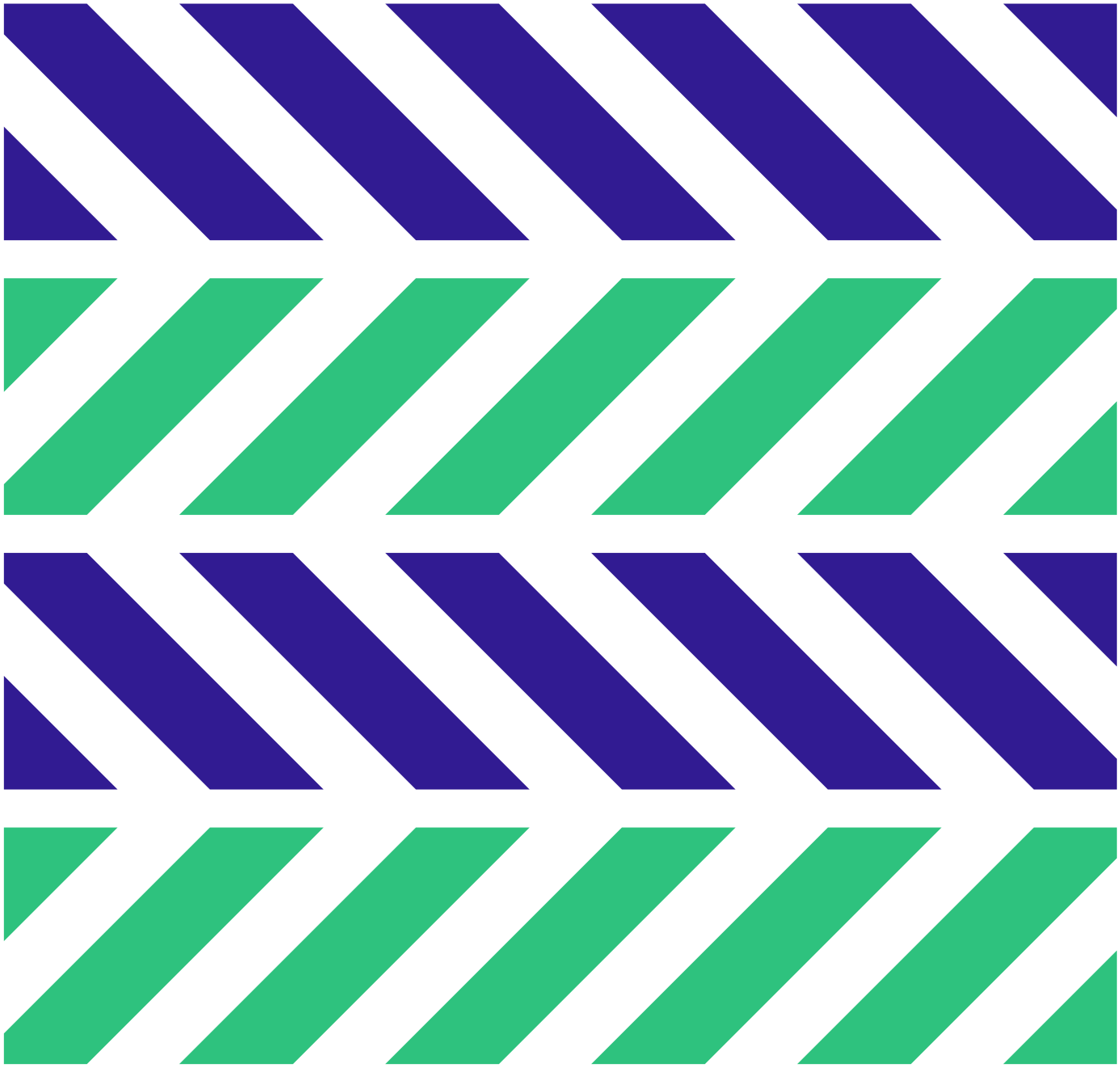
Biodose Tools

User Manual & Documentation

Alfredo Hernández



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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.

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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Contributors

Name	Institution	Role
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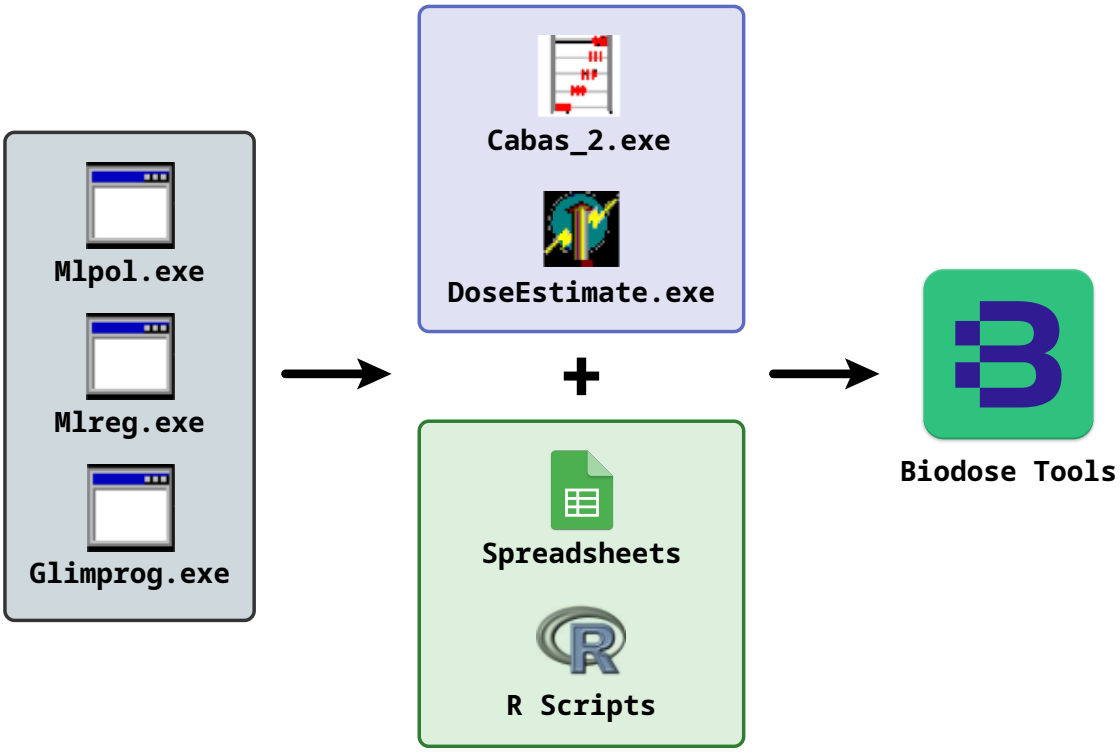
Ursula Oestreicher	BfS	Biologist
David Lloyd	PHE	Biologist

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

R

R is a general purpose package that includes support for a wide variety of modern statistical and graphical methods (many of which have been contributed by users). It is available for GNU/Linux, Mac OS X, and Windows. The R Foundation for Statistical Computing holds and administers the copyright of the R software and documentation. R is available under the terms of the Free Software Foundation's GNU General Public License in source code form.

R Shiny

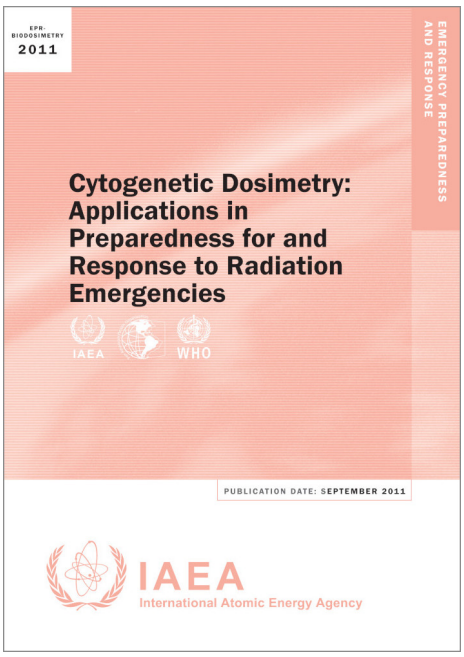
Shiny is an R package that makes it easy to build interactive web apps straight from R, combining the computational power of R with the interactivity of the modern web.

- 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.

To run Biodose Tools on your local machine, you need to install R (R Core Team, 2019). Additionally, we recommend to install RStudio (RStudio Team, 2015).

1.2.1. Installing R

1.2.1.1. Under Windows

Versions of R for Windows XP and later, including 64-bit versions, are available at CRAN. The distribution includes `Rgui.exe`, which launches a self-contained windowing system that includes a command-line interface, `Rterm.exe` for a command-line interface only, Rscript.exe for batch processing only, and `R.exe`, which is suitable for batch or command-line use.

More information on Windows-specific issues can be found in the CRAN R for Windows FAQ.

1.2.1.2. Under macOS

A version of R for macOS 10.6 and higher is available at CRAN. This is distributed as a disk image containing the installer. In addition to the graphical interface version, a command line version (particularly useful for batch operations) can be run as the command `R`.

More information on Macintosh-specific issues can be found in the CRAN R for Mac OS X FAQ.

1.2.1.3. Under GNU/Linux

R is available for most Linux distributions through your distribution's repositories. For example, R is provided on Debian-based distributions like Ubuntu by the `r-base` package. Many additional packages, such as `r-cran-rpart`, are provided at the maintainer's discretion.

To install R on Ubuntu, run the following commands on the Terminal:

```
sudo apt-get update
sudo apt-get install r-base r-base-dev
```

To install R on Fedora, run the following command on the Terminal:

```
dnf --refresh install R
```

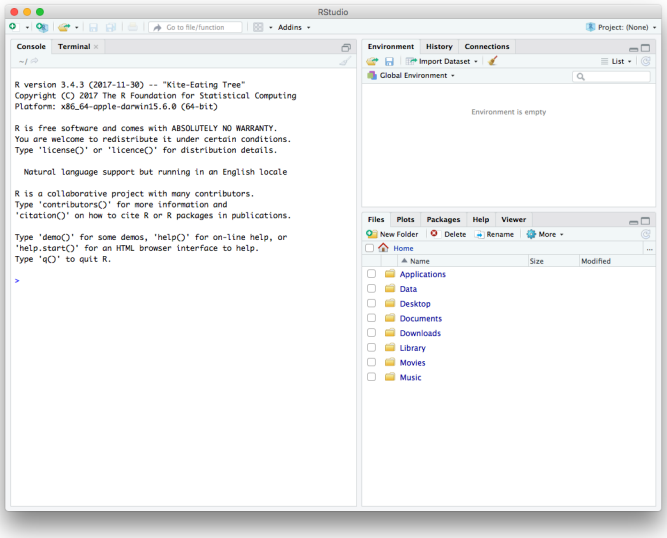
To install R on Arch Linux, run the following command on the Terminal:

```
sudo pacman -S r
```

1.2.2. Installing RStudio

RStudio for Windows, macOS, or GNU/Linux can be downloaded from https://www.rstudio.com/products/rstudio/download/. RStudio requires R to be installed on the local machine, so make sure to install it first.

Once installation is complete, the recommended next step for a new user would be to start RStudio and run a sample session.



The > character is the command prompt, and commands are executed once the user presses the RETURN or ENTER key.

1.2.3. Installing Biodose Tools

The application can be easily installed by runnning

```
install.packages("BiodoseTools")
```

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

```
devtools::install_github("biodosimetry-uab/biodose-tools-package")
```

1.2.4. Running Biodose Tools

Once it is installed, Biodose Tools can be easily run by typing

```
BiodoseTools::runApp()
```

Chapter 2. Usage

Stuff

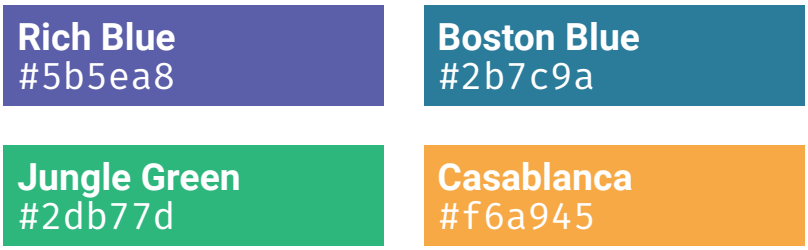
2.1. User interface

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)



Chapter 3. Feedback

Part II.

Statistical Methods

Chapter 4. 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 5. Dicentric analysis

5.1. 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

5.2. Dose estimation

Chapter 6. Translocation analysis

6.1. Dose-effect curve fitting

6.2. 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 Pere
  year = {2019},
  url = {https://biodosimetry-uab.github.io/documentation/},
}
```

References

Chang, W., Cheng, J., Allaire, J., Xie, Y., and McPherson, J. (2019). *shiny: Web Application Framework for R*. R package version 1.3.2.

Granjon, D. (2019). *bs4Dash: A 'Bootstrap 4' Version of 'shinydashboard'*. R package version 0.3.0.

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RStudio Team (2015). *RStudio: Integrated Development Environment for R*. RStudio, Inc., Boston, MA.

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