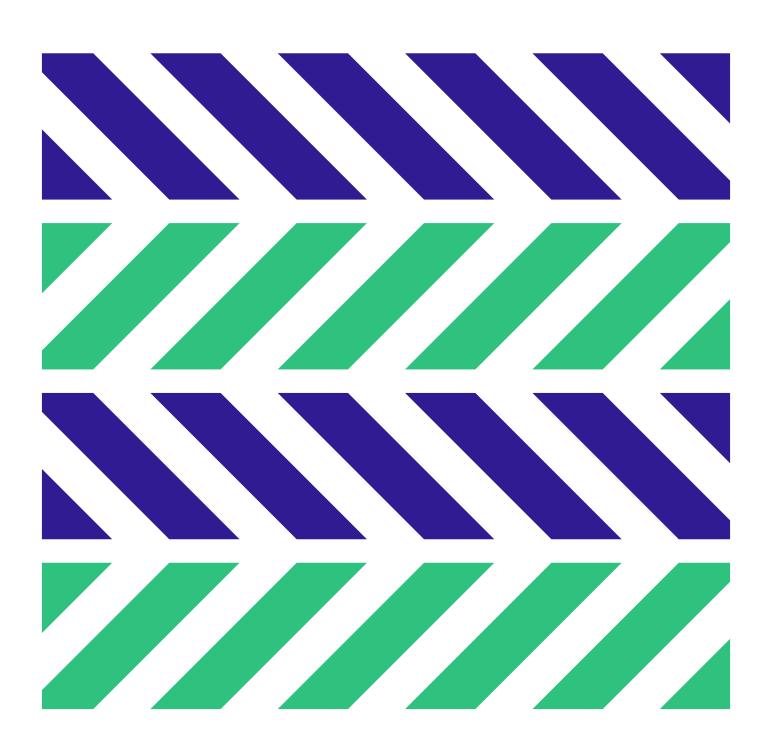


# User Manual & Documentation

Alfredo Hernández



# **Biodose Tools**

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Alfredo Hernández 2019-07-06

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#### **About**



This project in an app to be used by biological dosimetry laboratories. Biodose Tools is an open-source project that aims to be a tool to perform all different tests and calculations needed. The app is developed with R (R Core Team, 2019) together with Shiny (Chang et al., 2019) to offer an on-line, easy-to-use solution. Although the intention is to provide the application as a website, all R routines can be downloaded for improvement or personal use.

We also aim to clarify and explain the tests used and to propose those considered most appropriate. Each laboratory in its routine work should choose the optimum method, but the project aims to reach a consensus that will help us in case of mutual assistance or intercomparisons.

The project is initially developed by RENEB association, but contributions are always welcome.



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#### Structure of the book

Chapter 1 introduces the user to Biodose Tools and how to use it either online or with RStudio. 2 introduces the basic design principles behind the user interface, and the usage of the different modules.

. . .

In Appendix A, a technical review of the implementation of Biodose Tools is discussed.

## Acknowledgements

#### About the authors

The project is initially developed by RENEB association, as a collaboration between Universitat Autònoma de Barcelona (UAB), Bundesamt für Strahlenschutz (BfS), Durham University (DU), Institut de Radioprotection et de Sûreté Nucléaire (IRSN), Universidad de la Rioja (UdR), and Public Health England (PHE).

#### Principal contributors

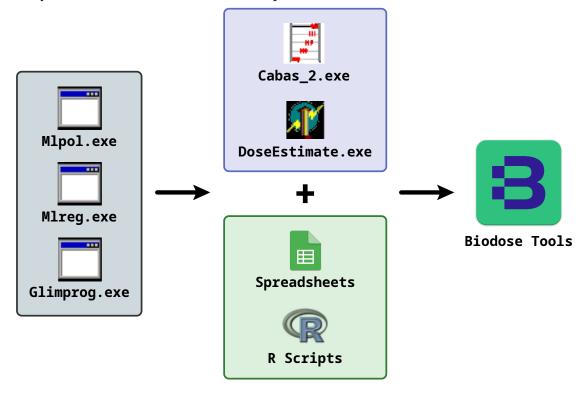
Name	Institution	Role
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## Background and goals

Over the years more powerful software has been developed to aid biologists in their daily work. Biodose Tools is the next step.



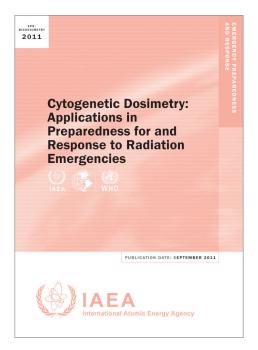
### R Shiny as a statistical tool

Shiny is an R package that makes it easy to build interactive web apps straight from R, combining the computational power of R with the interactivity of the modern web.

- Access to a powerful web framework for building web applications using R.
- Being in complete control of the mathematics and statistics behind.
- Rethink what biologists and laboratories need in their everyday workflow.
- Build a complete, fully documented tool.
- Provide an Open Source tool to the community.

#### **Modules**

Different modules can be built for each function (fitting, dose estimation, ...) while being totally independent from one another.



This opens up the possibility to implement statistical methods not included in the IAEA Manual (2011).

Part I.

**Using Biodose Tools** 

## **Chapter 1. Getting Biodose Tools**

Stuff

#### 1.1. Online

During the beta testing phase, the application is hosted on Shinyapps.io: https://aldomann.shinyapps.io/biodose-tools-beta/

#### 1.2. On RStudio

Many laboratories will prefer to use their own computers to run the app instead of relying on an external server, either for security reasons or better reliability.

The application can be easily installed by runnning

```
install.packages("biodose-tools")
```

Alternatively, if you want to download the development version, you can just run

devtools::install\_github("biodosimetry-uab/biodose-tools-package")

## Chapter 2. Usage

Stuff

#### 2.1. User interface

We describe the user interface (UI) components in this section.

#### 2.1.1. Design principles

Color is an effective, powerful and instantly recognizable medium for visual communications. In Biodose Tools color is used to identify different sections of information, a technique called *color-coding*.

Once users are attuned to the color schemes, they can use them. Even before then, they'll know when they've left one section for another, if they notice that the color scheme changed. So color-coding works to distinguish one section from another; it makes the boundaries clear.

- Jenifer Tidwell (Tidwell, 2010)

Rich Blue #5b5ea8 Boston Blue #2b7c9a

Lochinvar #2b9a7c Casablanca #f6a945

Part II.

**Statistical Methods** 

# Chapter 3. Introduction

Here is a review of existing statistical methods for the different implemented modules, i.e.,

- Dicentric analysis
- Translocation analysis

The primary objective of this section is to provide biologists with technical information about the statistical methods and tests used on Biodose Tools. The main source is (International Atomic Energy Agency, 2001)

# Chapter 4. Dicentric analysis

# 4.1. Dose-effect curve fitting

D	N	X	C0	C1	C2	C3	C4	C5	DI	u
0.00	5000	8	4992	8	0	0	0	0	0.9985997	-0.0748406
0.10	5002	14	4988	14	0	0	0	0	0.9974005	-0.1348939
0.25	2008	22	1987	20	1	0	0	0	1.0804910	2.6098032
0.50	2002	55	1947	55	0	0	0	0	0.9730135	-0.8614691
0.75	1832	100	1736	92	4	0	0	0	1.0259749	0.7898872
1.00	1168	109	1064	99	5	0	0	0	0.9992767	-0.0175514
1.50	562	100	474	76	12	0	0	0	1.0639572	1.0765604
2.00	333	103	251	63	17	2	0	0	1.1407182	1.8218931
3.00	193	108	104	72	15	2	0	0	0.8336227	-1.6377580
4.00	103	103	35	41	21	4	2	0	0.8823529	-0.8442765
5.00	59	107	11	19	11	9	6	3	1.1498550	0.8107914

Download dicentrics distribution

## **4.2.** Dose estimation

# **Chapter 5. Translocation analysis**

- 5.1. Dose-effect curve fitting
- 5.2. Dose estimation

## Chapter A. Implementation details

The Biodose Tools user interface is written in (Chang et al., 2019) using Bootstrap 4 (Granjon, 2019), analyses are implemented in the R programming language (R Core Team, 2019), with the resultant tables and plots rendered in HTML through JavaScript libraries. This is done by the browser of choice (Google Chrome, Firefox, Microsoft Edge, and Safari are officially suppored), or by an instance of QtWebKit if the app is run through RStudio.

# **Chapter B. How to cite Biodose Tools**

If you want to cite Biodose Tools, you can use the following BibTeX entry:

```
@Manual{BiodoseTools2019,
   title = {{Biodose Tools}},
   author = {Alfredo Hernández and Joan Francesc Barquinero and David Endesfelder and Peroyear = {2019},
   url = {https://biodosimetry-uab.github.io/documentation/},
}
```

## References

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- Tidwell, J. (2010). *Designing Interfaces: Patterns for Effective Interaction Design*. O'Reilly Media, Inc.