Convolutional Neural Network's Applications in Skin Cancer Diagnosis

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ELECTRICAL ENGINEERING
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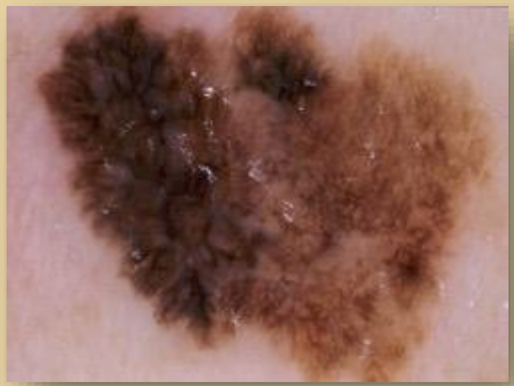
What is Melanoma?



What is Melanoma?

- Melanoma is the most aggressive type of skin cancer.
- Pathologists look at a skin biopsy slide and determine if its overall structure is normal, abnormal, or malignant.
- Diagnostic errors are much more frequently than in other tissues and can lead to under- and over-diagnosis of cancer.

Figure 1. An example of Invasive Melanoma Stage T1b with Hematoxylin and Eosin stain

What is Melanoma?

Cellular entities:

Nuclei

Melanocyte

Mitosis

Structural entities:

Dermis

Epidermis

Melanocyte nests

Diagnoses:

Benign

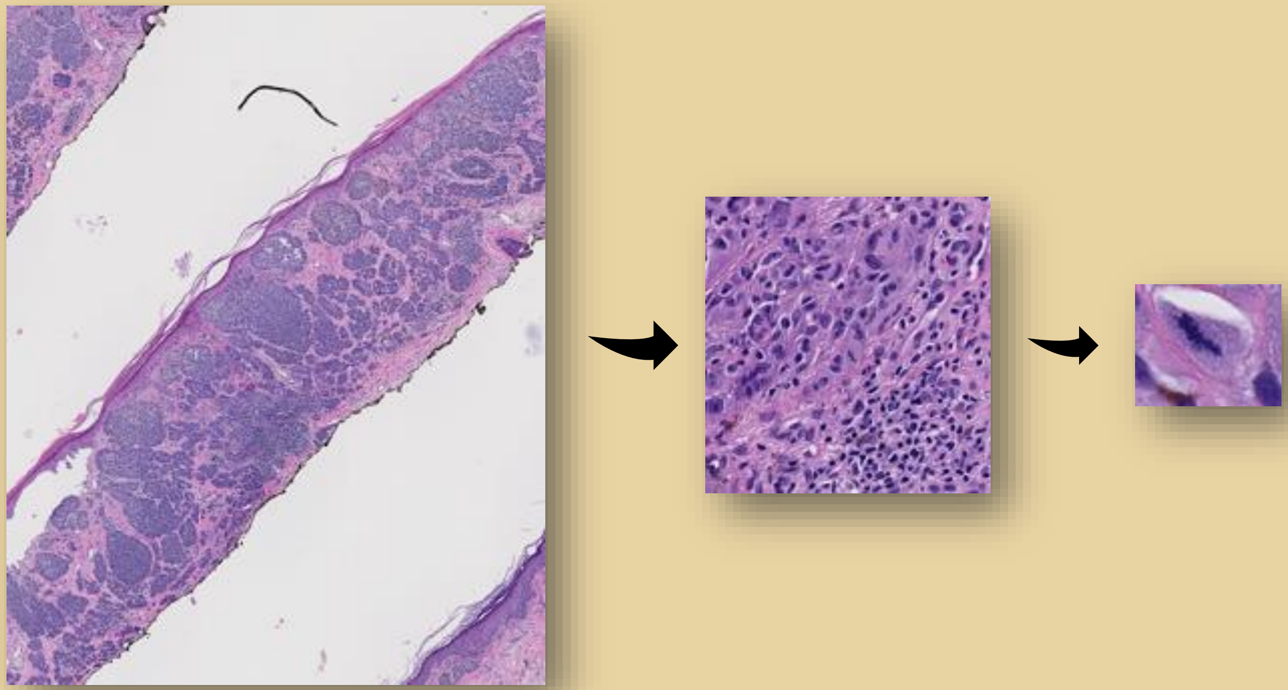
Atypia

Melanoma in situ

Invasive T1a

Invasive T1b

Cellular Level



Mitosis Detection

> Distinguishing **mitoses** from **normal nuclei** is a challenge.

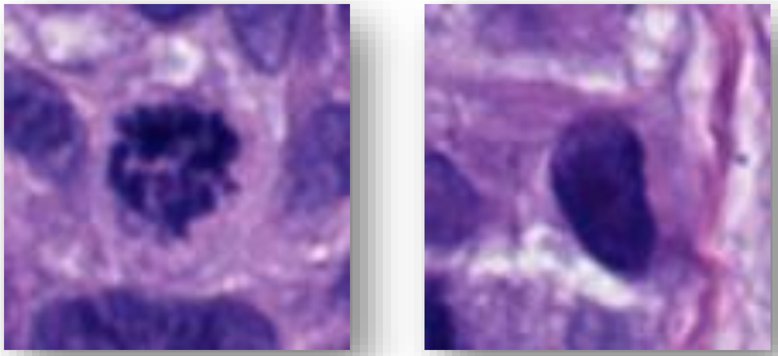


Figure 5. Examples of a sampled Mitosis (Left) and a sampled Nuclei (Right).

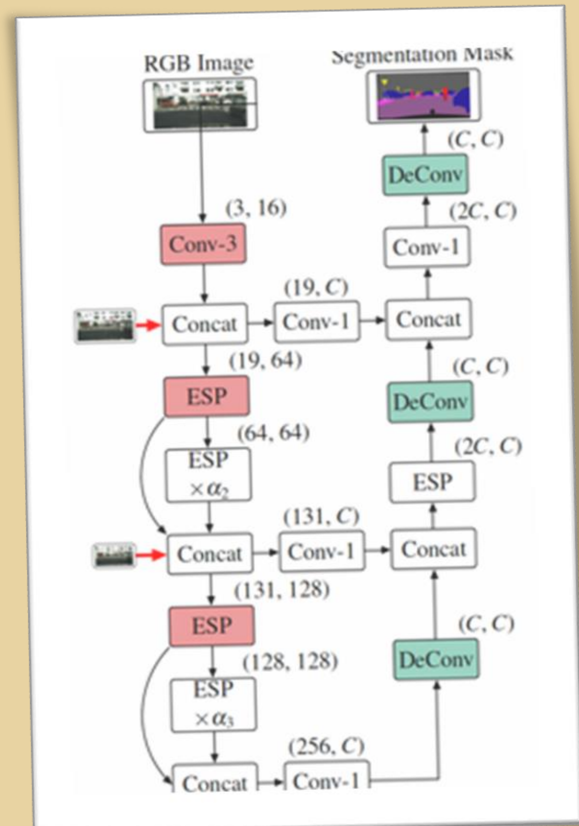
Preprocessing

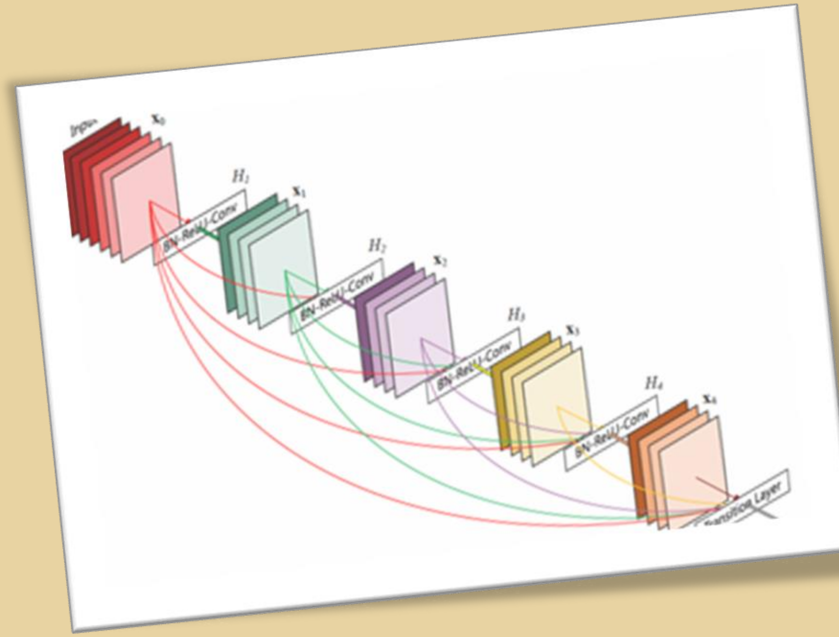
> **Data augmentation:**
  - Rotations of 45, 90, 135 or 225 degrees.
  - Mirroring horizontal and vertical.

> **The final dataset:**
  - 4364 mitosis samples.
  - 12640 non-mitosis samples.

> **Dataset randomly split:**
  - Training: 60%
  - Validation: 20%
  - Testing: 20%

Method and Models





Method and Model

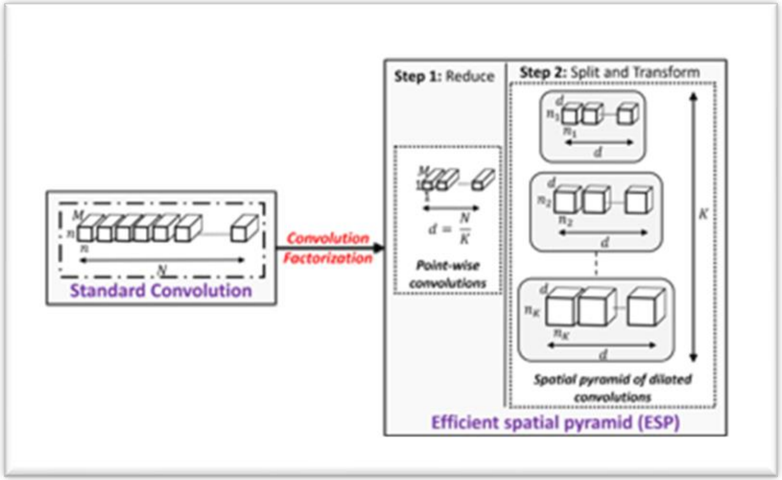
- In recent years, with the development of fast and accessible GPUs, Convolutional Neural Networks (CNNs) have dominated computer vision research due to their impressive performance, and mitosis detection is not an exception.

- We ran our experiment two separate times on two well-designed CNNs and compared their results:
  1. Efficient Spatial Pyramid of Dilated Convolutions (ESPNet)
  2. Densely Connected Convolutional Networks (DenseNet161)

Method and Model

> ESPNet

A fast and efficient convolutional neural network for high resolution inputs.



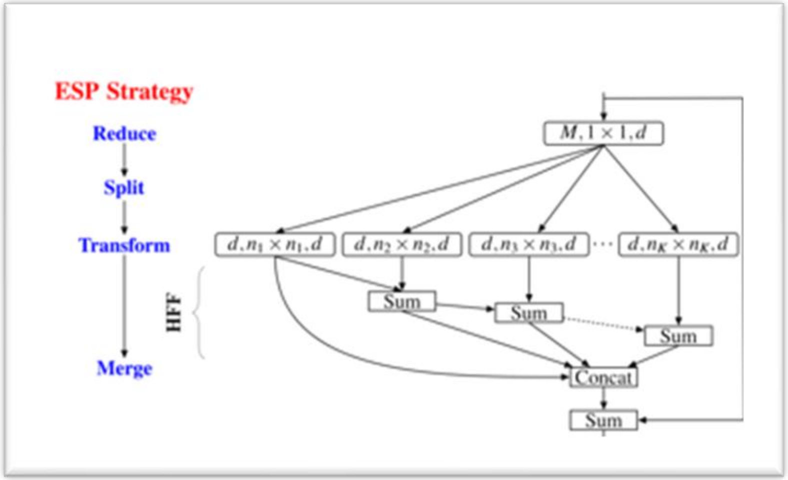


Figure 7. (Left) Comparing standard convolution and ESP. (Right) Block diagram of ESP module.

Method and Model

> DenseNet:

Whereas traditional convolutional networks with L layers have L connections—one between each layer and its subsequent layer—the DenseNet network has L(L+1)/2 direct connections.

Layers	Output Size	DenseNet-121	DenseNet-169	DenseNet-201	DenseNet-264
Convolution	112×112	7×7 conv, stride 2			
Pooling	56×56	3×3 max pool, stride 2			
Dense Block (1)	56×56	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 6$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 6$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 6$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 6$
Transition Layer (1)	56×56	1×1 conv			
	28×28	2×2 average pool, stride 2			
Dense Block (2)	28×28	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 12$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 12$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 12$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 12$
Transition Layer (2)	28×28	1×1 conv			
	14×14	2×2 average pool, stride 2			
Dense Block (3)	14×14	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 24$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 32$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 48$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 64$
Transition Layer (3)	14×14	1×1 conv			
	7×7	2×2 average pool, stride 2			
Dense Block (4)	7×7	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 16$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 32$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 32$	$\begin{bmatrix} 1 \times 1 \text{ conv} \\ 3 \times 3 \text{ conv} \end{bmatrix} \times 48$
Classification Layer	1×1	7×7 global average pool			
		1000D fully-connected, softmax			

Figure 8. DenseNet architectures for ImageNet.

Method and Model

- Hyperparameters
  - Adam optimizers.
  - learning rate decay schedule with step size = 5 and $\boldsymbol{\gamma} = 0.1$.
  - 20 epochs.
  - cross-entropy loss function.

- Evaluation Metrics
  - Accuracy = (TP+TN)/(TP+FP+FN+TN)
  - Precision = TP / (TP + FP)
  - Recall = TP / (TP + FN)
  - $\text{F1 score} = 2 \times \frac{(\text{Precision} \times \text{Recall})}{\text{Precision} + \text{Recall}}$
  - Sensitivity = TP / (TP + FN)
  - Specificity = TN / (TN + FP)

Results

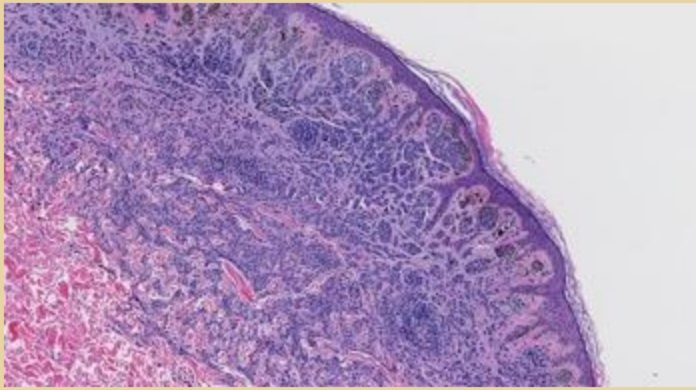
Results

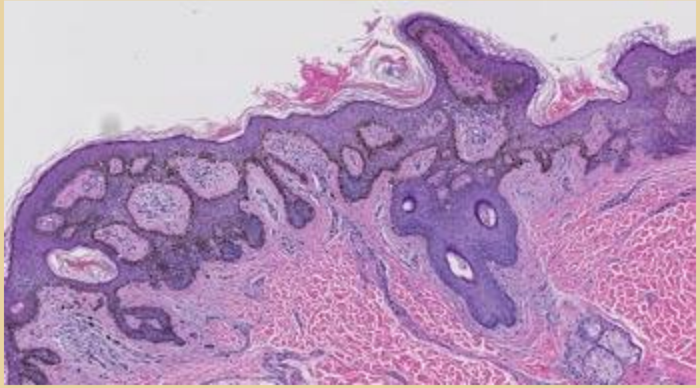
> Evaluation results of ESPNet and DenseNet161 on Melanoma

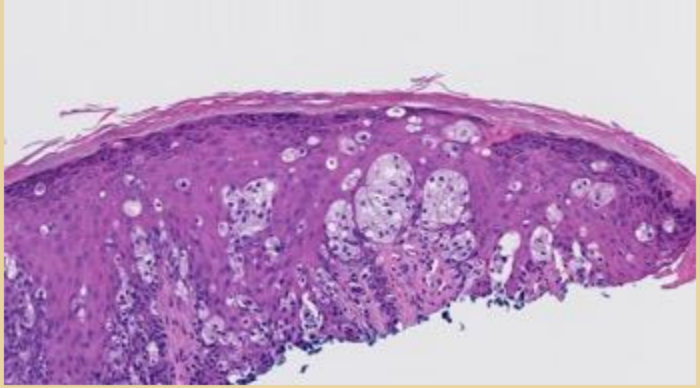
Table 1: Evaluation results of ESPNet and DenseNet161 on **Melanoma**

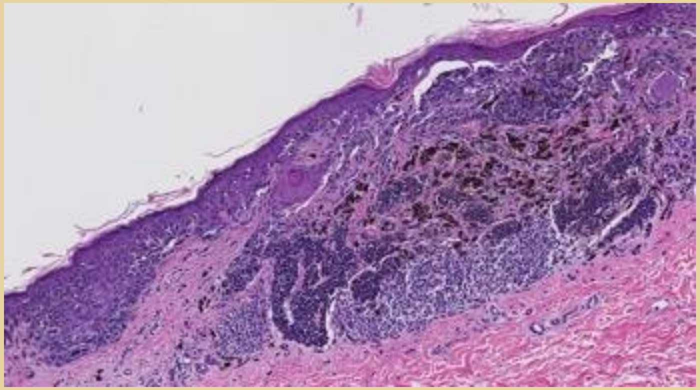
Metrics	**ESPNet**	**DenseNet161**
Accuracy	98.40%	98.80%
Precision	96.06%	98.37%
Recall	97.60%	96.80%
F1 Score	96.83%	97.58%
Sensitivity	97.60%	96.80%
Specificity	98.67%	99.47%
FP, FN	5, 3	2, 4
TP, TN	122, 370	121 , 373
Training time	35m & 6s	106m & 32s

Architectural Level







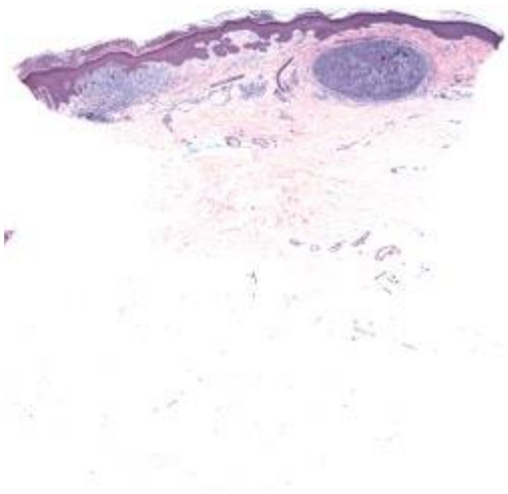


Dataset

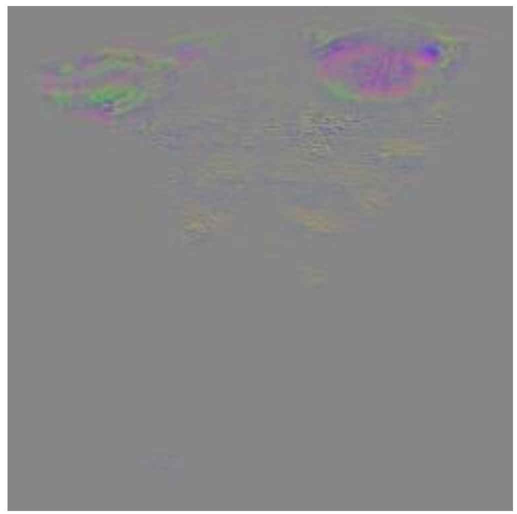
- Our dataset comes from 240 H&E stained slides of skin biopsy images, acquired by the University of Washington School of Medicine in the MPATH study (R01 CA151306).

- Our dataset contains five different diagnoses:
  1. Benign
  2. Atypia
  3. Melanoma in Situ
  4. Invasive Melanoma T1a
  5. Invasive Melanoma T1b.

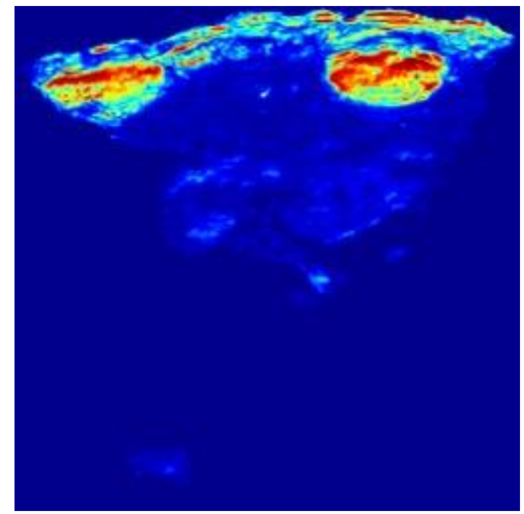
Benign vs. Invasive (1 vs. 5)



Normalized input



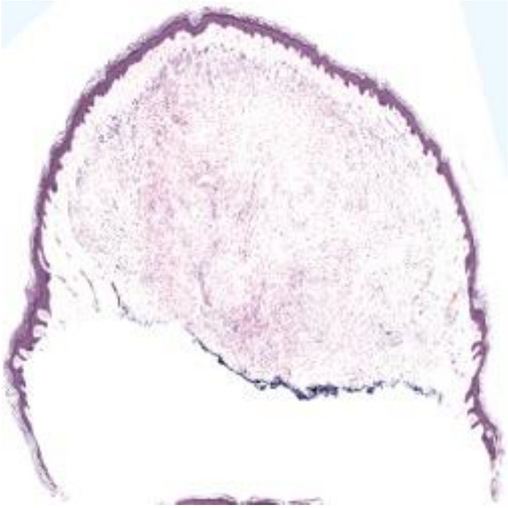
Gradient



Layer 5 heatmap

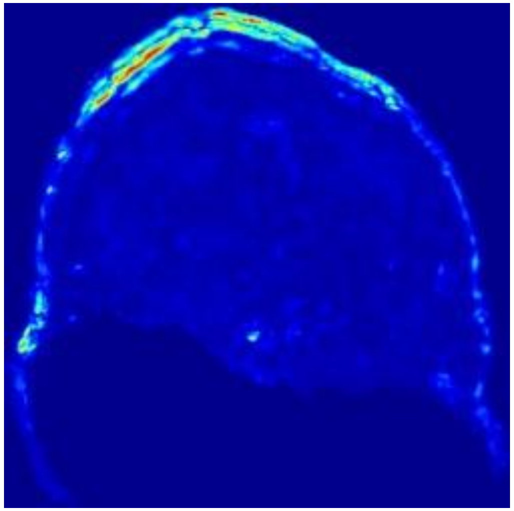
True Positive (Invasive)

Benign vs. Invasive (1 vs. 5)



Normalized input

Gradient

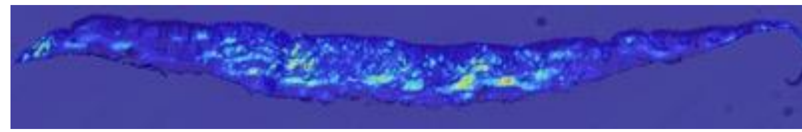


Layer 5 heatmap

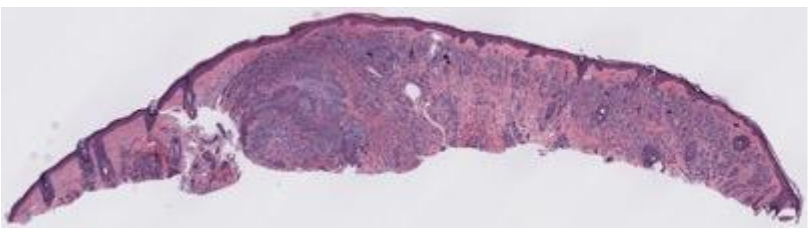
True Negative (Benign)

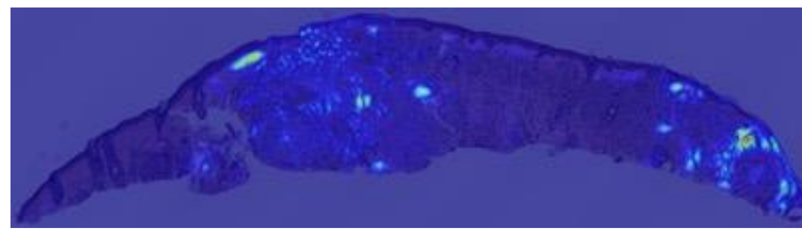
Benign & Atypia vs. Invasive

Atypia



Invasive





Invasive

Latest Results

Class 1 vs. 5

- **Train**: 1: 31 slices, 5: 72 slices
- **Test**: 1: 26 slices, 5: 74 slices

Class 1 &2 vs. 5

- **Train**: 1 & 2: 74 slices, 5: 72 slices
- **Test**: 1 & 2 : 75 slices, 5: 74 slices

	Accuracy	F1		Precision		Recall	
1 vs. 5	**Total**	**1**	**5**	**1**	**5**	**1**	**5**
	0.78	0.54	0.86	0.59	0.83	0.5	0.88
1&2 vs. 5	**Total**	**1&2**	**5**	**1&2**	**5**	**1&2**	**5**
	0.819	0.83	0.81	0.80	0.84	0.85	0.78

Thank you for your attention.

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