

Machine Learning for the classification of pigmented lesions in the skin

week 10-11 project



Pigmented Skin Lesions

Lesions that are brown, black or blue in colour under dermoscopy due to melanin (most often), blood or exogenous pigment

Melanocytic:

Melanocytic nevi (benign), Melanoma

Keratinocytic:

Seborrhoeic keratosis, lentigo, pigmented actinic keratosis, pigmented basal cell and squamous cell carcinoma

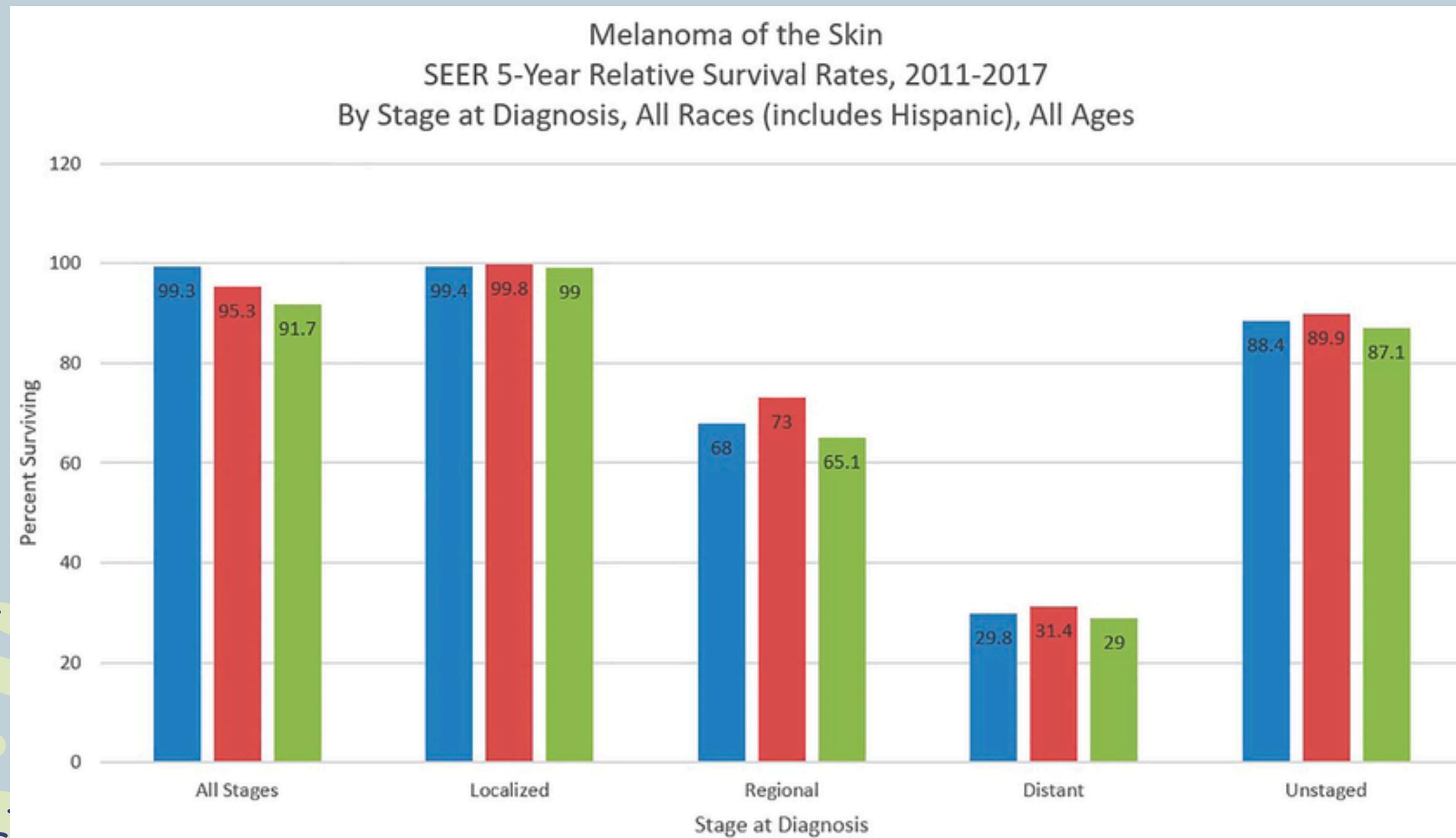
Vascular:

Trauma, vasculitis, angiomas

source: [dermnetnz](#)

SO..?

Pigmented lesions range from benign lesions such as nevi, to lesions associated to a very high mortality (melanoma). As such, correct diagnosis is important for patient outcome



Diagnostic Challenges



Skin lesions are usually examined and diagnosed using a dermascope or the naked eye

Difficult for primary care physicians

Need for technologies to aid diagnosis(?)

HAM10000

(Human Against Machine)

Dataset consists of 10015 dermatoscopic images which are released as a training set for academic machine learning purposes and are publicly available through the ISIC archive.

More than 50% of lesions have been confirmed by **pathology**, while the ground truth for the rest of the cases was either follow-up, expert consensus, or confirmation by in-vivo confocal microscopy.

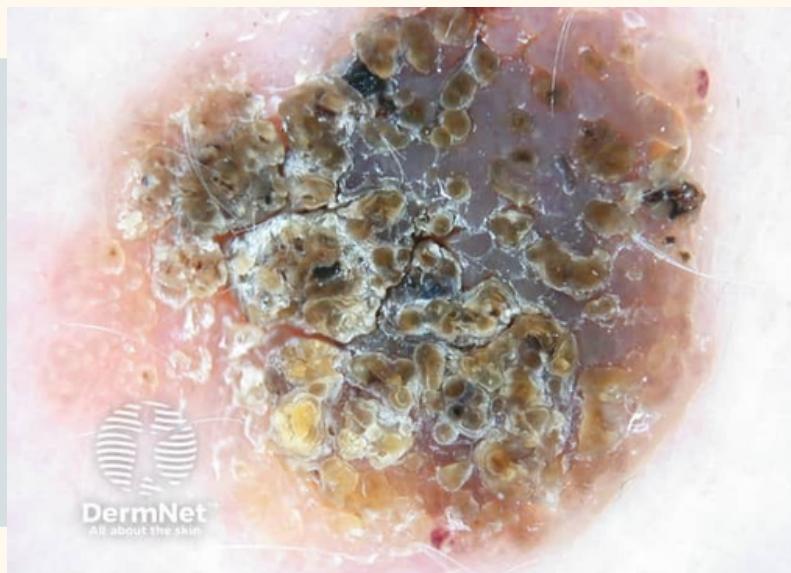
This benchmark dataset can be used for machine learning and for comparisons with human experts. Cases include a representative collection of all important diagnostic categories in the realm of pigmented lesions.

Categories in HAM10000

Actinic
Keratoses



Benign
keratoses



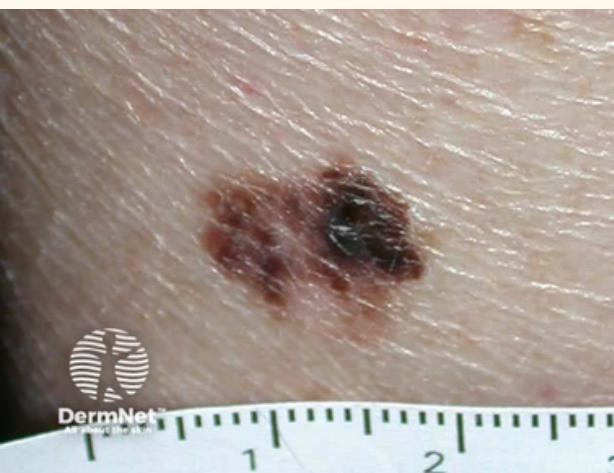
Basal cell
carcinoma



Melanocytic
nevi



Melanoma



Dermato-
fibroma



Vascular
skin
lesions



My little ML Model

Goal: Creating a deep learning model to classify seven types of skin lesions from images

Overview

Technical Approach & Architecture

- Data Preparation
- Model Architecture
- Training Process
- Results and Evaluation
- Model Interpretability
- Limitations and Challenges
- Future Improvements

Data Preprocessing Pipeline

- Standardization: All images resized to 224×224 pixels for consistent input to CNN
- Normalization: Pixel values normalized using ImageNet mean (0.485, 0.456, 0.406) and std (0.229, 0.224, 0.225)
- Training augmentations: RandomHorizontalFlip, RandomVerticalFlip, RandomRotation(20°), ColorJitter

```
# Use glob to find all jpg images in any subfolder of lesion_images
# The * wildcard will match both HAM10000_images_part_1 and HAM10000_images_part_2
def create_image_path_dict(base_dir=base_skin_dir):
    """Create a dictionary mapping image IDs to file paths"""
    imageid_path_dict = {os.path.splitext(os.path.basename(x))[0]: x
                         for x in glob(os.path.join(base_dir, 'lesion_images', '*', '*.jpg'))}
    return imageid_path_dict
```

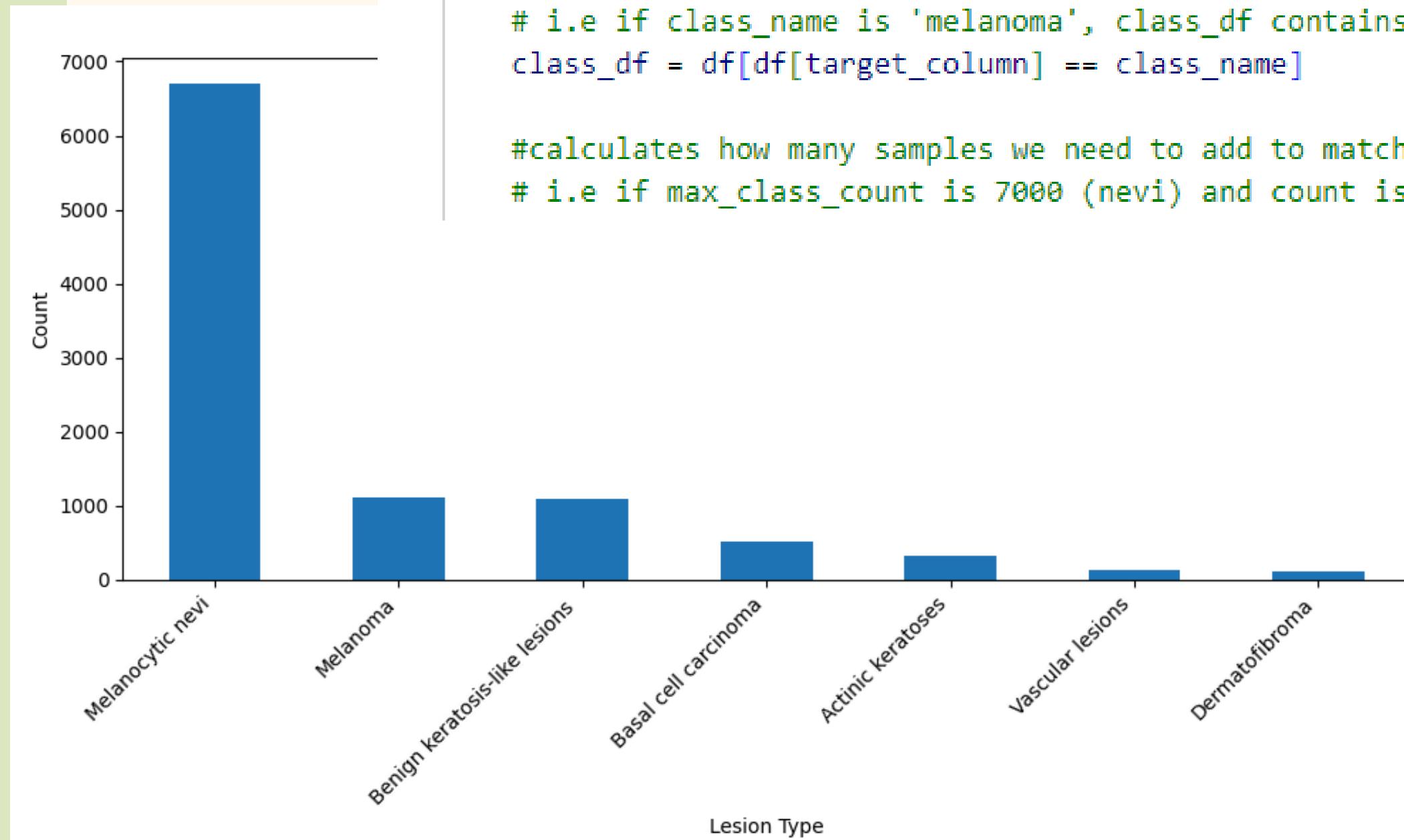
Data was stored as png. files in two folders and a separate metadata csv data sheet

```
data_transforms = {
    'train': transforms.Compose([
        transforms.Resize((224, 224)), # Takes an image of any size and resizes it to 224x224
        transforms.RandomHorizontalFlip(), # Flips the image horizontally
        transforms.RandomVerticalFlip(), # as above, just vertically
        transforms.RandomRotation(20), # Rotates the image by 20 degrees
        transforms.ColorJitter(brightness=0.1, contrast=0.1,
        transforms.ToTensor(), # Converts a PIL Image or numpy array to a tensor
        #Normalizes tensor images with mean and standard deviation
        # First parameter [0.485, 0.456, 0.406]: These are the
        # second parameter [0.229, 0.224, 0.225]: These are the
    ])
}
```

Data Preparation

Class imbalance strategy

- Oversampling minority classes to match majority class distribution
- Without oversampling, model would be biased toward the majority class



```
# This duplicates samples from minority classes to balance the dataset
def oversample_minority_classes(df, target_column):
    # Get the class counts
    class_counts = df[target_column].value_counts()
    max_class_count = class_counts.max()

    # Create a list to hold the balanced dataframe
    balanced_dfs = []

    # Loops through each class and its count (e.g., 'nevi': 7000, 'melanoma': 1000)
    for class_name, count in class_counts.items():
        # Creates a subset of the dataframe containing only rows of the current class
        # i.e if class_name is 'melanoma', class_df contains only melanoma rows
        class_df = df[df[target_column] == class_name]

        # calculates how many samples we need to add to match the majority class
        # i.e if max_class_count is 7000 (nevi) and count is 1000 (melanoma)
        needed_samples = max_class_count - count
```

Model Architecture

Transfer Learning Architecture

Base model: ResNet-18 pre-trained on ImageNet

ResNet-18 is a Convolutional Neural Network (CNN)

Reason: Relatively lightweight (18 layers) but still powerful and known to perform well with image classification

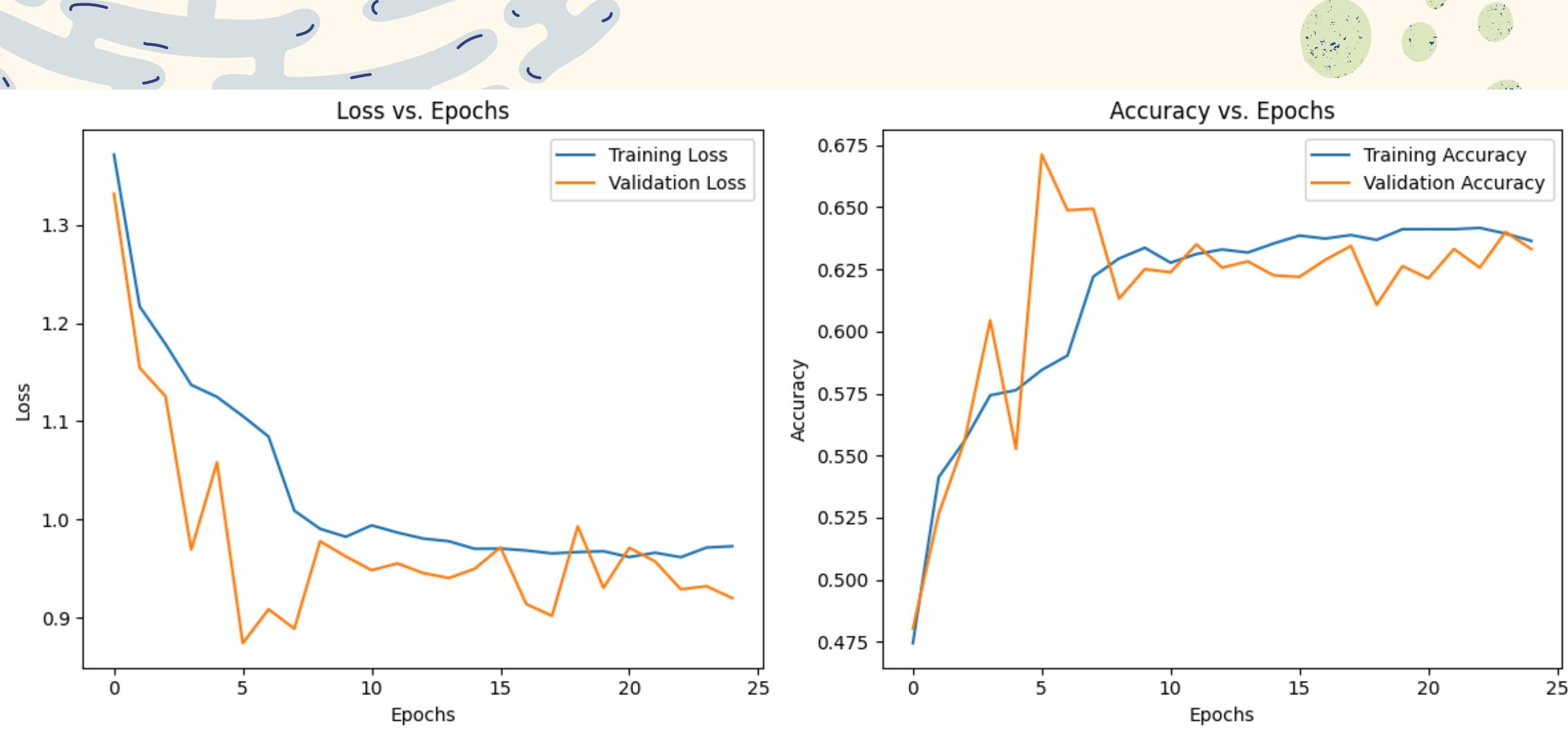
```
def create_model(num_classes):
    # first load a pre-trained ResNet-18 model
    resnet_model = models.resnet18(weights=models.ResNet18_Weights.IMAGENET1K_V1)

    # Freeze all the parameters to prevent them from updating
    # Preserve learned features -> pre-trained model has already learned useful features
    # Prevent overfitting -> with limited data, retraining all parameters might lead to overfitting
    # Efficiency: Training fewer parameters requires less computation
    # Basically: use the pre-trained features but adapt the final classification
    # Freezes: All convolutional layers: The feature extraction pipeline and All fully connected layers
    # --> freezing everything except the final fully connected layer: We're freezing the entire network except the last layer
    for param in resnet_model.parameters():
        param.requires_grad = False

    # This code replaces the original fully connected layer (which was designed for 1000 classes)
    # The last layer has 512 input features and outputs num_classes
    resnet_model.fc = nn.Sequential(
        nn.Linear(512, 256), #First fully connected layer -> 512 input features (from 512 learned features)
        nn.ReLU(), # Activation function (non-linearity), allows the network to learn complex functions
        nn.Dropout(0.5), # Randomly turns off 50% of neurons during training to prevent overfitting
        nn.Linear(256, num_classes) # Final output layer, has 256 input features, 1000 output classes
```

Training Process

- Batch size: 16 images per batch
- Optimizer: Adam with learning rate 0.001
- Learning rate scheduler: StepLR (reduces by factor 0.1 every 7 epochs)
- Loss function: CrossEntropy (standard for multi-class classification)



```
def create_optimizer(model, learning_rate=0.001):
    """Create an Adam optimizer for the model's FC layer"""
    return optim.Adam(model.fc.parameters(), lr=learning_rate)
```

```
#Learning Rate Scheduler: Adjusts learning rate during training
# -> Starts with lr=0.001
# -> Every 7 epochs, multiplies the learning rate by 0.1 -> Example: lr
# Large steps at the beginning for faster progress, Small steps later
def create_scheduler(optimizer, step_size=7, gamma=0.1):
    """Create a learning rate scheduler"""
```

Results and Evaluation

Overall Performance Metrics

Accuracy: 66.1% on the test set

Metric breakdown:

- Weighted avg precision: 0.751
- Weighted avg recall: 0.661
- Weighted avg F1-score: 0.692

Conclusion..

Model still performs remarkably better on majority classes

| Lesion Type | Precision | Recall | F1-Score | Support |
|----------------------|-----------|--------|----------|---------|
| Vascular lesions | 0.936 | 0.743 | 0.829 | 1341 |
| Dermatofibroma | 0.465 | 0.486 | 0.476 | 220 |
| Basal cell carcinoma | 0.338 | 0.345 | 0.341 | 223 |
| Melanocytic nevi | 0.377 | 0.670 | 0.483 | 103 |
| Benign keratosis | 0.298 | 0.477 | 0.367 | 65 |
| Actinic keratoses | 0.347 | 0.893 | 0.500 | 28 |
| Melanoma | 0.149 | 0.783 | 0.250 | 23 |

```
# calculate accuracy
# accuracy_score scikit-learn function that calculates proportion of correct predictions
accuracy = accuracy_score(all_labels, all_preds)
print(f"Test accuracy: {accuracy:.4f}")

#Generate a report
# classification_report: scikit-learn function that calculates multiple metrics:
# precision (% correct positive preds) -> True Pos / (True pos + False pos)
# recall (% correct positives id'ed) -> true pos / (true pos + false neg)
# F1: Balances precision and recall into a single score -> 2 * (precision * recall) / (precision + recall)
# support: Occurrences of each class in the test set
# target_names=class_names: Uses readable class names in the report (such as Melanoma instead of 0)

report = classification_report(all_labels, all_preds, target_names=class_names, output_dict=True)
report_df = pd.DataFrame(report).transpose() # .transpose() to flip rows and columns for better readability
print(report_df)
```

Results and Evaluation

Confusion Matrix

...Reflects class imbalances

```
cm = confusion_matrix(all_labels, all_predictions)
plt.figure(figsize=(10, 8))
plt.imshow(cm, interpolation="nearest")
plt.title("Confusion Matrix")
plt.colorbar() # color scale reference
# adding class labels:
tick_marks = np.arange(len(class_names))
plt.xticks(tick_marks, class_names, rotation=45)
plt.yticks(tick_marks, class_names) #
# adding value annotations:
thresh = cm.max() / 2. # calculates a threshold
for i in range(cm.shape[0]): # i for rows
    for j in range(cm.shape[1]): # j for columns
```

Higher sensitivity for some critical lesions (Melanoma: 78.3% recall,

Actinic keratoses: 89.3% recall)

But.. lower precision means many false positives (Melanoma precision only 14.9% ie many false positives)

Confusion Matrix



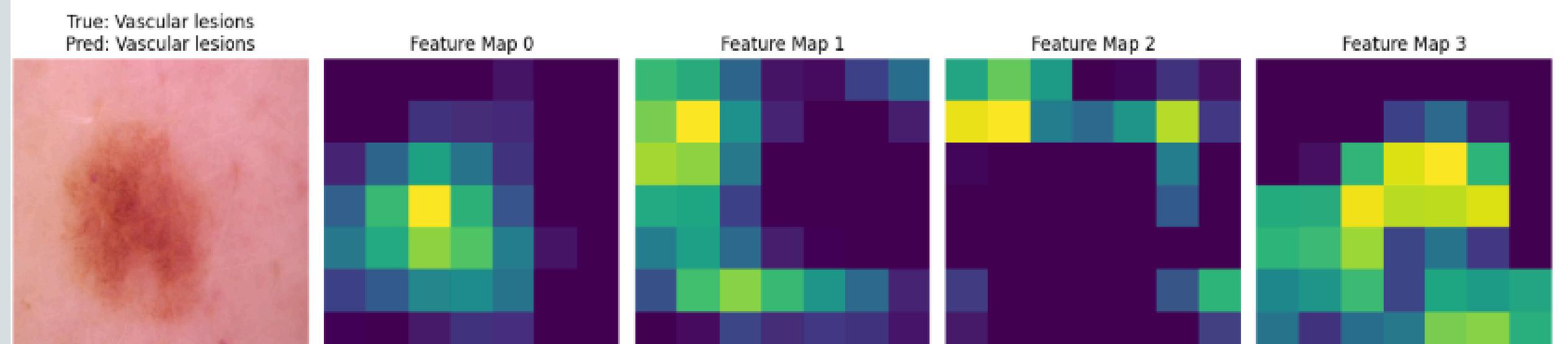
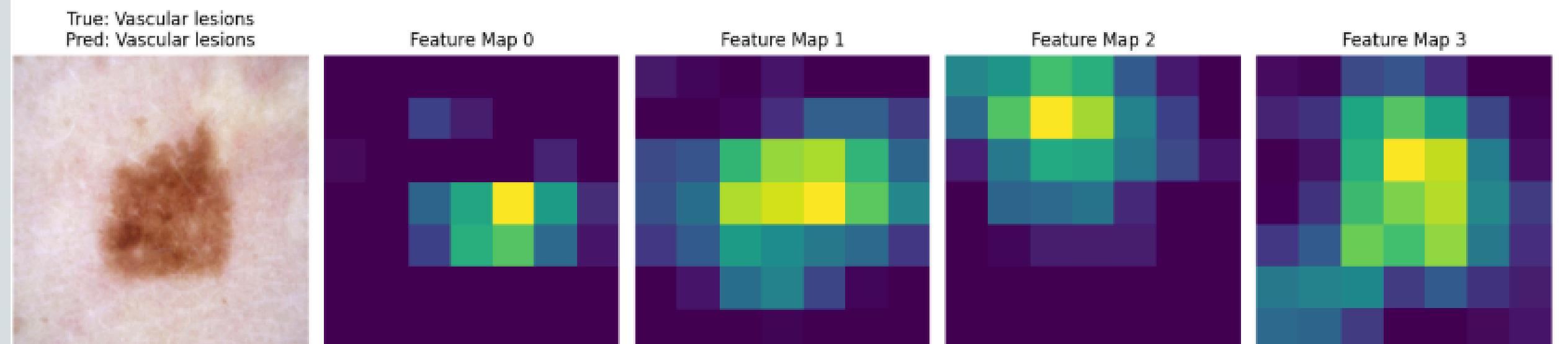
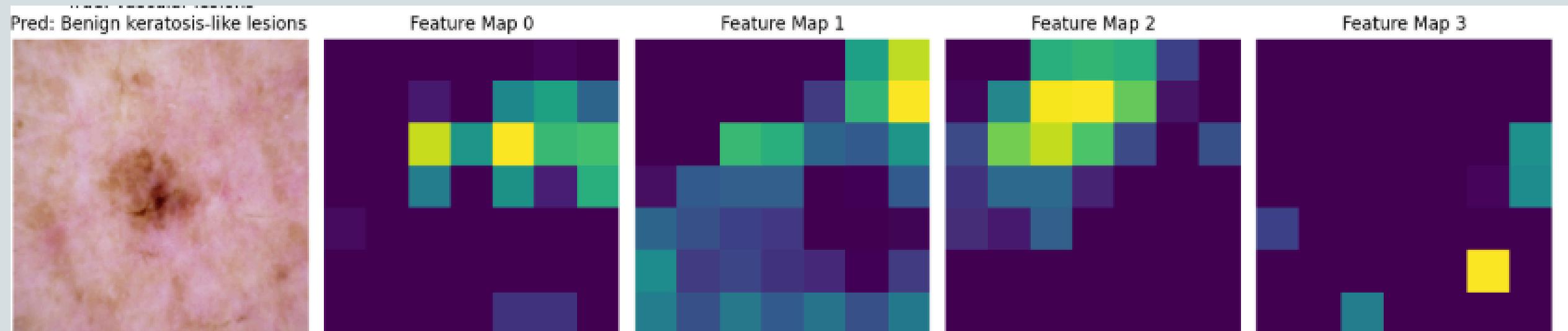
Interpretability – Feature Map Visualization

Visualization that helps understanding what the model "sees" internally..

Visualizes feature maps from an intermediate layer of the model:

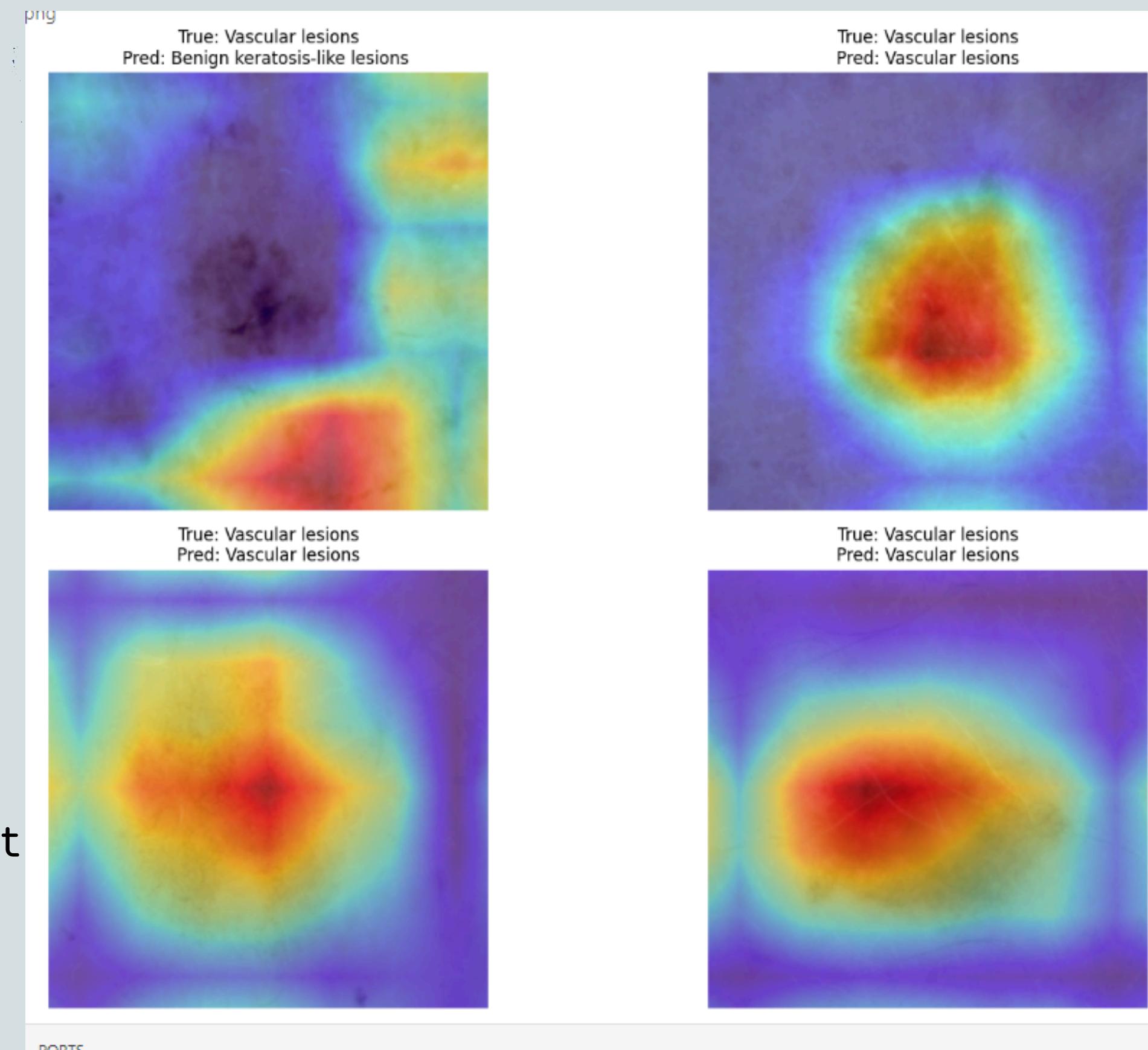
- What patterns it has learned to recognize
- Identify if it focuses on irrelevant features

Shows all features extracted, regardless of their importance to final classification



Interpretability - Grad-CAM visualization

- Grad-CAM = Gradient-weighted Class Activation Mapping
- Show which area of the lesion influenced the model's "diagnosis"
- Confirms whether the model focuses on the lesion itself rather than irrelevant background elements, shows biases
 - I.e for melanoma should highlight border and color irregularity, asymmetry etc
- In case of incorrect predictions, can help highlight how it was "misled"
- Combines feature activations with the gradients flowing back from the final classification



Limitations and Challenges

- Class imbalance effects on performance
- Limited dataset size for some classes (particularly melanoma)
- Frozen model limitations (transfer learning tradeoffs)
- Computational constraints affecting model complexity
- Generalizability concerns to real-world clinical settings

Future Improvements

- Architecture enhancements: use different premade model e.g. ResNet-50
- Training improvements: Fine-tuning more layers, enhanced augmentation
- Better handling of class imbalance
- Maybe combine multiple models specialized for different lesions
- Additional data sources to enhance training

Thank you for
you for your
attention!
(THE END)

