Microrheology with Optical Tweezers “MOT” virtual instrument (VI)

This program has been created by **Manlio Tassieri** and it is based on the analytical procedure introduced by M. Tassieri, R. M. L. Evans, R. L. Warren, N. J. Bailey and J. M. Cooper, "*Microrheology with optical tweezers: data analysis*", New J. Phys. **14**, 115032 (2012).

Installation

This program has been written in LabVIEW 2010 for Windows and 2013 for Mac.
Two scenarios are now possible:

(I) On your machine the related LabVIEW version **is installed**.

In this case, you can copy the executable “MOT” (.exe for Windows and .app for Mac) and use it straightaway.

(II) On your machine the related LabVIEW version **is not installed**.

In this case, you need: I) For Mac, to download a code from National Instrument that will be requested the first time you run the application; II) For Windows, to contact me and I will send you an “Installer” code, which emulates LabView on your machine.

Modus operandi

Pressing the white arrow button on the top toolbar can start the executable MOT.
A dialog box appears asking you to choose the file to read and analyse (i.e. the file containing the trajectory of the optically trapped bead). Note that the file to read must be of type .dat or .txt. It may contain more than three columns; however the executable reads only the first three columns of the file. These must be: {time [s], x [µm], y [µm]}. The file must not contain column headings *nor* time equal to zero.

Once the data have been loaded, both the coordinates are displayed on the top-left graph of the application’s front panel (Figure 1). On top of the trajectories one can choose: (I) the coordinate that has to be analysed (the default one is “x”); (II) the application of a high pass filter to remove a possible slow drift of the trajectory; the default one is “mean”, but you can choose also “raw data” (i.e. no filter) or “detrend” (a high pass filter).

On the left side of the VI there is a list of parameters that can be either read, like the number of data points of the loaded file, the variance of the two coordinates, the two trap stiffness, the bead mass and the ratio between the bead mass and the trap stiffness; or set, like the solvent (water in most of the cases) viscosity, the bead density, the temperature and the bead radius.

The trajectories are then analysed and the normalised position autocorrelation functions (NPAFs) are evaluated and displayed on the first page of the top-right Tab Control (Figure 1).
Move the graph cursor (i.e. the centre of the crossed blue lines) to the point where the NPAF goes to zero, this will discard all the zero values of the NPAF at long lag times. The same NPAF curves are also plotted in terms of the normalised mean square displacement (NMSD) on page two of the Tab Control. On page three the NPAF is plotted against the normalised lag-time (for further information see http://arxiv.org/abs/1403.6629). On page four the NPAF is plotted against the normalised lag-time, but the ordinate starts from e^{-1}; the intercept of the NPAF with the abscissa provides a *reading* of the solution's relative viscosity (for further information see http://arxiv.org/abs/1403.6629).
On the top-right of the VI one can set the point at which the down-sampling of the NPAF starts. The default is zero and with a base of 1.45; i.e. the first 5 points are linearly spaced in time and then they are quasi-logarithmically distributed on the time-scale: $\tau_n = ceil(1.45n)$, for non-negative integer n (see New J. Phys. **14**, 115032 (2012)). One can choose to distribute the data logarithmically with base 2. One can also choose the total number of data forming the NPAF by using the control named "Numeric" (the default is *50*).

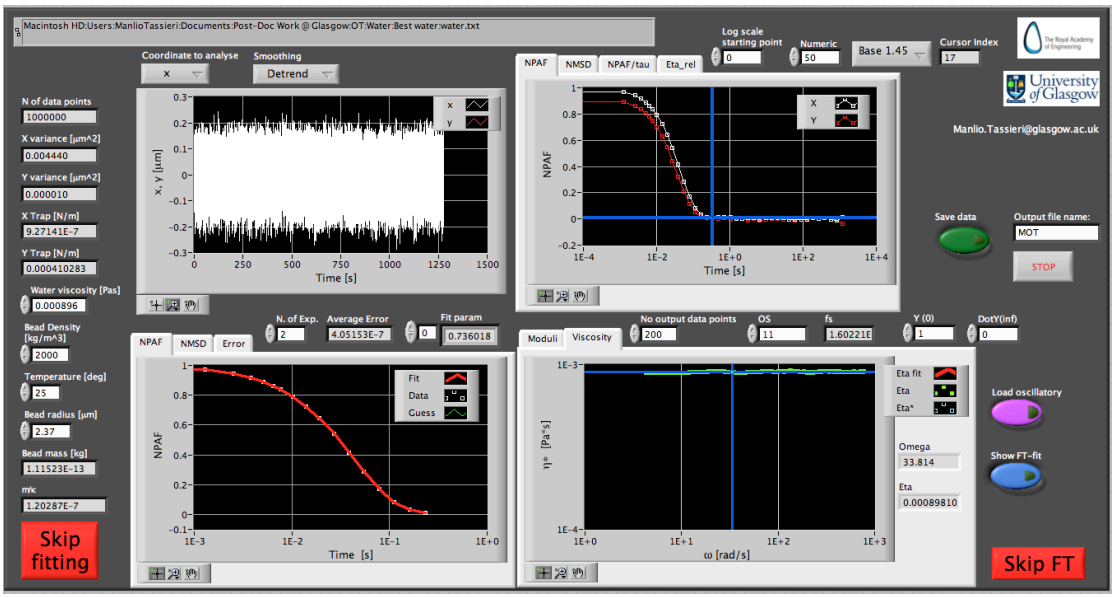

Figure 1. Front panel of the executable "MOT".

The bottom-left Tab Control visualises the fitting procedure of the NPAF (page one), the NMSD (page two) and the error of the fitting procedure (page three). The fitting function is a sum of stretched exponentials:

$$A(\tau) = \sum_{1}^{n} A_i e^{-(\lambda_i \tau)^{\gamma}}$$

where "n" can be set by using the control named "N. of Exp.". The values of the fitting parameters can be read from the indicator named "Fit param".

Once happy of the degree of accuracy achieved by the fitting process, which can be estimated by reading the displayer named “Average Error”, the red button named “Skip fitting” must be pressed to continue the data analysis.

The bottom-right Tab Control visualises the fluid’s linear viscoelastic (LVE) properties; i.e. both the viscoelastic moduli on the first page and the complex viscosity on the second page. It is possible to overlap the fluid’s LVE obtained from the fitting function by pressing the blue button named “Show FT-fit”.
The viscoelastic moduli obtained from the analysis of the NPAF can be compared with those obtained from an alternative measurement (e.g. bulk rheology), just by pressing the “Load oscillatory” button on the right side of the viscoelastic moduli graph. Note that the file to read must be of type .dat or .txt. It may contain more than three columns; however the executable reads only the first three columns of the file. These must be: {frequency [rad/s], G' [Pa], G'' [Pa]}. The file must not contain column headings *nor* time equal to zero. Moreover, within a single run it is possible to change the oscillatory data just by pressing again the “Load oscillatory” button; however, it is not possible to overlay more than one oscillatory measurement at one time.
The blue cursors on both the graphs allow a reading of the plotted functions from the displayers placed on the right of both the graphs.

The LVE are evaluated for 200 (by default) frequency values, which can be changed by using the control named “No output data points”. The range of frequency where the complex parameters are evaluated is based on the time window extremes of the measured NPAF. In particular, the longest lag-time (i.e. $\tau_{max}=t_{max}- t_0$) provides the lowest frequency w_{min} (i.e. $w_{min}=1/\tau_{max}$), whereas the shortest lag-time (i.e. $\tau_{min}=t_{min}- t_0$) provides the highest frequency w_{max} (i.e. $w_{max}=1/ \tau_{min}$).

As described in Tassieri et al. "*Microrheology with optical tweezers: data analysis*", New J. Phys. **14**, 115032 (2012), in order to obtain the fluid’s LVE properties, the NPAF requires to be *virtually* oversampled. This can be achieved by increasing the value of the control named “OS” (whose default value is 4) up to circa 10 or 12. The virtual oversampling frequency can be read from the displayer named “fs”. Note that, as the OS value increases the program will require more computational power; this may slow the machine.
The two parameters named “Y(0)” and “DotY(inf)” (whose default values are 1 and 0, respectively) are related to the Fourier Transform method explained in detail in the following two papers: Evans R.M.L. et al., Phys. Rev. E, 80, 012501 (2009) and Evans R.M.L., BSR Bulletin, 50, 76-86 (2009).

The whole process can be repeated by pressing the red button named “Skip FT”. Note that, you must change the parameters (e.g. position of the cursor on the NPAF or number of fitting exponentials or bead radius, etc.) before pressing the button.

The displayed NPAF, NMSD and moduli can be saved into a text file by pressing the “save data” button, which also terminates the program after saving. Note that, the button must be activated before pressing the “Skip FT” button. The output file is

saved in the same folder as the input file. The output file name is composed of the input file name plus what is written in the “Output file name” box (eg. Input file name = trajectory; Output file name box = MOT; Output file name = trajectory_ MOT.txt).

The effective number of output data points (i.e. number of rows in the output file) for the specific range of frequency can be chosen by changing the numeric value in the “No of output data” box (the default value is 200 points, equally spaced on a Log scale).

During execution, the program can be stopped at any time by pressing either the little red button on the top toolbar (preferred) or the “Stop” button on the right of the VI (which will execute after a complete loop).

The program can be re-started by pressing the white arrow button on the top toolbar.

Tips

Remember that the noise in the calculated complex parameters (e.g. *G', G''*) has its origin in the genuine noise of the experimental data (i.e. NPAF). This because the NPAF is an averaged function and it is exact only for an *infinitely long* measurement (which is practically impossible). In order to remove the noise in the final results, a fitting function of the experimental data could be used instead.

For further information or questions, please do not hesitate to contact me:
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