



Use Case 12

Lab 2: Skin Lesion Segmentation

Winter School 25/01/2022





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Skin Lesion Image Analysis



Introduction

- Skin cancer is a major public health issue, with malignant melanoma being the deadliest form of it and presenting millions of newly diagnosed cases every year.
- Dermoscopy is an imaging technique that eliminates the surface reflection of skin. By removing surface reflection, visualization of deeper levels of skin is enhanced.
- When used by expert dermatologists, dermoscopy provides improved diagnostic accuracy, in comparison to standard photography.









International Skin Imaging Collaboration

- The International Skin Imaging Collaboration (ISIC) contains the largest publicly available collection of quality controlled dermoscopic images of skin lesions.
- Collected from leading clinical centers internationally and acquired from a variety of devices within each center.
- Since 2016, ISIC has sponsored annual challenges for the computer science community







ISIC 2017 Challenge

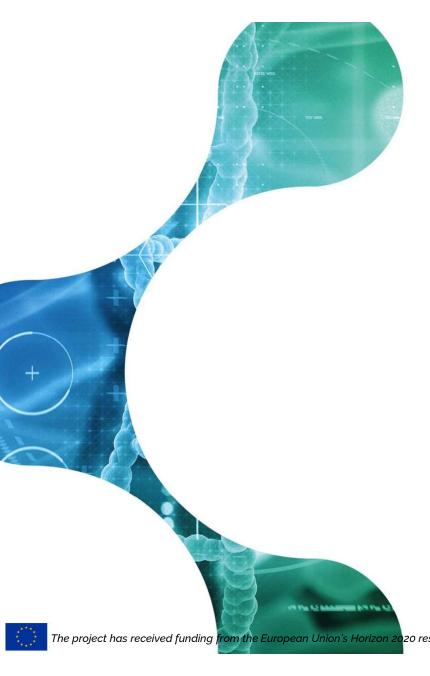


• Purpose of the challenge: develop image analysis tools to enable the automated diagnosis of melanoma from dermoscopic images.



- Part 1: Lesion Segmentation
- Part 2: Detection and Localization of Visual Dermoscopic Features/Patterns
- Part 3: Disease Classification
- Segmentation is defined as the recognition of the set of pixels that constitute the skin lesion within the image. It is employed in 2017 and 2018 challenges.
- The 2017 challenge was chosen because for the 2018 challenge test ground truth are still not provided.





Dataset

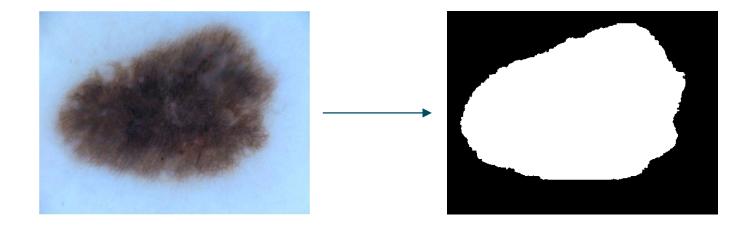




Segmentation Dataset



• Goal: automated predictions of lesion segmentation boundaries from dermoscopic images, in the form of a binary mask (0 background, 255 foreground).







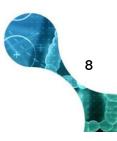
Segmentation Dataset





- Images are in .jpg format, while masks in .png format.
- Each image has only one lesion within it
- Dimensions of the images: from 576x768 to 6748x4439

Split	Number of images
Training	2000
Validation	150
Test	600





Models

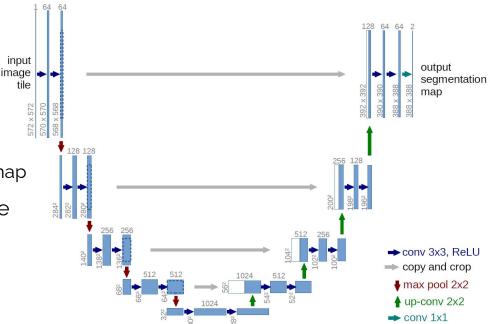


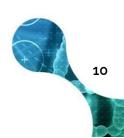
• Standard ap

UNet



- Standard approach: encoder-decoder convolutional neural network.
 - Encoder: increase the "what" and reduce the "where"
 - Decoder: create high-resolution segmentation map
- UNet, created specifically for biomedical image segmentation.
- Upsampling convolutions concatenate with features from contracting path
- Several modified UNet over the years, for example adding batch normalization and scaling the output segmentation map with the same resolution of the input.





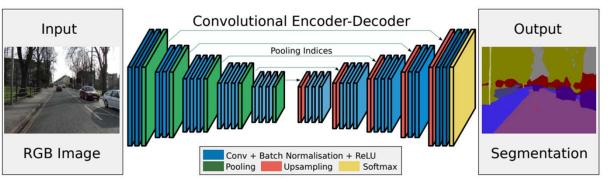


SegNet



- Same approach: encoder-decoder convolutional neural network.
 - Encoder: VGG16, with pooling layers that memorize the locations of the maximum feature value in each pooling window for each encoder feature map.
 - Decoder: for each encoder layer, there exists a corresponding decoder layer to upsample the feature maps to its original size, which uses the memorized max-pooling indices from the corresponding encoder feature map. In this way, SegNet uses less memory compared to UNet, which concatenate the entire feature map from the encoder.
- Actually, EDDL for now didn't retrieve the pooling indices, so the upsample is just a

resize of the image







Metric



- Metric: Jaccard index (Intersection over Union)
 - Quantify the percent overlap between the target mask and our prediction output
 - Number of pixels common between the target and prediction masks divided by the total number of pixels present across both masks.

$$IoU = \frac{|target \cap prediction|}{|target \cup prediction|} = \frac{|target \cap prediction|}{|target| + |prediction| - |target \cap prediction|}$$

• This metric is closely related to the Dice coefficient which is often used as a loss function during training.

$$Dice \ coefficient = \frac{2 \ |target \cap prediction|}{|target| \ + |prediction|}$$

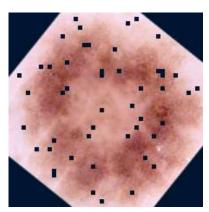


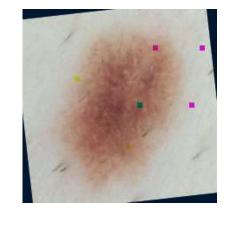


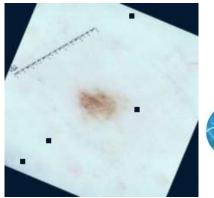
Pre Processing



Pre processing consists in several data augmentation functions:



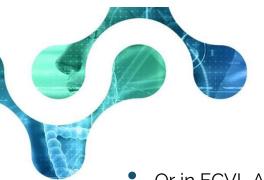








1)



Pre Processing



Or in ECVL Augmentation Language:

```
SequentialAugmentationContainer

AugResizeDim dims=(512,512) interp="cubic" gt_interp="nearest"

AugMirror p=0.5

AugFlip p=0.5

AugRotate angle=[-180, 180]

AugAdditivePoissonNoise lambda=[0, 10]

AugGammaContrast gamma=[0.5, 1.5]

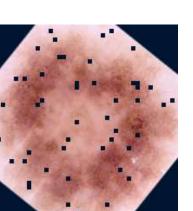
AugGaussianBlur sigma=[0, 0.8]

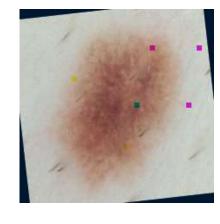
AugCoarseDropout p=[0, 0.03] drop_size=[0.02, 0.05] per_channel=0.25

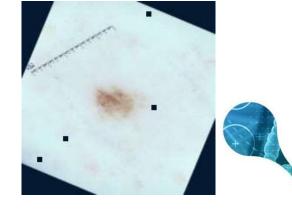
AugToFloat32 divisor=255 divisor_gt=255

AugNormalize mean=(0.6681, 0.5301, 0.5247) std=(0.1337, 0.1480, 0.1595)

end
```









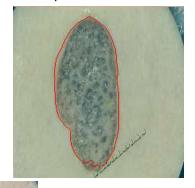


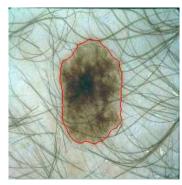
Post Processing



- To qualitatively evaluate the results, when the output of the neural network is saved, a little of post processing is added.
- ConnectedComponentsLabeling finds the connected components of the predicted mask
- Their contours are then colored red on the original image

```
tmp, labels = ecvl.Image.empty(), ecvl.Image.empty()
ecvl.ConvertTo(img_t, tmp, ecvl.DataType.uint8)
ecvl.ConnectedComponentsLabeling(tmp, labels)
ecvl.ConvertTo(labels, tmp, ecvl.DataType.uint8)
contours = ecvl.FindContours(tmp)
ecvl.ConvertTo(orig_img_t, tmp, ecvl.DataType.uint8)
tmp_np = np.array(tmp, copy=False)
for cseq in contours:
    for c in cseq:
        tmp_np[c[0], c[1], 0] = 255
        tmp_np[c[0], c[1], 1] = 0
        tmp_np[c[0], c[1], 2] = 0
```





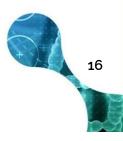




Results



Model	Loss	Optimizer	Initial LR	Epochs	Best epoch	Validation IoU	Test IoU
SegNet	Binary Cross Entropy	Adam	1e-5	100	49	0.725	0.708
SegNetBN	Binary Cross Entropy	Adam	1e-5	100	99	0.745	0.714
Unet	Binary Cross Entropy	Adam	1e-5	100	46	0.755	0.718
Unet	Dice	Adam	1e-3	100	74	0.750	0.733







Resources



Original Dataset

ISIC Challenge Datasets

Prepared Dataset

isic_segmentation.zip (11,3 GB) Option 1 Option 2

Pipeline Repository

<u>UC12_pipeline</u> <u>use-case-pipelines</u>





