

## ▼ Clone Data

```
1 !git clone https://github.com/EvilPickle-PCSHSPT/AJPom_cancer_data

Cloning into 'AJPom_cancer_data'...
remote: Enumerating objects: 1861, done.
remote: Total 1861 (delta 0), reused 0 (delta 0), pack-reused 1861
Receiving objects: 100% (1861/1861), 1.73 GiB | 54.01 MiB/s, done.
Resolving deltas: 100% (88/88), done.
Checking out files: 100% (1424/1424), done.
```

## ▼ Import Libraries

```
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/Ex3_ResNet50_nmVSpmd_nb.h5')

1 test_model.summary()

Model: "model"

Layer (type)           Output Shape        Param #     Connected to
=====
input_1 (InputLayer)   [(None, 224, 224, 3)]  0
conv1_pad (ZeroPadding2D)  (None, 230, 230, 3)  0         input_1[0]
conv1_conv (Conv2D)      (None, 112, 112, 64)  9472      conv1_pad[0]
pool1_pad (ZeroPadding2D) (None, 114, 114, 64)  0         conv1_conv[0]
pool1_pool (MaxPooling2D) (None, 56, 56, 64)  0         pool1_pad[0]
conv2_block1_preact_bn (BatchNormaliz (None, 56, 56, 64)  256      pool1_pool[0]
conv2_block1_preact_relu (Activat (None, 56, 56, 64)  0         conv2_block1_preact_bn[0]
conv2_block1_1_conv (Conv2D)      (None, 56, 56, 64)  4096     conv2_block1_preact_relu[0]
conv2_block1_1_bn (BatchNormaliz (None, 56, 56, 64)  256     conv2_block1_1_conv[0]
conv2_block1_1_relu (Activation (None, 56, 56, 64)  0         conv2_block1_1_bn[0]
conv2_block1_2_pad (ZeroPadding (None, 58, 58, 64)  0         conv2_block1_1_relu[0]
```

conv2_block1_2_conv (Conv2D)	(None, 56, 56, 64)	36864	conv2_bloc]
conv2_block1_2_bn (BatchNormali	(None, 56, 56, 64)	256	conv2_bloc]
conv2_block1_2_relu (Activation	(None, 56, 56, 64)	0	conv2_bloc]
conv2_block1_0_conv (Conv2D)	(None, 56, 56, 256)	16640	conv2_bloc]
conv2_block1_3_conv (Conv2D)	(None, 56, 56, 256)	16640	conv2_bloc]
conv2_block1_out (Add)	(None, 56, 56, 256)	0	conv2_bloc] conv2_bloc]
conv2_block2_preact_bn (BatchNo	(None, 56, 56, 256)	1024	conv2_bloc]
conv2_block2_preact_relu (Activ	(None, 56, 56, 256)	0	conv2_bloc]
conv2_block2_1_conv (Conv2D)	(None, 56, 56, 64)	16384	conv2_bloc]
conv2_block2_1_bn (BatchNormali	(None, 56, 56, 64)	256	conv2_bloc]
conv2_block2_1_relu (Activation	(None, 56, 56, 64)	0	conv2_bloc]
conv2_block2_2_pad (ZeroPadding	(None, 58, 58, 64)	0	conv2_bloc]
conv2_block2_2_conv (Conv2D)	(None, 56, 56, 64)	36864	conv2_bloc]
conv2_block2_2_bn (BatchNormali	(None, 56, 56, 64)	256	conv2_bloc]
conv2_block2_2_relu (Activation	(None, 56, 56, 64)	0	conv2_bloc]
conv2_block2_3_conv (Conv2D)	(None, 56, 56, 256)	16640	conv2_bloc]

## ▼ Grad-CAM

```
1 last_conv2d = 'conv5_block3_3_conv'
```

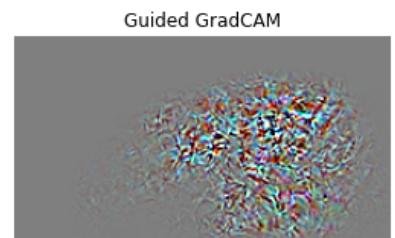
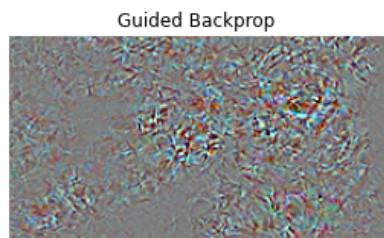
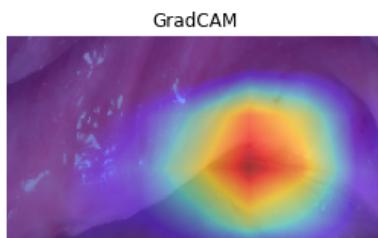
## ▼ Normal

```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/nor'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

```
/usr/local/lib/python3.7/dist-packages/tensorflow/python/keras/engine/training.py:100: UserWarning: `Model.state_updates` will be removed in a future version.
  Model prediction:
```

normal	(0)	with probability 0.835
pmd	(1)	with probability 0.165

Explanation for 'normal'

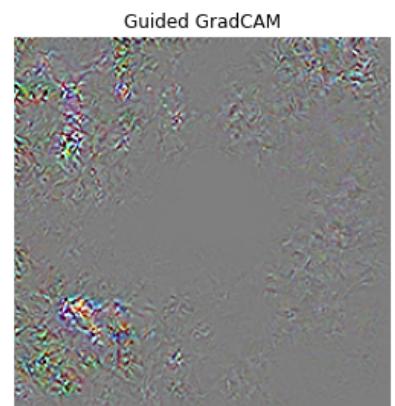
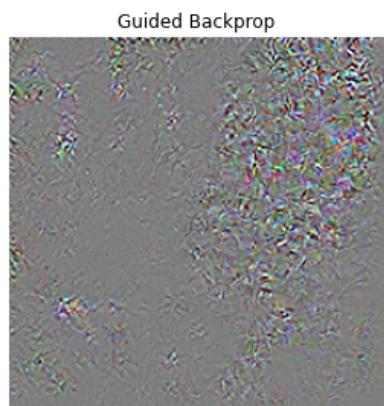
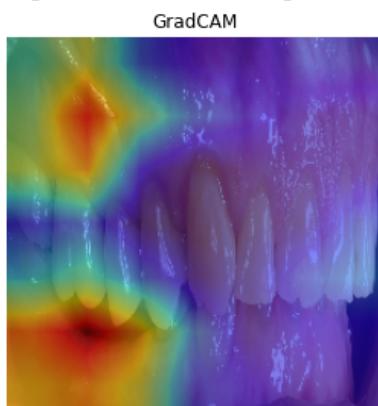


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.865
normal	(0)	with probability 0.135

Explanation for 'pmd'



```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

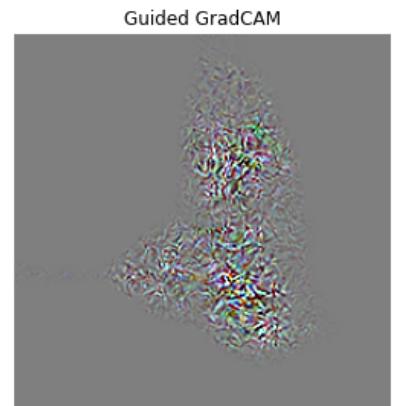
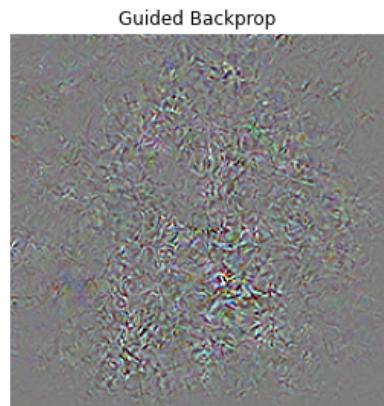
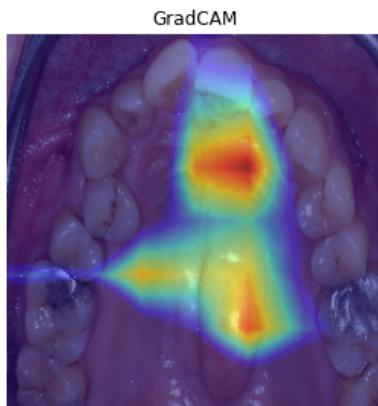
pmd	(1)	with probability 0.956
normal	(0)	with probability 0.044

```
1 test_img = '/content/AJPom_cancer_data/nmVSpmnd/split_images_clf/test/normal/00000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

normal	(0)	with probability 0.686
pmd	(1)	with probability 0.314

Explanation for 'normal'

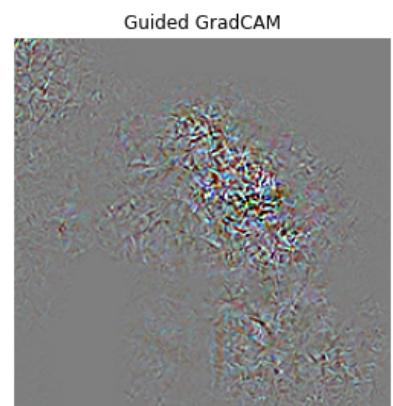
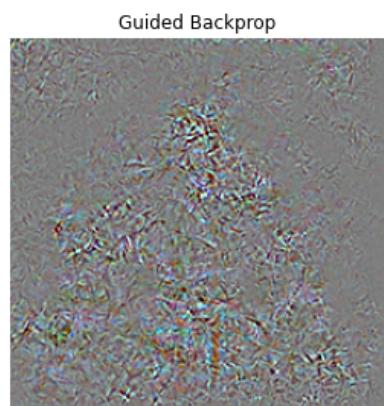
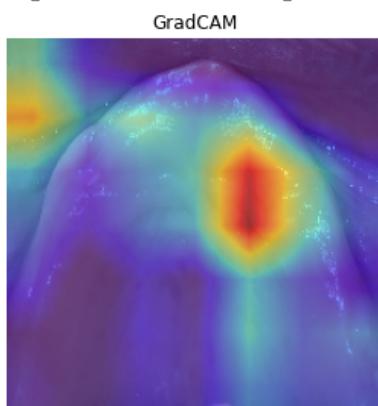


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmnd/split_images_clf/test/pmd/00000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

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

Explanation for 'pmd'

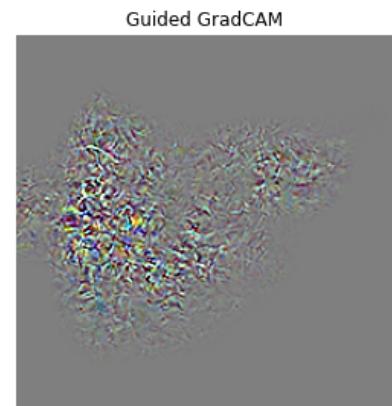
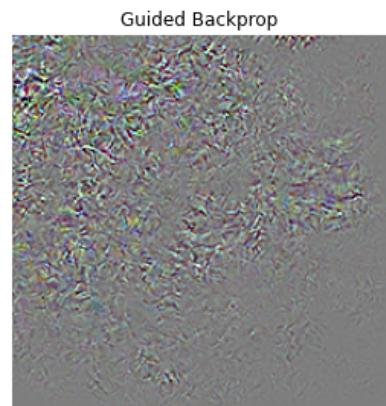
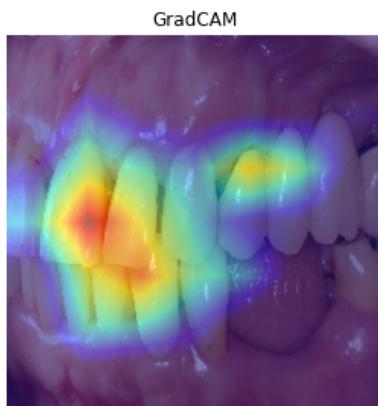


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmnd/split_images_clf/test/normal/00000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

normal	(0)	with probability 0.947
pmd	(1)	with probability 0.053

Explanation for 'normal'

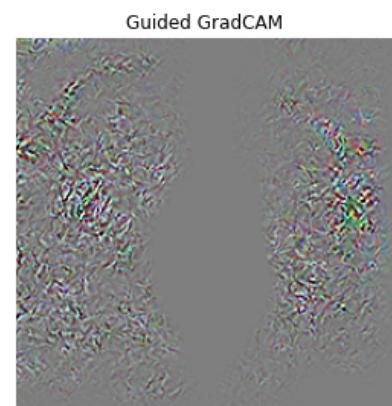
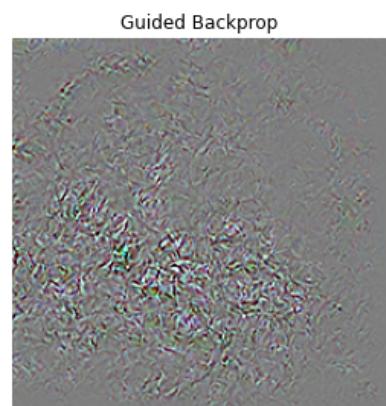
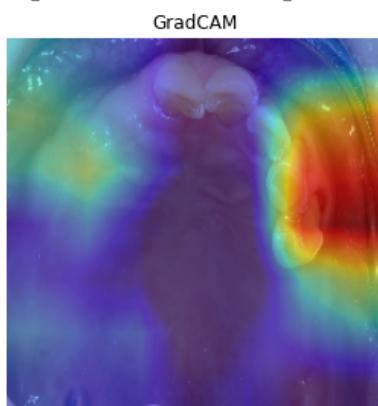


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmnd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.964
normal	(0)	with probability 0.036

Explanation for 'pmd'

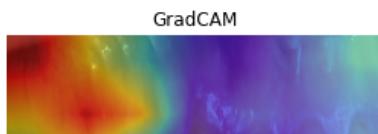


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmnd/split_images_clf/test/pmd/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.854
normal	(0)	with probability 0.146

Explanation for 'pmd'

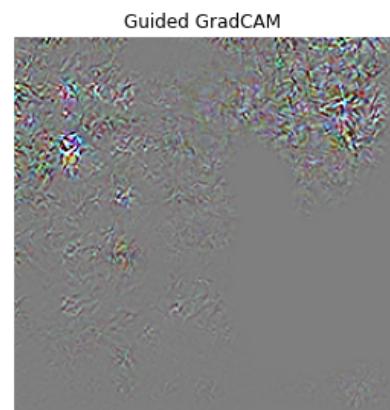
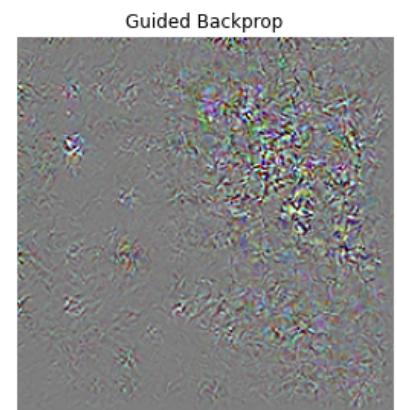


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.826
normal	(0)	with probability 0.174

Explanation for 'pmd'

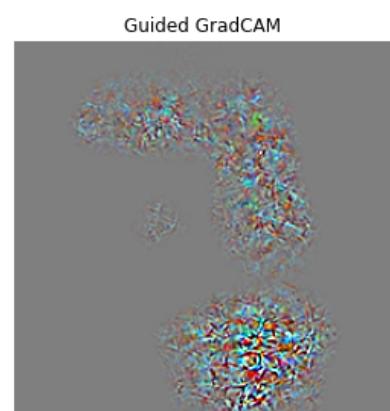
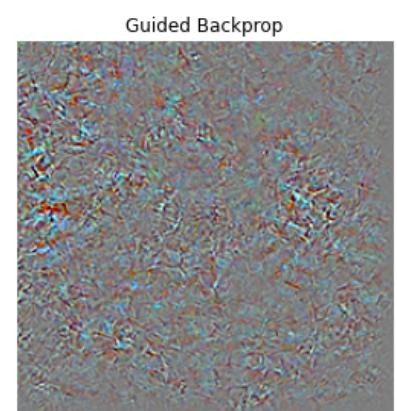
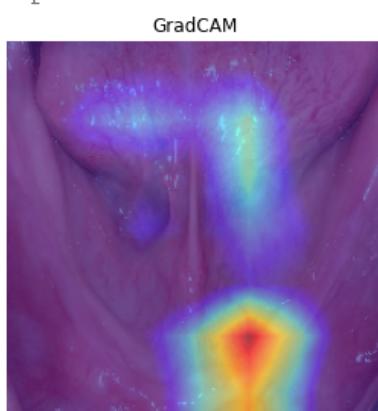


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

normal	(0)	with probability 0.816
pmd	(1)	with probability 0.184

Explanation for 'normal'



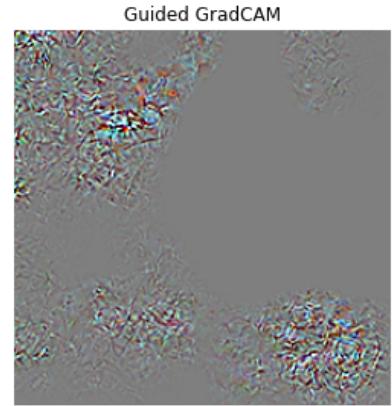
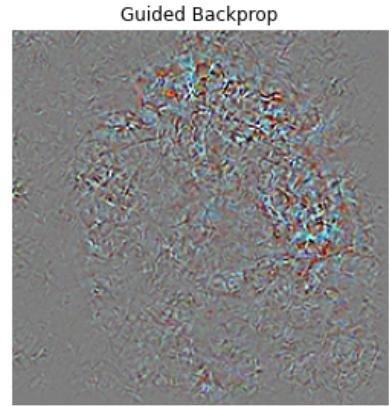
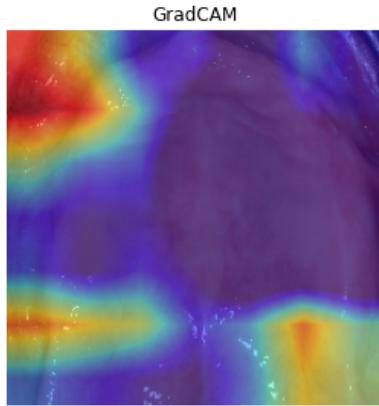
```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
```

```
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t)
```

Model prediction:

pmd	(1)	with probability 0.653
normal	(0)	with probability 0.347

Explanation for 'pmd'

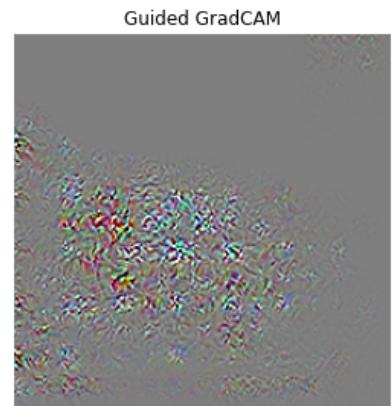
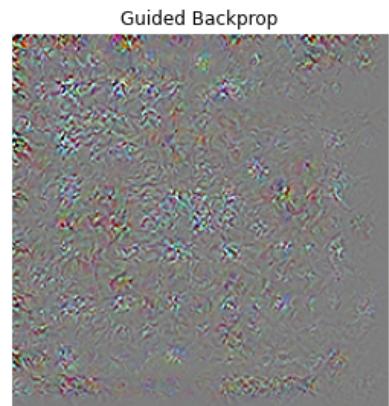
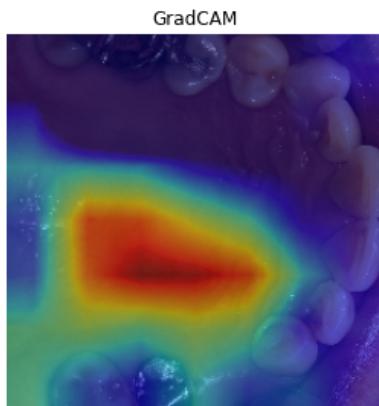


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/0.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t)
```

Model prediction:

normal	(0)	with probability 0.984
pmd	(1)	with probability 0.016

Explanation for 'normal'

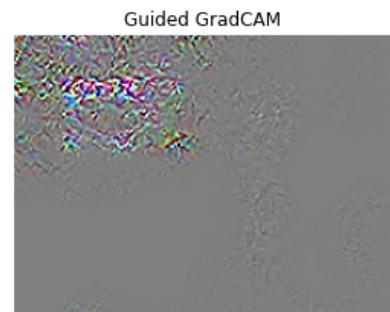
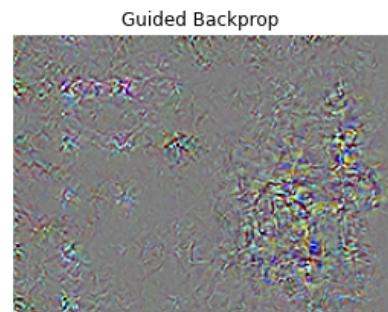
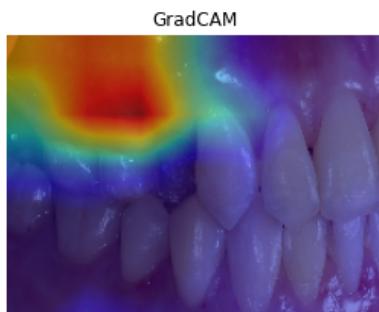


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/0.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t)
```

Model prediction:

pmd	(1)	with probability 0.515
normal	(0)	with probability 0.485

Explanation for 'pmd'

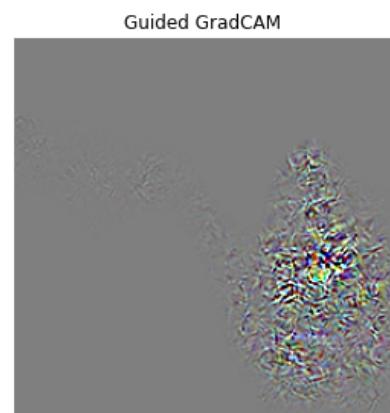
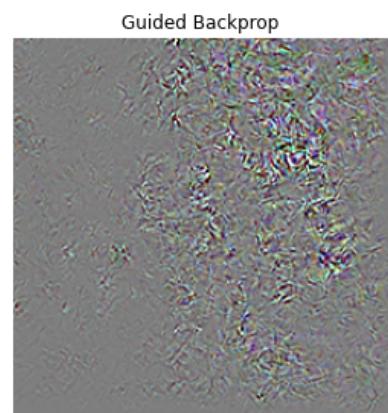
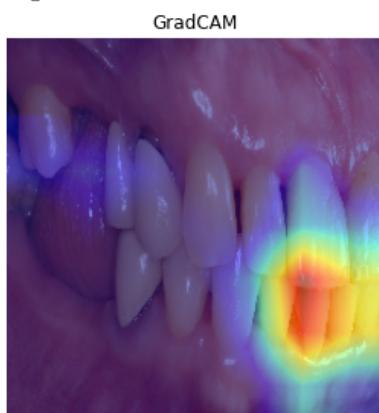


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

normal	(0)	with probability 0.785
pmd	(1)	with probability 0.215

Explanation for 'normal'



```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

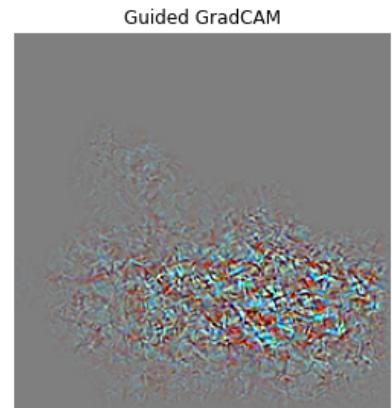
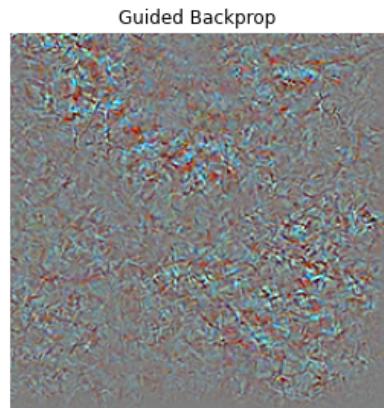
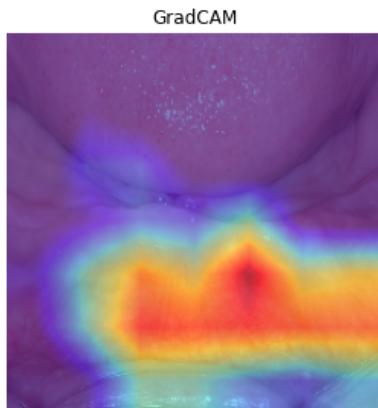
normal	(0)	with probability 0.987
pmd	(1)	with probability 0.013

```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/nor'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.839
normal	(0)	with probability 0.161

Explanation for 'pmd'

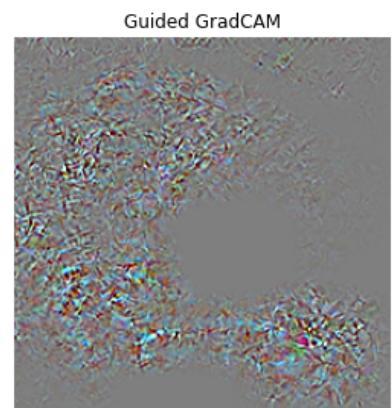
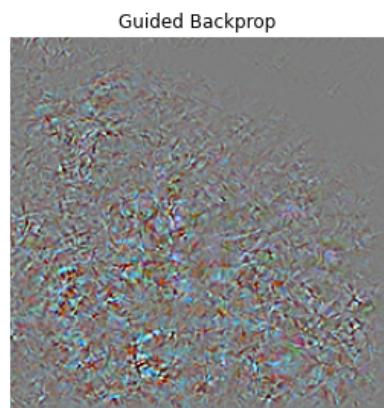
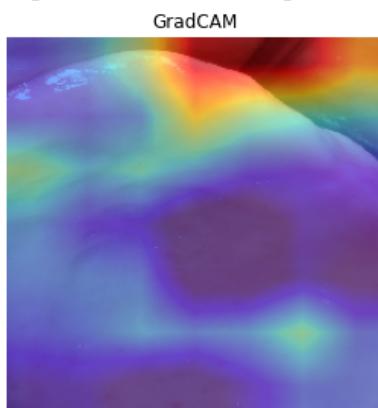


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/nor'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.969
normal	(0)	with probability 0.031

Explanation for 'pmd'

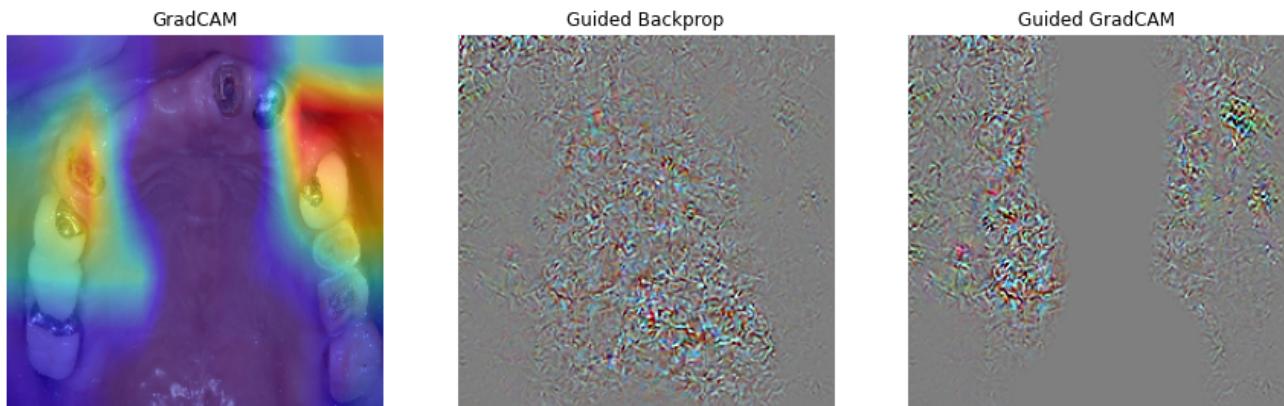


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/nor'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.842
normal	(0)	with probability 0.158

Explanation for 'pmd'

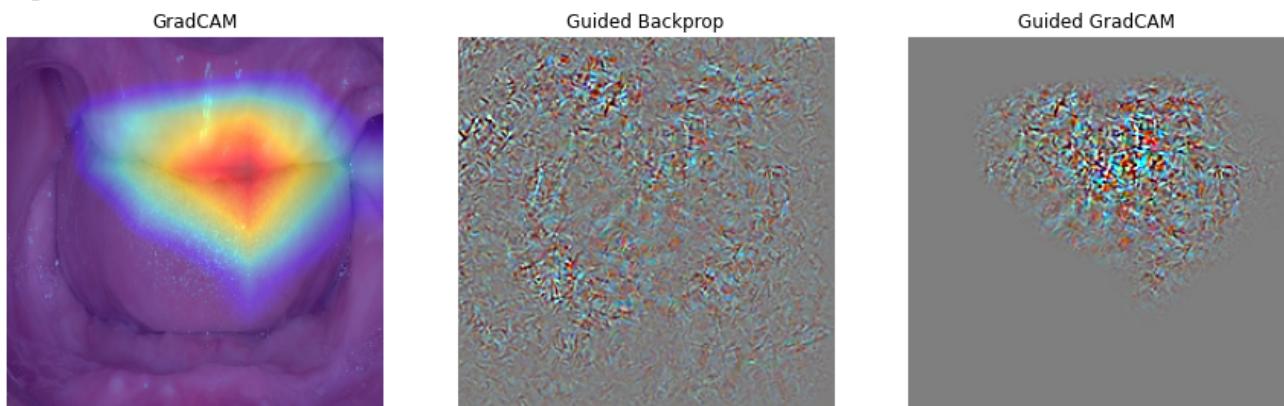


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

normal	(0)	with probability 0.985
pmd	(1)	with probability 0.015

Explanation for 'normal'

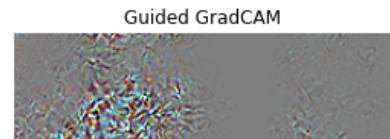
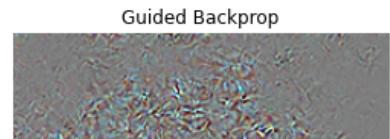


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.948
normal	(0)	with probability 0.052

Explanation for 'pmd'

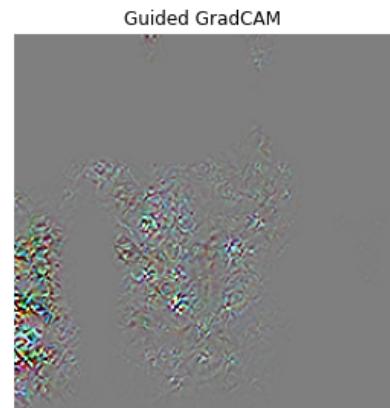
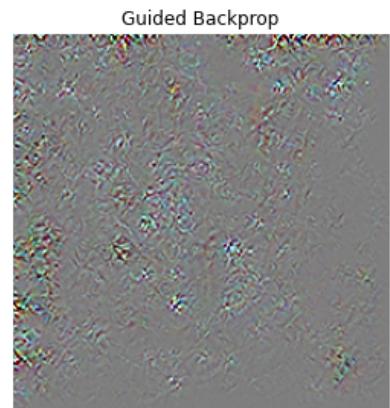
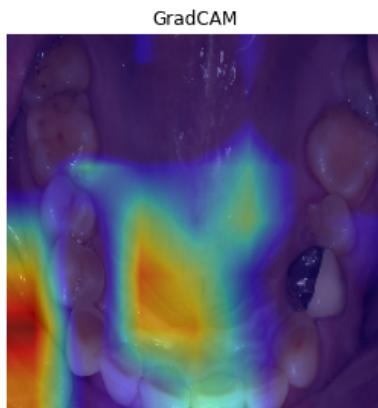


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

normal	(0)	with probability 0.758
pmd	(1)	with probability 0.242

Explanation for 'normal'

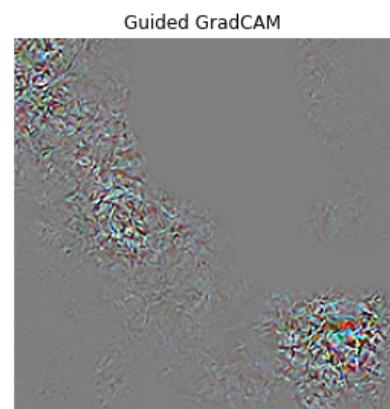
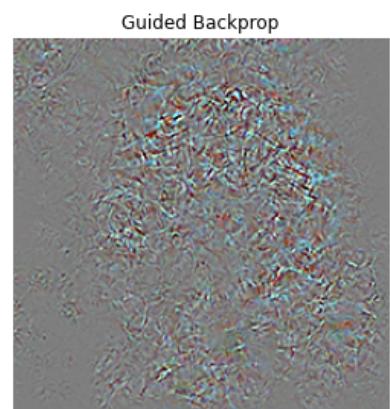
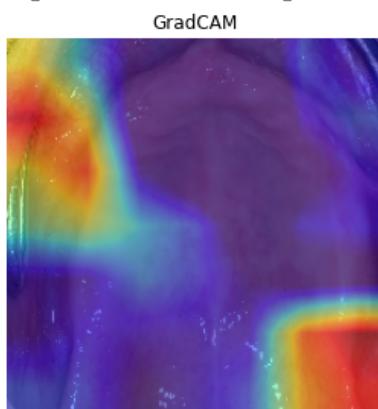


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.561
normal	(0)	with probability 0.439

Explanation for 'pmd'



```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
https://colab.research.google.com/drive/1aDWmNx7sFBZo02hr2s9RV48vutt-Cyla#printMode=true
```

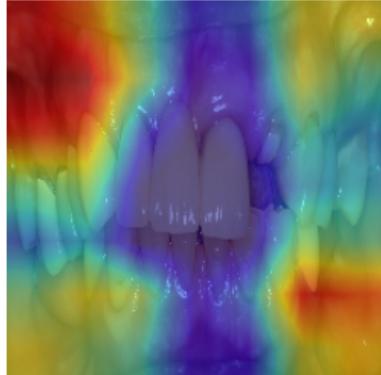
```
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t)
```

### Model prediction:

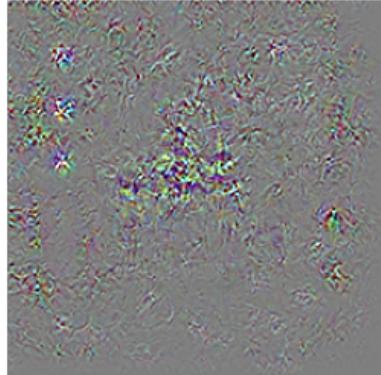
pmd (1) with probability 0.969  
normal (0) with probability 0.031

## Explanation for 'pmd'

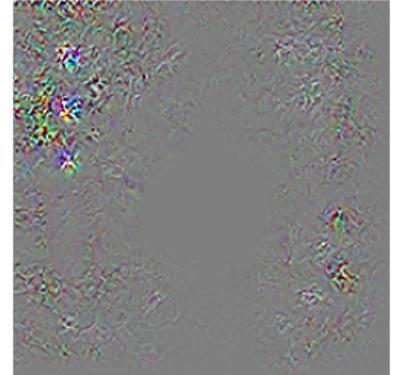
GradCAM



## Guided Backprop



### Guided GradCAM

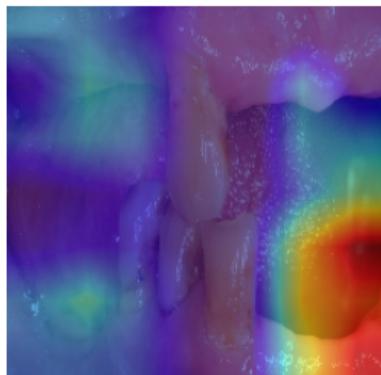


### Model prediction:

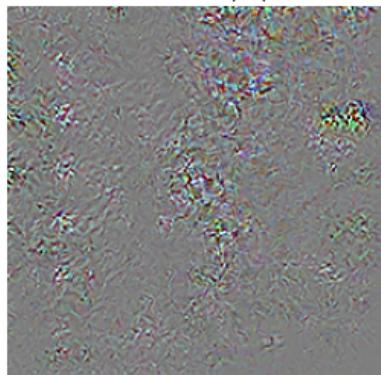
pmd (1) with probability 0.735  
normal (0) with probability 0.265

## Explanation for 'pmd'

## GradCAM



## Guided Backprop



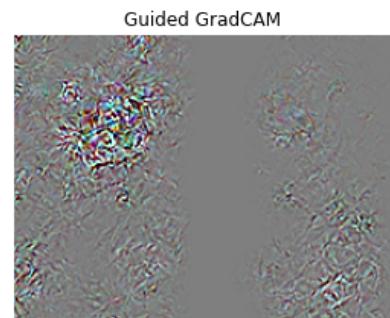
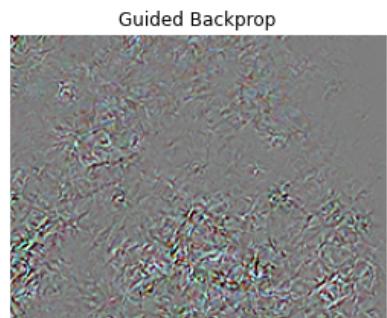
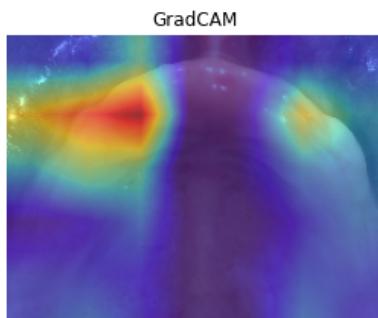
Guided GradCAM



Model prediction:

pmd	(1)	with probability 0.688
normal	(0)	with probability 0.312

Explanation for 'pmd'

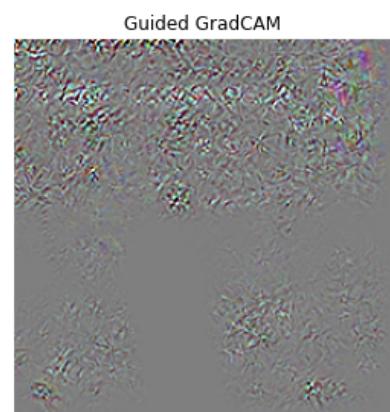
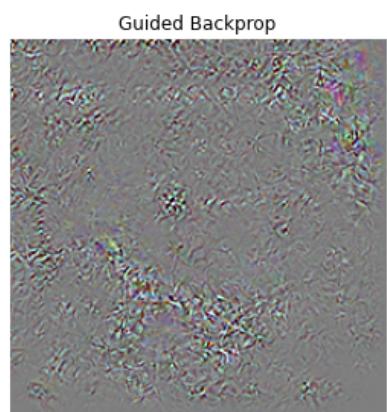
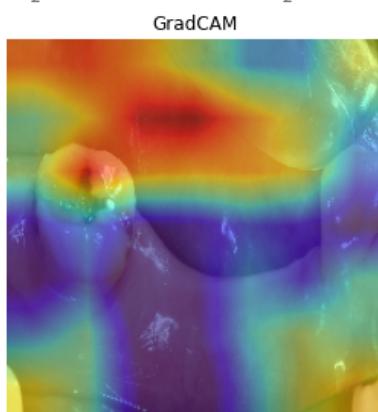


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal_00000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.849
normal	(0)	with probability 0.151

Explanation for 'pmd'



```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal_00000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

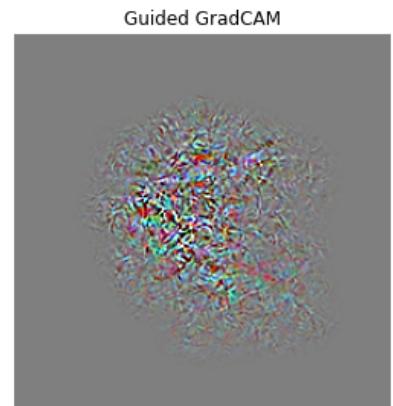
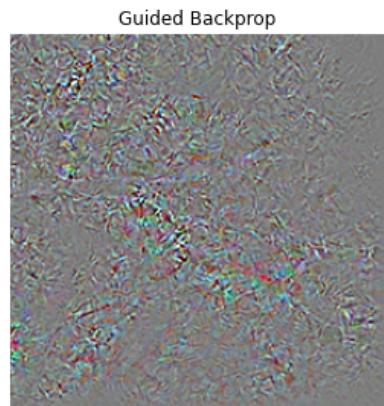
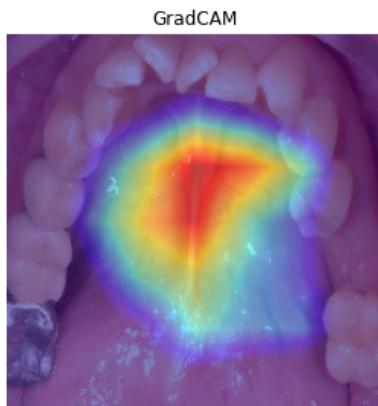
pmd	(1)	with probability 0.942
normal	(0)	with probability 0.058

```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

normal	(0)	with probability 0.995
pmd	(1)	with probability 0.005

Explanation for 'normal'

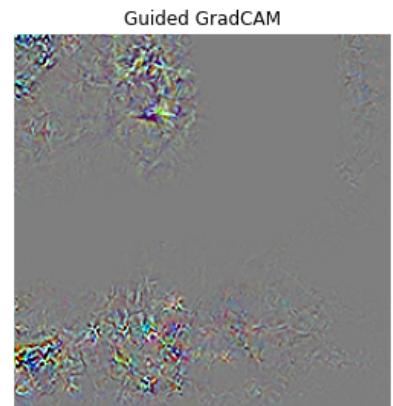
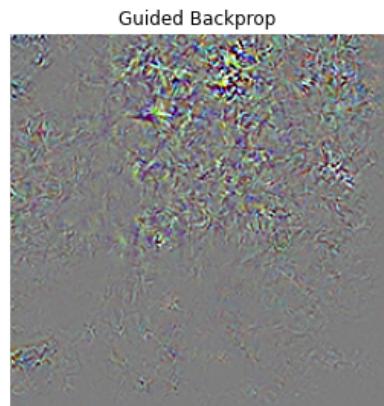
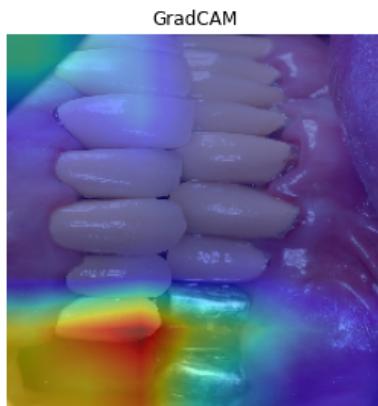


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.979
normal	(0)	with probability 0.021

Explanation for 'pmd'

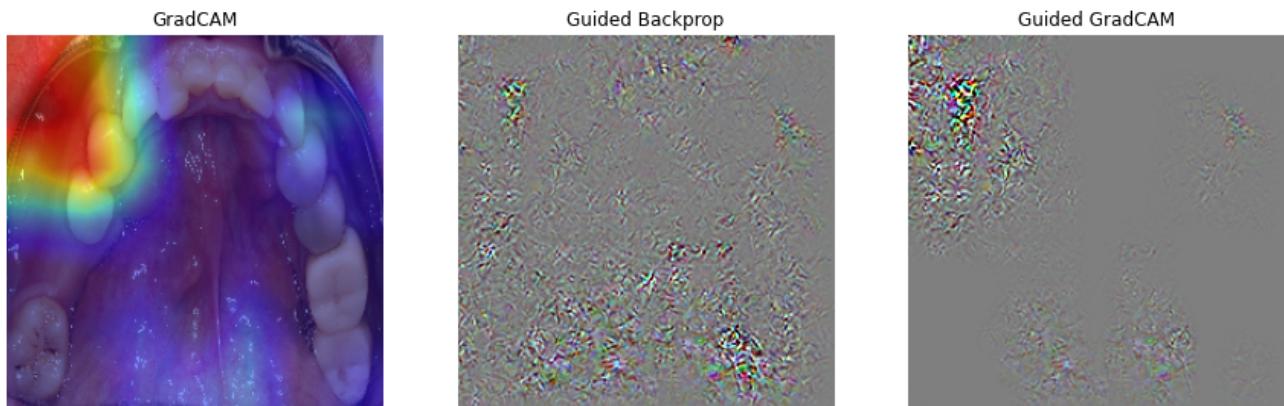


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.732
normal	(0)	with probability 0.268

Explanation for 'pmd'

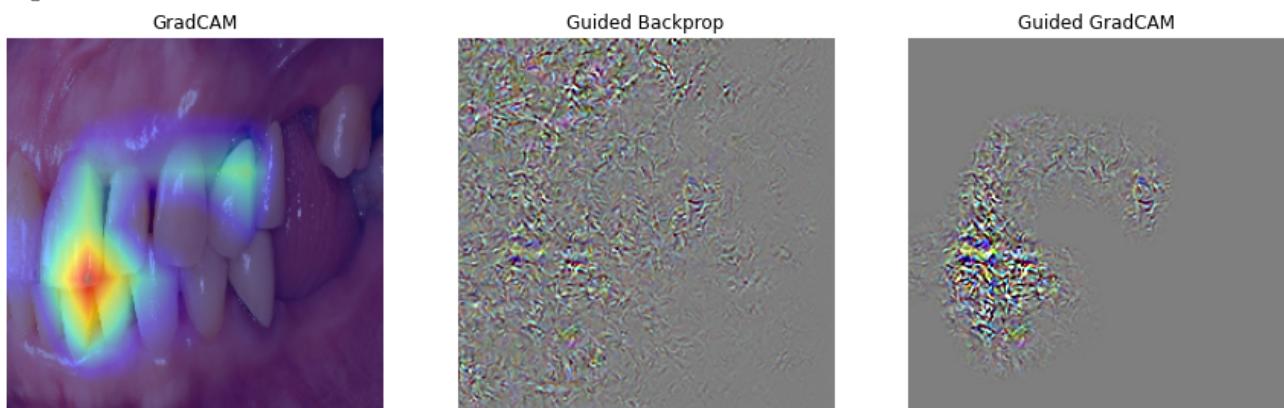


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

normal	(0)	with probability 0.834
pmd	(1)	with probability 0.166

Explanation for 'normal'

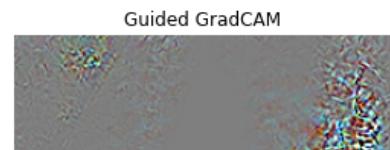
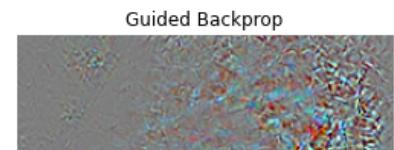


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.529
normal	(0)	with probability 0.471

Explanation for 'pmd'

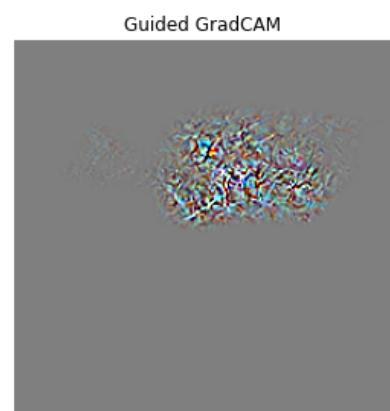
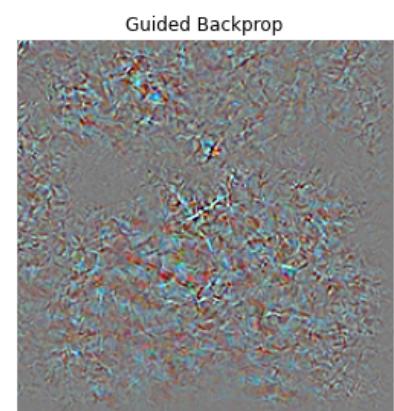
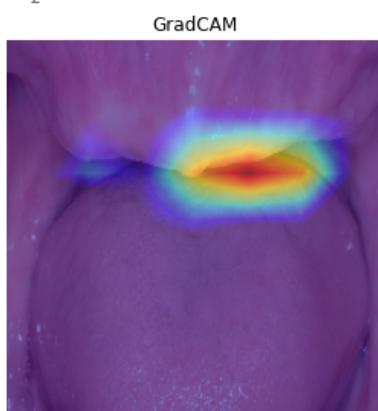


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal_00000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

normal	(0)	with probability 0.715
pmd	(1)	with probability 0.285

Explanation for 'normal'

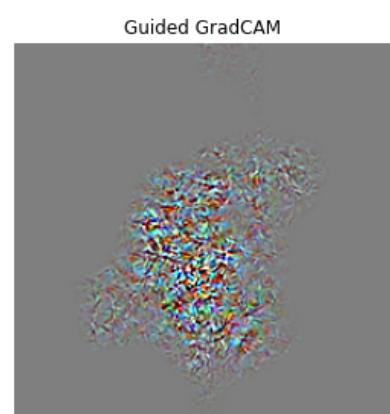
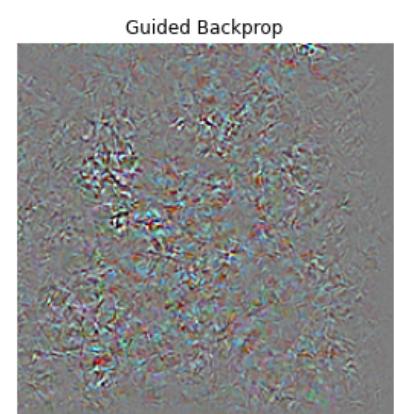
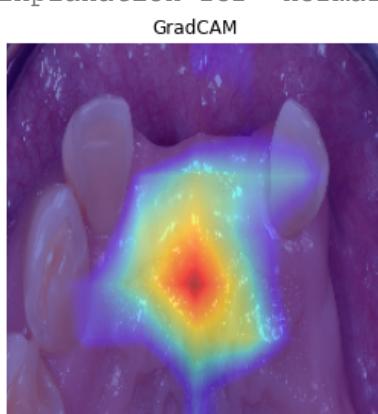


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal_00001.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

normal	(0)	with probability 0.776
pmd	(1)	with probability 0.224

Explanation for 'normal'

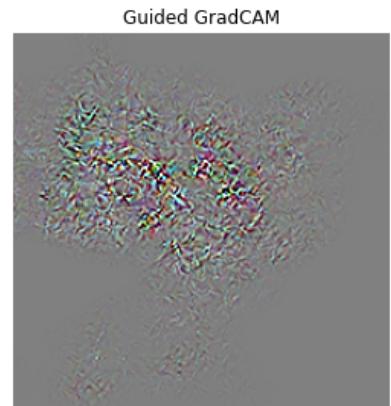
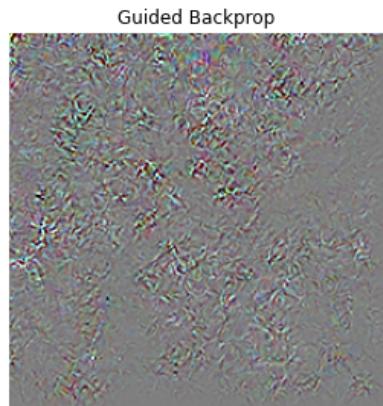
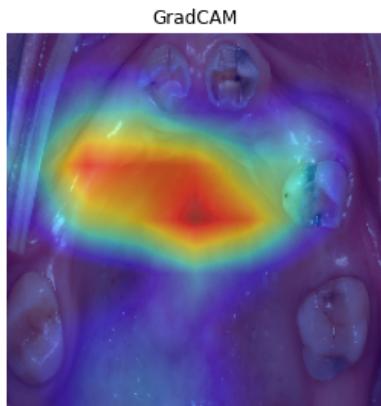


```
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.894
normal	(0)	with probability 0.106

Explanation for 'pmd'

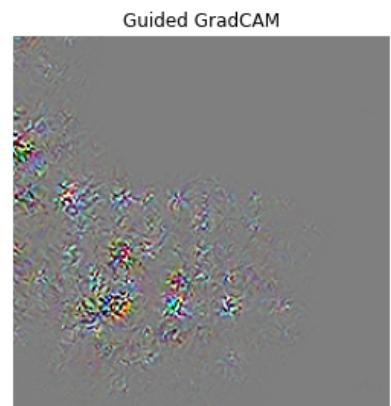
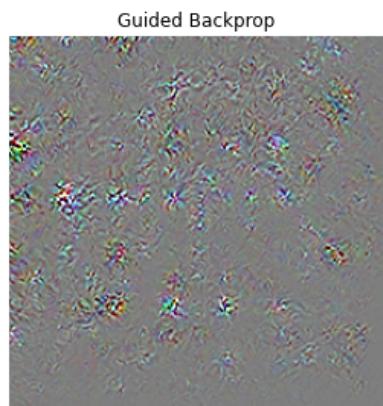
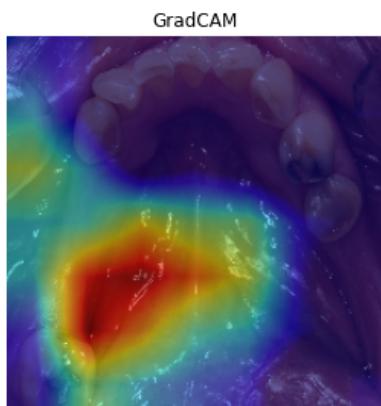


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/0.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

normal	(0)	with probability 0.976
pmd	(1)	with probability 0.024

Explanation for 'normal'

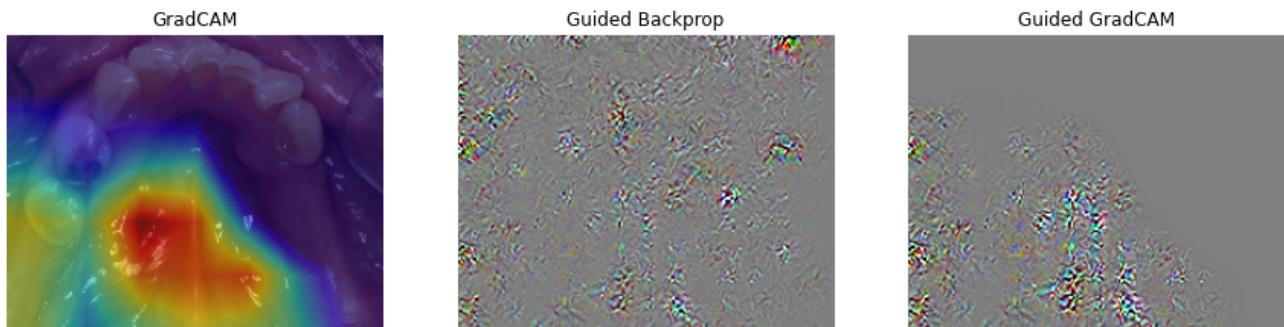


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/0.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

normal	(0)	with probability 0.962
pmd	(1)	with probability 0.038

Explanation for 'normal'

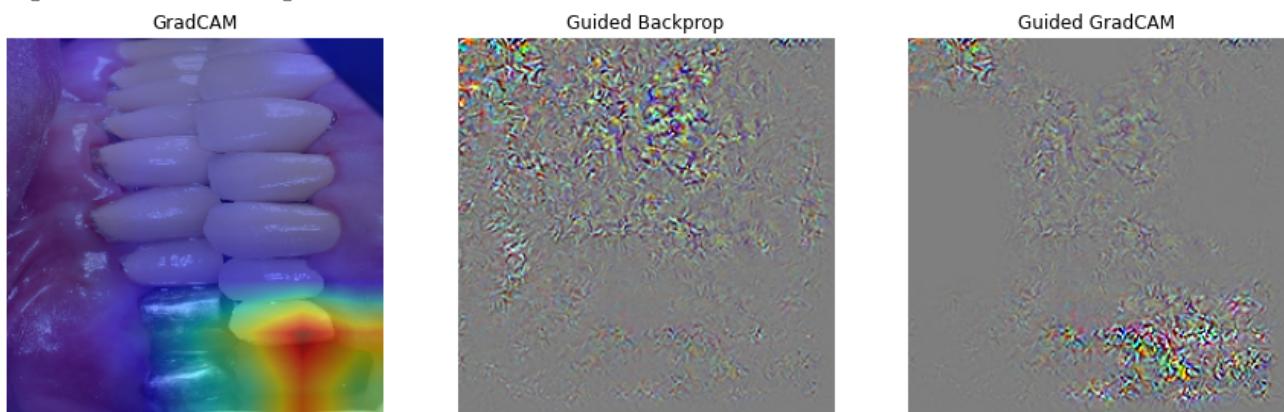


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.979
normal	(0)	with probability 0.021

Explanation for 'pmd'



```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

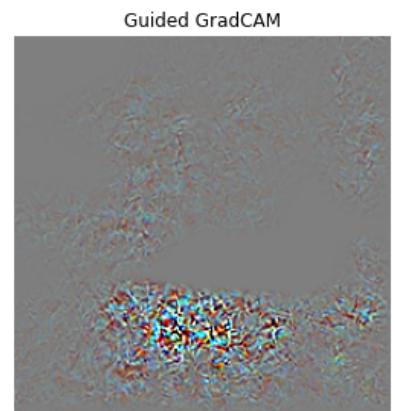
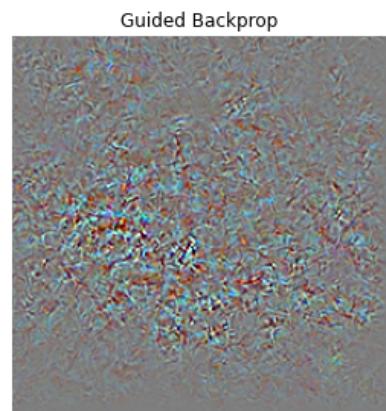
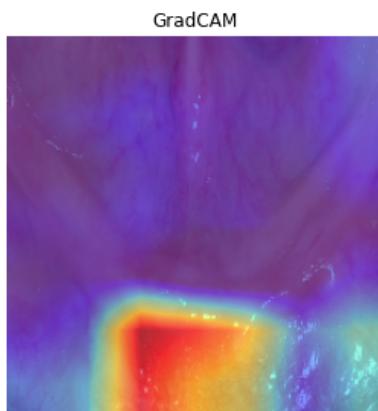
pmd	(1)	with probability 0.891
normal	(0)	with probability 0.109

```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.836
normal	(0)	with probability 0.164

Explanation for 'pmd'

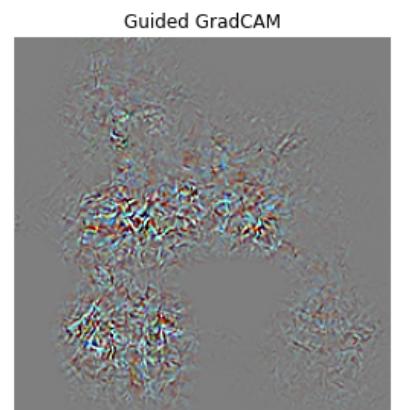
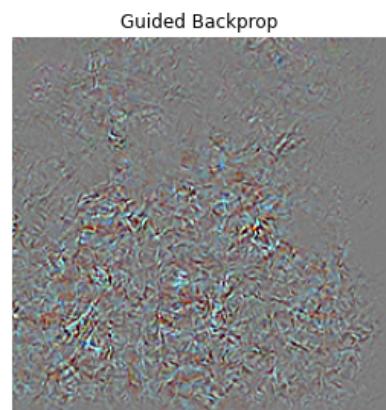
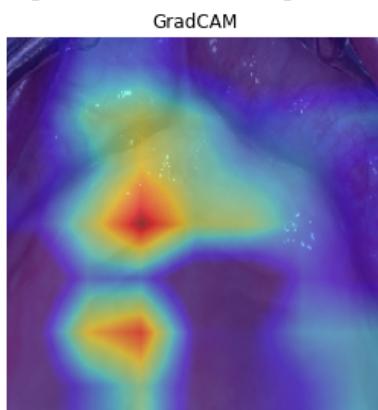


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.694
normal	(0)	with probability 0.306

Explanation for 'pmd'

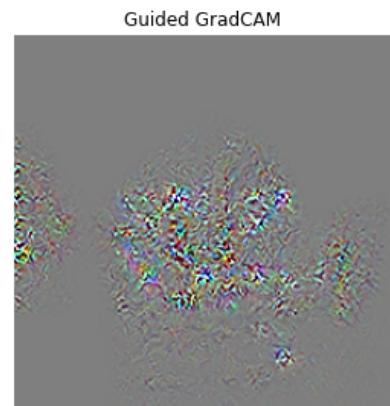
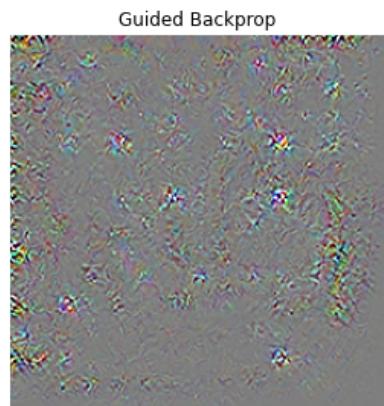
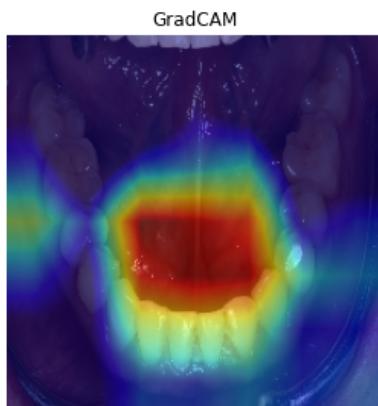


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

normal	(0)	with probability 0.927
pmd	(1)	with probability 0.073

Explanation for 'normal'

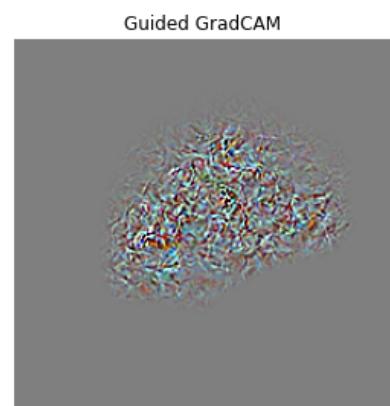
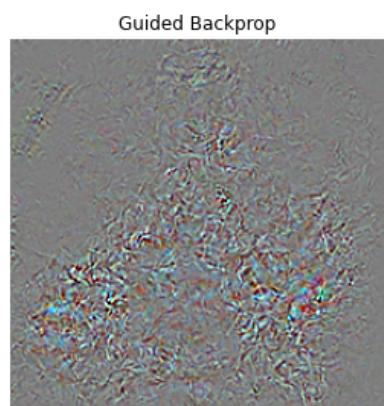
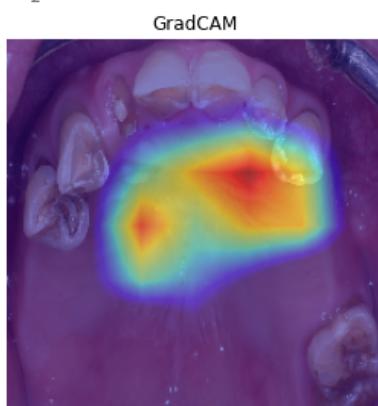


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

normal	(0)	with probability 0.861
pmd	(1)	with probability 0.139

Explanation for 'normal'



```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

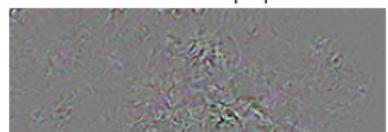
pmd (1) with probability 0.872  
 normal (0) with probability 0.128

## Explanation for 'pmd'

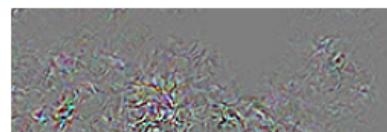
GradCAM



## Guided Backprop



## Guided GradCAM

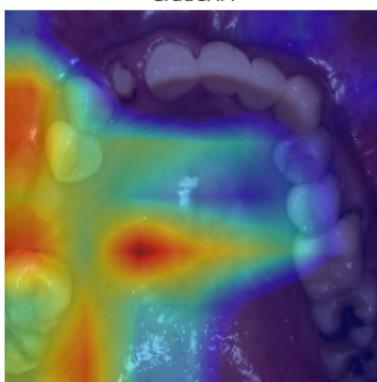


Model prediction:

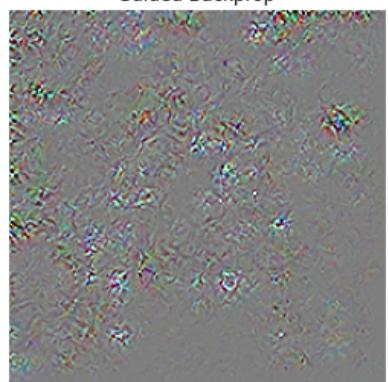
normal (0) with probability 0.787  
 pmd (1) with probability 0.213

## Explanation for 'normal'

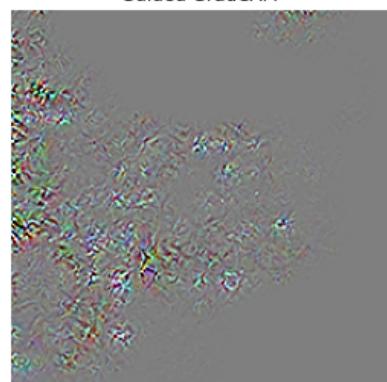
GradCAM



## Guided Backprop



Guided GradCAM



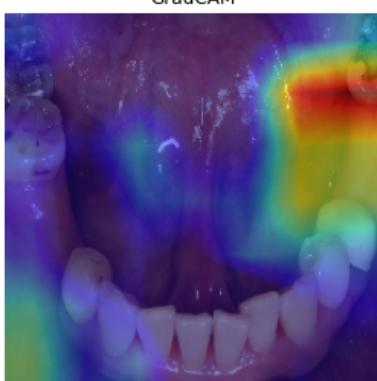
```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/norm'
2 qradcam, qb, quided_qradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

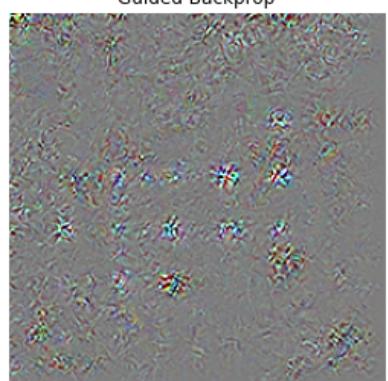
pmd (1) with probability 0.594  
normal (0) with probability 0.406

## Explanation for 'pmd'

GradCAM



Guided Backprop



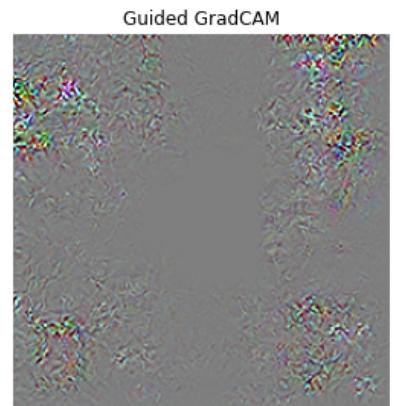
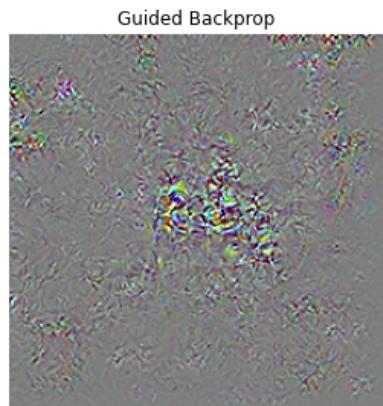
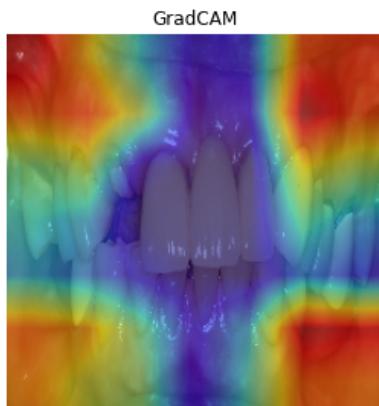
Guided GradCAM



```

1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/nor
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
Model prediction:
    pmd      (1)      with probability 0.980
    normal   (0)      with probability 0.020
Explanation for 'pmd'

```



```

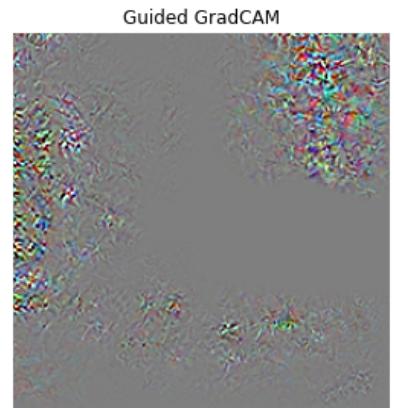
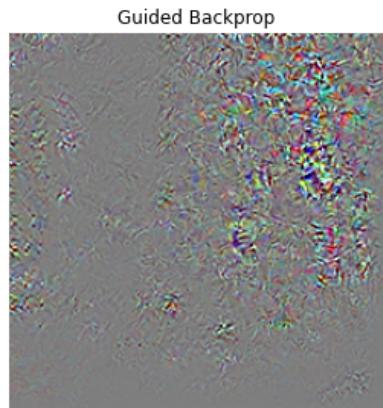
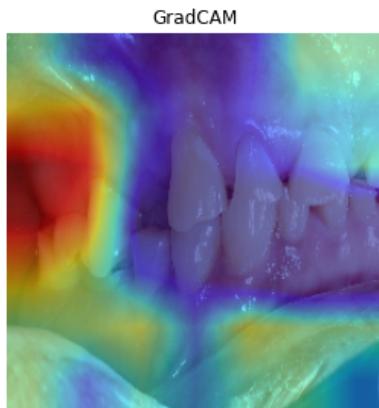
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/nor
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t

```

Model prediction:

pmd	(1)	with probability 0.807
normal	(0)	with probability 0.193

Explanation for 'pmd'



```

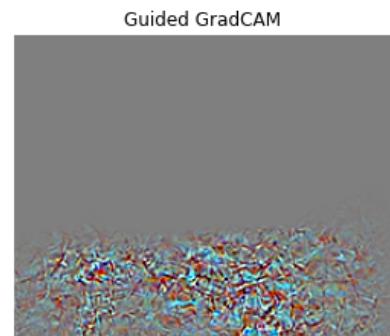
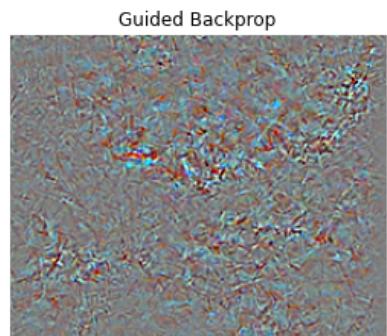
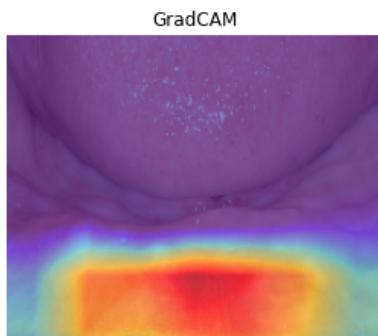
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/nor
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t

```

Model prediction:

pmd	(1)	with probability 0.840
normal	(0)	with probability 0.160

Explanation for 'pmd'

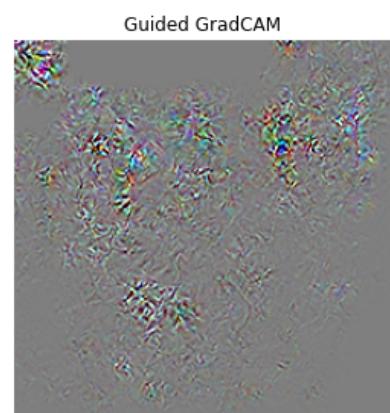
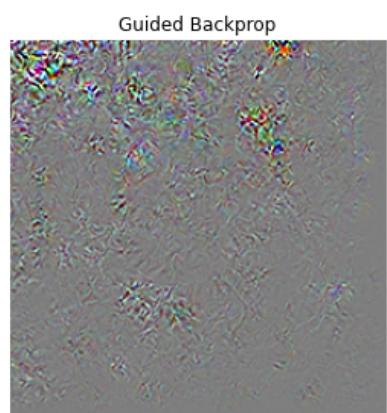
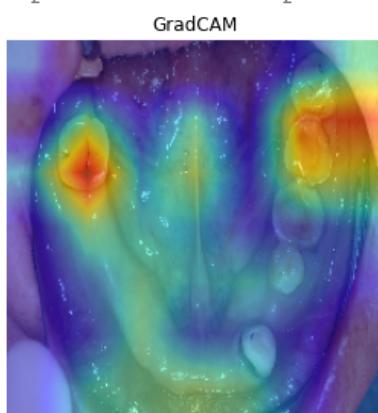


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.734
normal	(0)	with probability 0.266

Explanation for 'pmd'



```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

```
Model prediction:
```

normal	(0)	with probability 0.885
pmd	(1)	with probability 0.115

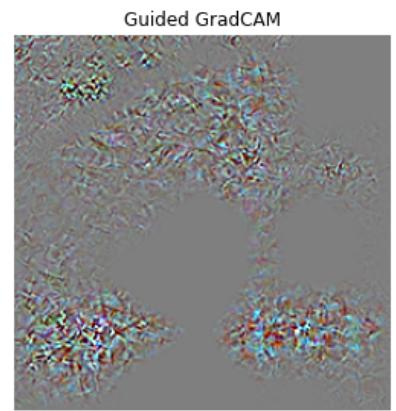
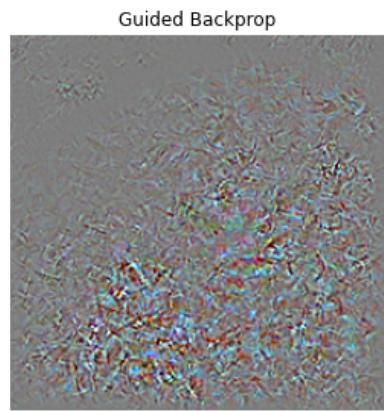
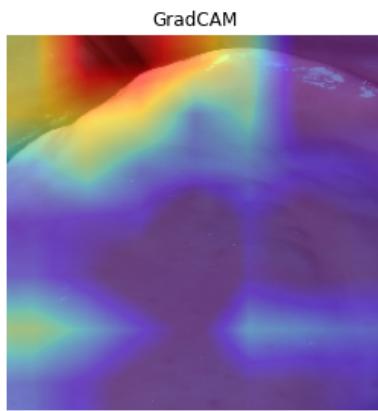
```
Explanation for 'normal'
```

```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

```
Model prediction:
```

pmd	(1)	with probability 0.987
normal	(0)	with probability 0.013

```
Explanation for 'pmd'
```

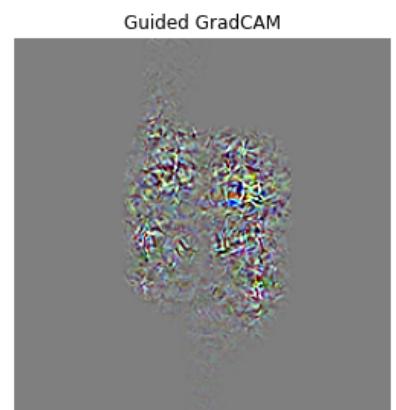
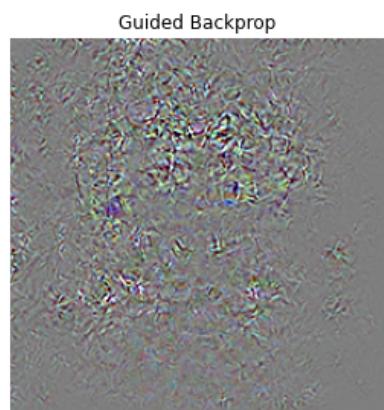
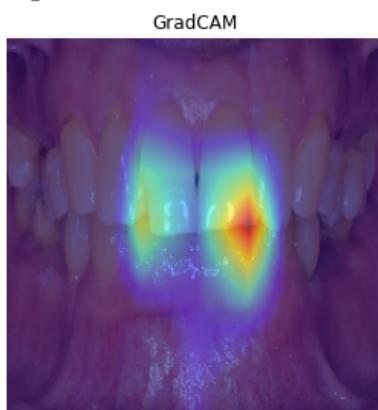


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

```
Model prediction:
```

normal	(0)	with probability 0.626
pmd	(1)	with probability 0.374

```
Explanation for 'normal'
```

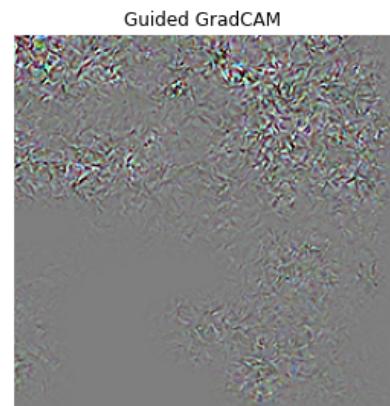
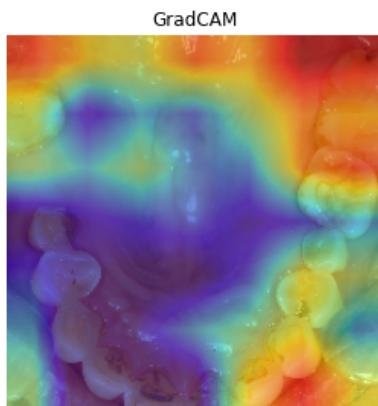


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.550
normal	(0)	with probability 0.450

Explanation for 'pmd'

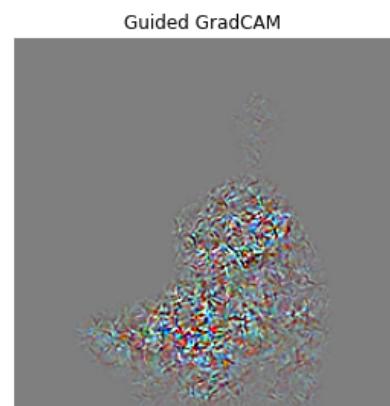
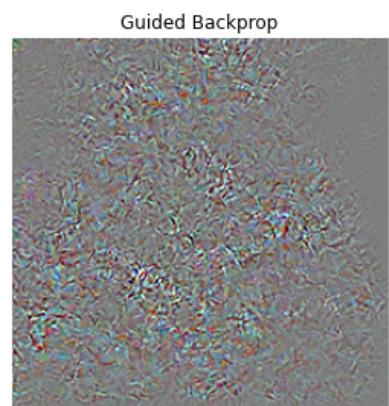
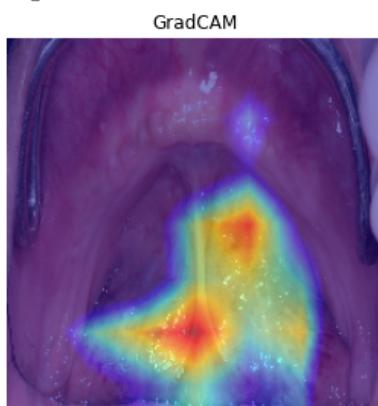


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

normal	(0)	with probability 0.851
pmd	(1)	with probability 0.149

Explanation for 'normal'

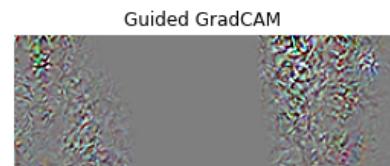
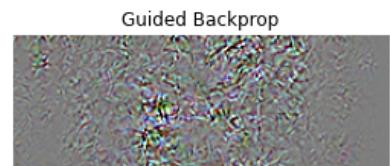


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.922
normal	(0)	with probability 0.078

Explanation for 'pmd'

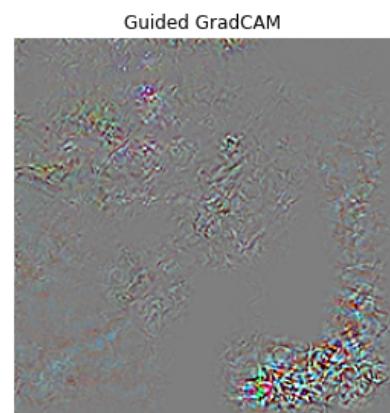
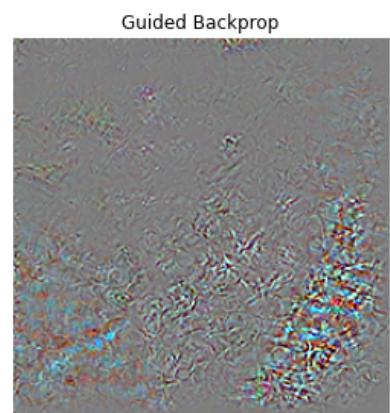
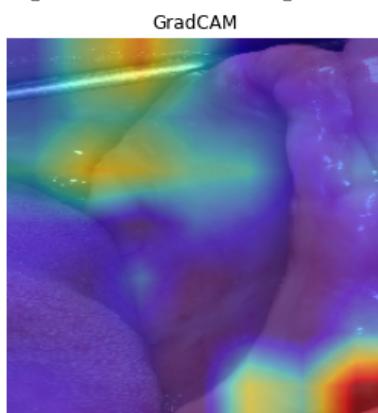


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.523
normal	(0)	with probability 0.477

Explanation for 'pmd'

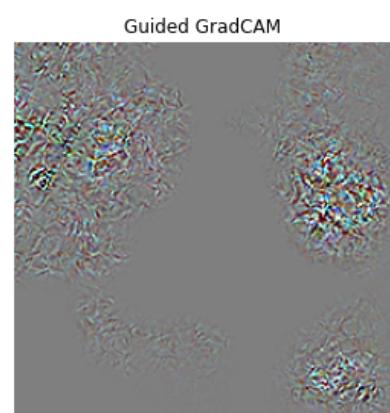
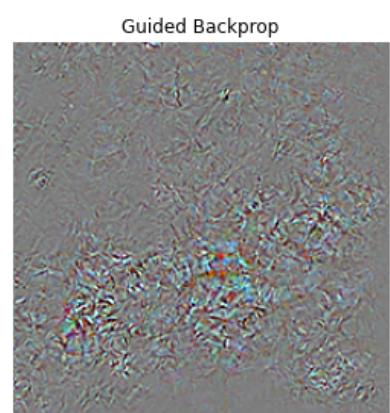
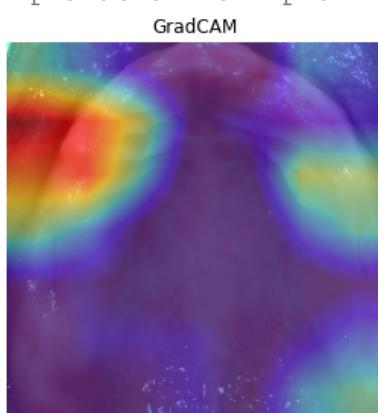


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/normal/00000000000000000000000000000000.jpg'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, test_img)
```

Model prediction:

pmd	(1)	with probability 0.827
normal	(0)	with probability 0.173

Explanation for 'pmd'

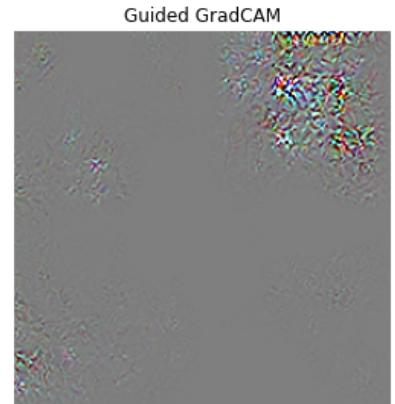
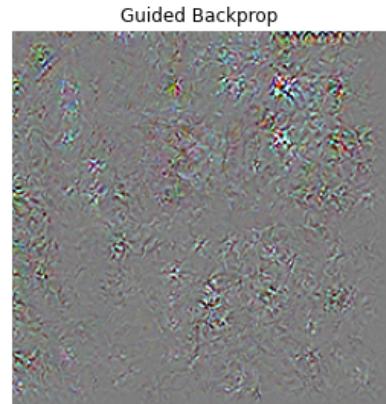
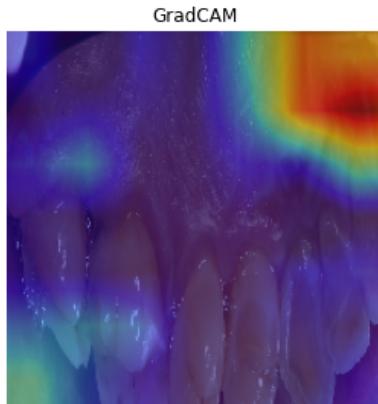


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/nor'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.691
normal	(0)	with probability 0.309

Explanation for 'pmd'

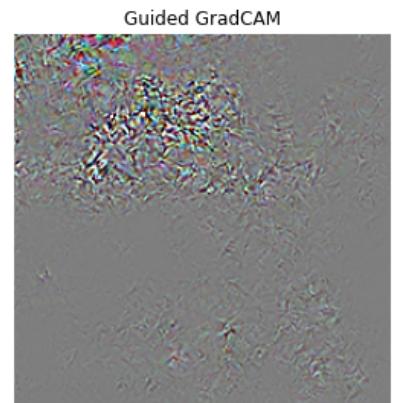
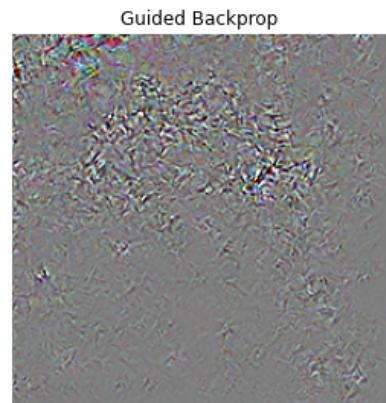
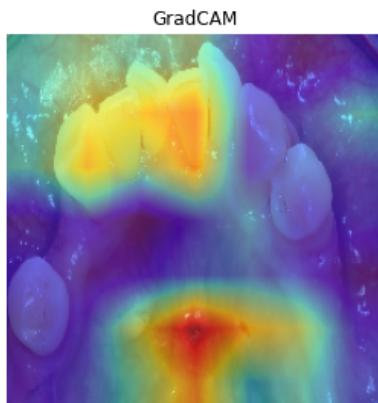


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/nor'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.549
normal	(0)	with probability 0.451

Explanation for 'pmd'



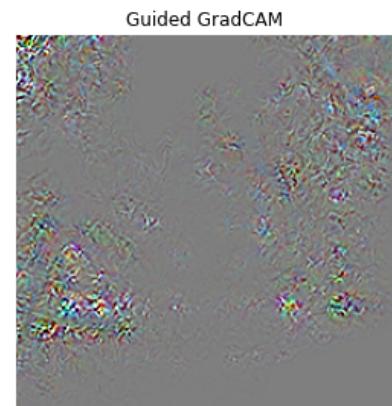
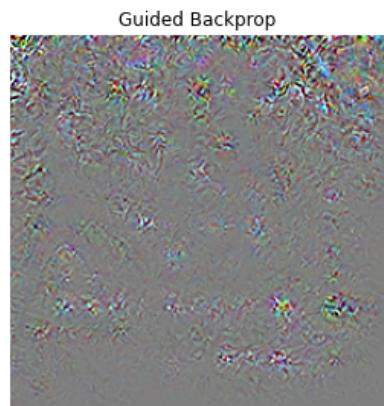
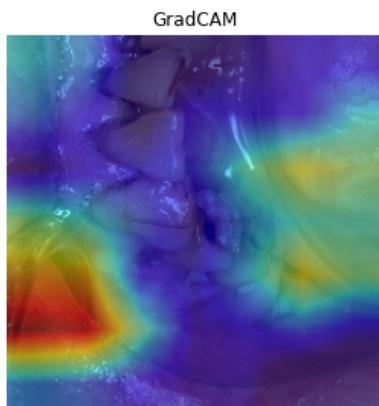
## ▼ PMD

```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.601
normal	(0)	with probability 0.399

Explanation for 'pmd'

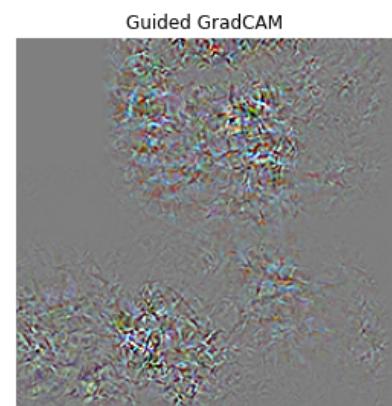
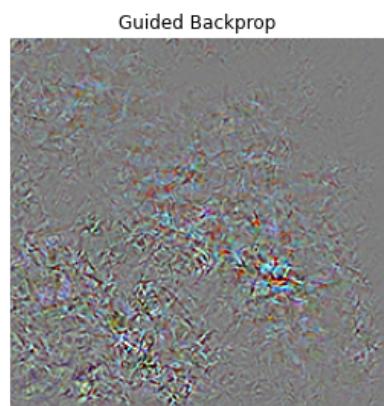
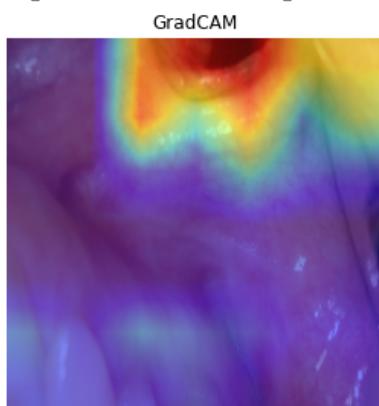


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.928
normal	(0)	with probability 0.072

Explanation for 'pmd'

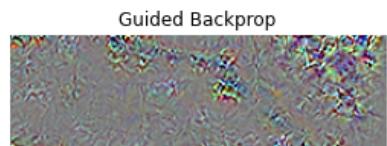
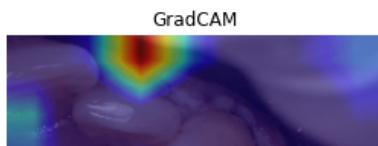


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

normal	(0)	with probability 0.623
pmd	(1)	with probability 0.377

Explanation for 'normal'

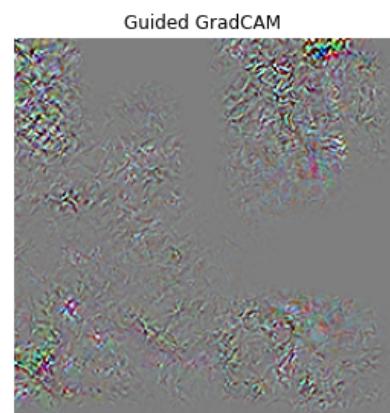
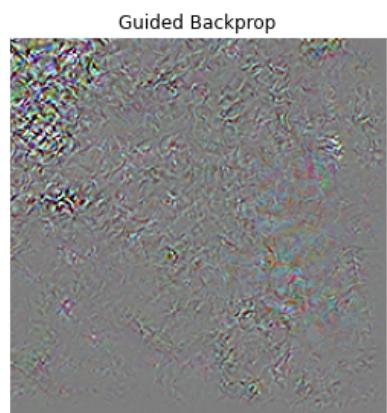
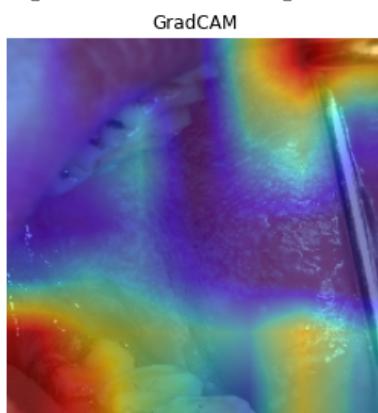


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.918
normal	(0)	with probability 0.082

Explanation for 'pmd'

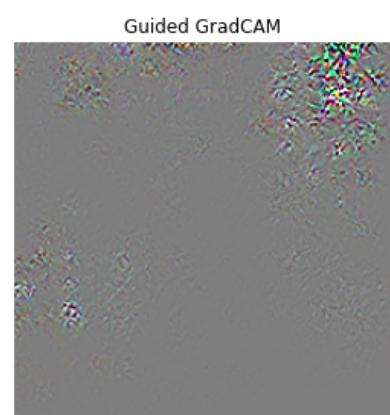
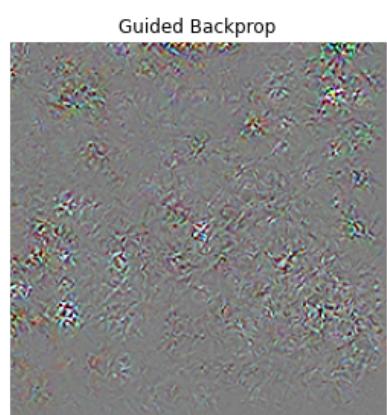
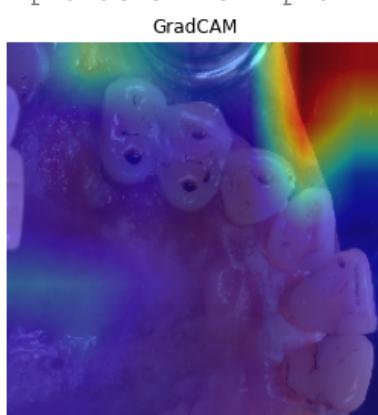


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.935
normal	(0)	with probability 0.065

Explanation for 'pmd'

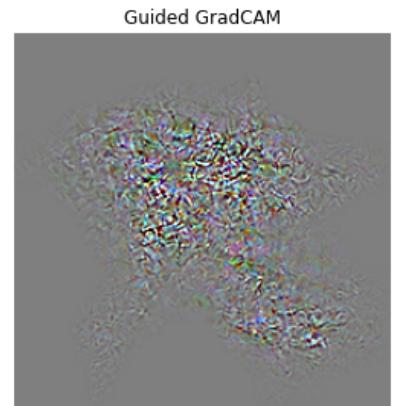
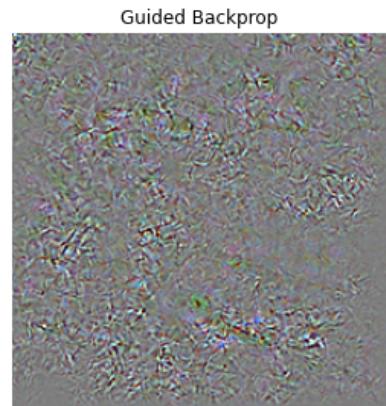
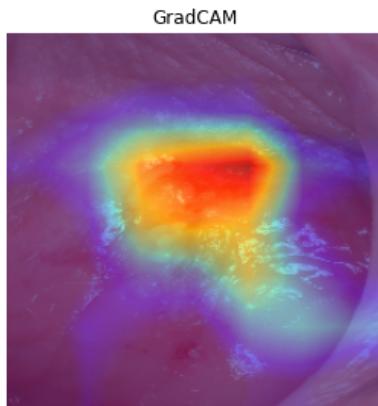


```
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.936
normal	(0)	with probability 0.064

Explanation for 'pmd'

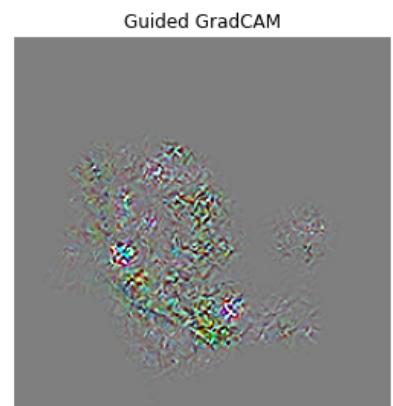
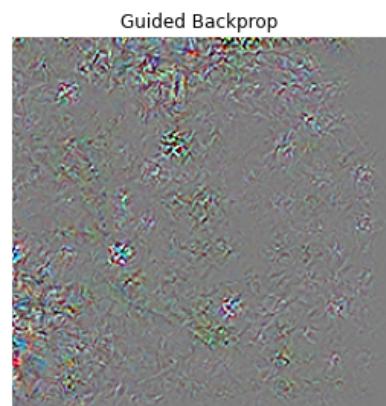
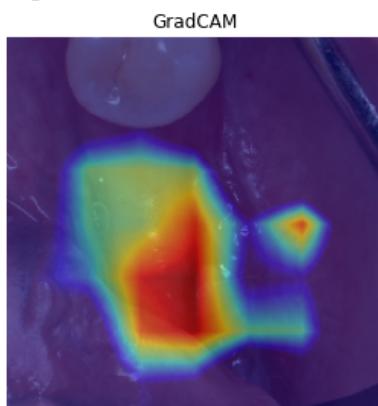


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

normal	(0)	with probability 0.627
pmd	(1)	with probability 0.373

Explanation for 'normal'

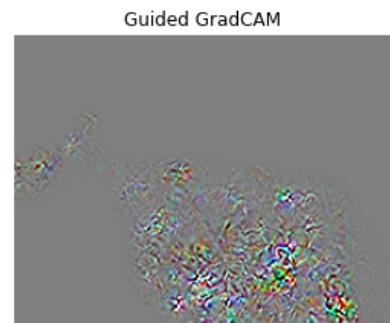
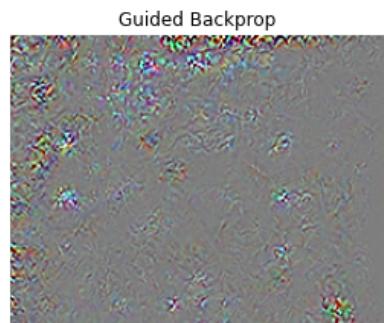
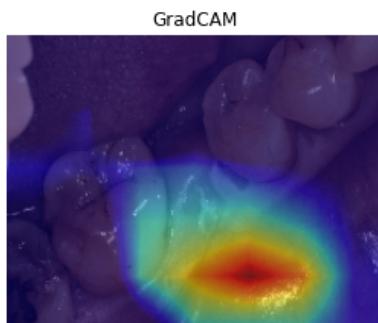


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

normal	(0)	with probability 0.668
pmd	(1)	with probability 0.332

Explanation for 'normal'

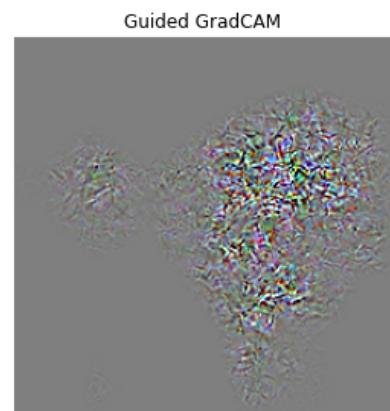
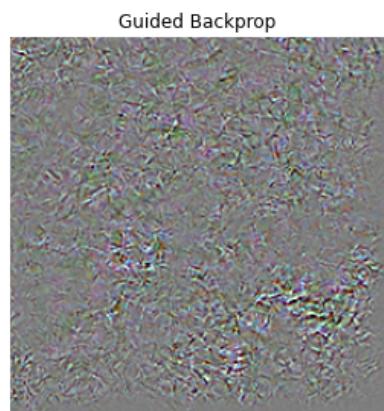
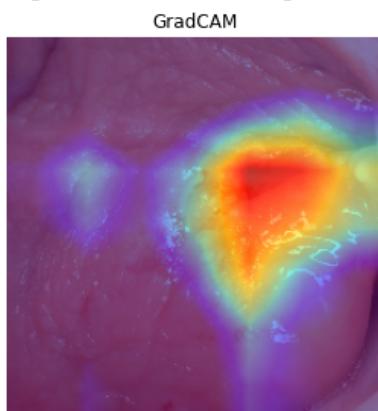


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.940
normal	(0)	with probability 0.060

Explanation for 'pmd'



```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

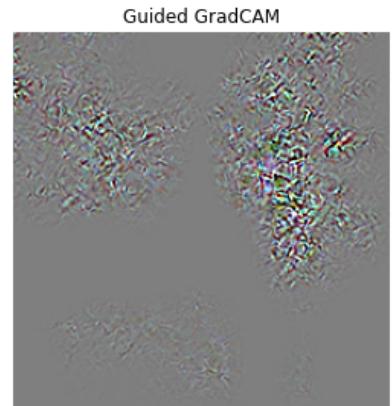
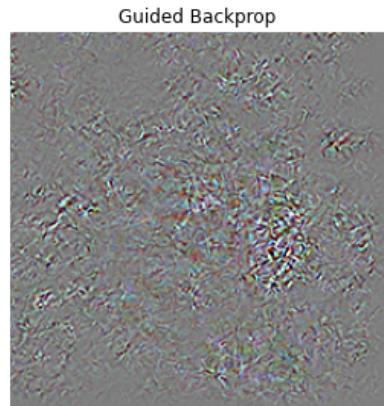
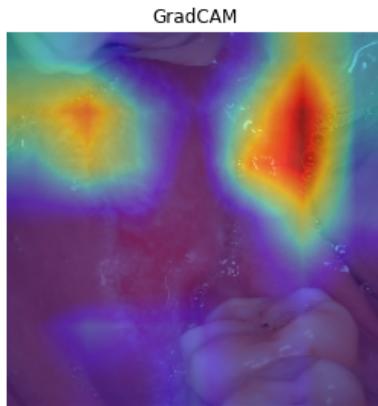
pmd	(1)	with probability 0.981
normal	(0)	with probability 0.019

```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.976
normal	(0)	with probability 0.024

Explanation for 'pmd'

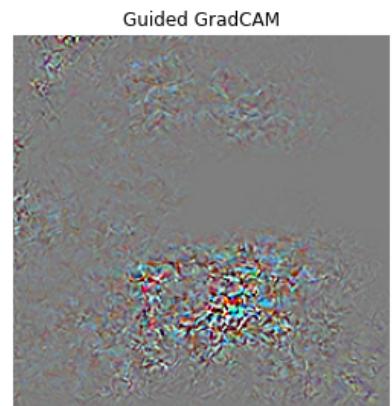
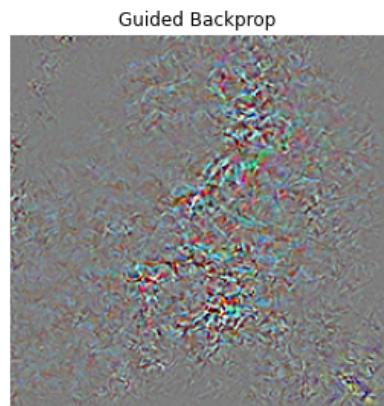
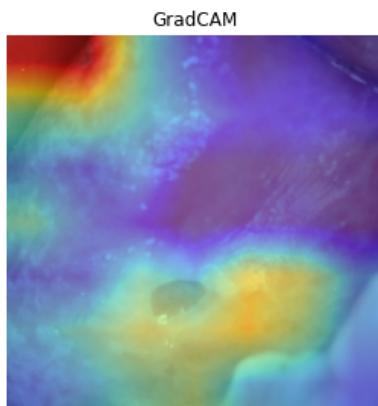


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.969
normal	(0)	with probability 0.031

Explanation for 'pmd'

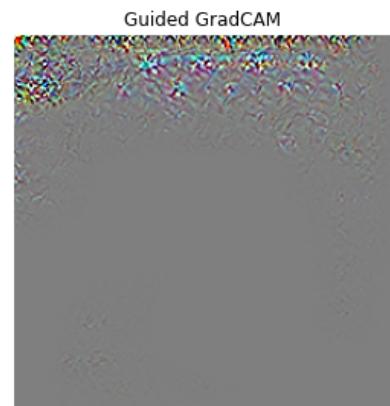
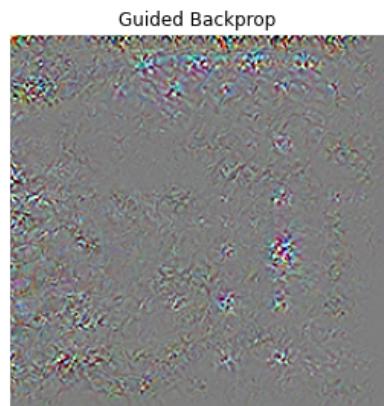
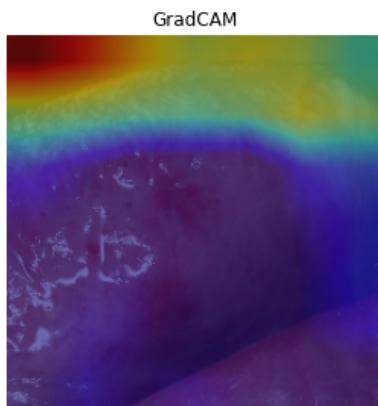


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.777
normal	(0)	with probability 0.223

Explanation for 'pmd'

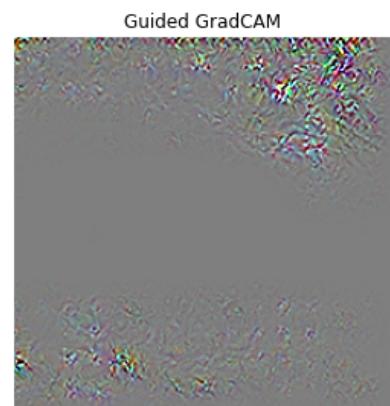
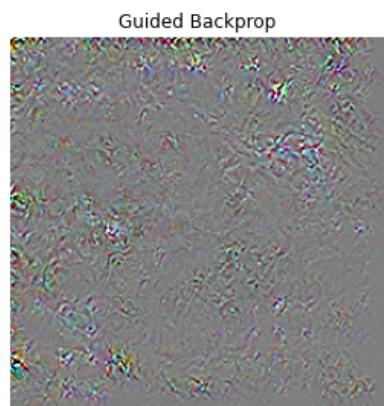
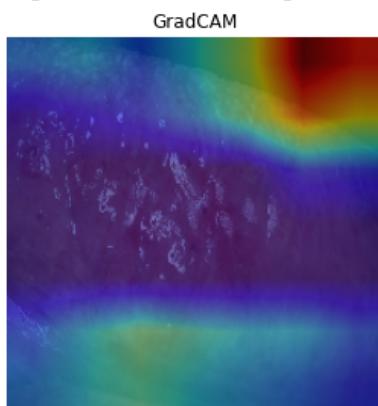


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.998
normal	(0)	with probability 0.002

Explanation for 'pmd'

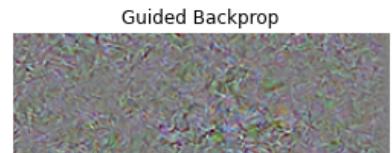
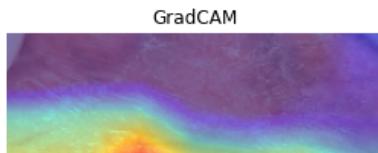


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.993
normal	(0)	with probability 0.007

Explanation for 'pmd'

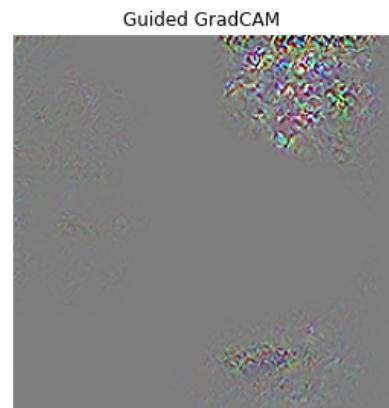
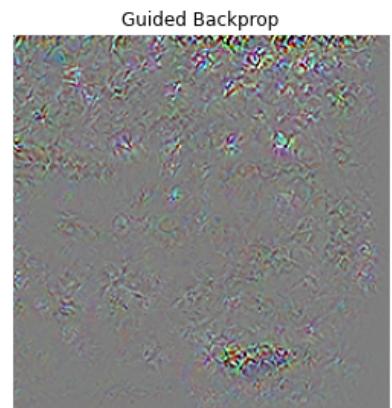
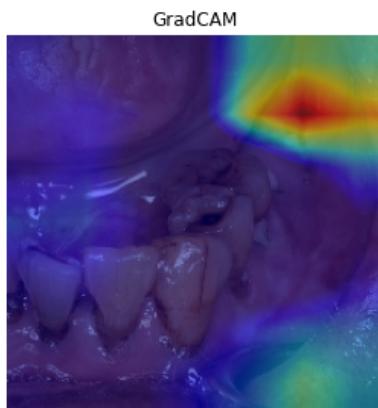


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.587
normal	(0)	with probability 0.413

Explanation for 'pmd'

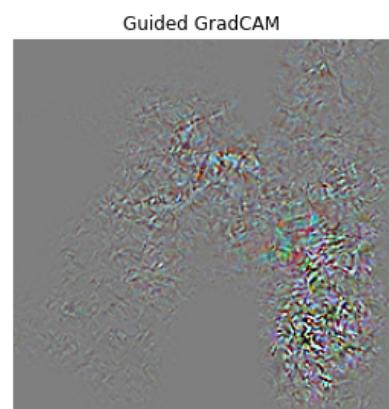
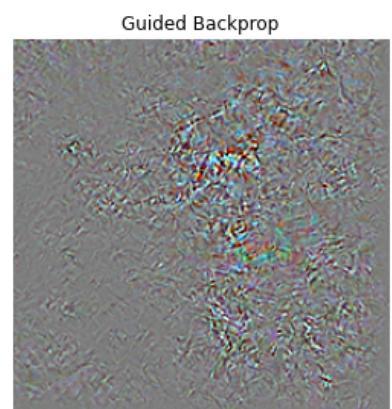
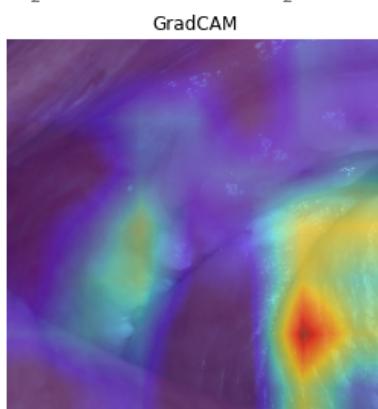


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.943
normal	(0)	with probability 0.057

Explanation for 'pmd'

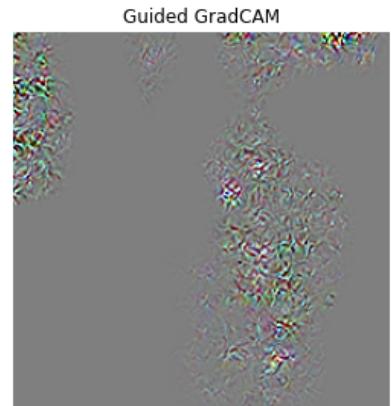
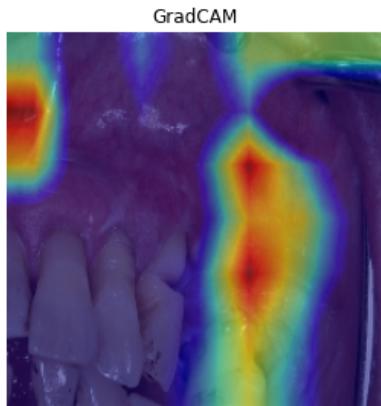


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

normal	(0)	with probability 0.706
pmd	(1)	with probability 0.294

Explanation for 'normal'

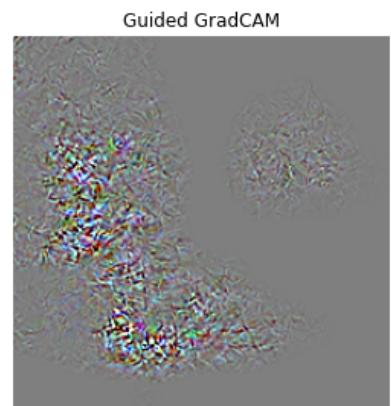
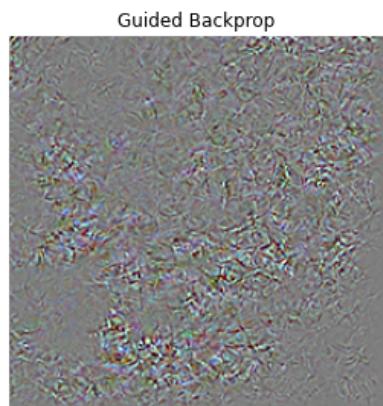
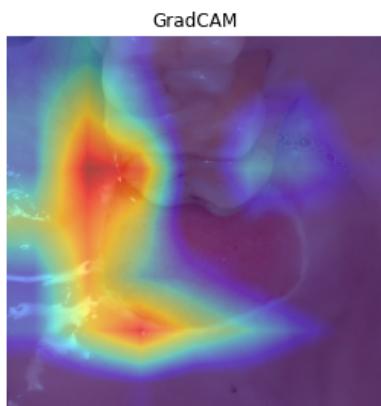


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.945
normal	(0)	with probability 0.055

Explanation for 'pmd'

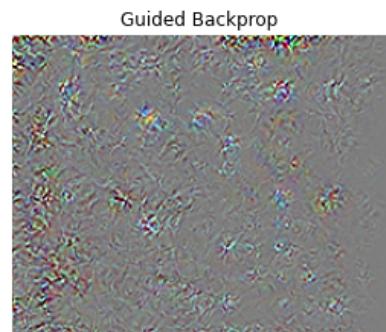
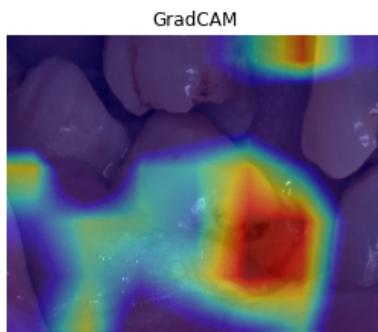


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

normal	(0)	with probability 0.557
pmd	(1)	with probability 0.443

Explanation for 'normal'

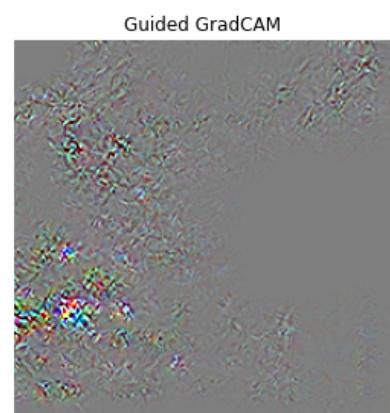
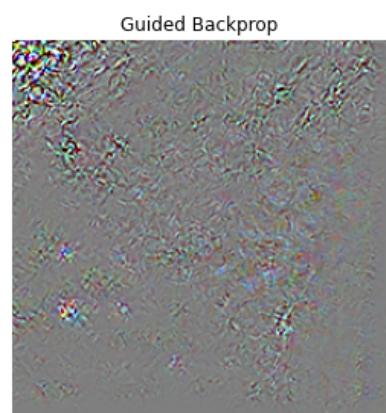
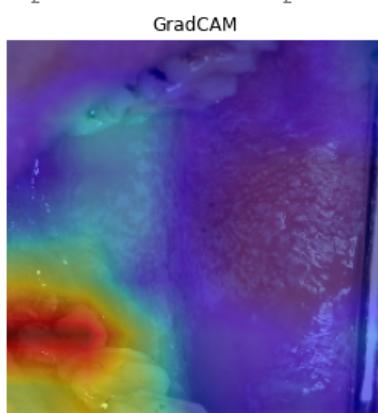


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.908
normal	(0)	with probability 0.092

Explanation for 'pmd'



```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.994
normal	(0)	with probability 0.006

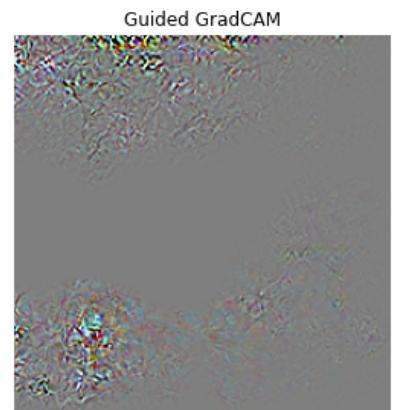
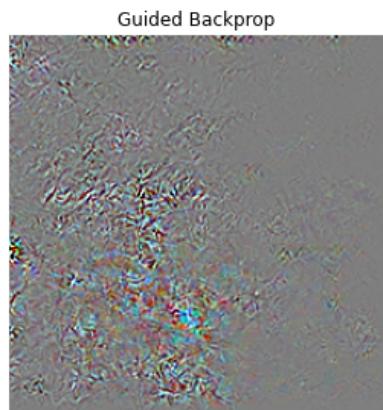
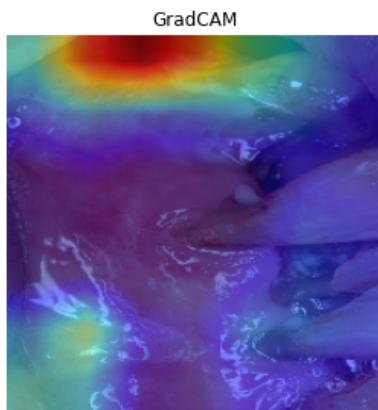
Explanation for 'pmd'

```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.973
normal	(0)	with probability 0.027

Explanation for 'pmd'

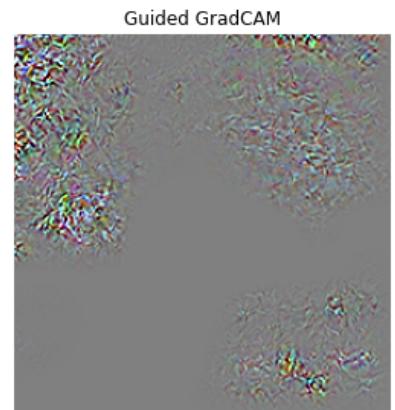
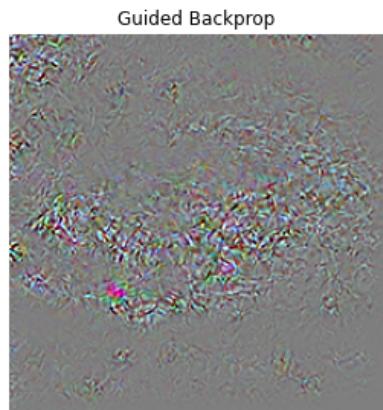
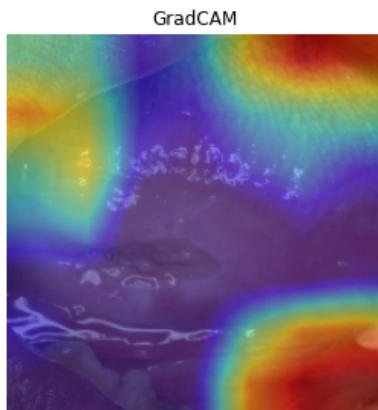


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.976
normal	(0)	with probability 0.024

Explanation for 'pmd'

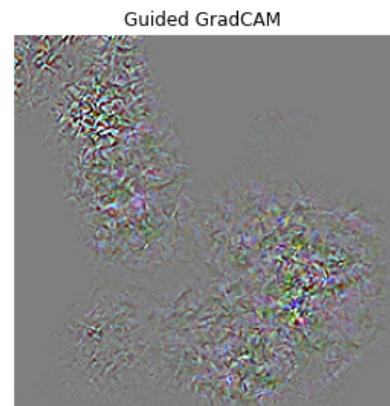
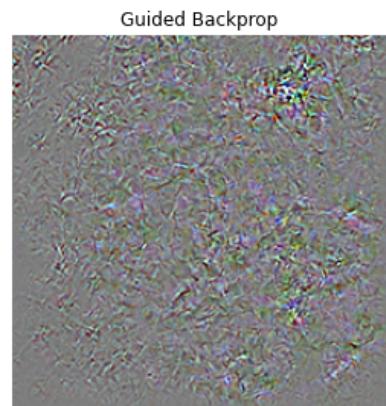
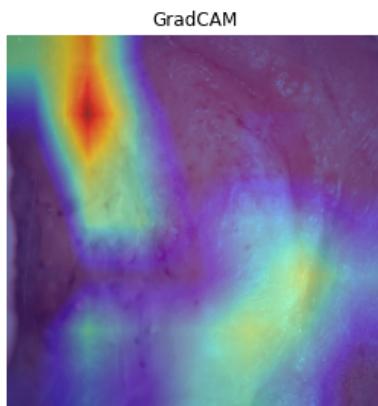


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.974
normal	(0)	with probability 0.026

Explanation for 'pmd'

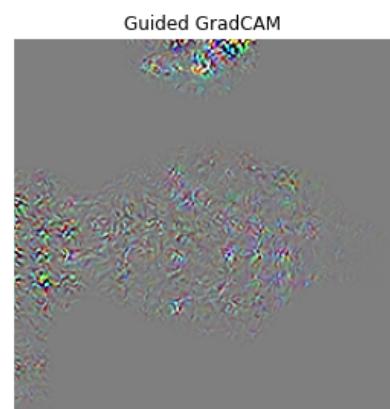
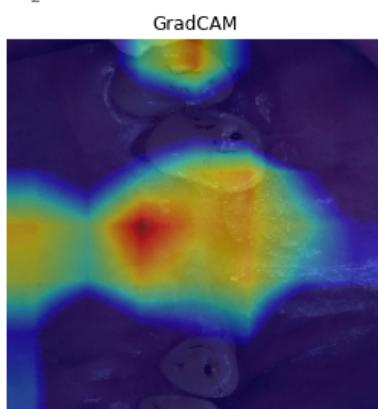


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

normal	(0)	with probability 0.860
pmd	(1)	with probability 0.140

Explanation for 'normal'

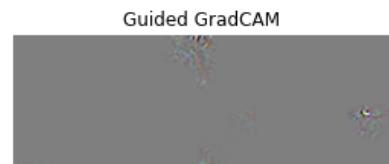
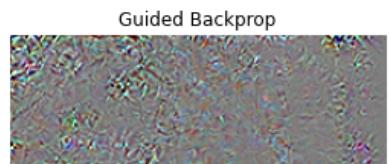


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

normal	(0)	with probability 0.672
pmd	(1)	with probability 0.328

Explanation for 'normal'

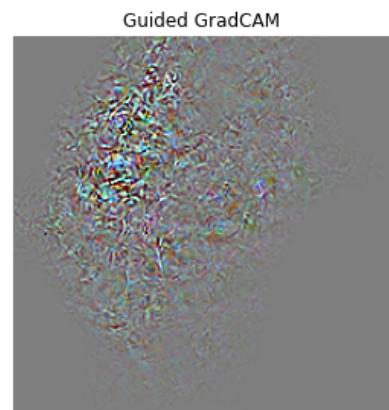
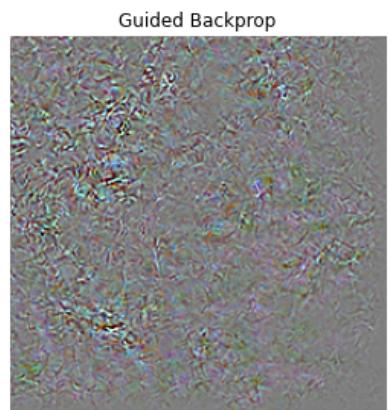
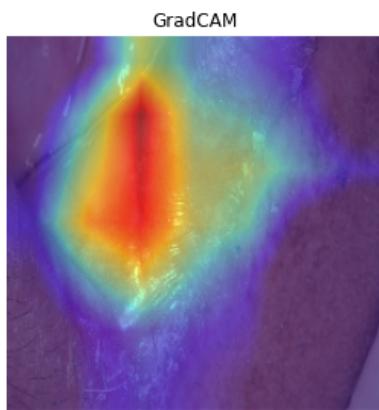


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.806
normal	(0)	with probability 0.194

Explanation for 'pmd'

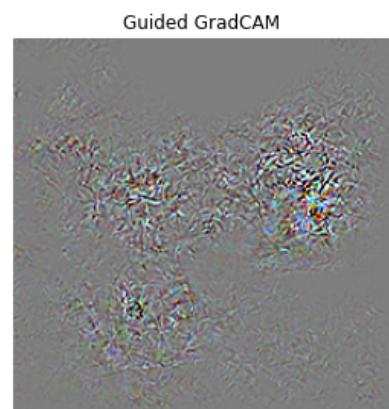
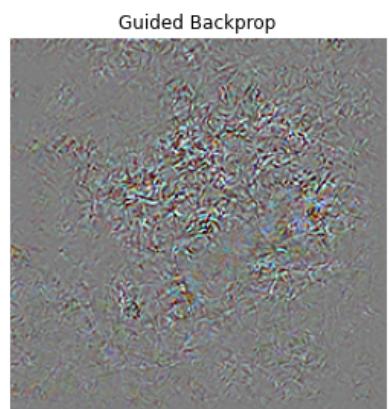
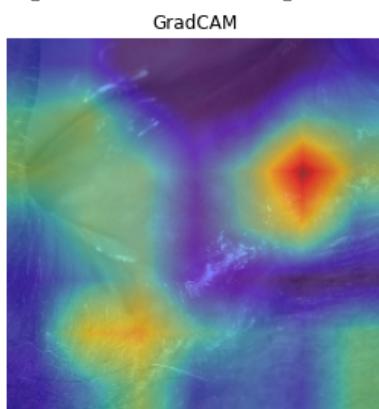


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

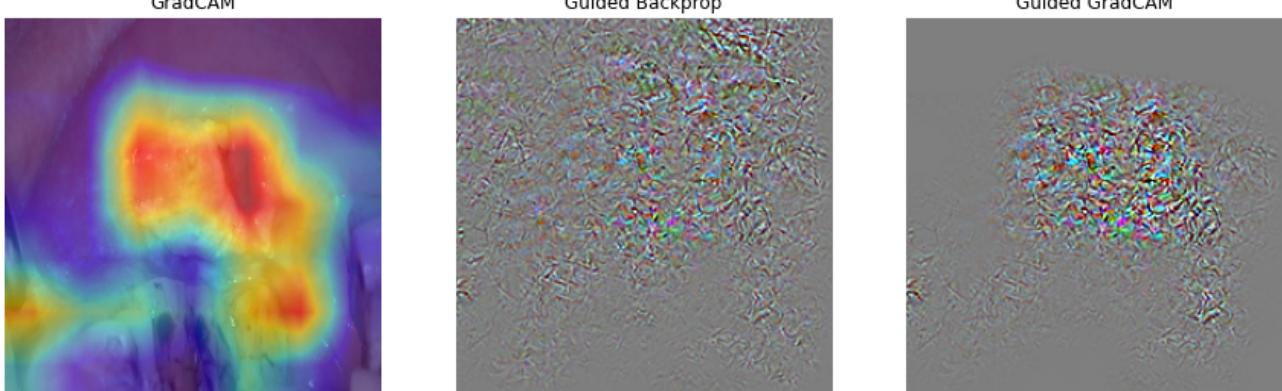
pmd	(1)	with probability 0.885
normal	(0)	with probability 0.115

Explanation for 'pmd'



```
1 test_img = '/content/AJ_Pom_cancer_data/nmvSpma/split_images_cir/test/pma'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
Model prediction:
    pmd          (1)      with probability 0.990
    normal       (0)      with probability 0.010
```

## Explanation for mild symptoms

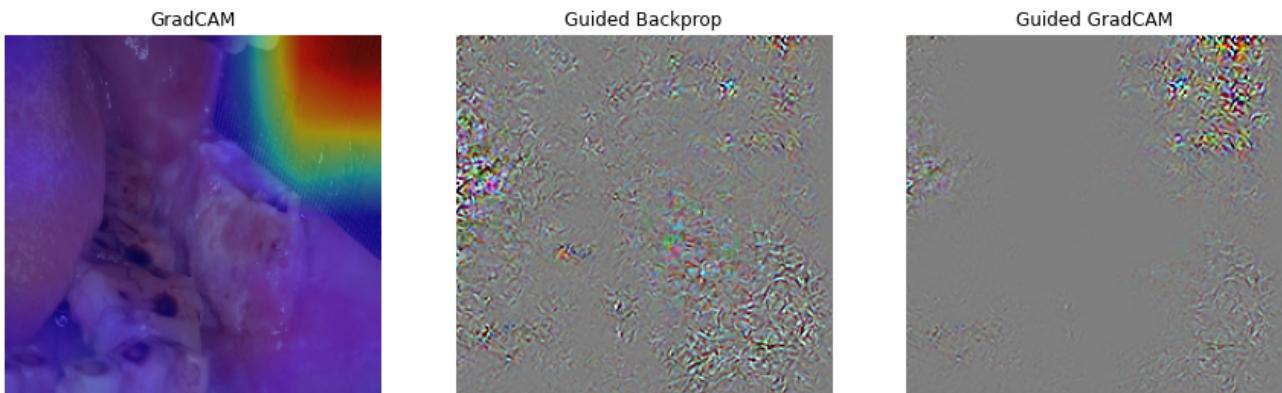


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd  
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd (1) with probability 0.665  
 normal (0) with probability 0.335

## Explanation for 'pmd'

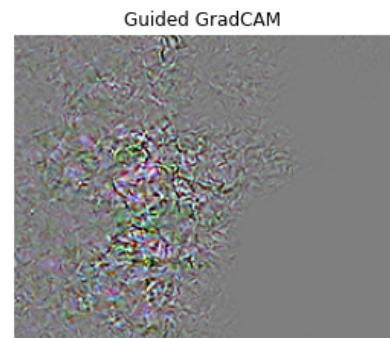
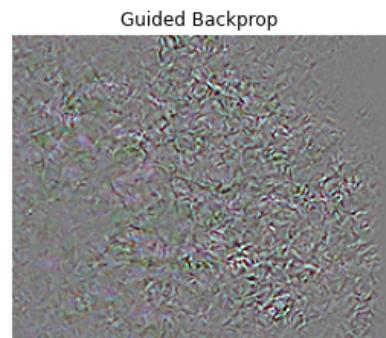
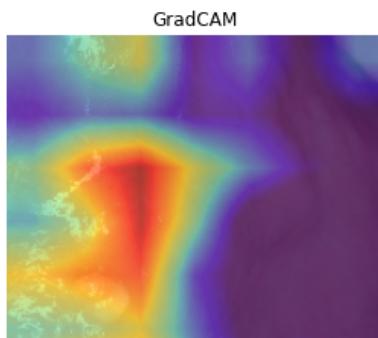


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd  
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.875
normal	(0)	with probability 0.125

Explanation for 'pmd'

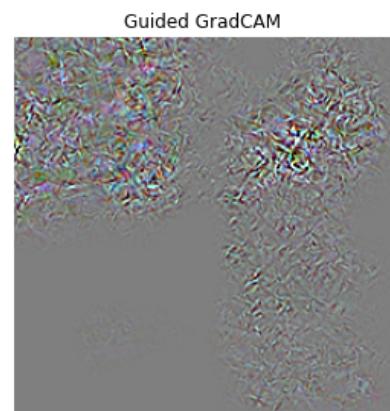
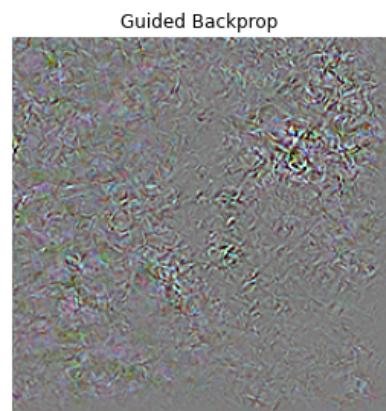
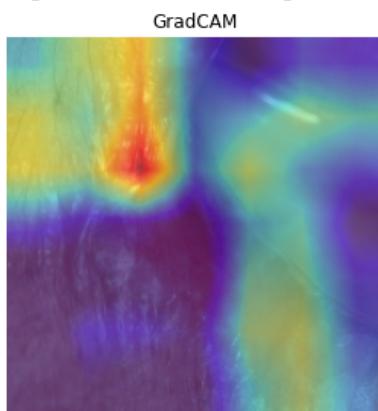


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.896
normal	(0)	with probability 0.104

Explanation for 'pmd'



```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.512
normal	(0)	with probability 0.488

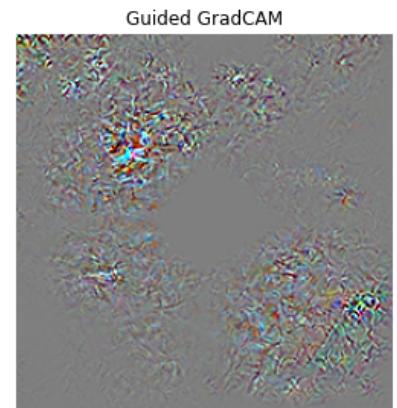
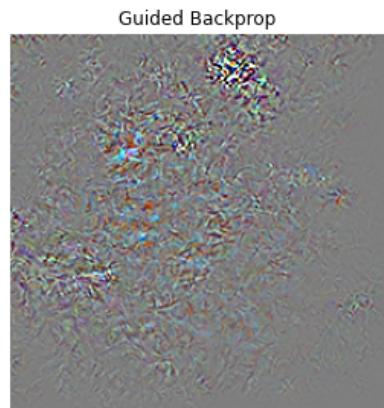
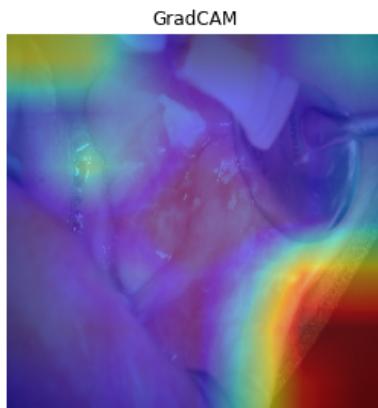
Explanation for 'pmd'

```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.993
normal	(0)	with probability 0.007

Explanation for 'pmd'

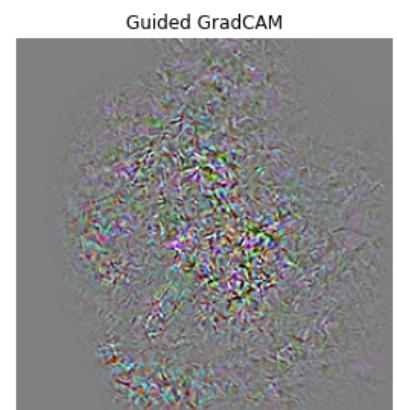
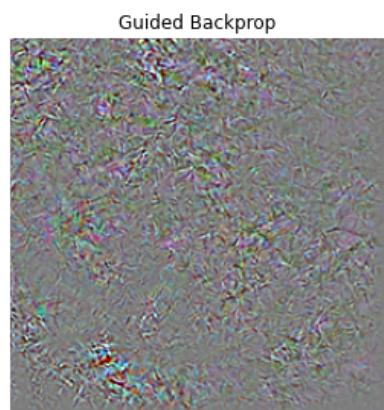
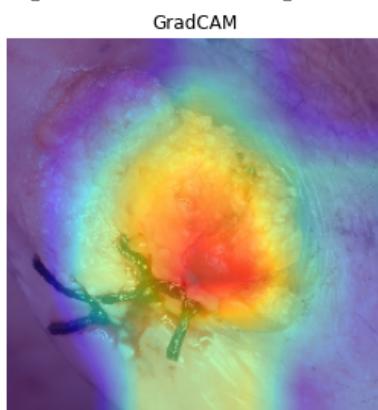


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.976
normal	(0)	with probability 0.024

Explanation for 'pmd'

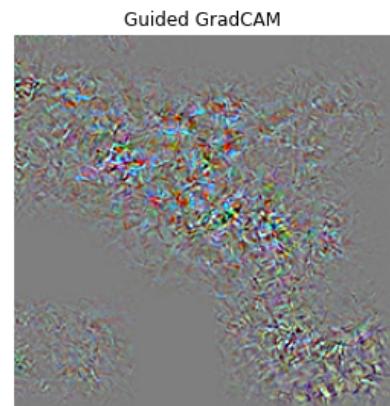
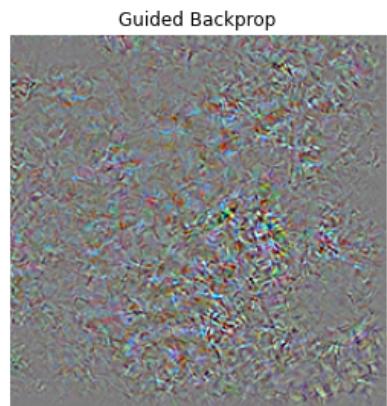
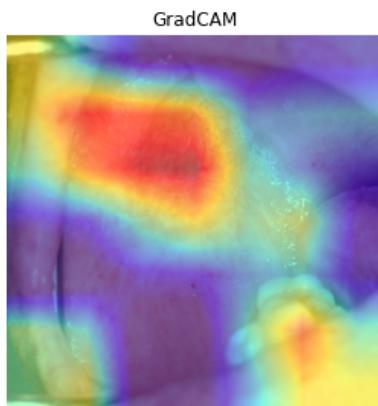


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.897
normal	(0)	with probability 0.103

Explanation for 'pmd'

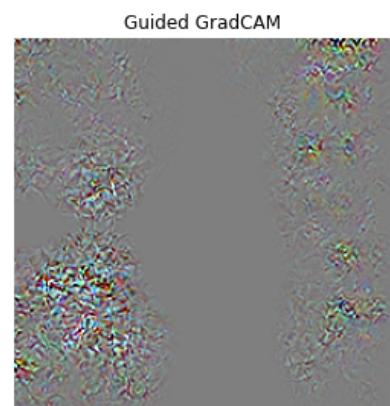
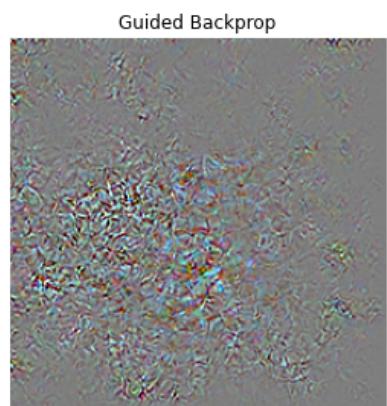
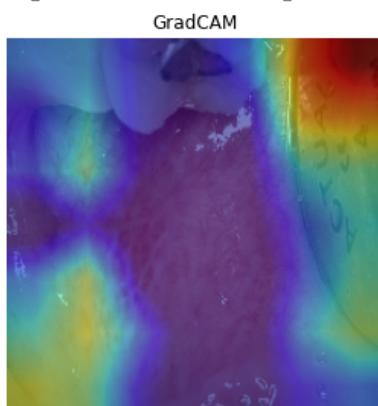


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmnd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.912
normal	(0)	with probability 0.088

Explanation for 'pmd'

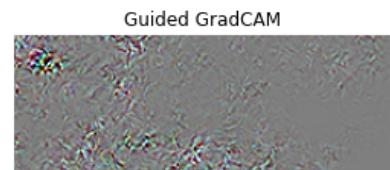
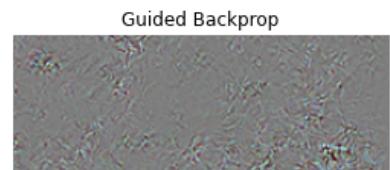


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmnd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.855
normal	(0)	with probability 0.145

Explanation for 'pmd'

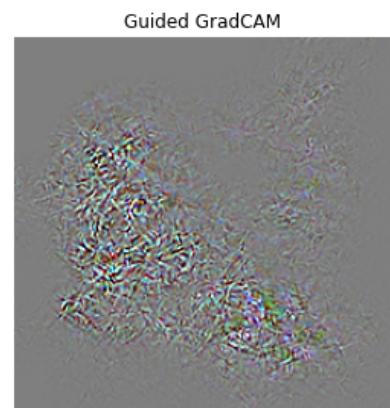
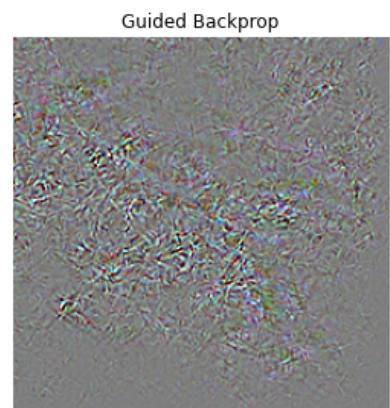
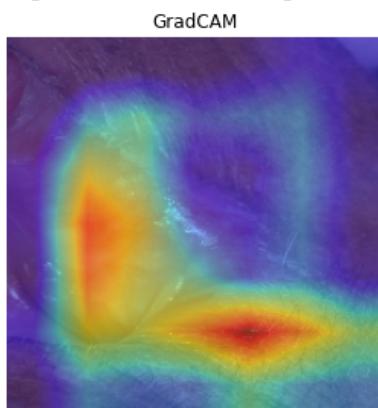


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.979
normal	(0)	with probability 0.021

Explanation for 'pmd'

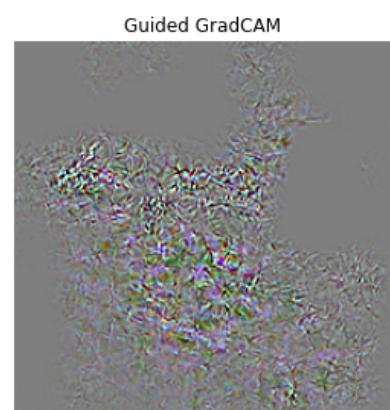
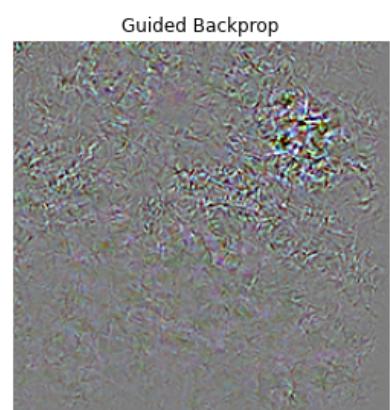
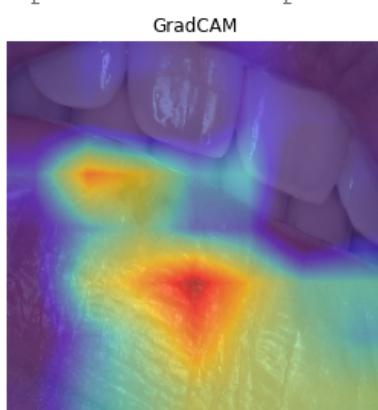


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.811
normal	(0)	with probability 0.189

Explanation for 'pmd'



```

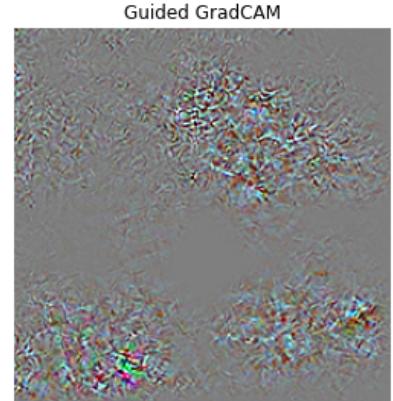
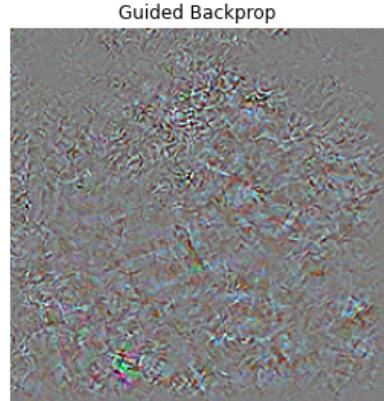
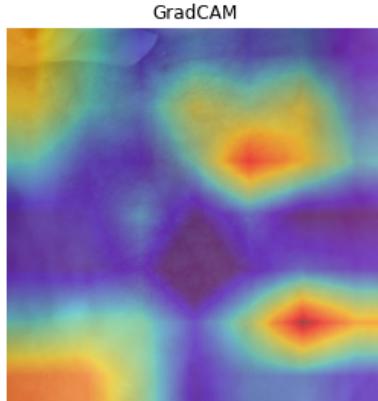
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t

```

Model prediction:

pmd	(1)	with probability 0.704
normal	(0)	with probability 0.296

Explanation for 'pmd'



```

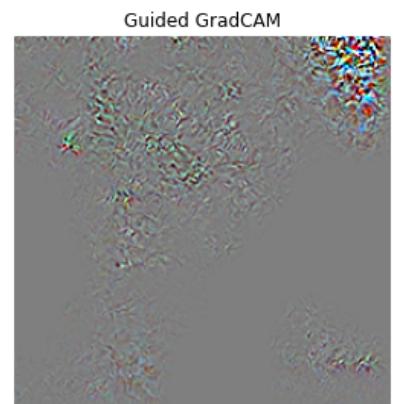
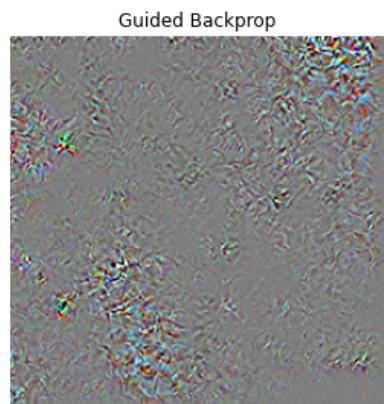
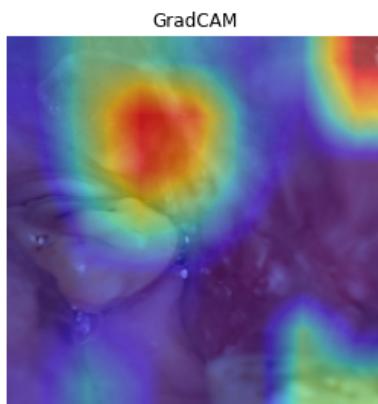
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t

```

Model prediction:

pmd	(1)	with probability 0.705
normal	(0)	with probability 0.295

Explanation for 'pmd'



```

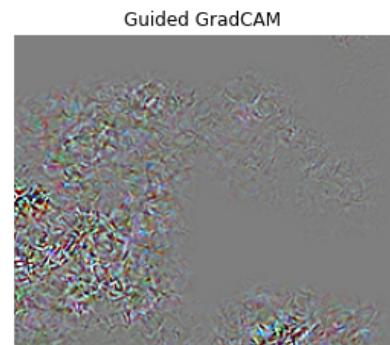
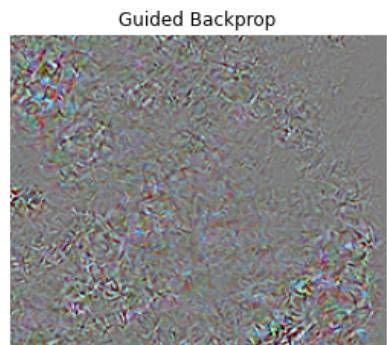
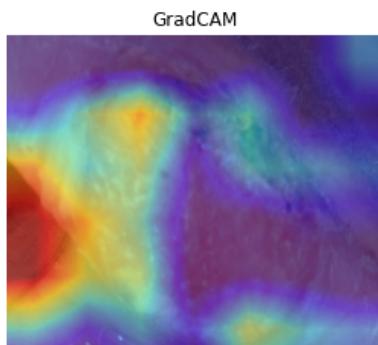
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t

```

Model prediction:

pmd	(1)	with probability 0.996
normal	(0)	with probability 0.004

Explanation for 'pmd'

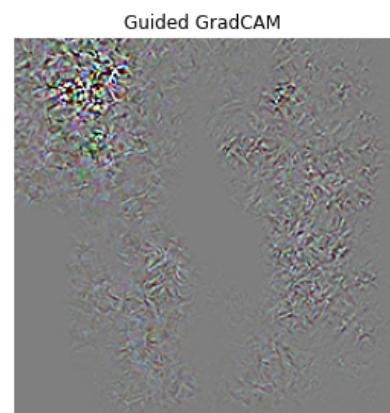
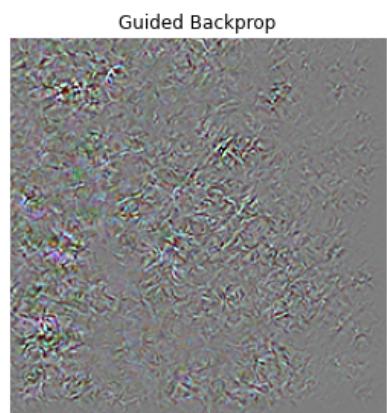
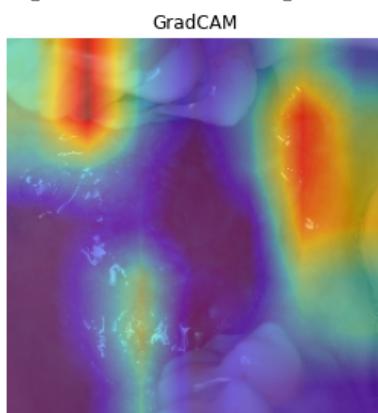


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.986
normal	(0)	with probability 0.014

Explanation for 'pmd'



```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.996
normal	(0)	with probability 0.004

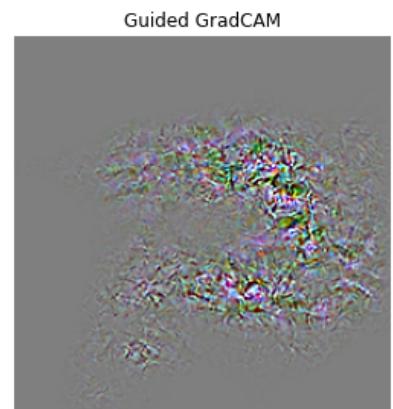
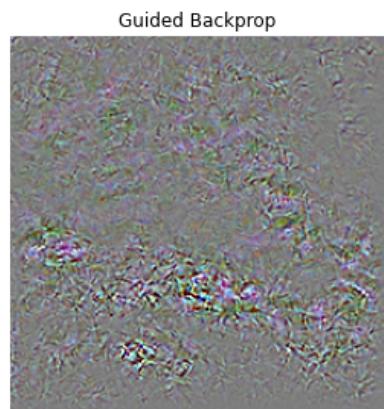
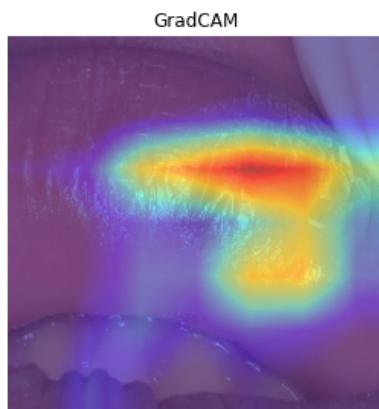
Explanation for 'pmd'

```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.950
normal	(0)	with probability 0.050

Explanation for 'pmd'

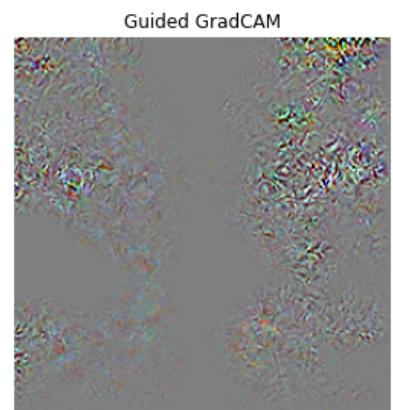
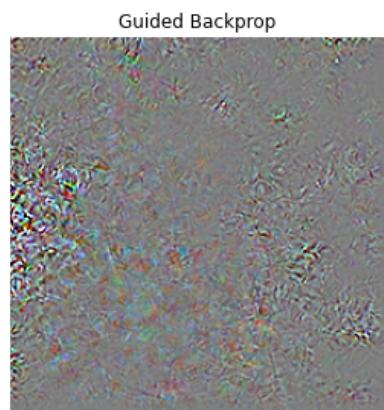
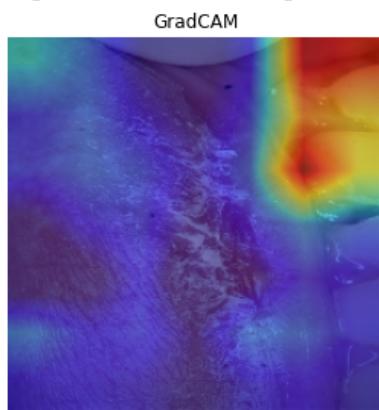


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.966
normal	(0)	with probability 0.034

Explanation for 'pmd'

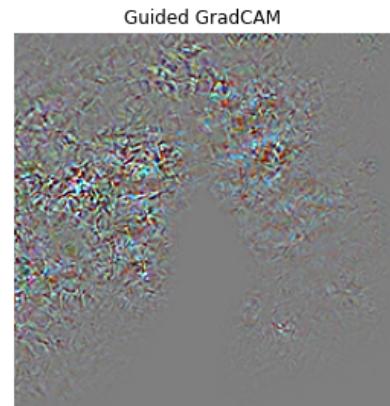
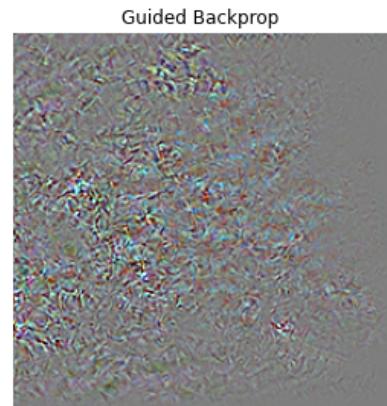
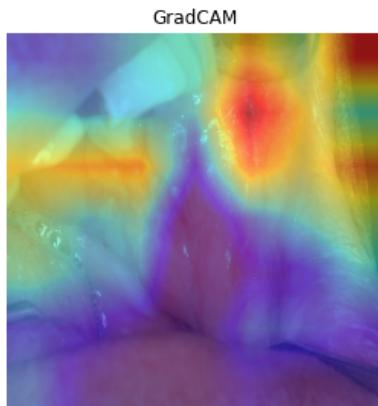


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.946
normal	(0)	with probability 0.054

Explanation for 'pmd'

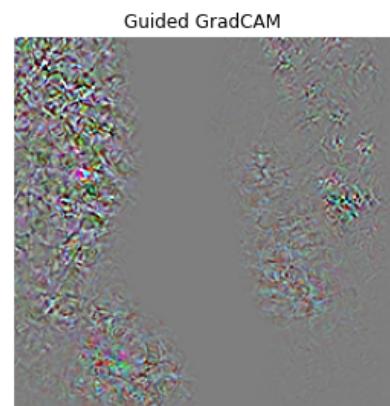
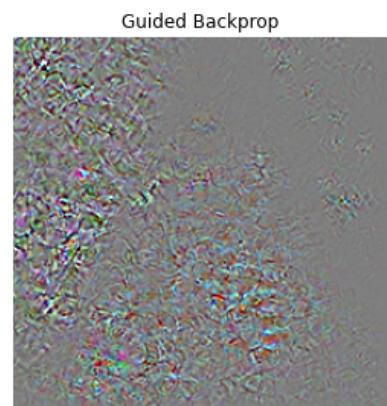
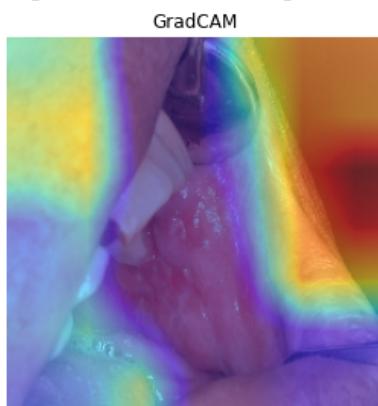


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.870
normal	(0)	with probability 0.130

Explanation for 'pmd'

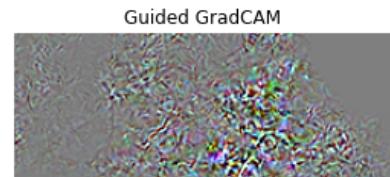
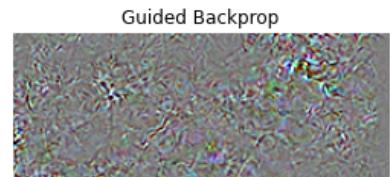
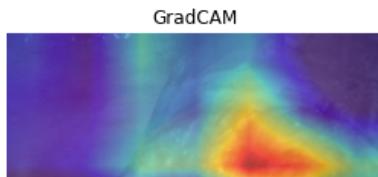


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.989
normal	(0)	with probability 0.011

Explanation for 'pmd'

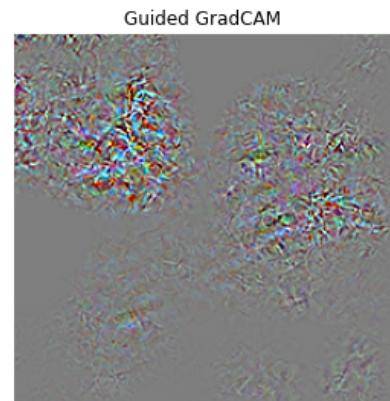
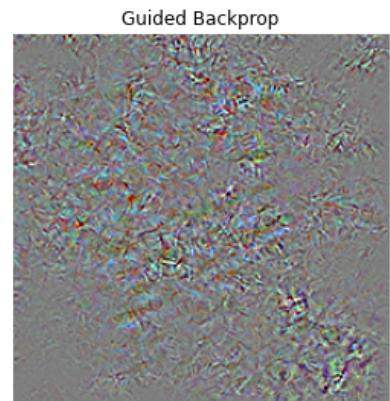
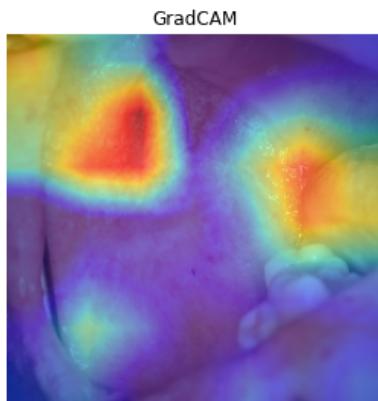


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.990
normal	(0)	with probability 0.010

Explanation for 'pmd'

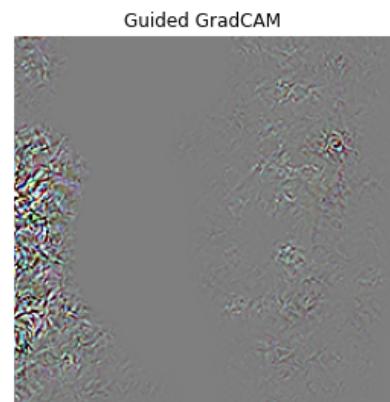
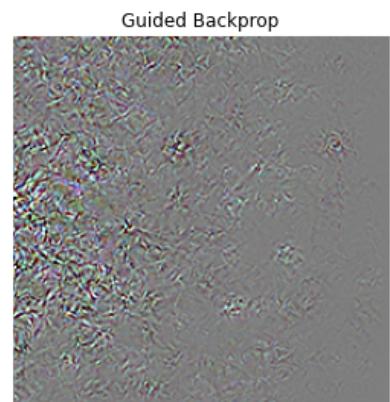
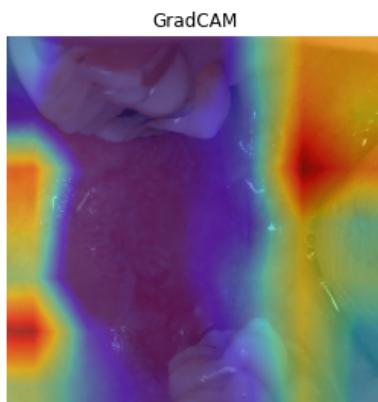


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.621
normal	(0)	with probability 0.379

Explanation for 'pmd'



```

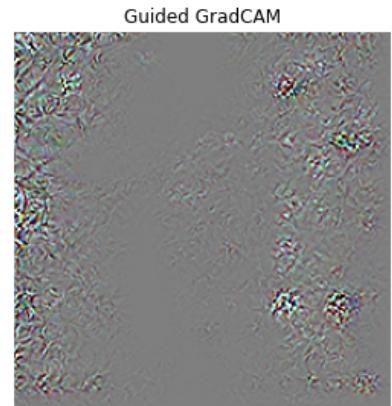
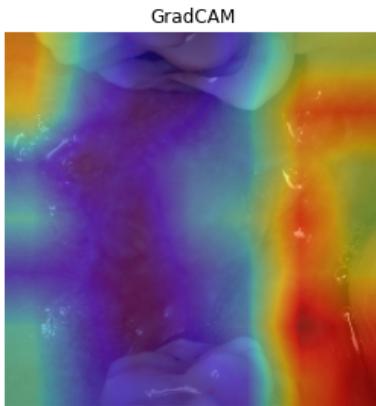
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t

```

Model prediction:

pmd	(1)	with probability 0.788
normal	(0)	with probability 0.212

Explanation for 'pmd'



```

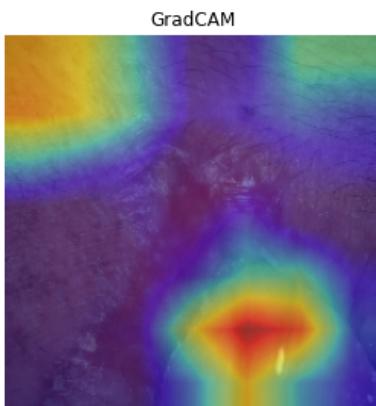
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t

```

Model prediction:

pmd	(1)	with probability 0.971
normal	(0)	with probability 0.029

Explanation for 'pmd'



```

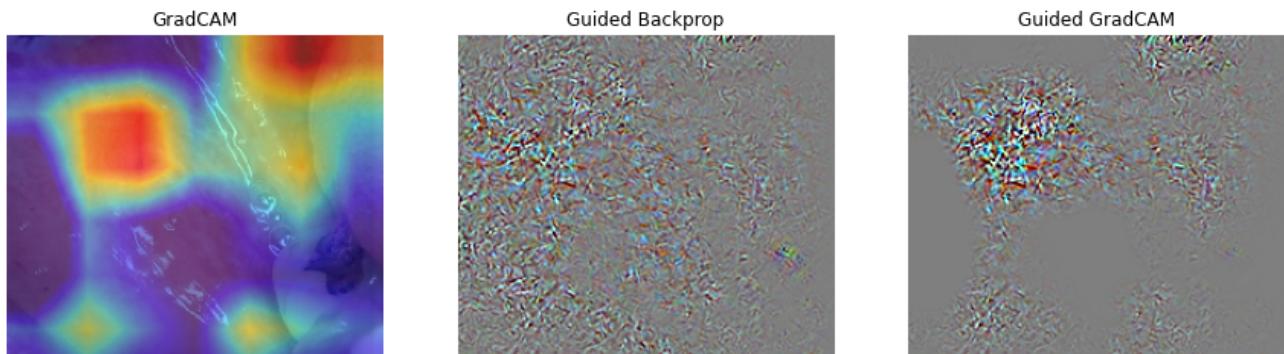
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t

```

Model prediction:

pmd	(1)	with probability 0.991
normal	(0)	with probability 0.009

Explanation for 'pmd'

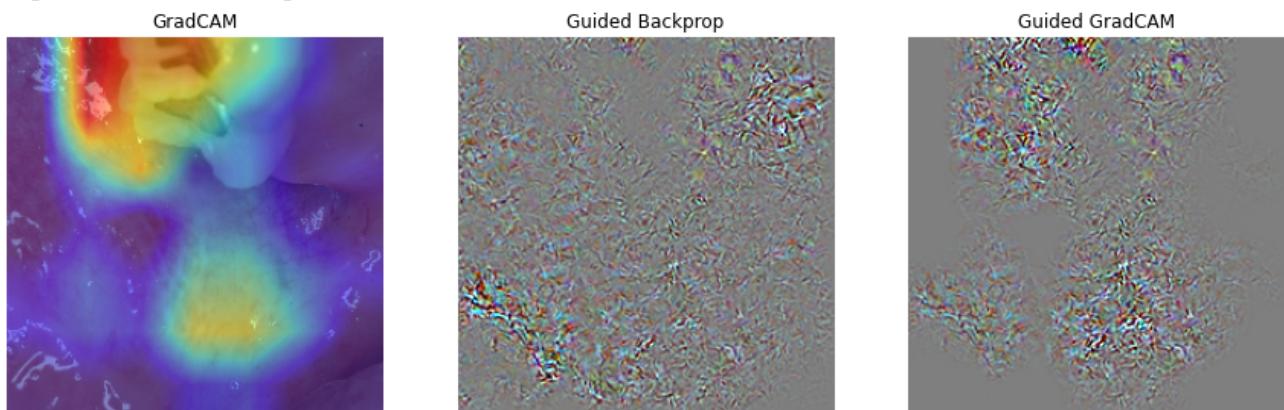


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.880
normal	(0)	with probability 0.120

Explanation for 'pmd'



```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.992
normal	(0)	with probability 0.008

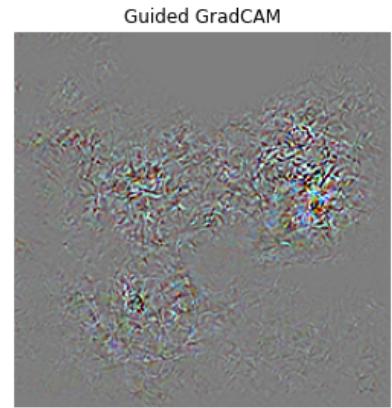
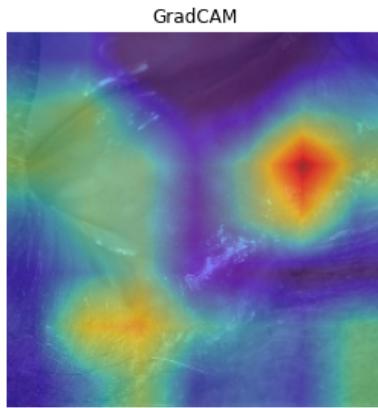
Explanation for 'pmd'

```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.885
normal	(0)	with probability 0.115

Explanation for 'pmd'

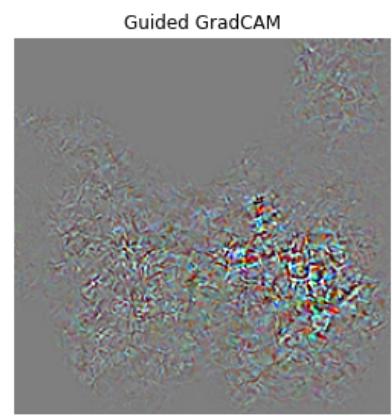
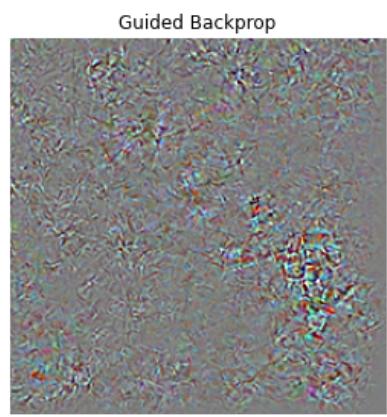
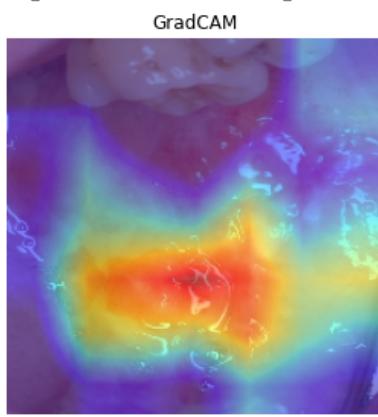


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.909
normal	(0)	with probability 0.091

Explanation for 'pmd'

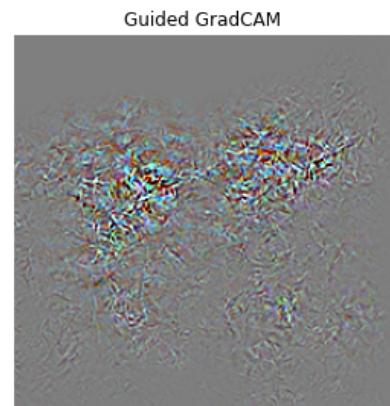
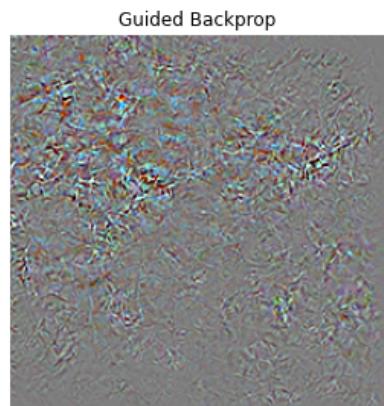
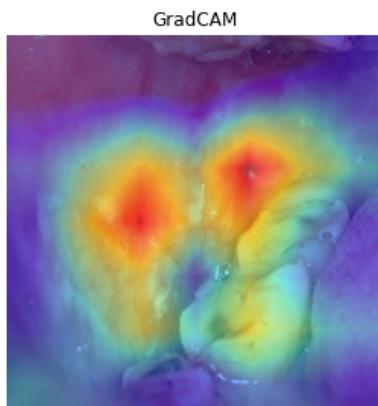


```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.964
normal	(0)	with probability 0.036

Explanation for 'pmd'



```
1 test_img = '/content/AJPom_cancer_data/nmVSpmd/split_images_clf/test/pmd'
2 gradcam, gb, guided_gradcam = compute_saliency(test_model, test_model, t
```

Model prediction:

pmd	(1)	with probability 0.653
normal	(0)	with probability 0.347

Explanation for 'pmd'

