

A Monte Carlo tool for raster-scanning particle therapy dose computation

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Abstract. Purpose of this work was to implement Monte Carlo (MC) dose computation in realistic patient geometries with raster-scanning, the most advanced ion beam delivery technique, combining magnetic beam deflection with energy variation. FLUKA, a Monte Carlo package well-established in particle therapy applications, was extended to simulate raster-scanning delivery with clinical data, unavailable as built-in feature. A new complex beam source, compatible with FLUKA public programming interface, was implemented in Fortran to model the specific properties of raster-scanning, i.e. delivery by means of multiple spot sources with variable spatial distributions, energies and numbers of particles. The source was plugged into the MC engine through the user hook system provided by FLUKA. Additionally, routines were provided to populate the beam source with treatment plan data, stored as DICOM RTPan or TRiP98's RST format, enabling MC recomputation of clinical plans. Finally, facilities were integrated to read computerised tomography (CT) data into FLUKA. The tool was used to recompute two representative carbon ion treatment plans, a skull base and a prostate case, prepared with analytical dose calculation (TRiP98). Selected, clinically relevant issues influencing the dose distributions were investigated: (1) presence of positioning errors, (2) influence of fiducial markers and (3) variations in pencil beam width. Notable differences in modelling of these challenging situations were observed between the analytical and Monte Carlo results. In conclusion, a tool was developed, to support particle therapy research and treatment, when high precision MC calculations are required, e.g. in presence of severe density heterogeneities or in quality assurance procedures.

1. Introduction

Scanned beam particle therapy, the most advanced ion beam delivery technique, combining magnetic beam deflection with active energy variation, offers the highest degree of target dose conformation attainable in external beam radiotherapy. To fully and safely exploit such delivery precision, accurate dose computation is required.

However, analytical algorithms employed in the treatment planning systems (TPS), typically involve some simplifications, e.g. in modelling of density effects or handling of lateral scattering [1], resulting in dose prediction uncertainties which may affect clinically relevant situations [2]. Furthermore, analytical algorithms offer limited facilities to model delivery-time uncertainties, like beam profile distortions [3].

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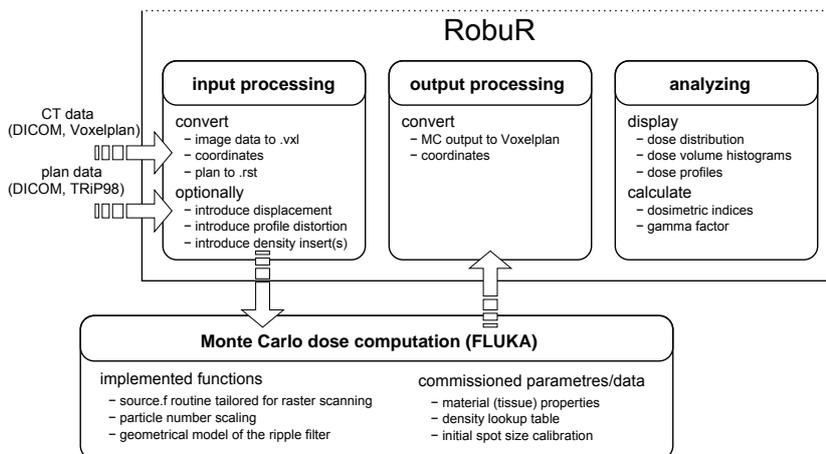


Figure 1. The workflow steps: data input from external sources, conversion and preprocessing, Monte Carlo dose computation with FLUKA, conversion and processing for display and analysis.

Monte Carlo (MC) methods have the potential to validate and complement analytical dose computations in complex situations, when high precision is required, supporting particle therapy scientific and clinical applications, as well as quality assurance procedures. Therefore, purpose of this work was to enable MC particle dose computation in patient geometries with raster-scanning and combine it, in a single platform, with flexible data input and preprocessing (to support a range of diverse computations) and comprehensive results display and analysis (e.g. to uniformly compare MC with analytical calculations in terms of DVHs or dosimetric indices).

2. Material and Methods

2.1. Monte Carlo tool

A general purpose Monte Carlo engine FLUKA [4], well-established in particle therapy applications [5, 6], was employed as core of our dose computation tool. For all calculations the default settings optimized for ion beam therapy applications (HADROTHERapy [7]) were used, which ensure the detailed transport of primary and secondary particles (e.g. 2% kinetic energy loss step, delta-ray production threshold 100 keV, particle transport threshold at 100 keV, except for neutrons at $1e-5$ eV, multiple scattering threshold at minimum allowed energy).

A complex beam definition was implemented, using the Fortran programming language, to model raster-scanning, i.e. delivery by means of multiple sources with variable spatial distributions, energies and numbers of particles. The beam source was plugged into the MC engine through the user hook system provided by FLUKA (stub routine `source.f`). Additionally, for carbon ion dose calculations, a geometrical model of the ripple filter [8], an element used to broaden the pristine Bragg peaks in depth, was defined.

Finally, the beam properties were adjusted to match the base data (definitions and values) used in comparative analytical computations, e.g. initial spot sizes were associated with the corresponding values at isocentre in air, used as references by the TRiP98 TPS [9]. Also, a Hounsfield unit lookup table, compatible with the one used for TRiP98, was defined, adopting material composition according to Schneider *et al* [10] expanded to account for metallic implants similarly to Parodi *et al* [5].

2.2. Data processing

The dose computation tool was interfaced (figure 1) with our radiotherapy toolkit RobuR [11], which handles input/output and processing of data in various formats, including converting computerized tomography (CT) data into FLUKA's VXL format and populating the beam source with treatment plan data (DICOM RTPlan or TRiP98's RST format). Additional input

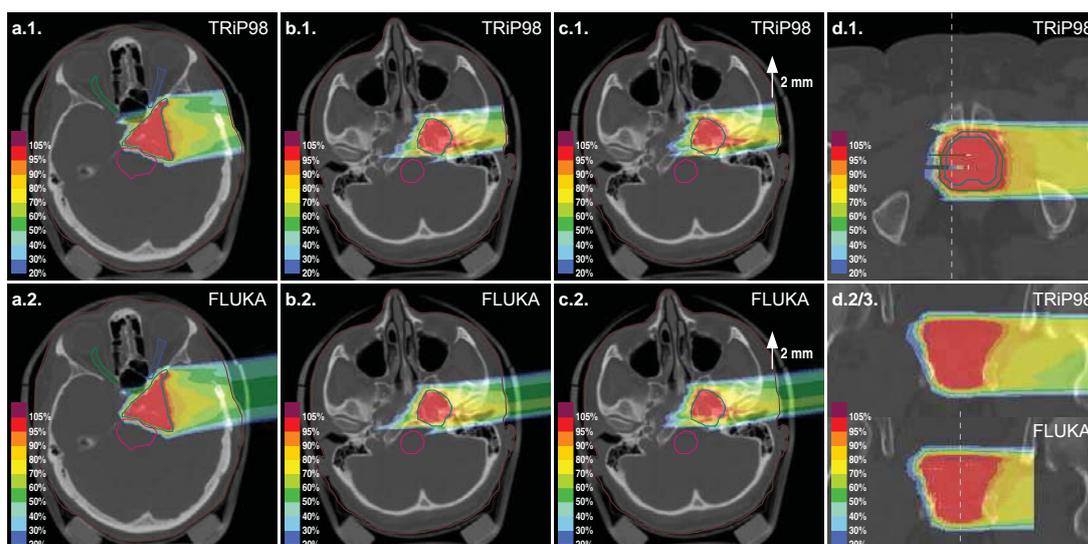


Figure 2. Dose distributions: a.1-2. and b.1-2. for skull base case (see also: figure 4), c.1-2. for a skull base case recomputed with a 2 mm set-up error (see also: figure 4), d.1. for prostate case with with two high density inserts introduced (see also: figure 5, a) and d.2/3. for prostate case with pencil beam distortions introduced (see also: figure 5, b).

data modification functionalities were provided, allowing to e.g. simulate (translational and rotational) positioning errors, introduce density inserts (by Hounsfield unit override in a specified contour or for selected pixels) and model beam profile distortions (e.g. width variations or profile asymmetry) through a user-controlled multiple-Gaussian parametrization, enabling accurate investigation of the resulting dosimetric effects. A direct comparison between MC and TRiP98 (or other systems adopting the DICOM format) dose distributions is possible through RobuR display and analysis capabilities, which were extended to directly support FLUKA data.

2.3. Comparison with analytical computations

The Monte Carlo tool was demonstrated on the recomputation of two representative carbon ion treatment plans (absorbed dose), a skull base and a prostate case, prepared with the TRiP98 TPS, employing analytical dose calculation models. Selected, clinically relevant issues influencing the dose distributions were chosen: (1) presence of positioning errors in skull base treatments (simulated by rigid CT displacement), (2) influence of high-density fiducial markers implanted in the prostate and (3) distortions of pencil beam profiles at extraction time.

3. Results

Figure 2 (a-c) shows dose distributions obtained for a skull base plan and demonstrates very good qualitative agreement between analytical and MC calculations in the homogeneous tissue regions (a), similarly to what was observed in water phantom calculations (figure 3), and slight discrepancies in the regions of heterogeneous tissue (b-c). The corresponding DVHs are presented in figure 4 showing differences in the order of 2%.

In figure 2 (d.1) the dose distribution is shown obtained through recalculation with the analytical TPS of the original prostate case plan, with two $1 \times 1 \times 3 \text{ mm}^3$ high-density inserts (obtained by Hounsfield unit override for selected pixels), simulating gold seeds. Due to limited modelling of the lateral scatter, nearly no dose is registered (distally) behind the inserts. The same case, recomputed with the MC tool, shows instead reduced, but substantial dose deposition

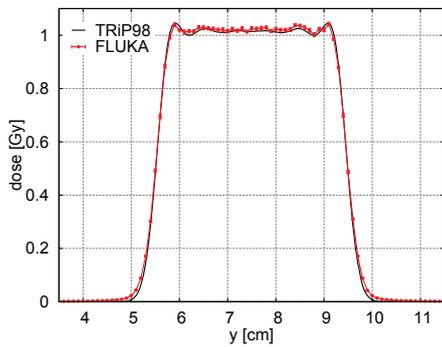


Figure 3. Dose profile of a $3.5 \times 3.5 \times 3.5 \text{ cm}^3$ target in a $7 \times 7 \times 7 \text{ cm}^3$ water phantom.

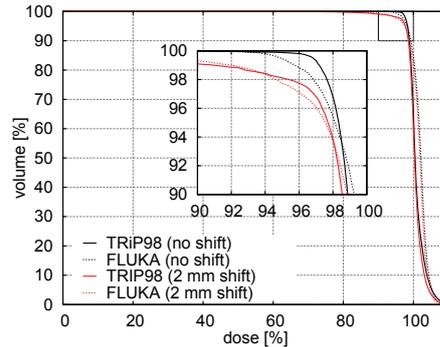


Figure 4. Dose volume histograms for the clinical target volume (CTV) for the skull base case.

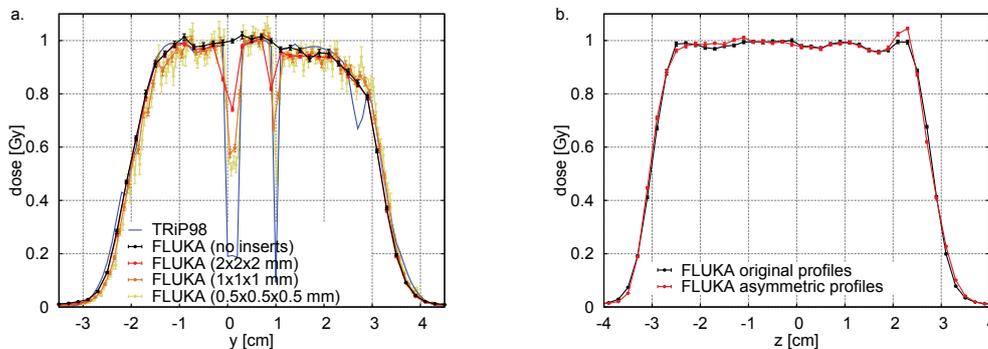


Figure 5. Dose profiles for the prostate case (indicated with dashed lines in figure 2, d): a. original plan and recomputation with high density inserts (for 3 scoring grids), b. recomputation with/without pencil beam distortions.

past the inserts, as visible in the dose profiles (figure 5, a). The MC computation results were scored at various dose grid resolutions ($2 \times 2 \times 2$, $1 \times 1 \times 1$ and $0.5 \times 0.5 \times 0.5 \text{ mm}^3$) to illustrate partial volume effects.

In figure 2 (d.2/3.) the coronal slice of the original prostate case plan (obtained with the analytical TPS) is compared with a recomputation, performed with the MC tool, with horizontal pencil beam profile distortions introduced (impossible to model within the TPS). The resulting dose deterioration, occurring predominately at field edge, is visualized in the cross-profiles in figure 5 (b).

4. Discussion and Conclusions

A tool was developed to enable dose recomputation of clinical scanned beam particle plans in patient and phantom geometries, with the FLUKA Monte Carlo code, and uniform comparison of the results within a single platform, also in terms of clinical parameters (DVH, dosimetric indices). Our work stems from the practical need, for our upcoming ion therapy centre, of including MC in QA procedures and from the research interest in the limitations of analytical dose computation algorithms. Therefore, the current implementation supports only computation of absorbed dose. However coupling of FLUKA with a radiobiological model has been

demonstrated [12] and represents one of the next priorities in the extension of our framework.

While the major features of the current implementation were demonstrated on relevant tests cases, where differences between analytical and MC results were observed, a quantitative comparison between dose calculations approaches is beyond the purpose of this study and is instead one of the planned future applications of the presented tool.

Other groups have worked on enabling MC recomputations of clinical treatment plans for QA and research purposes, including applications of FLUKA to carbon ion therapy. Notable is the work by Parodi *et al* [6], who investigated the suitability of FLUKA as clinical tool and applied it to relevant issues in proton and carbon ion therapy. Recently, integration of FLUKA within a planning software tool has been reported by Mairani *et al* [13]. The tight integration represents a common trait with the software platform we present in this manuscript, while the two projects appear to currently differ in focus. Where Mairani *et al* [13] privileged plan optimization and integration with a radiobiological model, creating a full-fledged clinical planning system, we have favoured flexibility in input data manipulation and output data analysis, to directly enable a broad range of simulations.

Finally, implicit in the design of our MC framework is the possibility to easily distribute it to other institutions, which could directly benefit from it at the sole cost of introducing their own facility-specific base data. It is in fact entirely written in standard Fortran (FLUKA interfaces) and C++, targeting GNU/Linux systems. Currently, its sole dependency is our radiotherapy software toolkit RobuR, which is scheduled for release under a permissive software licence [11].

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