Introducing the RadBioStat Educational Software: Computer-Assisted Teaching of the Random Nature of Cell Killing

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ABSTRACT

The interaction of radiation with cells and tissues has a random nature. Therefore, understanding the random nature of cell killing that is determined by Poisson distribution statistics is an essential point in education of radiation biology. RadBioStat is a newly developed educational MATLAB-based software designed for computer-assisted learning of the target theory in radiation biology. Although its potential applications is developing rapidly, currently RadBioStat software can be a useful tool in computer-assisted education of radiobiological models such as single target single hit, multiple target single hit and multiple target multiple hit. Scholars' feedback is valuable to the producers of this software and help them continuously improve this product, add new features and increase its desirability and functionality.

Keywords

Radiation Biology, Software, Computer-assisted Teaching, Cell Killing, Poisson distribution, Statistics

Introduction

Radiation biology is a branch of science that deals with the study of the action of ionizing radiation on living organisms. As radiation interacts randomly with cells and tissues, understanding the random nature of cell killing is an essential point in learning the basic concepts of radiation biology. RadBioStat is an educational MATLAB-based software designed for computer-assisted learning of the target theory in radiation biology. This software is developed as a research project at the Ionizing and Non-ionizing Radiation Protection Research Center (INIRPRC), Shiraz University of Medical Sciences (SUMS). The mathematical basis of target theory for radiation-induced cell damage was developed by Atwood and Norman in 1949 [1]. Target theory that is believed to be one of the essential concepts for understanding radiobiology, is based on inactivation of specific target(s) inside an organism by hits induced by ionizing radiation. We know that calculations of hit probability in such a radiobiological system are controlled by Poisson distribution statistics [2-4]. In this light, the probability of n events is given by:

$$p(n) = \frac{(e^{-x})(x^{n})}{n!} \qquad \text{Equation 1}$$

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where x = the average number of events
and n = the specific number of events

For better understanding of the concept of "mean lethal dose", i.e. random distribution of n hits (lesions) in n targets (1 hit per cell on average), RadBioStat uses a simple analogy. It draws a 10×10 matrix (100 squares) and randomly distributes 100 beads in these squares. As shown in figure 1, when there are 100 squares and 100 beads, 63% of the squares will be filled and 37% will remain empty (some of the squares will receive more than one bead). Now, if we replace the beads with radiation, there is a radiation dose that causes an average of one hit per cell (inactivation of one target per cell), the probability of survival can be easily calculated as:

$$p(0)=\frac{(e^{-1}.1^{0})}{0!}=e^{-1}=37\% \qquad \text{Equation 2}$$

Figure 1 shows the random distribution of 100 hits (lesions) in 100 targets (hit per cell = 1). As shown in this screenshot, Poisson statistics reveals that on average 37 cells will be survived because some cells will have more than one hit.For this reason, D0 (D37) that is usually called the "mean lethal dose", is the dose that on average. Figure 2 also shows that

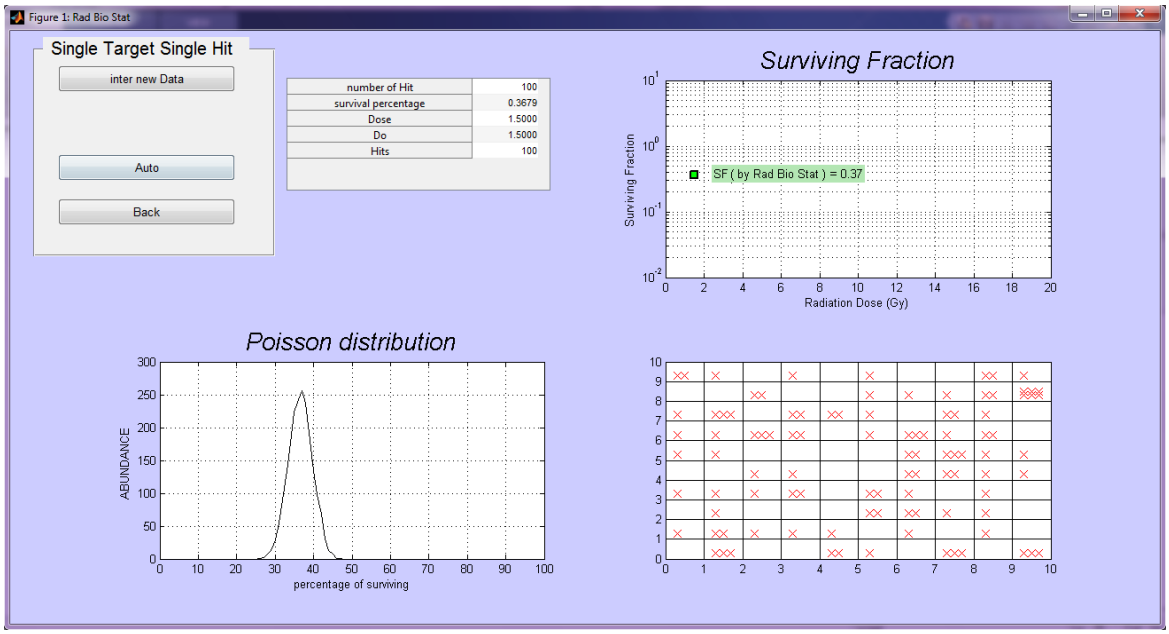

Figure 1: RadBioStat screenshot showing the concept of mean lethal dose (e.g. random distribution of 100 lesions in 100 cells will kill only 63% of the cells and 37% will survive). This test has repeated 2000 times (lower left panel).

in Single-Target Single-Hit model, there is no shoulder.

If we double the D37 dose, this time RadBioStat randomly distributes 200 beads in 100 squares and shows that 14% of the squares (cells) will be empty (will survive).

100 targets, 200 hits → x=1 → P=e-2=0.137

RadBioStat can also be used to draw typical cell survival curves in multiple target models. For example in the multiple target single hit model, m targets have to hit at least once for inactivation (equation 3).

$$P_m=(1-e^{-kD})^m \quad , \quad \frac{N}{N_0}=1-P_m=1-(1-e^{-kD})^m \qquad \text{Equation 3}$$

where k = 1/D37 and m is the number of targets.

On the other hand, in the multiple target multiple hit model, m targets have to hit at least n times for inactivation (equation 4).

$$\frac{N}{N_0} = [1-(1-e^{-kD})^m]^n \qquad \text{Equation 4}$$

Figure 3 shows a sample cell survival curve.

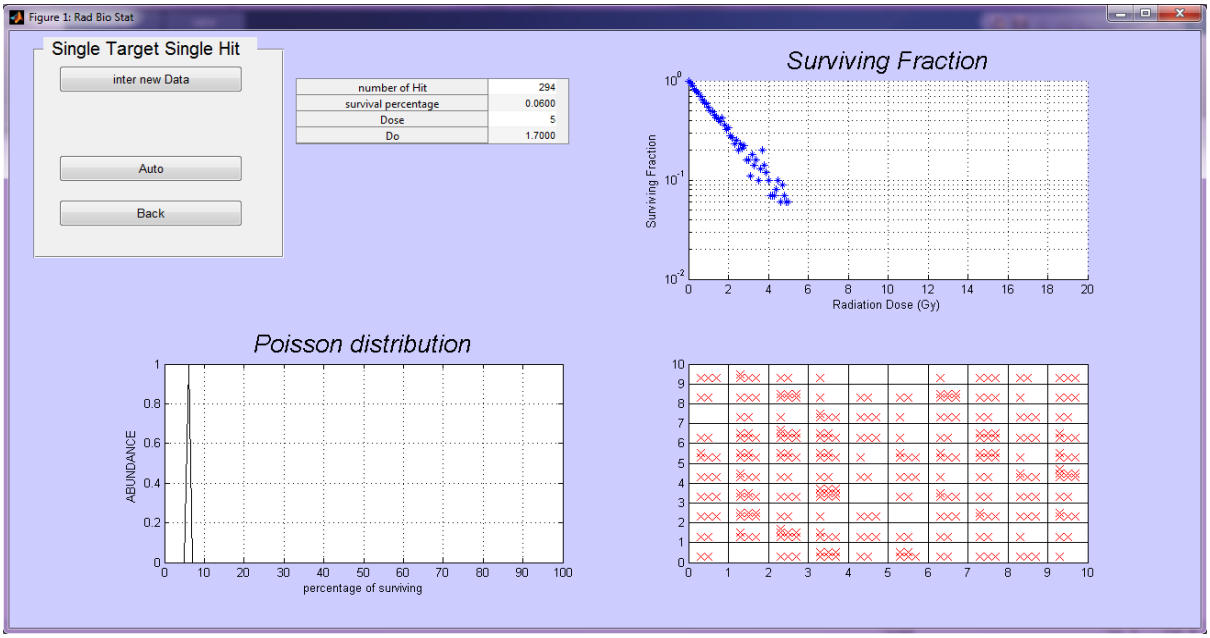

Figure 2: RadBioStat screenshot showing a typical cell survival curve. The software help students better understand why in Single-Target Single-Hit shoulder doesn't exist.

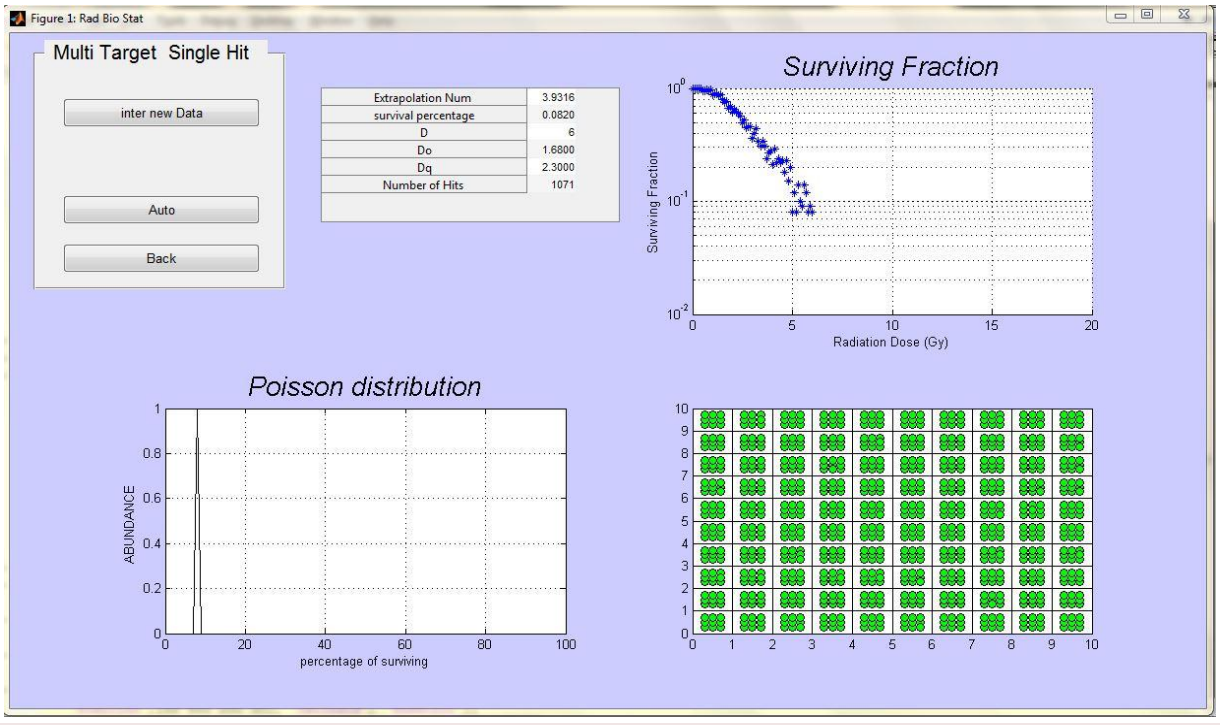

Figure 3: RadBioStat screenshot showing a typical cell survival curve. The software help students better understand why when the number of targets increases the shoulder width increases.

RadBioStat is developing rapidly by an expert team at the Ionizing and Non-ionizing Radiation Protection Research Center (INIRPRC). However, in its current status, this software can be a useful tool in computer-assisted teaching of the following radiobiological models:

- Single target single hit
- Multiple target single hit
- Multiple target multiple hit

It should be noted that this software is still in its preliminary stage and scholars' feedback is valuable to the producers of this software and will help them continuously improve this product, add new features and increase its desirability and functionality.

Acknowledgement

The development of this software was supported by the Ionizing and Non-ionizing Radiation Protection Research Center (INIRPRC), Shiraz University of Medical Sciences (SUMS), Shiraz, Iran.

Conflict of interest

None Declared.

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