

# Classification of a Melanoma with Deep Learning

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## 1 Introduction – Classes

Goal to classify three types of skin growth.

Class	Nevus	Seborrheic keratosis	Melanoma
<b>Appears at</b>	Birth (congenital)	Increased age	Increased age
<b>Risk</b>	Benign (harmless)	Benign (harmless)	malign (harmfull cancer)
<b>Characteristics</b>	<ul style="list-style-type: none"> <li>- hyperpigmented</li> <li>- mostly single colored</li> <li>- mostly arised skin</li> </ul> <p><b>Can turn into a Melanoma!</b></p>	<ul style="list-style-type: none"> <li>- Flat/raised papule /plaque</li> <li>- mostly one single</li> <li>- smooth, waxy or warty surface</li> </ul> <p>Can look similar to a Melanoma</p>	<p>ABCDE Rule (vs. Nevus)</p> <ul style="list-style-type: none"> <li>- <b>Asymmetry</b></li> <li>- <b>Border</b> irregular in shape.</li> <li>- <b>Color</b> multicolored</li> <li>- <b>Diameter</b> &gt; 6mm in diameter,</li> <li>- <b>Evolution</b> change characteristics over time.</li> </ul>

## 2 Data

Melanoma Detection Dataset from Kaggle.  
- *Unbalanced data*

	# total images
<b>test</b>	600
<b>train</b>	2000
<b>valid</b>	150

## 3 Models and Methods

1. Baseline Model (with RandomForest [RF])
2. Pretrained Neuronal Network [NN]
3. Train a ConvolutionalNN from scratch

RF and pretrained NN used the weights of the CNN VGG:

```
## Load base model weights ----
base_model <- application_vgg16(weights = "imagenet",
                                include_top = FALSE,
                                input_shape = c(image_size, image_size, 3L))

summary(base_model)

# i.e. freeze all convolutional VGG16 layers
freeze_weights(base_model)

## compile model
transfer_model %>% compile(
  optimizer = "adam",
  loss = "categorical_crossentropy",
  metrics = c("accuracy")
)
```

All models were compiled the same:

## 4 Results and Discussion

Model	Loss	Accuracy
Baseline model with RF	NA	0.70
Pretrained VGG	1.52	0.63
CNN from Scratch	0.80	0.68

### 1. Baseline model with RF

The Baseline model using the Random Forest as classification lead to the highest accuracy with 70 %.

RF uses no distribution assumption and can handle well imbalanced data sets (weighted random forest, balanced random forest).

### 2. Pretrained VGG with

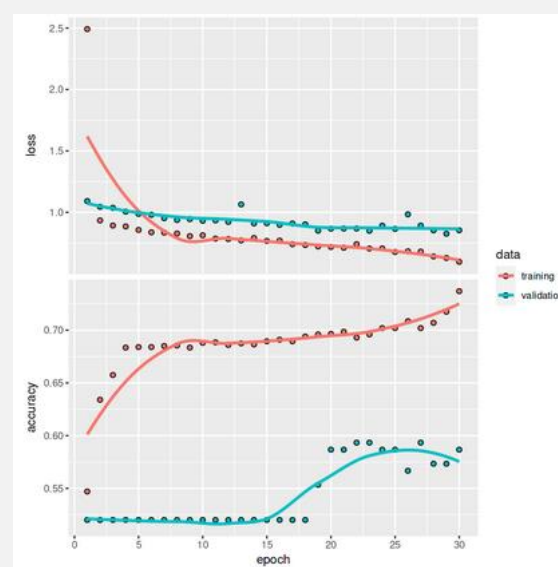
The pretrained VGG has the highest loss function and the lowest accuracy of all the trained models. This is surprising as the model provides 4096 features for the final densely connected classifier.

## [...] 4 Results and Discussion

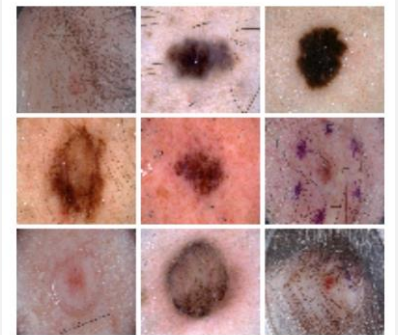
### 3. CNN from Scratch:

Overfitting (accuracy of Train data > test data)

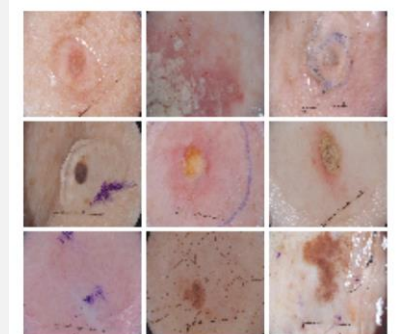
Solution: data augmentation, neuronal dropout



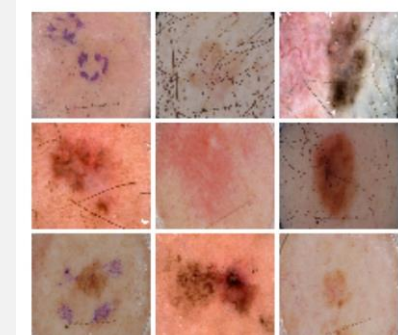
9 Sample Images of "Nevus" Missqualified



9 Sample Images of "Seborrheic Keratosis" Missqualified



9 Sample Images of "Melanoma" Missqualified



## 4 Conclusion

Data difficulties:

- Different pixel size/coloring of images
- Imbalanced data
- Cumbersome data load -> writing of new data import function

Language/Versioning difficulties:

- Tensorflow/Keras better documented for Python than for R
- Image data augmentation seems to depend on the version of keras and tensorflow. -> data augmentation skipped

Findings:

- Baseline model with RF best classification accuracy
- From scratch trained CNN: Minimization of loss and the accuracy vary among the batch\_sizes.
  - -> Effect is not completely understood.
  - Hypothesis: model optimization algorithm ADAM aims for solution with larger weights -> lower test accuracy

## 5 Base script

Skript: <https://github.com/hosts1/ethz-deepl-melanoma>

## References

1. <https://www.kaggle.com/datasets/wanderdust/skin-lesion-analysis-toward-melanoma-detection/code>.
2. [https://tensorchiefs.github.io/dl\\_course\\_2022/](https://tensorchiefs.github.io/dl_course_2022/).
3. <https://tensorflow.rstudio.com/>.
4. [https://tensorflow.rstudio.com/guides/keras/preprocessing\\_layers](https://tensorflow.rstudio.com/guides/keras/preprocessing_layers).
5. <https://medium.com/mini-distill/effect-of-batch-size-on-training-dynamics-21c14f7a716e>