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Analysis and Classification of Skin Lesions Using 3D Volume Reconstruction

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Abstract: *3D volume reconstruction is used to identify the skin cancer at earlier stage. Through the person may be preventing from death. The subsurface information such as blood layer thickness and blood volume components can be identifying by multispectral transillumination images of the skin lesions. Lesions are simulated by using volume reconstruction, thus the result shows excellent volume with accuracy rate. Preliminary validation is also done by the small set of clinical lesions. The lesion severity can be categorized by an expert dermatologist using two features average blood layer thickness and ratio of blood volume to total lesion volume. The lesion can be classified into three types moderate, mild and severe class with high accuracy. However, these methods do not perform efficiently over a large set of images. An inverse volume reconstruction method is presented which uses a genetic algorithm optimization procedure with a novel population initialization routine and nudge operator based on the multispectral images to reconstruct the melanin and blood layer volume components. In our system, it is expected to have the ability to differentiate classes of lesions' severity based on multispectral trans-illumination and it can be perform over a large set of images. Therefore it has features like fast screening, tracking and detection of early skin cancers such as melanoma.*

Keywords: *Multispectral imaging, Volume estimation, Genetic algorithm, Volume reconstruction.*

I. Introduction

The early detection of malignant skin lesions is critical to preventing death. Conventional analysis of suspicious skin lesions involves visual examination a trained expert aided with surface lighting and magnification to analyze the visible structure of a nevus. However, the deeper pigmentation structure is often overcome by the surface light reflection, and thus, important information regarding the depth extent of the malignancy is obscured. Deeper subsurface information, such as indications of increased blood flow (angiogenesis) is critical factors in early melanoma detection. As a result, much effort is being put into the evaluation of novel non-invasive optical imaging techniques as a way to detect and analyze the morphological changes associated with tumorigenesis, thereby improving patient diagnosis accuracy with minimal need for invasive and time consuming biopsy procedures.

Pigmented skin lesion consists of additional melanin compared to the background skin. A skin lesion may possess a distinct vascular pattern beneath the lesion. This network of blood vessels is more prevalent in malignant lesions than in benign lesions. With this in mind to assist in reconstruction, a two-layered skin lesion model is implemented.

The inverse volume reconstruction algorithm is used to the initial volume estimate provides a good "first guess" at the shape of the subsurface lesion and the size of the melanin and blood layers, a number of assumptions are involved which can lead to inaccurate estimates. Consequently, a more robust reconstruction must be undertaken while aided by knowledge of the initial volume estimate. Since the 3D reconstruction process is ill-posed, a GA-based optimization process is used to search the solution space for an optimal solution.

In a genetic algorithm, a population of strings which encode candidate solutions to an optimization problem is evolved toward better solutions. Traditionally, solutions are represented in binary as strings of 0s and 1s, but other encodings are also possible.

II. Related Work

Most optical techniques have had limited clinical exposure. Since many optical imaging techniques surpass the limits of resolution or sensitivity available to establish imaging techniques in vivo, the development of validation methods is especially challenging and important. Owing to the highly scattering nature of tissues at optical wavelengths, the development and interpretation of optical images requires complex mathematic models for image reconstruction it must be overcome to advance the use of optical imaging for diagnostic applications

and measurement of treatment response. Optical imaging may have its greatest clinical promise when it is combined with other imaging modalities. In this research, it is easily to identify the depth information of skin lesion, gives high accuracy and visualize subsurface information is more effective.

A.System Model

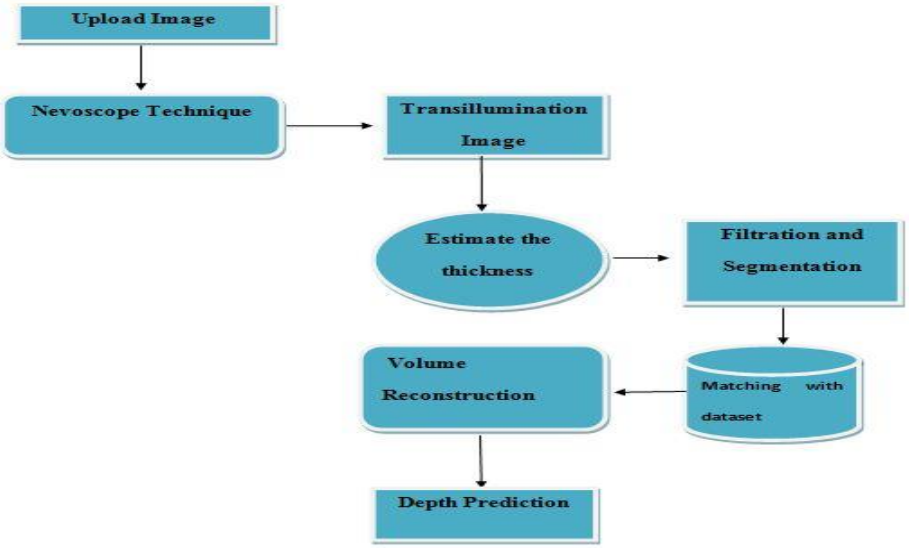

Fig 1.System Design

The user uploaded image. The Nevoscope contains a fiber optic ring light source that is placed against the skin. Light diffuses through the skin tissue beneath the lesion through scattering and absorption events, forming a backscattered transilluminated image of light which scatters up from behind the lesion. The accurate simulated Nevoscope transillumination images can be obtained for lesions of any size, shape, and composition in an acceptable amount of time and then filtration the image to remove the noise and segment the images based on similarities. The depth variation in order to evaluate the reconstruction and to predict the depth and identify the disease.

1.Multispectral Image

A multispectral image is one that captures image data at specific frequencies across the electromagnetic spectrum. The wavelengths may be separated by filters or by the use of instruments that are sensitive to particular wavelengths, including light from frequencies beyond the visible light range, such as infrared. Spectral imaging can allow extraction of additional information the human eye fails to capture with its receptors for red, green and blue. It was originally developed for space-based imaging

2.Tissue Viability Imaging Technique

It produces false red blood cell concentration values at the locations o pigmented lesions. It is used to find a tissue colour to histological parameter mapping, which is then applied pixel-by-pixel in the acquired images. These techniques are working with outside conventional methods. Its needs to deal with complex situations.

3.Initial Volume Estimation Technique

A good initial volume estimate is highly beneficial for a faster and more accurate final volume search through genetic algorithm optimization. By using the Monte Carlo simulation forward model, a Beer's law correction factor, specific to the Nevoscope geometry, was estimated in order to relate the pixel intensity seen in the surface transillumination images to the absorption coefficient and depth of an embedded object adjacent to the skin surface. Details of this procedure are discussed, but to summarize, an equation of the form I=I0 = f (μ_a, l) was developed where I is a pixel intensity value in an image with the object, I0 is the intensity of the same pixel in the background image without the object, μ_a is absorption coefficient of the object, and ` is the depth of the object. Scattering was assumed to be constant. The function was approximated by f (μ_a, l) ~ exp(R (μ_a , l)) where R (μ_a , l) was fit through Monte Carlo simulation over a range of values for μ_a and l.To find an estimate of the blood layer thickness. The wavelengths with smallest $\mu_a^{melanin}$/ μ_a^{blood} ratio is 600nm

$$\ell^{\mathrm{ML}}(x,y) = f^{-1}\left(\mu_a^{\mathrm{ML}}(680), \frac{I}{I_0}(680)\right)$$

The initial estimate the blood layer l^{bl} (x,y) and the thickness must be modified accordingly by the ratio of $C=\mu_a{}^{ml}(600)/\mu_a{}^{bl}(600)$.

$$\ell^{\mathrm{BL}}(x,y) = c \cdot (\ell^{\mathrm{ML}}_{600}(x,y) - \ell^{\mathrm{ML}}(x,y))$$

The above process is performed on l^{ml+bl} where $l^{ml+bl}=l^{ml}+l^{bl}$

$$\ell_f(x,y) = \sum_z L_f(x,y,z) \qquad L_f^{\mathrm{BL}}(x,y,z) = L_f^{\mathrm{ML+BL}}(x,y,z) - L_f^{\mathrm{ML}}(x,y,z)$$

The initial volume estimate and GA reconstruction procedure must be performed for each combination of parameter values within a desired range. The final estimated set of parameters is selected based upon the solution that produces the highest fitness.

B.Genetic Algorithm

In a genetic algorithm, a population of strings (called chromosomes or the genotype of the genome), which encode candidate solutions (called individuals, creatures, or phenotypes) to an optimization problem, is evolved toward better solutions. Traditionally, solutions are represented in binary as strings of 0s and 1s, but other encodings are also possible. The evolution usually starts from a population of randomly generated individuals and happens in generations. In each generation, the fitness of every individual in the population is evaluated, multiple individuals are stochastically selected from the current population (based on their fitness), and modified (recombined and possibly randomly mutated) to form a new population. The new population is then used in the next iteration of the algorithm. Commonly, the algorithm terminates when either a maximum number of generations has been produced, or a satisfactory fitness level has been reached for the population. If the algorithm has terminated due to a maximum number of generations, a satisfactory solution may or may not have been reached.

TYPICAL GENETIC ALGORITHM REQUIRES

1. A genetic representation of the solution domain,
2. A fitness function to evaluate the solution domain.

The fitness function is defined over the genetic representation and measures the quality of the represented solution. The fitness function is always problem dependent. For instance, in the knapsack problem one wants to maximize the total value of objects that can be put in a knapsack of some fixed capacity. A representation of a solution might be an array of bits, where each bit represents a different object, and the value of the bit (0 or 1) represents whether or not the object is in the knapsack. Not every such representation is valid, as the size of objects may exceed the capacity of the knapsack. The fitness of the solution is the sum of values of all objects in the knapsack if the representation is valid, or 0 otherwise. In some problems, it is hard or even impossible to define the fitness expression; in these cases, a simulation may be used to determine the fitness function value of a phenotype (e.g.,Computational fluid dynamics is used to determine the air resistance of a vehicle whose shape is encoded as the phenotype), or even interactive genetic algorithms are used.

Initialization

Initially many individual solutions are randomly generated to form an initial population. The population size depends on the nature of the problem, but typically contains several hundreds or thousands of possible solutions. Traditionally, the population is generated randomly, allowing the entire range of possible solutions.

Selection

During each successive generation, a proportion of the existing population is selected to breed a new generation. Individual solutions are selected through a *fitness-based* process, where fitter solutions (as measured by a fitness function) are typically more likely to be selected. Certain selection methods rate the fitness of each solution and preferentially select the best solutions. Other methods rate only a random sample of the population, as the former process may be very time-consuming.

Genetic Operators

The next step is to generate a second generation population of solutions from those selected through genetic operators: crossover (also called recombination), and/or mutation. For each new solution to be produced, a pair of "parent" solutions is selected for breeding from the pool selected previously. By producing a "child" solution using the above methods of crossover and mutation, a new solution is created which typically shares many of the characteristics of its "parents". New parents are selected for each new child, and the process

continues until a new population of solutions of appropriate size is generated. Although reproduction methods that are based on the use of two parents are more "biology inspired", some research suggests that more than two "parents" generate higher quality chromosomes.

These processes ultimately result in the next generation population of chromosomes that is different from the initial generation. Generally the average fitness will have increased by this procedure for the population, since only the best organisms from the first generation are selected for breeding, along with a small proportion of less fit solutions, for reasons already mentioned above.

Termination

This generational process is repeated until a termination condition has been reached. Common terminating conditions are:

- A solution is found that satisfies minimum criteria
- Fixed number of generations reached
- Allocated budget (computation time/money) reached
- The highest ranking solution's fitness is reaching or has reached a plateau such that successive iterations no longer produce better results
- Manual inspection

$$D_{600}(x,y) = \left[I_{600}(x,y) - I_{600}^{\text{real}}(x,y)\right] - \frac{\mu_a^{\text{ML}}(600) - \mu_a^{\text{BG}}(600)}{\mu_a^{\text{ML}}(680) - \mu_a^{\text{BG}}(680)} D_{680}(x,y)$$

The initial volume estimate and GA reconstruction procedure must be performed for each combination of parameter values within a desired range. The final estimated set of parameters is selected based upon the solution that produces the highest fitness. the location of the maximum difference due to blood error is found, and a nudge of ±1 is made in the blood thickness map in the proper direction based on D^{600} to find l^{BL}. Correct boundaries on the melanin and blood layers are enforced, the new chromosomes find its new fitness, and the GA proceeds.Consequently, a more robust reconstruction must be undertaken while aided by knowledge of the initial volume estimate. Since the 3D reconstruction process is ill-posed, a GA-based optimization process is used to search the solution space for an optimal solution. Volume error for the shallow melanin layer & deep blood layer (ΔV^{ML} and ΔV^{BL}) were calculated by

$$\Delta V = \frac{\left|\sum_{x,y} \ell_{\text{best}}(x,y) - \sum_{x,y} \ell_{\text{true}}(x,y)\right|}{\sum_{x,y} \ell_{\text{true}}(x,y)}$$

Where l^{best} is the thickness map for one layer in the best fit chromosome after the conclusion of the GA and l^{true} represents the true thickness map for that layer from the lesion model.

II. Results

Snapshots shown below explain transillumination image and calculate the estimation of blood thickness and predict the depth information.

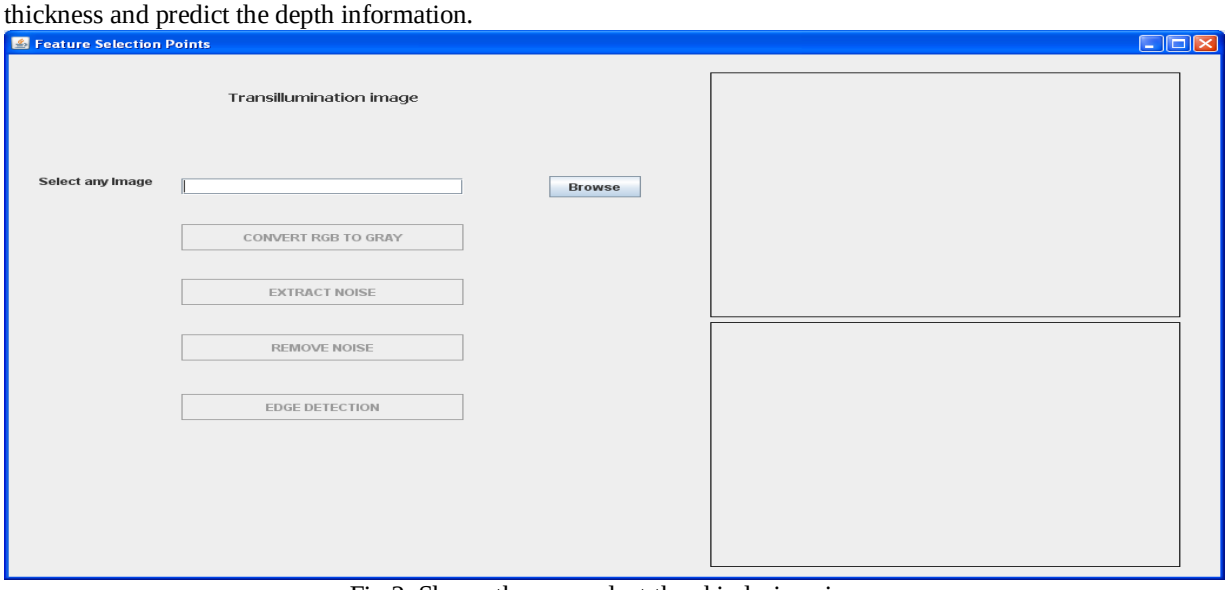

Fig 2. Shows the user select the skin lesions image

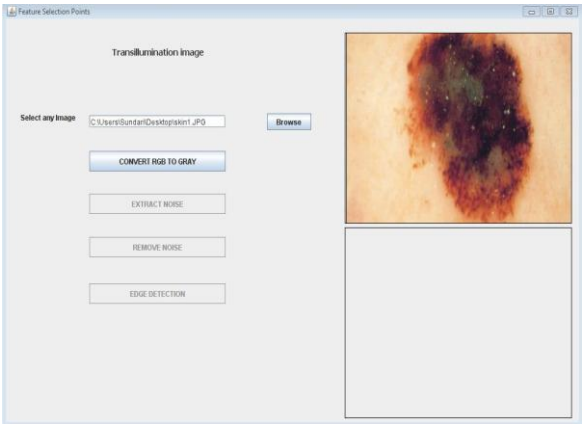

Fig 3. shows the upload the image

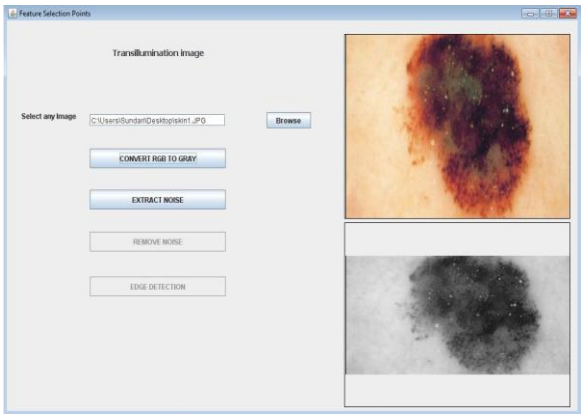

Fig 4. Convert RGB to gray scale image

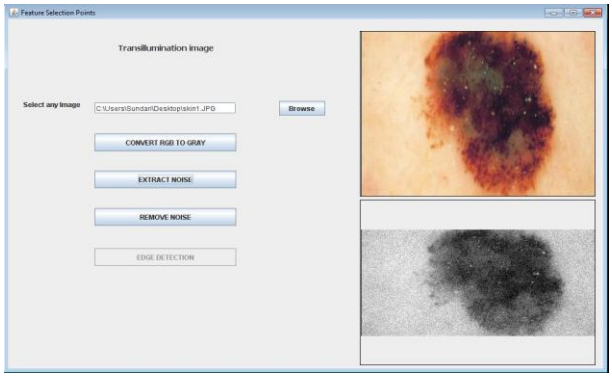

Fig 5. Extract the noise from the image

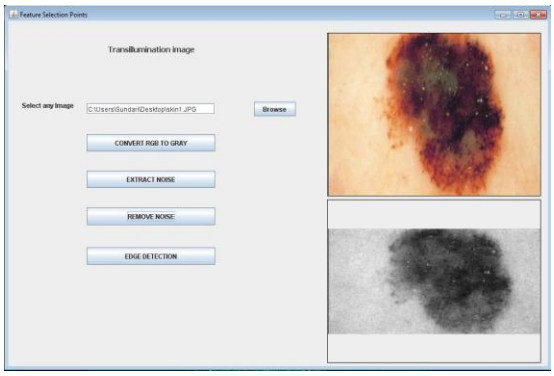

Fig 6. Remove the noise from the image

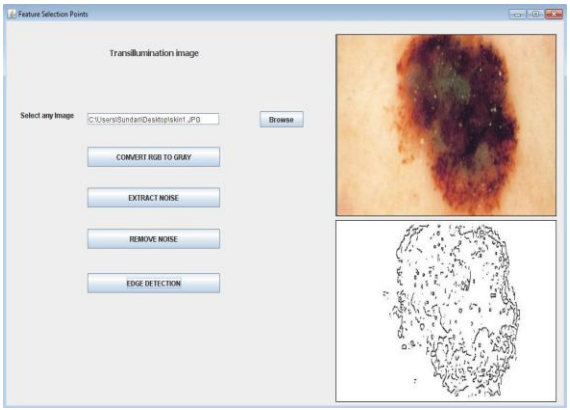

Fig 7. Shows the edge detection

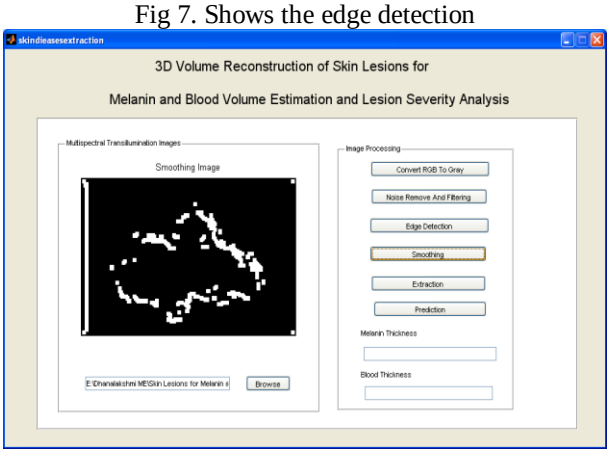

Fig 8. Calculate the estimation of blood layer thickness

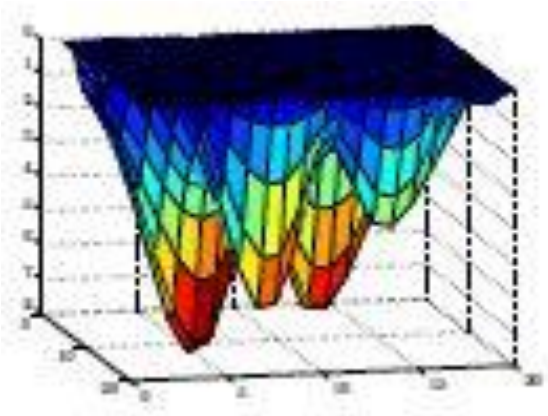

Fig 9. The graph shows the depth of skin lesion using volume reconstruction

V. Conclusion

The traditional methods demonstrate the features of volumetric reconstruction and chromospheres quantification for the analysis and classification of the pre-alignant lesions using multispectral imaging in a clinical setting. However, these methods do not perform efficiently over a large set of images. The proposed system is expected to have the ability to differentiate classes of lesions' severity based on multispectral trans-illumination. It makes use of the nevoscope imaging with the inverse value reconstruction. This could provide the proposed system with features like fast screening, tracking and detection of early skin cancers such as melanoma.

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