Dermal Radiomics for Melanoma Screening

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Abstract

Radiomics has shown considerable promise as a new, emerging approach to computer-aided cancer screening. However, the idea of adopting radiomics for melanoma screening has not been previously explored, with clinical screening relying solely on visual assessment of skin lesion, and thus suffers from low sensitivity and specificity. In this study, a dermal radiomics framework is proposed for computer-aided screening of melanoma, with the aim of improving screening accuracy. A radiomic sequencer is designed to generate radiomic sequences consisting of 367 dermal radiomic features based on extracted physiological biomarkers from dermatological imaging data. The extracted dermal radiomic sequences were then employed to classify benign and malignant melanoma via non-linear random forest classification, and showed superior results in terms of sensitivity, specificity and accuracy when compared to the-state-of-the-art feature models for melanoma classification.

1 Introduction

Radiomics is a newly emerged cancer diagnostic tool that centers around the high throughput extraction of quantitative features from medical images to quantify tumor phenotypes. While radiomics has shown great promise for screening and analysing different forms of cancer such as lung cancer and prostate cancer [1], to the best of our knowledge, radiomics has not been previously adopted for skin cancer, especially melanoma, which is the deadliest form of skin cancer. As such, radiomics could have great potential benefits for melanoma screening, especially since clinical screening currently relies solely on visual assessment of skin lesion, and thus suffers from low sensitivity and specificity. In this study, we propose a dermal radiomics framework for computer-aided melanoma screening, where a radiomic sequencer is designed to generate comprehensive radiomic sequences based on extracted physiological biomarkers from dermatological imaging data.

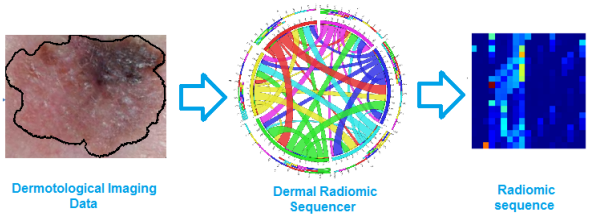

Fig. 1: Flowchart of the proposed dermal radiomics framework.

2 Methodology

The proposed dermal radiomics framework can be described as follows (see Fig. 1). Given a dermatological image of the skin lesion, physiological biomarkers such as eumelanin, pheomelanin and hemoglobin are extracted via non-linear random forest regression model [2], as such biomarkers play an important role in quantitatively characterizing skin tumor phenotypes. Next, a designed radiomic sequencer generates a comprehensive radiomic sequence consisting of 52 low-level features (LLF) [3], 9 high-level intuitive features (HLIF), which quantify the ABCD criteria [4], as well as 306 radiomic features generated from the extracted eumelanin, pheomelanin, and hemoglobin physiological biomarkers in the following manner:

1. For a given lesion segmentation, the lesion is further delineated as outer region and inner region to have a total of three distinct regions (outer region, lesion, and inner lesion) as shown in Fig. 2.
2. Two statistical features (mean and standard deviation) associated with these three regions are calculated over from eumelanin, pheomelanin, and hemoglobin physiological biomarkers extracted from 6 different colour spaces (RGB, XYZ, L*a*b*, L*u*v*, xyz, and rgb).

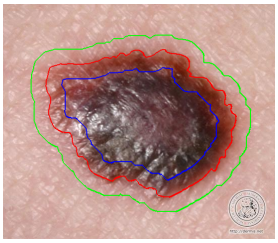

Fig. 2: Example skin lesion image with delineated boundaries of outer region(green), lesion(red), and inner region(blue)

3. The following ratios and differences between the three regions are calculated for each statistical feature: i) outer region(O) / lesion (L), ii) O / inner region (I), iii) L / I, iv) O - L, v) O - I, and vi) L - I.

Given the generated radiomic sequence, melanoma classification was then performed via random forest classification, with the classifier composed of using 1000 decision trees.

3 Results and Discussion

To study the efficacy of the proposed dermal radiomics framework (which we will denote as DRF), sensitivity, specificity, and accuracy of melanoma classification was measured based on a benchmark dataset consisting of 206 dermatological images (119 benign, 87 malignant) as shown in Table 1.

Table 1: Melanoma classification results (%)

Feature	Sensitivity	Specificity	Accuracy
LLF	82.9	72.9	78.4
HLIF + LLF	85.4	77.8	81.7
DRF	87.3	76.5	82.4

It can be observed from Table 1 that the proposed dermal radiomics framework can achieve noticeable overall classification accuracy and sensitivity improvements when compared to existing state-of-the-art LLF and HLIF feature models. These promising results show that such a dermal radiomics framework can aid clinicians and dermatologists for achieving better computer-aided melanoma screening.

Acknowledgments

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References

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