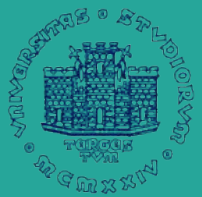
DATA SCIENCE &
SCIENTIFIC COMPUTING



UNIVERSITÀ
DEGLI STUDI DI TRIESTE

SIIM-ISIC Melanoma Classification

—

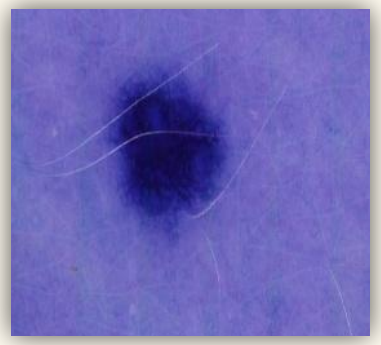
Statistical Machine Learning project by :
Abdalghani Azza M. N., Bartole Davide and Tedisco Francesca

Problem statement :

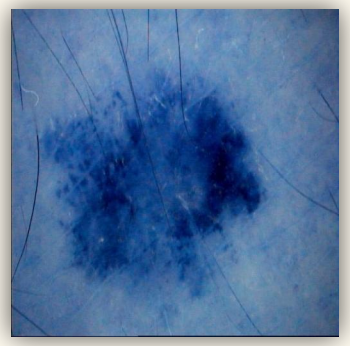
Melanoma is a common skin cancer.

Classification problem

?



No Melanoma



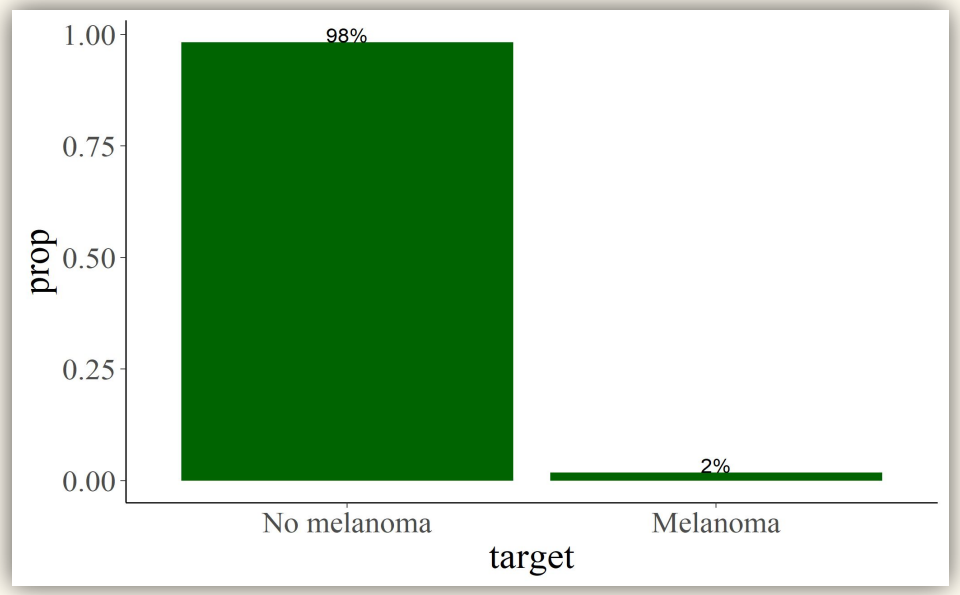
Melanoma

Data Description

The ISIC (International Skin Imaging Collaboration) archive contains the largest available collection of dermoscopic images of skin lesions.

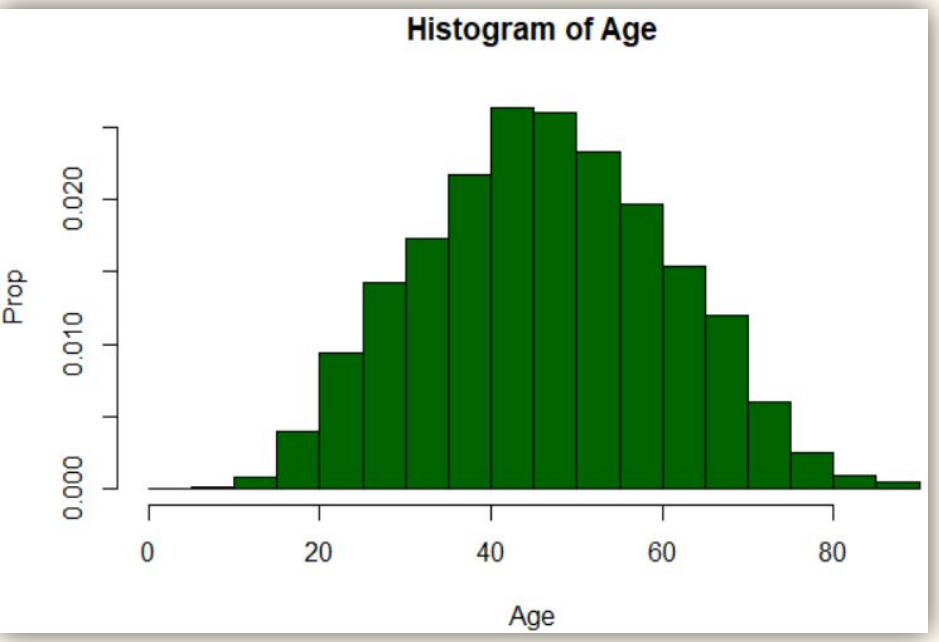
```
'data.frame':   33126 obs. of  5 variables:
 $ target    : Factor w/ 2 levels "No melanoma",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ age       : num  45 45 50 45 55 40 25 35 30 50 ...
 $ anatomy   : Factor w/ 7 levels "","head/neck",..: 2 7 3 2 7 3 3 6 6 3 ...
 $ sex       : Factor w/ 3 levels "","female","male": 3 2 2 2 2 2 3 2 3 2 ...
 $ image_name: chr  "ISIC_2637011" "ISIC_0015719" "ISIC_0052212" "ISIC_0068279" ...
```

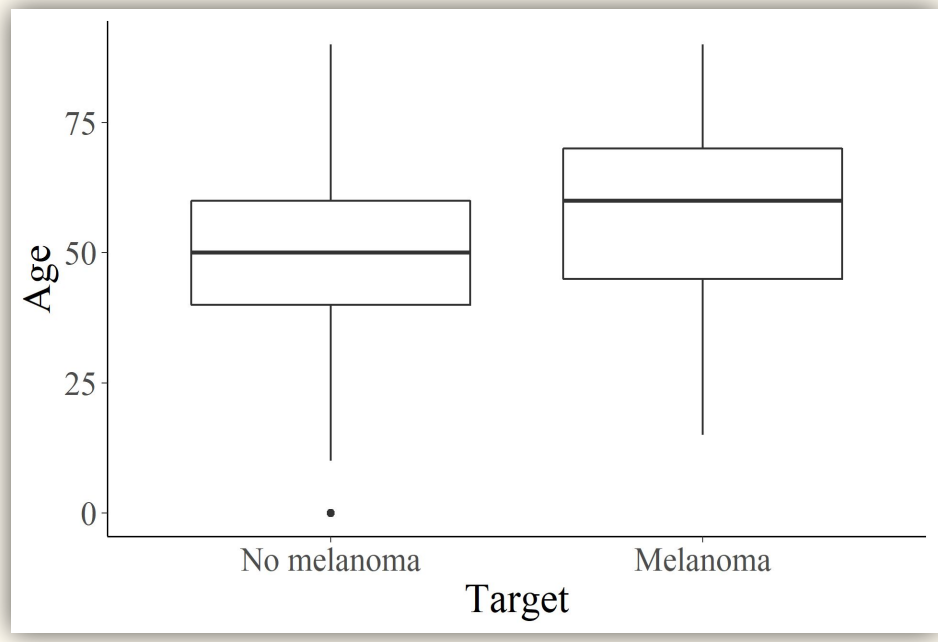
Data visualisation :



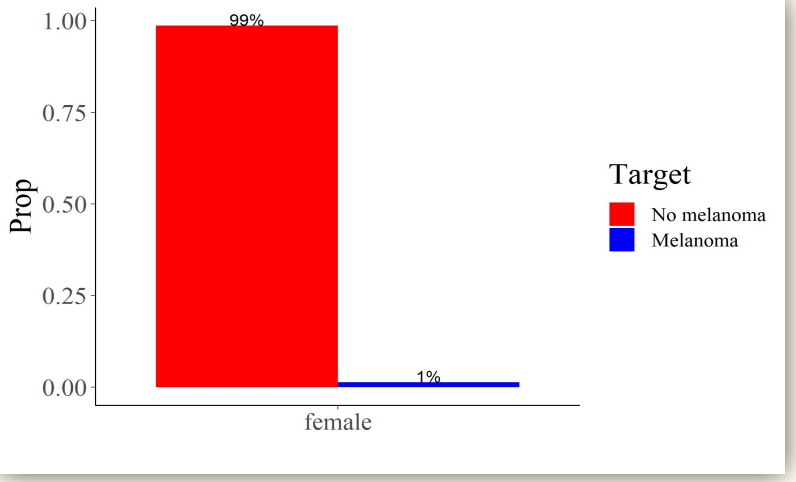

```
Final proportion:
0    0.532814
1    0.467186
```

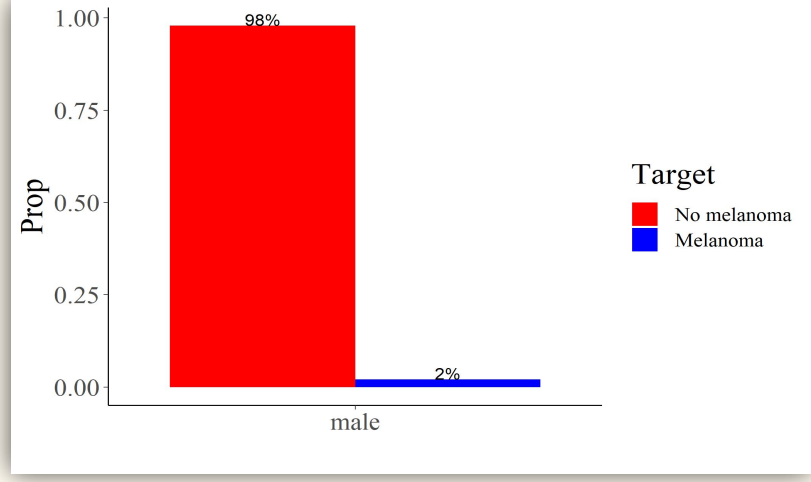
Age approximation

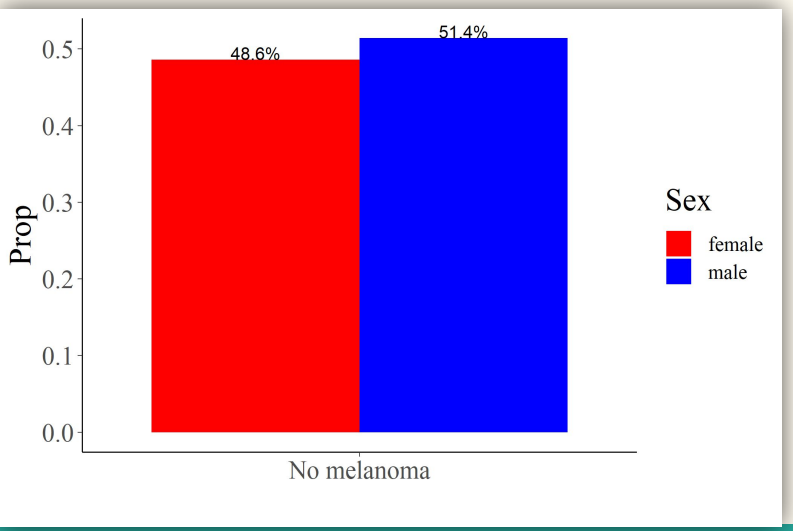


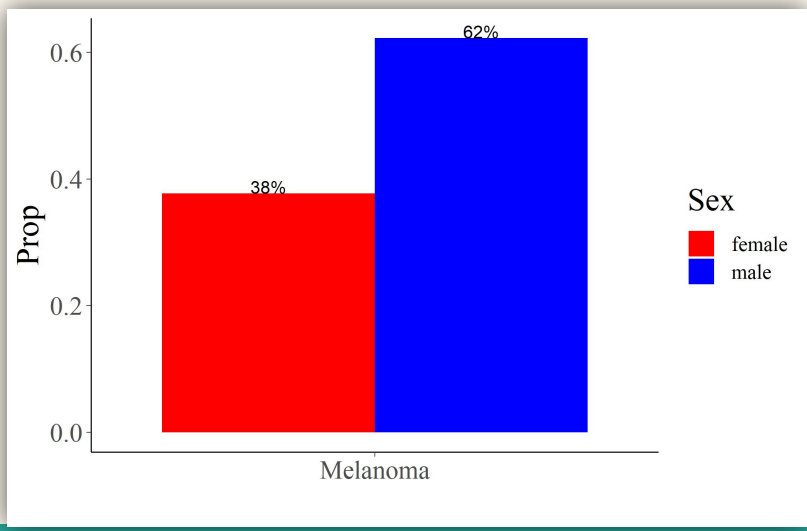


Sex

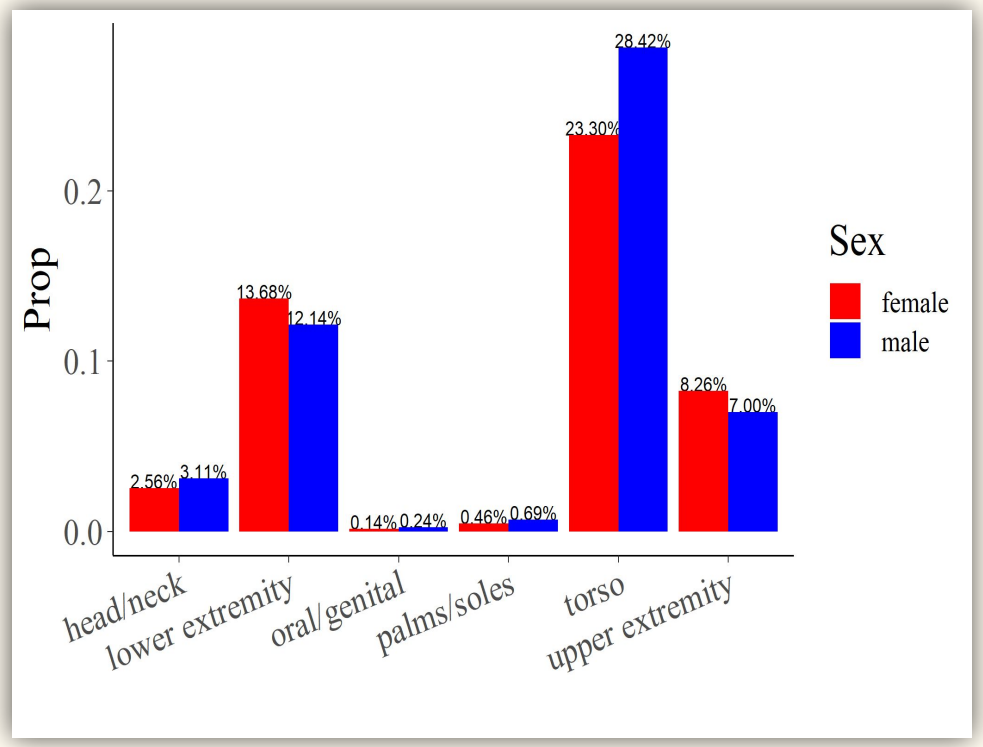

1.00
0.75
0.50
0.25
0.00
Prop
99%
1%
female
Target
No melanoma
Melanoma

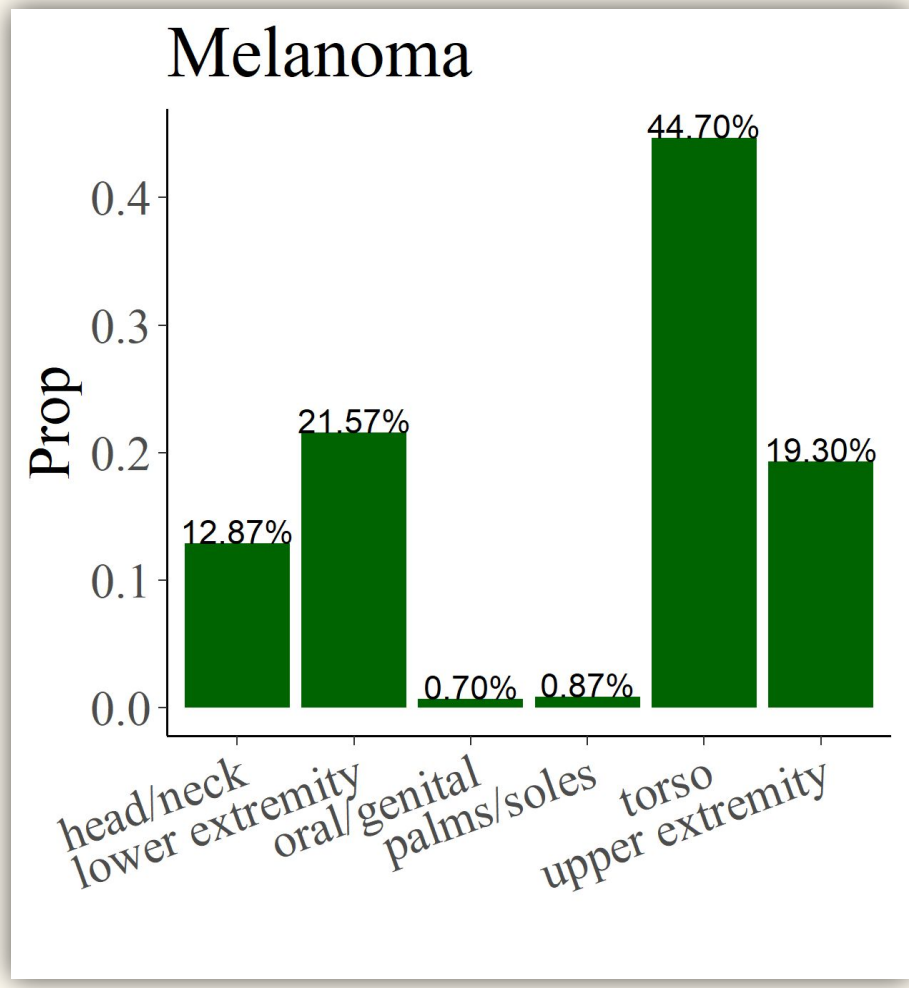

1.00
0.75
0.50
0.25
0.00
Prop
98%
2%
male
Target
No melanoma
Melanoma


0.5
0.4
0.3
0.2
0.1
0.0
Prop
48.6%
51.4%
No melanoma
Sex
female
male

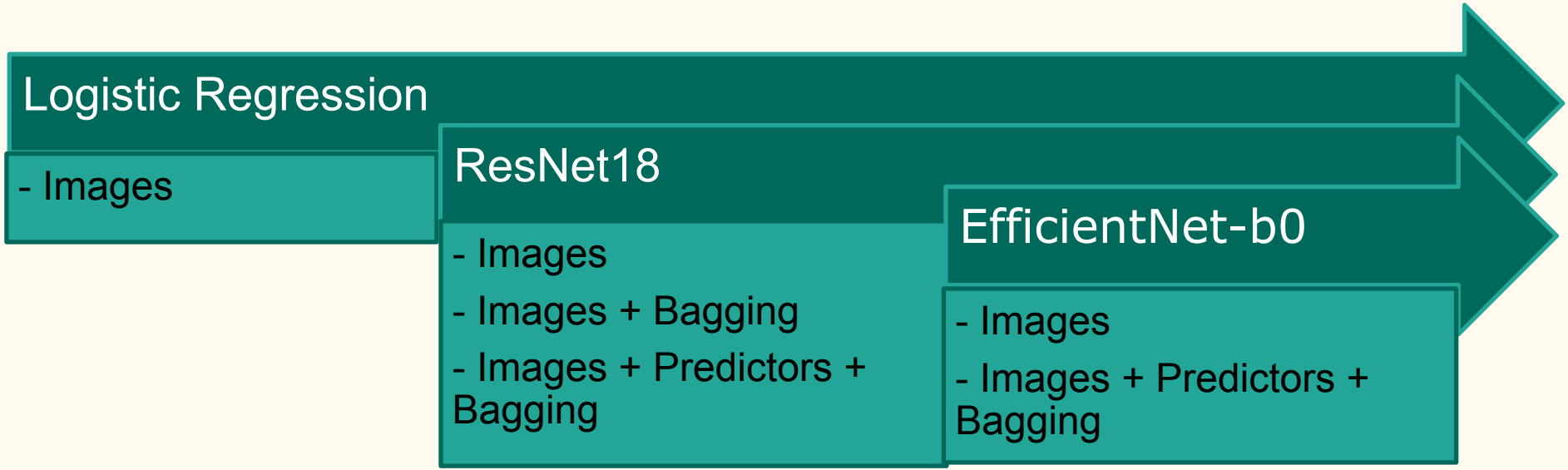

0.6
0.4
0.2
0.0
Prop
38%
62%
Melanoma
Sex
female
male

Anatomy = site of body





Proposed solutions :



1. Logistic Regression

- Images as input
- Target as output
- Logit function

- Train set
- Test set (15%)

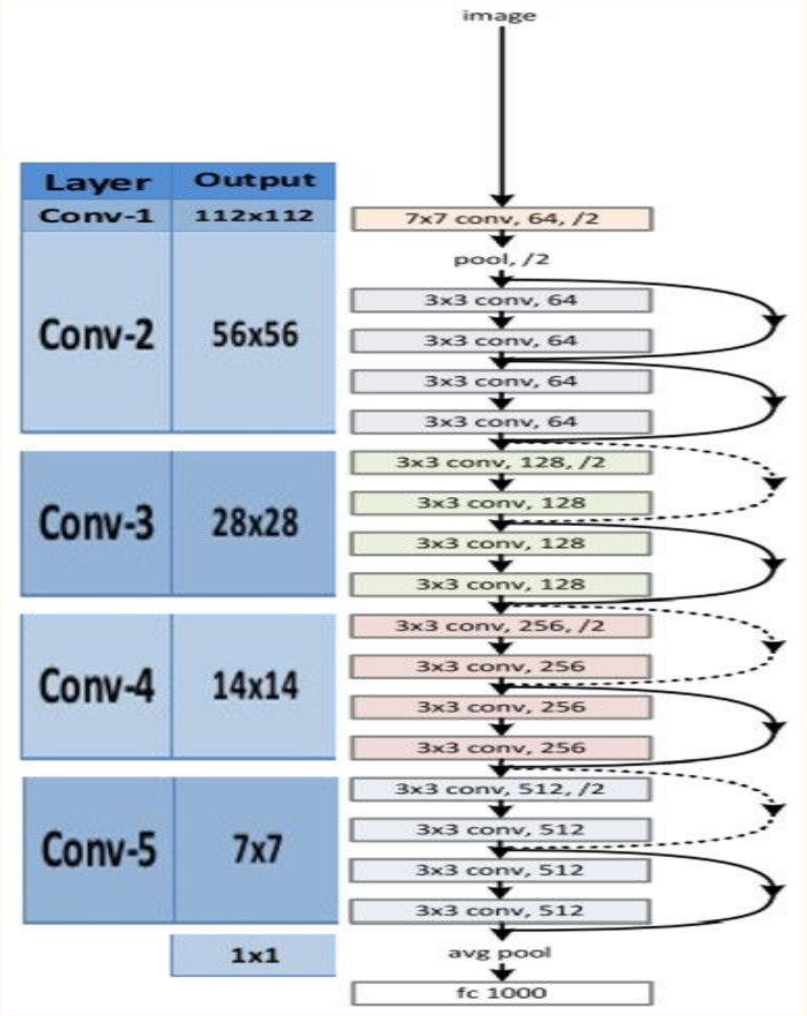
Accuracy=98,23%

False Positive Rate=0
False Negative Rate=1

	No Melanoma	Melanoma
No Melanoma	4881	88
Melanoma	0	0

2. ResNet18

- 18 layers
- Skip connections
- Winner of the ImageNet challenge 2015



Data transformation

Normalization with :

MU = [0.485, 0.456, 0.406]

S = [0.229, 0.224, 0.225]

- Vertical Flip (p=0.5)

- Horizontal Flip (p=0.5)

- To tensor

- Learning rate: 1e-3

- Predictions done with Test Time Augmentation

2.a. ResNet18: Images as Inputs

- CNN that envelopes the ResNet18

- Loss: BCE with logit loss
- Optimizer: Adam
- 10 epochs
- Dataset divided in 3 parts:
  - Training set (72%) → batch size: 64
  - Validation set (20%) → batch size: 16
  - Test set (8%) → batch size: 16

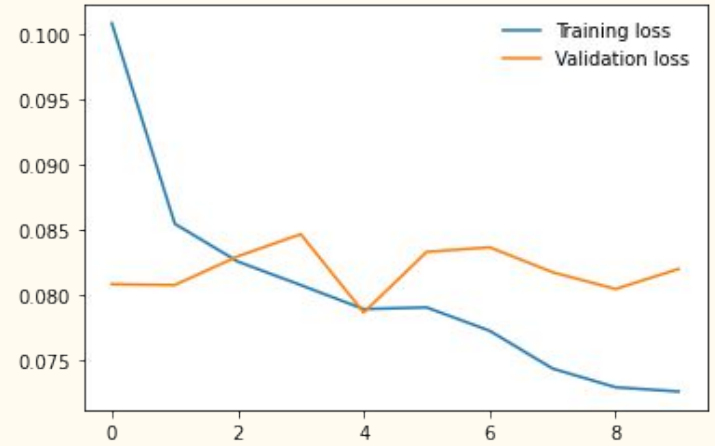
Results

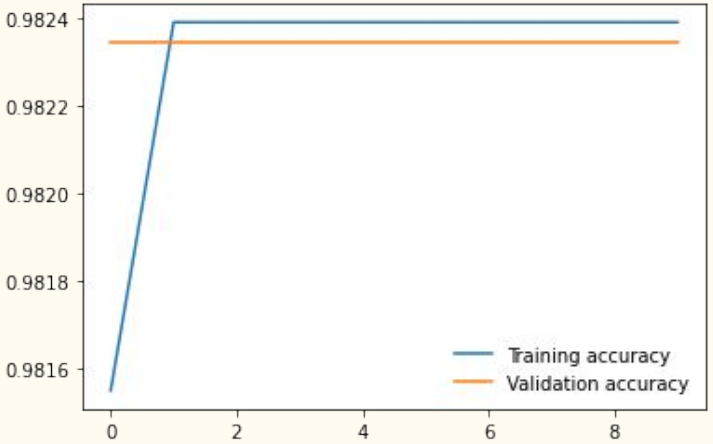
Accuracy: 98.23%

FPR: 0%

FNR: 100%

	No melanoma	Melanoma
No melanoma	2603	47
Melanoma	0	0





2.b. ResNet18: Images as inputs and bagging

- CNN that envelopes the ResNet18
- Bagging using 10 samples given by weighted bootstrap

- Loss: BCE with logit loss
- Optimizer: Adam
- 10 epochs
- Dataset divided in 3 parts:
  - Training set (72%) → batch size: 64
  - Validation set (20%) → batch size: 16
  - Test set (8%) → batch size: 16

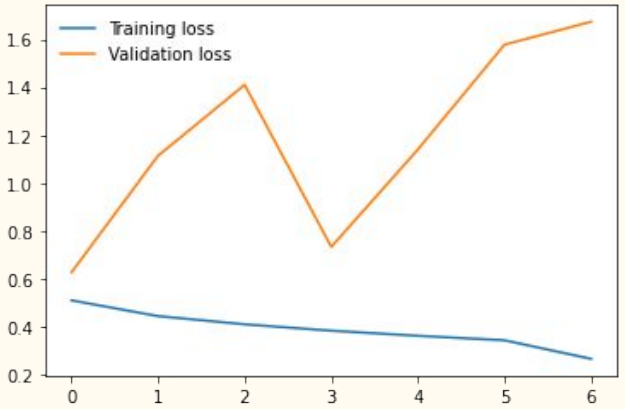
Results

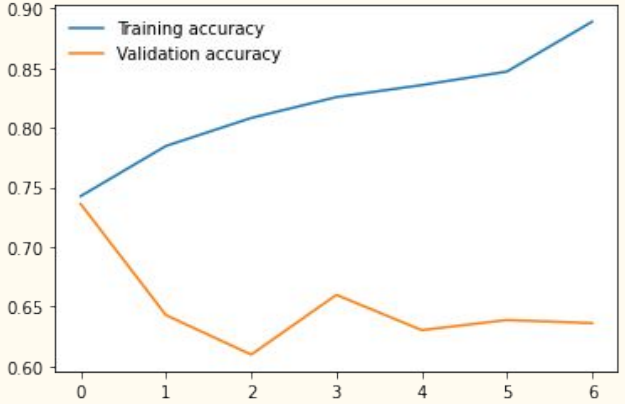
Accuracy: 83.51%

FPR: 19.05%

FNR: 13.6%

	No melanoma	Melanoma
No melanoma	1139	169
Melanoma	268	1074





2.c. ResNet18: Images, meta features and bagging

- 2 sets of layers
- Convolutional layers for the images
- Sequential layers for the meta features
  - Sex
  - Age
  - Site of the mole
- Bagging using 10 samples given by weighted bootstrap

- Loss: BCE with logit loss
- Optimizer: Adam
- 10 epochs

- Dataset divided in 3 parts:
  - Training set (72%) → batch size: 64
  - Validation set (20%) → batch size: 16
  - Test set (8%) → batch size: 16

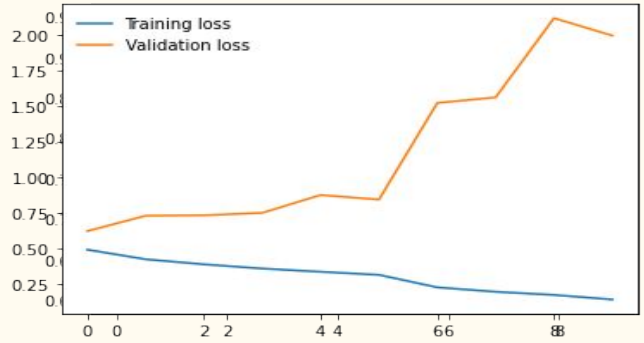
Results

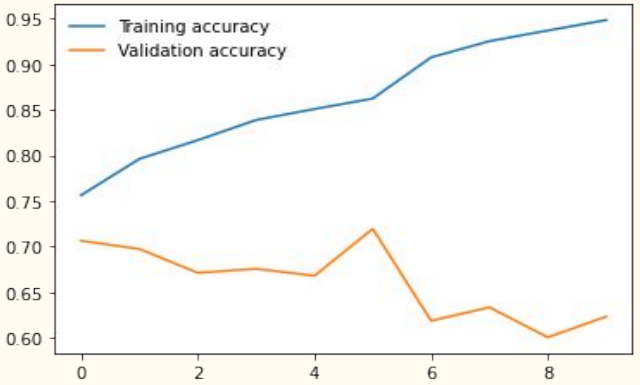
Accuracy: 96.53%

FPR: 6.25%

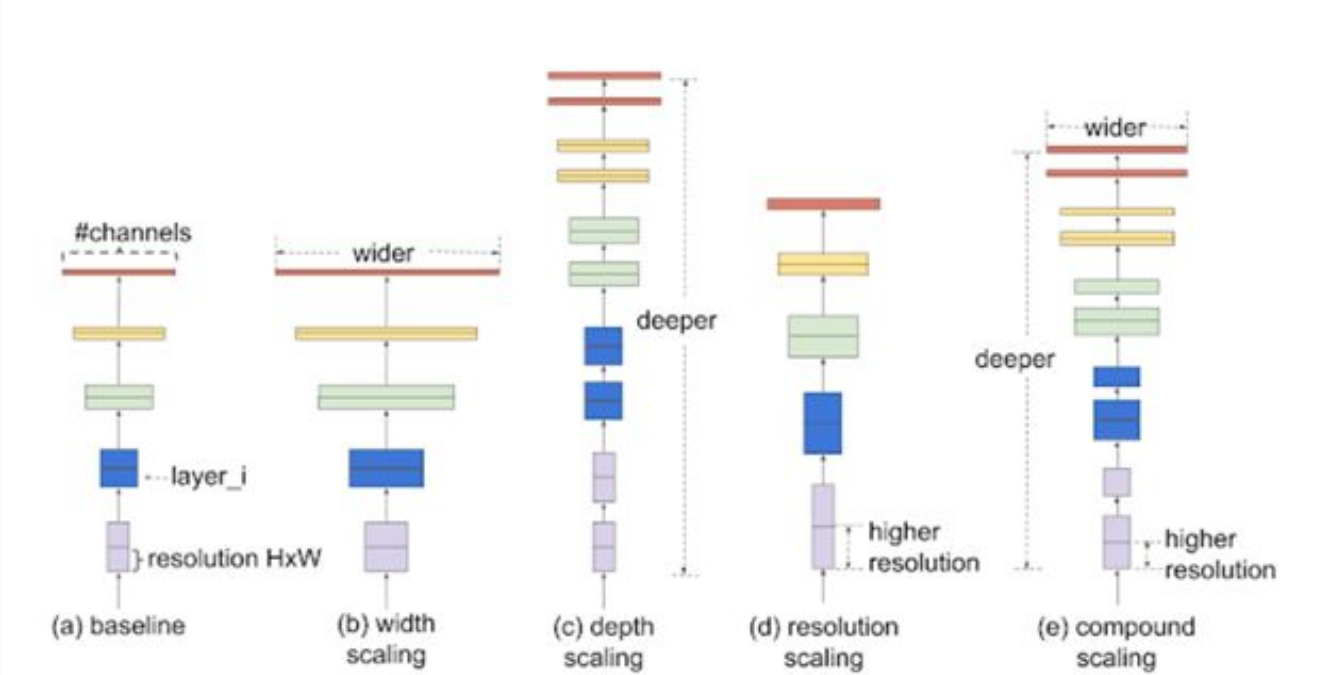
FNR: 0.32%

	No melanoma	Melanoma
No melanoma	1319	4
Melanoma	88	1239





3. EfficientNet : Scaling up CNN



Comparison of different scaling methods. Unlike conventional scaling methods (b)-(d) that arbitrary scale a single dimension of the network, our compound scaling method uniformly scales up all dimensions in a principled way.

EfficientNet-B0 :

Stage i	Operator $\hat{\mathcal{F}}_i$	Resolution $\hat{H}_i \times \hat{W}_i$	#Channels $\hat{C}_i$	#Layers $\hat{L}_i$
1	Conv3x3	224×224	32	1
2	MBConv1, k3x3	112×112	16	1
3	MBConv6, k3x3	112×112	24	2
4	MBConv6, k5x5	56×56	40	2
5	MBConv6, k3x3	28×28	80	3
6	MBConv6, k5x5	14×14	112	3
7	MBConv6, k5x5	14×14	192	4
8	MBConv6, k3x3	7×7	320	1
9	Conv1x1 & Pooling & FC	7×7	1280	1

Basic network structure of EfficientNet-B0

3.a. Images as inputs for EfficientNet-b0

Image Augmentation :

- Normalization with :

MU = [0.485, 0.456, 0.406]

S = [0.229, 0.224, 0.225]

- Vertical Flip (p=0.5)

- Horizontal Flip (p=0.5)

- To tensor

Hyperparameters:

Epochs = 20

LR = 1e-3

Batch_size = 32

B = 0.5

MelanomaNet :
- Pretrained EfficientNet-b0
- Global Average Pooling
- Droupout
- Dense output

- Split into 80% train and 20% val datasets.

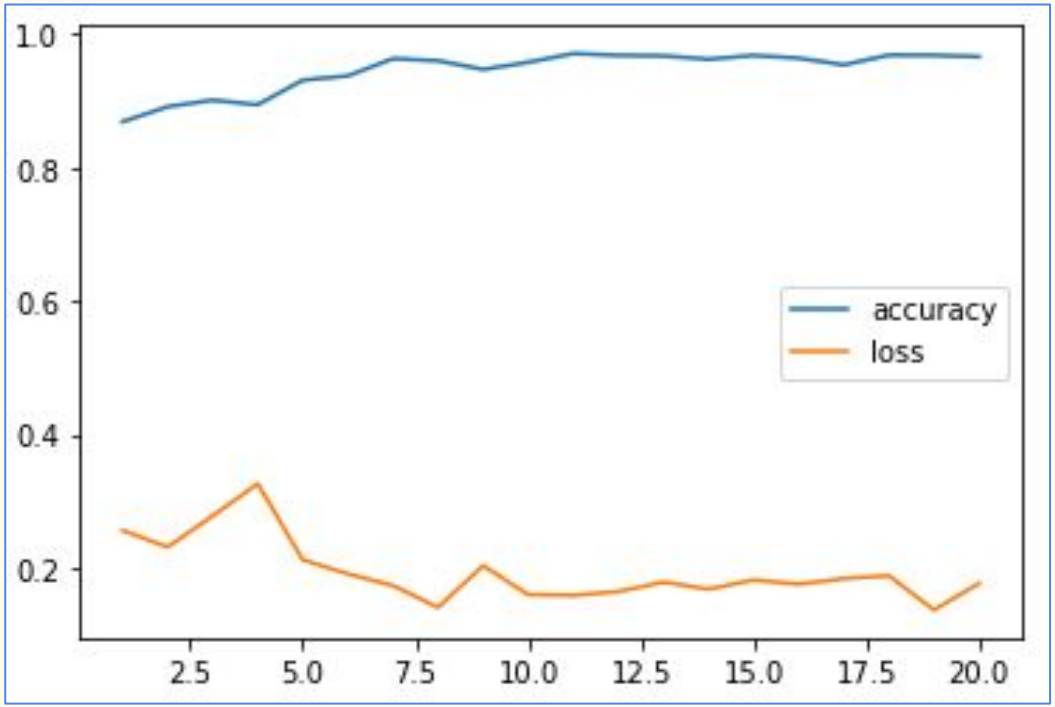
- WeightedRandomSampler

- Adam Optimizer

- Loss : Binary Cross-Entropy (BCEWithLogitsLoss)

- GPU device

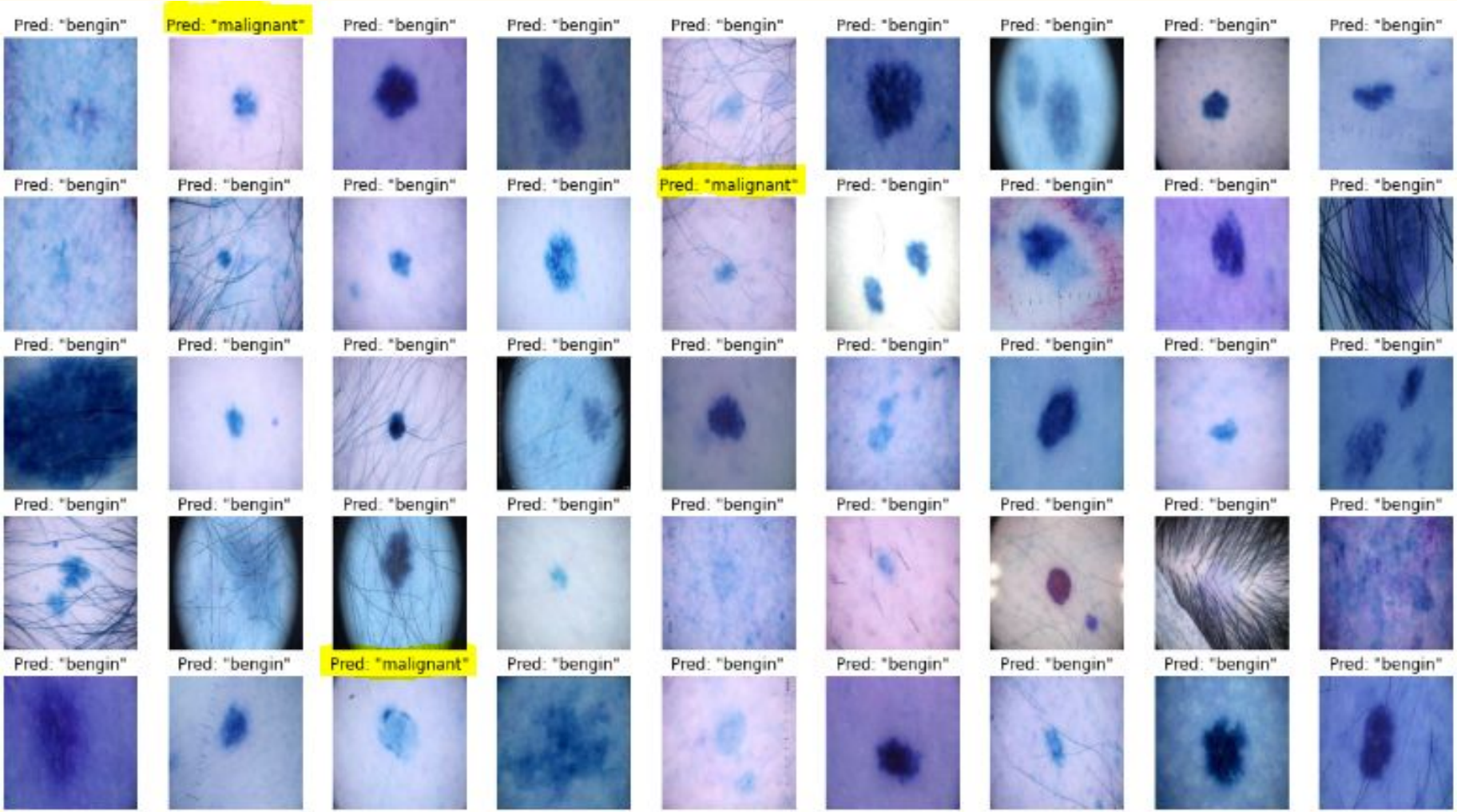
Results :



Validation accuracy and loss

- Accuracy : 96.6%
- Output Results :
  - 10605 benign
  - 377 malignant

	image_name	target	class
0	ISIC_0052060	1.710294e-14	"bengin"
1	ISIC_0052349	8.461608e-24	"bengin"
2	ISIC_0058510	3.301137e-23	"bengin"
3	ISIC_0073313	5.592170e-14	"bengin"
4	ISIC_0073502	9.411071e-10	"bengin"
5	ISIC_0074618	2.273408e-05	"bengin"
6	ISIC_0076801	1.325034e-12	"bengin"
7	ISIC_0077586	8.564031e-07	"bengin"
8	ISIC_0082004	1.457258e-04	"bengin"
9	ISIC_0082785	4.364880e-07	"bengin"


Pred: "bengin"
Pred: "malignant"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "malignant"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
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Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "malignant"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"
Pred: "bengin"

3.b. Images + meta features for EfficientNet-b0

- meta features : [sex, age_approx, anatom_site_general_challenge]

* Preprocessing the data :

    - Encoding

* Weighted bootstrap as bagging.

* split data into 3 parts (train, val, test).

3.b. Images + meta features for EfficientNet-b0

*hyper-parameters :

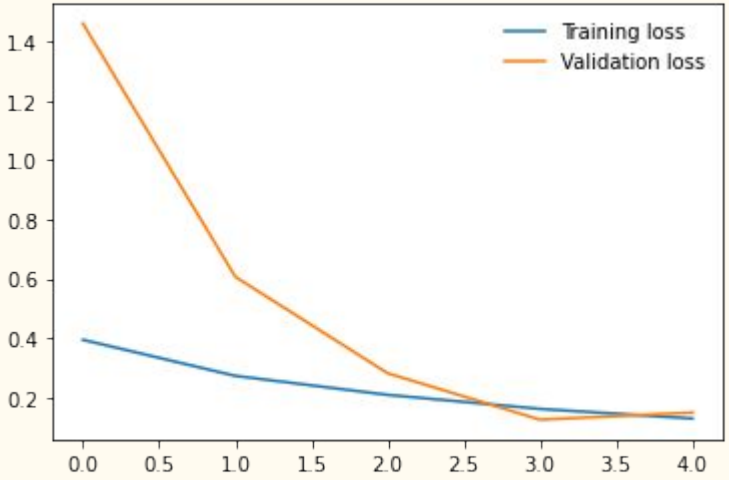
- Epochs = 5

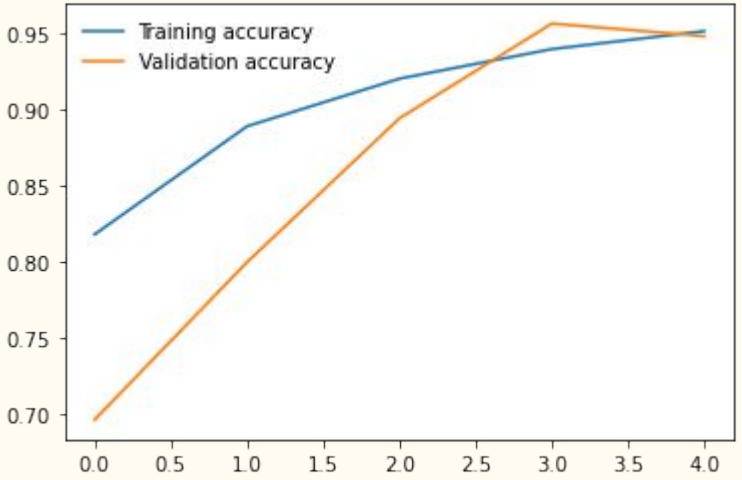
- Early stopping patience = 3

- batch_size = 64 , 16, 16

- Loss: BCE with logit loss
- Optimizer: Adam

Results

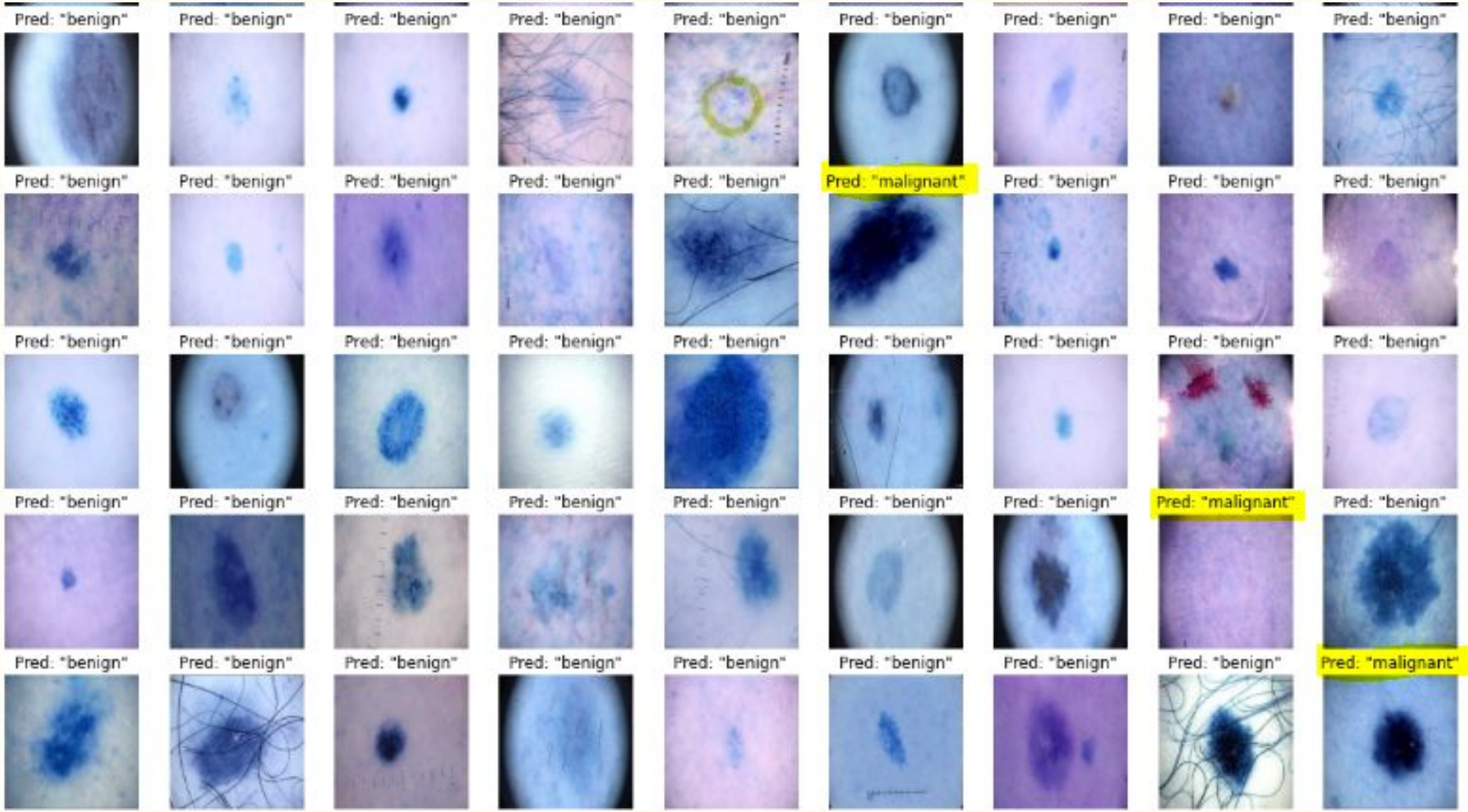




	No Melanoma	Melanoma
No melanoma	1374	44
Melanoma	33	1199

- Accuracy : 97.3%
- FPR = 0.0234
- FNR = 0.0354
- Output Results :
  - 10659 benign
  - 323 malignant

	image_name	prediction	target
0	ISIC_0052060	9.522337e-12	benign
1	ISIC_0052349	1.233248e-11	benign
2	ISIC_0058510	6.661144e-10	benign
3	ISIC_0073313	3.914397e-10	benign
4	ISIC_0073502	9.470966e-07	benign


Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "malignant"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign"
Pred: "benign

Predictions for Test file :

Comparison between EfficientNet and ResNet predictions:

	EfficientNet-b0		
ResNet18		No melanoma	Melanoma
	No melanoma	9873	86
	Melanoma	786	237

Predictions are done using Test Time Augmentation

Future work :

- Different Architectures
- Higher number of Bootstrap
- Different Cut-off for the classification
- Advance augmentation : e.g Hair augmentation
- Different size of images

Thanks for your attention !

References :

- EfficientNet : Rethinking Model Scaling for Convolutional Neural Networks (ICML 2019)
- Deep Residual Learning for Image Recognition