



Lesion Segmentation



Melanoma segmentation system



Summary

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What is Melanoma?

Melanoma occurs when the pigment-producing cells that give colour to the skin become cancerous. These cancerous growths develop when unrepaired DNA damage to skin cells (most often caused by ultraviolet radiation from sunshine or tanning beds) triggers mutations (genetic defects) that lead the skin cells to multiply rapidly and form malignant tumors. The majority of melanomas are black or brown, but they can also be skin-colored, pink, red, purple, blue or white. Melanoma is caused mainly by intense, occasional UV exposure (frequently leading to sunburn), especially in those who are genetically predisposed to the disease.

Symptoms might include a new, unusual growth or a change in an existing mole. Melanomas can occur anywhere on the body.

Treatment may involve surgery, radiation, medication or in some cases, chemotherapy.

Significance of the problem

Melanoma constitutes less than 5% of skin cancers but is responsible for around 95% of skin cancer deaths, and its incidence has been rising worldwide over recent decades. Melanomas often resemble moles; some develop from moles. In the United States, approximately 70,000 cases are diagnosed every year, with approximately 9,000 deaths. In Brazil, it is estimated that 6,000 new cases occur each year, resulting in 1,300 deaths.

In Brazil, estimates for the year 2015 indicated incidence rates of 3.47 new cases per 100,000 inhabitants for men and 3.07 for women. Mortality rates for the same year were 1.22 deaths per 100,000 inhabitants for men and 0.86 for women¹. In Brazil, skin cancer is the most incident, and melanoma is more aggressive than other types of cancer.

Objectives

- trainx - 2000 training RGB images of affected parts of skin resized to 192 x 256.
- trainy - 2000 segmented (Ground Truth) images of images in train resized to 192 x 256.
- validationx - 150 validation images of affected parts of skin resized to 192 x 256.
- validationy - 150 segmented (Ground Truth) images of images in train resized to 192 x 256.
- testx - 600 test images of affected parts of skin resized to 192 x 256.
- testy - 600 segmented (Ground Truth) images of images in train resized to 192 x 256.

All the images in all the folders are resized to 192 x 256 size.

Specifications

- ❖ Software specifications
 - Digital image processing using Keras and Tensorflow frameworks.
 - Jupyter notebook is used to run the code for convolution and deconvolution layers, training, etc.
- ❖ Hardware specifications
 - A computer with GPU : Nvidia Geforce on Windows 10
 - Anaconda navigator was installed with Spyder, Jupyter notebook were integrated into the development environment.

Proposed architecture

- ❖ The training dataset includes 2000 dermoscopic images in .jpg format and the corresponding lesion masks in .png format.
- ❖ The goal is to produce accurate binary masks of various skin lesions against a variety of background. Besides training set, the organizers provide a validation dataset that includes 150 images. The participants can submit the binary masks of these 150 images and evaluate the segmentation performance online. Additional test dataset with 600 images is provided for final evaluation. The final rank is based on Jaccard index.
- ❖ We train a CDNN to map from input dermoscopic image to a posterior probability map.
- ❖ The network contains 29 layers with about 5M trainable parameters.
- ❖ Rectified Linear Units (ReLUs) as the activation function.
- ❖ For each convolutional/deconvolutional layer. For output layer, we use sigmoid as the activation function. Pixel-wise classification is performed and CDNN is essentially served as a filter that projects the entire input image to a map where each element represents the probability that the corresponding input pixel belongs to the tumor. In order to address the conflict between multi-scale information aggregation and full-resolution pixel-wise classification, we implement a strategy of using upsampling and deconvolutional layers to recover lost resolution while carrying over the global perspective from pooling layers [3]. Batch normalization is added to the output of every convolutional/deconvolutional layer to reduce the internal covariate shift.

Architectural details of the proposed CDNN mode

Conv	Filter size	No. of features	Deconv	Filter size	No. of features
conv-1-1	3×3	16	deconv-1	3×3	256
conv-1-2	3×3	32	ups-1	2×2	256
pool-1	2×2	32	deconv-2-1	3×3	256
conv-2-1	3×3	64	deconv-2-2	3×3	128
conv-2-2	3×3	64	ups-2	2×2	128
pool-2	2×2	64	deconv-3-1	4×4	128
conv-3-1	3×3	128	deconv-3-2	3×3	128
conv-3-2	4×4	128	ups-3	2×2	128
pool-3	2×2	128	deconv-4-1	3×3	64
conv-4-1	3×3	256	deconv-4-2	3×3	32
conv-4-2	3×3	256	ups-4	2×2	32
pool-4	2×2	256	deconv-5-1	3×3	16
conv-5	3×3	512	output	3×3	1

Already existing detection systems

❖ SkinVision

- SkinVision is an application that allows users to upload images of their moles and helps them track their moles' evolution. It also helps users understand the symptoms and risk factors associated with skin cancer.[13] Our application is more diagnostic and goes beyond tracking to actually inform users of their probability of having skin cancer

❖ Doctor Mole

- Doctor Mole provides analysis of an image uploaded by the user instantaneously. It analyses the image based on the asymmetry, border, color, diameter, and evolution criteria of evaluating a moles and reports back numbers for each criteria independently. The application makes use of a "freemium" model and provides more detailed analysis for users who pay for it.[7]

Related work

Related work

Deadlines

- ❖ 1st week
 - Previous research and proposal submission
- ❖ 2nd week
 - Presentation and the commencement of project implementation.
- ❖ 3rd week
 - Project update
- ❖ 4th week
 -
- ❖ 5th week
 -
- ❖ 6th week
 - - Final presentation.

Bibliography and references

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Thanks for listening!

