AutoDecon Quick-Start

Version 2.001

Getting Started

AutoDecon is our newest software program. *AutoDecon* is basically an "automatic" algorithm which iteratively locates presumptive secretory event positions, adds these peaks to the current fit, automatically tests these secretion events for statistical significance, and automatically removes any non-significant secretory events, continuing this "loop" until no further statistically significant secretion events can be added. This document provides a cursory view of how this software operates.

Figure 1

After the software has been successfully downloaded and installed, an icon like the one shown in Figure 1 will appear on the user's desktop. Click on that icon to open the Pulse_XP folder. A window such as the one depicted in Figure 2 will appear on the screen. Locate and double-click on the *AutoDecon* icon.

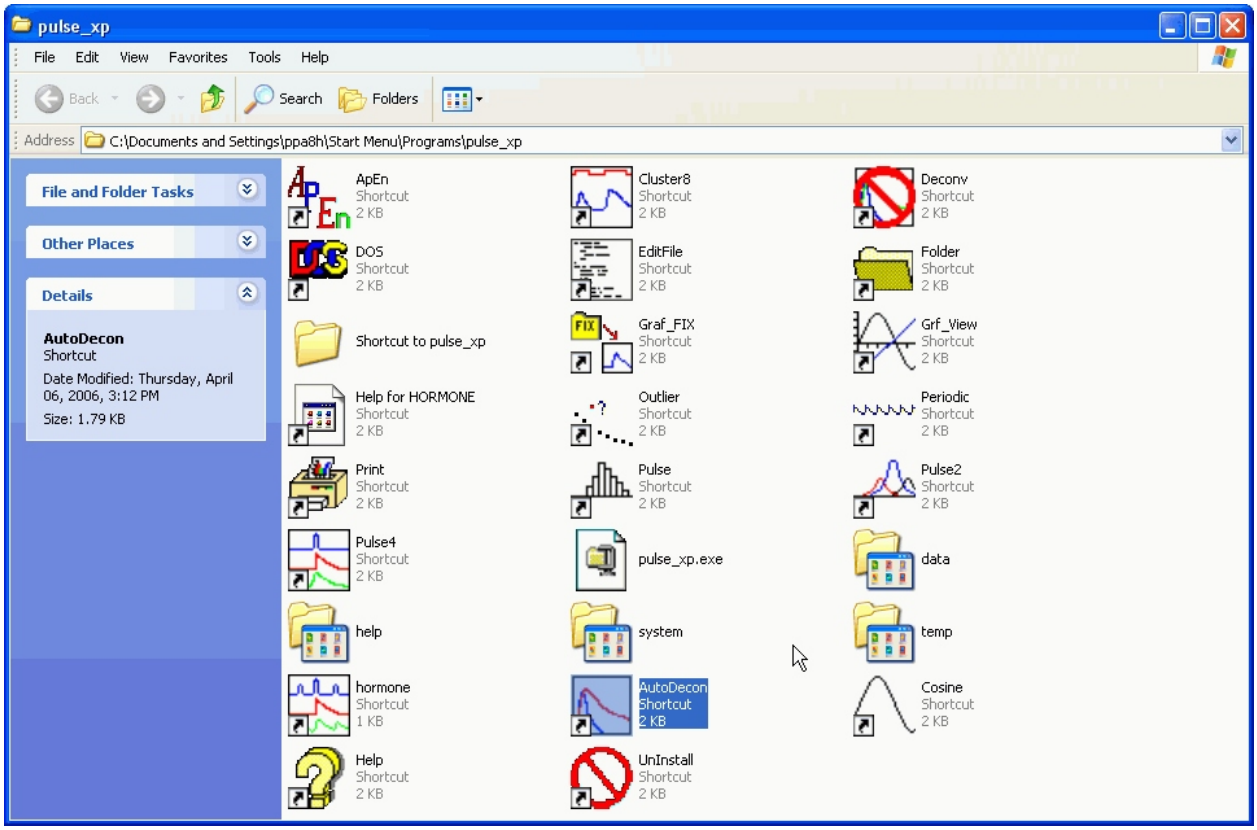


Figure 2

The Pulse_XP software suite's main window will appear. Note that a pre-existing data set must be opened before any analysis can be undertaken. This is done by clicking on the **File→Read A Data File→Fix Mode** [see Figure 3] (presuming the data file is in a *.fix format, see Chapter 1 for other file formats). As with other Windows' menu-driven programs, a new window will appear

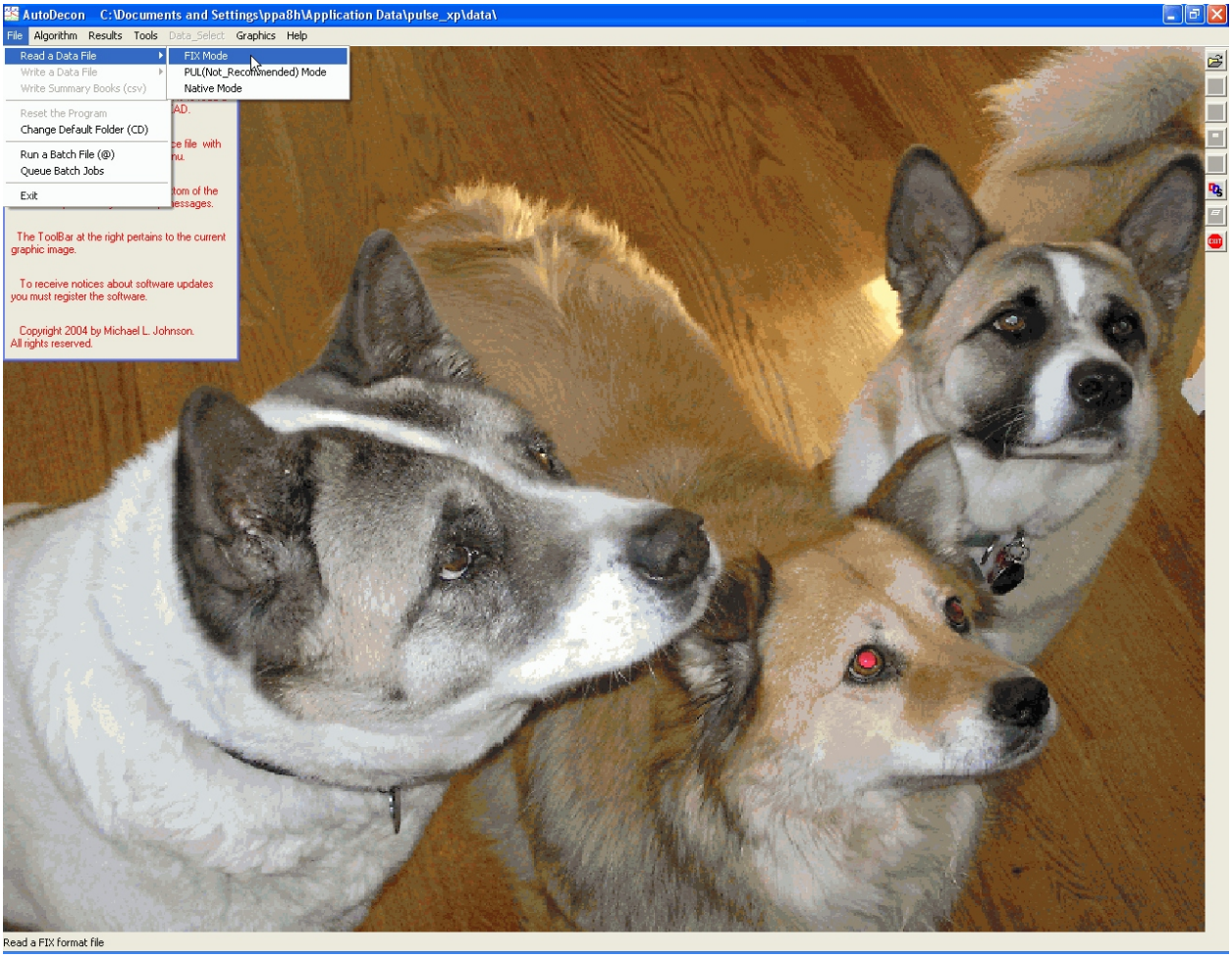


Figure 3

listing all of the *.fix files located in the currently selected subdirectory. We have chosen LHSim1.fix for the example presented here. LHSim1.fix contains data which was simulated to mimic luteinizing hormone (LH) data from a healthy young females. It is 10-minutely sampled data from over a 24-hour period which was assayed in duplicate.

Click on the file of choice (LHSim1.fix) and then click **Open**. The actual hormone concentration time-series data will now be displayed on the top right-hand side of the screen. Accompanying this on the screen is a data grid (Figure 4, upper left) which contains the numeric values of all parameters currently associated with the data. On the lower left-hand side of the screen is a graph depicting the autocorrelations. There should be only one or two red autocorrelations after the data has been fit. The residuals from the current fit are shown in the right middle graph. Note

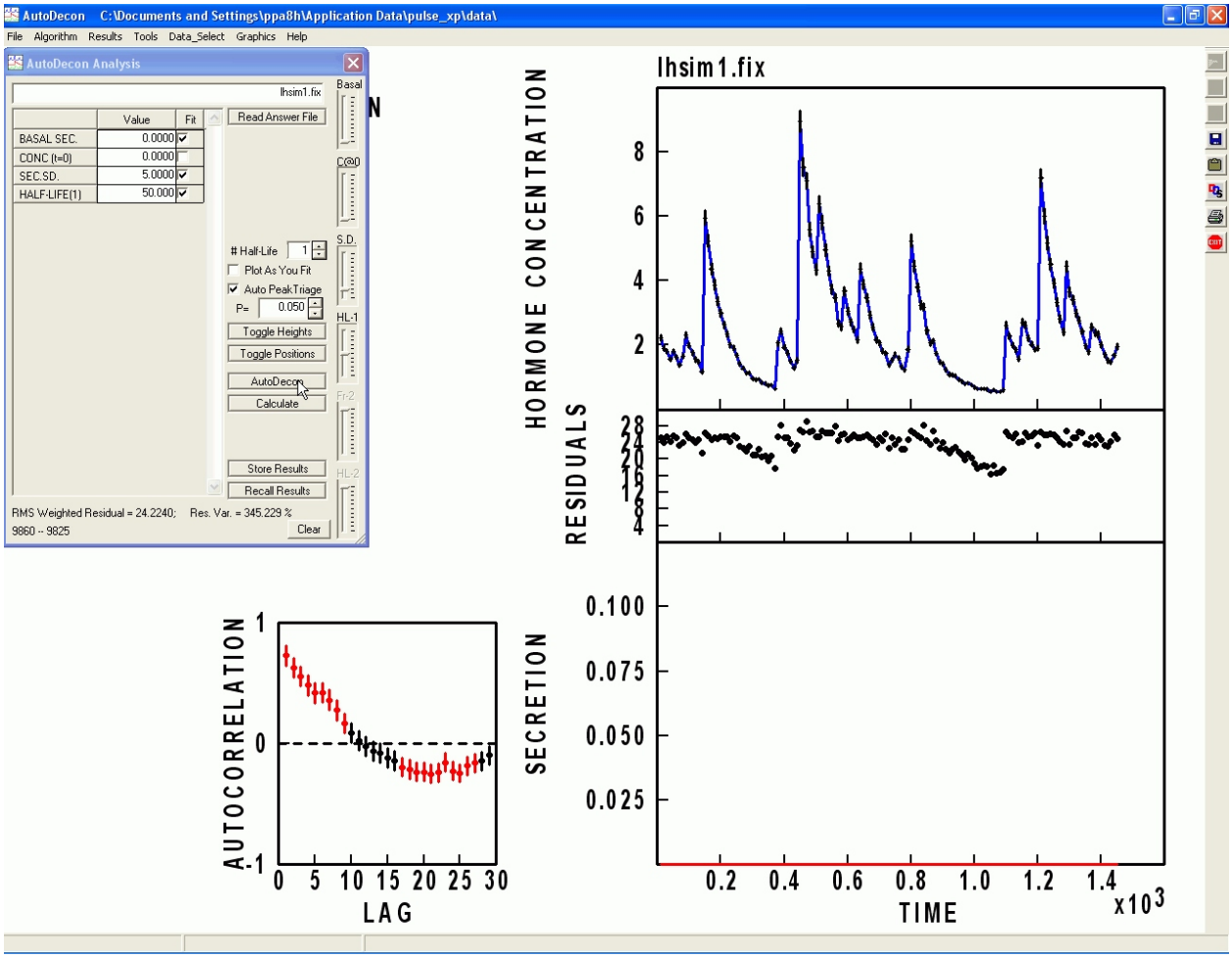


Figure 4

that these points should appear to be random once the fit has concluded. The lower right-hand graph is the actual secretion plot. Note that since there are no secretory events currently associated with the fit, there are no secretory events on this plot.

In the data grid there are several columns. The first column contains the titles of the parameters which may be currently fit: Basal Secretion, concentration at time zero, the Secretory Standard Deviation, and the Half-life(1). The next column contains the actual numeric values which correspond with the current parameters. The third column is labeled "Fit" and contains boxes which allow the user to select parameters to be varied during the upcoming fit.

Other items to note contained in the data grid include the "Read Answer File"option which allows a previously saved answer file to be read or superimposed onto the current data file. Also, the user can opt for more than one elimination half-life. The number of elimination half-lives can be varied by using the arrow adjacent to the radio box next to the half-life parameter. The default is for a single-component half-life.

The "Plot As You Fit" box remains unchecked by default as this option, when checked, allows the user to view the evolving graphic image every time the parameters are varied during a fit. This often significantly increases the time required for the completion of any particular fit. The "Toggle Heights" and "Toggle Positions" are useful when attempting to fit an entire series of estimated heights and/or positions of presumed secretory events.

Additionally, there are the options to "Store Results" and "Recall Results" for later use as well as to "Clear" the current parameters from the fit and refit the data. These tools are at times helpful and are explained in further detail in the User's Guide chapters.

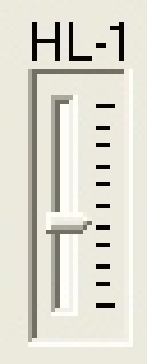


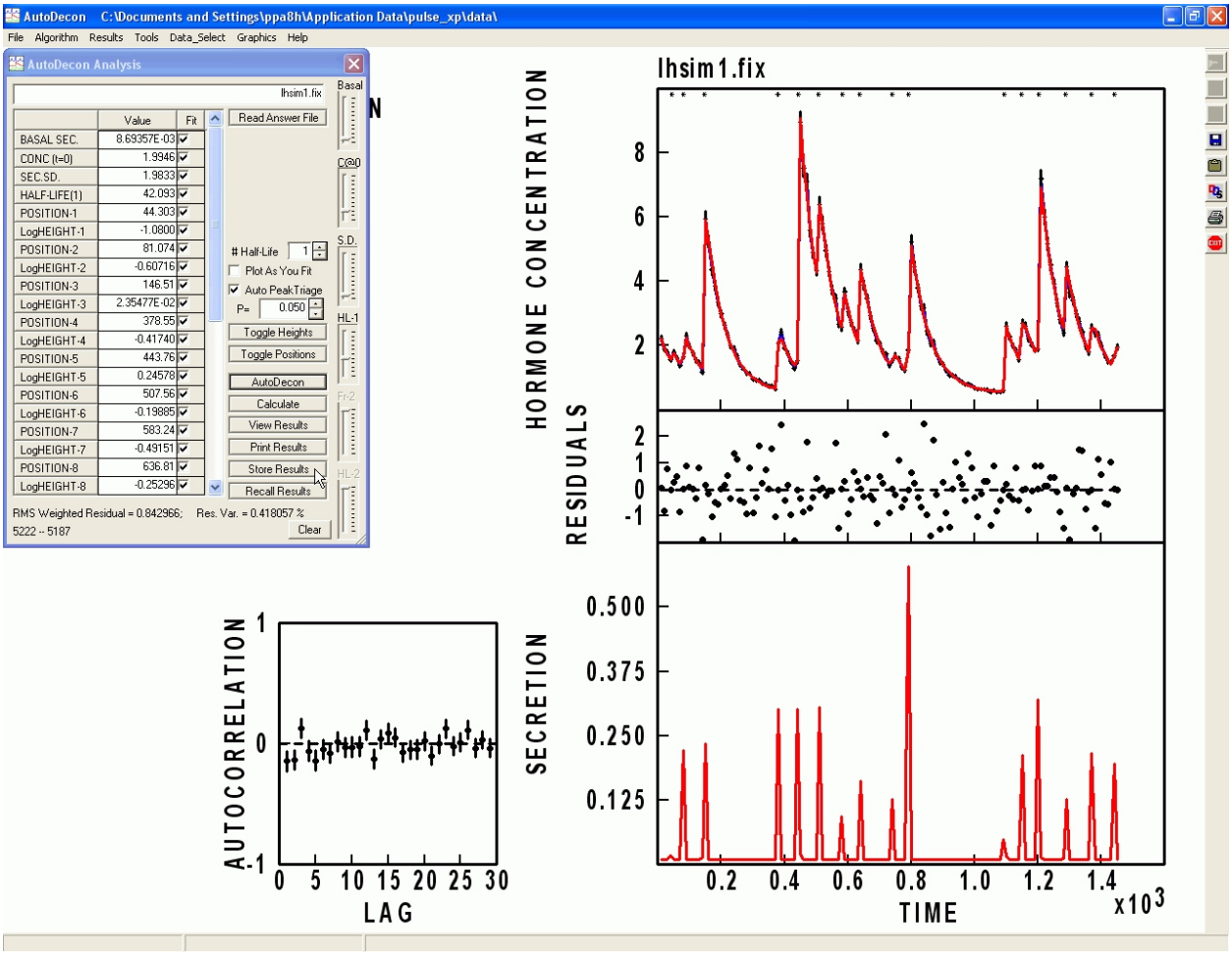
Figure 5

For the demonstration presented here of *AutoDecon* fitting a profile with no initialization file, click the boxes under the "Fit" column for the "Basal Sec.", "Sec. SD" and the "Half-Life(1)" parameters. The initialization values in the data grid are reasonable estimates for an LH data series with the secretory standard deviation being by default one-half of the sampling interval (half of ten minute sampling being 5 minutes) and the elimination half-life being approximately 50 minutes. If the values were not reasonable guesses for those parameters, the user would simply change them by clicking on the actual numeric values in the "Value" column and modifying the values or by using the sliders on the far right-hand side of the data grid (Half-life(1) shown enlarged in Figure 5). By clicking on the boxes under the "Fit" column, those parameters are marked as parameters to be varied during the subsequent fit.

To begin the fit, click on the ***AutoDecon*** box. *AutoDecon* is initialized and will calculate for several minutes or longer depending upon several factors including the density of hormone concentration data, the number of secretion events being estimated and the speed of the processor. The resultant fit is shown in Figure 6. The data grid now reflects the values for the 16 secretory events deemed statistically significant by the algorithm. The hormone concentration graph now also reflects the fitted curve (red solid line). The residuals in the middle right-hand column appear random. The secretion curve is shown in the lower right-hand panel while the autocorrelations (now all black) are in the lower left-hand side of the screen.

The results of this fit can be sent directly to the printer by clicking on "Print Results". The "View Results" box allows the user to open a text editor program where the data results may be viewed and edited. Parts of the file can be selected to highlight and print from the "View Results" box, as well.

The user can now also "Store Results" to the local data locker for use later during the same session of *AutoDecon*. Note that in order to permanently save the results to the computer's hard



drive, it is necessary to "Store Results" and then select either **File→Write A Data File→Native File** (to save the entire profile with its current fit) or **Results→Current Answers→Rename** (to save just the answer file, i.e. the basal secretion, conc @ t=0, sec. SD, half-life, positions and amplitudes).