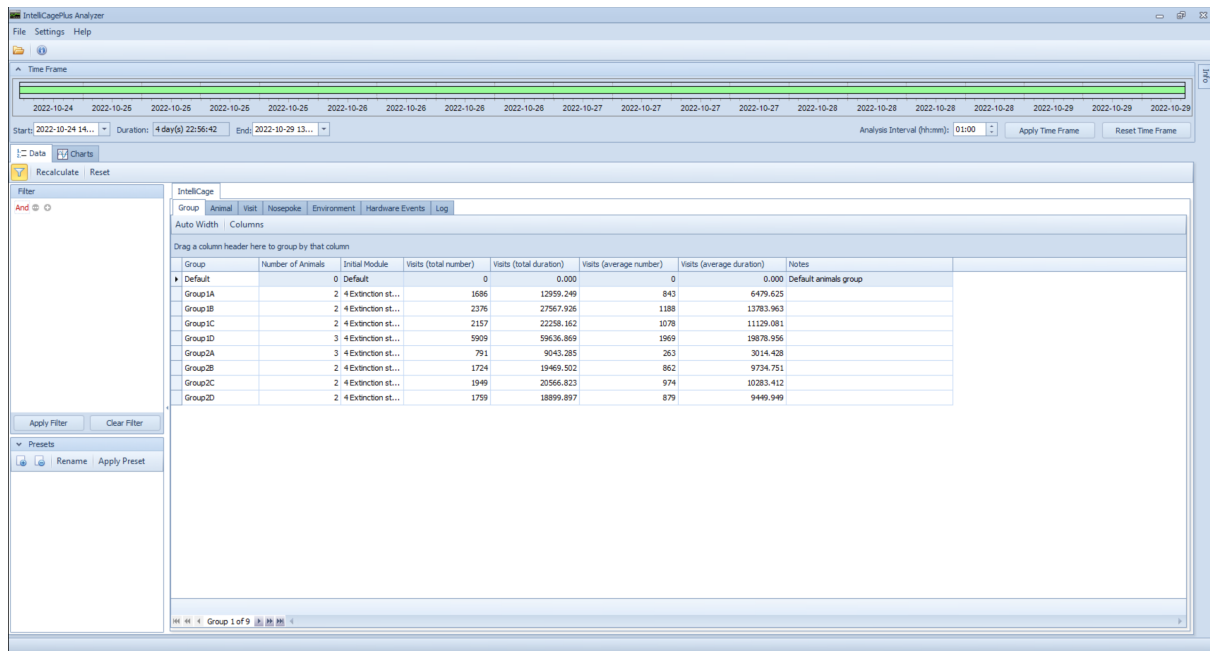


## IntelliCage automated analysis – Version 1

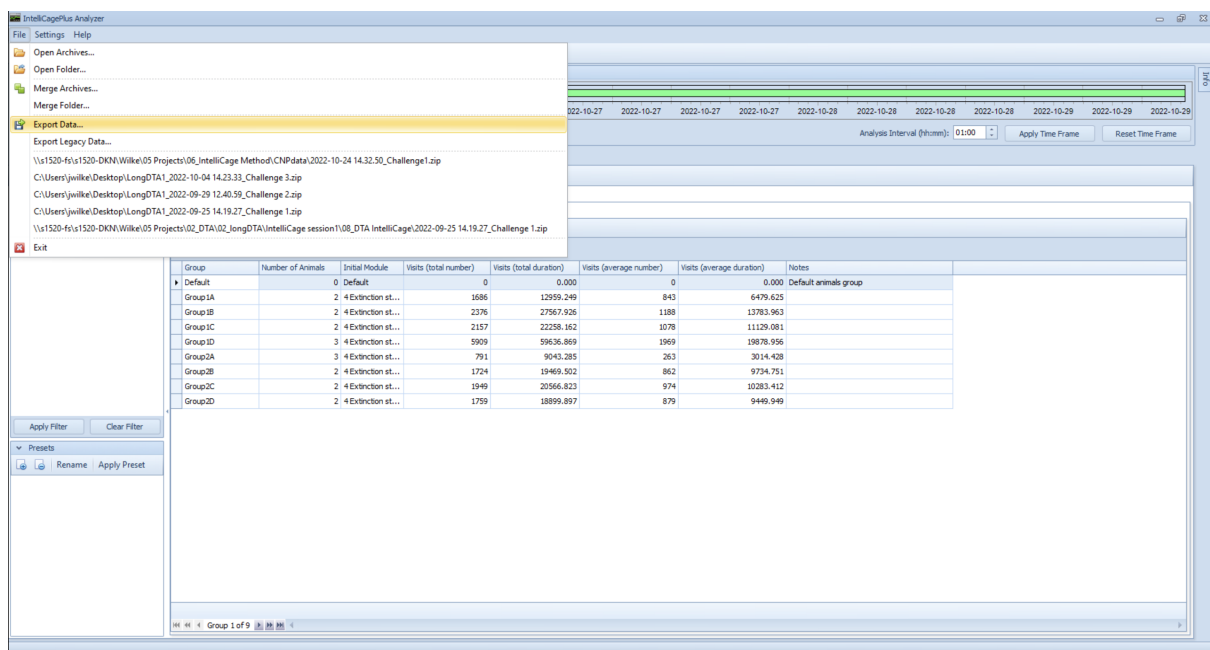
Hello! Thank you for taking the time to look at the readme file for IntelliR. In this file you will find basic instructions on how to run the analysis, including exporting the required files.

### File requirements:

After running the challenges, each individual IntelliCage Archive File (.zip) has to be open in the IntelliCage Analyzer Software.



After loading the file, click on the menu “File” and then “Export Data”. Double check that the whole session is selected as time frame.

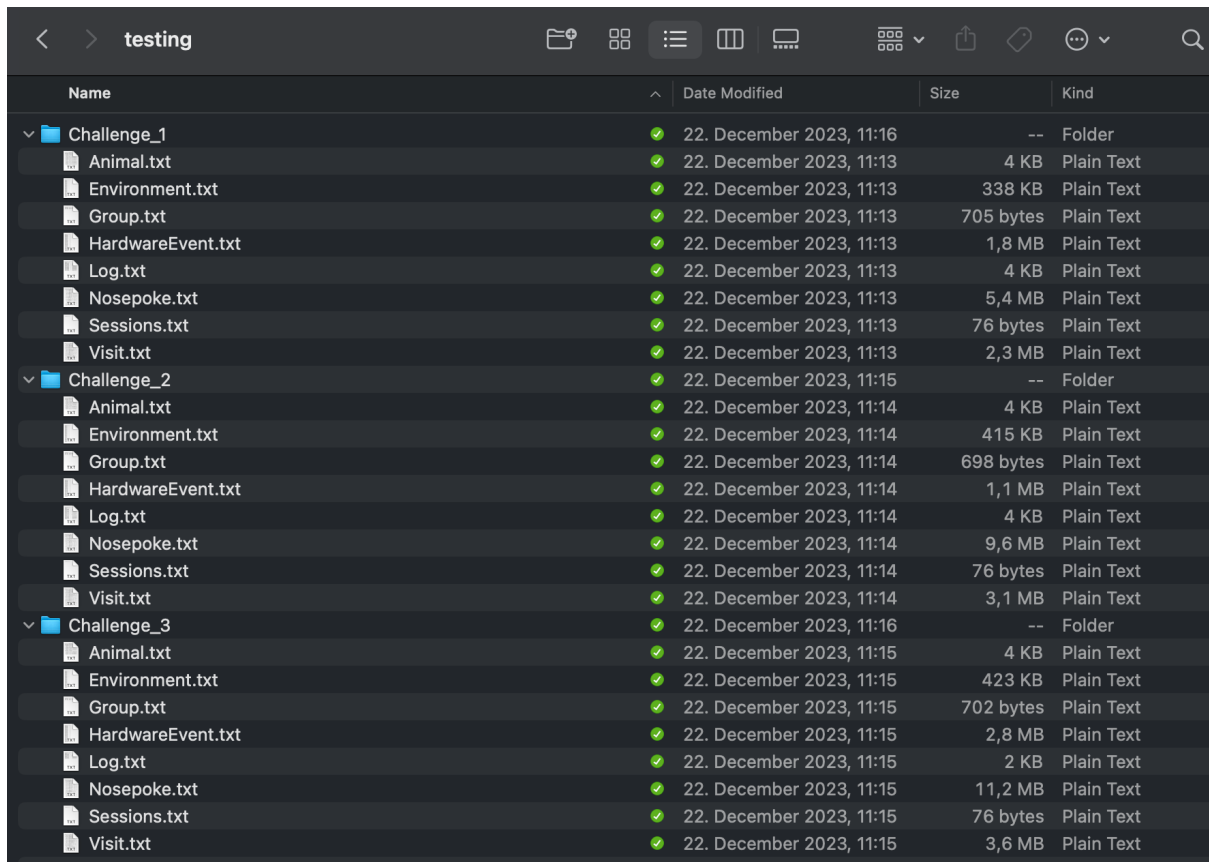


In the end you will have three exported folders that should be placed in one final folder with your project name. The folder exported from the IntelliCage Analyzer Software should be renamed as follows:

Challenge\_1  
Challenge\_2  
Challenge\_3

***Also note the location of the unblinding file to make sure it is easy to find it.***

See the screenshot below for how the files should be organized:



Name		Date Modified	Size	Kind
Challenge_1	✓	22. December 2023, 11:16	--	Folder
Animal.txt	✓	22. December 2023, 11:13	4 KB	Plain Text
Environment.txt	✓	22. December 2023, 11:13	338 KB	Plain Text
Group.txt	✓	22. December 2023, 11:13	705 bytes	Plain Text
HardwareEvent.txt	✓	22. December 2023, 11:13	1,8 MB	Plain Text
Log.txt	✓	22. December 2023, 11:13	4 KB	Plain Text
Nosepoke.txt	✓	22. December 2023, 11:13	5,4 MB	Plain Text
Sessions.txt	✓	22. December 2023, 11:13	76 bytes	Plain Text
Visit.txt	✓	22. December 2023, 11:13	2,3 MB	Plain Text
Challenge_2	✓	22. December 2023, 11:15	--	Folder
Animal.txt	✓	22. December 2023, 11:14	4 KB	Plain Text
Environment.txt	✓	22. December 2023, 11:14	415 KB	Plain Text
Group.txt	✓	22. December 2023, 11:14	698 bytes	Plain Text
HardwareEvent.txt	✓	22. December 2023, 11:14	1,1 MB	Plain Text
Log.txt	✓	22. December 2023, 11:14	4 KB	Plain Text
Nosepoke.txt	✓	22. December 2023, 11:14	9,6 MB	Plain Text
Sessions.txt	✓	22. December 2023, 11:14	76 bytes	Plain Text
Visit.txt	✓	22. December 2023, 11:14	3,1 MB	Plain Text
Challenge_3	✓	22. December 2023, 11:16	--	Folder
Animal.txt	✓	22. December 2023, 11:15	4 KB	Plain Text
Environment.txt	✓	22. December 2023, 11:15	423 KB	Plain Text
Group.txt	✓	22. December 2023, 11:15	702 bytes	Plain Text
HardwareEvent.txt	✓	22. December 2023, 11:15	2,8 MB	Plain Text
Log.txt	✓	22. December 2023, 11:15	2 KB	Plain Text
Nosepoke.txt	✓	22. December 2023, 11:15	11,2 MB	Plain Text
Sessions.txt	✓	22. December 2023, 11:15	76 bytes	Plain Text
Visit.txt	✓	22. December 2023, 11:15	3,6 MB	Plain Text

The files should be exactly what is obtained from the IntelliCage exporting software. No need for any changes.

### **But what if I have two sets of data that have to be analyzed together?**

No worries! Just run the `merging_intellicages` code! This is a fairly direct script and you only have to select the Visits.txt file from Challenge 1 for both sets of data. Remember to provide the new name of the folder your files will be placed to the variable **project\_merged**. The files for both separate sets have to be organized as described above!

Please let me know in case you have any questions.

## Running the analysis

For Windows users you still need to execute the code from *initial\_intellicages.R*. The source script (*start\_intellicages\_windows.R*) simply calls the starting script, so you may want to skip it. For Unix users you can double click the *run\_intellicages\_unix.sh* file. Otherwise just open the *initial\_intellicages.R* script or run it through the terminal using **Rscript** *initial\_intellicages.R*.

The code will install any required dependencies on its own, but please check the console in case of any errors.

After running the initial script, you will be greeted by the following screen (text changes according to operational system):

### Select Folders and Project Name

*Made by Vinicius Daguano Gastaldi*

Instructions:

- 1) Remember to follow folder structure as described in the readme file.
- 2) Type or paste the exact folder name where your files are.
- 3) Select the folder where all your projects, i.e., do not enter a specific project folder. You need to enter the directory before pressing OK.  
**It does not work if you simply select it and press OK.**
- 4) Select your results folder. This should be a general folder, a specific folder will be created for your project. You need to enter the directory before pressing OK.  
**It does not work if you simply select it and press OK.**
- 5) Current version of the script can only handle 2 or 4 groups.  
Your group names **should not contain spaces!** Use underscores, `_`, instead.
- 6) Your unblinding file should follow the instructions provided in the readme file.
- 7) Also check the readme file for possible color suggestions. Those have to be valid R color names.

Project name

Project folder

Results folder

Number of groups:

2

Name of group 1

Name of group 2

Select unblinding file

Browse...

Select IntelliCage script

Click to confirm

Color of group 1

Color of group 2

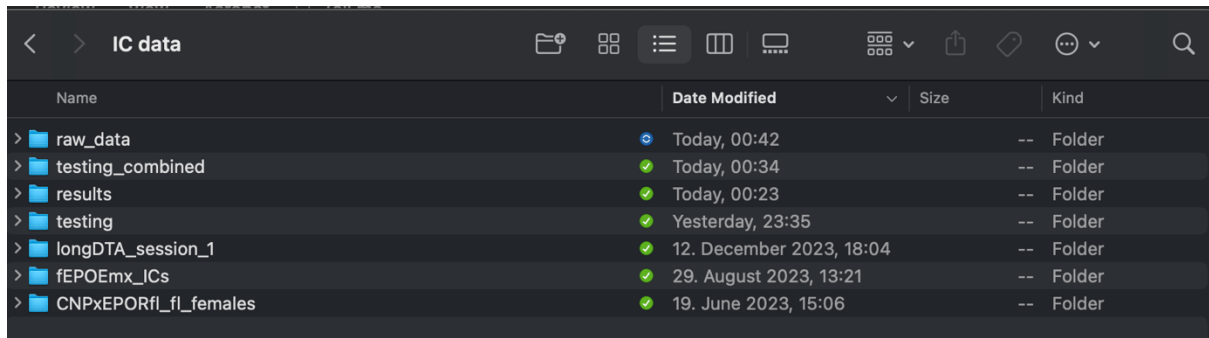
Please follow the instructions and provide all details needed for the code to run. The name of the project and groups **HAS to match what you have in your files**. The colors can be selected using their names or hex codes (recommended). To select hex codes, you can use the following website: <https://www.color-hex.com/>.

It is also important to provide a properly formatted unblinding file! The unblinding file contains only two columns: ID and Group. It should be saved as Tab-delimited Text (.txt) file. You can easily use Excel for this.

Everything else should run on its own!

In the next page you can find some examples of folder organization and one screenshot of the filled page.

One example of how folders should be organized:



Name	Date Modified	Size	Kind
> raw_data	Today, 00:42	--	Folder
> testing_combined	Today, 00:34	--	Folder
> results	Today, 00:23	--	Folder
> testing	Yesterday, 23:35	--	Folder
> longDTA_session_1	12. December 2023, 18:04	--	Folder
> fEPOEmx_ICs	29. August 2023, 13:21	--	Folder
> CNPxEPORfl_fl_females	19. June 2023, 15:06	--	Folder

Note that this folder contains all datasets with their appropriate names and a “results” folder where everything is saved.

Filling the page is also very straightforward. The main difference is that with Windows you will click on the folder for the projects and results and that is all. You should not actually “enter” them.

## Select Folders and Project Name

Made by Vinicius Daguano Gastaldi

Instructions:

- 1) Remember to follow folder structure as described in the readme file.
  - 2) Type or paste the exact folder name where your files are.
  - 3) Select the folder where all your projects, i.e., do not enter a specific project folder. You need to enter the directory before pressing OK.  
**It does not work if you simply select it and press OK.**
  - 4) Select your results folder. This should be a general folder, a specific folder will be created for your project. You need to enter the directory before pressing OK.  
**It does not work if you simply select it and press OK.**
  - 5) Current version of the script can only handle 2 or 4 groups.
- Your group names **should not contain spaces!** Use underscores, `_`, instead.
- 6) Your unblinding file should follow the instructions provided in the readme file.
  - 7) Also check the readme file for possible color suggestions. Those have to be valid R color names.

Project name

Number of groups:

Name of group 1

Color of group 1

Name of group 2

Color of group 2

Select unblinding file

## Observation!

ELM1A refers to ELM Acquisition, ELM2A to ELM Retrieval, ELM1R to ELM Reversal Acquisition, and ELM2R to ELM Reversal Retrieval. The different naming scheme in the script and the created files is to make it easier to identify differences between the created variables.