## From Noldus File to Visualisation part 5 : Phase Analysis with Biodare

Clair Chaigne

10 novembre 2021

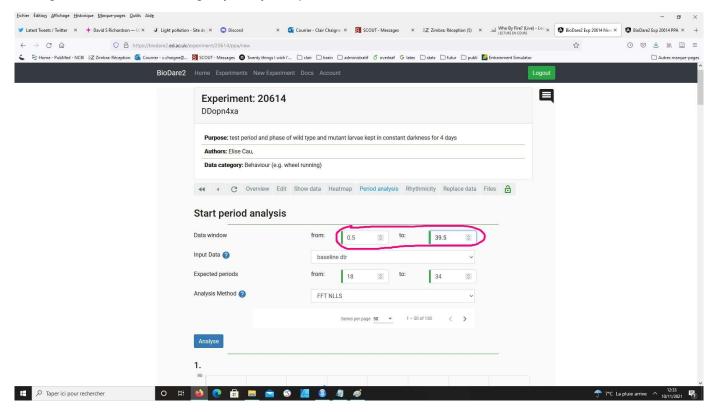
## 1. INSTRUCTIONS

This is a follow up from From Noldus File to Visualisation part 4: wakefish

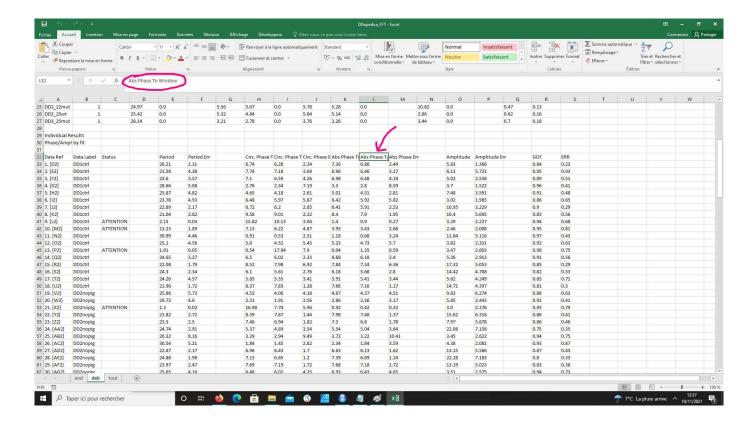
For this example I used the DDopn4xa experiments. It includes 3 independent experiments: PSDD1opn4xa, PSDD2opn4xa and PSDD3opn4xa, that I trimed so they all start at 23:30:00).

## 2. STEP BY STEP EXAMPLE

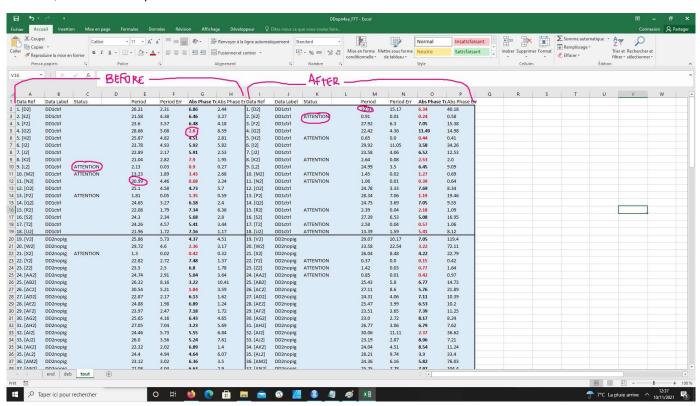
- 1-9. See steps 1 to 9 from part 4
- **10. Phases analysis**: for phases calculation, I use the default Expected periods, for Input Data I select baseline dtr and for Analysis Method I use the FFT-NLLS. For calculating the phase before the pulse, I use the Data window from 0.5 to 39.5 (corresponding to 9am/CT0 to midnight/CT15 of the following day in my data), and for the phase after the pulse the window is from 48.5 to 87.5 (corresponding to 9am/CT0 to midnight/CT15 of the following day in my data).



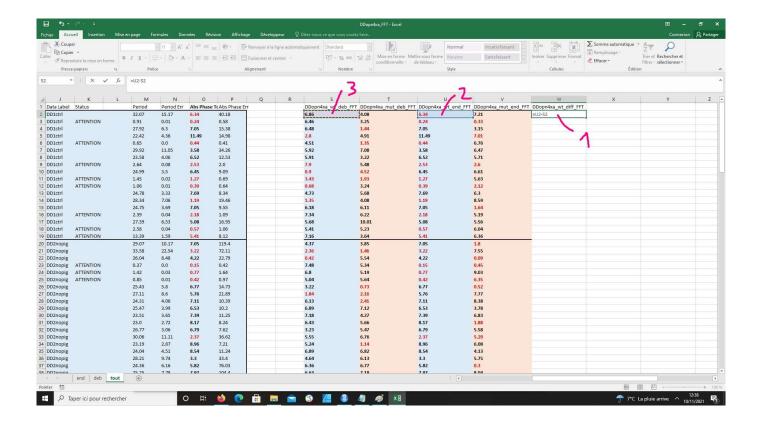
- 11-13. See septs 11 to 13 from part 4
- 14. Keep the Abs Phase to Window data



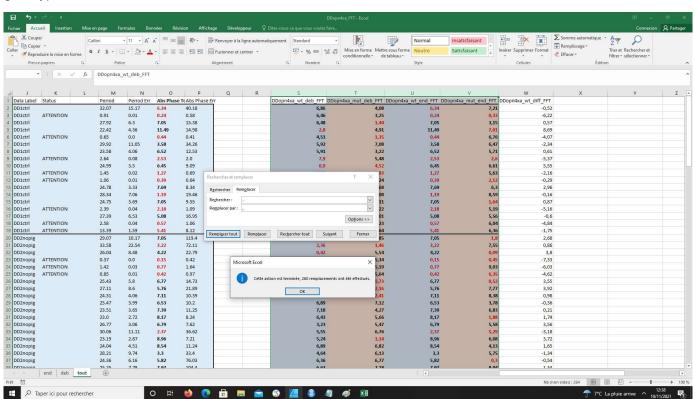
**15.** Labelling unwanted data After putting my data in the shape I want (colors, borders, putting before and after phases on the same sheet), I label in red the unwanted data: larvae with a period of more than 30 or less than 18, larvae with a phase of more than 24 or less than 3.

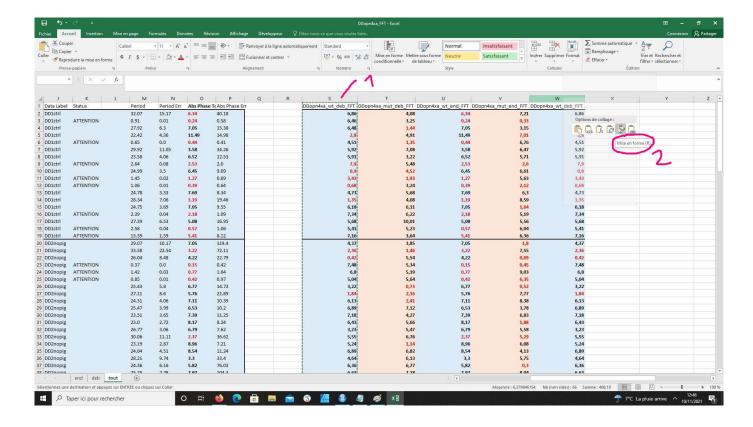


**16. Delta phase calculation** After ordering my data by genotype, I calculate the delta phase for each genotype: **(1)** in the correct cell, put the = sign to start a formula, **(2)** click on the cell corresponding to the after phase, **(3)** put a - in your formula and click on the cell corresponding to your before phase to do at the end =phaseafterthepulse-phasebeforethepulse



**17. Remove unwanted data**: to remove delta phase calculated from unwanted phases, if you have labelled your unwanted phases in red, you can **(1)** select and copy your before column and **(2)** paste it with the Mise en forme option label in red the delta phase to remove. do the same with the after column and for all the genotypes and voila!





18. Statistics: see part 4