An open-source software library for amorphous-track modeling

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1. Background: Amorphous track models

- Amorphous track models (ATMs) neglect the stochastic nature of track structure and replace it by a parameterized function of average dose around the track (Fig. 1).
- ATMs also postulate that the response of a system (detector, cells) is the same for X-rays and ions on a local scale. Therefore, the ion beam response can be solely derived from the system's X-ray response and the largely inhomogeneous pattern of ion dose deposition (Fig. 2).
- ATMs can predict
  - the relative efficiency of solid-state detectors (e.g. Alanine or TLDs)
  - the relative biological effectiveness (RBE) of cell survival
- ATMs are used clinically today to optimize treatment plans for ion radiotherapy.

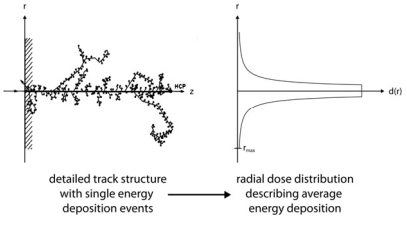

Figure 1: The detailed structure of a proton or ion track (left) is replaced by the 'radial dose distribution' (RDD).

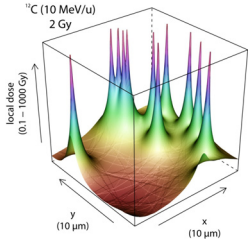

Figure 2: Local dose deposition pattern for Carbon ions at a typical clinical dose.

2. The libamtrack project

- A number of different flavors of ATMs exists, most notably [1]:
  - The 'Ion-Gamma-Kill' approach by R. Katz and co-workers
  - The 'Local effect model' by G. Kraft, M. Scholz and others
- In addition, various implementations and underlying physics assumptions are found.
- For the interested user it is therefore difficult to apply, compare, and further develop ATMs on a common basis.
- To overcome this problem, we started the software library 'libamtrack' [2].
- The latest version is 0.4.1r724, which includes
  - Three amorphous track model flavours:
    - Grid summation method (GSM)
    - Probability-based method (CPPSC, CPPSS)
    - Ion-Gamma-Kill method (IGK)
  - Various parametrizations for underlying physics:
    - 7 variants for radial dose distribution (RDDs, Fig. 3)
    - 7 variants for track-width / electron range
    - 6 variants for X-ray / gamma response

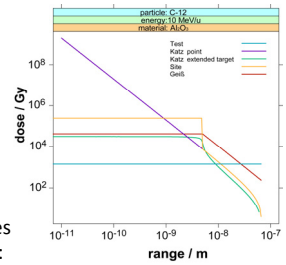

Figure 3: Some of the RDDs available in libamtrack.

- Main homepage, information, instructions, manuals and all relevant links:

http://libamtrack.dkfz.org

3. An application example

- For two spread-out Bragg peaks (SOBPs), the fluence differential in energy and depth for Carbon ions in water was computed using the FLUKA 2008.3d.0 transport code [3;4] (Fig. 4).
- Both SOBPs consist of five pristine Bragg peaks. One SOBP was generated using (active) energy variation between 220 and 270 MeV/u. For the second SOBP a primary beam of 350 MeV/u was (passively) degraded by a water column between 7.7 and 11.7 cm.
- For all following calculations, these data were read into the computing environment R (s. box 4) with libamtrack 0.5.0 (development) using the appropriate interface function (works also for the TRiP spc-format [5]).
- The data for the panels in Fig. 5 can be generated by executing a single function call of libamtrack. A second R call then produces the plot (using the lattice package [6]).
- For all fragments the fluence was higher for the passive SOBP (Fig. 5). In the tail, this leads to a significantly higher LET but does not translate into difference in cell survival other than from dose differences (for chosen model).

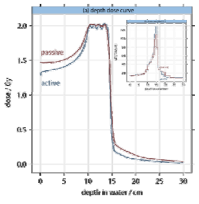

Figure 4: Depth-dose curve and LET (insert) for the active and passive SOBPs.

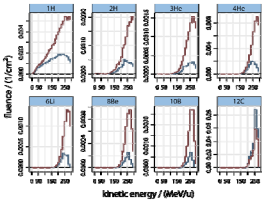

Figure 5: Fluence differential in energy for depth 1.5 cm. Note the different scales for the individual nuclides.

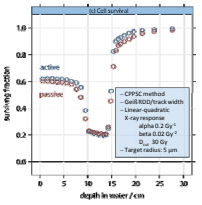

Figure 6: Cell survival as a function of depth for the active and the passive SOBP.

- **For more applications of libamtrack, please see also the posters by L. Grzanka et al. and R. Herrmann et al. (this conference).**

4. How to use libamtrack

- The most straightforward access is the libamtrack web interface (Fig. 7) which includes a selection of relevant functions.

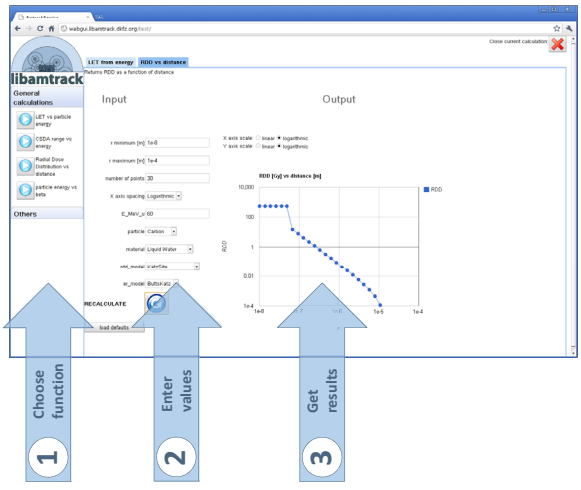

Figure 7: Three simple steps to get results from the libamtrack web interface.

- To utilize libamtrack's functionality in more detail and for customized calculations, an extension package for the R computing environment [7] is provided with extensive documentation and examples.
- libamtrack can also be called from script languages (Python), other software environments (e.g. [MATLAB™], [NI LabVIEW™] or similar) or within self-developed programs. This is the most complex approach as the user might have to develop their own access routines.

References

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