



Improving Skin Lesion Segmentation with Generative Adversarial Networks

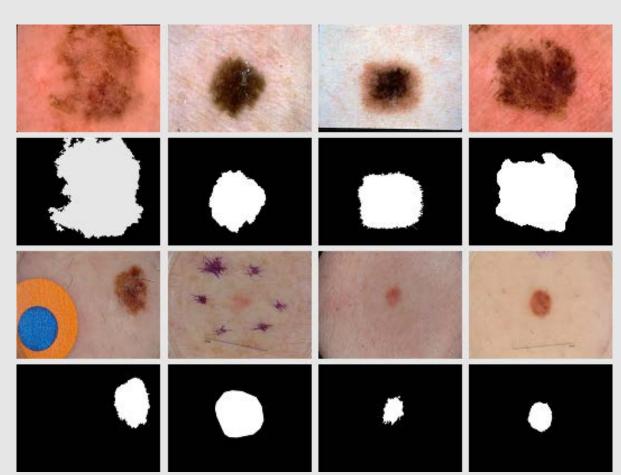
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Problem Statement

Malignant melanoma is the most dangerous skin cancer, with a substantial death rate. Automated skin lesion segmentation is a fundamental step to help experts in early diagnosis, but requires a huge amount of data to be performed. Unfortunately, manual image segmentation is a very time consuming job that demands the work of a competent specialist.



Samples from the ISIC dataset.

Goals:

- decrease the amount of manually segmented images required by automated analysis;
- support the clinical decision making.

Baseline Architecture Our model maps the input dermoscopic image into a posterior probability map, exploiting an architecture based on the CDNN which won the International Skin Imaging Collaboration (ISIC) challenge in 2017 [1]. 29 layers with about 5M trainable parameters probability map Conv* + Batch Norm + ReLU Dropout Pooling/Upsampling Conv* + Batch Norm + Sigmoid * fixed stride of 1 pixel. [1] Yuan, Yading, Ming Chao, and Yeh-Chi Lo. "Automatic skin lesion segmentation with fully convolutional-

Hyperparameters Analysis

The baseline CDNN is mainly affected by three hyperparameters, which are stressed in our analysis:

1) Input image size:

• 96x128 • 192x256

384x512

2) Image channels:

3) Loss function:

• RGB

• RGB + HSV + L* RGB + HSV + CIELAB

 $L = \frac{1}{n} \sum_{i,j} (t_{ij} - p_{ij})^2$ (MSE)

