glass slide. (Rickles, 1972)
- iii) The preparation, while still wet, is fixed on the slide by spraying a fixative solution. This is done to prevent the

slide from being altered by physical or environmental disturbance. (Rickles, 1972)

- iv) Following the above three steps of slide preparation, the staining steps follow to highlight the different features in a cell. In the first staining step the nuclei are stained by a haematoxylin solution. Nuclei are stained blue, dark violet to black.
- v) The second staining step is cytoplasm staining by orange staining solution, especially for demonstration of mature and keratinised cells. The target structures are stained orange in different intensities.
- vi) In the third staining step the so-called polychromatic solution is used, a mixture of eosin, light green SF and Bismarck brown. The polychromatic solution is used for demonstration of differentiation of squamous cells e.g. oral cancer and cycle diagnosis for examination under microscope.
- vii) Hence the method employs series of steps with each step comprising of particular solutions and each step being performed for designated period of time. Order of steps and quantities of chemicals used and time period can be vary in different protocols and it is up to the cytologist to decide upon which protocol to follow according to the requirements.
- viii) The results obtained by Pap can further be classified as: (Maraki *et al.*, 2004; Remmerbach *et al.*, 2003)

- (1) Normal Results (absence of abnormality in cells).
- (2) Abnormal Results (possible cancerous or pre-cancerous cells): Abnormal results can be further classified as:

- (a) ASCUS or AGUS: This result means there are atypical cells, but it is uncertain or unclear what these changes mean. The changes may be due to HPV. They may also mean there are changes that may lead to cancer.
- (b) LSIL (low-grade dysplasia) or HSIL (high-grade dysplasia): This means changes that may lead to cancer are present. The risk of cervical cancer is greater with HSIL.
- (c) Carcinoma in situ (CIS): This result most often means the abnormal changes are likely to lead to oral cancer if not treated.
- (d) Atypical squamous cells (ASC): Abnormal changes have been found and may be HSIL.

B. Image Processing

The image is first acquired from a microscope of resolution 0.63 μ meter per pixel. The image will be classified on the following parameters:

- Nuclear area
- Cytoplasm area
- Cytoplasmic-nucleic ratio

The following steps are performed on the image after it is acquired:

- i) A copy of the acquired image is then converted to grayscale for simplifying filtering, de-noising, sharpening and edge detection. (Rafael, 2002)

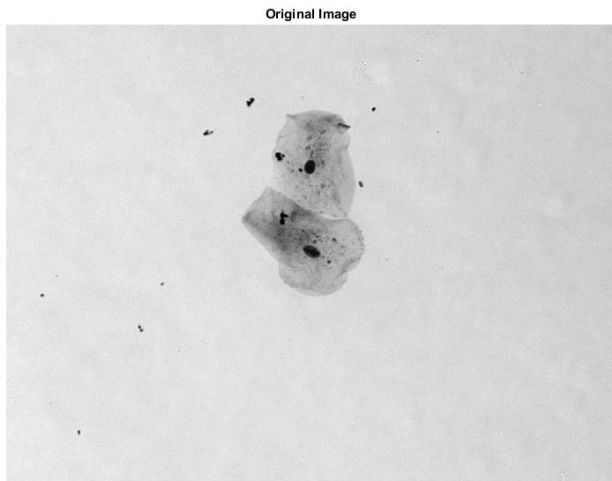


Figure 1. Grayscale image of the sample

- ii) In such a sanitised and controlled environment, the introduction of noise is generally minimal. The only aspects of the images we could consider as noise are blotted stains, dirt on the slide (lint, dust), etc.
- iii) The real challenge is to be able to program the machine to be able to differentiate the very obscure distinction in features. Often the cells are overlapping, cell is damaged, etc.
- iv) To be able to differentiate all of these features the image is put through various pre-processing stages like histogram equalisation, contrasting, filtering, sharpening etc. (Rafael, 2002)

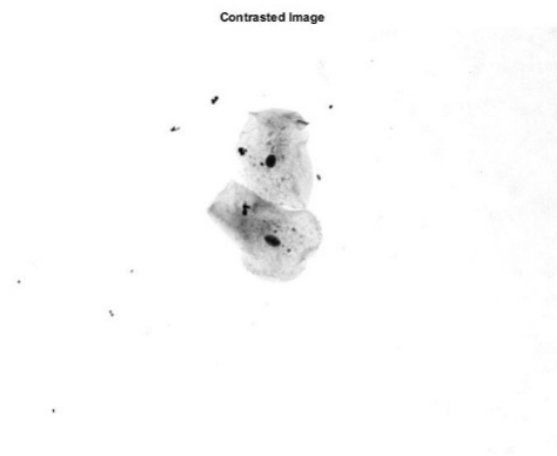


Figure 1. The contrasted image to filter out the noise and enhance edge detection

- v) The image is then converted into an edge image using the 'canny filter'. Canny filter is used since it retains the intricate edges of an image by using two thresholds to identify edges.
- vi) The image is segmented into regions using thresholding and M-connectivity criteria to be able demarcate the nucleus and cytoplasm based on pixel grey level intensities.

- vii) The edge image is compared with the region segmented image. On comparison the edge image is assigned the region codes from the previous image.
- viii) Finding areas enclosed within edges is made fairly easy now. Fourier descriptors are used to find image area since they can be programmed and varied to give us different levels of detail. (Rafael, 2002); Bergmeir and Garc'iaSilvente, 2010)

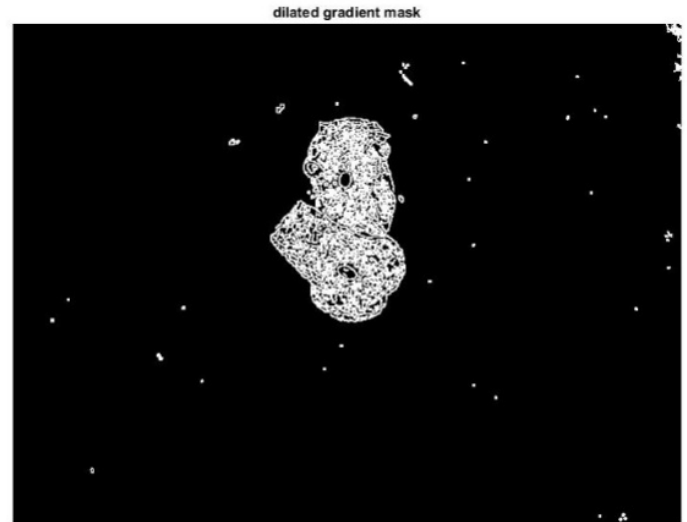


Figure 2. Edge image after applying canny filter and dilating the edges to form continuous edges



Figure 4. Image of only the cell body after various processing stages

- ix) The nucleus size can be evaluated from the region segmented image. A low threshold is set on the grayscale image and the nucleus regions are scanned on how many pixels on an average were falling below this threshold. (Bergmeir and Garc'iaSilvente, 2010; Haralick *et al.*, 1973)
- x) The Nuclear-Cytoplasmic ratio is evaluated by first finding out the areas of the cytoplasm and nucleus respectively. Then the area of nucleus is divided by area of nucleus to give the required ratio.

This ratio is tabulated and evaluated by the next machine learning process.

C. Machine Learning

- i) During training, nuclear-cytoplasmic ratios of 8 positive (diseased) samples and 10 negative (healthy) samples were collected
- ii) The training data were given three target values; two target values for positive samples (for low-grade dysplasia and high-grade dysplasia) and one for negative samples.
- iii) These samples are then trained using the Linear Vector Quantisation (LVQ) algorithm.
- iv) Learning Vector Quantization (LVQ), is a prototype-based supervised classification algorithm. LVQ is the supervised counterpart of vector quantization systems.
- v) LVQ maps each datum as an n-dimensional vector in a vector space. Then it assigns random centres and calculates their Euclidean distance from the remaining data points. Upon several epochs of the LVQ using these Euclidean distances are used to formulate the weights for the target values.
- vi) This algorithm classifies the samples into three groups according to the three targets assigned.

Once the training is complete, new samples can be evaluated as cancer positive and cancer negative (healthy).

RESULTS

The details extracted by the system like cytoplasm area, nucleus area and their ratios have been tabulated below. It should be noted that the areas have been calculated in terms of pixels and not in any SI units of sorts.

Table 1. Healthy Cells Data

Subject no.	Cytoplasmic Area	Nucleus Area	Cytoplasm-Nucleic Ratio
1.	36999.875000	744.250000	49.714310
2.	32720.875000	434.000000	75.393721
3.	31038.750000	415.000000	74.792169
4.	21946.250000	522.875000	43.693521
5.	38536.250000	764.750000	50.390651
6.	23767.906250	584.218750	40.683231
7.	20605.187500	580.750000	35.480305
8.	21244.500000	697.875000	30.441698
9.	28249.375000	450.250000	62.741532
10.	23975.075000	571.500000	41.951137

We can infer from the above table that the cytoplasm size of a normal healthy cell lie in the range of 20000-40000 pixels approximately, nucleus size of a normal healthy size lie in the range of 440-780 pixels approximately and their ratio in the range of 35-55 approximately.

Table 2. Diseased Cells

Subject no.	Cytoplasmic Area	Nucleus Area	Cytoplasm-Nucleic Ratio
1.	35587.000000	1494.000000	23.819946
2.	52973.250000	0.000000	Inf
3.	38139.125000	318.500000	119.746075
4.	31466.875000	0.000000	Inf
5.	133226.125000	692.125000	192.488532
6.	34971.780000	1483.000000	23.581780
7.	35912.920000	1212.560000	29.617437
8.	21372.310000	968.965000	22.056844

From the above table we can infer that there are instances where the size of cytoplasm or nucleus of healthy or diseased maybe similar but the difference in their ratios make their difference evident. Some diseased samples display the lack of nuclear development and are traditionally classified as LSIL. Their ratios are much above what the healthy cells display. Some samples display over development of nucleus and traditionally called HSIL. These are much lower than the healthy cells range.

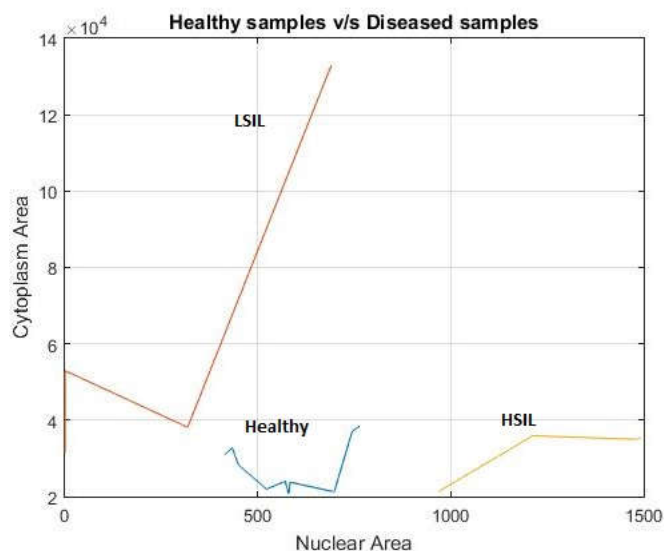


Figure 3. LSIL in red, healthy in blue and HSIL in yellow

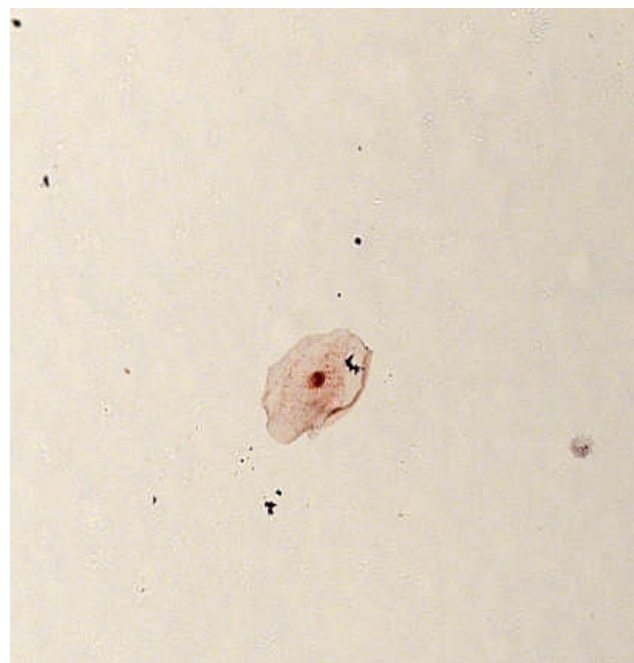


Figure 6. A healthy sample

The above graph uses data from healthy and diseased samples to represent the differences in the characteristics. The samples displaying LSIL are in red, healthy in blue and HSIL in yellow. Being able to differentiate between LSIL and healthy is fairly straightforward by looking at the graph. However, being able to

differentiate between HSIL and healthy isn't simple by simply observing the graph. At the end, the system prints a message stating whether the cyto-pathologist needs to examine that particular sample or not. The two images shown below show a healthy and diseased sample. The diseased sample shows the absence of nuclear development and irregularity in shape which are indicators of cancer.

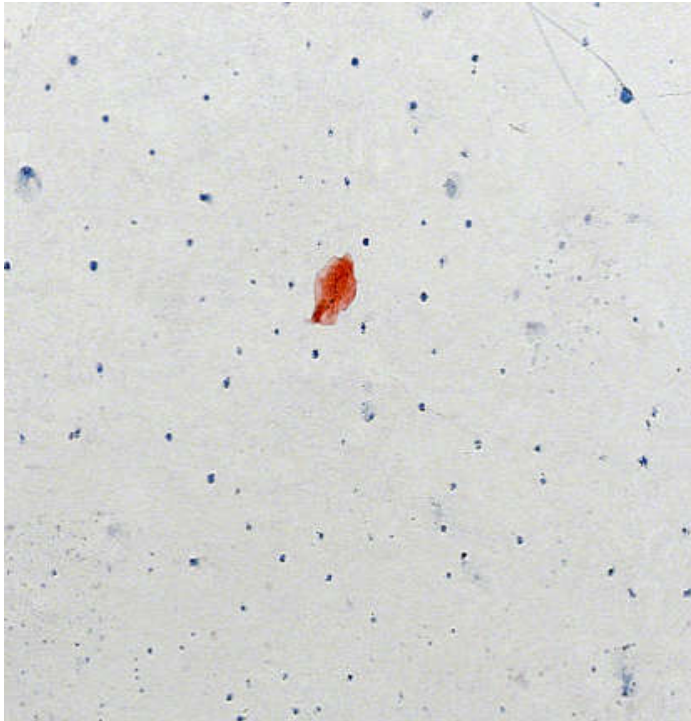


Figure 7. A diseased sample

Future Scope

The system has been able to successfully differentiate malignant and healthy cells in the oral cavity. This research can be further enhanced with more samples. Nonetheless, this paper is a milestone in cancer detection and the preventative screening process. The system described is a technology enabled effort in reducing oral cancer associated mortality amongst our countrymen. In the near future this system can be integrated as an assistive tool in pathology labs.

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