Nodule Classification using a Multi-Task Training

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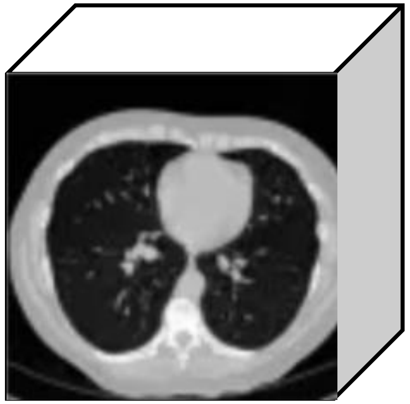
LUNA25 Team : MClab
https://github.com/dobe0715/LUNA25_MClab

Data set

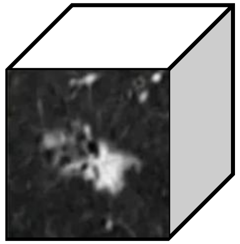
4069 patients



162x512x512

- Nodule ID
- Coordinates
- Malignant / Benign

6163 samples

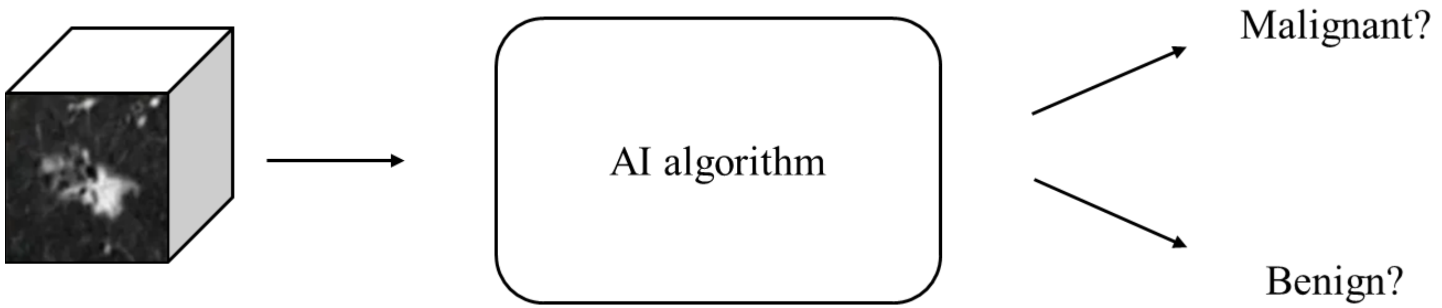


64x64x64

Problem definition and challenges

Problem

- Binary classification of malignant nodules in lung CT scans.



Challenges

- The complexity of 3D data
  - 3D datasets exhibit more complex spatial features than 2D images.
- Data imbalance
  - The dataset exhibits significant class imbalance, with only 555 malignant cases out of 6,163 total images (approx. 9%).

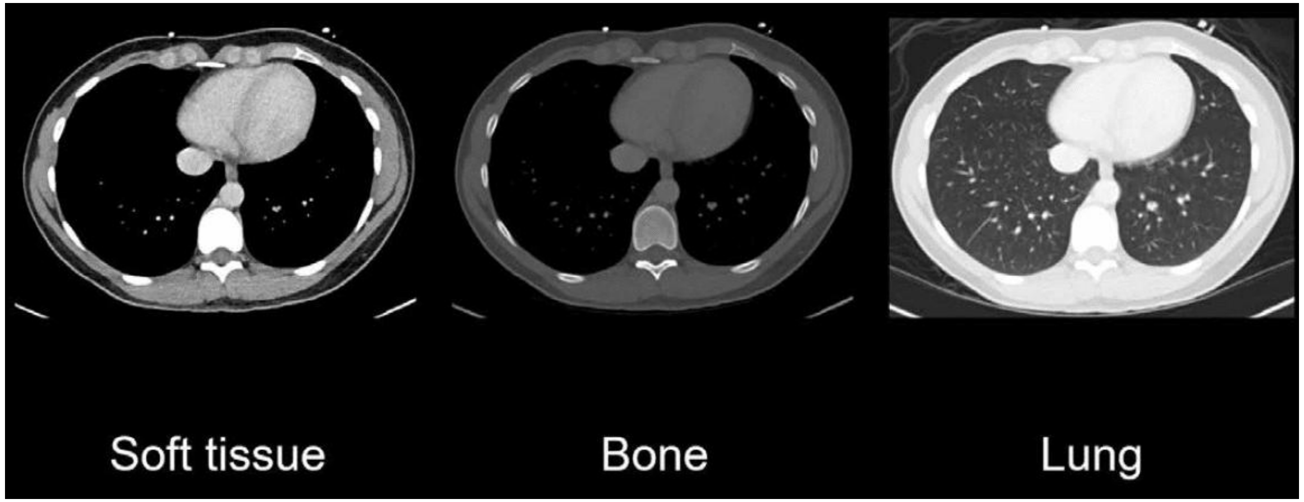
Overview

- Data Preprocessing
- Model architecture
- Inference strategy
- How to evaluate Model

Data preprocessing

Hounsfield Unit (HU) value

Substance	HU
Air	-1000
Lung	-500
Water	0
Blood	30~45
Soft tissue	100~300
~~bone~~	~~700~3000~~



https://litfl.com/abdominal-ct-windows-basics/

-1000 ~ 400 clipping!

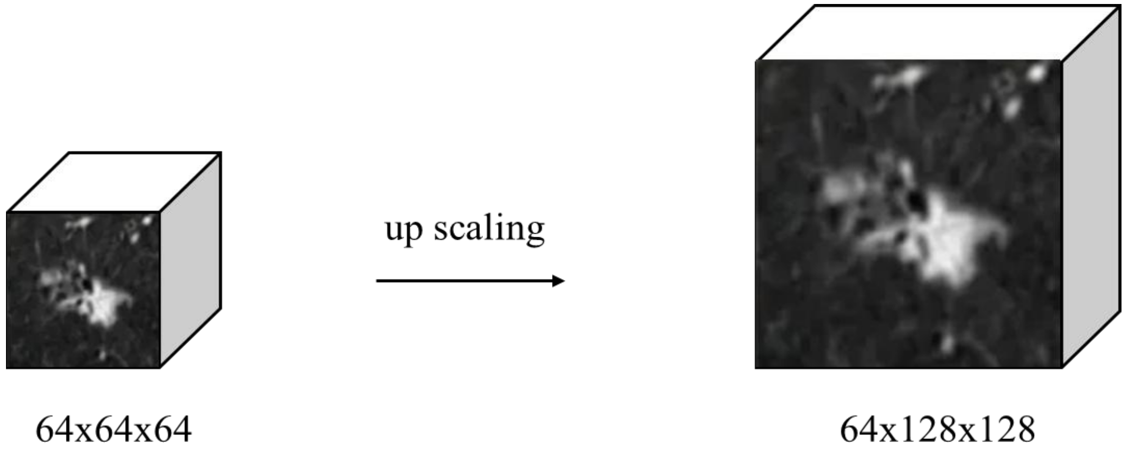
Data preprocessing

Our method

Upscaling nodule patches from 64×64×64 to 64×128×128

The I3D model reduces unnecessary down sampling in deeper layers and mitigates excessive loss of spatial detail.

Although simple, the approach is effective and deliberately designed.



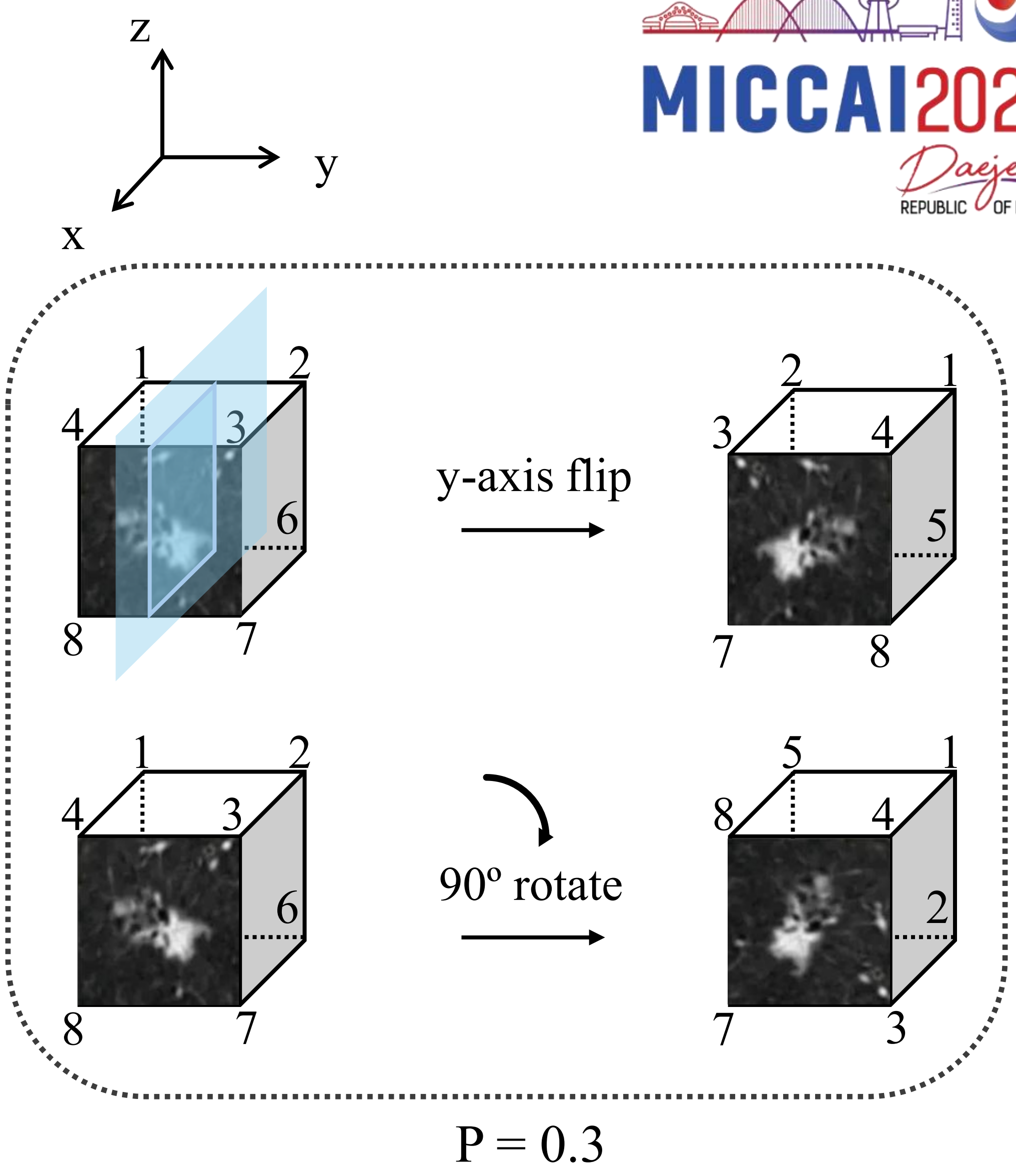
Data preprocessing

Our method

y- and z-axes **flips** and 90º **rotation**

These augmentations aim to enhance model robustness.

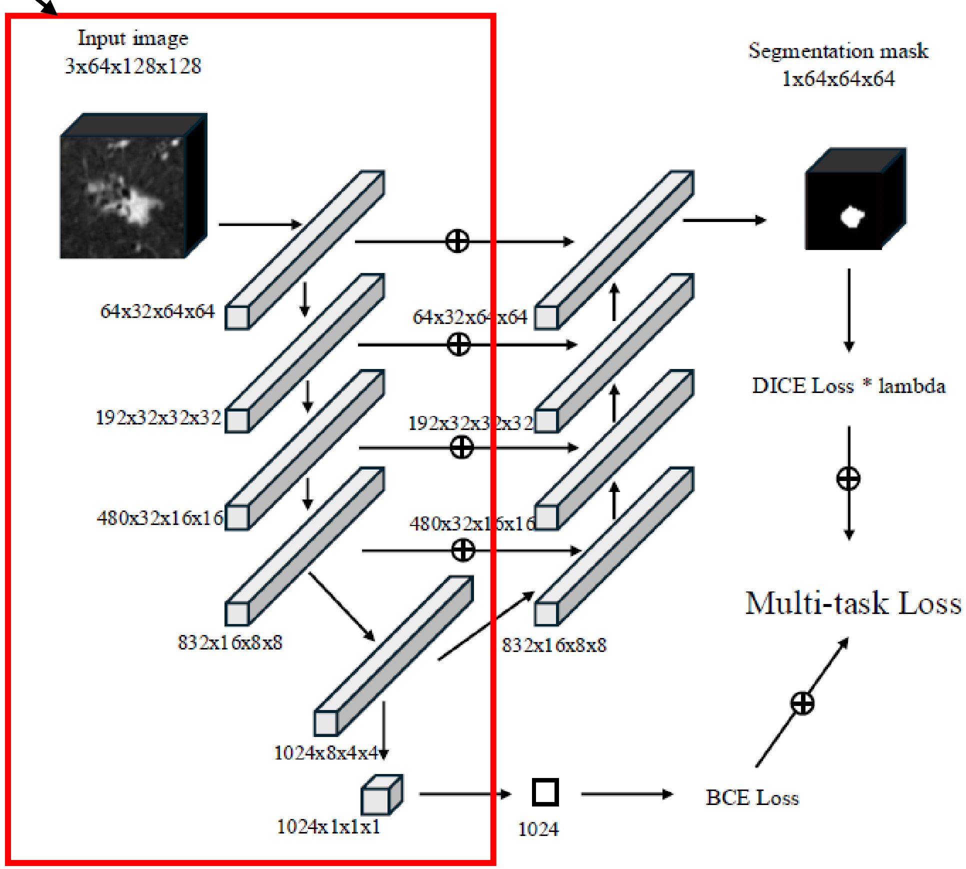
These augmentation choices are heuristic.



Model architecture

Model architecture : Multi-task learning

I3D model



Classification model (main task)

- An I3D model pre-trained on the Kinetics-400 dataset
- Final classification is performed using global average pooling and an MLP head.

Segmentation model (auxiliary task)

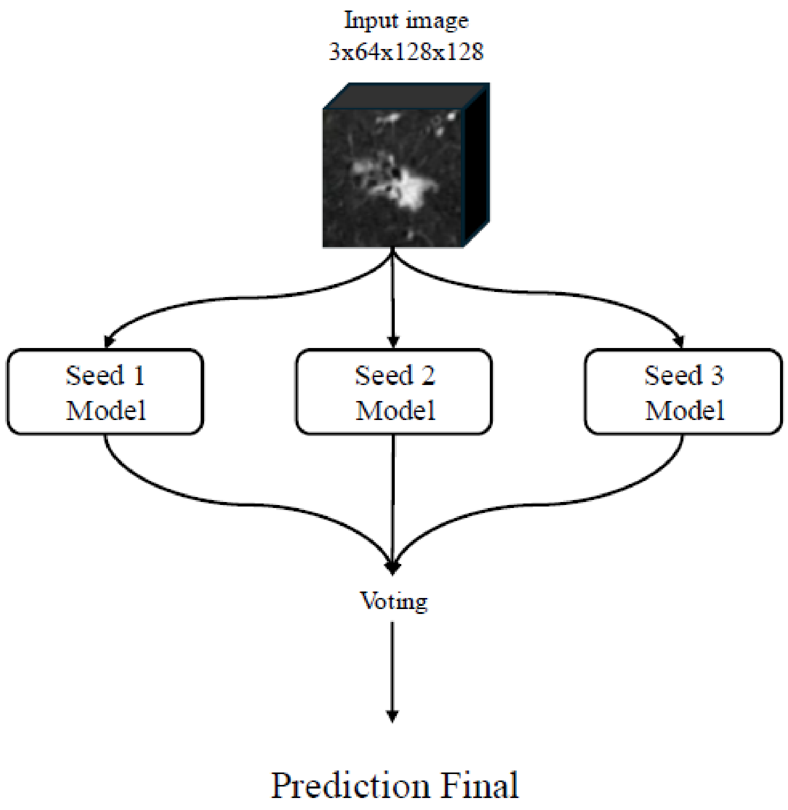
- To integrate I3D features, we use U-Net-like skip connections

The tasks are mutually complementary.

- nodule type ↔ shape
  (classification) (segmentation)

Inference strategy

Inference strategy



Goal: Reduce model bias and maximize generalization performances.

- Three identical models were trained independently, **each initialized with a random seed.**

- The final prediction was determined using soft voting. (Soft voting: weighted sum of the predicted probabilities of each model)

Model evaluation

Experimental setup

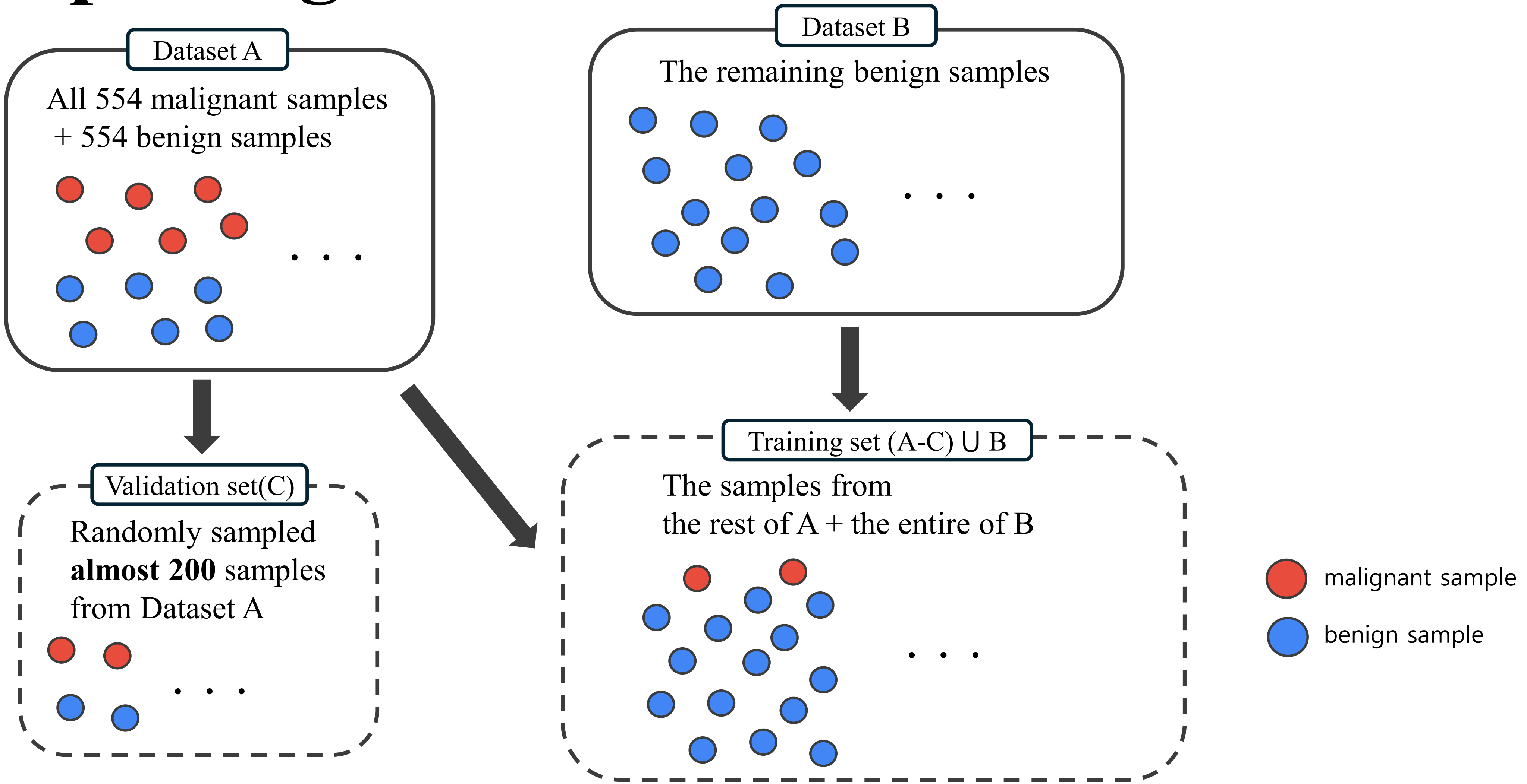
Goal

To address severe data imbalance and ensure reliable validation

Dataset

6157 CT patches with 554 malignant from the LUNA25 challenges (excluding 6 samples without masks)

Splitting method



Additional training method

- EMA(Exponential Moving Average) for weight updates
  - $\theta_{EMA}^{t} = \alpha \cdot \theta_{EMA}^{t-1} + (1 - \alpha) \cdot \theta^{t}$ (t : iteration)

- AMP(Automatic Mixed Precision) training
  - In calculation, using FP32 & FP16 mixing

Hyperparameters

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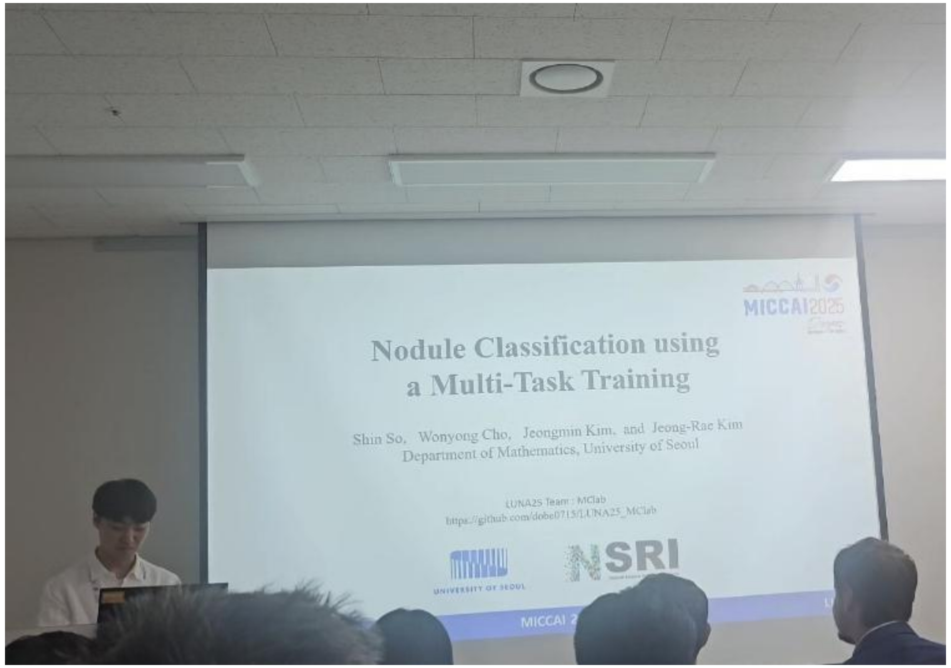
training config	our model
weight init (aux)	He-normal
optimizer	Adam
base learning rate	1×10^{-4}
weight decay	5×10^{-4}
optimizer momentum	$\beta_1 = 0.9, \beta_2 = 0.999$
batch size	32
training epochs	15
EMA	0.998
lambda (for aux loss)	0.5

Rank

1st	thomas.buddenkotte	v1	31 July 2025	0.7807	
2nd	vaicebine	Pulse-3D	25 July 2025	0.7466	
3rd	doobee (MClab)	NoduleMC	28 July 2025	0.7448	
4th	zry1054 (LUNA Summer)	FT	31 July 2025	0.7401	
5th	mx54039q (LUNA-Seeker)	LUNA-PN9	1 Aug. 2025	0.7336	

MICCAI Challenge



Q & A

Thank You ☺