









ORIGINAL ARTICLE



Biodose Tools: an R shiny application for biological dosimetry

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ABSTRACT

Introduction: In the event of a radiological accident or incident, the aim of biological dosimetry is to convert the yield of a specific biomarker of exposure to ionizing radiation into an absorbed dose. Since the 1980s, various tools have been used to deal with the statistical procedures needed for biological dosimetry, and in general those who made several calculations for different biomarkers were based on closed source software. Here we present a new open source program, Biodose Tools, that has been developed under the umbrella of RENEB (Running the European Network of Biological and retrospective Physical dosimetry).

Materials and methods: The application has been developed using the R programming language and the shiny package as a framework to create a user-friendly online solution. Since no unique method exists for the different mathematical processes, several meetings and periodic correspondence were held in order to reach a consensus on the solutions to be implemented.

Results: The current version 3.6.1 supports dose-effect fitting for dicentric and translocation assay. For dose estimation Biodose Tools implements those methods indicated in international guidelines and a specific method to assess heterogeneous exposures. The app can include information on the irradiation conditions to generate the calibration curve. Also, in the dose estimate, information about the accident can be included as well as the explanation of the results obtained. Because the app allows generating a report in various formats, it allows traceability of each biological dosimetry study carried out. The app has been used globally in different exercises and training, which has made it possible to find errors and improve the app itself. There are some features that still need consensus, such as curve fitting and dose estimation using micronucleus analysis. It is also planned to include a package dedicated to interlaboratory comparisons and the incorporation of Bayesian methods for dose estimation.

Conclusion: Biodose Tools provides an open-source solution for biological dosimetry laboratories. The consensus reached helps to harmonize the way in which uncertainties are calculated. In addition, because each laboratory can download and customize the app's source code, it offers a platform to integrate new features.

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1. Introduction

Biological dosimetry aims at estimating the absorbed dose in an individual in which an exposure to ionizing radiation (IR) is suspected, by means of analyzing biomarkers with a clear dose-effect relationship (IAEA 2011). A great majority of biomarkers of dose exposure come from the analysis of the induced DNA damage, most of them analyzed using cytogenetic techniques such as dicentric, translocation, or micronucleus assays. Dose assessment is based on converting

an observed yield of aberrations (e.g. the frequency of dicentrics present in peripheral blood lymphocytes) into an absorbed dose using a pre-established calibration curve. This process requires mathematical models and the assumptions on statistical probability distribution of the aberration in question. First, to establish a calibration curve, blood samples must be uniformly irradiated at several doses and the observed distribution of aberrations is mostly assumed to follow a Poisson distribution. More precisely, it is assumed that for low LET (linear energy transfer) radiation types,

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uniform exposures result in dicentric counts that follow a Poisson distribution (Bauchinger and Schmid 1973; Edwards et al. 1979). High LET radiation types tend to show overdispersion (Virsik and Harder 1981; Brame and Groer 2002; Puig and Barquinero 2011). Overdispersion also often arises in micronuclei counts and γ -H2AX foci data (Vral et al. 2011; Einbeck et al. 2018) and for semi-automatically sorted dicentrics (Endesfelder et al. 2020). Then the observed yields at different doses are used to construct a calibration curve assuming a Linear-Quadratic (LQ) or Linear (L) model, depending on the radiation quality. While low-LET exposures show a linear-quadratic dose-effect relationship, high-LET exposures tend to be linear, (Edwards et al. 1980). The coefficients of these models can be estimated using maximum likelihood or iteratively reweighted least squares approaches (Merkle 1983).

In case of a radiation accident, the observed distribution of aberration counts is tested for deviations from the Poisson distribution to distinguish between homogeneous and heterogeneous exposures. The observed count is inverse regressed by the calibration curve and uncertainties are usually calculated considering only the uncertainty relative to the yield observed or considering also uncertainties coming from the calibration curve (Edwards 1978; Merkle 1983; Savage et al. 2000). Procedures to consider both sources of uncertainties are not simple, as the error is made up of two components: (a) uncertainties from the distribution of observed counts, and (b) uncertainties from the LQ or L models of the calibration curve (Merkle 1983; Savage et al. 2000). In case of a heterogeneous exposure, additional distributional assumptions have to be made (Sasaki and Miyata 1968; Dolphin and International Atomic Energy Agency 1969; Pujol et al. 2016). Bayesian methods have been recently proposed to consider both sources of uncertainty, and for both, whole-body (homogeneous) and partial-body (heterogeneous) dose assessment (Ainsbury et al. 2014; Higuera et al. 2016; Morina et al. 2015).

1.1. Software implementations

The tools to deal with some or all of the statistical procedures used in biological dosimetry have evolved since the 1980s (Ainsbury and Barquinero 2009). These tools ranged from adapted Microsoft Excel sheets to specific programs (the later summarized in Table 1). The specific programs were based on closed-source software and, for example, used a single methodology to calculate uncertainties. Thus, improvements were restricted to those who manage the source code, and the end-user cannot modify or implement

any improvement. In addition, there is a possibility of misunderstanding or misuse of these closed programs.

Recently, using the R project for statistical computing (R Core Team 2022) some scripts have been written for biological dosimetry purposes. Although R programming is based on open-source code, most end-users performing biodosimetry are usually not familiar with programming and mathematical or statistical modeling that is required to use or implement R source code. It is therefore required to provide tools with GUIs that are easy to use and that provide the required functionality to obtain reliable dose estimates.

In this paper we present biodosetools (styled as Biodose Tools), an R package developed using shiny (Chang et al. 2022), to offer an online and easy-to-use solution to be used by biological dosimetry laboratories, as well as a tool for statisticians to manually perform the underlying calculations in R. The package is available from the Comprehensive R Archive Network (CRAN) at <https://cran.r-project.org/web/packages/biodosetools/index.html>, and GitHub at <https://github.com/biodosetools-team/biodosetools> and can be distributed under the GPL-3.0 license (GNU General Public License v3.0). Biodose Tools has been developed under the umbrella of RENEB (Running the European Network of Biological and retrospective Physical dosimetry).

2. Materials and methods

2.1. Statistical considerations

In biological dosimetry, the quantity being modeled is usually the *yield*, i.e. the mean aberration count per cell. For low-LET radiation, the yield (λ) of chromosome aberrations (e.g. dicentrics, translocations, micronuclei) is related to exposed dose (D) by the LQ equation:

$$\lambda = C + \alpha D + \beta D^2 \quad (1)$$

For high-LET radiation, as well as for highly protracted low-LET exposures (see Section 2.2.4.), the α -term becomes large, and eventually, the β -term becomes biologically less relevant and also statistically ‘not significant’ (Frome and DuFrain 1986; Sasaki 2003). In this situation, the dose-effect is approximated by the linear Equation (2):

$$\lambda = C + \alpha D \quad (2)$$

In both equations, C is interpreted as the background level.

2.1.1. Dose-effect curve fitting

The objective of dose-effect or curve fitting is to calculate the coefficients C , α and β which best fit the calibration data

Table 1. List of historical analysis software developed specifically for radiation biodosimetry.

Name	Language (s)	Framework (s)	Author (s)
MLPOL	Fortran 77	–	(Szłuińska et al. 2015)
MLREG	–	–	(Bundesamt für Strahlenschutz 1996)
DOSGEN	Pascal	Turbo Pascal	(García and Zequera 1996)
CABAS	Object Pascal	Delphi	(Deperas et al. 2007)
Dose estimate	Object Pascal	Delphi 6	(Ainsbury and Lloyd 2010)

points. For dicentrics (for more details see Section 2.2), simulated whole-body irradiation of ex vivo blood in test tubes with X-rays or γ -rays produces aberration counts which are very well represented by the Poisson distribution (Edwards et al. 1979). In contrast, neutrons and other types of high-LET radiation produce distributions which display overdispersion, where the sample variance exceeds the sample mean. Rather than choosing a more suitable distribution, this is usually dealt with by adjusting the calculating the overdispersion and then adjusting the uncertainty accordingly (IAEA 2011).

2.1.2. Testing for Poisson

Because most curve fitting methods rely on Poisson statistics (see Supplementary Materials Section 1.1), the dicentric cell distribution should be checked for Poisson compliance for each dose used to build the calibration curve. This should also be checked for the sample tested for an exposure. Although recently in the field of biological dosimetry different tests have been proposed to check the Poisson distribution (Duran et al. 2002; Higuera et al. 2018), the most widely used test is the u -test (Rao and Chakravarti 1956; Savage 1970). The u -test statistic (3) is a normalized unit of the dispersion index ($\hat{\sigma}^2/\bar{y}$), which for a Poisson distribution should be close to 1:

$$u = (\hat{\sigma}^2/\bar{y} - 1) \sqrt{\frac{N-1}{2(1-1/X)}} \quad (3)$$

When $-1.96 \leq u \leq 1.96$ the assumption of equidispersion is not rejected with a two-tailed significance level of $\alpha = 0.05$. A u -value higher than 1.96 indicates overdispersion, whilst u -values lower than -1.96 indicate underdispersion. Underdispersion is an extraordinary occurrence in Biodosimetry. However, Pujol et al. (2014) claimed that, after high dose exposure (>5 Gy), the underdispersion detected in their datasets was caused probably for two reasons. The first, due to the number of chromosomes that the cells possess and the limitation of forming cells with a very high number of dicentrics. The second is that at high doses fewer cells with 0 or 1 dicentric than expected were observed, possibly indicating a lower efficiency in repairing genetic damage at high doses.

2.2. Dose-effect curve fitting

2.2.1. Fitting method

Maximum likelihood is the method proposed for determining the best fit (Papworth 1975; Merkle 1983). Using this method, the best fit value for each coefficient is achieved by assuming a Poisson distribution and maximizing the likelihood of the observations by the method of iteratively reweighted least squares. In case of overdispersed distributions, as obtained after high LET radiation, the weights must take into account the overdispersion. Table 2 gives example data used to construct a dose-effect curve for low LET γ -radiation (Barquinero et al. 1995), while Table 3 shows the estimated coefficients when the data from Table 2 are fitted.

Table 2. Dicentric distribution within cells, dispersion index, and u -value of the dose-effect curve constructed from cytogenetic results obtained from blood samples irradiated with γ -rays (Barquinero et al. 1995).

D (Gy)	N	X	C ₀	C ₁	C ₂	C ₃	C ₄	C ₅	\bar{y}	$\hat{\sigma}^2$	$\hat{\sigma}^2/\bar{y}$	U
0.00	5000	8	4992	8	0	0	0	0	0.002	0.002	0.999	-0.075
0.10	5002	14	4988	14	0	0	0	0	0.003	0.003	0.997	-0.135
0.25	2008	22	1987	20	1	0	0	0	0.011	0.012	1.080	2.610
0.50	2002	55	1947	55	0	0	0	0	0.027	0.027	0.973	-0.861
0.75	1832	100	1736	92	4	0	0	0	0.055	0.056	1.026	0.790
1.00	1168	109	1064	99	5	0	0	0	0.093	0.093	0.999	-0.018
1.50	562	100	474	76	12	0	0	0	0.178	0.189	1.064	1.077
2.00	333	103	251	63	17	2	0	0	0.309	0.353	1.141	1.822
3.00	193	108	104	72	15	2	0	0	0.560	0.466	0.834	-1.638
4.00	103	103	35	41	21	4	2	0	1.000	0.882	0.882	-0.844
5.00	59	107	11	19	11	9	6	3	1.814	2.085	1.150	0.811

For each dose analyzed, the total number of cells scored (N), the total number of dicentrics observed (X), the cell distribution of dicentrics ($C_0 \dots C_5$), and the dispersion index ($\hat{\sigma}^2/\bar{y}$) and u -test statistic (u) are presented (a sample is considered overdispersed if $u > 1.96$).

Table 3. Fitted values of the coefficients of the LQ dose-effect calibration curve constructed from the dicentric distribution in Table 2.

Coefficient	Estimate	SE	t-Statistic	p-Value
C	0.00128	0.00047	2.716	0.007
α	0.02104	0.00516	4.079	<0.001
β	0.06303	0.00401	15.730	<0.001

The p -values of the t -test indicate that each parameter is statistically significant (see Supplementary Materials Section 1.2 for more details on testing goodness of fit).

2.2.2. Dose-effect calibration

Adequate curve fitting requires a sufficient number of evaluated dose points to minimize the error. A minimum of 7 doses should be evaluated, 5 of them at doses equal or lower than 1 Gy, including the 0 Gy dose. Usually, for low LET radiation (X-rays and γ -rays) the dose range evaluated is 0–5 Gy, at higher doses, evidence of saturation of the aberration yield exists. This saturation will result to a distortion of the β coefficient in Equation (1) (Lloyd and Edwards 1983; ISO 19328 2014). For high LET radiation, a range of 0–2 Gy is suggested (IAEA 2011). At higher doses, scoring should aim to detect 100 dicentrics at each dose. However, at lower doses this is difficult to achieve and instead several thousand cells per point should be scored; a number between 3000 and 5000 is suggested. In all cases, the actual number of cells scored should be dependent on the number of dose points in the low dose region, with the focus on minimizing the error on the fitted curve (Higuera et al. 2020).

Opinions vary on how to deal with the background level of chromosomal aberrations when fitting dose-effect data. In general, there are three approaches: (a) a dose point at 0 Gy is included in the curve fitting procedure, (b) the zero dose point is ignored, or else (c) the zero dose point is represented in every fitting procedure by a standard background value. Nowadays almost all laboratories include a 0 Gy dose point, and it should always be included for dicentrics, translocations and micronuclei. If the measured yield at zero dose is used as one of the data points for the curve fitting (as used in the curve fitting presented in Table 3), the background becomes a variable parameter. However, since the yield in unirradiated cells is usually low, often none are

observed so the measured yield at zero dose is zero. As discussed, at low doses, the statistical resolution of the data points is generally low. Thus, including the zero dose point in the curve fitting procedure can in some cases lead to negative estimated C and α coefficients, which obviously have no biological basis. A way to resolve this problem is to ignore the zero dose data point and constraining the curve to pass through the origin. Another way to solve this is to fit the calibration curve model with constrained maximum likelihood which forces the intercept parameter to be non-negative (Oliveira et al. 2016). Some experts have used a small positive background value as a data point and assigned a large percentage of uncertainty to it. Ideally each laboratory should generate its own background data. A consensus has emerged that the background level of dicentric is ~ 0.5 – 1.0 per 1000 cells (Lloyd et al. 1980) whilst for translocations (Sigurdson et al. 2008) and for micronuclei (Fenech 1993) the control values are higher.

2.2.3. Protracted and fractionated exposure

In case of a protracted or fractionated exposure to low-LET radiation the resulting chromosomal aberration yield may be lower than when receiving the same dose acutely (Edwards et al. 1980). Dose protraction reduces the dose squared coefficient, β , in Equation (1). It is assumed that this term refers to those aberrations generated by the interaction of two or more tracks. Exchange type aberrations, such as dicentric have a fast kinetics formation (Darroudi et al. 1998; Durante et al. 1996, 1998; Pujol-Canadell et al. 2020), and hence the effect on the interaction of two tracks can be modified by repair mechanisms that have time to function during chronic or intermittent acute exposures. In the early times of radiobiology and evaluating the effect of IR on *Tradescantia* Lea and Catcheside (1942) suggested a time-dependent factor called the G function (4) to allow change of the dose squared coefficient and so account for the impacts of dose protraction.

$$G(x) = \frac{2}{x^2} (x - 1 + e^{-x}), \quad \text{and } x = \frac{t}{t_0} \quad (4)$$

where t is the time over which the irradiation occurred, and t_0 is the mean lifetime of the breaks, which has been shown to be of the order of ~ 2 hours (Bauchinger et al. 1979; Lloyd et al. 1984).

Currently in biological dosimetry this approach is still accepted and that is why the LQ dose-effect Equation (1) may be modified as follows:

$$\lambda = C + \alpha D + \beta G(x) D^2 \quad (5)$$

Given a value of t , we can have three protraction cases:

- Acute exposure when t is approximately 0. In this case $\lim_{x \rightarrow 0} G(x) = 1$. Therefore, the dose-effect equation becomes (1).
- Highly protracted exposure when t is high. In this case $G(x)$ reduces virtually to zero. Therefore, even if a high dose (> 1.0 Gy) is involved, the dose-effect equation becomes linear (2).
- Protracted exposure for any case in between. In this case the effects of $G(x)$ need to be considered.

All dose estimation methods implemented in Biodose Tools consider protraction, with the extreme of $G(x) = 1$ or $G(x) \approx 0$ being just particular cases. For this reason, all methods described in Section 2.3 are derived using Equation (5) instead of (1).

2.2.4. Genomic equivalence for translocations

Curve fitting for translocations follow the same procedure as described for dicentric. However, Fluorescence *In Situ* Hybridization (FISH) analysis only evaluates the translocation frequency in a specific set of chromosomes painted. The conversion of this frequency to full genome equivalence is a recommended procedure to use when different data must be combined or when results using different combinations of whole chromosome paintings are compared, e.g. in the frame of interlaboratory comparisons.

When the DNA probes used to paint different chromosome pairs are labeled with different fluorochromes, the genomic conversion factor F_p/F_G is usually calculated by using the formula (6) for the painted fractions of the genome (Lucas and Deng 2000):

$$\frac{F_p}{F_G} = \frac{2}{0.974} \left[\sum_i f_i (1 - f_i) - \sum_{i < j} f_i f_j \right] \quad (6)$$

where F_G is the full genome aberration frequency, F_p is the translocation frequency detected by FISH, and f_i is the fraction of genome corresponding to each chromosome i used in the hybridization, taking into account the gender of the subjects (Morton 1991). The total number of interchromosomal exchanges is 0.974, using the same assumption of DNA proportionality (see calculations in Lucas et al. 1992).

Translocations have higher background levels than dicentric, which is partly due to the former being a persistent type of aberration. When attempting retrospective biological dosimetry, it is critical to account for the translocation background, especially at low doses. Because a pre-exposure control blood sample from the unintentionally irradiated person or a population study group is not available, an estimated value based on generic survey data must be utilized. Ideally, a laboratory would create its own control database, but this is a huge undertaking because it would have to cover a lot of confounding factors and, more importantly, a wide range of age groups. The greatest international database, split down by age, sex, ethnicity, geographic region, and smoking behaviors, is currently available thanks to a comprehensive meta-analysis published by Sigurdson et al. (2008). It is important to account for the background and subtract from the total number of translocations observed in an individual's lymphocyte the expected translocation rate given a set of confounding factors (7), the most important of which is age:

$$F'_G = \frac{X - X_c}{N(F_p/F_G)} \quad (7)$$

where F'_G is the corrected full genome aberration frequency, X is the total number of translocations observed, X_c is the total number of expected aberrations, N is the total number of cells, and F_p/F_G is the genomic conversion factor given by (6).

2.3. Uncertainty on dose estimation

While it is simple to determine a dose from a measured yield of dicentrics, the associated uncertainty can be calculated using a variety of methods. Calculating 95% confidence limits is a common procedure for expressing uncertainty in terms of a confidence interval. A frequentist 95% confidence interval means that with a large number of repeated samples, 95% of such calculated confidence intervals would include the true value of the dose. The problem in estimating confidence limits for dicentrics and translocations after low LET exposure comes from two sources of uncertainty: the uncertainty from the aberration yield of the person to be examined, and uncertainties associated with the calibration curve. This issue has been discussed in the literature (Merkle 1983; Savage et al. 2000; Szłuińska et al. 2007).

Depending on the type of exposure, methods for whole-body assessment, partial-body assessment, and assessments for heterogeneous exposures with two different doses were implemented in the biodosetools package, using the following methods. The biodosetools package implements the following assessment methods, which are indicated in IAEA 2001 and IAEA 2011:

- Whole-body assessment: Merkle's method (Merkle 1983).
- Whole-body assessment: delta method (IAEA 2001).
- Partial-body assessment: Dolphin's method (Dolphin and International Atomic Energy Agency 1969).

In addition biodosetools also includes a package to assess heterogeneous exposures using a mixed Poisson model (Pujol et al. 2016). That was used in a recent RENEB/EURADOS field exercise (Endesfelder et al. 2021). In-depth statistical descriptions of each method is available in Supplementary Materials Section 1.3.

3. Results

3.1. Package implementation

The development of biodosetools started in 2018 in the frame of RENEB (Running the European Network of Biological and retrospective Physical dosimetry), one of whose purposes is to standardize methodology for individualized dose estimation from biological methods to statistical ones. Since no unique method exists for the different mathematical processes involved in biological dosimetry, several meetings and periodic correspondence were held in order to reach a consensus on the solutions to be implemented and, in particular, the solutions to be proposed as default.

As of version 3.6.1 (November 2022), biodosetools supports dose-effect fitting and dose estimation for the following biodosimetry assays:

- Dicentric assay.
- Translocation assay.

The biodosetools package is available from CRAN <https://CRAN.R-project.org/package=biodosetools> and can be installed using the standard R tools. In Table 4 we list all the functions available to the user through the R API provided by biodosetools.

3.1.1. Used packages

Naturally, biodosetools is built on other packages. Data transformations and wrangling are done through dplyr (Wickham et al. 2022), tidyr (Wickham and Girlich 2022), rlang (Henry and Wickham 2022), and magrittr (Bache and Wickham 2022), while visualizations are done using ggplot2 (Wickham 2016). All of the aforementioned packages are part of the tidyverse meta-package (Wickham et al. 2019). While most statistical calculations are implemented ad-hoc with the stats (R Core Team 2022) package, we rely in additional packages for some statistical analyses, such as maxLik (Henningsen and Toomet 2011), mixtools (Benaglia et al. 2009), MASS (Venables and Ripley 2002), and msm (Jackson 2011). For improved legibility, messages and warnings in the command line interface are constructed using cli (Csárdi 2022).

3.1.2. User interface using shiny

The Biodose Tools user interface is written in R shiny (Chang et al. 2022) using Bootstrap 3, via the shinydashboard (Chang and Borges Ribeiro 2021), shinyWidgets (Perrier et al. 2022), and bsplus (Lyttle 2021) packages, and the golem (Fay et al. 2022) framework. Analyses are implemented in the R programming language (R Core Team 2022), with the resultant tables and plots rendered in HTML through JavaScript libraries, via either native shiny or rhandsonable (Owen 2021). This is done by the JavaScript engine shipped on browser of choice, or by an instance of QtWebKit if the app is run within RStudio. The shiny app allows to download processed count or case data via xtable (Dahl et al. 2019). Similarly, it allows to generate and download reports, which are rendered using rmarkdown (Allaire et al. 2022) and Pandoc (MacFarlane 2022) to convert a native .Rmd document directly into an Office Open XML .docx document, or a .pdf file built from an intermediary .tex file using LaTeX (Lamport 1994).

In Biodose Tools color is used to identify different sections of information, a technique called color-coding. In particular, Biodose Tools uses four colors to code information: (a) blue for options and settings, (b) purple for data input, (c) green for results, and (d) orange for exporting results. Figure 1 shows a simple mockup of how the four types of boxes and corresponding widgets would fit together in one of the shiny app's modules.

Table 4. List of available functions in the biodosetools package.

Usage	Functions
Fitting	fit(), plot_fit_dose_curve()
Estimation	estimate_whole_body_merkle(), estimate_whole_body_delta(), estimate_partial_body_dolphin(), estimate_hetero_mixed_poisson(), plot_estimated_dose_curve()
Auxiliary	calculate_aberr_table(), protracted_g_function(), calculate_genome_fraction(), calculate_trans_rate_manual(), calculate_trans_rate_sigurdson()
shiny app	run_app()

The comprehensive functions reference can be found on the project's website at <https://biodosetools-team.github.io/biodosetools/reference/>.

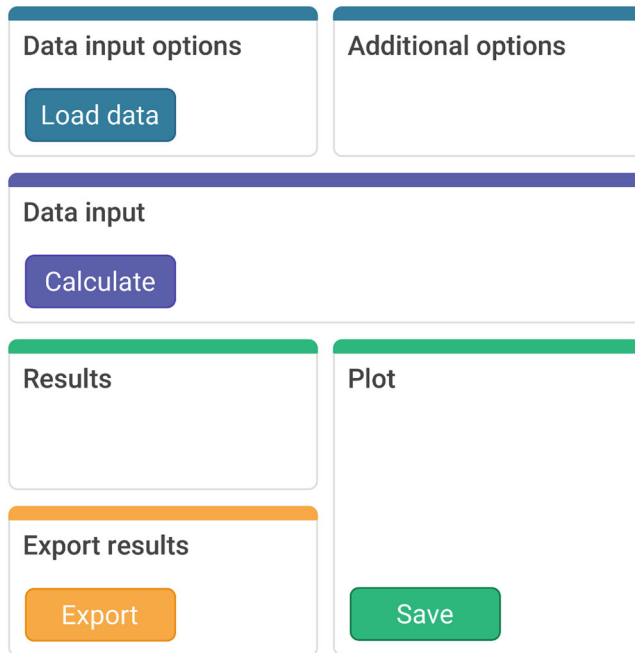


Figure 1. Mockup illustrating Biodose Tools' color coding to create an intuitive visual organization of the user interface.

3.1.3. Running Biodose Tools

For an offline use of Biodose Tools, we need to run the following commands in R console:

```
R > library(biodosetools)
R > run_app()
```

A series of video tutorials have been prepared with the aim of helping biodosetools users in the installation of R, RStudio, and the package itself, as well as in the usage of the shiny user interface to perform dose-effect fitting and dose estimation. They can be found on our YouTube channel: <https://www.youtube.com/@biodosetools>. The 'Installation Guide' tutorial has captions available in 8 languages. And as of 14 November 2022 the number of views of the three existing tutorials has been 508.

The following examples illustrate the functionality of biodosetools's shiny user interface to perform dose-effect fitting and dose estimation for the dicentric assay. The equivalent examples using the R API can be found in [Supplementary Materials 2](#). Additional examples are available on <https://biodosetools-team.github.io/documentation/>.

3.2. Dicentric dose-effect fitting

3.2.1. Input count data

The first thing to do is enter the count data. Biodose Tools allows to enter the count data from a file or manually (supported file formats are .csv, .dat, and .txt) (Figure 2). Once the table is generated and filled (Figure 3), the 'Calculate parameters' button will calculate the total number of cells (N), total number of aberrations (X), as well as mean (\bar{y}) variance (σ^2), dispersion index ($\hat{\sigma}^2/\bar{y}$), and u -value.

3.2.2. Irradiation conditions

As it is known that the irradiation conditions during calibration influence future dose estimates (Tromprier et al. 2017), and to improve their traceability, the user can enter the conditions in which the samples used to build the curve were irradiated. This option is only available in the shiny app (Figure 4), so that these can be saved into the generated reports.

3.2.3. Perform fitting

For the calibration adjustment it is necessary to select those options that are the most suitable, for example choosing between L or LQ adjustment (Figure 2), and then click on the 'Calculate fitting' button on the 'Data input' box (Figure 3). Fitting results and summary statistics will appear in the 'Results' tabbed box, and a graphical representation of the dose-effect curve is displayed in the 'Curve plot' box (Figure 5).

The 'Export results' box (Figure 5) displays two buttons: (a) 'Save fitting data', and (b) 'Download report'. The 'Save fitting data' will generate an .rds file that includes all information about the count data, irradiation conditions, and options selected when performing the fitting. This file can then be loaded in the dose estimation module to load the dose-effect curve coefficients. Similarly, the 'Download report' will generate a .pdf or a .docx report containing all inputs and fitting results.

3.3. Dicentric dose estimation

3.3.1. Load pre-calculated curve

The first step is to either load the pre-calculated curve in .rds format obtained in the dose-effect fitting module (Figure 6) or input the curve coefficients manually (Figure

Data input options

☒ Load data from file

☐ Only provide total number of dicentric

File input

Browse... count-data-barquinero-1995.csv

Upload complete

Generate table

Fitting options

Fitting formula

$\lambda = C + \alpha D + \beta D^2$

Fitting model

Automatic

Figure 2. 'Data input options' and 'Fitting options' boxes in the dose-effect fitting module. For dicentric, the 'Automatic' fitting model will select a quasi-Poisson model if there is overdispersion on the fitting, otherwise, it will select a Poisson model assuming equidispersion.

Data input													
	D (Gy)	N	X	C0	C1	C2	C3	C4	C5	mean	var	DI	u
1	0.000	5000	8	4992	8	0	0	0	0	0.00	0.00	1.00	-0.07
2	0.100	5002	14	4988	14	0	0	0	0	0.00	0.00	1.00	-0.13
3	0.250	2008	22	1987	20	1	0	0	0	0.01	0.01	1.08	2.61
4	0.500	2002	55	1947	55	0	0	0	0	0.03	0.03	0.97	-0.86
5	0.750	1832	100	1736	92	4	0	0	0	0.05	0.06	1.03	0.79
6	1.000	1168	109	1064	99	5	0	0	0	0.09	0.09	1.00	-0.02
7	1.500	562	100	474	76	12	0	0	0	0.18	0.19	1.06	1.08
8	2.000	333	103	251	63	17	2	0	0	0.31	0.35	1.14	1.82
9	3.000	193	108	104	72	15	2	0	0	0.56	0.47	0.83	-1.64
10	4.000	103	103	35	41	21	4	2	0	1.00	0.88	0.88	-0.84
11	5.000	59	107	11	19	11	9	6	3	1.81	2.09	1.15	0.81

Calculate parameters

Save count data .csv

Calculate fitting

Figure 3. 'Data input' box in the dose-effect fitting module.

Irradiation conditions

Name of the irradiator used

Whole blood or isolated lymphocytes

Radiation quality

X or gamma rays and energy

Temperature

Temperature during the irradiation

Dose rate (Gy/min)

Time incubations

Time incubations after sample irradiation

Dose quantity

In water or air kerma

Beam characteristics

Beam quality indicators, filtration (X-rays), energy (Gamma rays), ...

Figure 4. 'Irradiation conditions' box in the dose-effect fitting module.

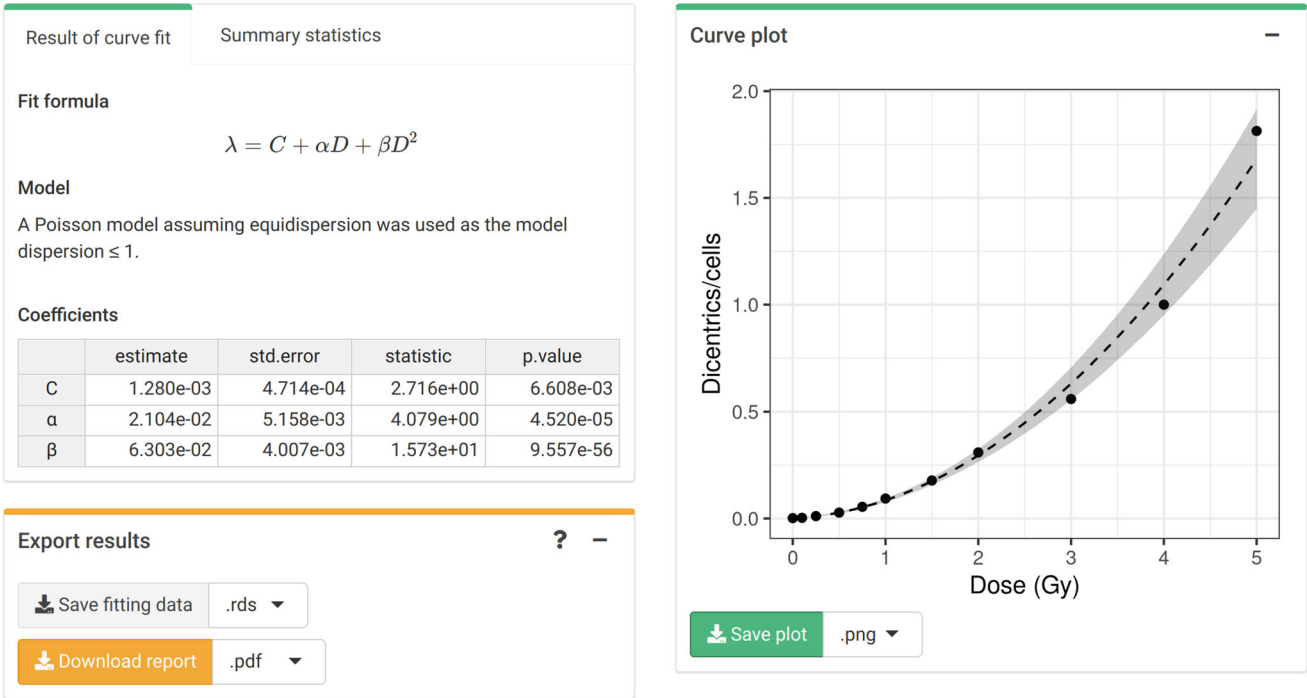


Figure 5. 'Results' tabbed box, 'Curve plot' and 'Export results' boxes in the dose-effect fitting module.

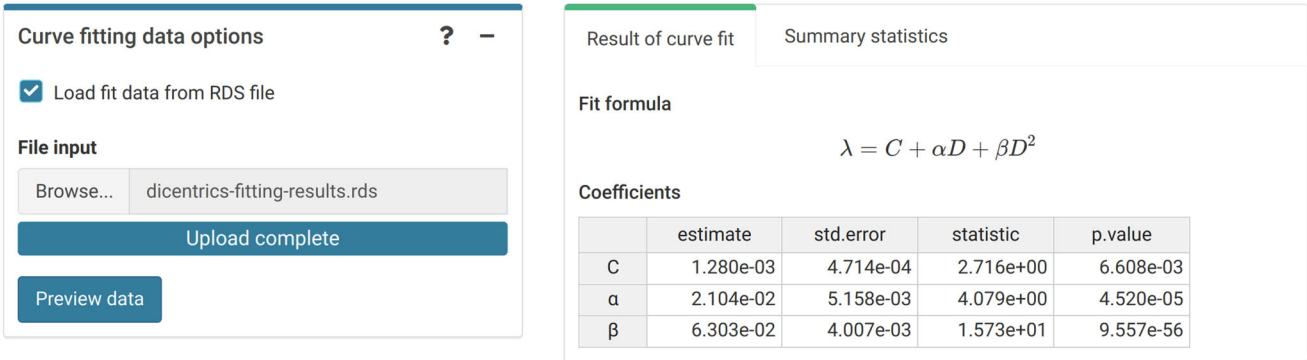


Figure 6. 'Curve fitting data options' box and 'Results' tabbed box in the dose estimation module when loading curve from an.rds file.

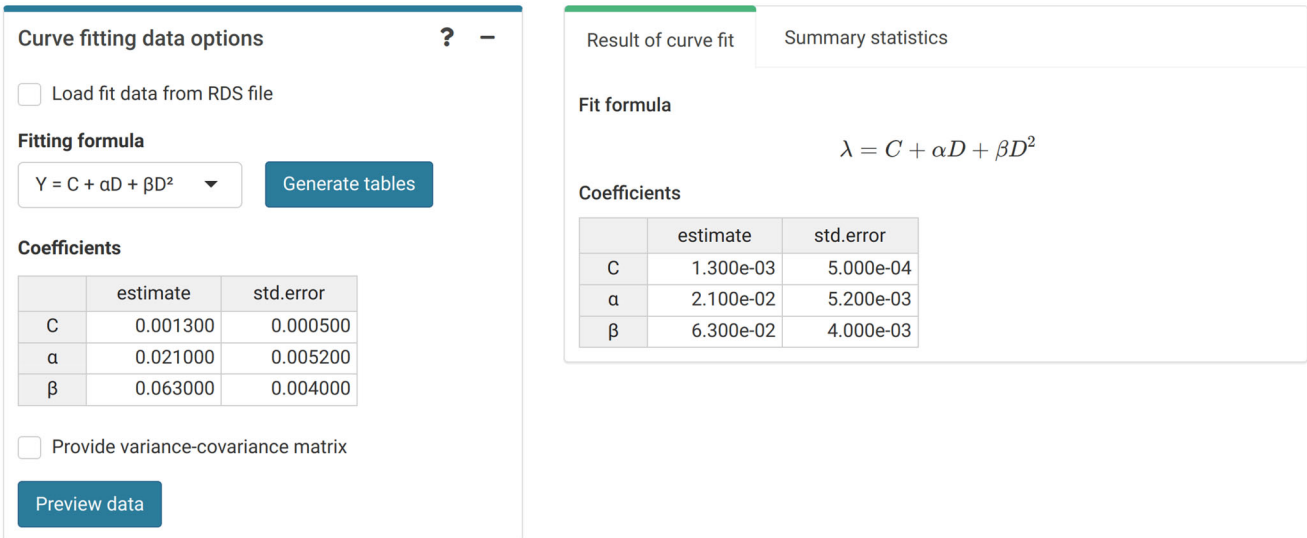


Figure 7. 'Curve fitting data options' box and 'Results' tabbed box in the dose estimation module when inputting curve coefficients manually. Note that if no variance-covariance matrix is provided, only the variances calculated from the coefficients' standard errors will be used in Equations (S1.6) (S1.9), and (S1.19).

Data input options

☐ Load data from file

Maximum number of dicentrics per cell

5

Case description

Short summary of the case

Generate table

Data input

	N	X	C0	C1	C2	C3	C4	C5	y	y_err	DI	u
1	361	100	302	28	22	8	1	0	0.28	0.04	1.77	10.35

Calculate parameters

Figure 8. 'Data input options' and 'Data input' boxes in the dose estimation module.

Dose estimation options

Exposure

Acute

Assessment

Partial-body

Whole-body error method

Merkle's method (83%-83%)

Partial-body error method

Dolphin (95%)

Survival coefficient

D0

D0

2.7

Estimate dose

Figure 9. 'Dose estimation options' box in the dose estimation module.

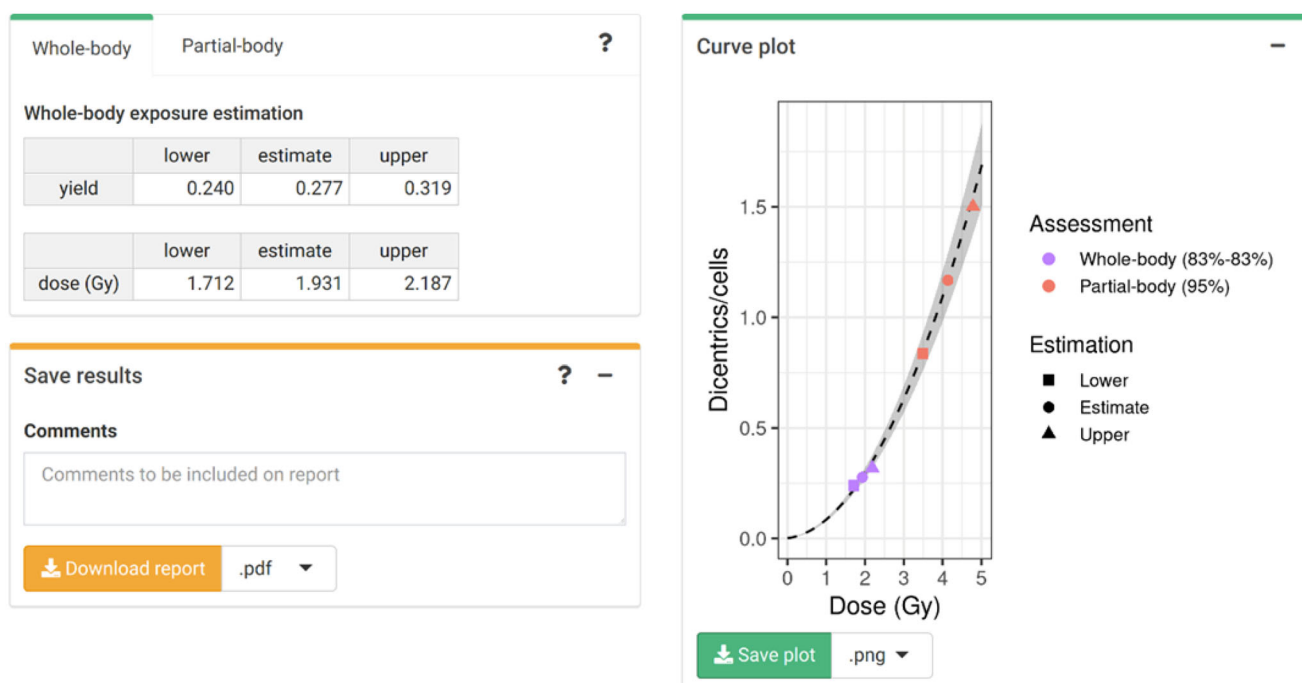


Figure 10. 'Results' tabbed box, 'Curve plot' and 'Save results' boxes in the dose estimation module.

Table 5. Example of a calibration data.

D (Gy)	N	X
0.00	100	0
0.25	200	1
0.50	161	6
1.00	88	10
1.50	131	28
2.00	74	23
2.50	189	70
3.00	141	61

D : dose in Gy. Number of cells analyzed, and X number of dicentrics observed.

7) in case the user wants to use a preexisting curve calculated outside of Biodose Tools. Clicking on ‘Preview data’ will load the curve into the app and display it on the ‘Results’ tabbed box.

3.3.2. Input case data

Next, we can choose to enter the count data from a file or manually (the supported file formats are .csv, .dat, and .txt) (Figure 8). Once the table is generated, clicking the ‘Calculate parameters’ button will calculate the total number of cells (N), total number of aberrations (X), as well as mean (\bar{y}), standard error (σ), dispersion index ($\hat{\sigma}^2/\bar{y}$), and u -value. The shiny app also includes the option to include the information about the incident that is being evaluated. This information may be relevant to explain the results obtained and is included in the generated reports.

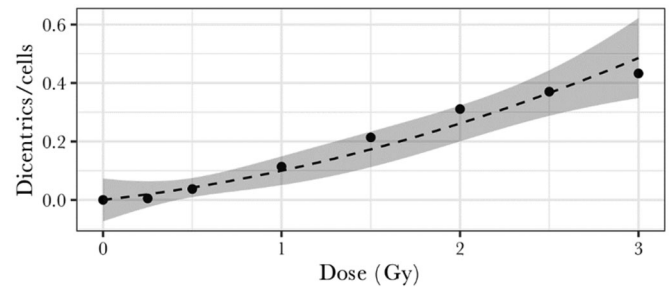
3.3.3. Perform dose estimation

The final step is to select the dose estimation options depending on the characteristics of the accident. In the ‘Dose estimation options’ box (Figure 9) we can select type of exposure (acute, protracted, and highly protracted), type of assessment (whole-body, partial-body, or heterogeneous), and error methods for each type of assessment.

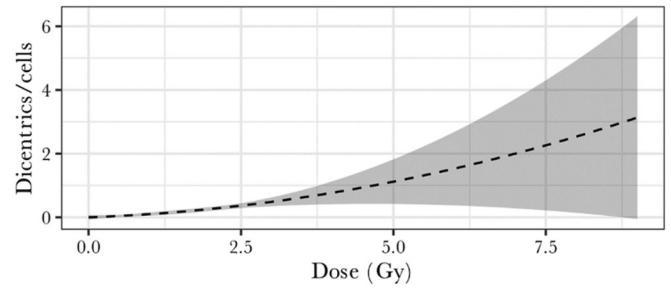
The dose estimation results are shown in Figure 10. Once the estimation is done the app also incorporates the possibility to describe the results obtained in the ‘Save results’ box. All information, the calibration curve used, the data of the case, the different estimated doses, as well as the description of the case and the interpretation of the results can be saved generating a .pdf or a .docx report via the ‘Download report’ button. It is important to note that biodosetools can be used not only to estimate the doses, but also to draft a report of the accident being evaluated with full traceability. This can be further adapted and customized to each laboratory’s internal needs thanks to the open-source nature of the project.

3.4. Technical matters

Biodose Tools has been developed following international guidelines of biological dosimetry (IAEA 2011; ISO 19238 2014; ISO 20046 2019). Despite our best efforts to ensure that biodosetools automatically handles mathematical errors behind the scenes, such as using a constraint maximum-likelihood optimization method (Oliveira et al. 2016) when the fitting using a generalized linear model (GLM) is not

**Figure 11.** Plot of dose-effect curve constructed from the dicentric distribution in Table 5.**Table 6.** Example of dicentric distribution within cells.

N	X	C_0	C_1	C_2	\bar{y}	SE	$\hat{\sigma}^2/\bar{y}$	u
148	13	136	11	1	0.088	0.025	1.073	0.654

**Figure 12.** Plot of dose-effect curve constructed from the dicentric distribution in Table 5 over an extended D range.

possible, or correcting negative dose estimates, the resulting curves may still result in errors (both using the shiny app or the R API) when performing dose estimation. As an example, let us consider the following curve, shown in Table 5 and Figure 11. Although at a glance we can already suspect that there is some kind of issue in the observed counts, due to the low number of evaluated cells, one may still decide to proceed and use it for dose estimations.

In Table 6 below we can see an example of a case we may want to estimate the dose for. If we try to estimate the dose using Merkle’s method, we encounter an error involving the uniroot() function. The function uniroot() searches for a root (i.e. zero) of the function $f(x_1, \dots, x_n)$ with respect to its first argument x_1 within a specified interval. In our example, this error occurs when projecting the upper 95% confidence limit of the yield λ_U into the lower curve (S1.6). The reason for this is that the lower 95% confidence band of the dose-effect curve is not a monotonically increasing function, meaning that D_L has multiple possible numerical solutions, as shown in Figure 12.

It is worth noting that this projection error is particular to Merkle’s method for whole-body assessment and could certainly be circumvented if one chooses to use the delta method instead. However, for optimal dose estimation we expect both the calibration curve and its confidence intervals to define monotonically increasing functions.

4. Discussion

Biological dosimetry has undergone a rapid evolution since the publication of the last IAEA manual (IAEA 2011). On the one hand, the potential of early biomarkers of exposure to ionizing radiation has been evaluated. Such as detection of γ -H2AX foci and gene expression (Kulka et al. 2017; Abend et al. 2021). In addition, new statistical approaches have been proposed: checking the Poisson distribution (Higueras et al. 2018); to estimate dose using Bayesian approaches (Ainsbury et al. 2014; Higueras et al. 2016; González et al. 2020); as well as being able to evaluate laboratory performance in interlaboratory comparison (ILC) exercises (González et al. 2022). In some cases these improvements have also been translated to shiny apps (<https://manu2h.shinyapps.io/InterLabComparison/>, https://manu2h.shinyapps.io/gof_poisson/).

The intention of the Biodose Tools team is to expand the capabilities of the app, and for Biodose Tools to serve as a platform to improve mathematical interpretation in biological dosimetry. Currently, there are a few improvements that we are already working on for future biodosetools releases, such as allowing .xlsx and .xls for data input, as well as full support for micronuclei assay analysis. Considering the periodic ILCs that the biological dosimetry community performs, another major future improvement is a specific module to standardize the dose estimation and data handling for ILCs. Last but not least, there are plans to integrate Bayesian dose estimation methods into biodosetools (Higueras et al. 2016), as well as to integrate existing software for γ -H2AX dose estimation (Einbeck et al. 2018) into biodosetools, and to add support for multiple count or case data inputs.

Biodose Tools is a joint international effort between mathematicians, statisticians, and cytogeneticists from different labs, which allowed us to arrive at a consensus on the classical or most commonly used statistical methods to be used in each step of the fitting and dose estimation processes. Due to the package and shiny application being open source and modular, expanding or changing the methods is a trivial matter. The shiny app, and the reports allow complete statistical traceability, which is very important for new laboratories that want to be accredited by the ISO standards: ISO 21243 2008 for triage, ISO 19238 2014 for dicentric, ISO 20046 2019 for translocations (ISO 21243 2008; ISO 19238 2014; ISO 20046 2019).

As of now, Biodose Tools is being used globally in different exercises and trainings, such as in the Lund exercise performed by RENEB and EURADOS working group 10 (between November 2019 and March 2020) (Endesfelder et al. 2021) as well as in a IAEA course in Thailand (30 July – 2 August 2019), where participants showed very positive feedback. The current RENEB 2021 interlaboratory comparison involving 85 specialized labs from 27 countries was performed exclusively using biodosetools 3.5; presented at RADRES's annual meeting (3–6 October 2021) (Port 2021).

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