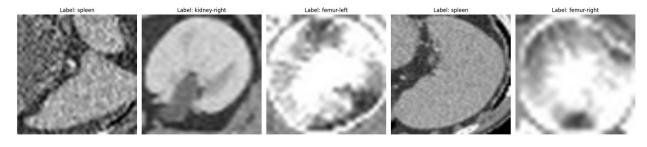
Homework (for 2 weeks)

Train a Vision Transformer model on any of MedMNIST datasets (except NoduleMNIST), followed by prediction and explanation.

Essentially apply the above steps with a different ViT model trained on one of the MedMNIST datasets.

```
import sys
import os
from torch.utils.data import DataLoader
from torchvision.transforms import v2
import torch
from torch import nn
import numpy as np
import gdown
import os
import matplotlib.pyplot as plt
from medmnist import INFO, OrganMNIST3D
sys.path.append("./obz")
def take middle slice(inpt: np.ndarray):
    inpt = inpt.squeeze()
    X, Y, Z = inpt.shape
    slice = inpt[:, :, Z // 2]
    slice = torch.Tensor(slice ).unsqueeze(0).repeat(3, 1, 1)
    return slice
TRANSFORMS = v2.Compose([v2.Lambda(take middle slice),
                         v2.Resize(size=(224,224))
                         1)
NORMALIZE = v2.Normalize(mean=[0.485, 0.456, 0.406], std=[0.229,
0.224, 0.225])
data dir = "./organ data"
os.makedirs(data dir, exist ok=True)
ref set = OrganMNIST3D(root=data dir, split="val", size=64,
transform=TRANSFORMS, download=True)
inf set = OrganMNIST3D(root=data dir, split="test", size=64,
transform=TRANSFORMS)
ref loader = DataLoader(ref set, batch size=32, shuffle=False)
inf loader = DataLoader(inf set, batch size=6, shuffle=True)
train set = OrganMNIST3D(root=data dir, split="train", size=64,
transform=TRANSFORMS, download=True)
```

```
train loader = DataLoader(train set, batch size=32, shuffle=False)
CLASS NAMES = list(INFO['organmnist3d']['label'].values())
LOGIT2NAME = INFO['organmnist3d']['label']
LOGIT2NAME
{'0': 'liver'.
 'l': 'kidney-right',
 '2': 'kidney-left',
 '3': 'femur-right',
 '4': 'femur-left',
 '5': 'bladder',
 '6': 'heart',
 '7': 'lung-right',
 '8': 'lung-left',
 '9': 'spleen',
 '10': 'pancreas'}
samples, labels = next(iter(ref loader))
fig, axes = plt.subplots(1, 5, figsize=(20, 5))
for i in range(5):
    image = samples[i].permute(1, 2, 0).numpy() # Convert tensor to
numpy array and rearrange dimensions
    axes[i].imshow(image, cmap='gray')
    axes[i].set title(f"Label: {CLASS NAMES[labels[i].item()]}")
    axes[i].axis('off')
plt.tight_layout()
plt.show()
```



```
from transformers import ViTConfig, ViTForImageClassification

DEVICE = "cuda" if torch.cuda.is_available() else "cpu"

config = ViTConfig.from_pretrained("google/vit-base-patch16-224-in21k")
 config.num_labels = len(CLASS_NAMES)

model = ViTForImageClassification.from_pretrained(
```

```
"google/vit-base-patch16-224-in21k",
    config=config
model = model.to(DEVICE)
Some weights of ViTForImageClassification were not initialized from
the model checkpoint at google/vit-base-patch16-224-in21k and are
newly initialized: ['classifier.bias', 'classifier.weight']
You should probably TRAIN this model on a down-stream task to be able
to use it for predictions and inference.
import torch.nn as nn
criterion = nn.CrossEntropyLoss()
optimizer = torch.optim.AdamW(model.parameters(), lr=1e-4)
def train(model, loader):
    model.train()
    total loss = 0
    for batch in tqdm(loader):
        imgs = batch[0].to(DEVICE)
        labels = batch[1].squeeze().long().to(DEVICE)
        optimizer.zero_grad()
        outputs = model(imgs).logits
        loss = criterion(outputs, labels)
        loss.backward()
        optimizer.step()
        total loss += loss.item()
    return total loss / len(loader)
for epoch in range(3):
    loss = train(model, train_loader)
    print(f"Epoch {epoch+1} loss: {loss:.4f}")
100%
            | 31/31 [13:40<00:00, 26.45s/it]
Epoch 1 loss: 1.6297
100%
            | 31/31 [12:25<00:00, 24.05s/it]
Epoch 2 loss: 0.7265
100%
            | 31/31 [12:22<00:00, 23.96s/it]
Epoch 3 loss: 0.4146
```

```
from sklearn.metrics import classification report
def evaluate(model, loader):
    model.eval()
    y true, y pred = [], []
    with torch.no grad():
        for batch in loader:
            imgs = batch[0].to(DEVICE)
            labels = batch[1].squeeze().long().to(DEVICE)
            outputs = model(imgs).logits
            preds = torch.argmax(outputs, dim=1)
            y true.extend(labels.cpu().numpy())
            y_pred.extend(preds.cpu().numpy())
    return y true, y pred
y true, y pred = evaluate(model, inf loader)
print(classification_report(y_true, y_pred, target_names=CLASS_NAMES))
              precision
                            recall f1-score
                                               support
       liver
                   1.00
                              1.00
                                        1.00
                                                     69
kidney-right
                   0.78
                              0.93
                                        0.85
                                                     68
                   0.78
kidney-left
                              0.87
                                        0.82
                                                     69
 femur-right
                   0.89
                              0.97
                                        0.93
                                                     65
  femur-left
                   0.97
                              0.89
                                        0.93
                                                     65
     bladder
                   1.00
                              0.77
                                        0.87
                                                     66
                   1.00
                              0.89
                                        0.94
                                                     28
       heart
  lung-right
                   1.00
                              1.00
                                        1.00
                                                     21
   lung-left
                   0.91
                              1.00
                                        0.95
                                                    21
      spleen
                   0.95
                              0.91
                                        0.93
                                                     69
    pancreas
                   1.00
                              0.96
                                        0.98
                                                     69
                                        0.92
                                                   610
    accuracy
   macro avq
                   0.93
                              0.93
                                        0.93
                                                   610
weighted avg
                   0.93
                              0.92
                                        0.92
                                                   610
# Move samples to the appropriate device
samples = samples[:5].to(DEVICE)
labels = labels[:5].to(DEVICE)
print(labels)
print(samples.shape)
# Dont normalize the LIDC data?
# Normalize the samples
#samples = NORMALIZE(samples)
# Perform inference using the model
```

```
with torch.no grad():
    logits = model(samples).logits
    predictions = torch.softmax(logits,
dim=1).argmax(dim=1).cpu().numpy()
# Map to class names
predicted classes = [LOGIT2NAME[str(pred)] for pred in predictions]
# Print the results
for i, pred class in enumerate(predicted classes):
    print(f"Prediction for Sample {i + 1}: {pred class}")
tensor([[9],
        [1],
        [4],
        [9],
        [3]], dtype=torch.int32)
torch.Size([5, 3, 224, 224])
Prediction for Sample 1: spleen
Prediction for Sample 2: kidney-right
Prediction for Sample 3: femur-left
Prediction for Sample 4: spleen
Prediction for Sample 5: femur-right
```

Extract features for outlier detection

```
# Setup OutlierDetector
from data_inspector.extractor import FirstOrderExtractor
from data_inspector.detector import GMMDetector
# Choose desired feature extractor. Chosen extractor will be used for
monitoring.
first_order_extrc = FirstOrderExtractor()

# Pass choosen extractor(s) to chosen OutlierDetector. Below we
utilize outlier detector based on Gaussian Mixture Models.
gmm_detector = GMMDetector(extractors=[first_order_extrc],
outlier_quantile=0.01)
# Call .fit() method with passed reference dataloader.
# Method will extract desired image features and fit outlier detection
model (in that case GMM).
gmm_detector.fit(ref_loader)
```

Explain the AI model

```
import importlib
import xai.xai_tool
importlib.reload(xai.xai_tool)

<module 'xai.xai_tool' from 'C:\\Users\\48601\\Desktop\\MCBS\\./obz\\
xai\\xai_tool.py'>
```

```
# Setup XAI Tools
from xai.xai tool import CDAM, AttentionMap
cdam tool = CDAM(model=model,
                                                     # CDAM mode
                mode='vanilla',
                gradient_type="from_logits", # Whether backpropagate
gradients from logits or probabilities.
                gradient reduction="average", # Gradient
reduction method.
                activation type="sigmoid")
                                                    # Activation
function applied on logits. (Needed when gradients are backpropagated
from probabilities.)
# In CDAM you need to specify on which layer you want to create hooks.
cdam tool.create hooks(layer name="vit.encoder.layer.11.layernorm befo
re")
attention tool = AttentionMap(model=model,
                              attention layer id=-1,# ID of an
attention layer from which to extract attention weights
                             head = None
                                                    # ID of
attention head to choose. If None, attention scores are averaged.
```

! IMPORTANT!

I had to modify the AttentionMap.explain method as follows to match models output

```
def explain(self, batch: torch.Tensor):
    """
    Provides an attention map for a batch of input images.

NOTE: target_idx is there only for compatibility with other XAI Tools
    """
    _, _, img_H, img_W = batch.shape

# PREVIOUS VERSION: preds, all_atts = self.model(batch, output_attentions=True)
    out = self.model(batch, output_attentions=True)
    all_atts = out.attentions
```

```
with torch.no_grad():
    output = model(samples, output_attentions=True)
    attentions = output.attentions

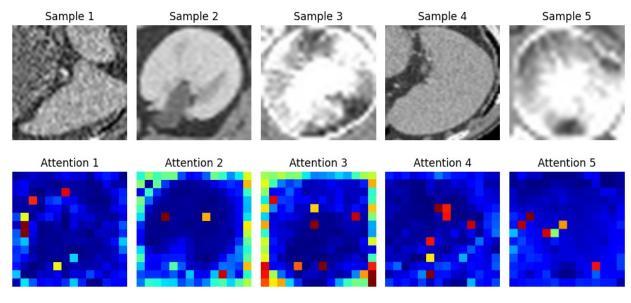
attention_tool.attentions = list(attentions)
attention_maps = attention_tool.explain(samples)

# Visualize samples and attention maps
fig, axes = plt.subplots(2, 5, figsize=(10, 5))
```

```
# First row: Original samples
for i in range(5):
    original_image = samples[i].permute(1, 2, 0).cpu().numpy() #
Convert tensor to numpy array and rearrange dimensions
    axes[0, i].imshow(original_image, cmap='gray')
    axes[0, i].set_title(f"Sample {i + 1}")
    axes[0, i].axis('off')

# Second row: Attention maps
for i in range(5):
    attention_map = attention_maps[i].cpu().numpy()
    axes[1, i].imshow(attention_map, cmap='jet')
    axes[1, i].set_title(f"Attention {i + 1}")
    axes[1, i].axis('off')

plt.tight_layout()
plt.show()
```

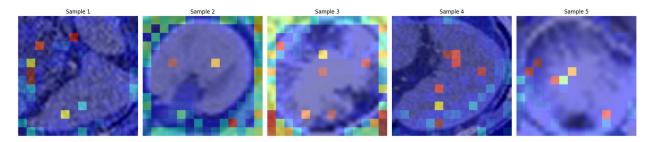


```
# Visualize attention maps overlaid on samples
fig, axes = plt.subplots(1, 5, figsize=(20, 5))

for i in range(5):
    original_image = samples[i].permute(1, 2, 0).cpu().numpy() #
Convert tensor to numpy array and rearrange dimensions
    attention_map = attention_maps[i].cpu().numpy() # Convert
attention map to numpy array

# Overlay attention map on the original image
    axes[i].imshow(original_image, cmap='gray')
    axes[i].imshow(attention_map, cmap='jet', alpha=0.5) # Use alpha
for transparency
    axes[i].set_title(f"Sample {i + 1}")
```

```
axes[i].axis('off')
plt.tight_layout()
plt.show()
```



! IMPORTANT!

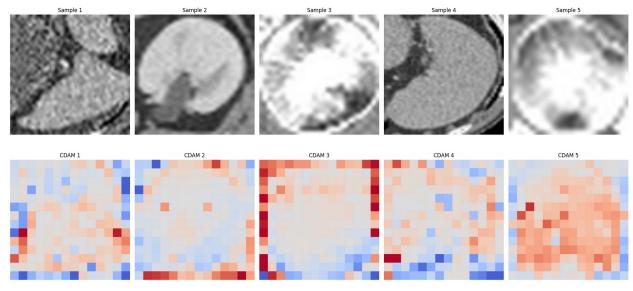
I also had to modify the CDAM._compute_cdam method as follows to match models output

```
with self.hook_manager():
    outputs = self.model(batch)
    self.model.zero_grad()

if self.gradient_type == "from_logits":
    # PREVIOUS VERSION: outputs[range(B), target_idx].sum().backward()
    outputs = outputs.logits if hasattr(outputs, "logits") else outputs
    outputs[range(B), target_idx].sum().backward()
```

```
cdam maps = cdam tool.explain(samples, target idx=[0,0,0,0,0])
# Visualize samples and CDAM maps
fig, axes = plt.subplots(2, 5, figsize=(20, 10))
# First row: Original samples
for i in range(5):
    original image = samples[i].permute(1, 2, 0).cpu().numpy() #
Convert tensor to numpy array and rearrange dimensions
    axes[0, i].imshow(original image, cmap='gray')
    axes[0, i].set title(f"Sample {i + 1}")
    axes[0, i].axis('off')
# Second row: CDAM maps
for i in range(5):
    cdam map = cdam maps[i].squeeze().cpu().numpy() # Convert CDAM
map to numpy array
    axes[1, i].imshow(cdam map, cmap='coolwarm', vmin=-
cdam maps.abs().max(), vmax=cdam maps.abs().max()) # Diverging
colormap
    axes[1, i].set title(f"CDAM {i + 1}")
    axes[1, i].axis('off')
```

```
plt.tight_layout()
plt.show()
```



```
# Visualize CDAM maps overlaid on samples with histogram and color bar
fig, axes = plt.subplots(2, 5, figsize=(20, 10),
gridspec kw={'height ratios': [4, 1]})
# First row: Original samples with overlaid CDAM maps
for i in range(5):
    original image = samples[i].permute(1, 2, 0).cpu().numpy() #
Convert tensor to numpy array and rearrange dimensions
    cdam map = cdam maps[i].squeeze().cpu().numpy() # Convert CDAM
map to numpy array
    # Overlay CDAM map on the original image
    im = axes[0, i].imshow(original image, cmap='gray')
    im = axes[0, i].imshow(cdam_map, cmap='coolwarm', alpha=0.5,
vmin=-cdam maps.abs().max(), vmax=cdam maps.abs().max()) # Use alpha
for transparency
    axes[0, i].set title(f"Sample {i + 1}")
    axes[0, i].axis('off')
# Second row: Histogram of CDAM map values
for i in range(5):
    cdam map = cdam maps[i].squeeze().cpu().numpy() # Convert CDAM
map to numpy array
    axes[1, i].hist(cdam map.ravel(), bins=30, color='blue',
alpha=0.7)
    axes[1, i].set_title(f"Histogram {i + 1}")
    axes[1, i].set xlabel('Value')
    axes[1, i].set ylabel('Frequency')
```

plt.tight_layout() plt.show()

