RadCalc's 3D Monte Carlo and 3D Collapse Cone algorithms

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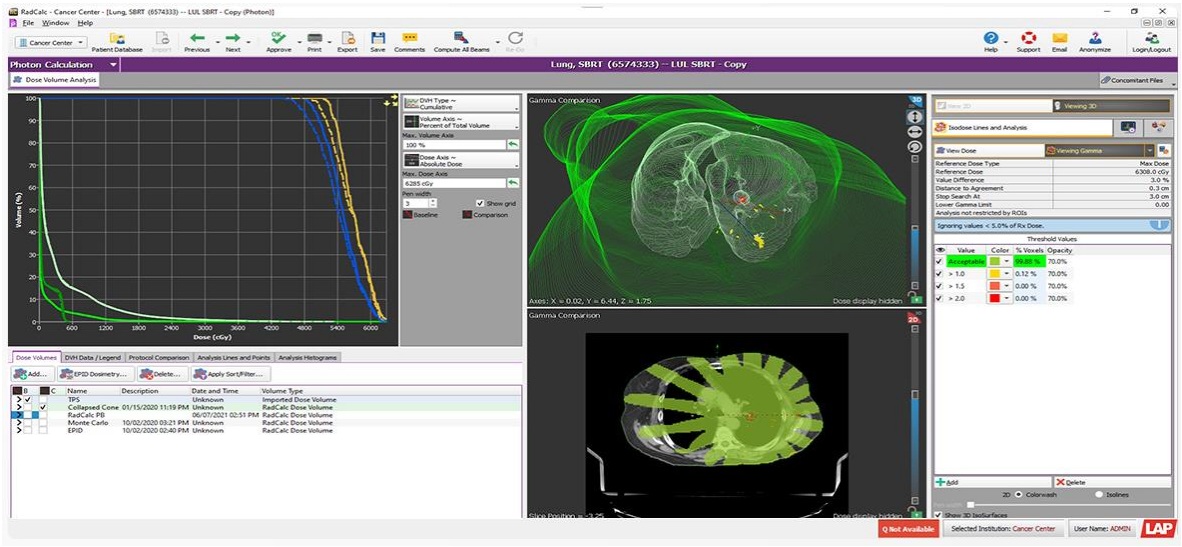
RADCALC

This whitepaper explores RadCalc's 3D dose algorithms. The 3D Collapsed Cone module was first introduced in version 7.0 released in beta in Aug of 2019, with clinical release in November. The 3D Monte Carlo module was released in version 7.1, with the beta release happening in September of 2019 and clinical release in January of 2020.

Extensive clinical evaluations were performed to validate RadCalc's new 3D modules' increasing the commitment to accuracy and reliability.

RadCalc's 3D modules provides confidence and reliability for all field sizes in a single model with both the Collapsed Cone Superposition Convolution and BEAMnrc Monte Carlo.



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1.1 Introduction

Collapsed Cone Superposition algorithms have been the most commonly used in treatment planning systems for nearly a quarter century and are the most trusted model-based dose calculation algorithm.

The Collapsed Cone dose computation process involves computing the incident fluence with a 1mm resolution. The computation is sped up by the use of poly-energetic dose kernels optimized at a depth of 10 cm from a weighted fit of monoenergetic PDD curves, along with a set of beam hardening factors to account for spectrum changes with depth. The TERMA is determined using the same 1mm resolution of the incident fluence. Electron contamination parameters are added into the calculation during the dose computation process. The energy deposited into a given location in the dose grid is determined by 256 or 160 collapsed cones, which is then summed to determine the final dose for each voxel within the volume.

Monte Carlo is widely considered to be the gold standard in terms of dose accuracy and our goal is to build confidence in the most uncertain planned doses.

Modern day Monte Carlo methods benefit from more affordable computing power and powerful variance reduction techniques. These techniques are used to reduce calculation times. One such technique is directional bremsstrahlung splitting which involves only transporting photons that will contribute to the useful radiation field. The variance reduction methodologies employed by RadCalc minimize the time to compute dose without sacrificing accuracy. RadCalc's Monte Carlo algorithm offers benefits in the dose volume calculation for small heterogeneous cases, as well as highly modulated plans with large dose gradients where sparing normal healthy tissues can be more critical.

1.2 Key 3D Features in RadCalc

RadCalc enhances clinical practice by providing advanced tools for precise and efficient verification. Its seamless integration with treatment planning systems optimizes workflow efficiency, enabling clinicians to concentrate on patient care.

DVH Protocols

Any number of DVH protocols can be defined from the analysis screen within RadCalc. Using rules in RadCalc, different DVH protocols can be automatically selected and applied to the specific plan. RadCalc automatically checks whether the DVH objectives are met for critical structures using both the TPS and RadCalc's 3D dose. Analysis reports are automatically attached to your verified plan and sent to your workstation via email or to a directory of your choice on your server.

3D Dose Analysis

RadCalc provides Percent difference, DVH, Distance to Agreement, and Gamma analysis tools to evaluate 3D computations. The functionality includes RadCalcAIR (Automated Import & Reporting) providing a fully automated process for plan import, computation, 3D dose analysis and report generation. RadCalc's fully automated process immediately alerts you to plans that fail to pass your pre-set Gamma analysis acceptance

criteria. RadCalc allows automatically applying different Gamma calculation defaults and acceptance criteria based on user defined rules.

Auto Modeling

The RadCalc 3D modules utilize an automated beam commissioning process in conjunction with the users measured data to produce a customized beam model, the user only needs to press a button to generate the necessary models based upon their existing data.

The collapsed cone modeling process fully utilizes the existing measured data within RadCalc, therefore there are no new data requirements required from users.

The Monte Carlo modeling process partially uses the existing measured data within RadCalc. This data is used strictly as part of a simple matching process to identify the best matching RadCalc Monte Carlo machine file using a pre-computed set of PDD and Off Axis Profile data. Once this is determined, a reference dose calculation is performed in order to determine the reference dose conversion factor which converts the deposited energy to absorbed dose in the patient.

Standard beam geometries can easily be reviewed and analyzed within the same simple user interface during the commissioning process.

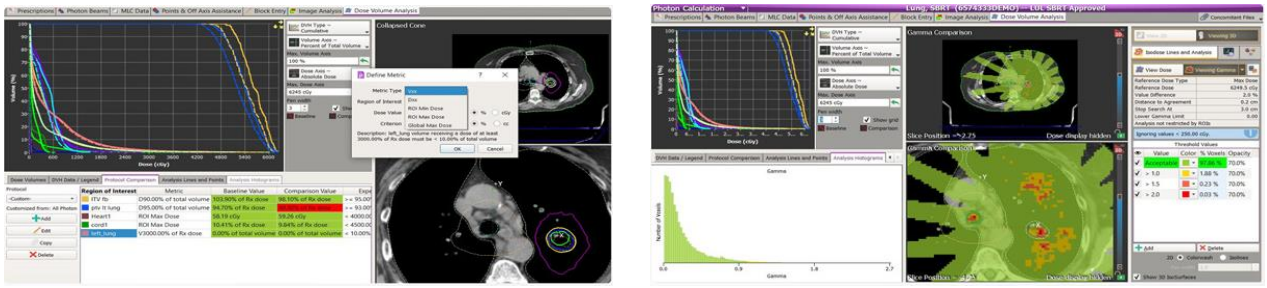

Image 1 RadCalc key 3D analysis features

1.3 Clinical Evaluation Evidence

As RadCalc has continuously evolved it has incorporated new recommendations from the American Association of Physicists in Medicine (AAPM) to enhance its accuracy and reliability. These include the recommendations of the AAPM TG-218 and TG-219[1,2].

Despite the evolving standards, the foundational criteria of achieving agreements within +/- 5.0% have remained a benchmark, ensuring consistency in its performance. The development team at RadCalc has always aimed to tighten these criteria as much as possible, striving for the highest levels of precision in dose verification[3]. This commitment to accuracy is reflected in the robust clinical evaluations and consistent performance improvements seen in RadCalc's subsequent versions.

By integrating these rigorous standards and adapting to new guidelines, RadCalc has solidified its reputation as a trusted and reliable tool in radiation therapy, ensuring that patients receive the safest and most effective treatments possible.

1.3.1 3D Collapsed Cone Module

3D Collapsed Cone

The collapsed cone algorithm originates from the Dosimetry Check technology acquired from Math Resolutions, LLC and is now fully owned by LifeLine Software, Inc.

Support for CT images was added to RadCalc to convert a CT voxel from a Hounsfield Unit to density for 3D collapsed cone dose computations.

The fluence files used for the calculations are based on the fluence that has been utilized since the release of RadCalc version 4.0 in 2001. The dose algorithm involves a simple attenuation process of the primary radiation (i.e., the fluence) through the patient based on the density determined by the CT numbers. This process is similar to the existing ray traces used in the regions of interest module that has been available beginning with version 6.1. Collapsed cones, which are ray traces in 256 directions (160 starting in RadCalc version 7.3.2.0), cover the 3D space surrounding the dose point of interest and are used to determine the energy deposited to the dose point of interest from the various steps along each cone. A 3D dose matrix of points is used to define the entire area of the patient, allowing for a 3D dose distribution to be determined.

The validation testing was performed initially on an IMRT Thorax heterogeneous phantom from CIRS[4]. The purpose of the test was to verify the accuracy with which the algorithm can compute the dose to the lung by comparing the dose computed with the Collapsed Cone algorithm to a measured point.

A phantom with inhomogeneity inserts was used to create a curve of CT number to density in gm/cc. The density in the phantom water equivalent tissue material varied from 1.00 to 1.009 due to the beam hardening of the kVp energy x-ray used for CT scanning. In the lung area, the density was measured at 0.156, while in the bone area, it was 1.482. These values vary with position within the phantom but are noted to demonstrate the order of magnitude of the three density types. The phantom was irradiated with two different treatment plans: a four field “box” and a 460-degree arc, both using the same isocenter.

The four field “box” plan consisted of four radiation fields, 10x10 cm in size, anterior, posterior, right and left lateral, with 200 monitor units for each field.

The 360-degree arc plan consisted of a single full arc of a 10x10 cm field size with 200 monitor units total. The rotation computation was simulated for the CC computation with a beam every 10 degrees.

The phantom was irradiated on a Varian Medical Linear Accelerator (Varian, USA) at 6MV. The dose was measured with pinpoint ionization chamber from PTW, model 31006 (PTW –Freiburg, Germany) at the isocenter point in the left lung. The dose was also computed on the Varian Eclipse treatment planning system with two different algorithms, AAA and Acuros, for comparison purposes.

Four field box, dose cGy at isocenter:

Field	Meas (cGy)	RadCalc CC (cGy)	% Diff	AAA (cGy)	% Diff	Acuros (cGy)	% Diff
AP (0)	194	192.4	-0.80%	193.5	-0.30%	188.9	-2.70%
PA (180)	177	175.1	-1.10%	176	-0.60%	172.5	-2.60%
Left (90)	189.1	187	-1.10%	184.8	-2.30%	183.3	-3.20%
Right (270)	123.5	124.9	1.10%	113.9	-8.40%	120.8	-2.20%
Total	**683.6**	**679.4**	**-0.60%**	**668.2**	**-2.30%**	**665.5**	**-2.70%**

360 degree arc, dose cGy at isocenter:

Field	Meas (cGy)	RadCalc CC (cGy)	% Diff	AAA (cGy)	% Diff	Acuros (cGy)	% Diff
Arc	169	167	-1.20%	162.9	-3.70%	164.4	-2.80%

Table 1: The above data illustrate that in the most complicated treatment scenario for radiation oncology (dose in lung), the percent difference between the RadCalc collapsed cone algorithm and measurement was within +/-1.2% for all beams. In comparison, Varian's AAA algorithm was -2.3% off and Acuros was -2.7% off. For an arc plan, Varian's AAA was -3.7% off and Acuros was -2.8% off while RadCalc CC was -1.2% off.

The evaluation of these results from the collapsed cone calculations demonstrate that the standard phantom calculations were all within 2% of their expected value. Additionally, anonymized patient data freely provided from customers for testing purposes all demonstrated point dose comparisons within 2% and the Gamma Analysis Index for these plans were above 90%.

1.3.2 The 3D Monte Carlo Module

3D Monte Carlo

The Monte Carlo algorithm used to perform the 3D dose calculations comes in the form of off-the-shelf software, BEAMnrc (a.k.a. EGSnrc), and DOSXYZnrc. These software programs were developed by the National Research Council of Canada and are widely considered the standard against which all dose calculation algorithms are compared. Although not developed by LifeLine Software, Inc., BEAMnrc and DOSXYZnrc are utilized in the dose calculation process. They are used to transport particles through the machine components and then the patient. The uncertainty for the computations utilizes the history by history approach described by Walters et al.[5]

The dose computation process is very straightforward. The CT dataset is first converted into a density and material matrix using a CT to-density table with air and water as the two materials. Aside from that, the beam parameters are written into the format needed by BEAMnrc and DOSXYZnrc. These parameters are used to perform a Monte Carlo simulation, which produces a dose matrix with energy deposited into each voxel. This dose is then converted into RadCalc's internal format. The conversion process involves applying a reference dose conversion factor to the deposited energy, converting it into absorbed dose.

The uncertainty for Monte Carlo computations uses the history by history approach

Over eighty patient calculations were performed, and the dose calculations were within acceptable ranges, with an average percent difference of 1% to 3% between the primary treatment planning system and the high passing Gamma Index values (i.e., 96% and above using 3% and 3mm as the criteria).

1.4 Additional 3DCC and 3DMC publications

RadCalc's exceptional accuracy provides confidence and reliability for all field sizes in a single model with both the Collapsed Cone Superposition Convolution and BEAMnrc Monte Carlo. Two papers are summarized here:

1: Evaluation of RadCalc 3DCC against Measured Data[6]

- **Focus**: Verification of RadCalc's 3D Calculation Module (3DCC) against clinical data.
- **Methodology**: Compared 3DCC dose calculations to measured data in various treatment plans, primarily using a water phantom.
- **Key Metrics**: Gamma pass rate, comparison between calculated and measured doses.
- **Results**: Showed a high level of agreement between RadCalc's 3DCC and measured data for most cases.
- **Main Findings**:
    - Gamma pass rates for 3%/3mm criteria ranged from 90-98%, depending on the complexity of the treatment plan.
    - Performance was slightly worse for highly modulated plans and cases with tissue inhomogeneities.

Summary:

> The accuracy of the RadCalc 3D Collapsed Cone algorithm for all field sizes was validated directly with measurements for both simple and complex geometries, with and without heterogeneities, using international guidelines and published criteria such as TG 114 and TG 219. The modelling was performed with the user's custom beam data and with independent validation of the machine characteristics, including the Radiation Light Field Offset. The calculations were performed with both NVIDIA Tesla K20 and RTX 3080 GPUs, demonstrating RadCalc's hardware flexibility.
>
> RadCalc's Collapsed Cone algorithm from version 7.1.4.1 was evaluated, as well as the changes implemented in version 7.2.2.0. The newest improvements in version 7.2.3.1 were not evaluated as part of this work. However, it is not surprising to see that even with version 7.2.2.0, the complex IMRT and VMAT deliveries met the recommendations of TG 219 with IMRT fields using a 2% and 2mm criteria and for the most complex nasopharynx VMAT plan meeting 3%/2mm criteria. Overall, for the modulated fields there was especially good agreement of less than 1mm DTA in the areas of steep dose gradients.
>
> Open fields had PDD comparisons of less than 0.5% differences, and Off Axis Ratios (OAR) within 2% in the central 80%. Additionally, the researchers performed dose comparisons for heterogeneous phantoms, including a 2cm stepped phantom on top of the water surface for an enface and oblique beam geometry, as well as utilizing Lung, Bone, Air and Mediastinum geometries, of which the results were generally within 3.5% of the measured dose. These results are better than the 2.5% dose differences recommended for simple open or MLC shaped static fields in homogenous medium and the action limits that are recommended when doses exceed 5% difference for heterogeneous calculations.

2: Tuning and Validation of the New RadCalc 3DMC Based Pre-Treatment Verification Tool[7]

- **Focus**: Development and validation of RadCalc's Monte Carlo (3DMC) module for radiotherapy pre-treatment verification.
- **Methodology**: Dosimetric comparison between 3DMC and clinical measurements on phantom and patient data. Validation was performed on 70 VMAT plans.
- **Key Metrics**: Gamma pass rate, tuning of Additional Radiation to Light Field Offset (ARLF) parameter for dose accuracy.
- **Results**:
    - Gamma pass rates for 3%/3mm criteria were above 95% after tuning for all energy types.
    - Improved dose accuracy for complex cases, especially in lung cancer patients due to better handling of tissue inhomogeneity.
- **Main Findings**:
    - RadCalc 3DMC achieved higher accuracy compared to 3DCC, particularly for complex treatment sites.
    - The ARLF tuning significantly improved the agreement between 3DMC calculations and measured data.

Summary:

The results of RadCalc's 3D Monte Carlo algorithm secondary check on the patient's heterogeneous CT datasets were compared against on-couch homogeneous phantom measurements after fine tuning the models in RadCalc with a Gamma criteria of 2%/2mm and low dose thresholds of 50%. 70 VMAT plans were used for clinical validation of RadCalc's 3D Monte Carlo algorithm for 6x, 10x, 6FFF and 10FFF against Eclipse v13.7 for both AAA and Acuros XB. Of the 70 plans, 20 were used for tuning and the other 50 were utilized as a validation set.

The RadCalc MC modeling process allows the user to choose the spot size and mean energy that best fits three open fields. Using this spot size and mean energy combination, a BEAMnrc-modeled machine is loaded, and every physical component is modeled. The unique auto-modeling method provides near-instantaneous beams with only one parameter that needs to be fine-tuned: the additional Radiation Light Field Offset (ARLF), also known as the Dosimetric Leaf Gap (DLG) in Varian terminology.

The authors quote their DLG for each energy and the resulting ARLF from the model tuning performed. The authors demonstrate the accuracy of RadCalc's Monte Carlo against the Eclipse algorithms, and the on-couch homogenous phantom measurements against the Eclipse algorithms. As is the topic of the up-and-coming TG 360, the authors performed statistical methods on the comparison of the gamma passing rates. They utilized ROC curve analysis to set the acceptable plans for the on-couch measurements and the RadCalc Monte Carlo calculations as the 95th and 90th percentile, respectively. The confusion matrix, including the number of True Positives/Negatives and False Positives/Negatives, demonstrates Gamma Passing Rate comparisons against

AAA/Acuros XB and a box chart that includes the on-couch measurements. In summary, these data show a high degree of agreement between the RadCalc MC and Acuros XB calculations, especially for the lung subset used.

As the authors conclude, after tuning, RadCalc's 3D Monte Carlo Algorithm provides a solution to independently verify treatment plans directly on the patient's CT with sensitivities and specificities similar to those of on-couch phantom solutions. It also detects inaccuracies in tissue inhomogeneities that homogeneous on-couch phantoms are unable to detect.

Aspect	**Paper 1: Evaluation of RadCalc 3DCC against Measured Data[4]**	**Paper 2: Tuning and Validation of the New RadCalc 3DMC Based Pre-Treatment Verification Tool[5]**
Module Type	3D Calculation (3DCC)	3D Monte Carlo (3DMC)
Verification Focus	Comparison of 3DCC with measured data	Validation of 3DMC using phantom and clinical plans
Methodology	Measured vs calculated doses (water phantom)	Tuning and validation using VMAT plans (phantom + patient)
Key Metric	Gamma pass rate	Gamma pass rate, ARLF tuning
Main Energy Types	6X, 10X	6X, 10X, 6FFF, 10FFF
Results	Gamma pass rates: 90-98% for 3%/3mm	Gamma pass rates: >95% after tuning
Inhomogeneity Handling	Performance affected by tissue inhomogeneity	Better performance for lung and complex inhomogeneous sites
Clinical Validation	Slight reduction in accuracy for complex cases	High accuracy across all complex plans, especially lung
Improvement/Innovation	-	ARLF parameter tuning improves dose agreement

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Addendum: GPU-based fast Monte Carlo dose calculation using electron pre-calculated tracks

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INTRODUCTION

The RadCalc implementation of its fast Monte Carlo dose calculation algorithm is based on the Pre-calculated Monte Carlo (PMC) technique published by Jabbari et al. in 2009 [1]. In this technique, the stochastic trajectory of an electron could be pre-sampled ahead of time and then used as look-ups at run time. Using the established EGSnrc Monte Carlo code [2], electrons would be generated in an identical initial direction and energy and transported through a homogeneous medium of interest. For each electron, in pre-determined step sizes, the position, direction and energy would be recorded until the electron reached their minimum threshold energy *ecut*. Any events along its path that would set in motion a new particle such as secondary electrons or bremsstrahlung photons would also be recorded. The compilation of these step information and events constitutes an electron track. A sufficiently high number of these tracks would be generated for each medium and at differing energy intervals such as to cover the whole energy range of clinical electron beams. At run time, to transport an electron, a track is randomly selected at a suitable initial energy and used to transport the electron by raytracing from each track step to the next. Any secondary particles created along the track would be added to a stack to be transported subsequently. The dose deposited is assumed to be uniform along an electron step. If an electron travels a pathlength r_v within a voxel v, then the dose deposited to the voxel e_{dep}, v can be calculated as:

$$e_{\mathrm{dep},v} = e_{\mathrm{dep}} \frac{r_v}{r}, \qquad (1)$$

where r is the total length of the step of the electron track along which the electron travelled through v and e_{dep} is the total energy deposition along that step. As the electron is assumed to be going in a straight line along each step, a larger step size would induce a larger error in the location of the dose deposition. However, smaller step sizes would result in larger track sizes which must fit within the video random access memory (VRAM) at run time.

Although the generation of a track bank is done with EGSnrc, this time-consuming step is only performed once ahead of time and is independent of the treatment machine or the patient geometry. The time spent during this step can therefore be ignored for practical timing comparison. This method would provide a significant speed-up compared to conventional Monte Carlo methods as no costly interaction sampling would then have to be performed during run time. The only significant computation time would be stemming from raytracing the electron voxel-by-voxel along the pre-calculated steps. Jabbari et al. observed speedups by a factor of 40 with PMC compared to EGSnrc calculations with dose discrepancies on the order of 2%.

In 2015, Renaud et al. [3] published a graphics processing unit (GPU) implementation of the PMC technique which handled both electron and proton transport. The statistical uncertainty (Type A) arising from the finite number of particles simulated at run time can be estimated by calculating the voxel-wise standard error across multiple calculation batches:

$$\sigma_{A,v} = \frac{1}{\bar{D}_v\sqrt{B}}\sqrt{\frac{1}{B}\sum_{b}^{B}(D_v - \bar{D}_v)^2}, \quad (2)$$

where $\sigma_{A,v}$ is the relative Type A uncertainty on the mean across B batches of equal history, and $\bar{D}_v$ is the mean dose for a voxel v across all B batches. Renaud et al. quantified the systematic uncertainty due to the finite size of the track bank as a latent uncertainty on PMC dose calculations. While the statistical uncertainties can be reduced by increasing running more histories, the latter is constant for a pre-generated track bank. If a PMC calculation is performed at sufficiently high histories N such that the statistical uncertainty can be ignored, then the latent uncertainty σ_L can be estimated as the root mean square deviation of local residuals between PMC doses D^{PMC} and benchmark doses D^b, calculated using a conventional Monte Carlo code such as EGSnrc:

$$\sigma_L = \lim_{N\to\infty}\sqrt{1/N\sum_{v}\left(\frac{D_v^{\mathrm{PMC}} - D_v^b}{D_v^b}\right)^2}, \quad (3)$$

where the summation is performed over all voxels v. In RadCalc's implementation, the history by history method utilized with the original BEAMnrc Monte Carlo Module is utilized as described in "The 3D Monte Carlo Module" section above.

Although the PMC code had been validated to provide accurate electron dose calculations when compared with EGSnrc by Renaud et al. [3], it was done without accounting for photon transports. However, in megavoltage external electron beam, bremsstrahlung photons and contamination photons generated in the gantry head account for a significant portion of the patient dose and must be corrected for. Therefore, to be adequate for external beam radiotherapy purposes, a photon transport method was added to the PMC code.

METHOD

A. Photon transport

Bremsstrahlung photon creation events in electron tracks were recorded at pre-generation time in EGSnrc. During live calculations, each GPU thread loads up a particle from a phase space source file. If the particle is an electron, it is transported according to its track data until they either reach $E < ecut$ or cross to a different medium. For all calculations presented in this paper, an electron total energy cutoff of $ecut$ = 0.7 MeV was used. If secondary electrons or bremsstrahlung photons are generated along the track, they are added to a stack of particles for the thread to transport subsequently. For photon transport, a method similar to the ones used in the EGS4 report [4] and by Fippel [5] is applied. The mass attenuation coefficient for photoelectric, Compton and pair production interactions in water are obtained from NIST [6] and are initialized on the GPU as texture objects. For each photon of energy E, its corresponding total mass attenuation coefficient $\mu(E)/\rho$ is fetched from the texture objects based on its energy E. Let $z(E)$ be the distance to be travelled by a photon. The probability that a photon interaction occurs within this distance $z(E)$ can be written as:

$$P(z(E)) = 1 - e^{-\mu(E)z(E)}. \quad (4)$$

Using the direct sampling method, we let $P(z(E))$ be represented by a uniformly distributed random number ξ between 0 and 1. By directly inverting Eq. 4, we obtain:

$$z(E) = -\frac{1}{\mu(E)} \ln(1 - \xi). \quad (5)$$

As 1 - ξ is also uniform between 0 and 1 for $\xi \in (0, 1)$, the density-normalized distance $z(E)/\rho$ to be travelled by the photon before an interaction occurs can then be sampled as:

$$z(E)/\rho = -\frac{1}{\mu(E)/\rho} \ln(\xi'), \quad (6)$$

where ξ' is a uniformly distributed random number between 0 and 1. The photon is then ray-traced by accounting for each voxel's density ρ until the distance $z(E)$ has been fully travelled. Photons are transported as long as their energy is higher than *pcut* = 0.01 MeV and while they remain within the phantom geometry. Photons below the cutoff energy *pcut* are forced to deposit all their energy in the voxel they are found in. Once the photon has travelled the full distance $z(E)$, one of the three interaction types is sampled from the interaction-specific mass attenuation coefficients. The methods described in EGSnrc [2] to sample energy and scattering angle of the secondary particles generated by each interaction type are applied. For pair production, secondary positrons are handled as if they were electrons.

Each GPU thread is responsible for transporting one particle sampled from the initial source. Any ensuing secondary particle is appended to the thread's stack of particles and transported subsequently. In the current implementation, all body materials are treated as density scaled water. However, as the initial particle source must be transported from outside the patient body, the PMC code must also handle transporting particles in air. For electrons, the tracks are pre-generated in air with a larger maximum step size of 1 cm and lower history of 4000 tracks per energy. This is in contrast to tracks in water being generated with a maximum step size of 0.5 mm and with 40,000 tracks per energy [3]. This reduces the memory size of the air track bank such that it can be loaded onto the GPU simultaneously. If an electron is found to be outside the patient geometry (i.e. in air), the track segment is first verified to intersect the patient's bounding box [7] before performing more costly voxel-by-voxel raytracing. Any particle found to exit the phantom geometry is immediately discarded. For photon plans, the particles sampled are impacted by the computed transmission maps used at each control point. Particles are also discarded here based on the transmission values. The number of particles discarded are reflected in the number of history differences reported between the calculations in RadCalc's BEAMnrc and PMC implementation.

B. Beam model

The PMC algorithm only handles particle transport within the phantom geometry and surrounding air. It effectively replaces the DOSXYZnrc user-code in EGSnrc. Special considerations must be taken to model the transport of particles in the linac head. For photon beam dose calculations, the RadCalc implementation of PMC starts by sampling particles from a statistical source model, identical to the one used for a BEAMnrc calculation in RadCalc. Their transmission through downstream collimation system is modelled by using a fluence map obtained from RadCalc's Collapsed Cone Algorithm. This map is used to calculate the probability for a particle to be transmitted through a 2D plane at the MLC height. For electron dose calculations, pre-calculated electron phase space files are collected upstream of the electron insert for all applicator size and beam energy using BEAMnrc. Particles are then sampled directly from the phase space file and transmitted through the cutout insert by using a binary map that models the cutout shape. Particles are projected at the cutout height and the value of the binary map at the particle's projected position dictates whether the particle is transmitted.

VALIDATION

To validate the accuracy of PMC dose calculation, external beam dose calculations in water of photon and electron fields are compared to EGSnrc calculations. Phase space sources of particles are collected below all collimation devices of a TrueBeam linac using BEAMnrc for both a 6 MV 5x5 cm^2 photon field and a 9 MeV 10x10 cm^2 electron field. These phase space sources are then used as input to both PMC calculations and ground truth DOSXYZnrc calculations in a homogeneous water phantom at 100 cm SSD. PDDs and transverse profiles of the 2 corresponding calculation methods are compared. All calculations are run to less than 1% statistical uncertainty. In this validation, all particle transport within the linac head is performed by BEAMnrc. As such, only the accuracy of PMC's dose calculation within the patient or phantom geometry is herein validated, and not its source model.

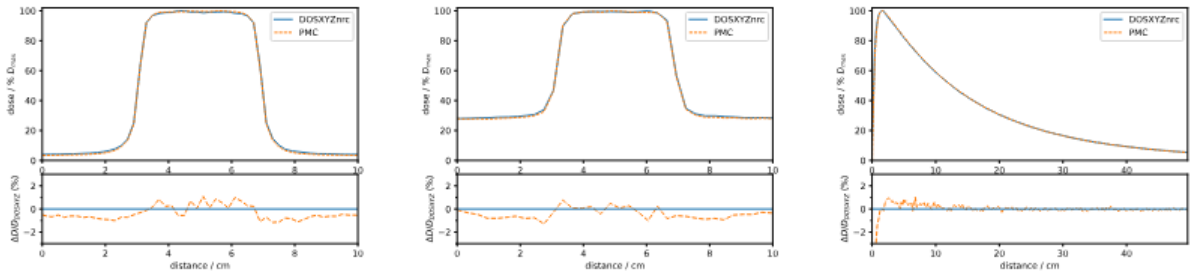

FIG. 1: Validation of a 6 MV 5x5 cm^2 photon field in a homogeneous water phantom. Residual plots are global residuals. Transverse profiles are taken at a depth of 5 cm. In-line profile-offset to go through middle of an MLC (Left). Cross-line profile-through abutting leaf gap (Center). PDD (Right).

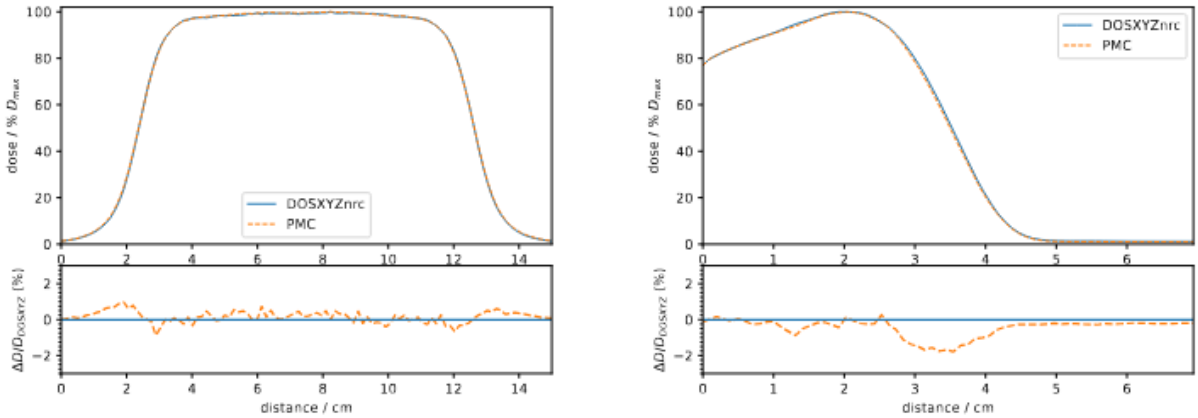

FIG. 2: Validation of a 9 MeV 10×10 cm^2 electron field in a homogeneous water phantom. Residual plots are global residuals. Transverse profiles are taken at a depth of 2 cm. Transverse Profile (Left). PDD (Right).

A 12 static field lung SBRT plan is used to benchmark PMC, both in terms of dose calculation accuracy and computation time against EGSnrc. Similarly, an intermediate phase space file is collected below the MLC using BEAMnrc and used as input to both calculation methods. A strict 1%/0 mm gamma analysis is used to compare the 2 dose distributions with a global low dose threshold of 10%. The two calculations agreed with a passing rate of 99.8%. The EGSnrc calculation is run on a parallel CPU workstation (2× Intel(R) Xeon(R) Gold 6140 – 36 cores) while the PMC calculation is run on an NVIDIA RTX A5500 card. A Type A uncertainty of 1% was achieved with PMC in under 50 seconds while it took 6 minutes and 40 seconds with EGSnrc.

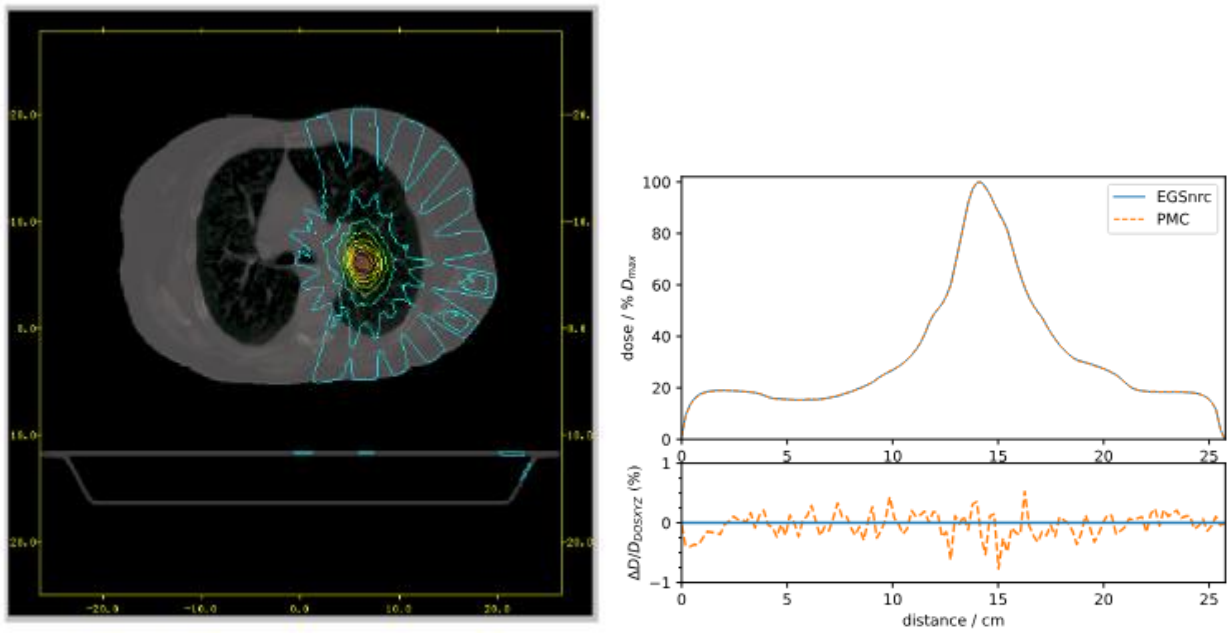

FIG. 3: Validation of PMC accuracy for an SBRT plan in a heterogeneous lung patient. Axial CT slice as displayed using dosxyz_show. (Left) Vertical dose profile through one of the static fields. (Right)

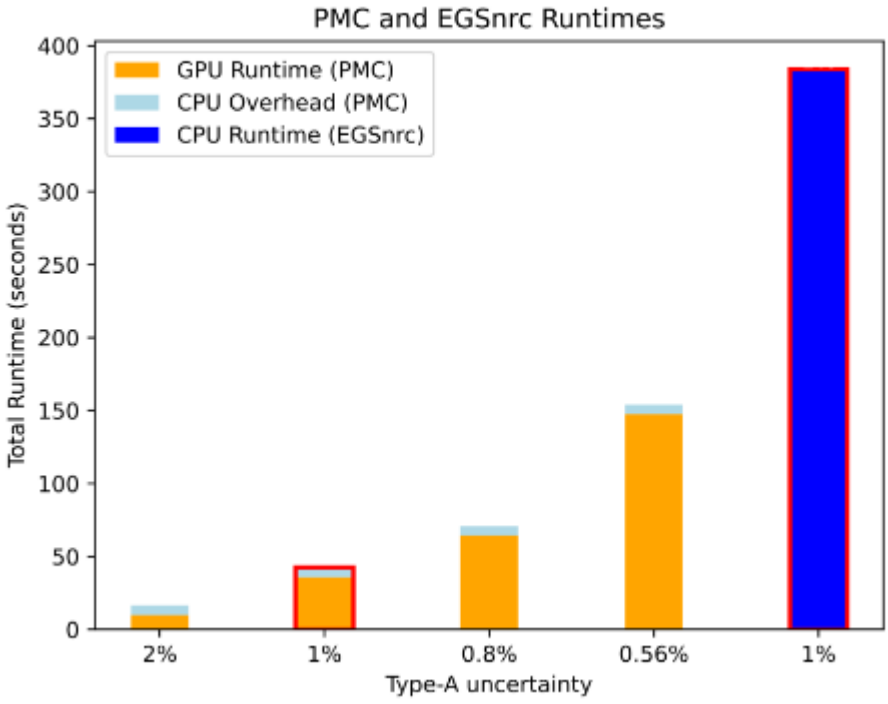

FIG. 4: Runtime comparison of the lung SBRT plan.

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