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"Survival": a radiobiological simulation toolkit for ion beam therapy

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Purpose: One major rationale for the application of heavy ion beams in tumor therapy is their increased relative biological effectiveness (RBE). The complex dependencies of RBE on the dose, biological endpoint, position in the field etc. require the use of biophysical models. This study aims at introducing a new software, named "Survival", to facilitate the radiobiological computations needed in ion therapy.

Methods: The proposed code was written in C++ and it was developed with a modular architecture in order to easily incorporate different models. The following radiobiological models were successfully implemented: the Local Effect Model (LEM, version I, II and III) [1,2] and variants of the Microdosimetric Kinetic Model (MKM) [3,4]. Different numerical evaluation approaches were also implemented: Monte Carlo (MC) numerical methods and a set of faster analytical approximations. [5,6]

Results: As examples of possible applications, the toolkit was used to reproduce the RBE versus LET for different ions (proton, He, C, O, N) and different cell lines (CHO, HSG). Intercomparison between different models (LEM and MKM) and computational approaches (MC and fast approximations) were performed.

Conclusions: The developed software could represent an important tool for the evaluation of the biological effectiveness of charged particles in ion beam therapy, in particular when coupled with treatment simulations. Its modular architecture facilitates benchmarking and intercomparison between different models and evaluation approaches. The code is open source (GPL2 license) and can be downloaded at <https://github.com/batuff/Survival>.

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