

深度學習於醫學影像分析—Deep learning in medical image analysis  
Fall 2024

**Homework 3, due on 2024/11/18**

1. In Homework 2, each SPECT image is assigned to one of the three Parkinson's disease (PD) stages. In fact, these three PD stages are merged from the original six stages: 0=normal, 1=PD stage 1, 2=PD stage 2, 3=PD stage 3, 4=PD stage 4, and 5=PD stage 5.
  - a. The distribution of our training data over 6 PD stages (classes) is relatively imbalanced, which could result in a distortion of the classification model. Also, our data seem not large enough to construct a powerful image classifier. Please adopt appropriate approaches to address these issues.
  - b. This homework provides a new file “**train\_hwk02\_new.csv**”, where the variable “Stage\_New” represents the original 6 PD stages that the SPECT images belong to. Use this new file, which can be downloaded from e3 (<https://e3.nycu.edu.tw/>) under “Homework 3”, for the deep learning with the ResNet50 architecture that we did in Homework 2.
  - c. Load your created prediction models with the test images and generate their predicted probabilities for 6 PD stages and predicted disease stages. Upload a file “**ResNet50\_6c.csv**” for these prediction results. Please also upload the Python codes of your solution (saved as a .ipynb file) and its compiled html file.
2. In the second part of this Homework, you are asked to analyze magnetic resonance imaging (MRI) images. We have a total of 120 three dimensional (3D) brain MRI images, where 60 of them are from normal participants and 60 are from patients with brain tumors.

The goal is to predict whether the 3D MRI images are from normal participants or from patients with brain tumors.

3. The zipped file “**hwk03\_data.zip**”, which can be downloaded from e3 (<https://e3.nycu.edu.tw/>) under “Homework 3”, contains all MRI datasets for this homework.

In the folder “DICOM”, you can find 120 sub-folders that are named by persons’ ID’s. Under each person ID sub-folder, there are two sub-sub-folders “T1” and “T2”, which contain T1-weighted and T2-weighted two dimensional (2D) MRI images at different brain positions from that person, respectively. Notice that the numbers of 2D MRI images differ from person to person, but the numbers of T1-weighted and T2-weighted images from the same person are the same. Also, there is an “InstanceNumber” tag in each slice’s DICOM header. Please use the InstanceNumber to be the index of locations for 3D MRI, NOT use the order of filenames.

The file “**train.csv**” can be used to build up your prediction models and the file “**test.csv**” is for testing models’ accuracy. Please read the file “**README.pdf**” first for the meaning of each data item in “**train.csv**” and “**test.csv**”.

4. To build the prediction models for normal/brain-tumors classification using 3D MRI images, you are asked to perform the following analyses:

- a. Image contrast adjustment: The header of the DICOM file provides the window width (WW) and window center/level (WC) values:

$$WW = \text{highest\_visible\_value} - \text{lowest\_visible\_value}$$

$$WC = (\text{highest\_visible\_value} + \text{lowest\_visible\_value})/2$$

We then adjust each pixel value (imval) in the image to be

$$\text{imval\_adj} = \begin{cases} \text{highest\_visible\_value} & \text{if } \text{imval} > \text{highest\_visible\_value} \\ \text{imval} & \text{if } \text{lowest\_visible\_value} \leq \text{imval} \leq \text{highest\_visible\_value} \\ \text{lowest\_visible\_value} & \text{if } \text{imval} < \text{lowest\_visible\_value} \end{cases}$$

These imval\_adj values are further normalized to a range of [0,255] for regular computer screen display:

$$\text{im} = 255 \times [(\text{imval\_adj} - \text{lowest\_visible\_value})/WW]$$

Please perform the above normalization process for each 2D MRI image.

These normalized images are the used for the following analyses.

- b. Notice that the numbers of 2D MRI images differ from person to person. You are asked to apply the **trilinear interpolation approach** ([https://en.wikipedia.org/wiki/Trilinear\\_interpolation](https://en.wikipedia.org/wiki/Trilinear_interpolation), <https://pytorch.org/docs/stable/generated/torch.nn.functional.interpolate.html>) to down/up sample images to unify the depth dimension of all persons’ 3D MRI images. **We set the target image number to be 22.** After applying trilinear interpolation, the size of each person’s 3D MRI image is unified as

(height × width × depth) = (512 × 512 × 22).

- c. Use convolutional neural networks (CNNs) to extract features in 3D MRI images. Utilize transfer learning to adopt the pre-trained model whose weights are trained from a large source dataset to improve prediction accuracy.

Perform the **single slice**, **late fusion**, **early fusion**, and **3D CNNs**. Output the prediction results for the test dataset based on each of the 4 CNN approaches.

The pre-trained models require input images with three channels (e.g., color). Our input data are grayscale medical imaging, and we thus represent three channels for pre-trained models with T1 grayscale, T2 grayscale, and the average of T1 and T2 grayscales.

- d. Upload 4 files “**single.csv**”, “**late.csv**”, “**early.csv**”, and “**3D.csv**” for prediction results based on single slice, late fusion, early fusion, and 3D CNNs, respectively. Please also upload the Python codes of your solution (saved as a .ipynb file) and its compiled html file.
  - e. Select a **best** model from d. for the Kaggle competition.
5. Kaggle submission: **Only for the 3D MRI analysis**
- a. Kaggle link:  
<https://www.kaggle.com/t/06eda64654bd4ff9829c6d7c6cb1be89>
  - b. Display team name: <studentID>
  - c. The scoring metric is accuracy.
  - d. You can submit at most 5 times each day.
6. Report submission: **Please submit 2 reports—one for the first part of the SPECT image analysis and the other for the second part of the 3D MRI analysis**
- a. How did you address the problems of imbalanced data and insufficient sample size? (5 pts)
  - b. Reproducibility of the results (the first part 2 pts and the second part 4 pts)
  - c. Number of parameters: Please write the parameter count of your final selected model to the Kaggle competition (2 pts)
  - d. The difficulty during training (the first part 3 pts and the second part 8 pts)

- e. Briefly explain the structures of the models you are using for the second part: You are required to do analyses of single slice, late fusion, early fusion, and 3D CNNs (16 pts)
  - f. You should submit compiled HTML file and ipynb notebook with name prefix to e3 platform. Also, submit the prediction result csv file.
    - The first part: {studentID}\_1.ipynb, {studentID}\_1.html, {studentID}\_1.pdf, ResNet50\_6c.csv
    - The second part: {studentID}\_2.ipynb, {studentID}\_2.html, {studentID}\_2.pdf, single.csv, late.csv, early.csv, 3D.csv
7. Grading policy
- a. Kaggle: **60 pts based on your final selected model for the 3D MRI analysis**  
 The public leaderboard is calculated with approximately 50% of the test data. The final score will be based on the other 50% (private leaderboard), so the final scorings may be different.
    - Basic score (30 pts):  
Over baseline: 30 pts
    - Ranking score (30 pts):  
 Accuracy:  $\left(1 - \frac{\text{rank}-1}{\text{num\_participated}}\right) \times 20$  pts (the larger the accuracy, the higher the ranking)  
 Number of parameters:  $\left(1 - \frac{\text{rank}-1}{\text{num\_participated}}\right) \times 10$  pts (the smaller the number of parameters, the higher the ranking)
  - b. Report: **The first part 10 pts and the second part 30 pts**
8. Error submission
- If you submit the wrong format of files to e3, your score may be reduced.
- a. Team name error: 0 pts
  - b. Late submission: -10 pts per day