RADIANCE

Radiotherapy Survival Rate Modeling Interface

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Source code available at: https://github.com/RiPires/DTRP_Project.git

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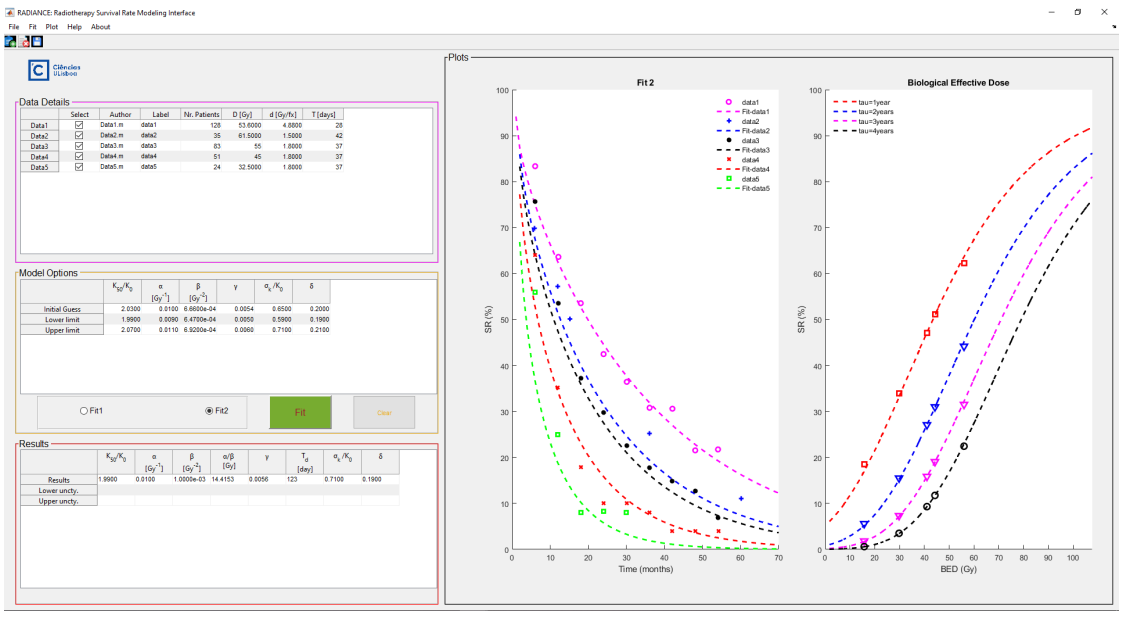
What is RADIANCE?

RADIANCE is a GUI (Graphical User Interface) to estimate radiobiological parameters by fitting different survival rate models to clinical data, with the aim of evaluating the radiobiological equivalence between different treatment regimes and designing new optimised dose fractionation schemes.

In the first release, two survival models, here called "Fit1" and "Fit2", are available. These models are used by Tai A, Erickson B, et al., in their study to "Estimate radiobiologic parameters from clinical data for biologically based treatment planning for liver irradiation". In our project, we automate the implementation of these formalisms in the form of the RADIANCE interface, that produce comparable results of the estimated parameters with the ones obtained by Tai A, Erickson B, et al.



Fit 1:

$$SR(D,d,\tau) = e^{-Kexp(-p)}, \tau > T$$
$$p = \alpha(1 + \frac{d}{\alpha/\beta})D - \gamma T - (a(\tau - T))^{\delta}$$

The survival rate, SR (%), depends on the elapsed time since the beginning of the treatment, **τ** (months), the total prescription dose, D (Gy), the dose per fraction, d (Gy/fx) and the total treatment time, T (day). **γ** = ln2/Td, **α** and β characterise the intrinsic radiosensitive of the cells. Td is the potential doubling time (day). K, a and δ are the remaining fit parameters.

Fit 2:

$$SR(D,d,\tau) = 1 - \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{t} e^{-\frac{z^2}{2}} dz = \frac{1}{2}(1 - erf\frac{t}{\sqrt{2}})$$
$$t = \frac{e^{-p} - K_{50}/K_0}{\sigma_k/K_0}$$
$$p = \alpha(1 + \frac{d}{\alpha/\beta})D - \gamma T - (\gamma(\tau - T))^{\delta}$$

On the second model, K50 is the critical number of tumour clonogens corresponding to death in 50 % patients. σk is the gaussian width for the distribution of critical clonogen numbers.

BED:

$$\mathtt{BED} = (1 + \frac{d}{\alpha/\beta})D - \frac{\gamma T}{\alpha}$$

The RADIANCE interface has a straightforward way of use. In this first release, the user starts by running the "radiance.m" script, with the latest version of MATLAB (remember that it was tested using version R2023a, we don't guarantee that it will perfectly run with older or newer versions of MATLAB). In the same path of the "radiance.m" file should also be present the following files:

- bedfunction.m
- BED.m
- fit1.m
- fit2.m
- perform_fit1.m
- chi2_residuals.m
- sample.m
- uncertainty_quocient.m
- perform_fit1.m
- perform_fit2.m
- secondfitting.m
- calculate_n.m
- fit1bed.m
- fit2bed.m
- Ciencias_ul_azul_h_s-ass.png
- AddFileIcon.png
- DeleteFileIcon.png
- SavePlotIcon.png
- ClearPlotIcon.jpg
- help.txt
- about.txt

The data files to be imported should also be in this path! Otherwise, the program will fail.

Inside the interface, the user will find 5 different areas to interact with: menu and toolbars on the top left; a "Data Details" panel with a table containing information about the clinical data; a "Model Options" panel with a table containing input parameters to guarantee the convergence of the fits, a model selection radio-button feature that allows to choose the model to be applied and a "Perform Fit" button to run the fitting algorithm once the set-up is done; a "Results" panel with a table that will be filled with the fitted parameters; a "Plots" panel with two axes, one for survival rate over time plot and the other for survival rate over BED plot.

How to use it?

The first step is to import the clinical data to be used. For that purpose, the user can click on the "AddFile" icon on the toolbar, or go to the menu "File/Add Files…". Each file should correspond to a different study, with its own parameters N, D, d and T.

The files should have an appropriate name, with a ".m" extension (e.g. "Study1.m"), formatted in a four column way (Tau SR up_error bot_error), being Tau the elapsed time from the beginning of the treatment (in months), SR the survival rate (in %), up_error the upper error associated to the SR and bot_error the bottom error associated to the SR. In the backend of the program, importing the files only keeps their names stored in the row header of the "Data Details" table, that are then used to read the content of the files, when called by "Fit1.m", "Fit2.m" or "BED" functions.
In any case, if the input file doesn't contain error bar values, these will be considered zero.

After importing the data files, the user should fill in the remaining information about the studies (N, D, d and T) in the corresponding fields of the “Data Details” table (warning and error messages are activated if the user prompts certain inputs such as characters in a numeric cell or negative numbers). **These parameters are mandatory to be filled before performing the fit**.

At any time, the user can delete studies using either the “Delete unselected files” icon in the toolbar, or in the menu “File/Delete files”. All the information in the table related to the studies is deleted.

One way to avoid adding files and filling in the table by hand every time the user closes and launches the interface is to save its current state on the menu “File/Save”. The information is saved in a “.mat” binary file, in the current path, with a name chosen by the user. Afterwards, this information can be loaded via the menu “File/Open”.

If the user intends to have a graphical look at the clinical data selected on the table before performing the fit this can be done using the menu “Plot”, “Plot selected clinical data”.

At any time, the user can clear the axes using the menu “Plot”, “Clear axes”.

With all the details regarding the clinical data set up, the user may focus on the “Model Options” panel. This starts by choosing the model to apply, either “Fit1” or “Fit2” as defined previously (apart from the “Model Options panel” this can also be done in the menu “Fit”, “Select model”). The headers on the corresponding table will change according to the selected model. A set of values is assumed by default taking into account the results shown byTai A, Erickson B, et al. A more realistic and accurate set of values for “Initial guess”, “Lower limit” and “Upper limit” should be inputted by the user, based on its clinical expertise (warning and error messages are activated if the user prompts certain inputs such as negative numbers).

At this point, the program is ready to perform the fit using the “Fit” button on the “Model Options” panel or on the menu “Fit “, “Perform fit”. After performing the fit, the fitted SR vs Time and SR vs BED curves are displayed in the “Plots” panel, together with the clinical data, and the results of the fitted parameters are displayed on the “Results” panel.

The axes can be saved in a separate file using the menu “Plot”, “Save”, where the user is prompted to choose which axes to save, the name and the extension of the file.

References

- Tai A, Erickson B, Khater KA, Li XA. Estimate of radiobiologic parameters from clinical data for biologically based treatment planning for liver irradiation. Int J Radiat Oncol Biol Phys. 2008 Mar 1;70(3):900-7. doi: 10.1016/j.ijrobp.2007.10.037. PMID: 18262101