1 !git clone https://github.com/fxlmer/AJPom cancer

```
Cloning into 'AJPom_cancer'...

remote: Enumerating objects: 73, done.

remote: Counting objects: 100% (73/73), done.

remote: Compressing objects: 100% (35/35), done.

remote: Total 217 (delta 56), reused 52 (delta 38), pack-reused 144

Receiving objects: 100% (217/217), 351.85 MiB | 47.47 MiB/s, done.

Resolving deltas: 100% (122/122), done.

Checking out files: 100% (30/30), done.
```

1 !git clone https://github.com/EvilPickle-PCSHSPT/AJPom cancer data

```
Cloning into 'AJPom_cancer_data'...
remote: Enumerating objects: 51, done.
remote: Counting objects: 100% (51/51), done.
remote: Compressing objects: 100% (25/25), done.
remote: Total 1854 (delta 26), reused 51 (delta 26), pack-reused 1803
Receiving objects: 100% (1854/1854), 1.73 GiB | 52.19 MiB/s, done.
Resolving deltas: 100% (82/82), done.
Checking out files: 100% (1426/1426), done.
```

## Import

```
1 import tensorflow as tf
```

- 2 from google.colab import files
- 3 from Ex2 DenseNet121 nmVSpmd utils import \*

```
1 tf.compat.v1.disable eager execution()
```

- 1 test model = tf.keras.models.load model('/content/AJPom cancer/Ex/Ex2 nm'
- 1 # test\_model.summary()

## Grad-CAM

last conv2d = 'conv5 block16 2 conv'

## Normal

```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/nor
```

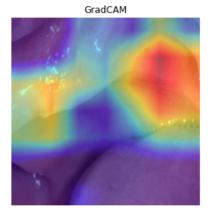
<sup>2</sup> gradcam, gb, guided gradcam = compute saliency(test model, test model, te

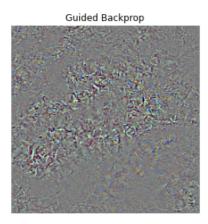
/usr/local/lib/python3.7/dist-packages/tensorflow/python/keras/engine/training warnings.warn('`Model.state\_updates` will be removed in a future version.' Model prediction:

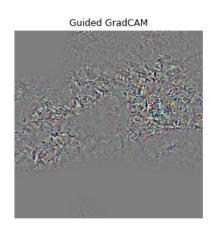
normal pmd

1 (0) with probability 0.833
(1) with probability 0.167

Explanation for 'normal'







1 test\_img = '/content/AJPom\_cancer\_data/nmVSpmd/split\_images\_clf/test/norm
2 gradcam, gb, guided gradcam = compute saliency(test model, test model, test model)

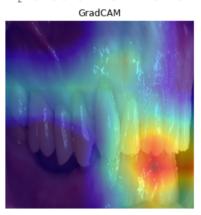
Model prediction:

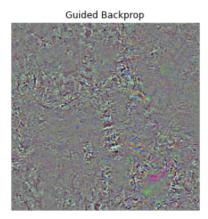
pmd

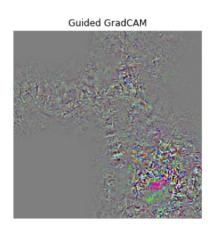
normal

- (0) wit (1) wit
- with probability 0.985 with probability 0.015

Explanation for 'normal'



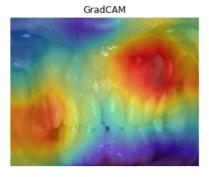


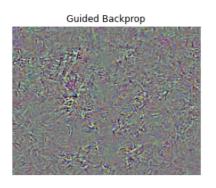


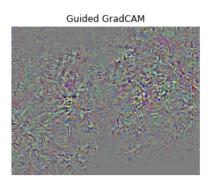
- 1 test\_img = '\_/content/AJPom\_cancer\_data/nmVSpmd/split\_images\_clf/test/norm
- 2 gradcam, gb, guided gradcam = compute saliency(test model, test model, test

Model prediction:
normal (0) with probability 0.997
pmd (1) with probability 0.003

Explanation for 'normal







1 test\_img = '/content/AJPom\_cancer\_data/nmVSpmd/split\_images\_clf/test/norm
2 gradcam, gb, guided\_gradcam = compute\_saliency(test\_model, test\_model, test\_model)

<sup>1</sup> test\_img = '/content/AJPom\_cancer\_data/nmVSpmd/split\_images\_clf/test/nor

<sup>2</sup> gradcam, gb, guided gradcam = compute saliency(test model, test model, test model, test model, test model, test model)

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- PMD

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