PULSE_XP User's Guide

Chapter 7

Approximate Entropy

ApEn

Version 2.001

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Approximate Entropy (ApEn)

Approximate Entropy (ApEn) is a fairly new statistic which was developed to quantify the orderliness of serial data. ApEn provides a statistical measure for the determination of this regularity. Approximate Entropy is a model-independent regularity measure which monitors sample-by-sample pattern irregularity. Higher ApEn values denote greater irregularity (or process randomness) while lower ApEn values indicate greater regularity or orderliness in the data. Thus, values close to zero denote a high degree of orderliness in the data while higher values nearer to 1.0 indicate a great degree of disorderliness.

Approximate Entropy is complementary to the pulse-detection algorithms in that it evaluates both dominant and subordinate patterns in the data. ApEn can detect changes in underlying episodic behavior which may not be reflected in peak occurrences or amplitudes and provides an explicit barometer of feedback system changes in coupled systems.

Note that ApEn is scale-dependent meaning that "getting more data" does not necessarily enhance the results. For example, if the expected pattern is approximately one minute, then sampling every 1 second will mask that pattern and be of little use. A sampling interval closer or equal to one minute would be the appropriate interval.

ApEn assigns a non-negative number to a time series, with larger values corresponding to greater apparent serial irregularity in the hormone release patterns over time. ApEn is from a two-parameter family of statistics (m and r) with m being the length of compared runs and r the filter width. These two parameters (m and r) must be specified to compute approximate entropy, which then measures the logarithmic likelihood that runs in the patterns that are close (within r) for m contiguous observations remain close (within the same tolerance with r) on the next incremental comparisons. The r value used for the various endocrine hormone profiles is generally 20%.

ApEn is performed on individual hormone concentration time-series. Normalizing r to each time-series SD gives approximate entropy a translation in scale and variance. The distribution of "random" maximal ApEn values is determined by 1,000 random shuffles of ordered sample values within a given time series. Thus, the ApEn of each "observed" (unshuffled) data series is also evaluated as a mean ratio of the observed-to-random ApEn and also as a calculated z-score (number of SD's) removed from the maximally random ApEn.

For a more in-depth understanding of Approximate Entropy, we recommend reading: *Pincus SM, 1991, Approximate entropy as a measure of system complexity. Proc Natl Acad Sci USA; 88: 2297-301.*and *Veldhuis JD, Johnson ML, Veldhuis OL, Straume M, and Pincus SM, 2001, Impact of Pulsatility on the Ensemble Orderliness (Approximate Entropy) of Neurohormone Secretion. Am J Physiol. Integr. Comp. Physiol. Regul., 281, R1975-R1985.*

Execution of ApEn

As with the other programs in this suite, ApEn can be executed several ways: 1) by clicking on **Algorithm→ApEn** after the program has already been opened (as shown in Figure 1); 2) by double-clicking on the Desktop icon of pulse_xp and then double-clicking on the ApEn icon; or 3) by using the Windows "start" menu and selecting the pulse_xp program suite and then scrolling up to the ApEn icon.

Figure 1

As with the other programs, a data file must always be read into the program from under **File→Read a Data File→*.fix** before the analysis can begin. We have again selected the data series Set1.fix for the example presented in this guide.

Figure 2 shows the data grid for the Approximate Entropy statistic. The data series name is on the top line. The first box is labeled "First Difference Detrend". If the user checks this box, the data will be first-differenced - meaning that any underlying trend in the data will be removed before the analysis begins. This is not the method which we recommend. The next box is labeled "Use R as a Fraction of the Data's SD" and should remain checked. Under the R value column, the default of 0.20000 or 20% and will generally remain that value. The number of Monte Carlo Cycles (MC Cycles) here is 10,000. This value needs not be changed either before performing the analysis.

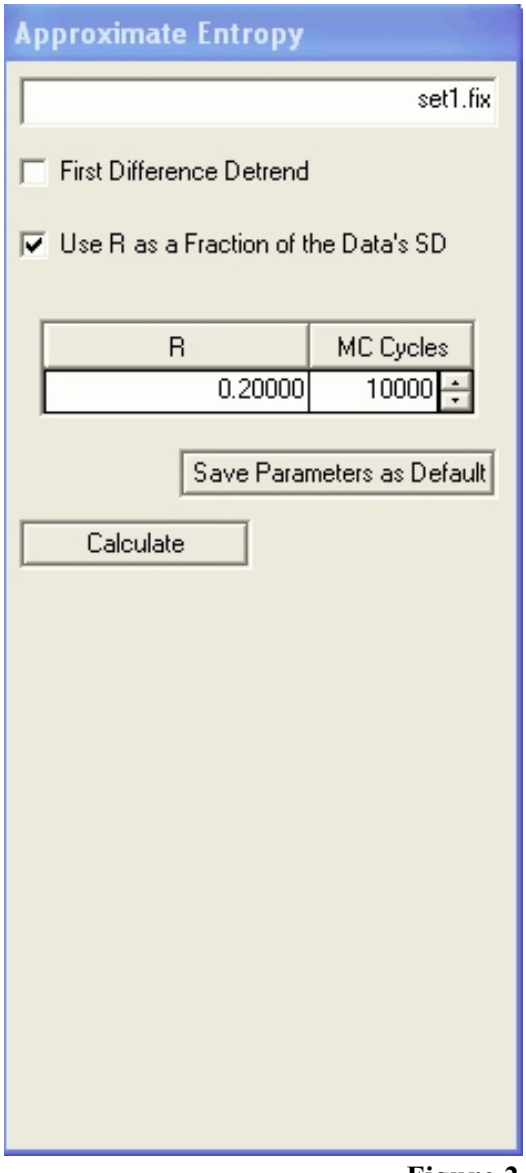

Figure 2

"Save Parameters as Default" allows the user to save the current selection of parameters for upcoming sessions of Hormone.exe. Note that even if the current parameters are "saved" as the default values, they can always be changed again during any upcoming analyses.

For our example here, set1.fix, we will go ahead and click on the **Calculate** box. This calculation could take a few seconds (depending on the speed of your processor) as there are going to be 10,000 MC Cycles performed on the data.

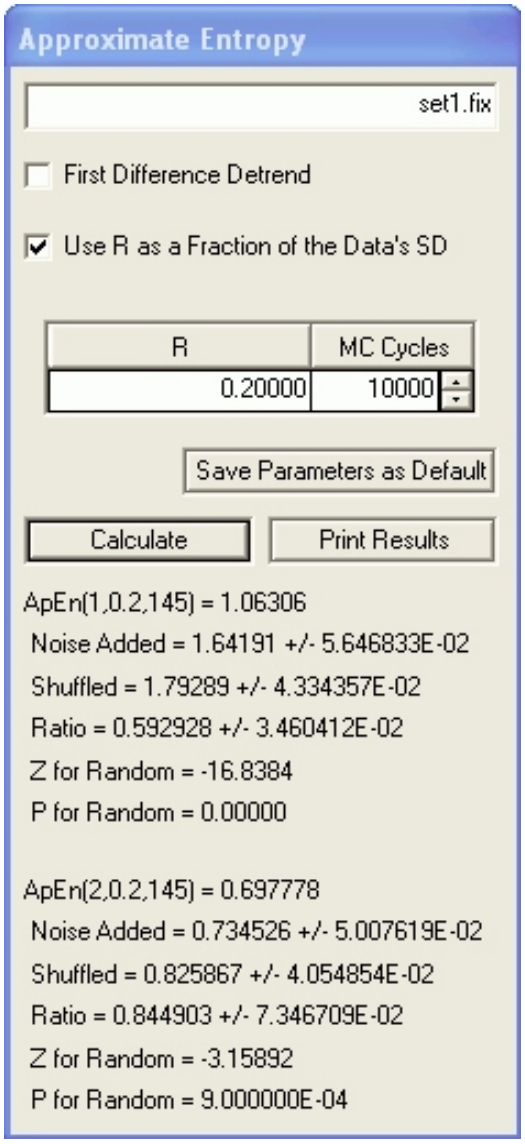

Figure 3

Figure 3 depicts the data grid after the calculations have concluded. The results are printed directly under the **Calculate** and **Print Results** boxes. The ApEn(1,20%,145) is presented first. Its actual value is 1.06306. Summarized next is the Noise Added and the Shuffled ApEn value as well as the ApEn Ratio and the *Z* score for the Random ApEn. Also provided is the *P* value for the Random ApEn.

ApEn(2,20%,145) results are provided for the user in the same format just below the ApEn(1) results.

By clicking on **Print Results**, the user can have a hard copy of these results.

If there is a clear reason to analyze the data after first detrending it, check the box next to "First Difference Detrend" and then click on **Calculate**. Again, this analysis will undoubtedly take several seconds to conclude. When the calculations are complete, a screen as shown in Figure 4 will be depicted. These results are just the 1st-differenced results and can also be printed.

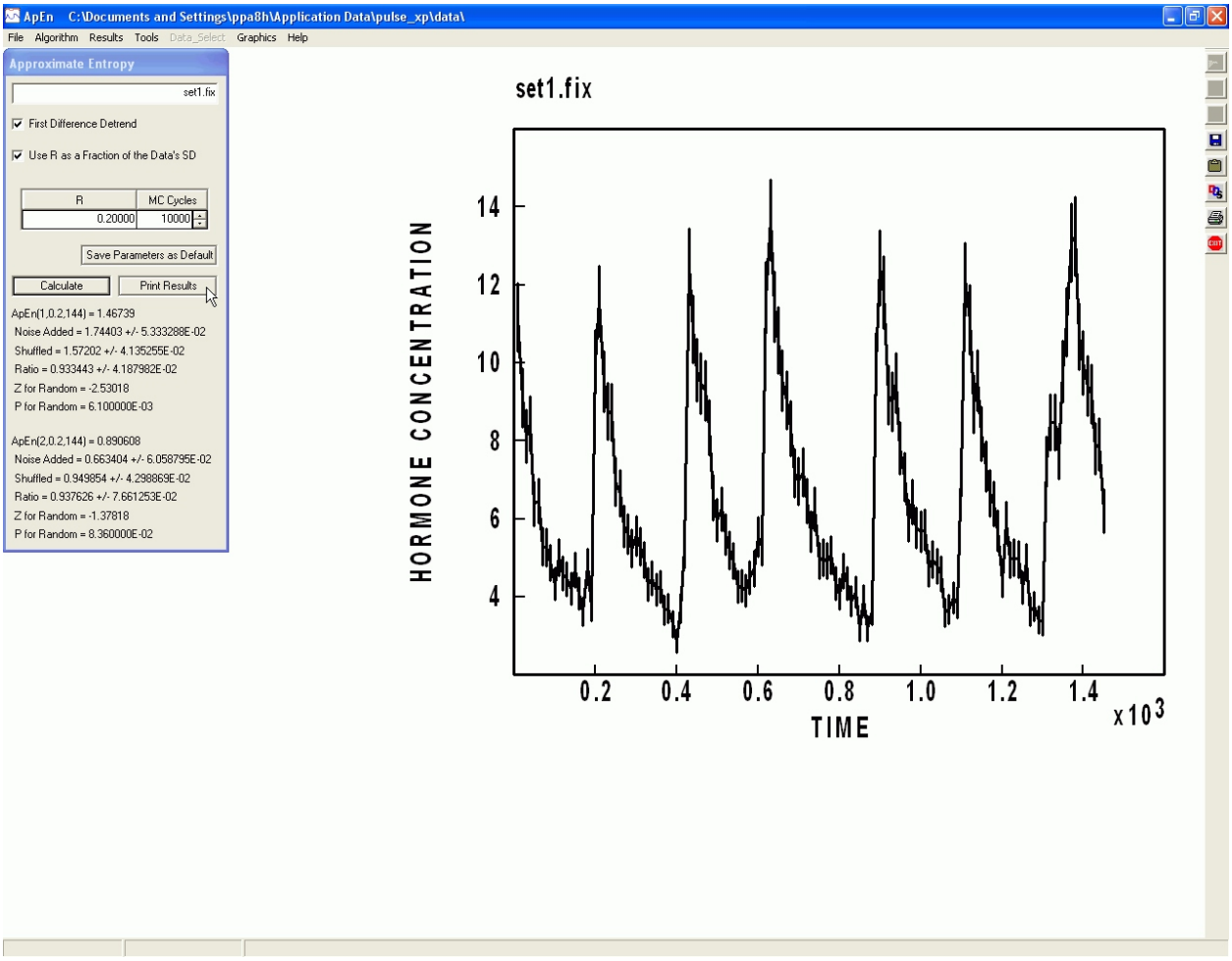
ApEn C:\Documents and Settings\ppa8h\Application Data\pulse_xp\data\
File Algorithm Results Tools Data_Select Graphics Help
Approximate Entropy
set1.fix
First Difference Detrend
Use R as a Fraction of the Data's SD
R
MC Cycles
0.20000
10000
Save Parameters as Default
Calculate
Print Results
ApEn(1,0.2,144) = 1.46739
Noise Added = 1.74403 +/- 5.333288E-02
Shuffled = 1.57202 +/- 4.135255E-02
Ratio = 0.933443 +/- 4.187982E-02
Z for Random = -2.53018
P for Random = 6.100000E-03
ApEn(2,0.2,144) = 0.890608
Noise Added = 0.663404 +/- 6.058795E-02
Shuffled = 0.949854 +/- 4.298869E-02
Ratio = 0.937626 +/- 7.661253E-02
Z for Random = -1.37818
P for Random = 8.360000E-02
set1.fix
HORMONE CONCENTRATION
14
12
10
8
6
4
0.2
0.4
0.6
0.8
1.0
1.2
1.4
TIME
x10 3

Figure 4