

Technical Report: “CWRU-UH-Cornell” on GDP-HMM Challenge

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1. Motivation

Current state-of-the-art dose-distribution prediction falls into two broad families:

1. 3D segmentation backbone – e.g. cascaded U-net in the OpenKBP “C3D” [1] method; the organizer’s baseline for GDP-HMM [2] uses a MedNeXt-Base network [3].
2. 2D diffusion-based generators – DoseDiff [4], DiffDP [5], etc.

Given the limited challenge timeline and the lack of decisive evidence demonstrating one method is better than the other due to nature of stacking multiple innovations in a single approach, we chose a straightforward 3D segmentation backbone strategy. Our goal was to identify a strong segmentation backbone architecture, keep the data preprocessing and loading *identical as provided in the challenge*.

2. Experiments and Findings

2.1 Experiment 1 – SegMamba backbone [6]

Hypothesis: With larger parameters, network learns richer representations of complex inputs, thus SegMamba (66M) segmentation network should outperform the MedNeXt-base (10M)

Outcome: best validation loss 0.2231 (MAE=2.561, ID: 2475) at epoch 388 – worse than the organizer’s baseline. Limited time precluded an in-depth ablation, but two explanations are plausible: (i) Specialized segmentation network may be ill-suited to sharply peaked dose distribution prediction; (ii) Heterogenous multi-input information is not well-utilized by SegMamba

2.2 Experiment 2 – MedNeXt-Large (kernel 5)

We reverted to MedNeXt and selected “Large, k=5” variant, strongest configuration in the original paper.

Hypothesis: MedNeXt-Large (k5) should outperform the MedNeXt-base (10M)

Outcome: best validation loss 0.2090 (MAE=2.411, ID: 2566) at epoch 308 – a clear improvement over both the baseline (MAE=2.54) and SegMamba.

2.3 Experiment 3 – Physics-informed composite loss

We prototyped a combination of Dice, L1, MAE loss to improve PTV coverage and OAR sparing. Implementation bugs and time pressure prevented a stable run; the idea was shelved.

2.4 Experiment 4 – Smooth-L1 loss

Observation: validation L1 plateaued near 0.20 with smaller and slower decrease. We replaced L1 with Smooth-L1(beta=0.25) to emphasize sub-2.4 Gy voxels while retaining robustness to larger errors.

Outcome: best validation L1 loss 0.2116, Smooth-L1 loss 0.1115 (MAE=2.405). We expect a lower beta (=0.15) would have pushed MAE further down, but the validation phase has already been completed. This experiment is our team’s final submission for the challenge.

Links to code and Docker Hub: [GitHub Code Link](#), [Docker Hub Link](#)

3. Future work

Our immediate next step is to prototype a **cascaded MedNeXt** workflow, mirroring the two-stage C3D design: a coarse-resolution MedNeXt generates an initial dose volume, which a second, finer-resolution MedNeXt then refines. Because MedNeXt accepts an arbitrary number of channels, this cascade can be assembled with minimal engineering effort and, judging from C3D’s success, should push voxel-wise MAE below our single-stage result.

Yet MAE alone is not a perfect proxy for clinical plan quality. In our own study the **SegMamba model recorded the top plan-quality score (Metric-2 = 118.44) despite a higher MAE (2.561)**, underscoring that backbone choice—and perhaps the broader CNN-versus-diffusion paradigm—affects deliverability metrics differently from mean absolute error. A systematic sweep that disentangles MAE from Metric-2 across MedNeXt cascades and representative diffusion models is therefore warranted.

Another promising lever is the **use of distance maps** in place of binary masks. DoseDiff attributes much of its gain to this richer geometric encoding. In a sub-study of Experiment 2 we replaced OARs with distance maps and reached a best validation loss of 0.2246 (epoch 322)—encouraging but not yet superior to the binary baseline. A more thorough integration of distance-encoded PTV and OAR channels into MedNeXt can be further investigated.

Finally, future work should examine the eight-channel input stack itself—some elements may be redundant—and expand **physics-informed loss** so the optimizer is driven not only by MAE but also by structural fidelity and plan-quality surrogates. Together, these directions aim to close the remaining gap between algorithmic accuracy and clinically actionable dose plans while keeping inference costs modest compared with diffusion-based pipelines

4. Implementation Details

All experiments were executed on a Linux HPC cluster, Python 3.11.3, PyTorch 2.3.1 compiled with CUDA 12.1. The job used 4 A40 GPUs (48GB VRAM each). Apart from our efficient dataloader, the training pipeline is the same as organizer’s implementation (“train_lightning.py”). Memory limited train batch size to 2, but with efficient dataloader, was able to increase it to 4. However, 2 was still used for sake of comparison with previous experiments. The default train budget was set to 120 hours or max epoch 400; for the final run (“Experiment 5”) extended to 144 hours or max epoch 600.

5. References

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