Lab5: Image segmentation (MONAI)

3099704 AI for Digital Health (2025/2)

Outline

Objective

Material

MONAI: What is it? Built-in models?

Lab 5.0: YOLOv8s (Bonus!)

Dataset: kvasir dataset (2017)

Lab 5.1: UNet (2D segmentation)

Dataset: Skin Cancer MNIST (HAM10000)

Lab 5.2: UNet (3D segmentation)

Dataset: Brain Tumor Segmentation 2020 Dataset (BraTS2020)

3D Slicer

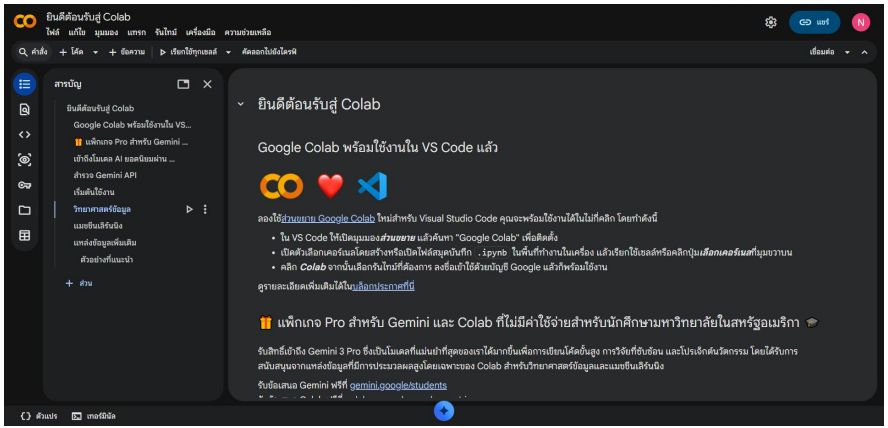
Objective

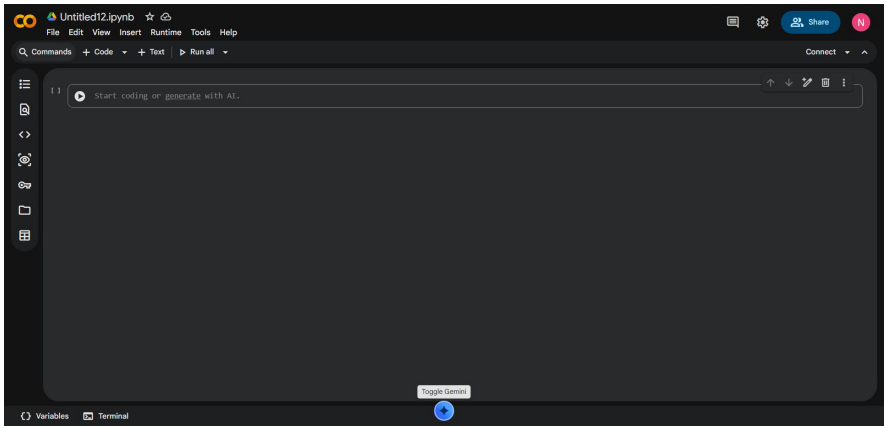
- Create segmentation model

- Use the **MONAI library** to build deep learning model (UNet)

Material

- With **Google Colab**, you don't need to install any software. All you need is a Google account, and you can start using it right away. Simply visit: https://colab.research.google.com/ or select NEW NOTEBOOK to start a new file.



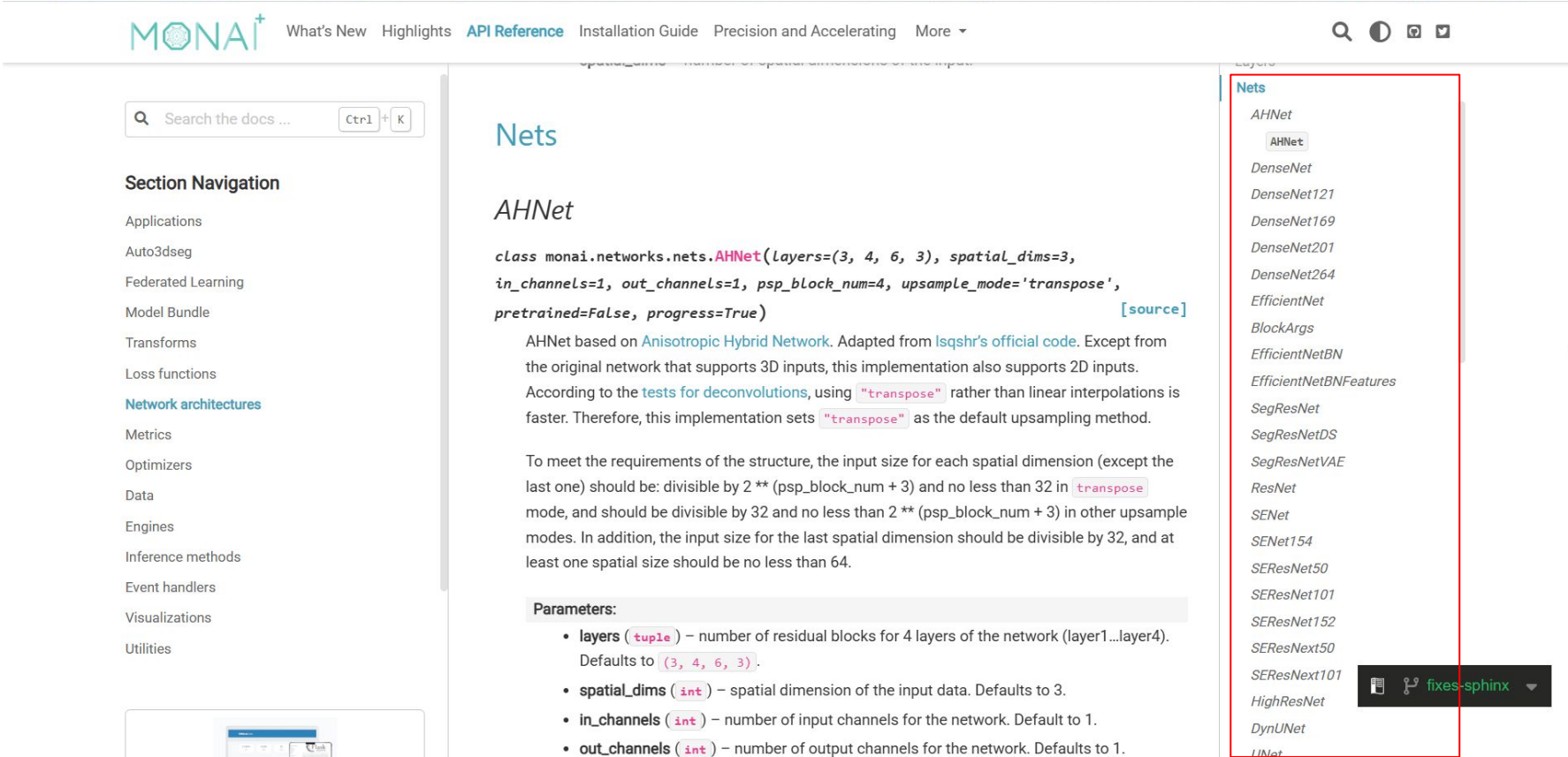


MONAI: What is it? Compare to Pytorch?

MONAI is an open-source medical imaging AI framework initiated by NVIDIA in 2020. PyTorch is a general-purpose framework for deep learning, while MONAI is built on PyTorch but adds specialized functions for medical imaging tasks, such as

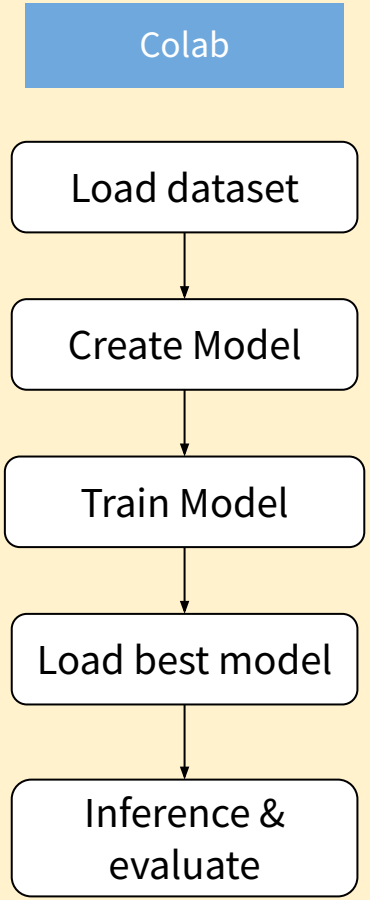
- **Data Loading:** CacheDataset supports big data and caching
- **Transforms:** monai.transforms supports 3D medical volume
- **Networks:** build-in models, such as UNet and SegResNet
- **Inferers:** sliding_window_inference enable inference 3D volumes by 2D models

MONAI: Built-in models



Lab5.0: YOLOv8s (Bonus!)

In this lab, you will create a polyp segmentation model **(YOLOv8s)** and evaluate its performance using **Ultralytics library** in Google Colab.

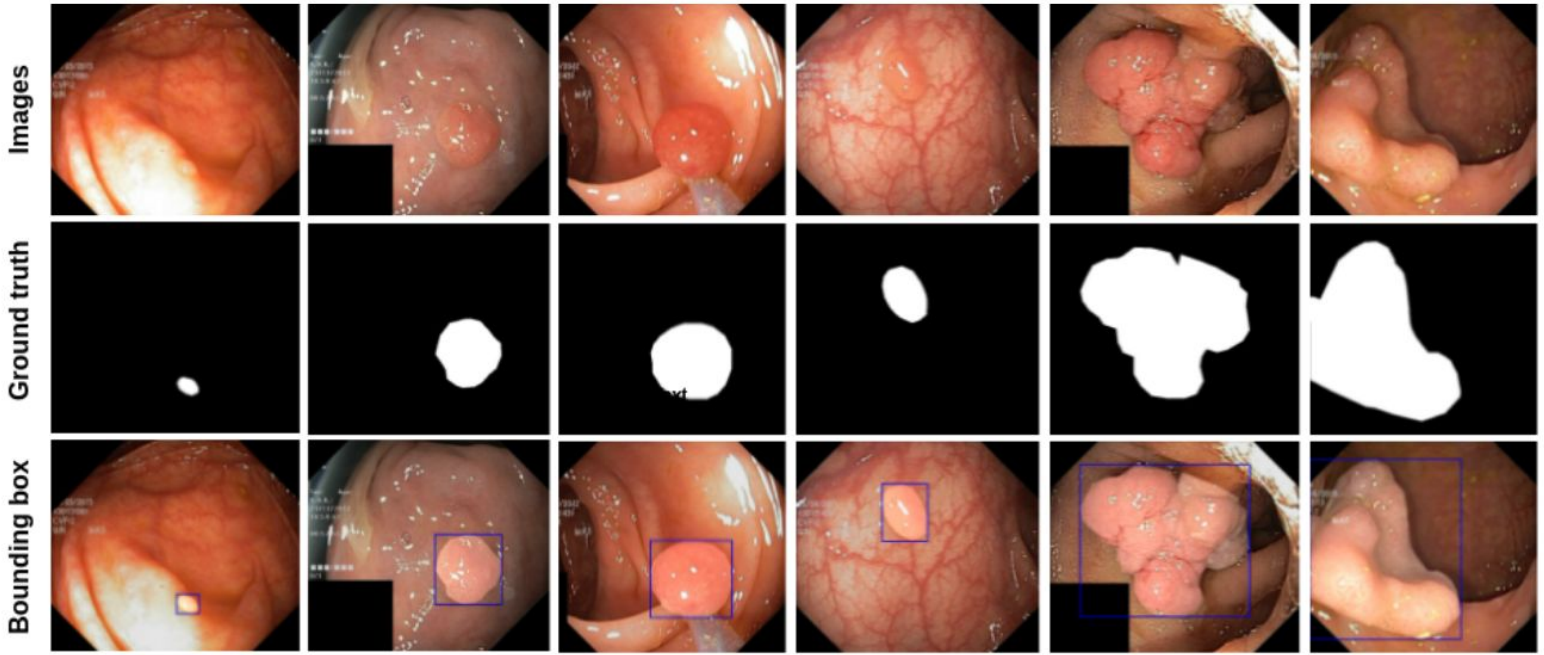


Dataset: kvasir dataset (2017)

- **Kvasir dataset** consists of 4,000 annotated images, including 8 classes showing anatomical landmarks, pathological findings, or endoscopic procedures in the GI tract.
- The dataset consists of the images with different resolutions, from 720x576 up to 1920x1072 pixels in JPG format, and documents in JSON format.
- The dataset was released in 2017 by the **Simula Research Laboratory, Norway.**

- To simplify the experiment, we selected only **500 images** containing polyps and prepared the dataset in a format compatible with YOLO training.

Dataset: kvasir dataset (2017)

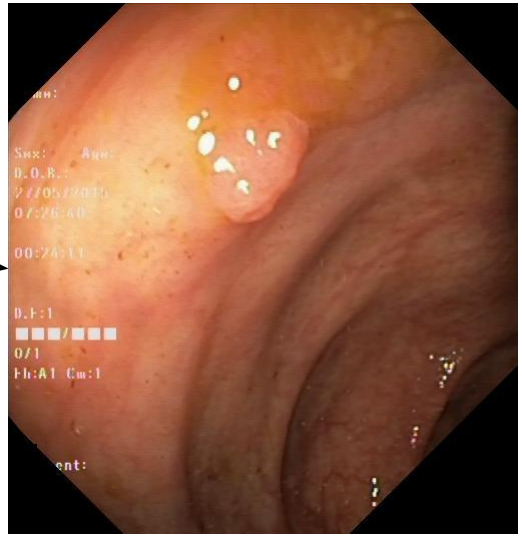


The figure shows the example images, bounding box, and mask from Kvasir-SEG. The white mask shows the area covered by the polyp region, and the background regions contain non-polyp tissue pixels.

Lab5.0: YOLOv8s (Bonus!)

- Dataset format

```
polyp_seg/
├── images/
│   ├── train/
│   │   └── img1.jpg
│   ├── val/
│   │   └── img2.jpg
│   └── test/
│       └── img3.jpg
├── labels/
│   ├── train/
│   │   └── img1.txt
│   ├── val/
│   │   └── img2.txt
│   └── test/
│       └── img3.txt
├── mask/
│   └── test/
│       └── img1.png
└── Kvasir_seg.yaml
```



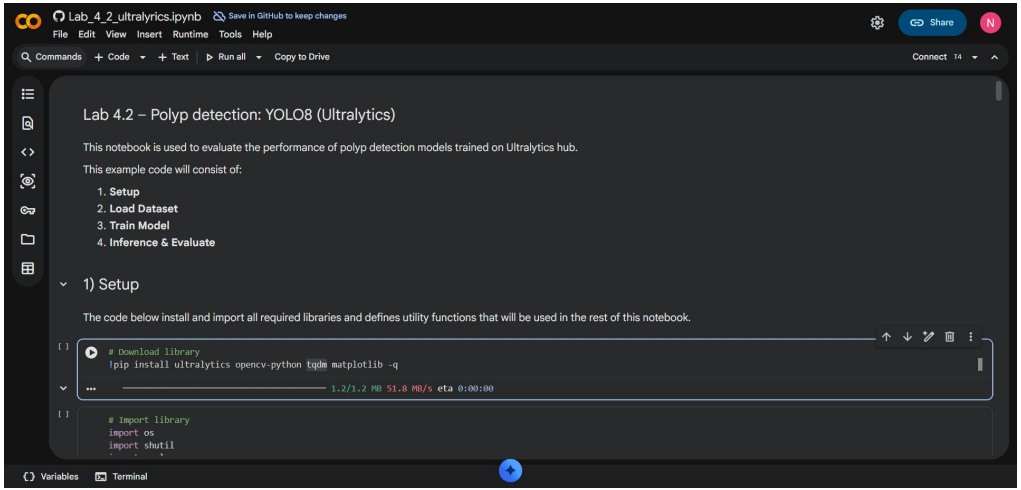
```
train: images/train
val: images/val
test: images/test

names:
  0: polyp
```

<class_index> <x1> <y1> <x2> <y2> ... <xn> <yn>

Lab5.0: YOLOv8s (Bonus!): 4 steps

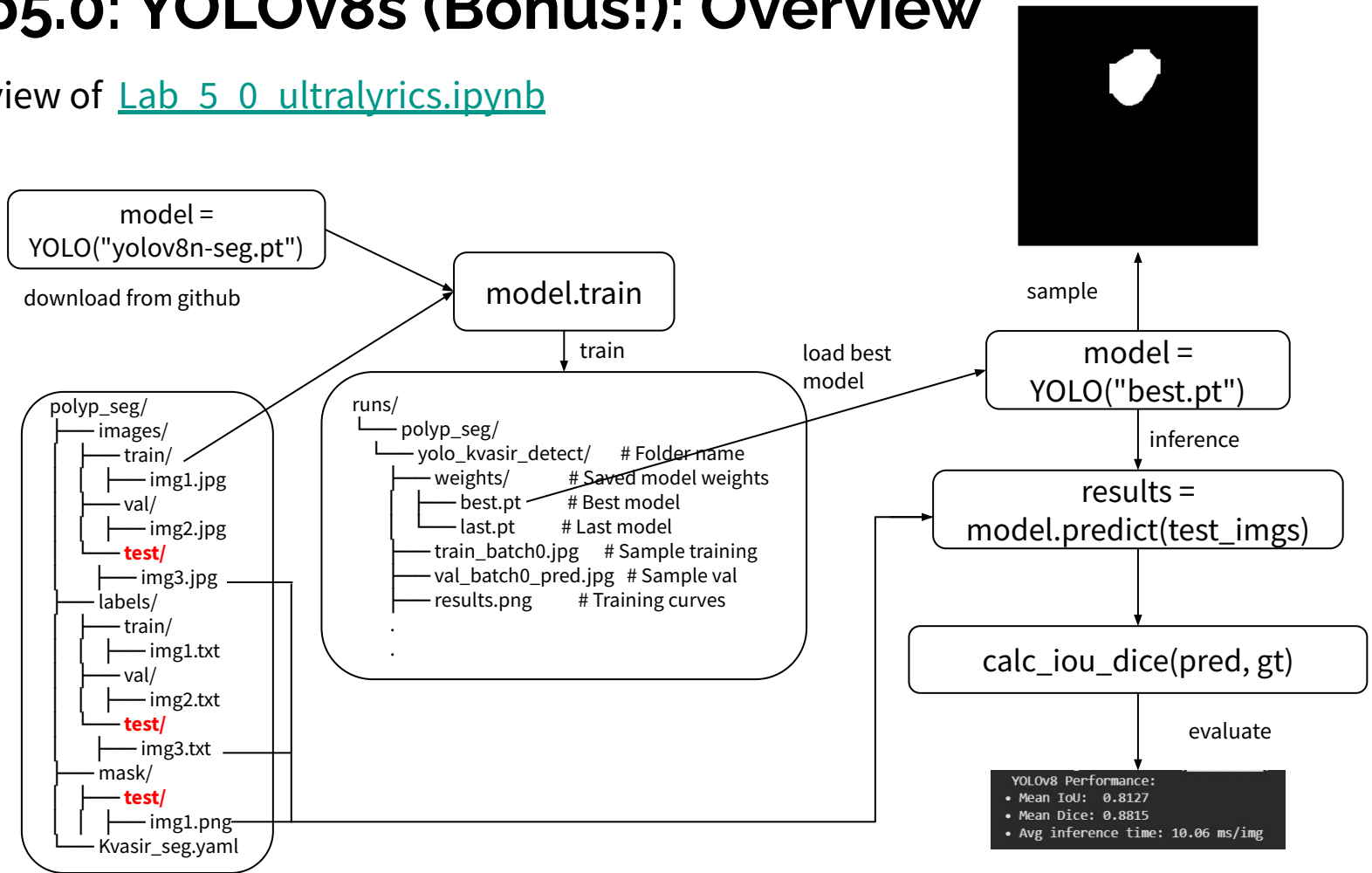
Run Lab_5_0_ultralyrics.ipynb (in colab)

1) Setup
2) Load Data
3) Train model
4) Inference & Evaluate



Lab5.0: YOLOv8s (Bonus!): Overview

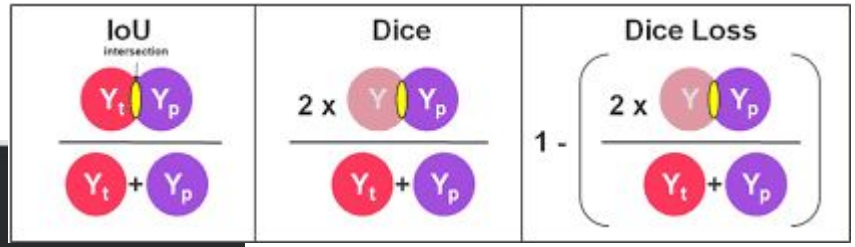
Overview of [Lab_5_0_ultralyrics.ipynb]



Lab5.0: YOLOv8s (Bonus!): Results

Results may vary between runs due to random seed initialization and hyperparameter tuning; however, the overall performance should be similar to the results shown on this page.

```
YOLOv8 Performance:
• Mean IoU:  0.8127
• Mean Dice: 0.8815
• Avg inference time: 10.06 ms/img
```



$$\text{IoU} = \frac{TP}{TP + FP + FN}$$

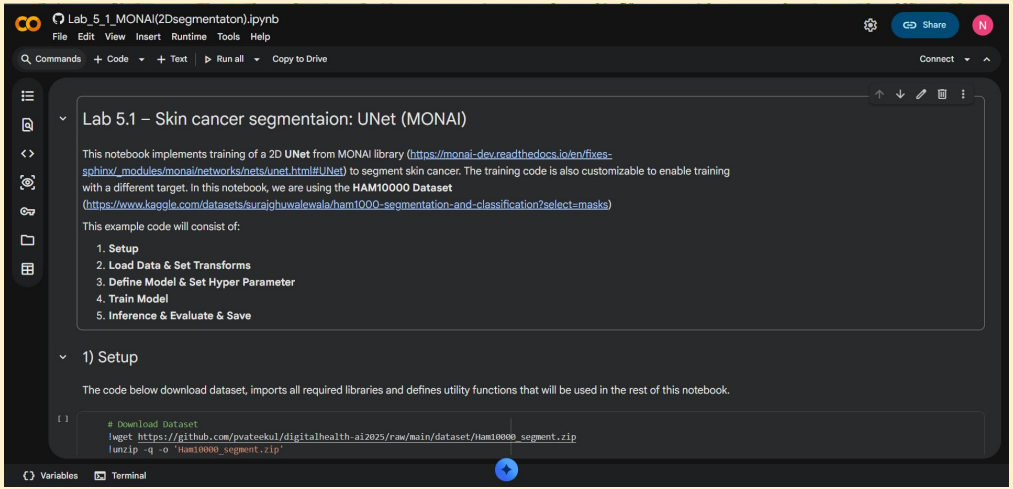
$$\text{Dice} = \frac{2TP}{2TP + FP + FN}$$

Lab5.1: UNet (2D segmentation)

In this lab, you will create and evaluate an skin cancer segmentation model (UNet) using the **MONAI library**. Code can be executed in Lab_5_1_MONAI(2Dsegmentaton) on Google Colab.

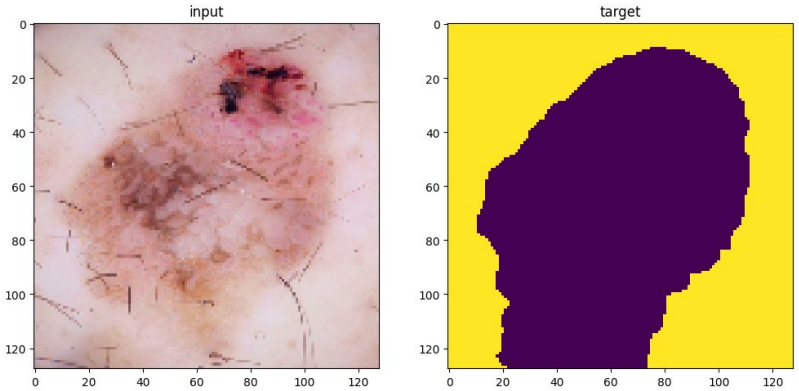
This notebook will consist of:

1) Setup
2) Load Data & Set Transforms
3) Define Model & Set Parameter
4) Train Model
5) Inference & Evaluate & Save

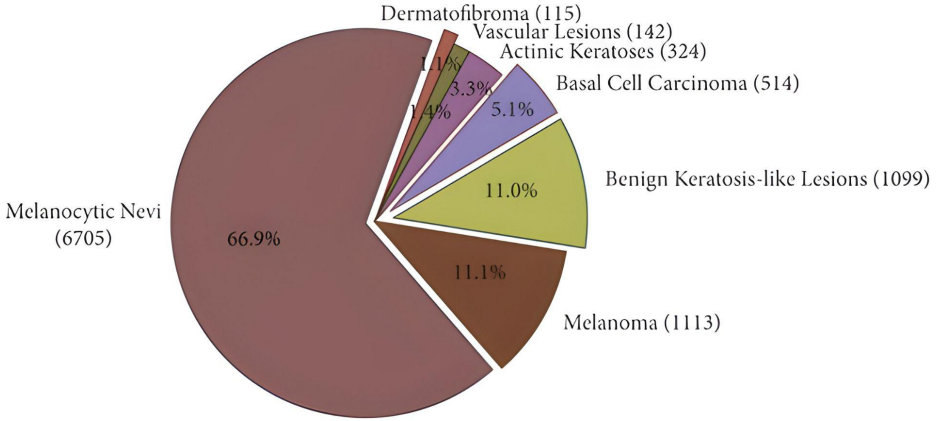


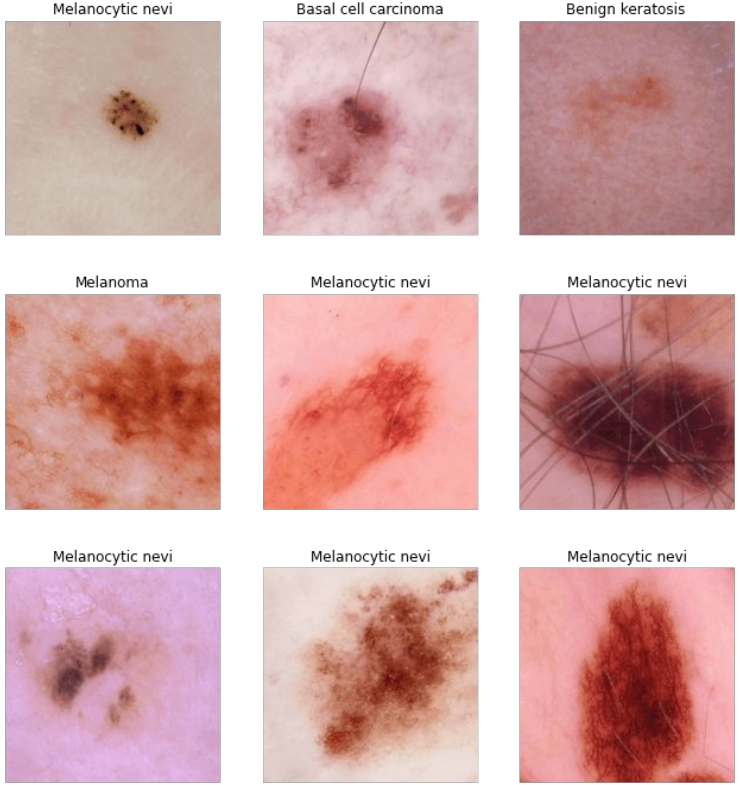
Dataset: Skin Cancer MNIST (HAM10000)

- The dataset consists of 10,015 images with 10,013 labeled objects belonging to **7 skin cancer classes**.
- The data contains image in JPG format, masks in PNG format and documents in JSON format
- The dataset was released in 2018 by the Medical University of Vienna and the University of Queensland.
- To simplify the experiment, we selected only **200 cases** containing images and masks.



Dataset: Skin Cancer MNIST (HAM10000)

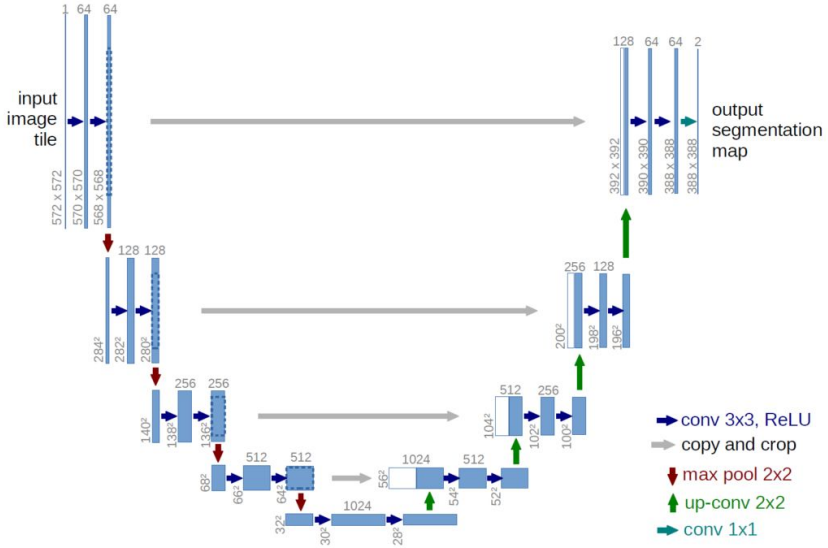




Model: UNet (Ronneberger O, 2015)

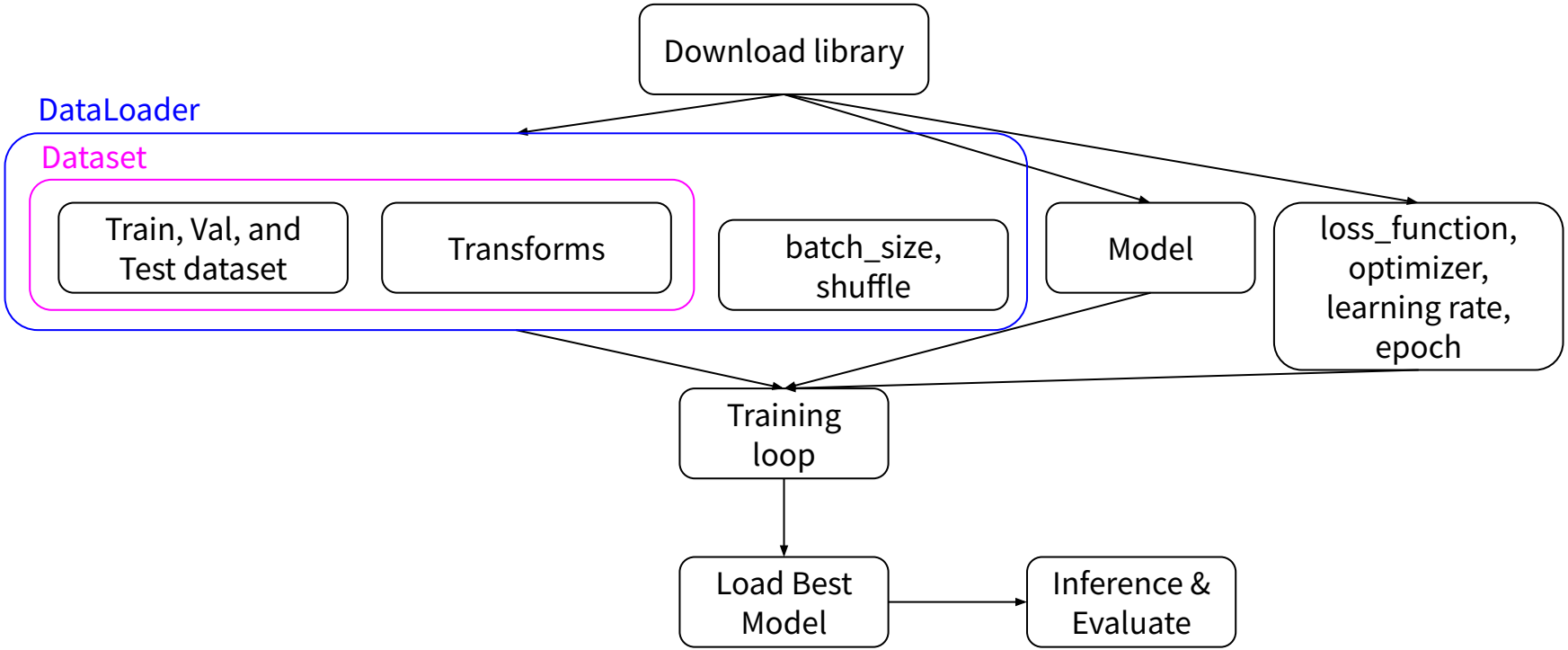
In this lab, we chose to use Unet, which has the following key architectural innovations:

- The left side (**encoder**) progressively downsamples the image to capture context.
- The right side (**decoder**) upsamples to recover spatial resolution for pixel-level predictions.
- **Skip connections** are directly connected feature maps from the encoder to the decoder at corresponding levels.



Lab5.1: UNet (2D segmentation)

Overview of Lab_5_1_MONAI(2Dsegmentaton)



Lab5.1: UNet (2D segmentation)

Overview of Lab_5_1_MONAI(2Dsegmentaton)

Train, Val, and Test datasets

```
# Dataset
train_images = sorted(glob.glob(os.path.join("/content/images", "*.jpg")))
train_labels = sorted(glob.glob(os.path.join("/content/masks", "*.png")))
data_dicts = [{"image": image_name, "label": label_name} for image_name, label_name in zip(train_images, train_labels)]
train_files, val_files, test_files = data_dicts[:120], data_dicts[120:160], data_dicts[160:]
```

```
train_files[:5]

[{'image': '/content/images/ISIC_0024306.jpg',
  'label': '/content/masks/ISIC_0024306_segmentation.png'},
 {'image': '/content/images/ISIC_0024307.jpg',
  'label': '/content/masks/ISIC_0024307_segmentation.png'},
 {'image': '/content/images/ISIC_0024308.jpg',
  'label': '/content/masks/ISIC_0024308_segmentation.png'},
 {'image': '/content/images/ISIC_0024309.jpg',
  'label': '/content/masks/ISIC_0024309_segmentation.png'},
 {'image': '/content/images/ISIC_0024310.jpg',
  'label': '/content/masks/ISIC_0024310_segmentation.png'}]
```

Lab5.1: UNet (2D segmentation)

Overview of [Lab_5_1_MONAI(2Dsegmentaton)]

Transforms (pre)

```python
# Transforms (pre&post proceeding)
roi_size = (128, 128)
train_transforms = Compose(
        [ # 1) Load data path -> tensor
          LoadImaged(keys=["image", "label"],ensure_channel_first=True,image_only=True,dtype=torch.float),
          # 2) scale intensity [0-255] -> [0-1]
          ScaleIntensityRanged(keys=["image", "label"], a_min=0, a_max=255, b_min=0.0, b_max=1.0, clip=True),
          # 3) Resize tensor [HxW] -> [128x128]
          Resized(keys=["image", "label"], spatial_size=roi_size, mode=["bilinear", "nearest-exact"]),
          # 4) Augment (Random flip in each epoch.)
          RandFlipd(keys=["image", "label"], prob=0.5, spatial_axis=0),
        ]
    )
val_transforms = Compose(
        [
          # 1) Load data path -> tensor
          LoadImaged(keys=["image", "label"],ensure_channel_first=True,image_only=True,dtype=torch.float),
          # 2) scale intensity [0-255] -> [0-1]
          ScaleIntensityRanged(keys=["image", "label"], a_min=0, a_max=255, b_min=0.0, b_max=1.0, clip=True),
          # 3) Resize tensor [HxW] -> [128x128]
          Resized(keys=["image", "label"], spatial_size=roi_size, mode=["bilinear", "nearest-exact"]),
        ]
    )

test_transforms = Compose(
        [
          # 1) Load data path -> tensor
          LoadImaged(keys=["image", "label"],ensure_channel_first=True,image_only=True,dtype=torch.float),
          # 2) scale intensity [0-255] -> [0-1]
          ScaleIntensityRanged(keys=["image", "label"], a_min=0, a_max=255, b_min=0.0, b_max=1.0, clip=True),
          # 3) Resize tensor [HxW] -> [128x128]
          Resized(keys=["image", "label"], spatial_size=roi_size, mode=["bilinear", "nearest-exact"]),
        ]
```

Lab5.1: UNet (2D segmentation)

Overview of Lab_5_1_MONAI(2Dsegmentaton)

Transforms (post)

```
post_transforms = Compose(
        [
            Invertd(
                keys="pred",
                transform=test_transforms,
                orig_keys="image",
                meta_keys="pred_meta_dict",
                orig_meta_keys="image_meta_dict",
                meta_key_postfix="meta_dict",
                nearest_interp=False,
                to_tensor=True,
            ),
            AsDiscreted(keys="pred", argmax=True, to_onehot=2),
        ]
    )
```

Lab5.1: UNet (2D segmentation)

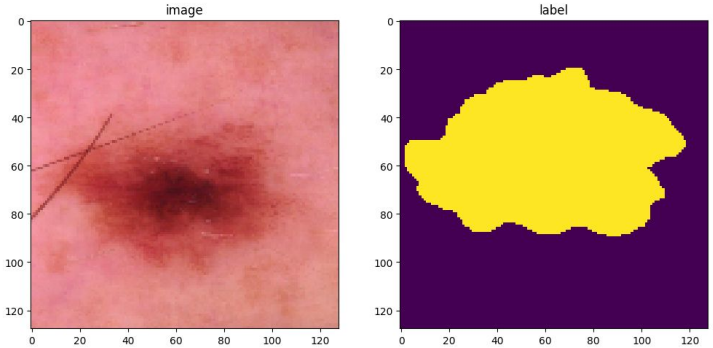
Overview of [Lab_5_1_MONAI(2Dsegmentaton)]

Dataset

Train, Val, and Test dataset

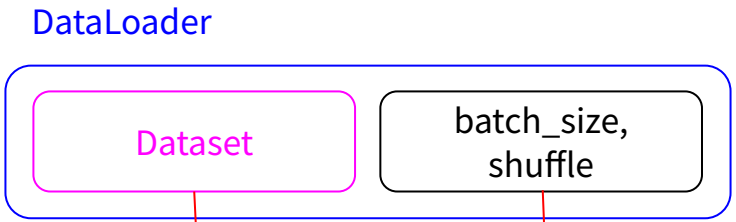
Transforms

```
# Dataset
train_ds = CacheDataset(data=train_files, transform=train_transforms, cache_rate=1.0, num_workers=20)
val_ds = CacheDataset(data=val_files, transform=val_transforms, cache_rate=1.0, num_workers=20)
#Use 20 processes to prepare the data and 100% of the dataset is cached.
```



Lab5.1: UNet (2D segmentation)

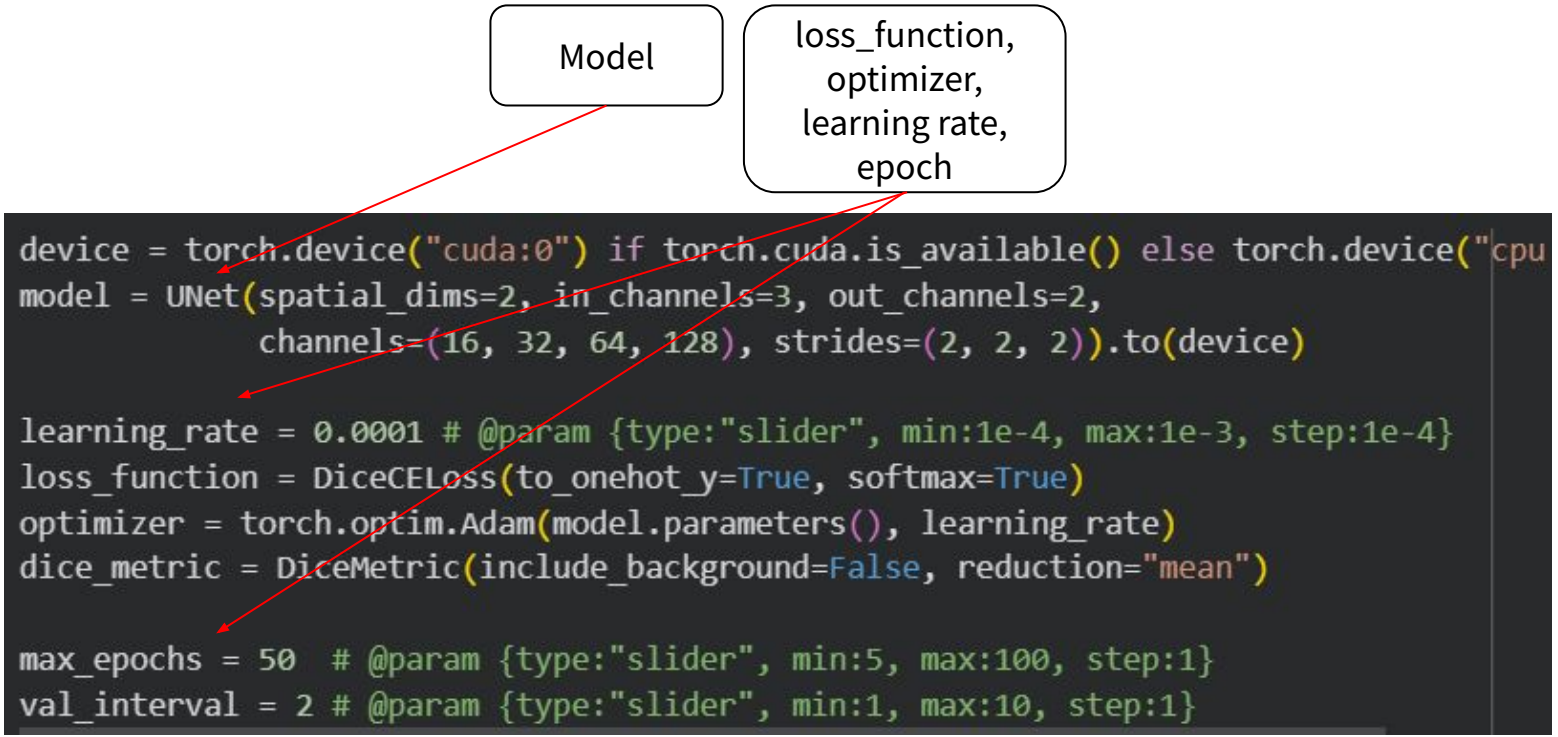
Overview of Lab_5_1_MONAI(2Dsegmentaton)




```
# DataLoader
train_loader = DataLoader(train_ds, batch_size=4, shuffle=True, num_workers=20)
val_loader = DataLoader(val_ds, batch_size=1, num_workers=20)
```

Lab5.1: UNet (2D segmentation)

Overview of Lab_5_1_MONAI(2Dsegmentaton)



Lab5.1: UNet (2D segmentation)

Overview of Lab_5_1_MONAI(2Dsegmentaton)

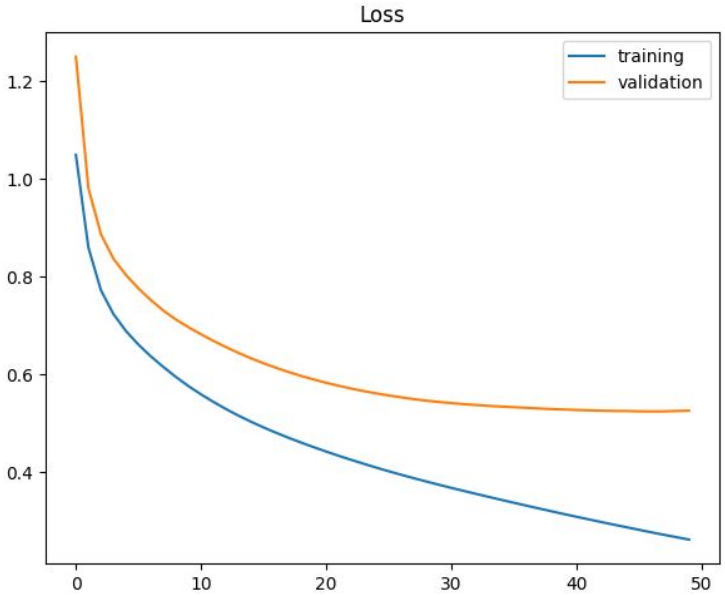
Training loop

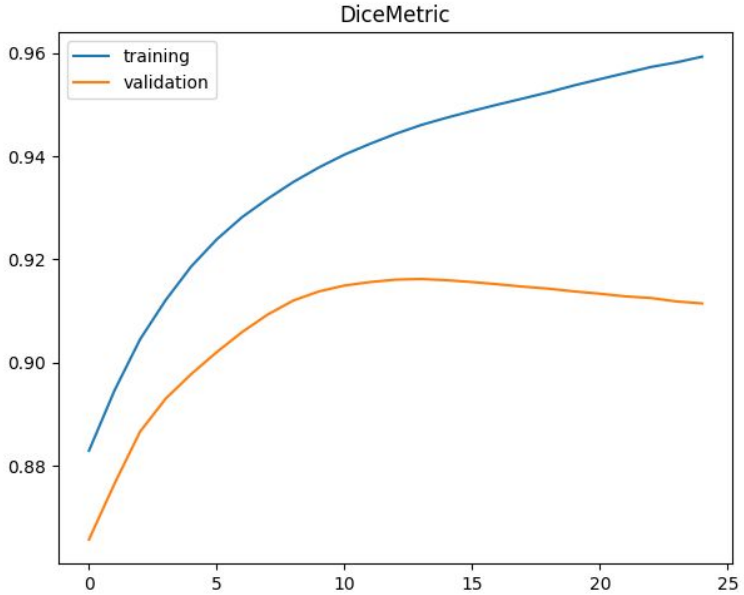
```
for epoch in range(max_epochs):
    print("-" * 10)
    print(f"epoch {epoch + 1}/{max_epochs}")
    model.train()

    epoch_loss = 0
    step = 0
    for i, batch_data in enumerate(train_loader):
        step += 1
        inputs, labels = (batch_data["image"].to(device), batch_data["label"].to(device))

        optimizer.zero_grad()
        outputs = model(inputs)                # predict outputs
        loss = loss_function(outputs, labels)  # calculate loss
        loss.backward()                        # backpropagation
        optimizer.step()
        optimizer.zero_grad()
```

Lab5.1: UNet (2D segmentation)

Overview of Lab_5_1_MONAI(2Dsegmentaton)

Training loop





Lab5.1: UNet (2D segmentation)

Overview of Lab_5_1_MONAI(2Dsegmentaton)

Load Best Model

Evaluate

Inference

```python
# Example & Save (.png)
# Load best model
model.load_state_dict(torch.load(os.path.join("/content/UNet_best_metric_model.pth")))
model.eval()

DSC_all = []
with torch.no_grad():
    for i, batch in enumerate(test_loader):
        img = batch["image"].to(device)
        label = batch["label"].to(device)

        output = model(img)
        pred = torch.argmax(output, dim=1, keepdim=True)

        dice_metric = DiceMetric(include_background=False, reduction="mean")

        dice_metric(y_pred=pred[0], y=label[0].to(device))
        DSC_all.append(dice_metric.aggregate().item())

        if i % 5 == 0:
            visualize_rgb_with_dice(
                image=img[0],
                gt=label[0],
                pred=pred[0],
                dice_value=dice_metric.aggregate().item()
            )
        dice_metric.reset()
```

Lab5.1: UNet (2D segmentation)

Overview of Lab_5_1_MONAI(2Dsegmentaton)

Load Best Model

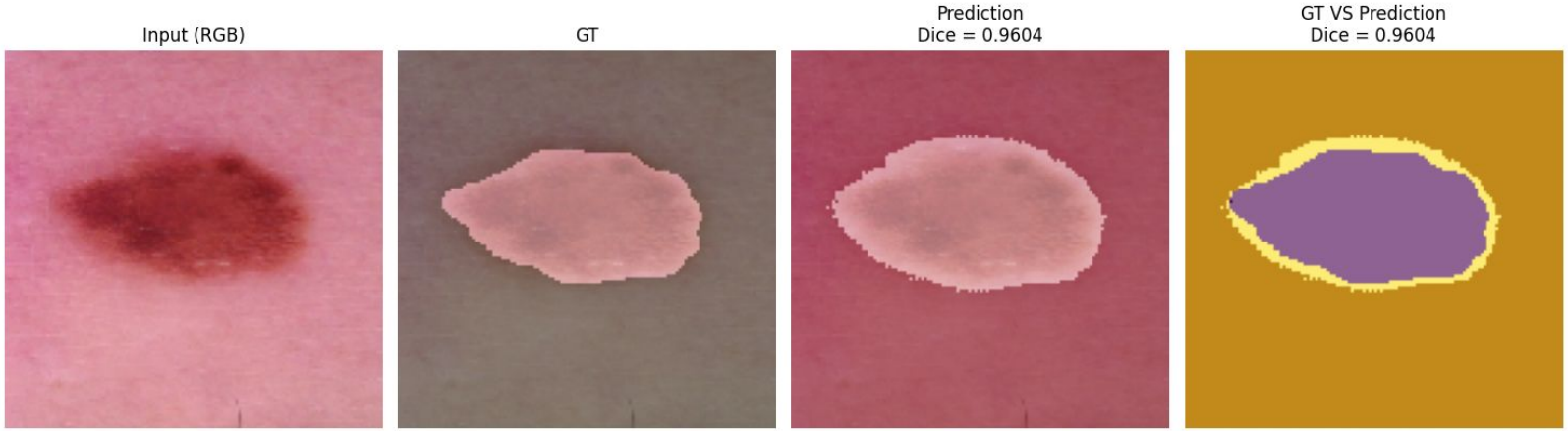
Evaluate

Inference

```
batch["pred"] = pred
batch = [post_transforms(i) for i in decollate_batch(batch)]

# Create the output directory if it doesn't exist
output_dir = "output/UNet"
os.makedirs(output_dir, exist_ok=True)

# Create a tensor (e.g., a simple example tensor)
tensor = torch.argmax(batch[0]["pred"], dim=0).detach().cpu()

# Metadata for saving the NIfTI file
metadata = {
          "filename_or_obj": os.path.join(output_dir, "example.nii.gz")
          }

# Initialize the SaveImage transform
saver = SaveImage(output_dir=output_dir, output_postfix="_UNet", output_ext=".png", resample=False)

# Save the tensor as a NIfTI file
saver(tensor, meta_data=metadata)

print(f"NIfTI file saved in {output_dir}")
```

Lab5.1: UNet (2D segmentation)

Results may vary between runs due to random seed initialization and hyperparameter tuning; however, the overall performance should be similar to the results shown on this page.



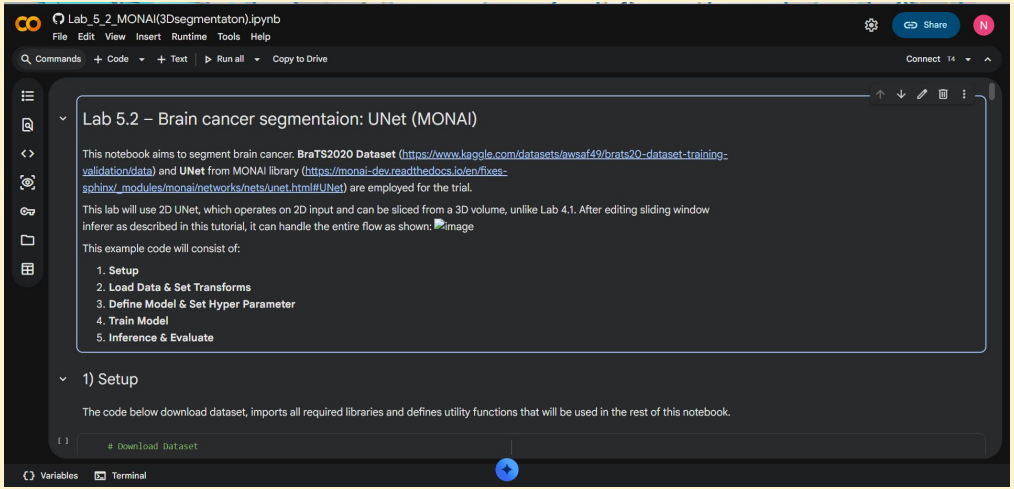

```
Mean Dice: 0.7297
```

Lab5.2: UNet (3D segmentation)

In this lab, you will create and evaluate a brain tumor segmentation model (UNet). Unlike Lab 5.1, this lab focuses on a 3D segmentation task, with the main differences in the DataLoader and inference process. All code can be executed in Lab_5_2_MONAI(3Dsegmentaton.

This notebook will consist of:

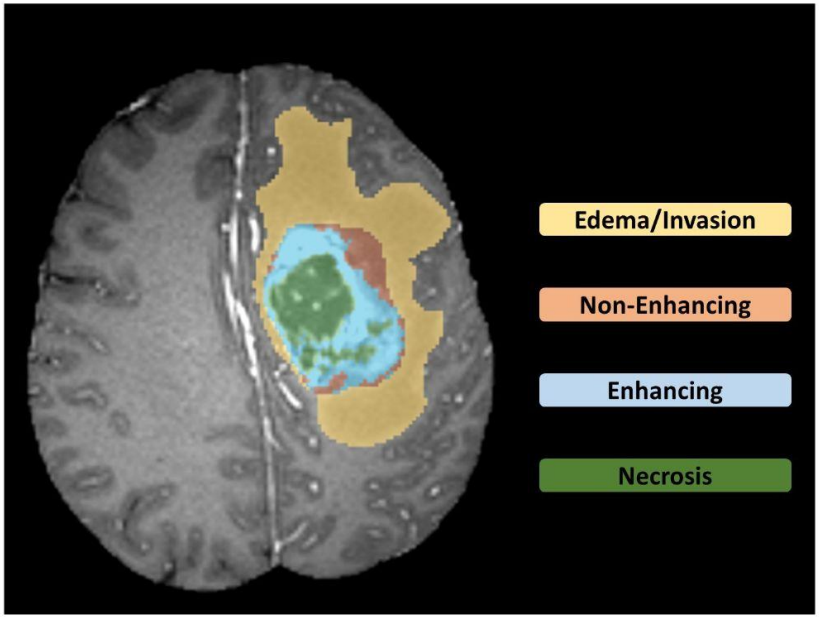
1) Setup
2) Load Data & Set Transforms
3) Define Model & Set Parameter
4) Train Model
5) Inference & Evaluate & Save

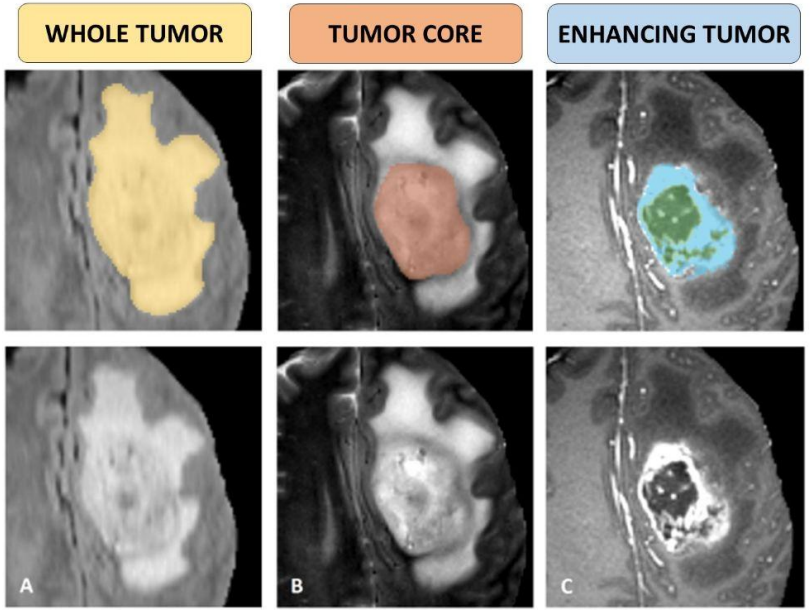


Dataset: Brain Tumor Segmentation 2020 Dataset (BraTS2020)

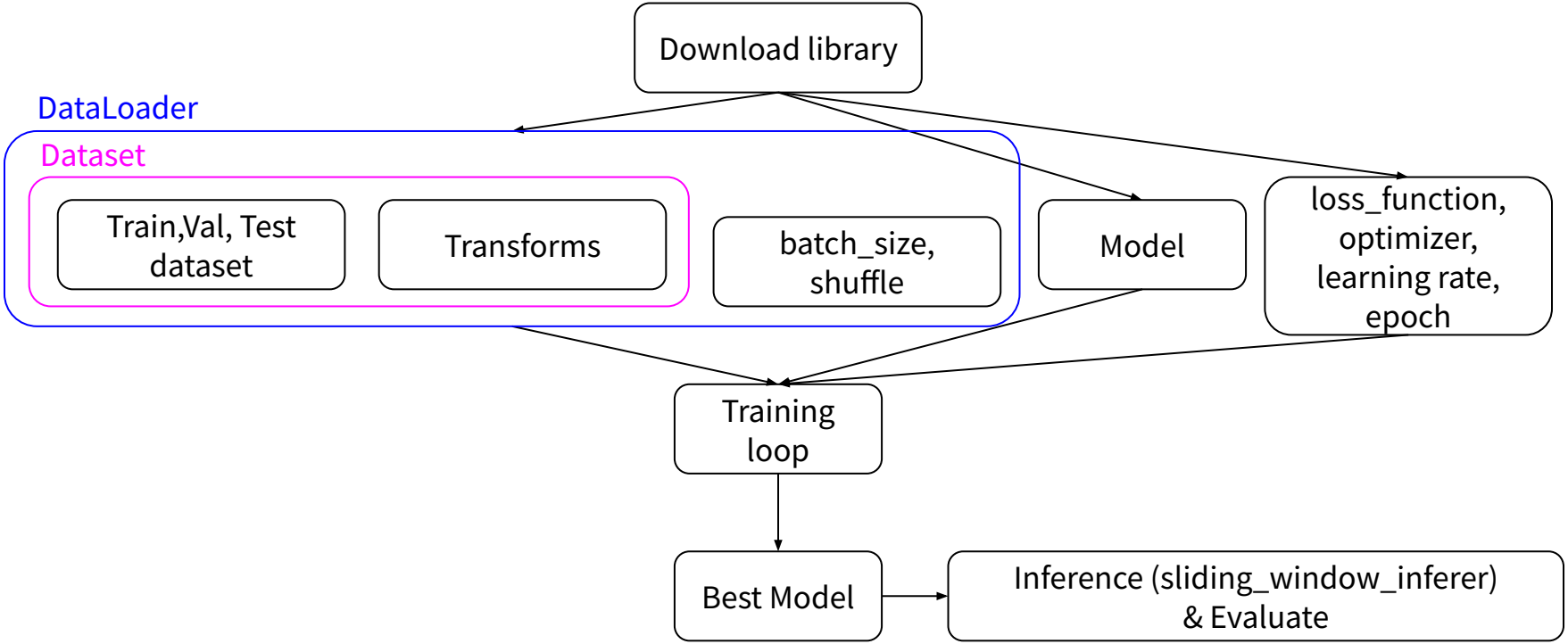
- BraTS 2020 is dataset for brain tumor segmentation, consisting of T1, T1ce, T2, FLAIR with tumors (4 classes), which contains image in nii.gz format
- BraTS 2020 includes **369 training cases**, with further validation/test subjects provided for evaluation.
- BraTS 2020 dataset was released by the Multimodal Brain Tumor Segmentation Challenge organizing team
- To simplify the experiment, we selected only **20 cases** containing FLAIR images and tumor masks.

Dataset: Brain Tumor Segmentation 2020 Dataset (BraTS2020)





Lab5.2: UNet (3D segmentation)



Lab5.2: UNet (3D segmentation)

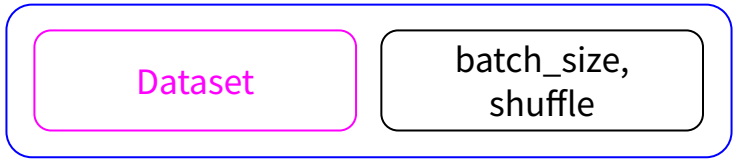
Lab 5.2 is similar to Lab 5.1 in many cells; however, there are several key differences:

Transforms (pre)

```
class ConvertToTumorChannel(MapTransform):
        def __call__(self, data):
            d = dict(data)
            for key in self.keys:
                d[key] = torch.isin(d[key], torch.tensor([1, 2, 3, 4], device=d[key].device)).float()
            return d

# Transforms (pre&post proceeding)
roi_size = (128, 128, 128)

train_transforms = Compose(
        [# 1) Load data path -> tensor
        LoadImaged(keys=["image", "label"],ensure_channel_first=True,image_only=True,dtype=torch.float),
         # 2) Orient the image to the standard coordinate system
        Orientationd(keys=["image", "label"], axcodes="RAS"),
         # 3) scale intensity [0-1023] -> [0-1]
        ScaleIntensityRanged(keys=["image"], a_min=0, a_max=1023, b_min=0.0, b_max=1.0, clip=True),
         # 4) merged all tumor classes into a single class to simplify
        ConvertToTumorChannel(keys="label"),
         # 5) Resize tensor [HxWxD] -> [128x128x128]
        Resized(keys=["image", "label"], spatial_size=roi_size, mode=["bilinear", "nearest-exact"]),
         # 6) Augment (Random flip in each epoch.)
        RandFlipd(keys=["image", "label"], prob=0.5, spatial_axis=0),
        ]
    )
```

Lab5.2: UNet (3D segmentation)

DataLoader



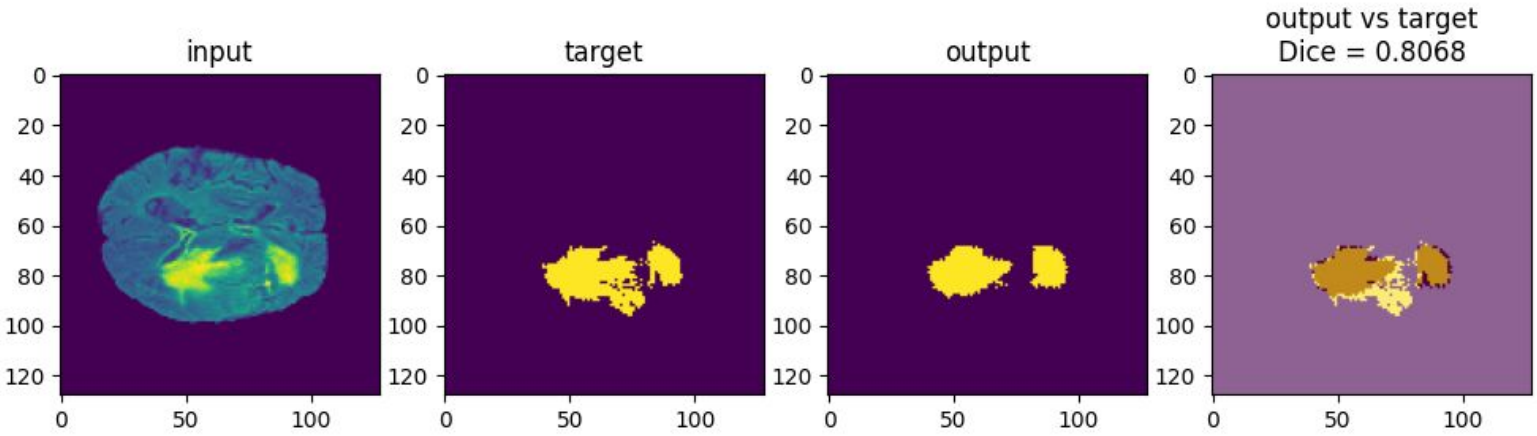
Since the data used in this lab is 3D, but we want to use it in conjunction with a 2D model, MONAI has a specific function for this.

```
# DataLoader 3D -> 2D
train_ds = CacheDataset(data=train_files, transform=train_transforms, cache_rate=1.0, num_workers=4)
val_ds = CacheDataset(data=val_files, transform=val_transforms, cache_rate=1.0, num_workers=4)

patch_func = monai.data.PatchIterd(keys=["image", "label"], patch_size=(None, None, 1), start_pos=(0, 0, 0))
patch_transform = Compose([
            SqueezeDimd(keys=["image", "label"], dim=-1),  # squeeze the last dim
            Resized(keys=["image", "label"], spatial_size=[128, 128]),
    ])

train_patch_ds = monai.data.GridPatchDataset(data=train_ds, patch_iter=patch_func, transform=patch_transform, with_coordinates=False)
train_shuffle_ds = monai.data.ShuffleBuffer(train_patch_ds, buffer_size=30, seed=0)
train_loader = DataLoader(train_shuffle_ds, batch_size=4, num_workers=4, pin_memory=torch.cuda.is_available())

val_patch_ds = monai.data.GridPatchDataset(data=val_ds, patch_iter=patch_func, transform=patch_transform, with_coordinates=False)
val_shuffle_ds = monai.data.ShuffleBuffer(val_patch_ds, buffer_size=30, seed=0)
val_loader = DataLoader(val_shuffle_ds, batch_size=4, num_workers=4, pin_memory=torch.cuda.is_available())
```

Mean Dice: 0.7252 Mean Dice: 0.7252

Lab5.2: UNet (3D segmentation)

Results may vary between runs due to random seed initialization and hyperparameter tuning; however, the overall performance should be similar to the results shown on this page.

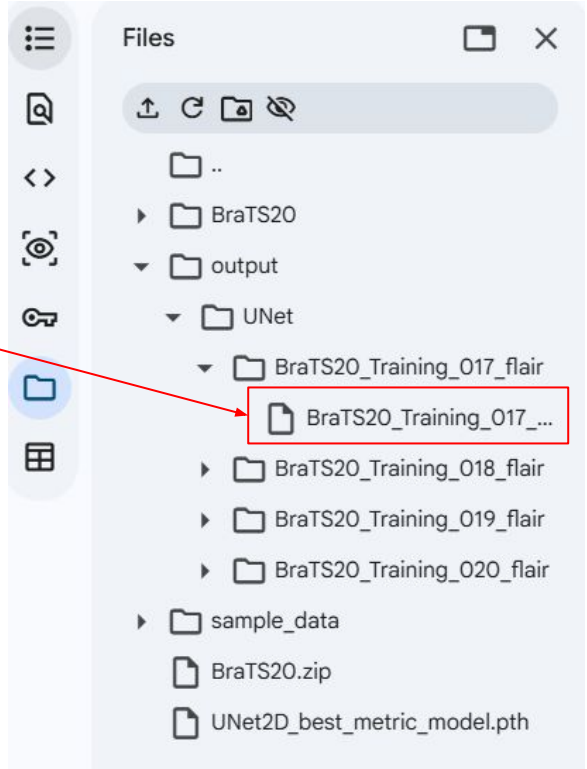



```
Mean Dice: 0.7252
```

Mean Dice: 0.7252 Mean Dice: 0.7252

Lab5.2: UNet (3D segmentation)

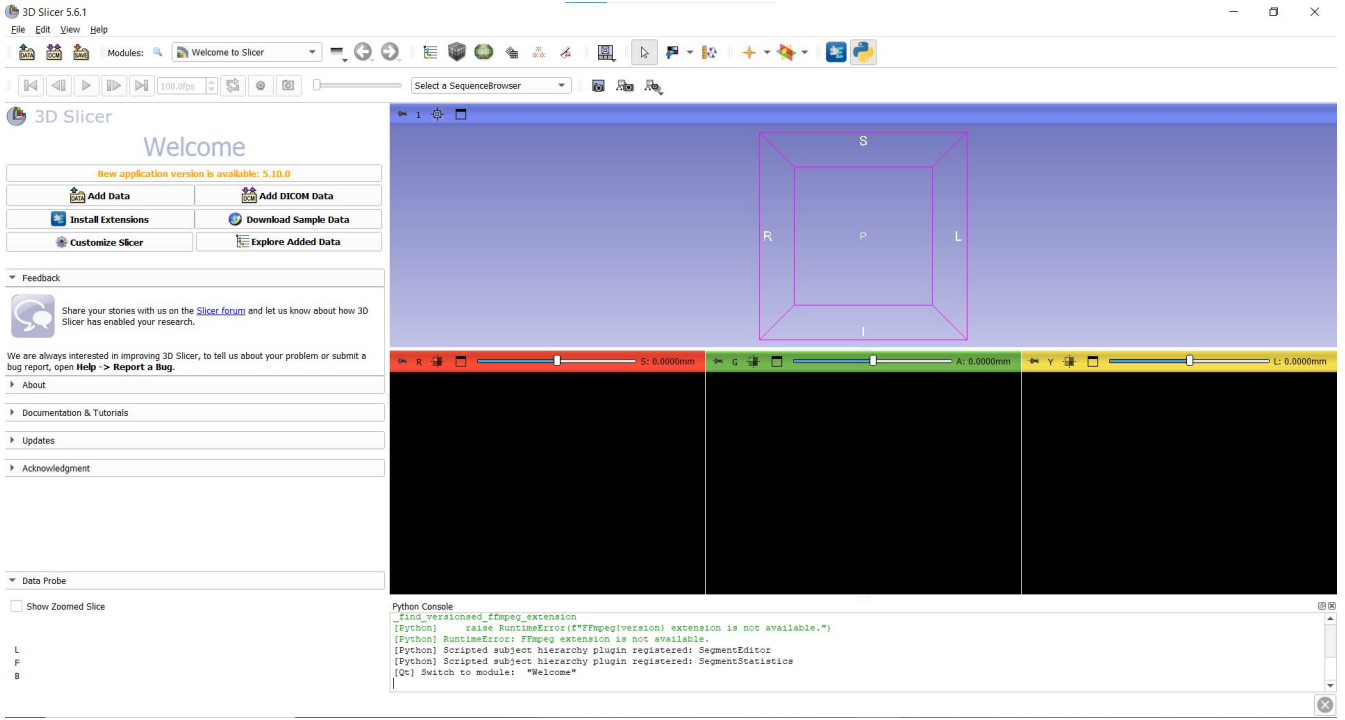
The outputs generated from the test dataset are saved as .nii.gz files. These files can be downloaded and opened for visualization in 3D Slicer.



3D Slicer

- **3D Slicer** is a free, open-source software platform for medical image analysis and visualization
- Supports **3D/4D imaging data** such as CT, MRI, and ultrasound
- Provides tools for **segmentation, registration, and 3D visualization**
- **Download**

3D Slicer (cont.)

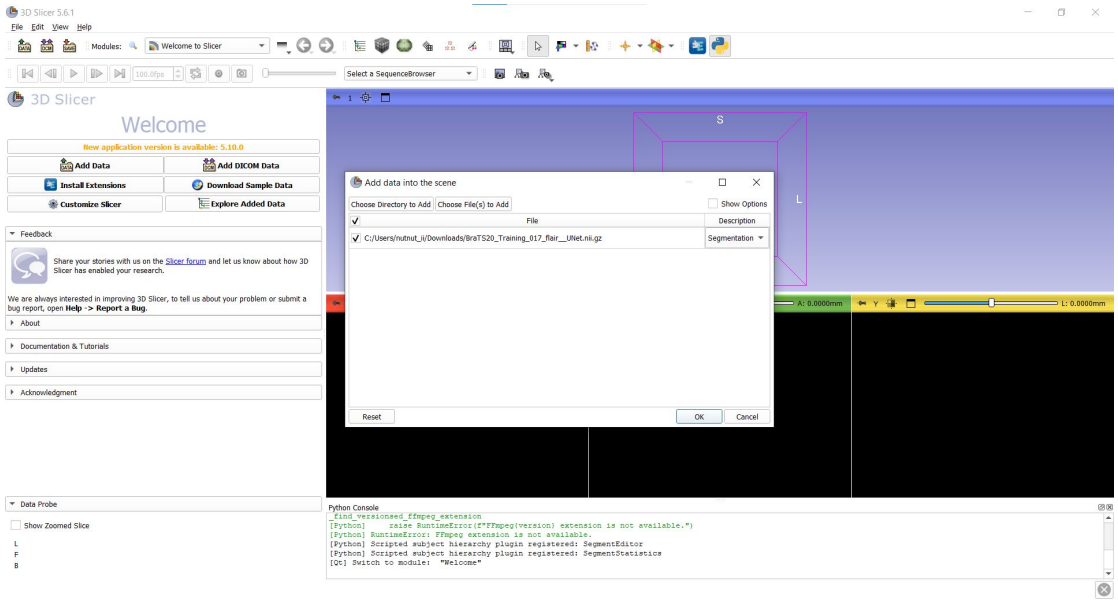


Example image of the 3D slicer program.

3D Slicer: Load a segmented data to the program

Steps to Load a Segmentation (.nii.gz) in 3D Slicer

1. **Load the .nii.gz file** using *File → Add Data*
2. In the **Add Data** window, set the file type to **Label Map**.
3. Click **OK** to load the segmentation.
4. Right-click the label map and select **Convert to Segmentation**.
5. The segmentation will appear in the **Segment Editor** and 3D view.



3D Slicer: Load a segmented data to the program

Steps to Load a Segmentation (.nii.gz) in 3D Slicer

1. **Load the .nii.gz file** using *File → Add Data*
2. In the **Add Data** window, set the file type to **Label Map**.
3. Click **OK** to load the segmentation.
4. Right-click the label map and select **Convert to Segmentation**.
5. The segmentation will appear in the **Segment Editor** and 3D view.