New approaches for ABCD analysis

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Introduction

- Existing color algorithms [1] do not sufficiently account for colors associated with melanin distribution or inflammation
- We propose **two alternative methods for color calculation** that better adhere to melanin distribution and inflammation

Due to current shortage of labeled wide-field images, lesion evolution algorithms rely on ABCD methods, rather than utilizing more advanced Deep Neural Network algorithms

Background

- RGB color space is insufficient for accurately discerning dominant colors
- **LAB color space more consistent with** the way human vision perceives color
- **CIELAB2000 distance** approximates human perception of color differences
- We used Hierarchical Agglomerative Clustering (HAC) with CIELAB2000 distances to extract dominant colors

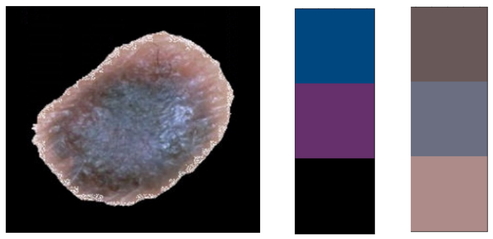

Fig.1: segmented lesion (left); predominant colors found in RGB color space (middle); predominant colors found in LAB color space (right)

Dataset

- Testing: The clinical images within 7-point criteria evaluation database [2]
- Segmentation: ISIC 2018 challenge dataset [3] [4]

Method

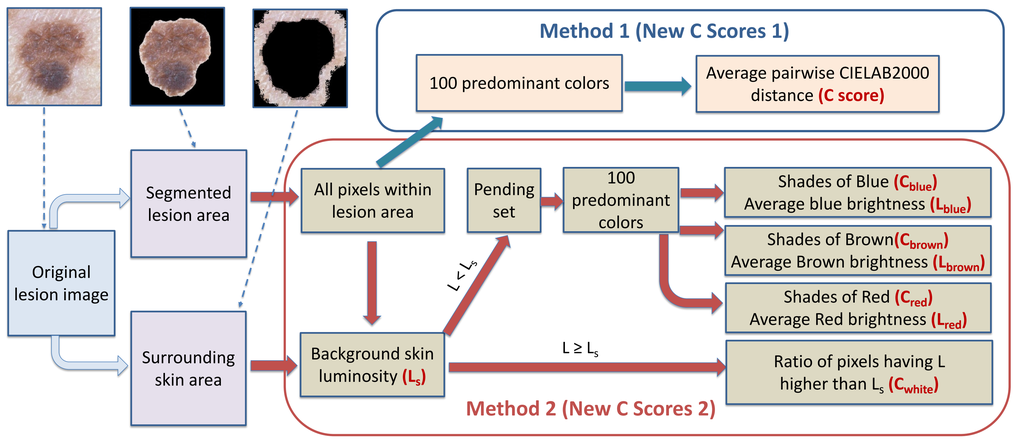

Fig.2: Pipeline of Method 1 and Method 2

Method 1: Pairwise distances between dominant colors

1) Segment the skin lesion but only use the central 80%
2) Extract 100 dominant colors within the lesion
3) Compute pairwise distances between the 100 dominant colors as C score

Method 2: Color Variances

1) Identify Blue, Red and Brown (including Black) sub-spaces within LAB color space
2) Use labeled images to refine the color subspaces
3) Compute the variance and luminosity of all blues, reds and brown pixels

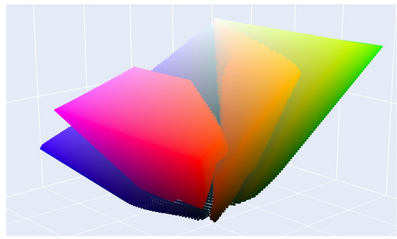

Fig.3: Color subspaces in LAB

Method 2 Algorithm:

1) Segment the skin lesion, use the central 80% as lesion area; use region between the central 100% - 120% as the surrounding skin area
2) Extract background skin luminosity L_s from the surrounding skin area
3) For each pixel with color (L, A, B) within the lesion area, if $L \geq L_s$, save in the white cluster; else save it in the pending set
4) C_{white} = (# of pixels in white cluster) / (# of pixels in lesion area); save L_s as white brightness
5) For pixels in pending set, use HAC to extract 100 dominant colors
6) For each dominant color, measure its distance to blue, red, brown, and other subspaces based on the CIELAB2000 distance. Allocate all pixels represented by each dominant color to the color of the closest subspace
7) Compute the variance of Blue, Red and Brown pixels (C_{blue}, C_{red}, C_{brown}), and average luminosity for the same pixels (L_{blue}, L_{red}, L_{brown})

Results

Table 1: Models Performance with sensitivity = 0.9

Model	Specificity	Precision	Accuracy
DNN [a]	0.30240	0.30952	0.69642
New C Scores 1	0.32068	0.31597	0.75959
New C Scores 2	0.36551	0.33090	0.75959
Old C Scores [b]	0.21034	0.28437	0.74680

(a) Deep Neural Network: An ensemble model of Xception, InceptionV3 and EfficientB7
(b) Old C scores represent 3 standardized variance for the values in R, G, B channels

Using regression models the newly proposed C indices can extract more relevant information from clinical images than the traditional C algorithm.

Future work will implement the proposed New C Scores 2 for lesion evolution analysis. With the availability of labeled clinical evolution data, Deep Networks are likely to produce superior results.

Conclusion

The proposed approach allows us to better track color changes in clinical lesions images. As a next step, we will investigate if the proposed C indexes can extract quality information form various skin tones.

We are actively seeking collaborations for collecting temporal clinical data - preferably with **Fitzpatrick metadata –** in order to enable better tracking of lesion evolutions across various skin tones.

Reference

[1] She Z, Liu Y, Damatoa A. Combination of features from skin pattern and ABCD analysis for lesion classification. Skin Res Technol. 2007 Feb;13(1):25-33. doi: 10.1111/j.1600-0846.2007.00181.x. PMID: 17250529.
[2] J. Kawahara, S. Daneshvar, G. Argenziano and G. Hamarneh, "Seven-Point Checklist and Skin Lesion Classification Using Multitask Multimodal Neural Nets," in IEEE Journal of Biomedical and Health Informatics, vol. 23, no. 2, pp. 538-546, March 2019, doi: 10.1109/JBHI.2018.2824327.
[3] Noel Codella, Veronica Rotemberg, Philipp Tschandl, M. Emre Celebi, Stephen Dusza, David Gutman, Brian Helba, Aadi Kalloo, Konstantinos Liopyris, Michael Marchetti, Harald Kittler, Allan Halpern: "Skin Lesion Analysis Toward Melanoma Detection 2018: A Challenge Hosted by the International Skin Imaging Collaboration (ISIC)", 2018; https://arxiv.org/abs/1902.03368
[4] Tschandl, P., Rosendahl, C. & Kittler, H. The HAM10000 dataset, a large collection of multi-source dermatoscopic images of common pigmented skin lesions. Sci. Data 5, 180161 doi:10.1038/sdata.2018.161 (2018).