

PULSE_XP User's Guide
Chapter 12
Gold's Deconvolution

Version 2.002

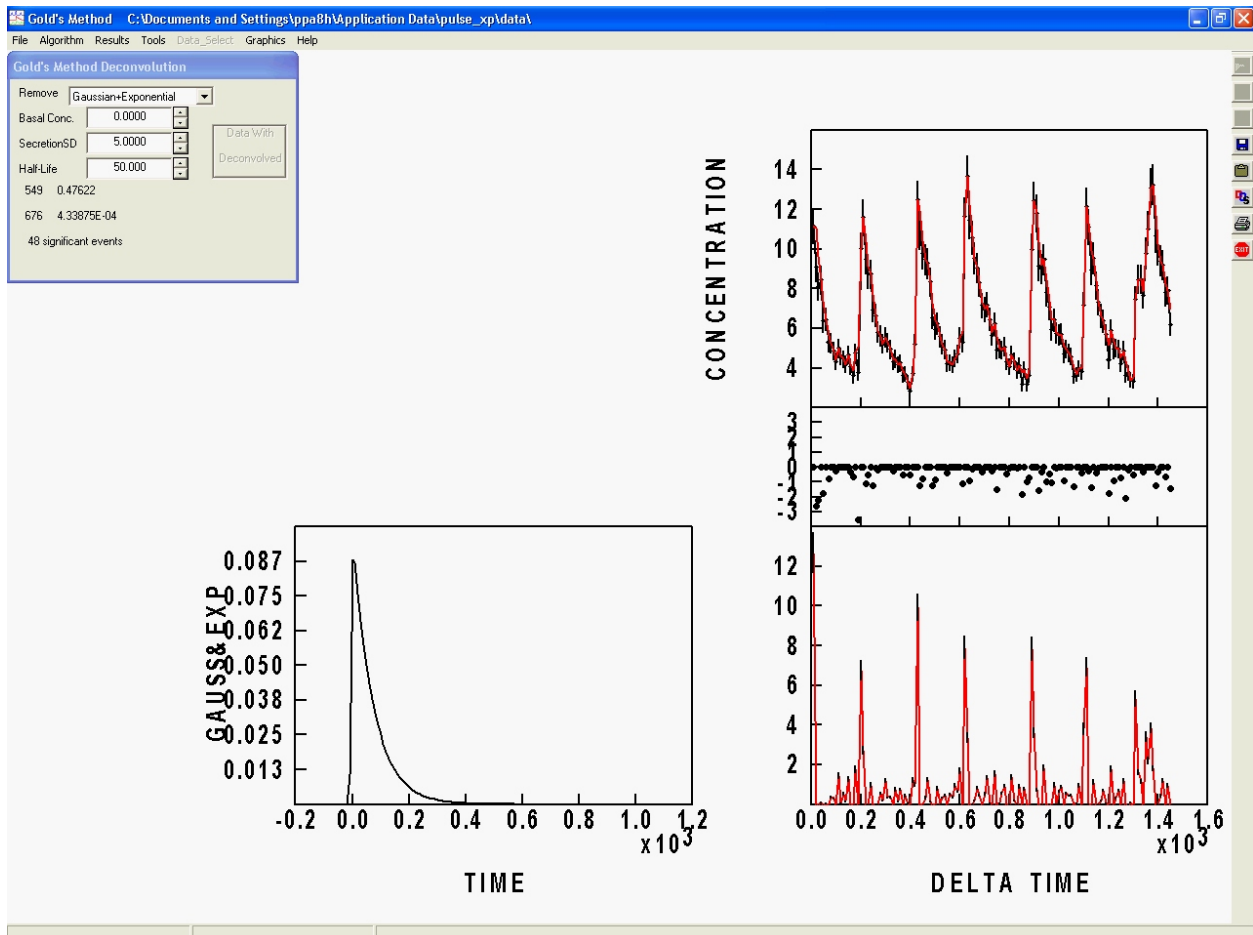
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Gold's Method Deconvolution

An early deconvolution algorithm (1964) was the Gold's method. This standard deconvolution method utilizes an iterative approach. The iterative method starts with an initial estimate and then subsequently proffers a better estimate based on the actual data. This process is repeated until the iterations do not significantly change from one cycle to the next.

Unfortunately, Gold's method does not provide a statistical basis for any presumptive secretory bursts. In addition, there is no clear method for propagating the errors inherent in the data and thus no way to provide the valid uncertainty for the secretion rates. This is the case in many deconvolution methods where there is the assumption that the data is always equally spaced in time and that there are no experimental measurement errors. Another serious flaw with the Gold's deconvolution method is that there is a requirement for a specified half-life. Additionally, Gold's Method also transmits back the same number of data points for the secretion time series as were in the original time series. Newer methods have partially addressed these shortcomings. For more reading regarding Gold's method please refer to "Deconvolution With Applications in



Spectroscopy”, Peter A. Jansson, 1984; and the newly released undergraduate textbook, “An Invitation to Biomathematics”, Raina S. Robeva, James R. Kirkwood, Robin L. Davies, Leon S. Farhy, Michael L. Johnson, Boris P. Kovatchev, & Marty Straume, 2007.

The operation of the program entails selecting the Gold’s Method and then opening a data set. By default the program will open with Gaussian+Exponential in the Remove box. There is a choice to select either Gaussian, Exponential or a combination of the two. The basal secretion is set to zero and the secretory standard deviation is determined as one-half of the sampling interval of the data. The default half-life is 50.0 minutes.

The file used in the example in Figure 1 is an LH data series sampled every 10-minutes and assayed in duplicate. Using the default values, Gold’s Method returns 48 secretory bursts. The top right hand inset depicts the hormone concentration curve with a curve superimposed. The middle right panel shows the residuals while the lower right hand figure is the returned secretion series. The lower left hand figure is the shape of the curve after selecting the Gaussian+Exponential box.