

PULSE_XP User's Guide
Chapter 10
X-ApEn

Version 2.002

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Cross-Approximate Entropy (X-ApEn)

Cross-Approximate Entropy is a recently developed analysis statistic which is a two-variable extension of the ApEn statistic. X-ApEn is a lag-, scale- and model-independent measure of two-signal synchrony which provides a quantifiable distinction of both feedforward and feedback control mechanisms without having to determine the precise underlying processes. X-ApEn uses the same “m” and the “r” which are found in the approximate entropy statistic. The “r” of 0.200 is the default and generally accepted as the correct value for this parameter. This value can be modified by the user, though.

Serial hormone concentration time series data are utilized to assess X-ApEn. Two series of data must be read into the Hormone program before the analysis may be performed. For the example provided here, two simulated growth hormone data sets [ghsim1.fix and ghsim2.fix] have been selected. After the appropriate data series have been read into the software, select **Algorithm** → X-

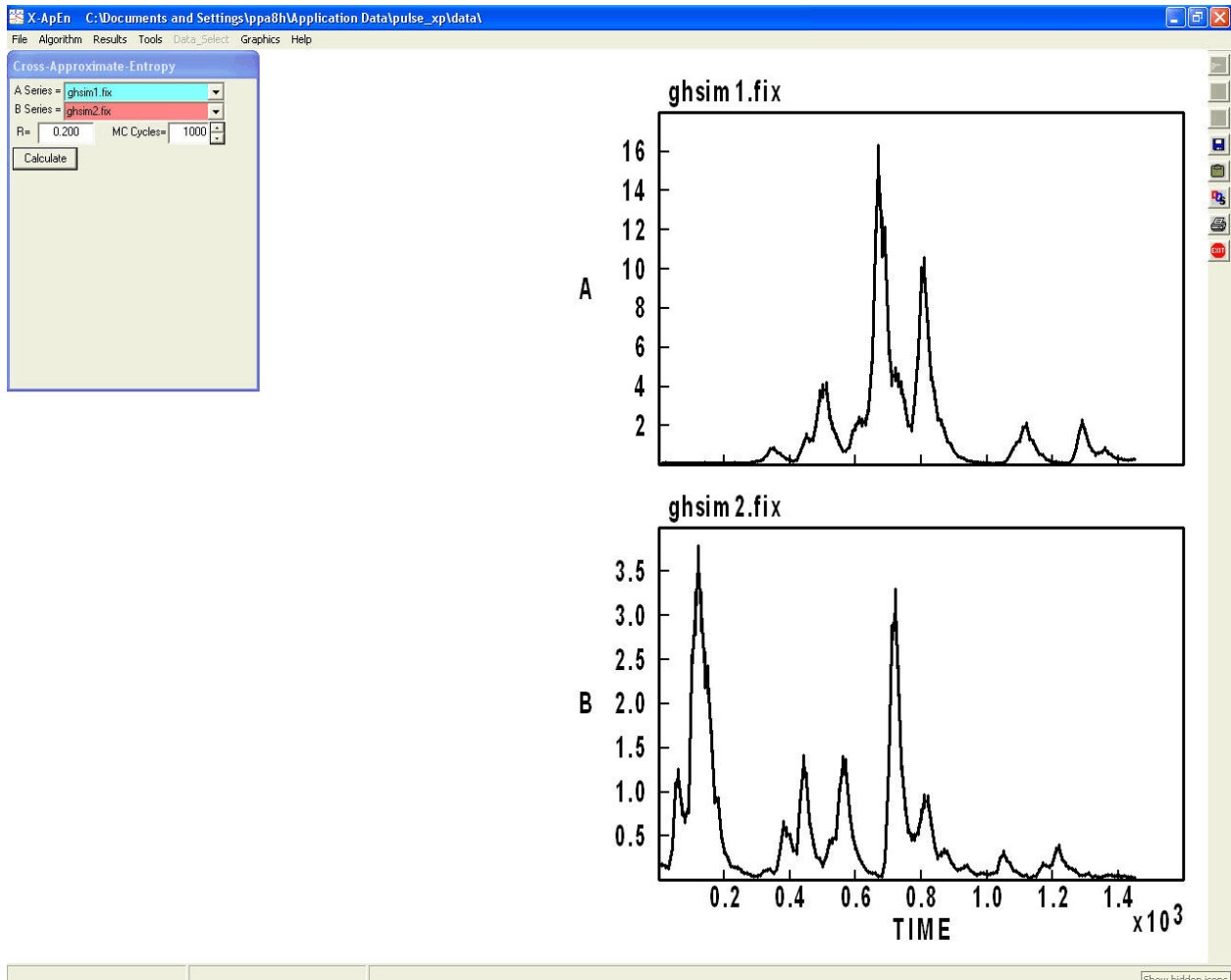


Figure 1

ApEn. A screen as seen in Figure 1 will be displayed. It is very important to mention that the order of the selected files for analysis is very important for this statistic. The analysis of A file versus B file will not yield the same results as opting for B file versus A file.

Once the files are selected and in the proper order, the user must simply click on **Calculate** to perform the cross-approximate entropy calculations. The results are provided in the dialog box on the top right-hand side of the screen. The graphic output as shown in Figure 2 is given at values 0, 1, and 2 for the m value.

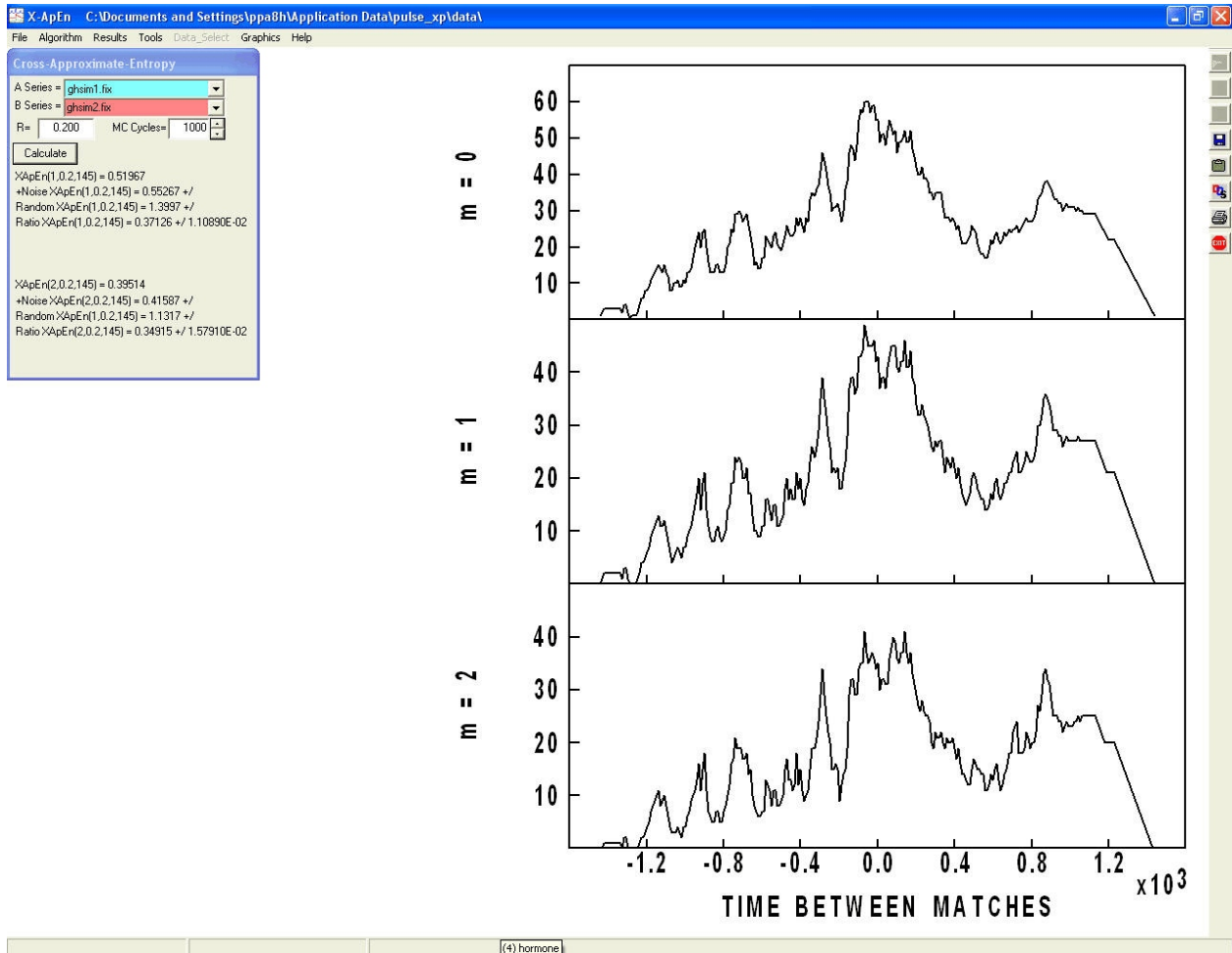


Figure 2