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The Pulse_XP software has evolved over the last 20-plus years primarily for the analysis of hormone pulsatility time-series data ([Installation](#), [Introduction](#), [Data File Format](#), [Frequently Asked Questions](#), [AutoDecon QuickStart](#)).

Cluster analysis ([Pub](#), [Quick Start](#), [UserGuide](#)) is still utilized by many users to locate “peaks” in hormone time-series concentration data.

We strongly recommend the **AutoDecon** algorithm ([Pub](#), [Pub2](#), [Quick Start](#), [UserGuide](#), [Tutorial](#)) over our previous deconvolution programs though we do provide a comprehensive overview to the analysis algorithms. Now included in the software is the ability to [Queue](#) data for analysis and to [Simulate](#) data for the evaluation of the ability of the algorithm to perform on the actual experimental data.

We still have several other deconvolution algorithms available for download:

Pulse analysis ([UserGuide](#)) is an our early wave-form independent algorithm which was designed with the assumption that secretory events were not Gaussian. **Pulse2** ([UserGuide](#)) is a modification of the Pulse algorithm and is both a pulse-detection and deconvolution algorithm which now includes terms for the basal secretion of the hormone.

Pulse4 ([Pub](#), [UserGuide](#)) is an automated recursive parametric deconvolution algorithm which addresses the issue of basal and pulsatile hormone secretory processes while also providing an estimate of the endogenous hormone elimination half-life.

Gold's Deconvolution Method ([UserGuide](#)) is one of the earliest (1964) deconvolution algorithms and is provided here for historical purposes.

Though our original deconvolution (**Deconv**) algorithm ([Pub](#)) is still available for use, we **strongly** recommend against its use in favor of **AutoDecon** ([Pub](#), [Pub2](#), [UserGuide](#), [Tutorial](#)) which is an automated program that inserts presumptive peaks, tests them for significance and either retains or removes them, depending upon their statistical validity.

Other algorithms included in the suite:

Approximate Entropy (ApEn) ([Pub](#), [Quick Start](#), [UserGuide](#)) analysis is utilized to quantify temporal irregularity in data.

Cross-Approximate Entropy (X-ApEn) ([UserGuide](#)) is a two-variable extension of the *ApEn* statistic.

The **Periodic** ([UserGuide](#)) algorithm is based on the assumption that the physiological signal occurs at a regular interval without assuming that the waveform is a sine or cosine wave.

Cosine analysis ([UserGuide](#)) examines both circadian and ultradian rhythms which may underlie pulsatile hormone secretion and which are assumed to be of the form of a cosine.

SRQuant ([Pub](#)) is based upon convolution integrals and tests whether several simultaneously measured input signals can be individually delayed, spread in time, transformed, combined, and discretely convolved with an elimination function to predict the time course of the concentration of an output hormone.

Concordance ([UserGuide](#)) is used to examine how much agreement there is between multiple hormone-concentration time-series data.

An accepted method by which to compare two time series has classically been that of **Cross-Correlation** ([UserGuide](#)). Correlation is used to evaluate nonrandom coincidences. The conditional probability equations utilized here assess this coupling issue. It is of utmost importance to remember that the results are difficult to interpret if there is significant auto-correlation between the series.