From Noldus file to Visualisation part 2 : prepare for wakefish

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1. INSTRUCTIONS

This is a follow up from `From Noldus File to Visualisation part 1 : Noldus`

For this example I used the `PSDD2opn4xa` experiment (8 movies labelled PSDD2opn4xaF1 to F8).
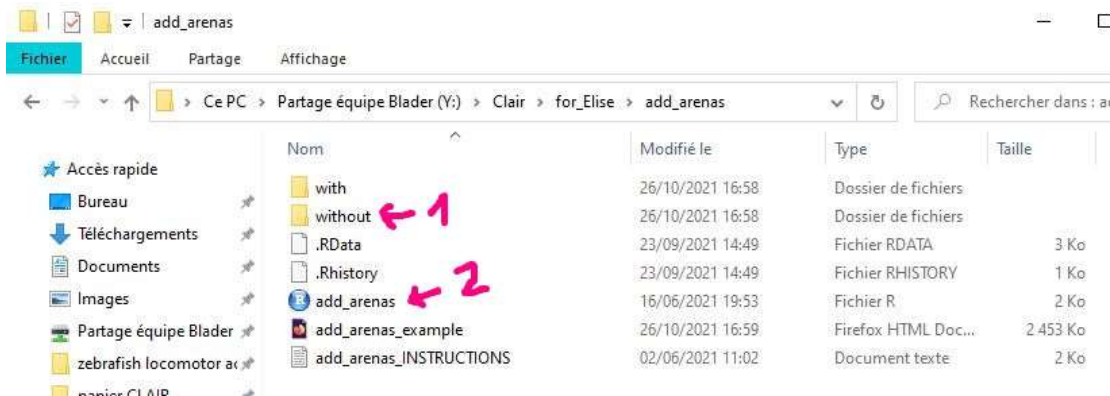
2. STEP BY STEP EXAMPLE

1. At the end of the Noldus processing, you should end up with one excel file for each one of your movies *(here 8 excel files for "PSDD2opn4xa")*. For each type of experiment (*opn4xaDD*), I create a folder for each one of my experiments (*opn4xaPSDD1, opn4xaPSDD2, opn4xaPSDD3, etc...*). In the folder corresponding to my experiment (*opn4xaPSDD2*), I like to create a folder called `1.*nameofmyexperiment*` where I put the original excel files I directly extracted from the Noldus.
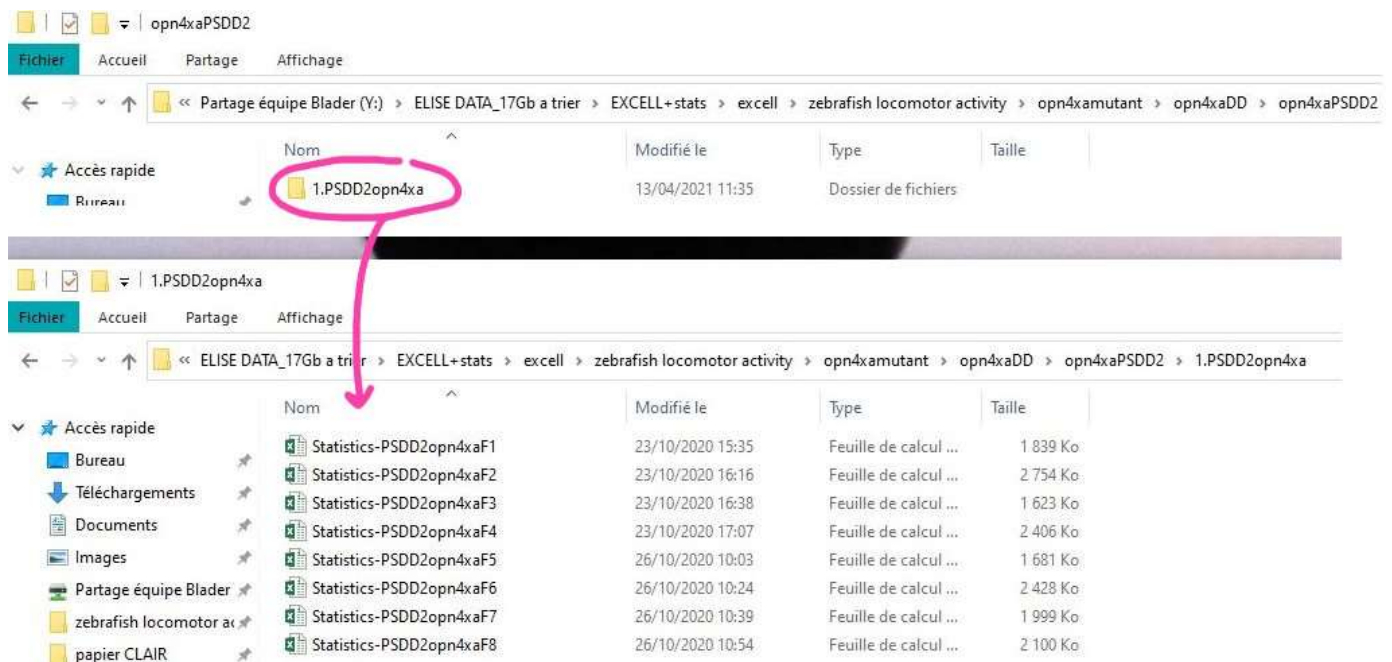
2. (if you have more than 24 fishes). Prepare the files for wakefish processing : to be able to process the files, the wakefish program (program writen by L.Sanchou to extract the distance moved per min over x minutes from several files into one final file) needs to detect several column thanks to specific keywords in the excel files, so make sure you have these : `Distance moved` for the column containing the distance moved, `< User-defined 1 >` for the column containing the genotypes, `Arena` for the column containing the Arena names, `Start` for the column containing the time. With 96 arenas, the Noldus files contain *"1,2,3,..."* instead of *"Arena 1, Arena 2, Arena 3,..."*, this is why you need an extra step before being able to process them with the wakefish program.

2.a : **(1)** in `Y://Clair//for_Elise//add_arenas` , copy your excel files in the `without` folder, **(2)** open the `add_arenas` R file (you need to have R installed in your computer). You can follow the add_arenas_example if you have any issues or check add_arenas_INSTRUCTIONS.
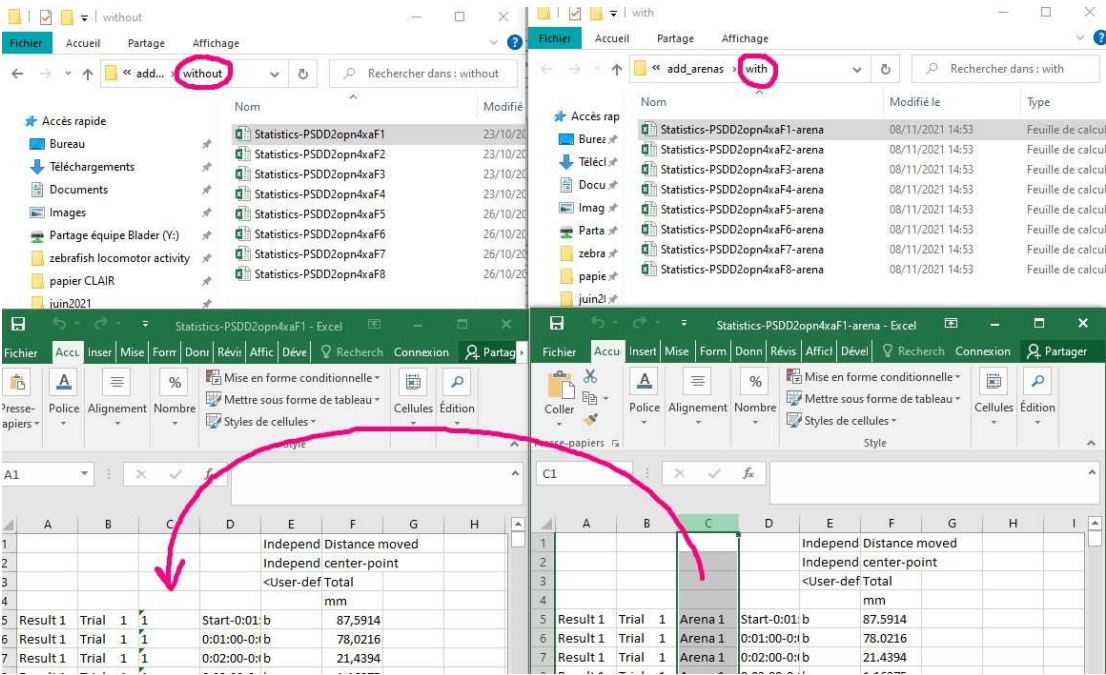

**2.b** Run the `add_arenas` R file (select all the code with `CTRL+A` and run it with `CTRL+ENTER`)

2.c for each file in the `with` folder *(Statistics-PSDD2opn4xaF1-arena)*, copy and paste the Arena column in the corresponding file in the `without` folder *(Statistics-PSDD2opn4xaF1)*.

2.d I like to put the modified files ready to go to be processed in another folder called

`2.*nameofmyexperiment*_pour_wakefish`
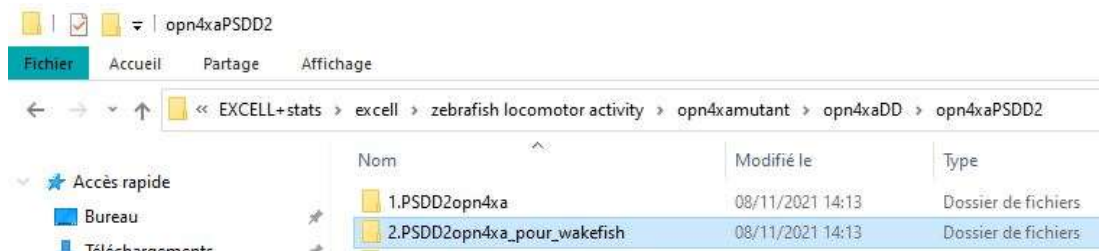
3.a If you forgot to put a genotype column, the wakefish program will not like it. But do not worry, you can add it manually ! Open each file, do a `right click` on a column name (`E` for example) and click on `Insertion` (Insert a column)
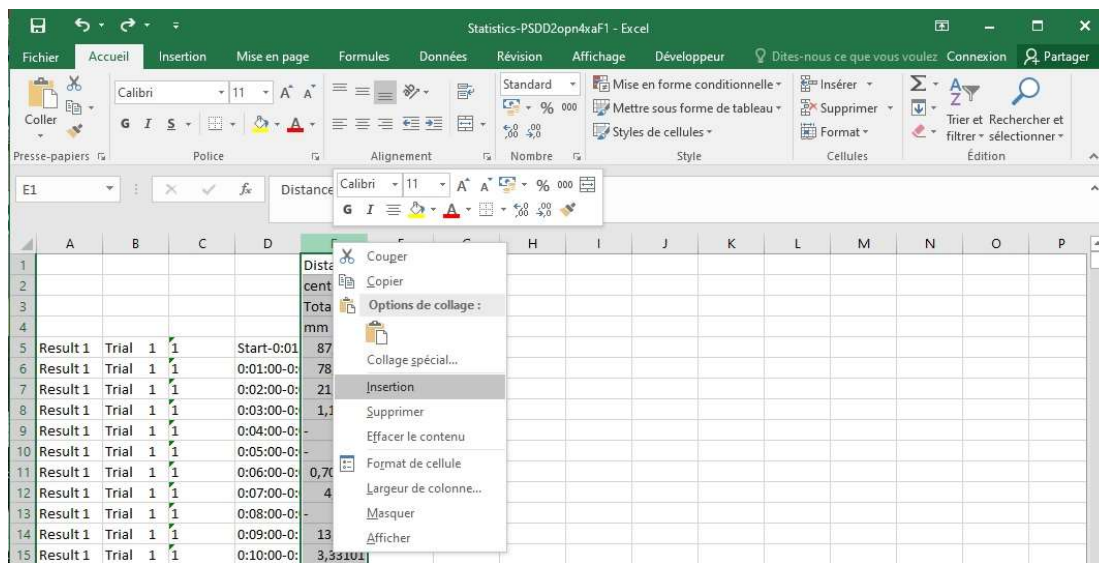
3.b with the column still selected, click on `Rechercher et selectionner` (Search and Select), `Remplacer` (Replace)
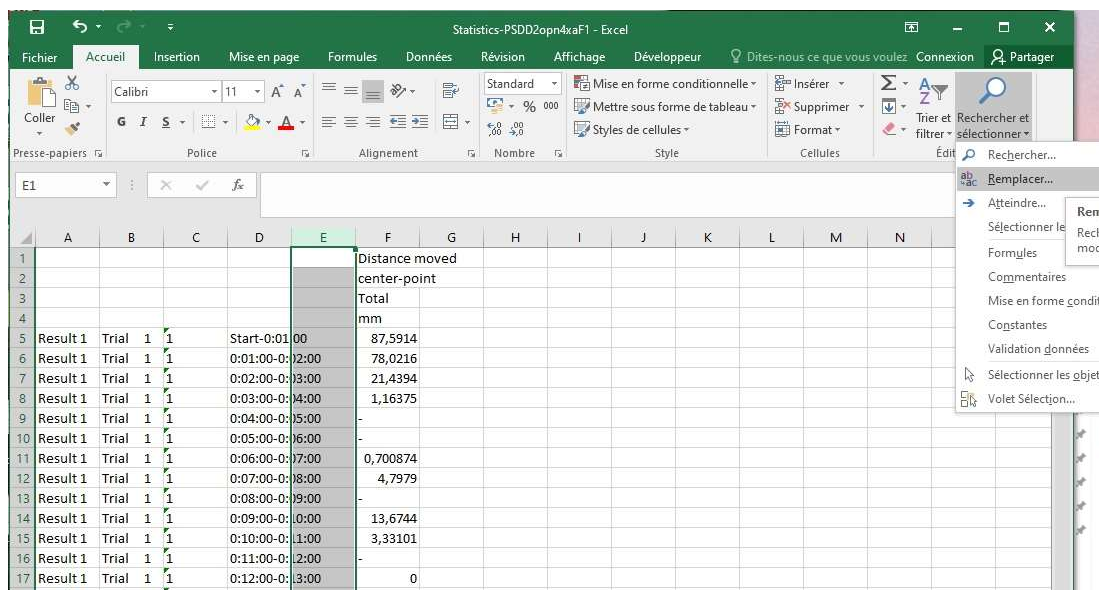
3.c keep the `Rechercher` box empty, and put a random letter in the `Remplacer par` box, click on `Remplacer tout`

3.d copy and past the first 4 lines of a file with a genotype in your file, and voila !