

Diaphysator: an online application for the exhaustive cartography and user-friendly statistical analysis of long bone diaphyses

Supplement: Technical documentation for the R-Shiny application

1. Use Diaphysator online

Diaphysator can be used simply as an online application:

```
https://diaphysator.shinyapps.io/maps/
```

This can be easier for users who are not familiar with R, but Diaphysator will be slightly slower.

2. Install steps for local use

Diaphysator is also available as an R package, hosted on GitLab. Using Diaphysator as a local application is recommended, as it runs faster and offline, and allows a full access to the source code.

2.1. Install prerequisites

First, download the R software in its latest version¹. It can be freely obtained on Comprehensive R Archive Network, CRAN:

- direct link for Linux: <https://cran.r-project.org/bin/linux/>
- direct link for Mac OS: <https://cran.r-project.org/bin/macosx/>
- direct link for Windows: <https://cran.r-project.org/bin/windows/base/>

Depending on your operating system, additional operations may also be required:

- Windows users should install the latest version of Rtools: <https://cran.r-project.org/bin/windows/Rtools>
- Mac OS users should install XCODE: <https://developer.apple.com/xcode/>

Finally, the R package `devtools` must also be installed. This can be done by running the following command into the R console:

```
install.packages("devtools", dep=TRUE, repos="http://cran.uib.no/")
```

2.2. Install the R package Diaphysator

Open an R console and type (or copy-paste) the following command lines at the prompt:

```
library(devtools)  
install_git('https://gitlab.com/f.santos/Diaphysator.git')
```

¹Please note that the package presented in this article is only available for R 3.4.0 or newer

2.3. Run Diaphysator

- To load the package, type the following command line into the R console:
`library(Diaphysator)`
- Then, the graphical user interface can be launched by typing:
`StartDiaphysator()`
- For further technical documentation, please open the help page by typing:
`help(Diaphysator)`
or visit the Diaphysator webpage on GitLab:
<https://gitlab.com/f.santos/Diaphysator>

Notes

- As for any other R-Shiny application, the R console does not respond as long as the graphical user interface is active. To exit Diaphysator, press `Ctrl+C` when being on the R console (on Linux systems), or `Echap` (on Windows systems).
- Regardless of the size and resolution of your screen, it is advisable to adjust the zoom level of your web browser (for Firefox, press simultaneously `Ctrl` and `-`), and/or switch it to fullscreen mode (for Firefox, press `F11`).

3. How to prepare the data input files

Diaphysator functions in symbiosis with a software, the Extractor, published in 2017². As input files, Diaphysator requires the data files generated by the Extractor, or CSV files manually created and formatted in the same way.

Two types of files are required: one single “information file” (which always has to be manually created), and several “diaphyses data files” (such as those generated by the Extractor). Example data files can be downloaded on Diaphysator webpage.

3.1. Information file

The information file is a CSV sheet whose the first column must be labeled “ID”. This column provides a unique identifier for each studied individual.

Any number of other columns can be freely added and labeled by the user, in order to provide additional details about the individuals. Those columns can be qualitative variables (e.g. sex, country or age class) or quantitative variables (e.g. age in years, stature, body mass, or body composition variables such as fat mass and fat-free mass). These variables can then be correlated to the cortical thickness and cortical area in Diaphysator user interface.

An example of valid information file is given in Figure 1.

²Dupej, J., Lacoste Jeanson, A., Pelikán, J., & Brůžek, J. (2017). Semiautomatic extraction of cortical thickness and diaphyseal curvature from CT scans. *American Journal of Physical Anthropology*, 164(4), 868–876. DOI: 10.1002/ajpa.23315

	A	B	C	D	E	F	G	H	I	J
1	ID	sex	age	stature	biiliac_breadth	body_mass	fat_mass	fat-free_mass	body_fat_percent	body_mass_index
2	F01	F	33	171	285.04841693565	40.4	46.6	87	46.4367816091954	29.75
3	F02	F	62	165	288.582814430035	38.4	47.6	86	44.6511627906977	31.59
4	F03	F	70	167	306.316374721463	37.8	15.2	53	71.3207547169811	19
5	F04	F	51	165	265.910509622467	36.9	31.1	68	54.2647058823529	24.98
6	F05	F	60	160	275.844123259496	33.4	35.6	69	48.4057971014493	26.95
7	F06	F	82	158	272.368796559371	48	24	72	66.6666666666667	28.84
8	F07	F	55	160	280.28	19.3	32.7	52	37.1153846153846	20.31
9	F08	F	54	157	278.728181412214	61.3	28.7	90	68.1111111111111	36.51
10	F09	F	23	156	254.934207389769	20.9	36.1	57	36.6666666666667	23.42
11	F10	F	59	157	289.67608897976	17.4	72.6	90	19.3333333333333	36.51
12	F11	F	45	167	278.484466855299	15.7	37.3	53	29.622641509434	19
13	F12	F	25	156	268.626407970624	27.7	26.3	54	51.2962962962963	22.19
14	F13	F	55	168	264.20286654359	53.6	34.4	88	60.9090909090909	31.18
15	F14	F	50	161	251.799863453656	19.4	47.6	67	28.955223880597	25.85
16	F15	F	45	160	274.349368086898	26	28	54	48.1481481481482	21.9
17	F16	F	46	176	307.79859713293	72.6	47.4	120	60.5	38.74
18	F17	F	67	166	272.877110381798	47.3	40.7	88	53.75	31.93
19	F18	F	69	167	307.442458535398	27.5	34.5	62	44.3548387096774	22.23
20	F19	F	47	150	260.975589094478	28.7	24.3	53	54.1509433962264	23.56
21	F20	F	62	160	277.250014018539	37.5	32.5	70	53.5714285714286	27.34

Figure 1: Example of valid CSV sheet for the “information file”, with the first column labeled “ID”.

3.2. Diaphyses data files

The simplest way is to generate these files with the Extractor.

3.2.1. Description of the possible types of files

Two types of files can be loaded in Diaphysator.

- Cortical thickness files are CSV files without headers nor row names. With the default parameters of the Extractor, 100 slices are considered within a diaphyseal segment, and thickness is measured in 50 directions per cross-section. Then, the CSV files will have 100 rows (one per slice) and 50 columns (one per direction).
- Cortical area files are CSV files without headers nor row names. Still with the default parameters of the Extractor, those files will have 100 rows (one per slice) and two columns: the first one indicates the medullary area on the given slice, the second one indicates the total area. Please note that the rows must be ordered in decreasing order of percentage of biomechanical length: with default parameters, the first row corresponds to 80%, and the last row correspond to 20%.

It is recommended to load both types of files in Diaphysator (i.e. two files per individual), but one can also choose to submit only one given type of file per individual (e.g. cortical thickness). The tabs of Diaphysator related to the other type of files are then disabled.

3.2.2. Naming and organizing the data files

The names of the diaphyses data files, and the “ID” column of the information file, must match exactly. For instance, a given (female) individual “F01” is declared in the information file displayed on

Figure 1. Then, her associated CSV file for cortical thickness must be named “F01_thickness.csv”; and her associated CSV file for cortical area must be named “F01_CA.csv”.

This is a mandatory naming convention for Diaphysator: all cortical thickness files must end with “_thickness.csv”, and all cortical area files must end with “_CA.csv”. Furthermore, the name of each file must begin with the exact ID of the associated individual, as specified in the information file.

As previously said, one may import only cortical area related files, or only cortical thickness related files, or both types of files. But please note that for each type of file loaded in Diaphysator (“_CA” and/or “_thickness”), the number of CSV files imported must be equal to the number of individuals declared in the information file. If one diaphysis data file is missing, or if an individual has been omitted in the information file, Diaphysator will display an error popup.

Importing diaphyses data files through the user interface is done by selecting all data files at once. Consequently, all the data files (“_CA” and/or “_thickness”) must have been placed in the same folder on your computer. A correct scheme of organization and naming, in coherence with the information file displayed in Figure 1, is given in Figure 2.

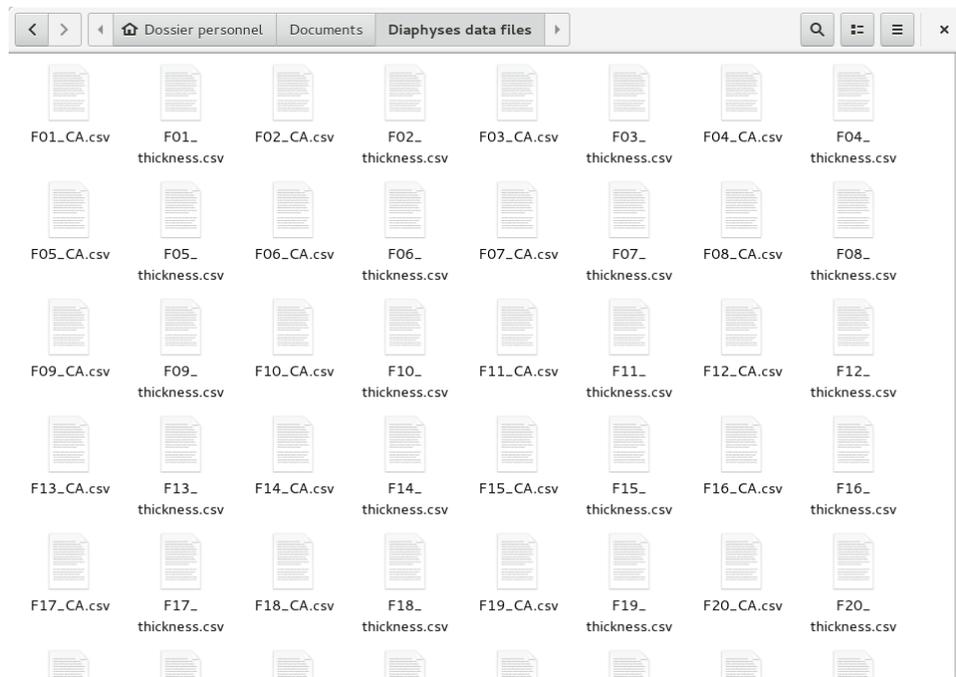


Figure 2: Proper organization and naming of diaphyses data files for Diaphysator.