Deep Learning for Automatic Cancer Segmentation and Classification in 3D CT Scans

The task covers various aspects of the deep learning fundamentals, including convolutional neural networks (CNNs), image preprocessing, data augmentation, model evaluation, and specific challenges associated with medical image analysis (heterogeneous appearances and resolutions).

We provide a de-identified pancreas CT dataset with segmentation annotations and lesion subtype labels. (three classes). The objective is to build a multi-task deep learning model for pancreas cancer segmentation (label 1: normal pancreas (red), label 2: pancreas lesion (green)) and classification.

The model should have a shared encoder to extract image features and two separated decoder head for segmentation and classification, respectively. Please develop the model based on the popular nnUNetv2 (MIC-DKFZ/nnUNet) framework, which already provides state-of-the-art segmentation networks and out-of-the-box image preprocessing and model training pipelines. You only need to modify the architecture to implement a classification head.

After finished the network design, you can train it on the provided training dataset followed by inferring on the validation and testing sets.

Dataset

In order to enable tasks to be completed on publicly available free computing resources (e.g., T4 on Colab and K80GPUs on Kaggle), the original large 3D pancreas CT scans have been cropped to small region of interests (ROIs).

Dataset Splits

Split Subtype 0 Subtype 1 Subtype 2
Train 62 106 84
Validation 9 15 12

Folder Structure

```
data
├── train
│  ├── subtype0
│  │  ├── quiz_0_041.nii.gz # mask (0-background; 1-pancreas; 2-lesion)
│  │  ├── quiz_0_041_0000.nii.gz # image
│  │  ├── ...
│  ├── subtype1
│  └── subtype2
└── validation
│  └── subtype0
│  │  ├── quiz_0_168.nii.gz # mask (0-background; 1-pancreas; 2-lesion)
│  │  ├── quiz_0_168_0000.nii.gz # image
│  │  ├── ...
│  ├── subtype1
│  └── subtype2
├── test # only images are provided
│  ├── quiz_037_0000.nii.gz
│  ├── quiz_045_0000.nii.gz
│  ├── quiz_047_0000.nii.gz
```

```
| ├── ...
```

In train and validation folders, images and masks are separated based on the subtypes. Each image and mask is named with the format: quiz_subtype-id_case-id_0000.nii.gz and quiz_subtypeid_case-id.nii.gz, respectively. In the test set folder, only images are provided with the format quiz_case-id_0000.nii.gz.

Submission

_results.pdf: A technical report that describes your methods and validation results.

results.zip: segmentation and classification results of testing cases

```
├── your_name_results.zip
| ├── quiz_037.nii.gz
| ├── quiz_045.nii.gz
| ├── quiz_047.nii.gz
| ├── ...
| subtype_results.csv
```

Please save the classification results as subtype_results.csv with the following two columns

Names	Subtype
quiz_037.nii.gz	0
quiz_045.nii.gz	1
quiz_045.nii.gz	2
...	...

Remarks

Finishing with the nnUNetv2 framework (nnU-Net ResEnc M model) is a mandatory requirement because it provides SOTA segmentation performance and has great flexibilities for network extensions.
It is not allowed to use any publicly available datasets or pre-trained weights.
Please also don't use the validation set as training set during model development. The role of validation set is to debug or moniter the performance during training.

The default number of training epoch is 1000 in nnU-Net. Considering the limited runtime on Colab/Kaggle, you don't need to train so many epochs. The model training can be stopped when the loss converges.

Expectations

segmentation performance
whole pancreas (normal pancreas (label==1) + pancreas lesion (label==2)
np.uint8(label > 0)) DSC: 0.85+,
pancreas lesion DSC (np.uint8(label==2)): 0.27+
classification performance: macro-average F1: 0.6+