

An analytical model for proton beam collimator scattering dose calculation

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Introduction

Proton therapy is a state-of-the-art technique of radiotherapy which delivers protons to the tumor volume. The Institut Curie - Centre de Protonthérapie d'Orsay (ICPO), currently uses the passive beam spreading (Double Scattering) technique in 2 horizontal fixed beam lines and our new treatment room featuring an IBA gantry. Personalized collimators are routinely used to tailor the field to the tumor shape in order to spare surrounding critical structures and reduce the dose to the healthy tissue with small lateral penumbra. Unfortunately, some protons interact with the collimator and create an undesired additional amount of dose. This contamination, of about 10% of the maximum dose, perturbs the determination of the dose at the calibration point (Titt, 2008), and has to be included in the TPS dose calculation. The aim of this study is to describe the aperture contamination with a fast analytical model.

Materials and Methods

Measurements:

Measurements were performed on one of the horizontal passive beam lines at IC-CPO, described in Fig. 1. The energy of different Bragg Peaks is adjusted with the range binary filter, while the second scatterer laterally enlarges the beam size. 201 MeV **pristine Bragg Peaks** were used through brass divergent half-block collimators located at various off-axis distances (Fig. 2) in order to get the contamination from only one side of the collimator, but also for circular apertures.

Monte-Carlo simulations:

Simulations were run with the GATE platform based on the GEANT4.9.2 release (Grevillot, 2010) in order to investigate the influence of different beam parameters on the contamination function, e.g. the beam energy spectrum and angular distribution.

Contamination definition and computation:

- 1 The collimator contamination is defined as the difference between the measured profile and an ideal uncontaminated profile. The latter is analytically computed by the Treatment Planning System (TPS) ISOGRAY by DOSIsoft as shown in Fig. 3.
- 2 The **contamination function** is computed only for the **entrance face of collimator** with a fast analytical algorithm, depending on the following parameters : energy, aperture size and distance between the collimator and the dose calculation point.
- 3 The computation of the real (contaminated) profile is achieved in summing the contamination function to the ideal calculated profile. The final contaminated profile is then compared to the measurements.

The new analytical representation of the contamination function is developed using experimental data. It relies on a physical model which has been validated using the Monte-Carlo simulations.

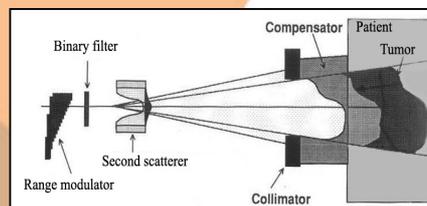


Fig. 1: Simple scheme of a Double Scattering beam line

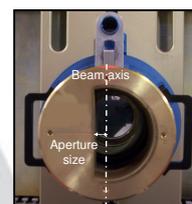


Fig. 2: Picture of half-block collimator located at 15 mm off-axis distance

Results

The developed analytical model describes well the phenomenon of the aperture contamination. Fig. 3 shows a comparison between an analytically calculated profile and the measured corresponding one at 2 cm depth in water. Fig. 4 points out that the contamination decreases with depth and confirms the good agreement of the analytical model with the measurements in 2-D.

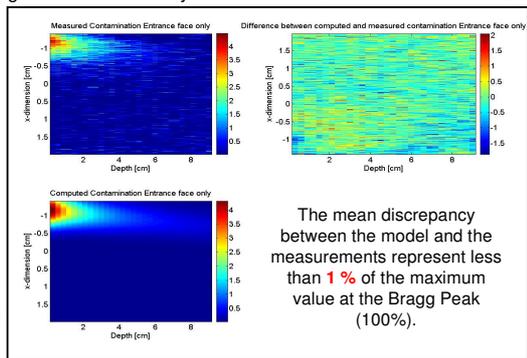


Fig. 4: 2-D comparison between the analytical model and the measurements

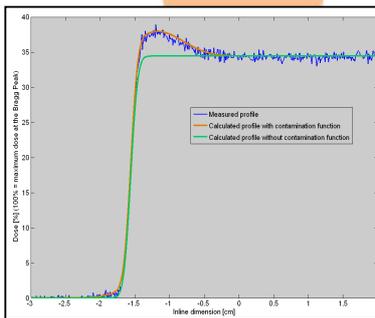


Fig. 3: Comparison between the measured profile and the calculated profiles with and without the contamination function computation at 2 cm depth in water

Fig. 3 demonstrates that the real dose is not computed properly without the contamination function. The latter is essential to accurately calculate proton dose distributions using apertures.

The analytical model is being implemented in Treatment Planning System ISOGRAY by DOSIsoft for **complex apertures**, to better take into account the collimator contamination with both algorithms : Ray Tracing and Pencil Beam.

Discussion and Conclusion

The collimator contamination is accurately described by a fast analytical model. However the study was run for pristine peaks only using divergent collimators. Consequently, further investigations will be lead with **Spread Out Bragg Peaks**, as well as a comparison between **divergent and non divergent** collimators. Moreover, measurements were performed for a Double Scattering beam line, but collimators could also be used for **Pencil Beam Scanning** to improve lateral penumbra (Safai et al., 2008). Therefore, the analytical model will be broaden to this beam delivery technique.

References

- [1] Titt U, Zheng YS, Vassiliev ON, Newhauser WD (2008) Monte Carlo investigation of collimator scatter of proton-therapy beams produced using the passive scattering method. Physics in Medicine and Biology 53: 487-504
- [2] Grevillot L, Frisson T, Zahra N, Bertrand D, Stichelbaut F, Freud N, Sarrut D (2010) Optimization of GEANT4 settings for Proton Pencil Beam Scanning simulations using GATE. Nuclear Instruments and Methods in Physics Research B, Article in press.
- [3] Safai S, Bortfeld T, Engelsman M (2008) Comparison of the lateral penumbra of a collimated double-scattered beam and uncollimated scanning beam in proton radiotherapy. Physics in Medicine and Biology 53: 1729-1750.