Improving TG-43 dose accuracy with Deep Learning

S. QUETIN [1,2], **B. BAHORIC** [3], **F. MALEKI** [4,5,6], **S.A. ENGER** [1,2,7]

1. Medical Physics Unit, Department of Oncology, McGill University, Montreal, QC, Canada
2. Montreal Institute for Learning Algorithms, Mila, Montreal, QC, Canada
3. Department of Radiation Oncology, Jewish General Hospital, McGill
4. Department of Computer Science, University of Calgary, Calgary, AB, Canada
5. Department of Diagnostic Radiology, McGill University, Montreal, QC,Canada
6. Department of Radiology, University of Florida, Gainesville, FL, USA
7. Lady Davis Institute for Medical Research, Jewish General Hospital,Montreal, QC, Canada

INTRODUCTION

- Radiotherapy is an important component of cancer treatment with approximately 50% of all cancer patients receiving radiotherapy during the course of their treatment.
- High dose rate brachytherapy is a form of radiotherapy, where a sealed highly radioactive photon emitting radiation source is temporarily placed inside or in proximity of the tumor via thin hollow implanted catheters/applicators irradiating the tumor from inside out.
- Current clinical treatment planning software treat the patient's body as a large water sphere, ignoring attenuation of the radiation by the patient's tissue and inserted needle/applicators.
- The most accurate method and the gold standard to calculate absorbed dose to the tumor and radiation sensitive healthy tissues in radiotherapy is the Monte Carlo method.
- However, the Monte Carlo method is computationally expensive and too slow for use in the time-sensitive clinical workflow.

AIM

This study aims to provide a solution to the accuracy-time trade-off for high dose rate brachytherapy dosimetry by using deep learning.

METHOD

Database:
Currently retrospective data from 98 patients that underwent Iridium-192 based high dose rate breast brachytherapy were used to build the Deep Learning model.

Monte Carlo simulations:
- Research treatment planning system RapidBrachyMCTPS[1] was used.
- 10^7 decay events were simulated for each dwell position, with a voxel size of 1x1x1 mm^3
- Computations were performed on Compute Canada cluster and lasted between 10 to 15 minutes parallelized on a 64 cores CPU.

Data for training:
- The patients data was randomly split in training (70 patients), validation (14) and test sets (14).
- 25 dwell positions were used to create 3D dose maps for training and validation sets and all the dwell positions were used to create the dose maps for the Test set.
- Volumes were resampled to a voxel size of 1x1x1 mm^3.
- The first input to the model was the TG43 dose to water[2]. The second input to the model represented patient body composition. It was either the patient tissue composition, or the respective mass densities derived from the CT Hounsfield units. We also investigated the concatenation of the volume of the inverse squared distance to the dwell position to the patient body composition volume.
- Outputs were dose to medium calculated with Monte Carlo.

Preprocessing:
- We studied the minimum volume size that we could use to crop around the dwell positions while retaining the same dosimetric indices information. (see Figure 1)
- Non relevant interpolated dose values inside the source of TG-43 dose to water maps[4] were capped to maximum Monte Carlo dose values to ease the training task.
- Categorical patient tissues volume and patient tissue mass densities volume were scaled to 0:1.

Deep Learning model:
- U-Net architecture[3] was benchmarked to newly developed 3D Deep Learning regression model architecture designed to handle multi-input problem. (see Figure 2)
- The sum of absolute errors was minimized during the training.
- Adam optimizer was used with a learning rate of $1e^{-3}$ and a polynomial scheduler.

Workflow:
- Train a model to predict dose maps in medium.
- Test the model predictions on never seen patient data:
  - For each patient, predict dose maps with the trained model for each dwell position, then build the combined dose map with all the dwell positions contributions weighted by their dwell times.
  - Compute relevant dosimetric indices from the ground truth Monte Carlo calculated dose maps and the Deep Learning model-based predicted dose maps.
  - Compare dosimetric indices between ground truth dose maps and predicted dose maps. (See Table 2)

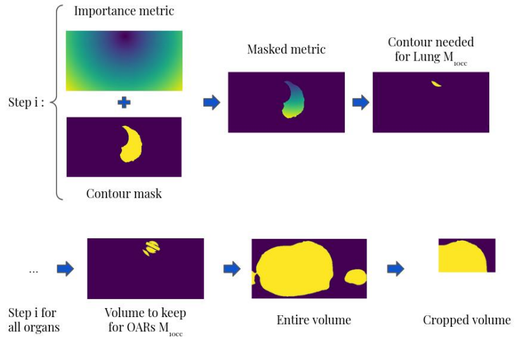

Figure 1. Proposed cropping strategy. Voxels closer to the dwell positions are kept to define the smallest cropping boundaries that one can crop with to keep the same dosimetric indices information inside the cropped volume. M_{10cc} defines the voxels that make the 10 cm^3 closer to the center of all dwell positions. We assumed that dosimetric indices of interest would be included in this M_{10cc} volume. Using this method, volume size was set to 160 x 128 x 112 and volumes cropped around the center of the dwell positions..

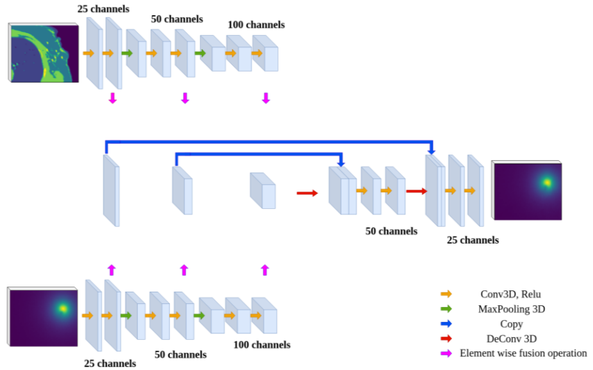

Figure 2. Proposed layer level fusion network called C-Net. In this network, features are learned separately for the two different inputs via two different Convolutional Neural Networks and the second ReLU outputs of each convolution block of both inputs are multiplied together element wise. The decoder part uses skip connection from the multiplied features and not individual features. Fusion operation can be a multiplication : $f(x,y)= x*y+x$, or an addition : $f(x,y)=x+y$. The figure shows the shallow version of the C-Net which we benchmarked with a U-Net. Shallow U-Net has [32,64,128] channels, deep U-Net [16,32,64,128,256] and deep C-Net [12,24,48,96,192].

RESULTS

	Whole predicted volume	CTV	Lung	Heart	Skin	Chest wall
TG43	403.383±941.960	7.97±3.531	7.026±1.255	9.531±2.363	22.18±2.177	9.626±2.148
U-Net shallow w patient tissues	1.906±1.320	0.644±1.203	2.073±1.434	3.286±3.422	1.278±0.303	1.844±1.386
U-Net deep w patint mass densities	1.496±1.138	0.703±1.131	1.740±1.150	2.72±3.773	1.176±0.234	1.680±1.373
C-Net deep add w patient tissues and distance to dwell	1.926±1.199	0.746±1.217	2.078±1.101	2.631±1.742	1.545±0.673	2.077±1.141
C-Net shallow add w p0atient mass densities	2.202±1.199	0.702±1.174	2.492±1.470	3.726±3.276	1.779±0.370	2.177±1.365
C-Net shallow mul w patient tissues	1.994±1.319	0.637±1.171	2.109±1.438	3.976±4.269	1.213±0.293	2.212±1.786
C-Net deep mul w patient mass densities	2.023±1.450	0.772±1.113	1.953±1.379	2.372±1.650	1.932±1.407	2.093±1.458

Table 1. Mean absolute percent error between Monte Carlo single dwell position dose maps and TG43 dose in water and Deep Learning predicted dose maps for our patient test set. From each architecture presented in Figure 2 and trained with all different models, best performing models on the validation set were used to make prediction on the test set and obtained the presented results.

	CTV D_{90}	Lung D_{2cc}	Heart D_{2cc}	Skin D_{2cc}	Chest wall D_{2cc}
TG43	5.693±1.157	9.595±1.783	5.418±2.540	7.482±3.282	6.778±2.388
U-Net shallow w patient tissues	0.134±0.190	0.633±0.874	1.302±2.233	0.203±0.200	0.366±0.384
U-Net deep w patint mass densities	0.229±0.162	0.442±0.483	1.065±1.905	0.175±0.16	0.328±0.276
C-Net deep add w patient tissues and distance to dwell	0.315±0.245	0.767±0.745	0.985±0.681	0.290±0.324	0.345±0.318
C-Net shallow add w patient mass densities	0.236±0.185	0.435±0.402	1.312±2.184	0.311±0.199	0.409±0.377
C-Net shallow mul w patient tissues	0.170±0.129	0.588±0.861	2.060±3.660	0.145±0.102	0.438±0.446
C-Net deep mul w patient mass densities	0.323±0.311	0.646±0.538	0.726±0.615	0.408±0.505	0.388±0.430

Table 2. Mean absolute percent difference between dosimetric indices obtained with Monte Carlo combined dose maps and obtained with TG43 and Deep Learning predicted combined dose maps. D_x : Minimum dose received by x % of the volume, D_{xcc} : Maximum dose received in x cm^3

- From the above two tables, we can see that Deep Learning predicted dose maps are much closer to Monte Carlo dose maps than TG43 water dose maps. For instance, TG43 CTV D_{90} difference with Monte Carlo D_{90} is higher than five percent whereas it is lower than 0.5 percent for any Deep Learning model prediction.
- The prediction time with the Deep Learning solution is on average less than 0.1 second for a dwell position dose map, which correspond to a combined dose predicted with Deep Learning in on average 15 seconds for a complete treatment plan. For the same resolution Monte Carlo method takes between 10 to 15 minutes per dwell position to achieve type A uncertainties below 0.1% inside the CTV.

CONCLUSIONS

- Deep learning-based solutions can provide accurate and fast dose prediction for high dose rate brachytherapy applications.
- Accurate dose predictions in seconds is a step towards patient-specific brachytherapy dosimetry.
- Any desired radiation quantity can be obtained with accuracies arbitrarily close to those of the source Monte Carlo algorithm, but with much faster computation times.

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CONTACT INFORMATION

sebastien.quetin@mail.mcgill.ca