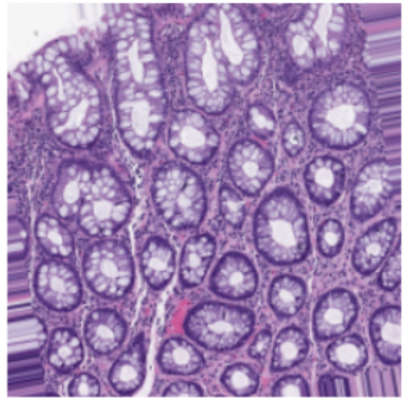
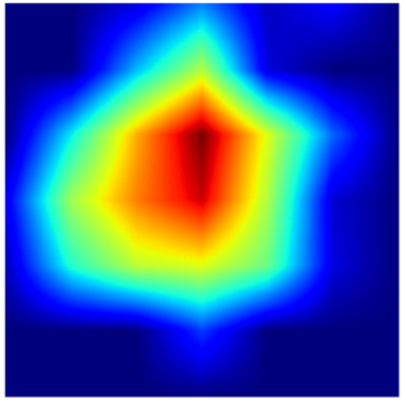
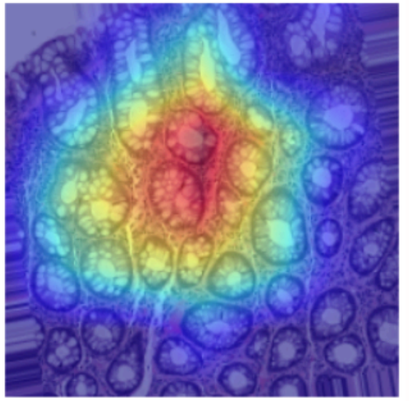




2025

ColoVision

AI with a gut feeling.

Team

CAU Kiel MSc students

Mikhail Melnichenko
Daria Fedorova

Models

Image classification

Basic CNN
DenseNet121

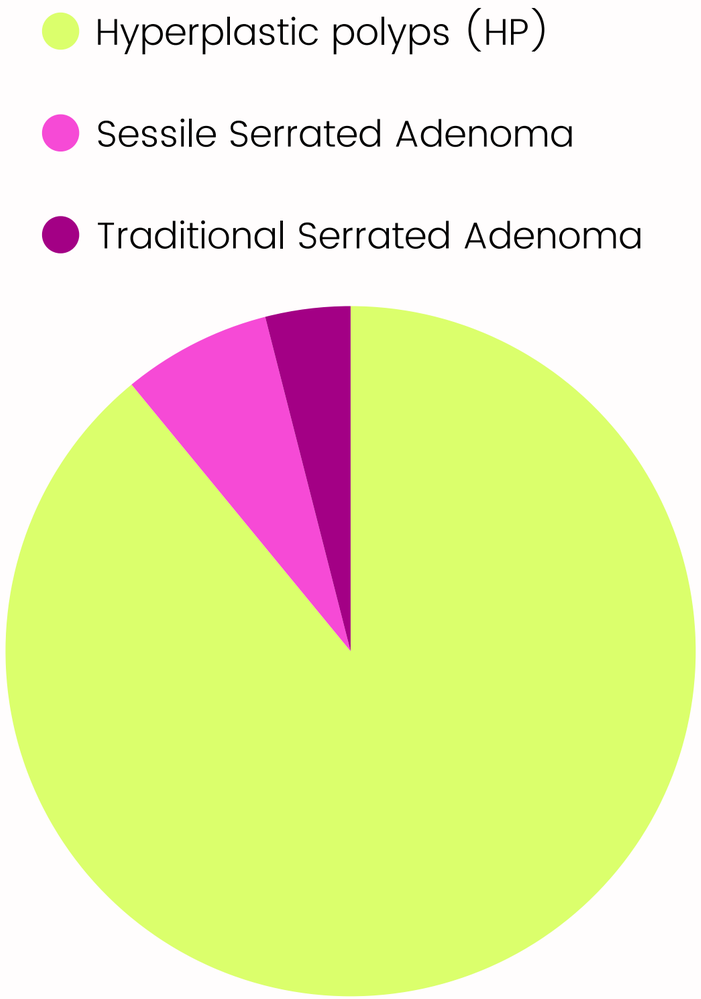
Sessile serrated adenoma (SSA) and hyperplastic polyps (HP)

PREVALENCE

SSA, now often referred to as sessile serrated lesions (SSLs) are precursors to 15-30% of colorectal cancers.
Overall prevalence of SSAs is 8.2%. [1]

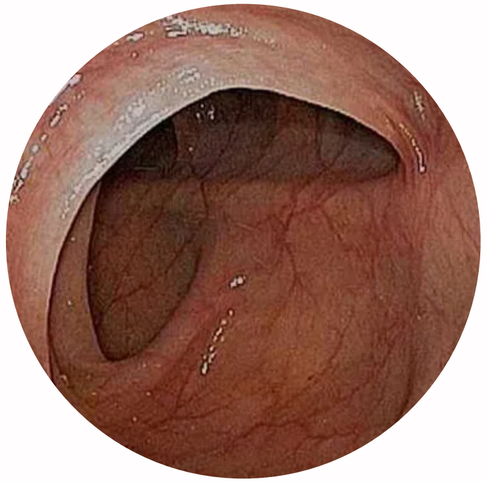
CHALLENGE

HPs are typically benign.
Distinguish HP from SSA → "a challenging problem with considerable inter-pathologist variability." [2]



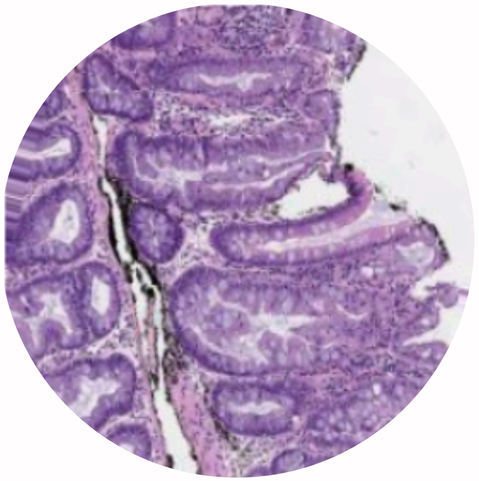
1- IJspeert JE et al, 2016
2 - Wei J. et al, 2021
Chart - Jaravaza, D.R., Rigby, J.M. 2020

Cancer diagnosis and AI



ENDOSCOPY

https://mantasmd.com/endoscopy-colon-splenic-flexure-normal/



HISTOLOGY

MHIST dataset

MOLECULAR DIAGNOSTICS

https://www.istockphoto.com/de/search/2/image?mediatype=illustration&phrase=dna+sequence+icon

Literature

ACCURATE AND REPRODUCIBLE INVASIVE BREAST CANCER DETECTION IN WHOLE-SLIDE IMAGES: A DEEP LEARNING APPROACH FOR QUANTIFYING TUMOR EXTENT

2017 BY CRUZ-ROA, A. ET AL

Demonstrates CNNs' effectiveness in cancer region identification on Whole slide images (WSIs)

DEEP LEARNING IN CANCER GENOMICS AND HISTOPATHOLOGY

2024 BY UNGER, M. ET AL

Informs the selection of appropriate architectures and supervision strategies for colon polyp classification

---

A PETRI DISH FOR HISTOPATHOLOGY IMAGE ANALYSIS (MHIST DATASET)

2021 BY WEI, J. ET AL

Provides a directly relevant dataset for developing and testing computer vision models to distinguish benign from malignant colon polyps. ...and we want to **BEAT THE MODEL FROM THIS PAPER :)**

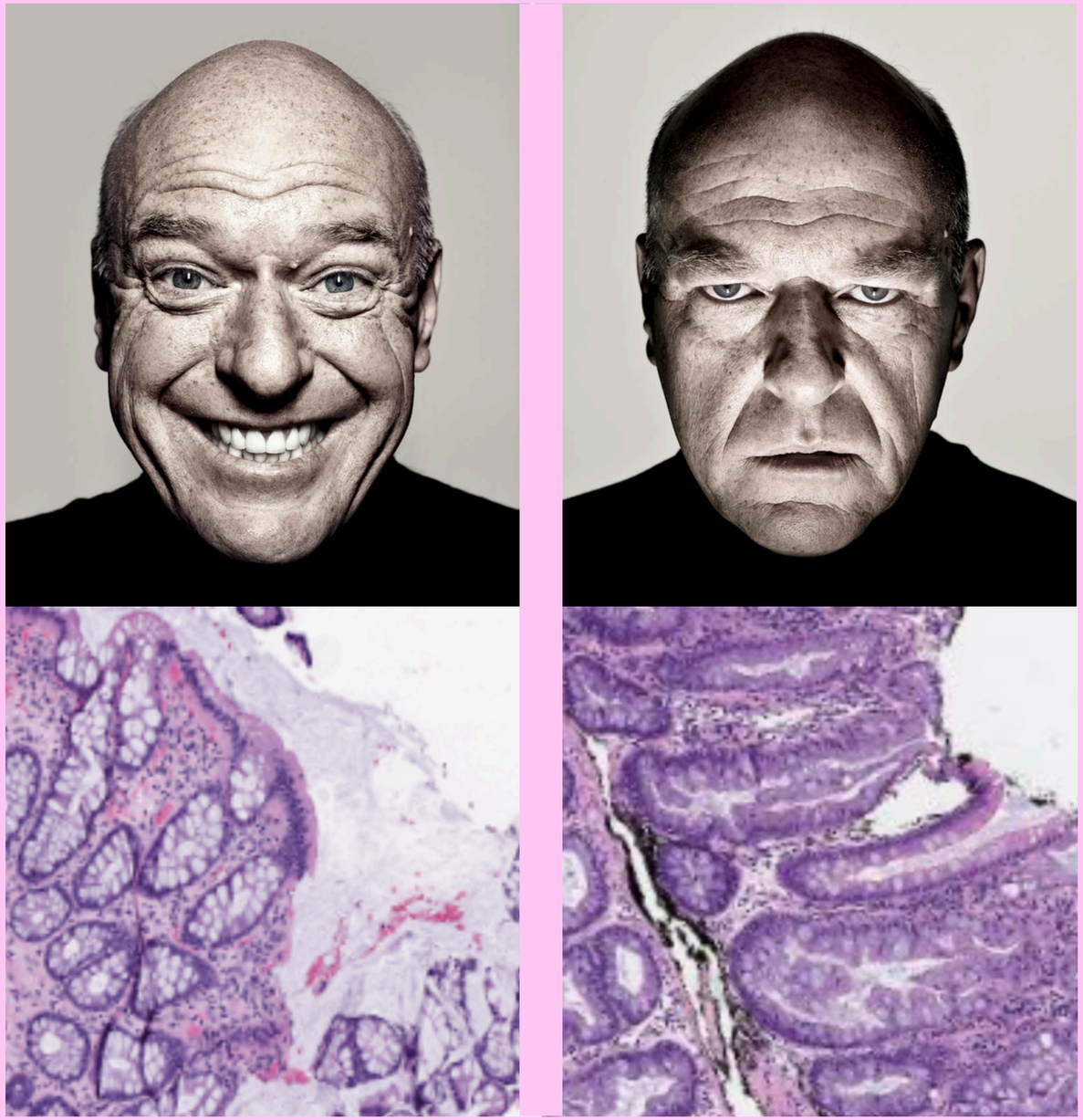
AUC = 92.7 ± 0.4

Good or bad?

MHIST dataset:

3,152 RGB images 224×224 px
from 328 clinical slides

- benign or **HP**, **polyp**
- malignant or **SSA**, **adenoma**



Feature engineering

- 7 pathologists voting
  - 3/7 (43%) and 4/7 (57%) excluded

- Augmentation
  - rescaling (0-255)
  - zoom (up to 10%)
  - rotation (up to 15°)
  - horizontal flip

GENERAL SCHEME

1. RANDOM SEARCH

CNN:

- number of **filters/neurons** in each layer (**conv/dense**)

Transfer learning (DenseNet121):

- number of **neurons** in the dense layer
- **dropout rate**
- **alpha & gamma in focal loss function**

2. RANDOM SEARCH FINE TUNING

- number of frozen layers

3. TRAIN MODEL WITH THE BEST PARAMETERS

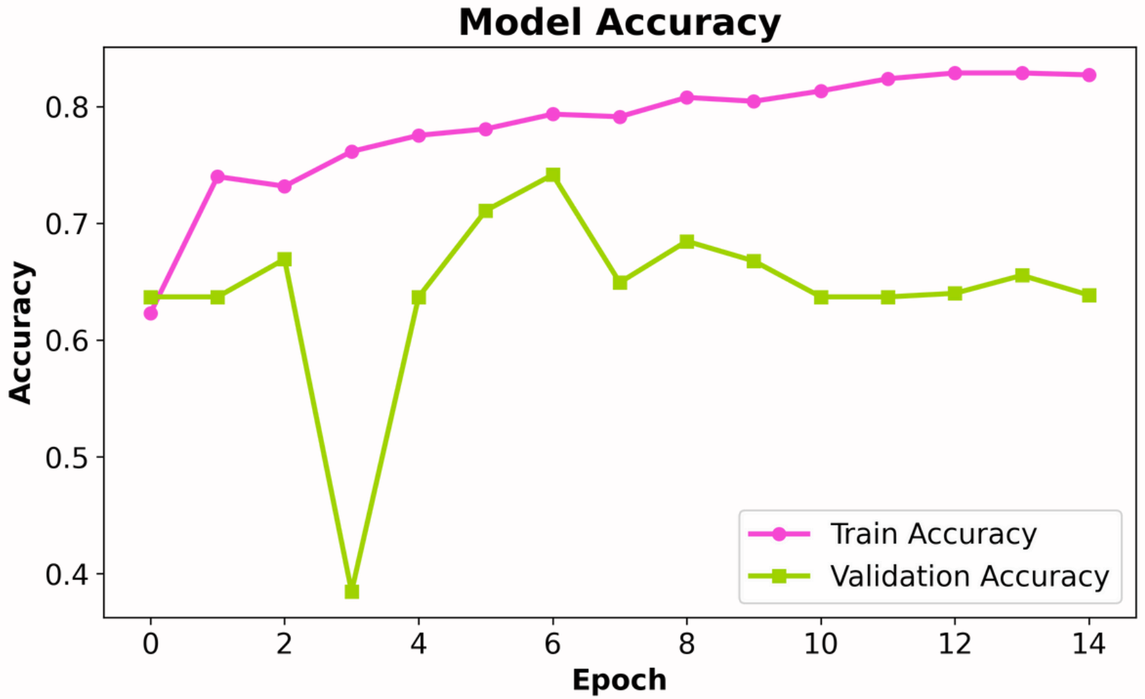
- CALLBACK function: automatic learning rate correction using **ReduceLROnPlateau**

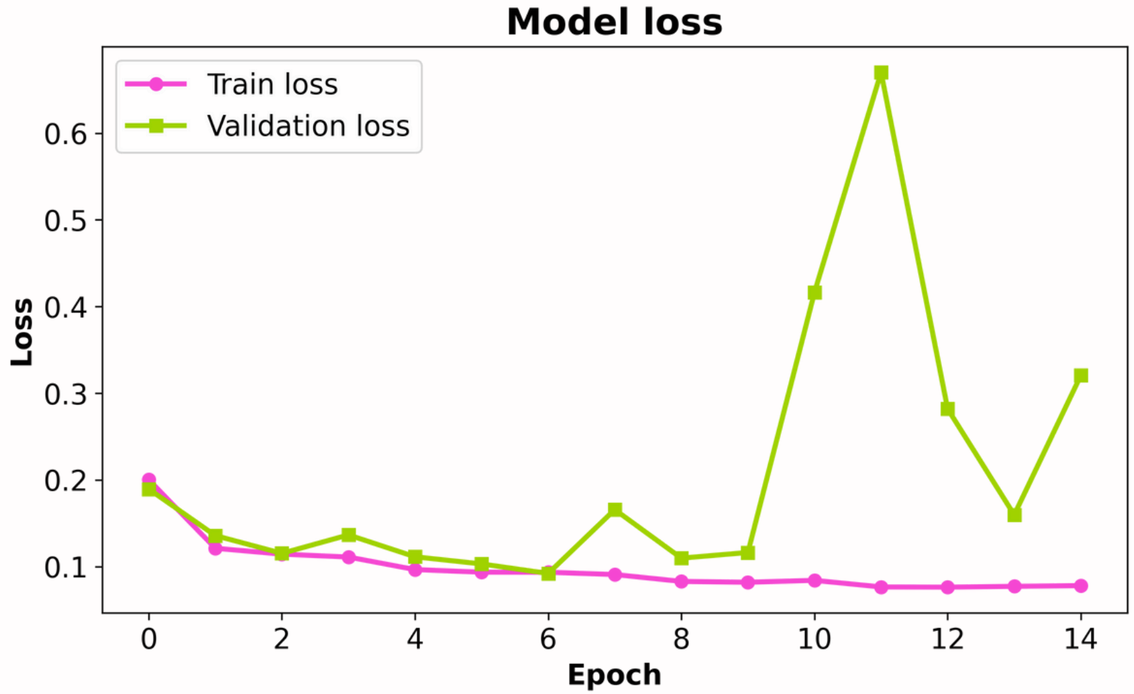
```python
def focal_loss(gamma=2.0, alpha=0.75):
    def loss(y_true, y_pred):
        y_pred = K.clip(y_pred, K.epsilon(), 1. - K.epsilon())
        alpha_t = tf.where(tf.equal(y_true, 1), alpha, 1 - alpha)
        pt = tf.where(tf.equal(y_true, 1), y_pred, 1 - y_pred)
        return -alpha_t * K.pow(1. - pt, gamma) * K.log(pt)
    return loss
```

Baseline: CNN → focal loss

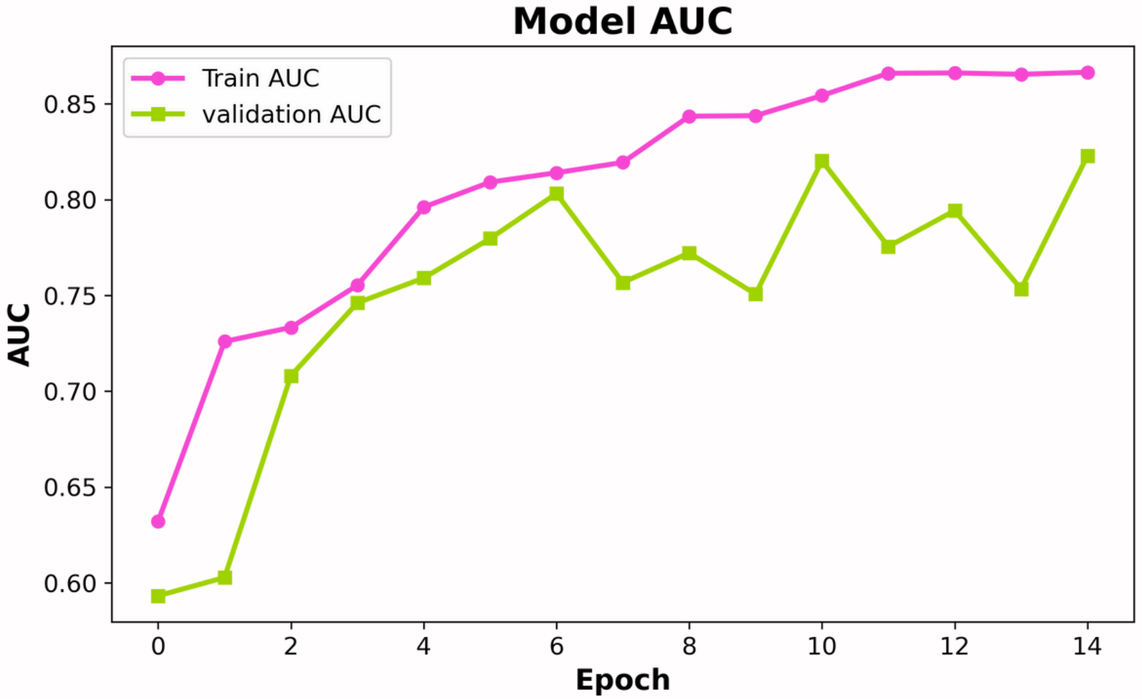
Baseline: CNN

```python
def build_model(hp):
    model = models.Sequential([
        layers.Input(shape=(224, 224, 3)),

        layers.Conv2D(hp.Int('conv1_filters', 32, 128, step=32), (3, 3), padding='same'),
        layers.BatchNormalization(),
        layers.ReLU(),
        layers.MaxPooling2D(),
        layers.Dropout(hp.Float('dropout1', 0.2, 0.5, step=0.1)),

        layers.Conv2D(hp.Int('conv2_filters', 64, 256, step=64), (3, 3), padding='same'),
        layers.BatchNormalization(),
        layers.ReLU(),
        layers.MaxPooling2D(),
        layers.Dropout(hp.Float('dropout2', 0.2, 0.5, step=0.1)),

        layers.Conv2D(hp.Int('conv3_filters', 128, 512, step=128), (3, 3), padding='same'),
        layers.BatchNormalization(),
        layers.ReLU(),
        layers.MaxPooling2D(),
        layers.Dropout(hp.Float('dropout3', 0.2, 0.5, step=0.1)),

        layers.Flatten(),
        layers.Dense(hp.Int('dense_units', 128, 512, step=64)),
        layers.BatchNormalization(),
        layers.ReLU(),
        layers.Dropout(hp.Float('dropout4', 0.2, 0.5, step=0.1)),

        layers.Dense(1, activation='sigmoid')
    ])
```



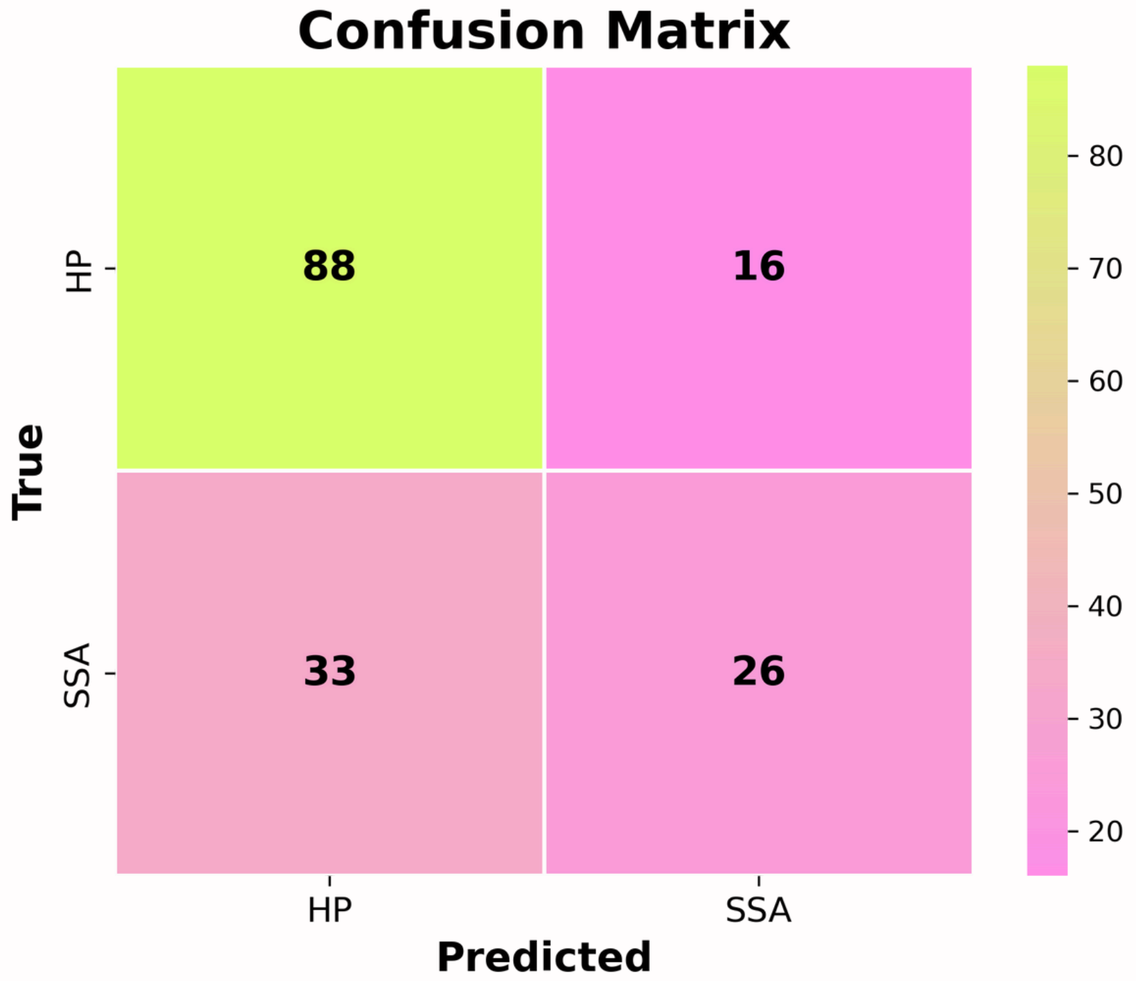


Baseline: CNN



	Training	Validation
Accuracy	0.8216	0.6385
Loss	0.0819	0.3205
AUC	0.8574	0.8229

Baseline: CNN



Transfer learning

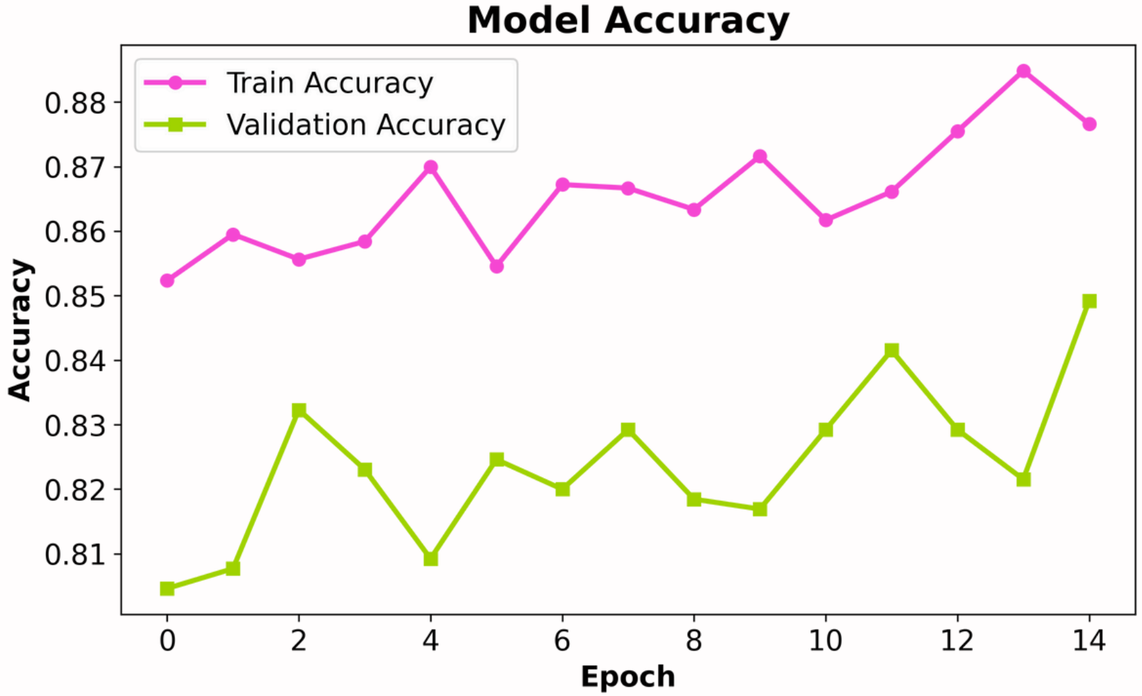
DenseNet121

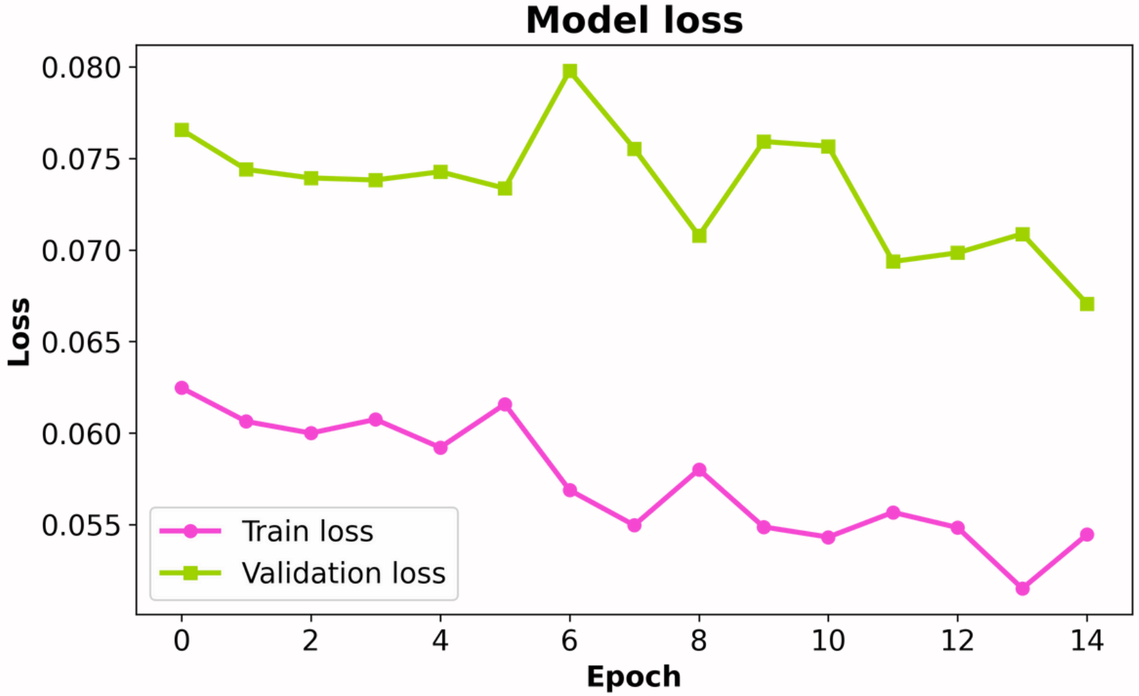
```python
def build_feature_extraction_model(hp):
    base_model = DenseNet121(weights='imagenet', include_top=False,
input_shape=(224, 224, 3), name='densenet121_base')
    base_model.trainable = False

    x = base_model.output
    x = GlobalAveragePooling2D()(x)
    x = Dense(hp.Int('dense_units', 64, 256, step=64))(x)
    x = BatchNormalization()(x)
    x = tf.keras.layers.ReLU()(x)
    x = Dropout(hp.Float('dropout', 0.2, 0.5, step=0.1))(x)
    output = Dense(1, activation='sigmoid')(x)

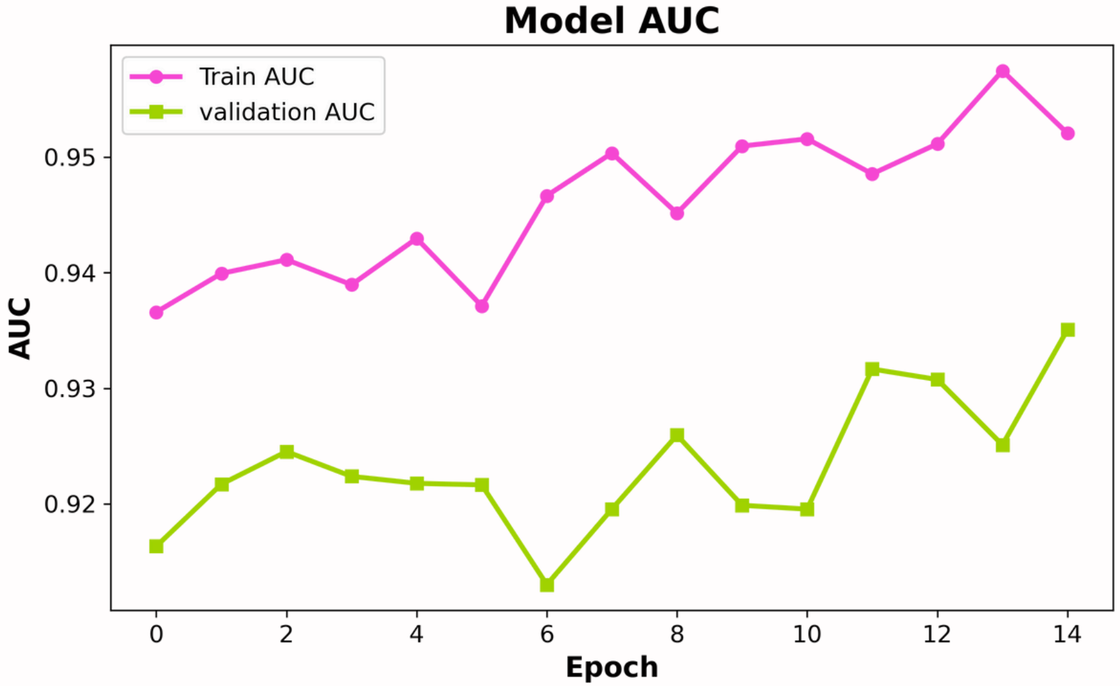
    model = Model(inputs=base_model.input, outputs=output)

    model.compile(
        optimizer=Adam(learning_rate=hp.Choice('lr', [1e-5])),
        loss=focal_loss(gamma=hp.Choice('gamma', [1.5, 2.0]),
alpha=hp.Choice('alpha', [0.5, 0.75])),
        metrics=['accuracy', tf.keras.metrics.AUC(name='auc')]
    )
    return model
```



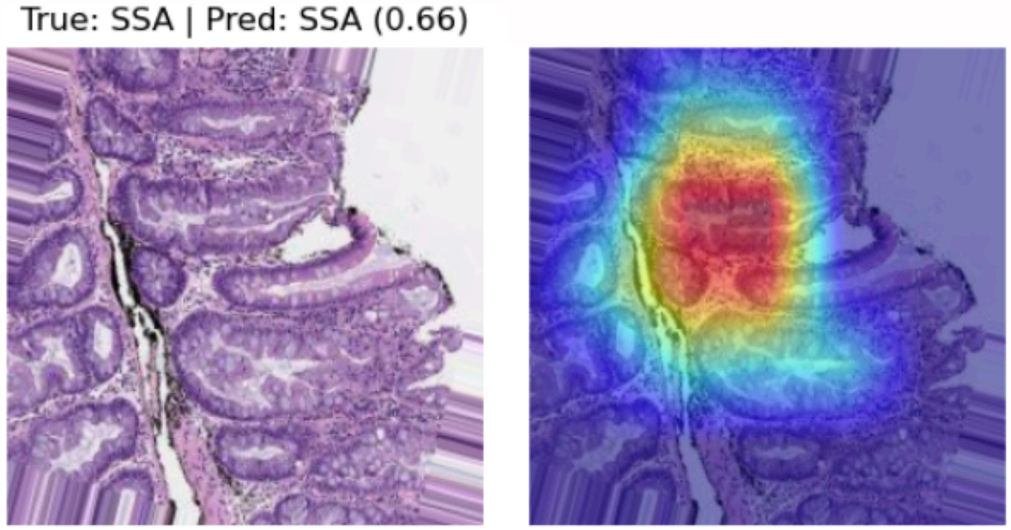


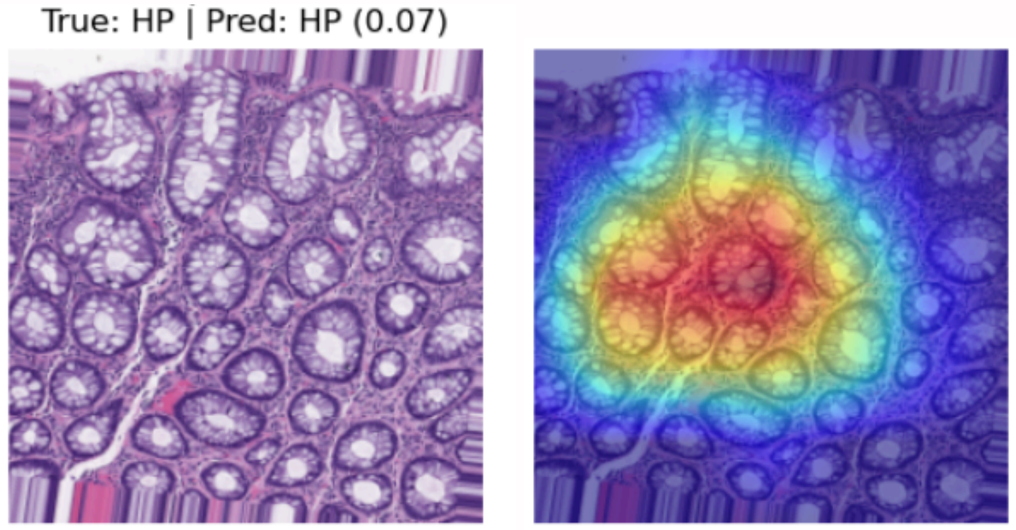
DenseNet121: after search and fine-tuning



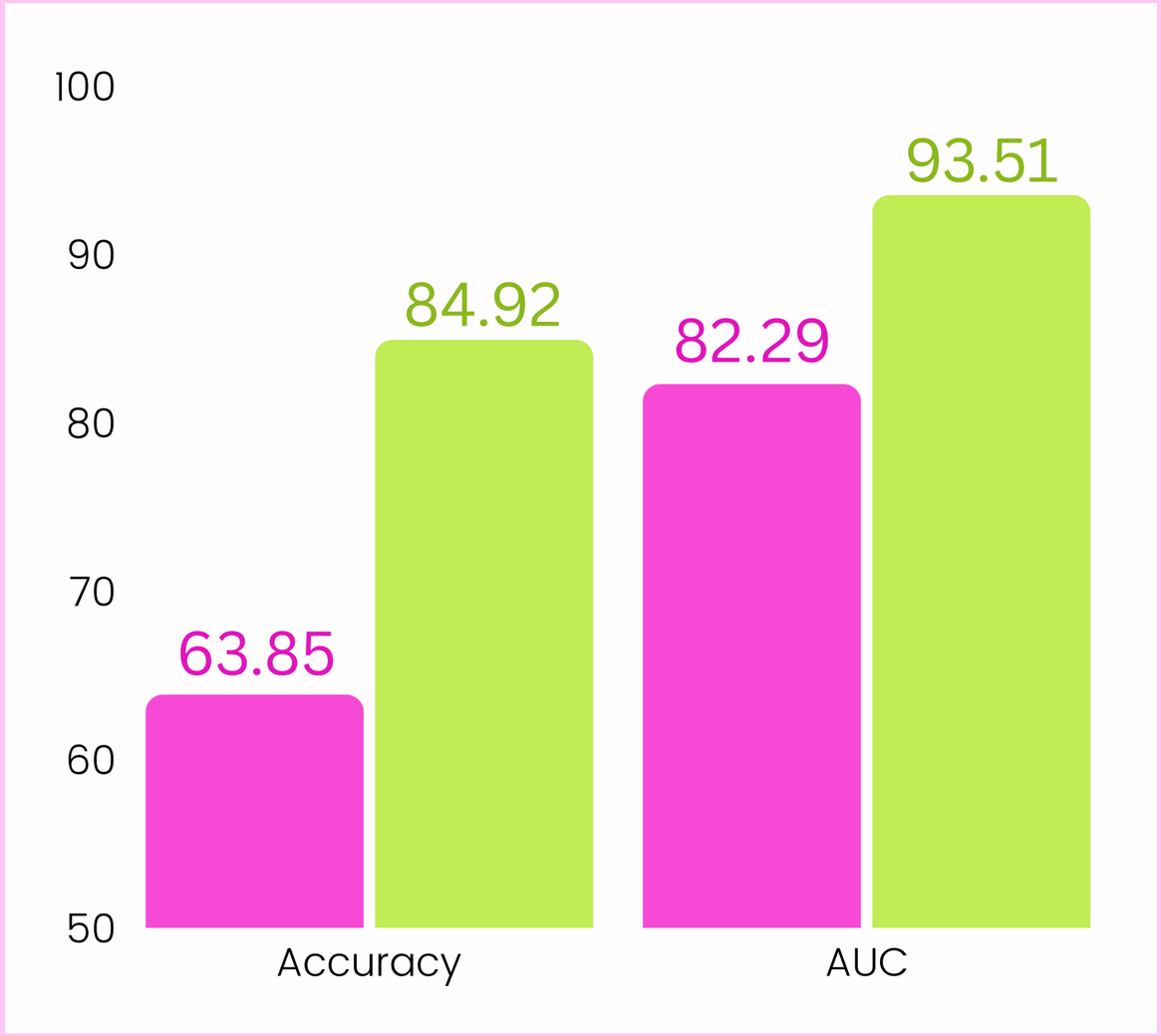
DenseNet121: after search and fine-tuning

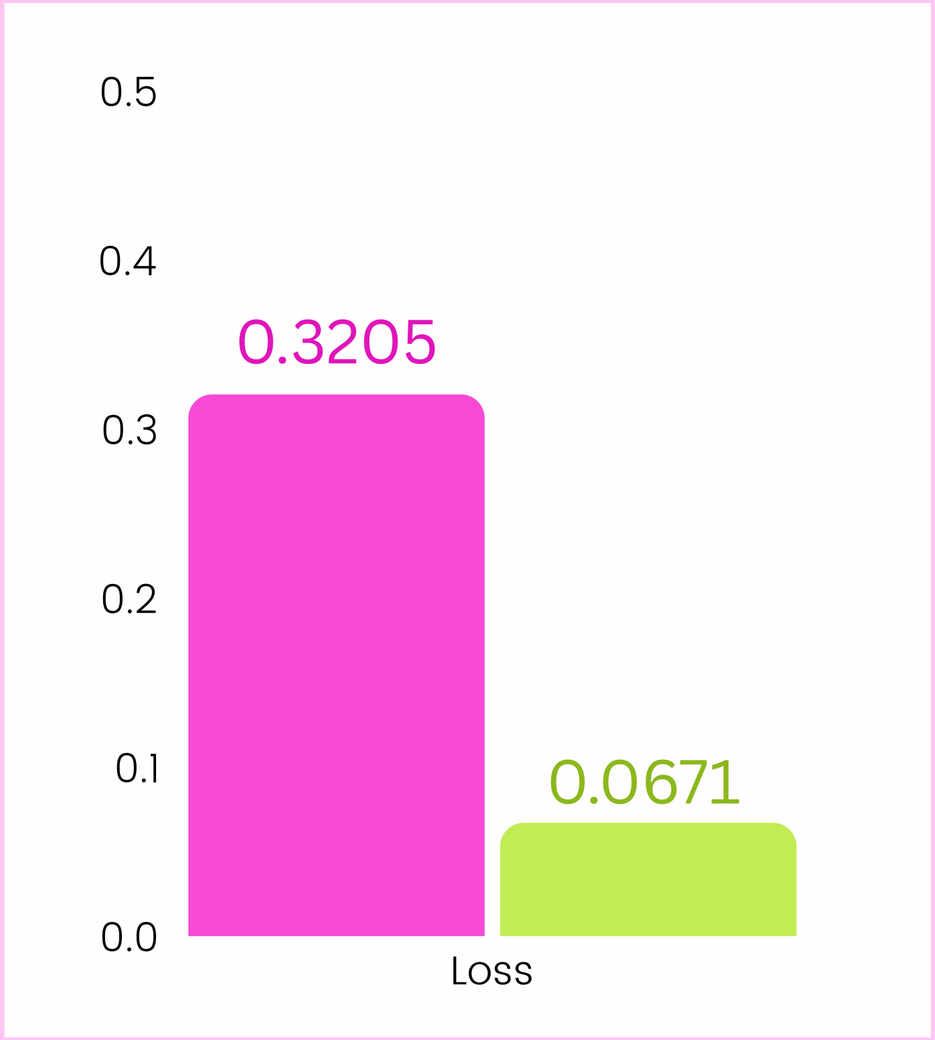
	Training	Validation
Accuracy	0.8868	0.8492
Loss	0.0537	0.0671
AUC	0.9544	0.9351



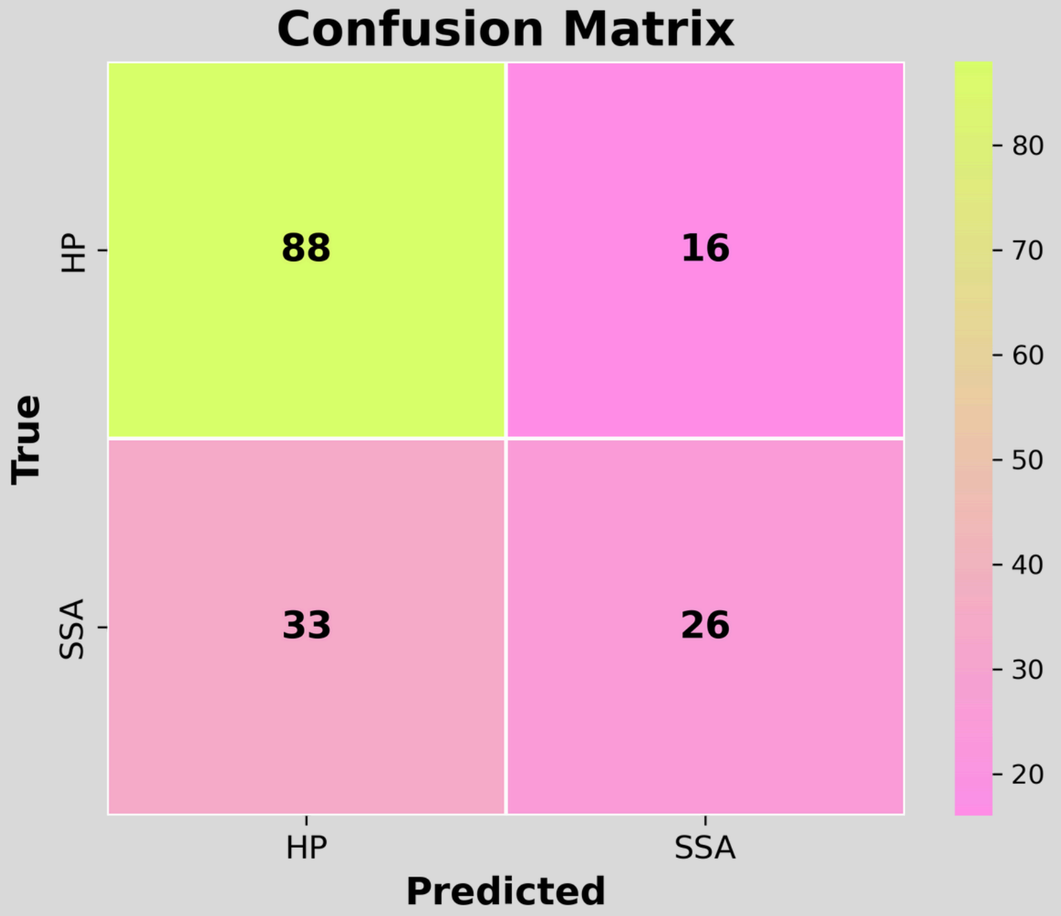


CNN vs DenseNet121

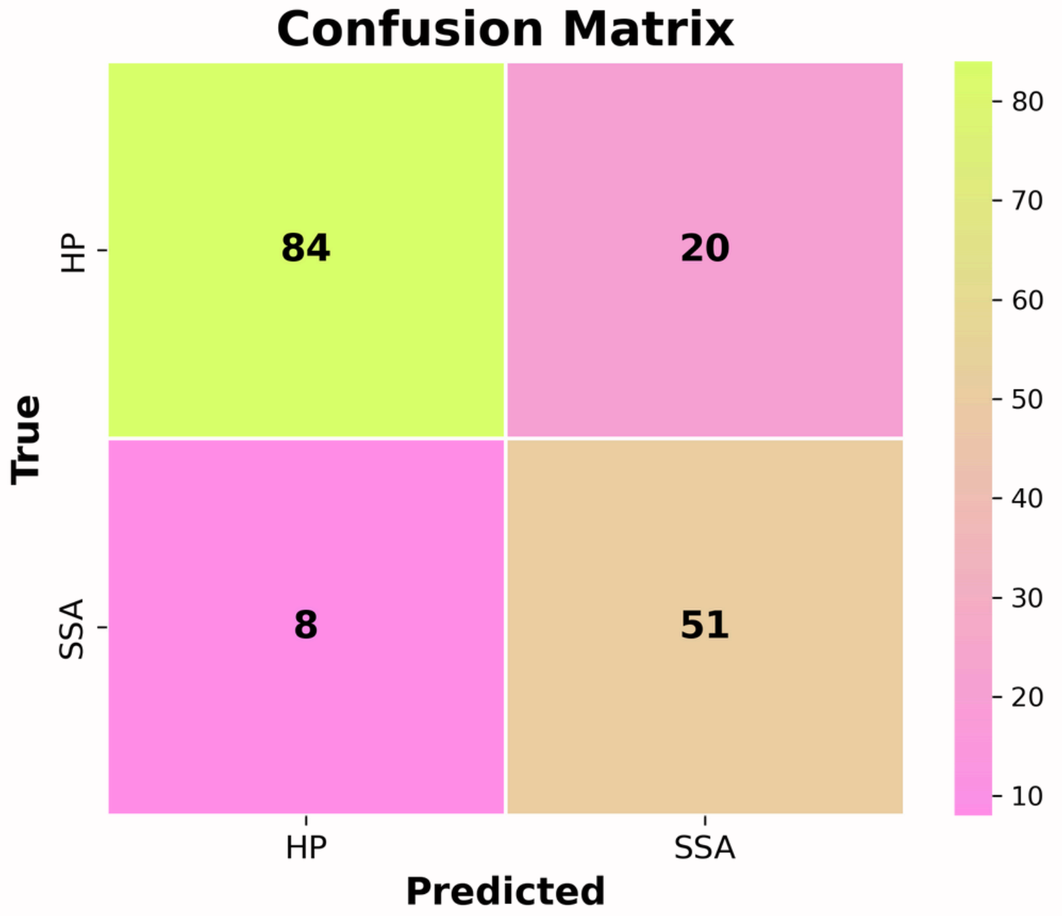




CNN



DenseNet121



Challenges

✓ **UNCERTAIN LABELING**

Votes:
3 (4) out of 7 pathologists

↓

Exclude uncertain cases

✓ **IMBALANCE OF CASES**

Less SSA in the dataset - model is biased

↓

Focal loss function: alpha=0.75

✓ **PREFER WORSE DIAGNOSIS**

Prefer SSA over HP: SSA needs urgent treatment, we do not want to miss it

↓

Focal loss function: gamma = 2

Conclusion & perspective

- Model may support pathologist's conclusion
- Needs additional work to eliminate false negatives to be more reliable as a diagnostic tool

Outcompeted:

- **2021 original MHIST dataset paper using ResNet18 by 0,41% AUC;**
- **2023 paper [1] using DenseNet (84.39% AUC) by 9,12%**

Did not reach:

- **[1]'s ConvNeXt** 93,91%

REDUCE IMPACT OF COLOR

RGB to YUV (or YCbCr) to separate the color information into luminance and chrominance.

MORE COMPUTATIONAL POWER

More epochs for longer training and better results

FIND AND COMBINE DIFFERENT DATASETS (HP & SSA HISTOLOGY)

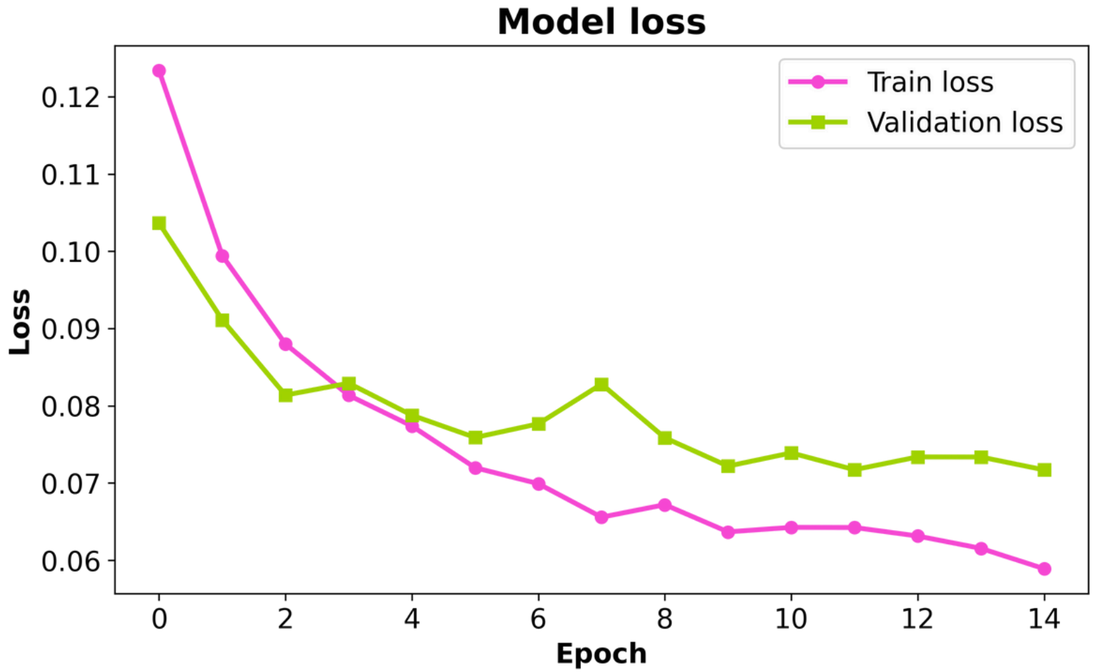
Get more information for a fully usable model

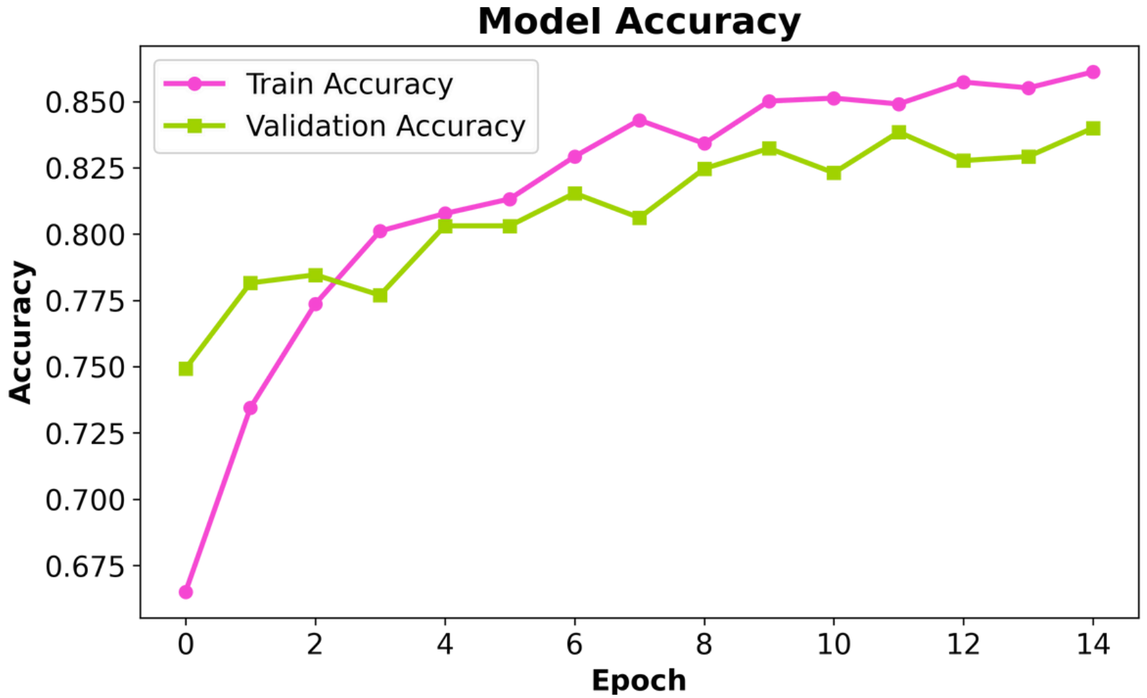
1 - Negriz M. 2023

Q & A

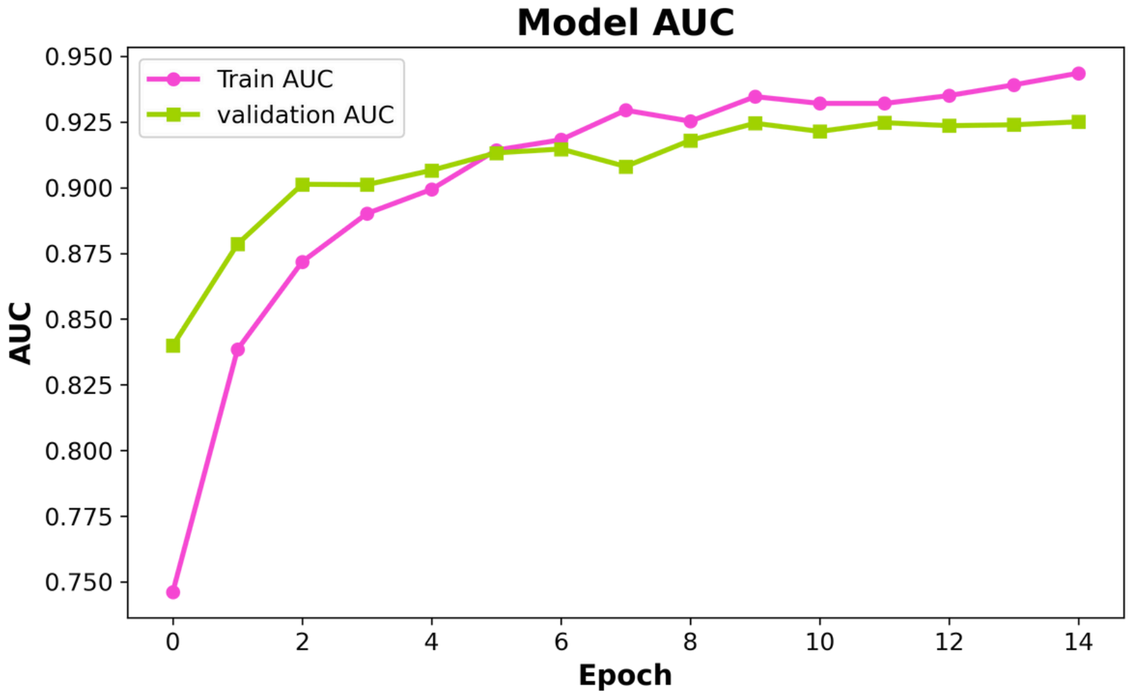
Comments and suggestions are welcome!

Mikhail Melnichenko,
Daria Fedorova





DenseNet121: after search and before fine-tuning



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        layers.BatchNormalization(),
        layers.ReLU(),
        layers.MaxPooling2D(),
        layers.Dropout(hp.Float('dropout1', 0.2, 0.5, step=0.1)),

        layers.Conv2D(hp.Int('conv2_filters', 64, 256, step=64), (3, 3), padding='same'),
        layers.BatchNormalization(),
        layers.ReLU(),
        layers.MaxPooling2D(),
        layers.Dropout(hp.Float('dropout2', 0.2, 0.5, step=0.1)),

        layers.Conv2D(hp.Int('conv3_filters', 128, 512, step=128), (3, 3), padding='same'),
        layers.BatchNormalization(),
        layers.ReLU(),
        layers.MaxPooling2D(),
        layers.Dropout(hp.Float('dropout3', 0.2, 0.5, step=0.1)),

        layers.Flatten(),
        layers.Dense(hp.Int('dense_units', 128, 512, step=64)),
        layers.BatchNormalization(),
        layers.ReLU(),
        layers.Dropout(hp.Float('dropout4', 0.2, 0.5, step=0.1)),

        layers.Dense(1, activation='sigmoid')
    ])
    model.compile(
        optimizer=optimizers.Adam(learning_rate=hp.Choice('lr', [1e-5])),
        loss=focal_loss(gamma=hp.Choice('gamma', [1.5, 2.0]), alpha=hp.Choice('alpha', [0.5, 0.75])),
        metrics=[
            'accuracy',
            metrics.AUC(name='auc'),
            metrics.Recall(name='tpr'),
            metrics.FalsePositives(name='fp'),
            metrics.TruePositives(name='tp'),
        ]
    )
    return model
```