

Extension of the treatment planning system TRiP by the beam mixing model proposed by Lam*[§]

O. Steinsträter¹, T. Friedrich¹, U. Scholz¹, M. Krämer¹, M. Durante¹, and M. Scholz¹

¹GSI, Darmstadt, Germany

The treatment planning system TRiP [1,2] developed at GSI for heavy ion radiotherapy predicts the biological effect of an ion beam based on the Local Effect Model (LEM), also developed at GSI [3]. Here, LEM is used to derive the biological effect of monoenergetic ion beams, typically provided as parameters according to the Linear-Quadratic-Linear (LQL) model (α , β and threshold dose D_t). Since for the treatment planning the effect of mixed radiation (the primary projectile and its fragments in a wide energy range) has to be predicted, in addition a beam mixing model is required. Currently a monte-carlo based model [1] and a model based on the Theory of Dual Radiation Action (TDRA) [2] are implemented in TRiP. The monte-carlo based model is highly flexible but for many application too time consuming. On the other hand, the calculation time for the TDRA based model could substantially be reduced by moving a significant part of the total calculation into a pre-processing step which has to be performed only once [2]. Unfortunately the TDRA based model cannot directly use ion specific threshold parameters D_t , which are provided by the most recent version of the LEM [4]. Although an extension of the TDRA based model is possible [5], this model is significantly more complex and does not allow a comparable pre-processing technique as in the original model. We therefore introduced the beam mixing model provided by Lam [6], which is independent of the underlying model for the dose-response curves of the contributing monoenergetic ions and therefore highly flexible. In addition, similar to the implemented TDRA based model, a significant part of the calculation could be moved to a pre-calculation step.

The beam mixing model proposed by Lam [6] relates the slope of the effect of the mixed beam, ϵ_{mix} , to the slopes of the effects of the contributing monoenergetic beams, ϵ_i : $\frac{d\epsilon_{\text{mix}}}{dD} = \sum_i \frac{D_i}{D_{\text{mix}}} \frac{d\epsilon_i}{dD}$ (total dose $D_{\text{mix}} = \sum_i D_i$).

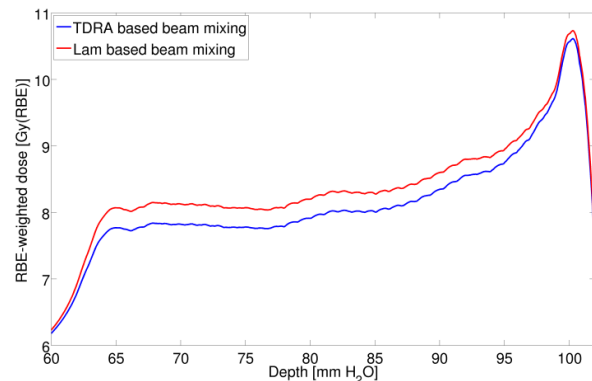
The irradiation system developed at GSI uses an active dose shaping technique which superimposes many narrow ion beams (pencil beams). The irradiation field at a position (x, y, z) can therefore be expressed in terms of the initial fluences of the contributing pencil beams, F_{i_v} , comprised as vector $\mathbf{F} = (F_1, \dots, F_N)$. Hence, TRiP internally calculates effects with respect to \mathbf{F} : $\epsilon(\mathbf{F})$. In addition, for the optimization of the target dose, the algorithms implemented in TRiP also need the derivatives of ϵ with respect to the fluences: $\partial\epsilon/\partial F_{i_v}$. For the Lam based beam mixing method this results in a weakly-coupled system of ordinary differential equations (ODE) for $t \mapsto \epsilon(t\mathbf{F})$ and $t \mapsto \partial\epsilon(t\mathbf{F})/\partial F_{i_v}$, $0 \leq t \leq 1$,

* Work supported by Siemens Healthcare.

§ Work is part of HGS-HIRE.

$$\frac{d}{dt}\epsilon = f_0(\epsilon), \quad \frac{d}{dt}\left(\frac{\partial\epsilon}{\partial F_{i_v}}\right) = f_v\left(t, \epsilon, \frac{\partial\epsilon}{\partial F_{i_v}}\right), 1 \leq v \leq n,$$

which have to be solved for each position (x, y, z) . The functions f_v are quite complicated and depend on the depth z and on other more general properties of the irradiation field, but not on the fluence vector \mathbf{F} . Therefore, significant parts of the calculation of the f_v can be moved to a pre-calculation step, which only has to be repeated if general parameters like the initial projectile or the irradiated cell type have to be changed.



In the figure, TRiP estimations for the RBE-weighted dose of a carbon irradiation of CHO (Chinese Hamster Ovary) cells with an SOBP (Spread Out Bragg Peak) of 4 cm are shown (the plot is restricted to the SOBP region). Whereas both curves have been based on the same LEM data, the beam mixing models were different: TDRA model in blue, the newly implemented Lam model in red.

Conclusion

Although significantly more complex than the TDRA based method, especially the pre-calculation technique reduces the calculation time for the Lam based method to a value acceptable for the most applications.

The new beam mixing model tends to emphasize higher β values (around 5% higher RBE-weighted dose values in the SOBP) which might be of particular interest for the new full simulation LEM method [4].

References

- [1] M. Krämer et al., Phys. Med. Biol., 45 (2000) 3319.
- [2] M. Krämer et al., Phys. Med. Biol., 51 (2006) 1959.
- [3] T. Elsässer et al., Int. J. Radiation Oncology Biol. Phys. 78 (2010) 1177.
- [4] U. Scholz et al., GSI Sci. Report, (2011) 517.
- [5] O. Steinsträter et al., GSI Sci Rep, (2011) 524.
- [6] G. K. Y. Lam, Radiat. Res., 110 (1987) 232.