Universität Augsburg
Fakultät für Angewandte Informatik

Praktikum BioMedProg

Abschlusspräsentation Team C - Medical Image Analysis

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Agenda

The task

Pneumonia Classification with X-Rays

Pneumonia:

- Inflammatory condition of the lung.
- Caused by infection with bacteria or viruses.
- Affecting primarily small air sacs (alveoli).
- Pneumonia affects
  - 450 million people (7%)
  - Result in ~ 4 million deaths per year.

Fig.1

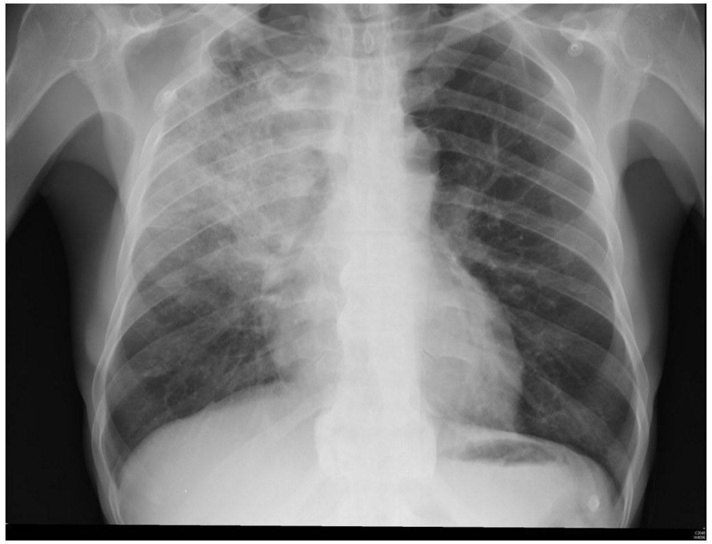


Fig.2

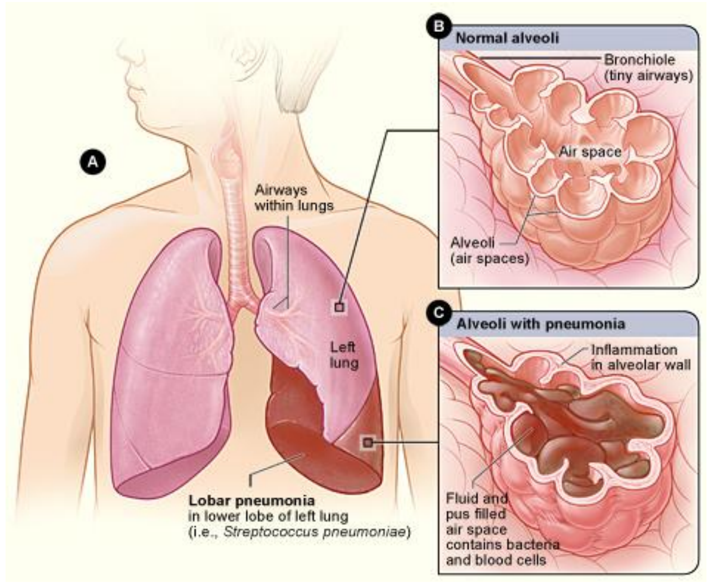

A
Airways within lungs
Left lung
Lobar pneumonia in lower lobe of left lung (i.e., *Streptococcus pneumoniae*)
B
Normal alveoli
Bronchiole (tiny airways)
Air space
Alveoli (air spaces)
C
Alveoli with pneumonia
Inflammation in alveolar wall
Fluid and pus filled air space contains bacteria and blood cells

Fig.1: https://www.flickr.com/photos/pulmonary_pathology/7471755378
Fig.2: https://commons.wikimedia.org/wiki/File:Lobar_pneumonia_illustrated.jpg

Implementation

- Framework:
  - PyTorch

- API:
  - MONAI (https://www.monai.io)

Implementation

1. Dataset analysis
2. Preprocessing
3. Model building
4. Training and evaluation

Implementation

Dataset analysis

- Dataset:

  - 2686 2D images Thorax X-Ray Scans (1024 x 1024 px)
  - Classes:
    - Normal (1341 x-rays)
    - Viral Pneumonia (1345 x-rays)
  - Dataset consists of both single channel (grayscale) and triple channel (RGB) images!

Implementation

Data preprocessing

- Image preprocessing:

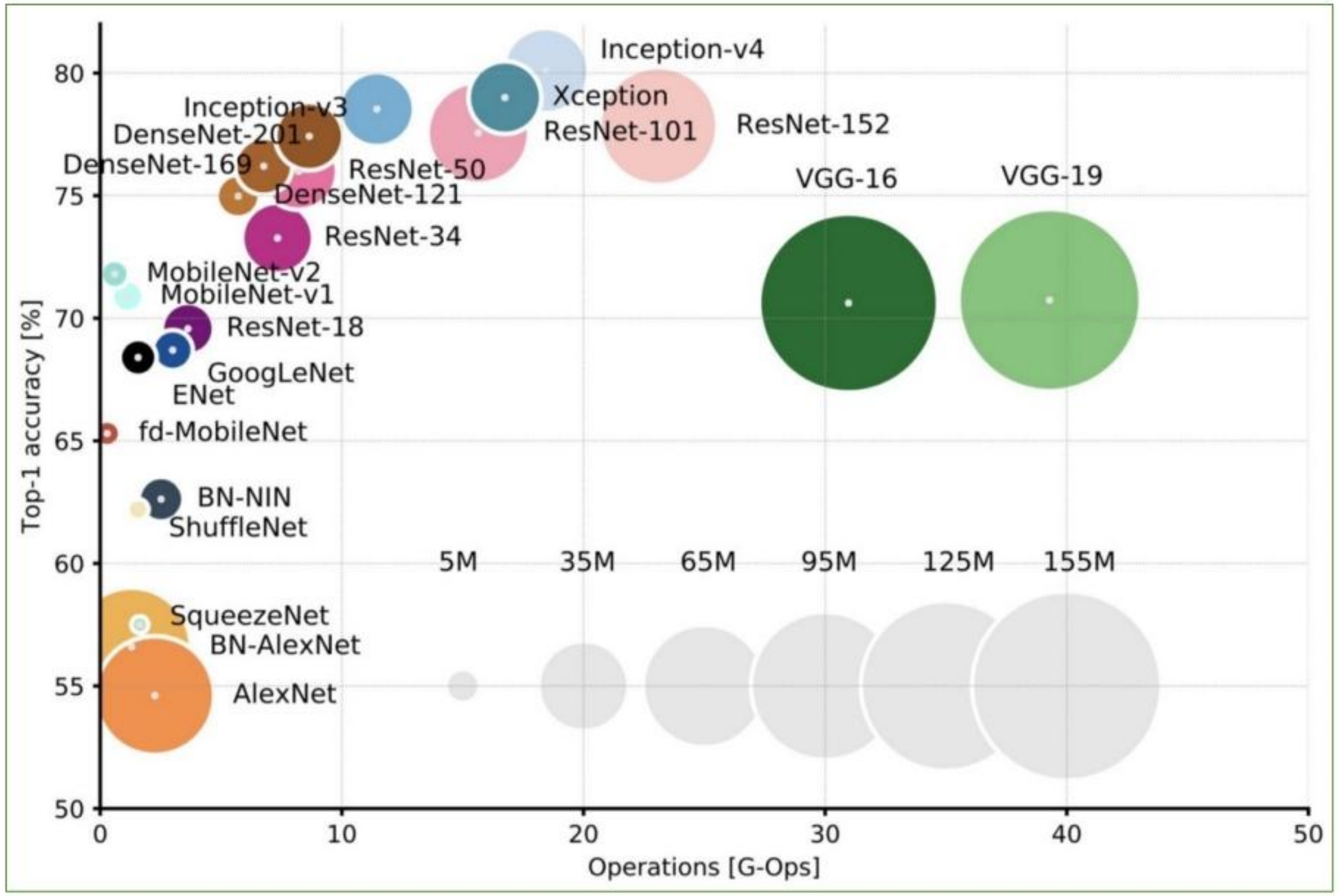
  - convert RGB to grayscale or the other way
    - DenseNet and ResNet require single channel grayscale
    - Inceptionv4 requires RGB
  - Resize
  - Augmentation (randomly rotate, flip and zoom)

Implementation

Model building

- Three different architectures:
  - DenseNet-121
  - Inception v4
  - ResNet-50

- Two optimizers:
  - Adam
  - SGD



Implementation

Training and evaluation

Training:
- Epochs: 200
- Batch size: 48
- Resize to 224 x 224 px
- Learning rate: 0,0001

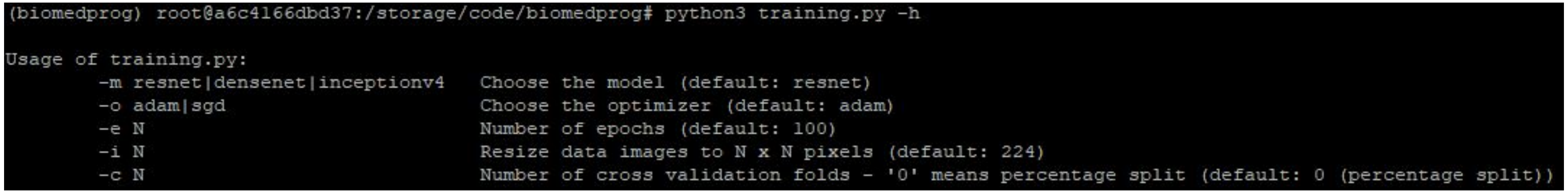
Validation:
- 3-fold cross validation

Evaluation metrics:
- Loss
- Accuracy
- Sensitivity
- Specificity

Implementation

How to run

- Requires Python3 environment with pip package manager
- Install the required packages as in the requirements.txt (`pip install -r requirements.txt`)
- Adapt settings such as the dataset location in the `parameters.py`
- See usage via `python3 training.py -h`



```
(biomedprog) root@a6c4166dbd37:/storage/code/biomedprog# python3 training.py -h

Usage of training.py:
        -m resnet|densenet|inceptionv4   Choose the model (default: resnet)
        -o adam|sgd                      Choose the optimizer (default: adam)
        -e N                             Number of epochs (default: 100)
        -i N                             Resize data images to N x N pixels (default: 224)
        -c N                             Number of cross validation folds - '0' means percentage split (default: 0 (percentage split))
```

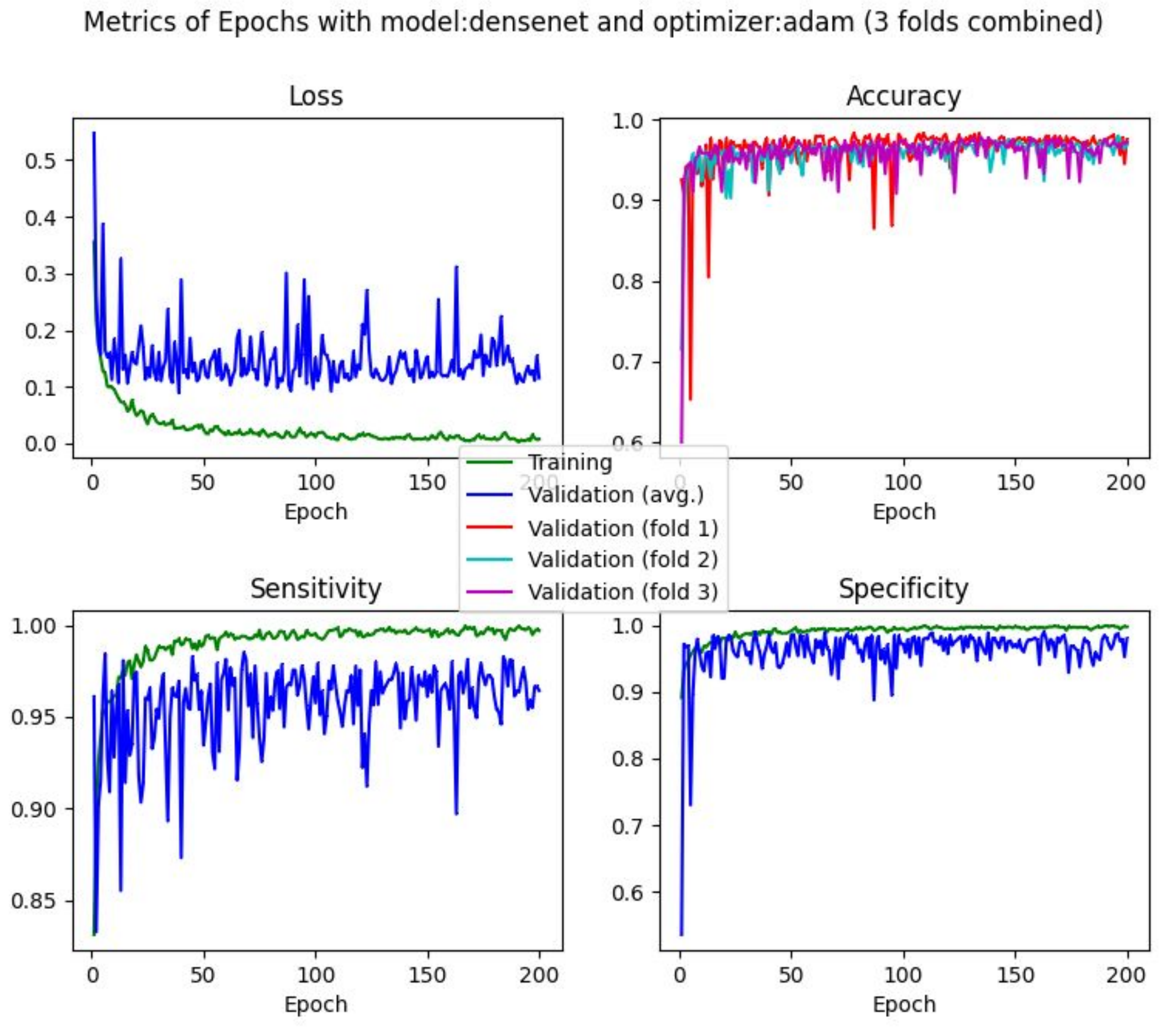
- Example with DenseNet-121, Adam optimizer, 200 epochs and resize to 224px with 3-fold cross validation:

  `python3 training.py -m densenet -o adam -e 200 -i 224 -c 3`

Results

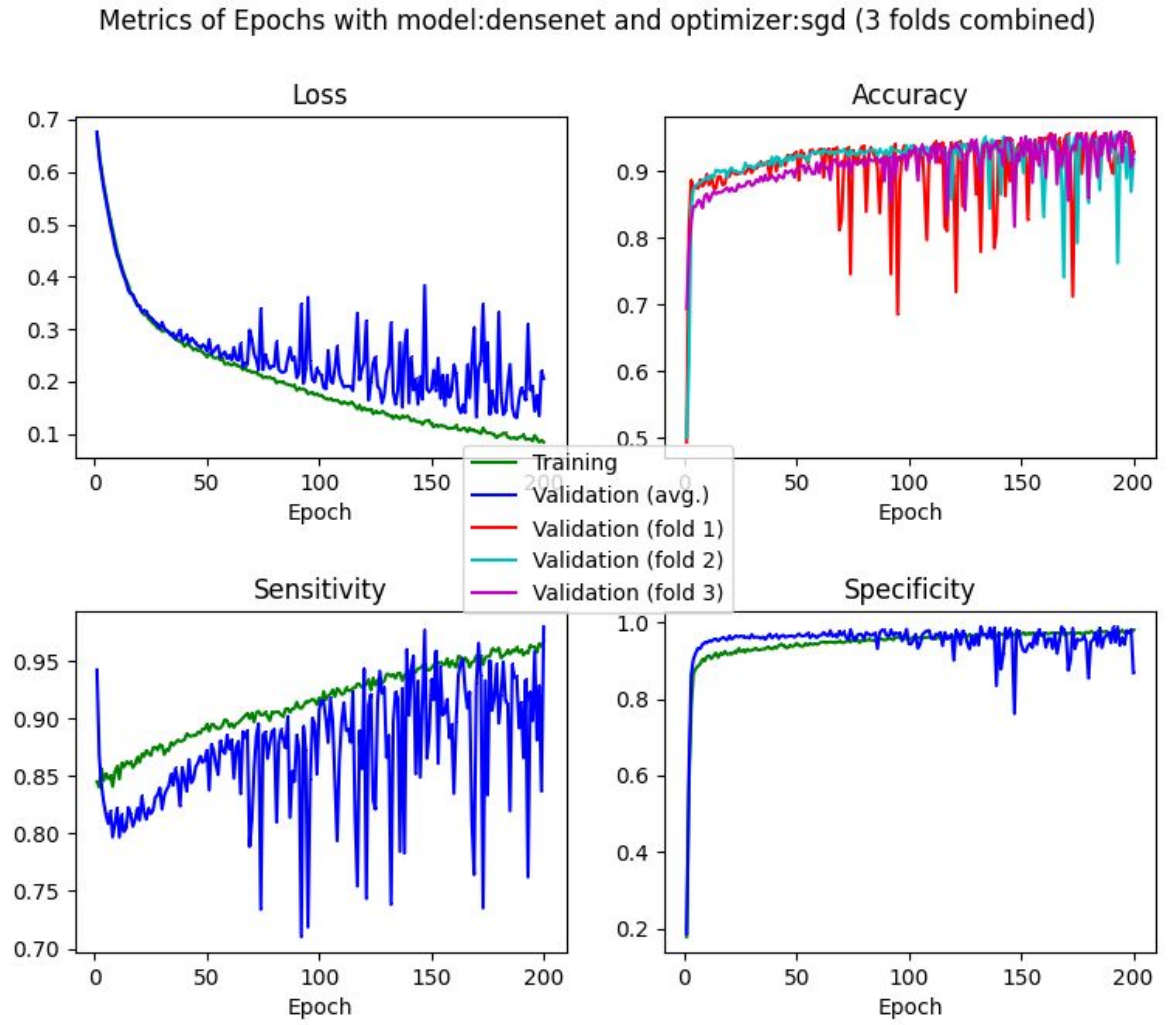
Evaluation metrics

DenseNet-121 with Adam



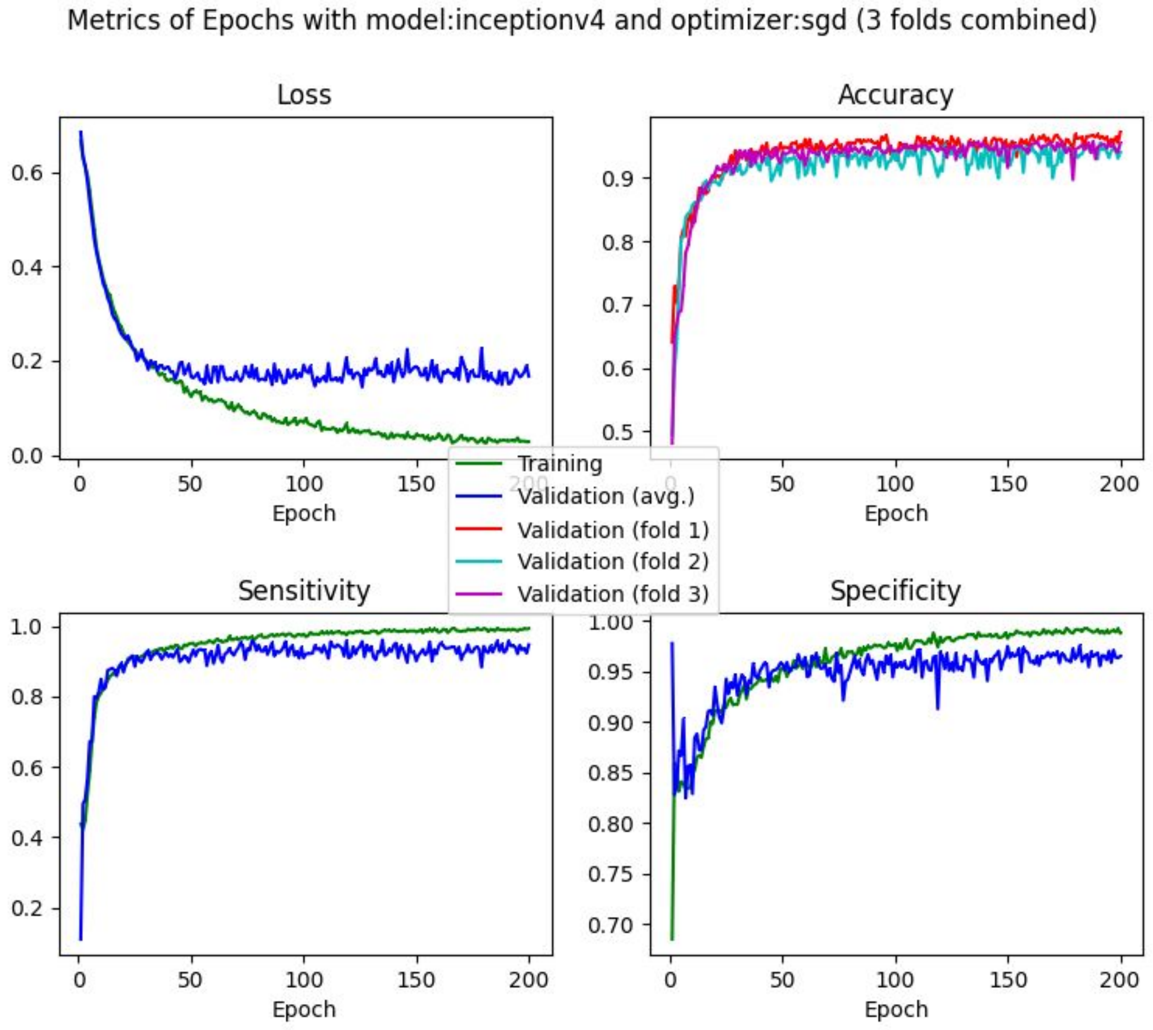
Evaluation metrics

DenseNet-121 with SGD



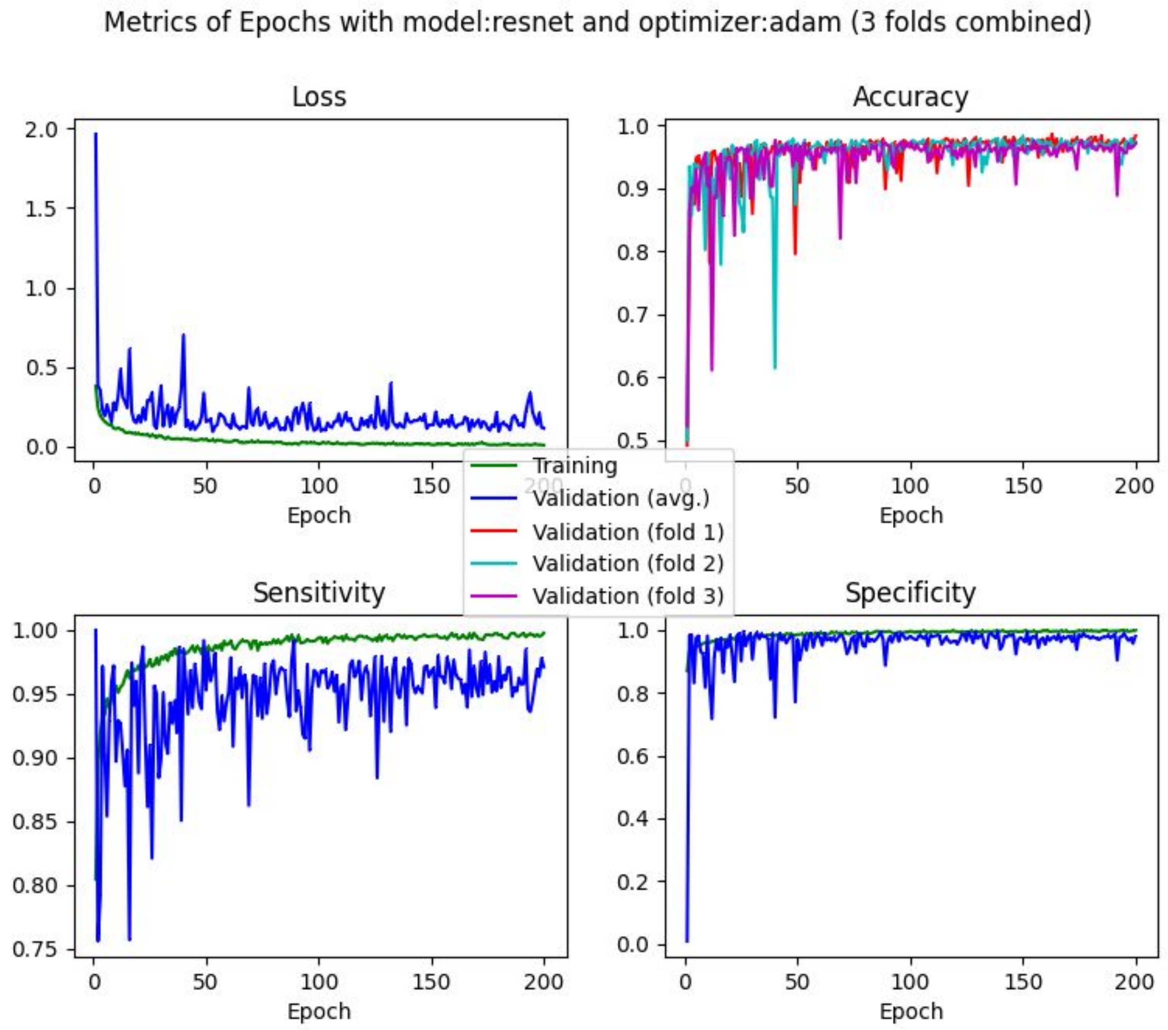
Evaluation metrics

Inception v4 with SGD



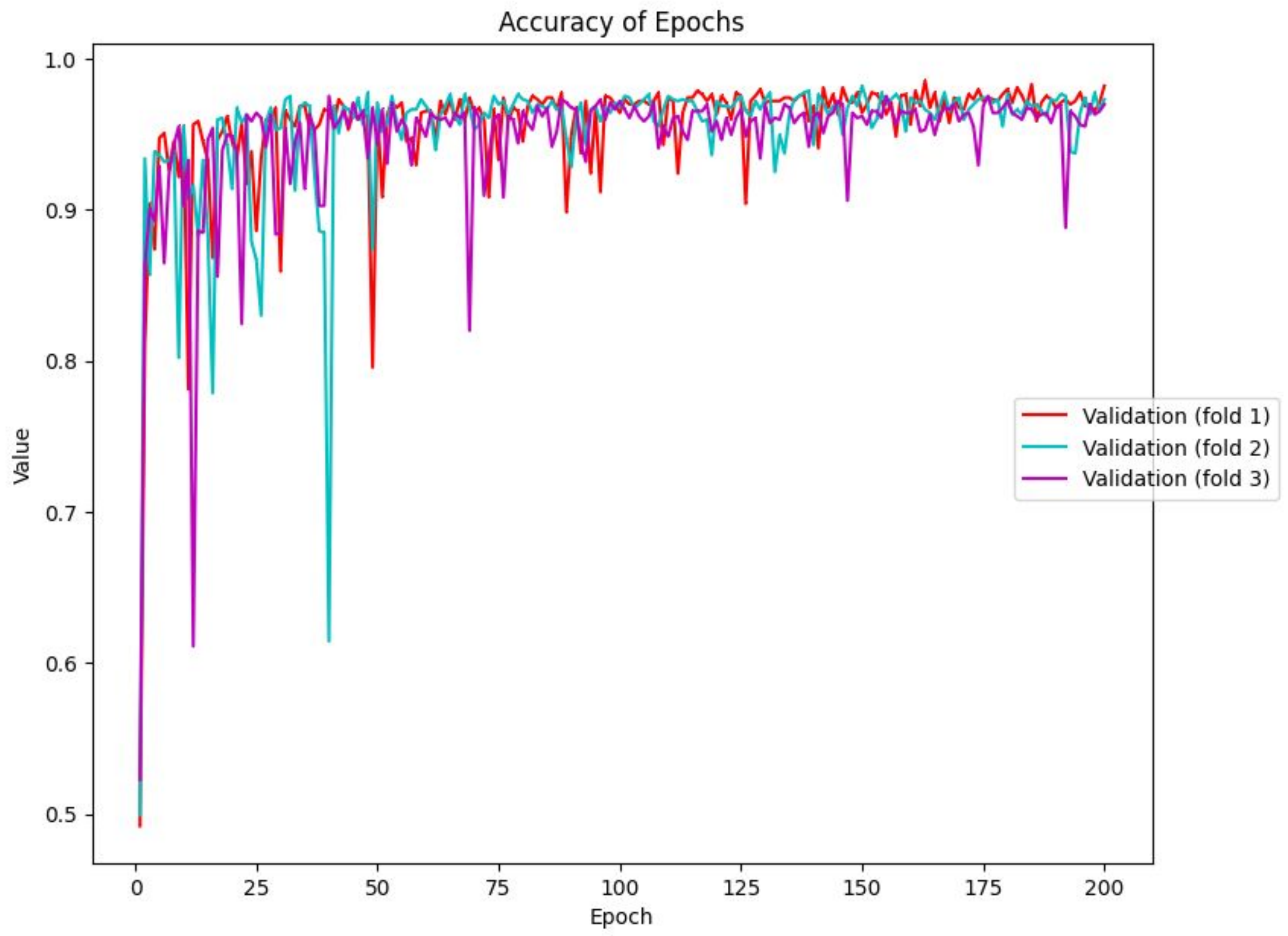
Evaluation metrics

ResNet-50 with Adam

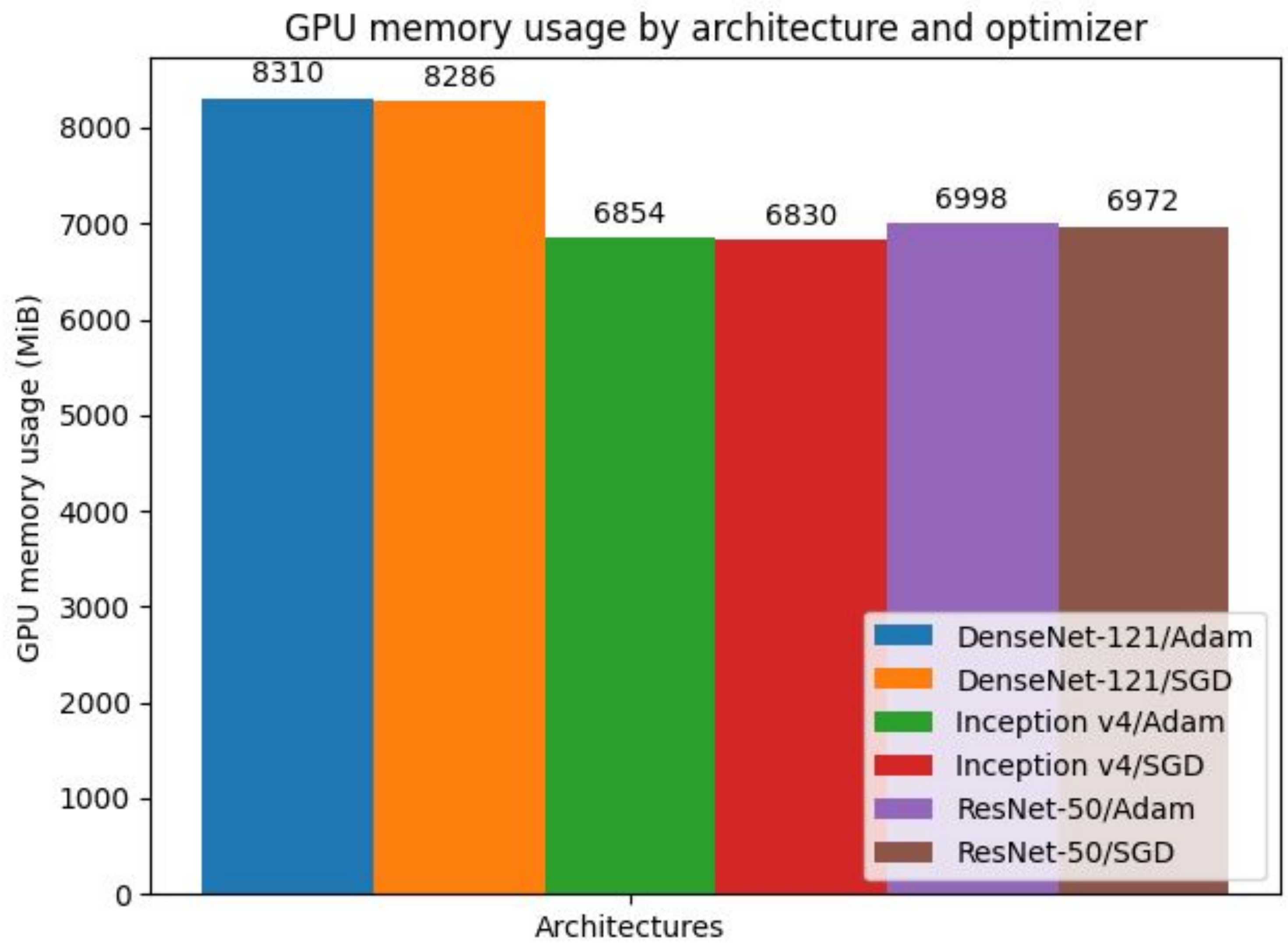


Evaluation metrics

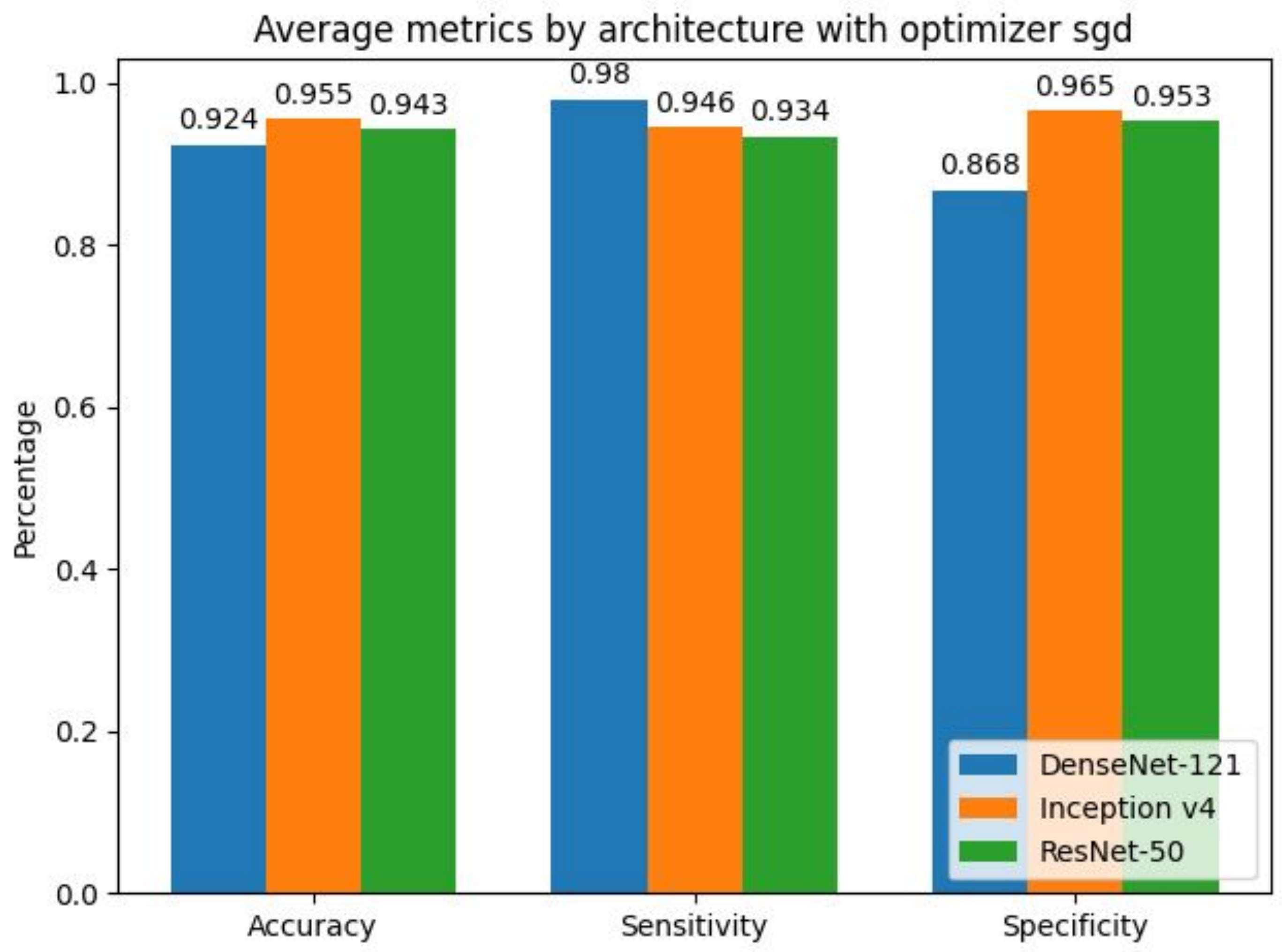
ResNet-50 with Adam



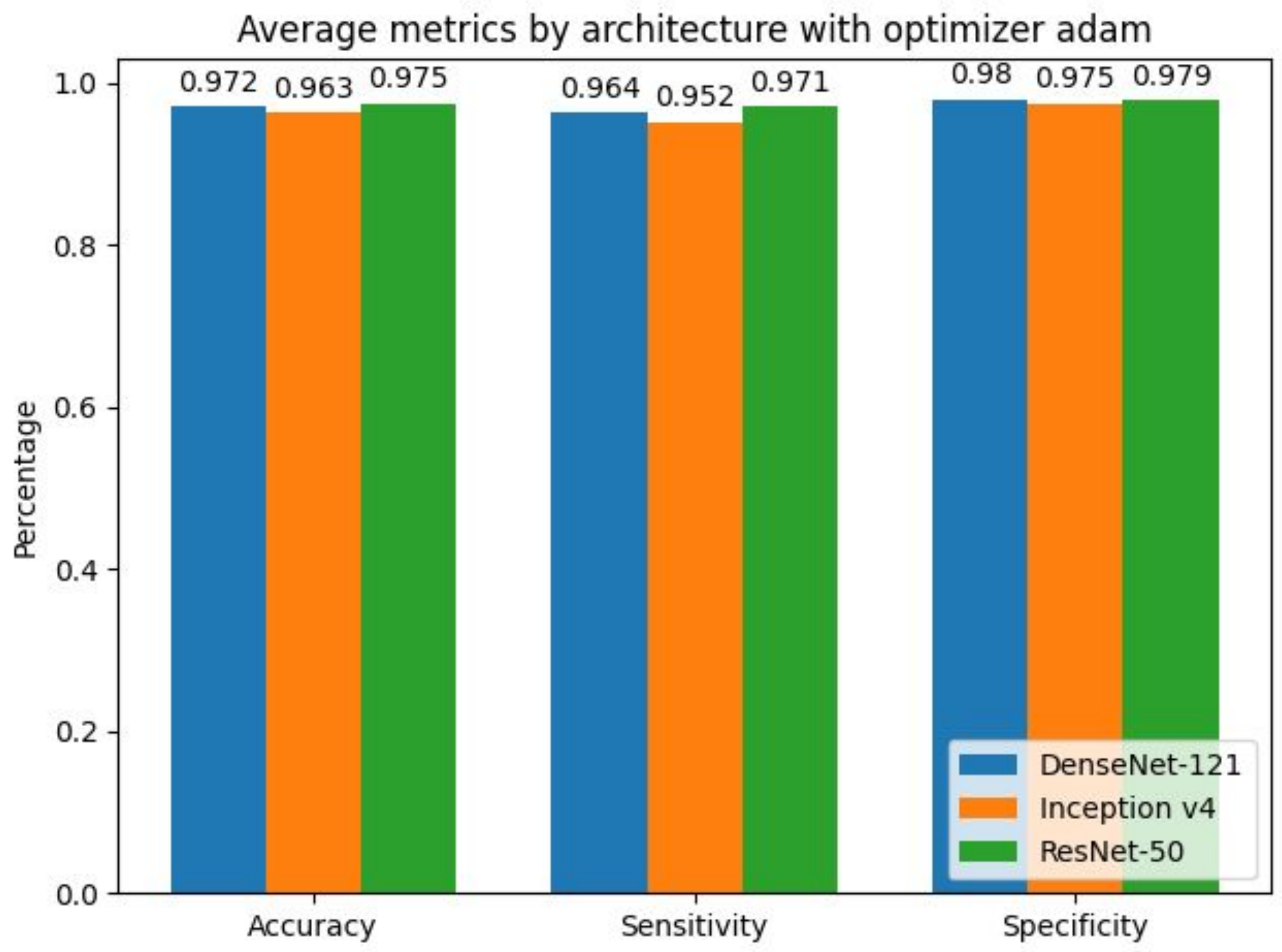
GPU memory usage



Results with SGD optimizer



Results with Adam optimizer



Conclusion

1. DenseNet-121 with SGD is beginning to overfit after 75 epochs.
2. ResNet-50 with SGD is overfitting after around 150 epochs.
3. Adam is performing better than SGD.
4. ResNet-50 with Adam optimizer achieves the most stable results and overall the best performance.

Implementing the project was quite straightforward using PyTorch and MONAI. Only if you have to mix plain PyTorch with MONAI functions, for example during preprocessing, you have to be cautious regarding the data types of parameters and shapes and arrangement of matrices - they often do not match.

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Thank you for your attention!