

DEMO program for time-resolved fluorescence analysis

User's manual

1. Open a DOS window in the directory where DEMO_P5web.zip is stored
2. Unzip automatically the file DEMO_P5web.zip by typing demo_p5web. The executable DEMO_P5.exe and companion files are automatically unzipped (or use your favourite package to extract the files).
3. Type demo_p5: the following menu asks you to select one data set:

```
=====
===          MENU : DATA          ===
=====

          SELECT DATA TO ANALYZE
1  => 4 exponential decay - 2048 points - 4 ps/channel
2  => 5 exponential decay - 4096 points - 18 ps/channel

          Enter your choice :
```

4. Type 1

```
=====
===          MENU : LIFETIME DOMAIN          ===
=====

Lifetime domain for distribution search
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150 Lifetimes from  0.015  to  1.500ns

Do you want to change the values? [Y/N]
```

5. At this stage you may change the lifetime domain to scan and the number of lifetimes in the distribution. In a first trial answer N (or "n") to continue.

```
=====
===          MENU : FIT ZONE          ===
=====

*** WARNING: reversed curves ***

Convolution zone spans between channel  701 and 1945

Fitting zone spans      between channel  701 and 1937

Do you want to display data ? [Y/N]
```

6. These markers define limits for convolution and fit. You can see that the fitting zone should always start after the convolution domain and ends at the same point (here the data have been recorded in a reverse way).

- 6.1. You answer Y (or "y") to display the data, to check the time domain you want to fit and therefore to change the marker's position accordingly. You should pay attention to start the convolution BEFORE the leading edge of the IRF.

6.2 Answer N again and continue.

Do you want to change the fitting zone ? [Y/N]

6.2.1 You answer N and the analysis starts. It can be stop at any iteration in using ESC button.

6.2.2 You answer Y

- Enter new_FIRST_FIT_channel
- Enter new_LAST_FIT_channel

You enter the new marker values and the dialog restarts from point 6.1.

Note: all parameters for lifetime domain, convolution and fitting zone are initialized in file test-1.go

The demo program uses and writes several files:

Input files :

test-1.go: Input parameter file for running the example as a demo. It contains all the necessary responses to the questions asked by the program and the required filenames. We detail how to modify this for your specific analysis below.

excit1.fl, test-1.im : Files containing data used in our demo example, IRF and decay respectively

test-1.prm : Parameter file with all options for the instrument configuration and the experimental method.

memsys.prm : Parameter file contains all MemSys control variables (see MemSys5 manual)

Output files :

test-1.log : Output result file from demo data analysis

test-1.dis : Output file containing τ and $h(\tau)$ distribution for further use and plot.

test-1.crv : Output file containing data , fitting values, residuals and autocorrelations.

test-1.dec : Output file containing fluorescence decay corresponding to each peak in the lifetime distribution.

test-1.tab : Output file containing a table of the parameters of the $h(\tau)$ distribution

test-1.txt : Output file containing all results for Igor® procedure to print analysis data sheet