

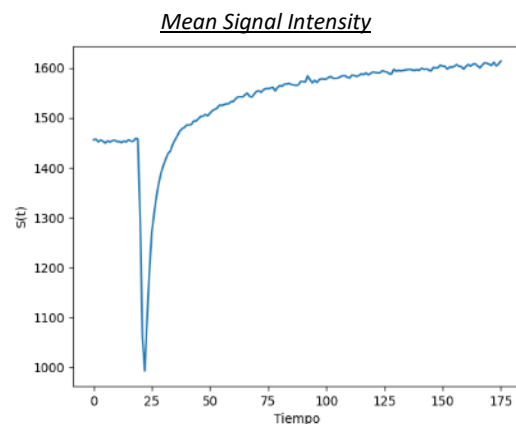
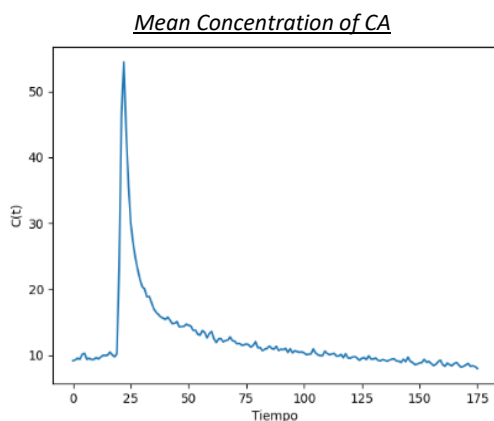
## PERFUSION-NOBEL: USER GUIDE

### 1. PREVIOUS NOTES

- I. Software and files needed for the correct execution of the Python project
  - a) Downloads
    - Python (version > 3.7)
    - Python interpreter (Optional. This project was developed using PyCharm)
  - b) Inputs needed and their corresponding preprocessing steps
    - Masks of the brain and AIF/VOF regions in .png/.npy format.
      - Any manual or semi-automatic method can be used for this task. Both ITK-Snap and ImageJ are possible external tools to extract the ROIs.
    - DSC-MRI images in DICOM format.
      - It is already stated in the code but there are some lines written specifically for files with the naming structure "MRI[num]".
    - $S_{min}$ : Frame corresponding to the minimum in signal intensity (integer number).

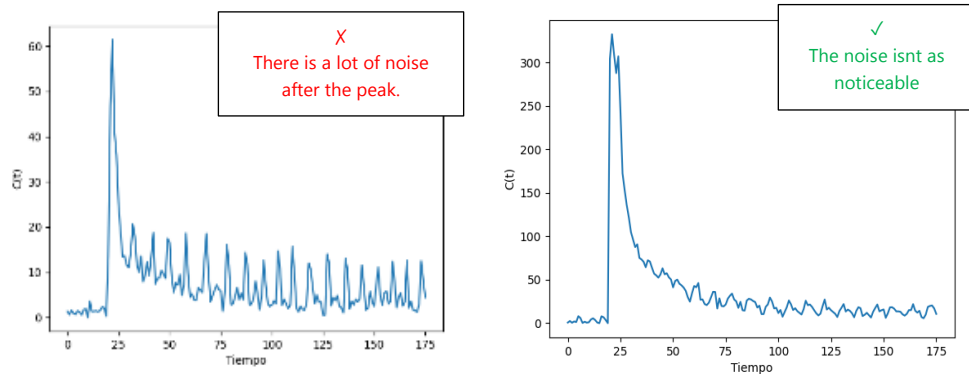
### 2. PERFUSION MAP CALCULATION

- I. The parametric maps will all be automatically saved (.tiff format) in the same directory where the python scripts are located. Any other image displayed during the program execution must be manually saved.
  - a) **BE CAREFUL!** The .tiff files are always saved with the same name. Thus, any map from previous runs will be rewritten if it is not moved to another directory.
- II. The script that must be executed is called PerfusionMain.py. It can be run either through the terminal or using a Python interpreter.
  - a) **BE CAREFUL!** It must be located in the same directory as PerfusionClass.py and InitialParametersClass.py.
- III. Once PerfusionMain.py is executed, a window like the one shown in **Figure 1** will pop up, asking for the user inputs.
  - a) Other inputs not included in this window, such as echo time (TE), time between frames... must be changed modifying the code in InitialParametersClass.py.
- IV. After clicking the Start button, the Signal Recovery (SR) and Percentage Signal Recovery (PSR) will be calculated and displayed.
  - a) The PSR map often contains a wide range of values, resulting in maps with little to no apparent variation. The color bar range should be modified to fix this.
- V. Next, the mean concentration curve and mean signal intensity are displayed. Example curves are shown in the next pictures:

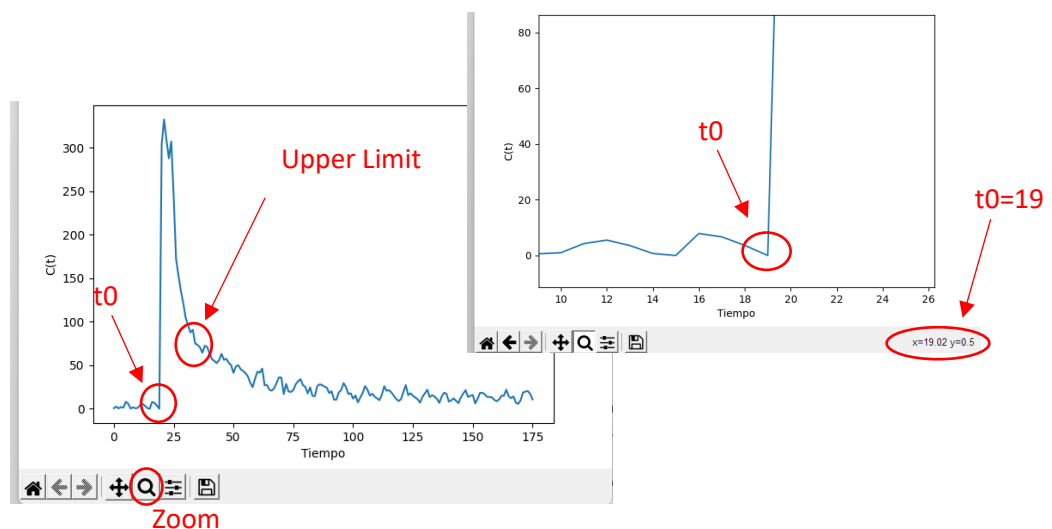


VI. The next few steps are those regarding the parametrization of the Arterial Input Function (AIF) / Venous Output Function (VOF).

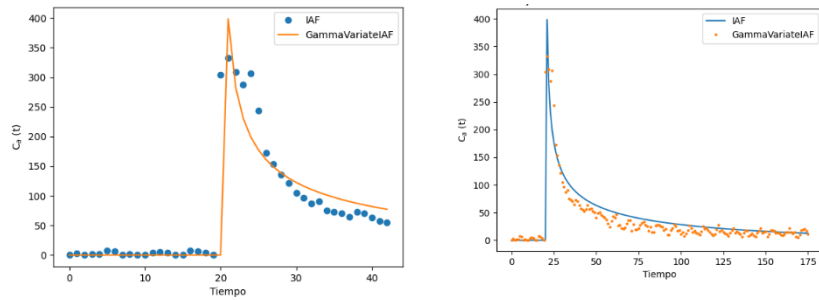
- a) The program shows the mean concentration curve in the masked region corresponding to the reference vessel. The shape of this curve is pretty similar to the concentration curve in the whole tissue, one of the main differences being that the former is noisier due to having less pixel values when doing the average. The next figures show two concentration curves in different AIF/VOF masked regions.



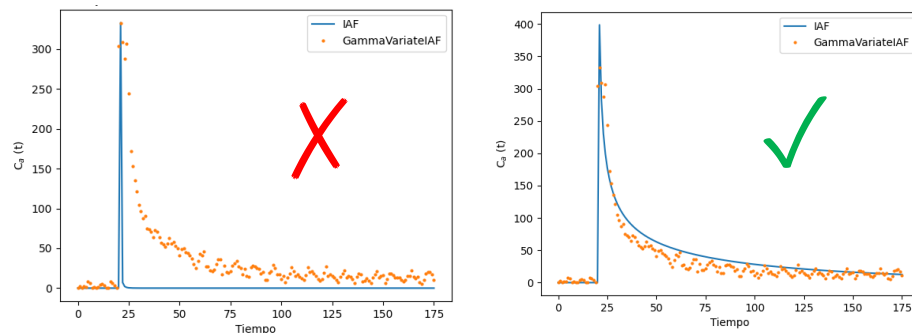
- The shape of this curve is quite sensitive to the ROI selected and, in many cases, odd shapes will be related to it. Because of this, the software will give the option to stop the process after displaying the concentration curve in the AIF/VOF region in case the ROI selected doesn't give the expected curve shape.
- b) Choosing to continue the program execution will display the concentration curve in the AIF/VOF region for a second time. The initial parameters needed for the following fitting of the curve to a gamma variate function must be extracted from this graph. The parameters needed and where to find them can be seen in the following pictures:



- c) After extracting the values and closing the graph, another window will appear asking for them.
- d) The curve fitting process will then start and the result will be displayed in two different plots: One only included values inside the interval  $[0, \text{Upper Limit}]$  and another graph including the whole range of values.
- e)
- f)



- g) A proper curve fitting result is critical to obtain accurate values of the parametric maps. Both describing the shape of the curve and its maximum value are important, so it will be important to keep a balance between these two factors. An example of “bad” and “good” curve fitting results is shown in the following pictures



- h) After the fitting process is finished, the analysis tool will give the option to redo it, changing the initial parameters in case the result isn't the desired one.

VII. Choosing not to reintroduce the initial fitting parameters will trigger all the parametric map calculations. The parametric maps will then be displayed and automatically saved in *.tiff* format.

- a) In total there will be six parametric maps displayed:
- **Two** Cerebral Blood Flow (CBF) maps in [ml/(100g\*s)] and [ml/(100g\*min)] units.
  - **Two** Cerebral Blood Volume (CBV) maps, both in [ml/100g] units, calculated through non deconvolution and deconvolution-based methods.
  - **Two** Mean Transit Time (MTT) maps, both in [s] units, obtained from the two CBV maps.