## From Noldus file to Visualisation part 3 : wakefish

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## 1. INSTRUCTIONS

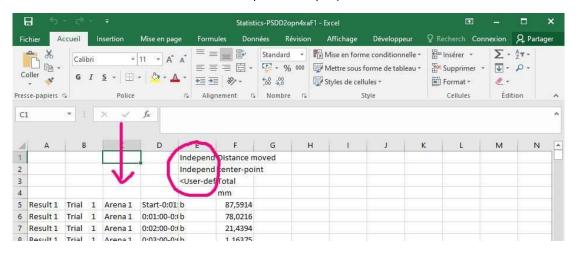
This is a follow up from From Noldus File to Visualisation part 2: prepare for wakefish

For this example I used the PSDD2opn4xa experiment (8 movies labelled PSDD2opn4xaF1 to F8).

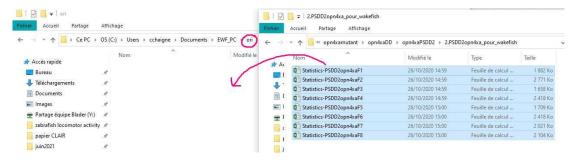
## 2. STEP BY STEP EXAMPLE

**1.** For processing to wakefish, your files should all look like this (make sure your Arenas are labelled "Arena 1, Arena 2, ..." and not just "1, 2, ..." and that you have a genotype column). If not check the

From Noldus File to Visualisation part 2 : prepare for wakefish



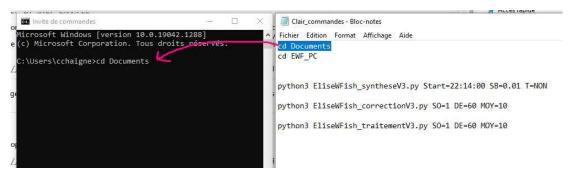
2. copy your files in your EWF\_PC//ori folder (be sure this folder is empty before your copy your files).



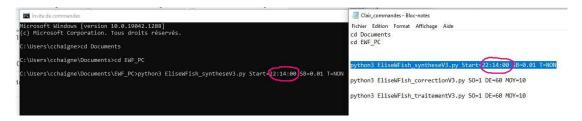
3. open the "terminal"



**4.** copy and paste the coding lignes cd Documents and cd EWF\_PC (or directly cd Documents\EWF\_PC) in the terminal to go in the correct folder



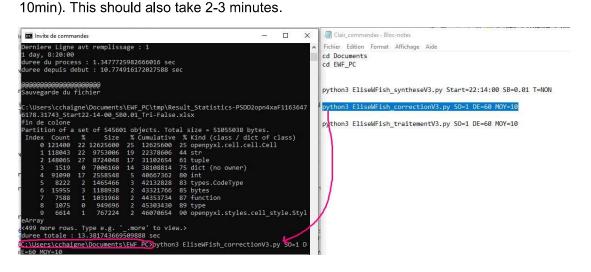
**5. Synthese part**: copy and paste the synthese part with the correct parameters python3 EliseWFish\_syntheseV3.py Start=22:14:00 SB=0.01 T=NON, put the correct Starting Time (Start=HH:MM:SS): 23:00:00 correspond to 8am, beware do not put anything over 23:00:00; SB= (binarisation threshold in mm to consider that the larva is moving), T=OUI ou T=NON to sort out by genotype or not



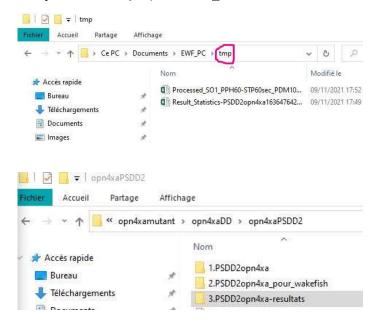
This part takes 2-3min. For each file, it should say something like this if it's able to detect every column it needs:

For example if you forgot to put the genotype column, it will look like that and it would work:

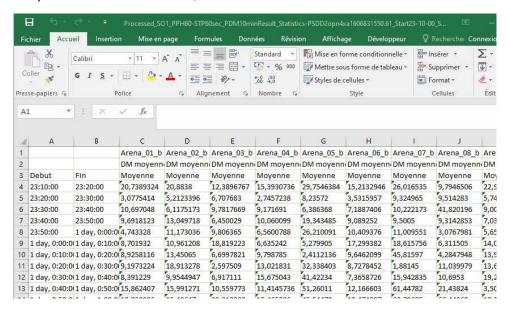
**6. Correction part** When the Synthese part is over (you should get a single line saying C:\Users\votre\_login\Documents\EWF\_PC\ori ), copy and paste the synthese part with the correct parameters python3 EliseWFish\_correctionV3.py SO=1 DE=60 MOY=10, put the correct threshold time in minutes where you consider that the larva is sleeping (**SO=1** for 1min), bining time in the Noldus file seconds (**DE=60** for distance moved per minute), mean to do (**MOY=10** to have to distance moved by minute over



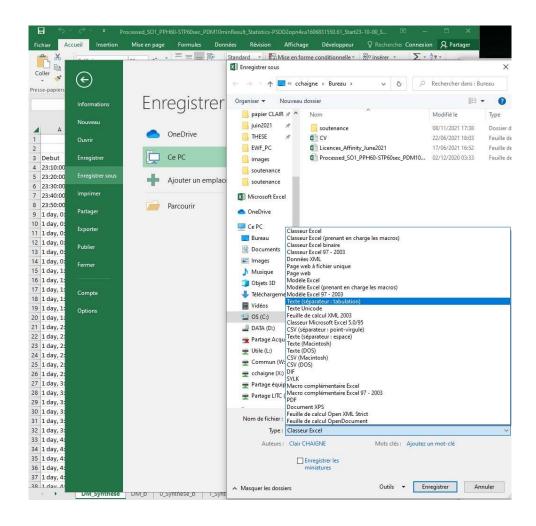
- **6. Traitement part** when the Correction part is over, copy and paste the traitement part with the correct paramters python3 EliseWFish\_traitementV3.py S0=1 DE=60 MOY=10, ut the correct threshold time in minutes where you consider that the larva is sleeping (**SO=1** for 1min), bining time in the Noldus file seconds (**DE=60** for distance moved per minute), mean to do (**MOY=10** to have to distance moved by minute over 10min). This part can take several hours.
- 7. when the traitement part is over, I like to copy and paste the Processed and Result files in the tmp folder in my 3.\*nameofmyexperiment\*\_resultats folder



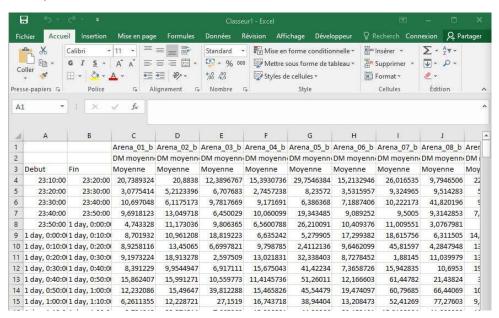
8. open the Processed file, it should look like this:



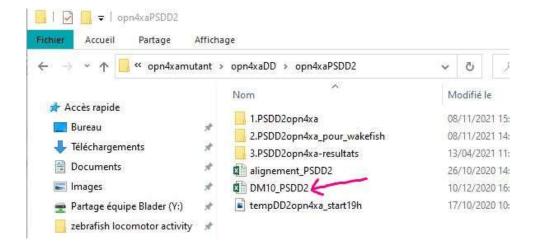
**9.** copy and paste the DM\_Synthese sheet in another excel file (CTRL+A to select everything, CTRL+C to copy and CTRL+V to paste). Save this new file as a Texte (separateur : tabulation) file.



10. Open this new file in Excel, it should now look like this:



**11.** Save this file as an excel file (Classeur Excel). I like to save name this file DM10\_nameofmyexperiment for 10min means.



## 3. Issues you can have

- Do not put a starting time over 23:00:00
- If you have too many different genotypes, the wakefish won't be able to generate the final excel files (too many sheets to generate)
- Check that there is not any very very small data (the wakefish program should then give an error message with the line number where this very very small data is such as e^-0.006), replace it with 0
- If when you try to open the processed file, it says the name is too long to be opened, you can trim its name and/or try to copy it on your desk and open it from it.