

## Comment on “Multiscale Entropy Analysis of Complex Physiologic Time Series”

The purpose of this Comment is to show that the recently introduced multiscale entropy (MSE) approach [1], while aiming at measuring entropy at different scales, measures both variation and entropy.

The MSE algorithm is based on the application of approximate entropy (AE) [2] or sample entropy (SE) [3] for different scales of the same process. AE and SE are measures of regularity (orderliness) in serial data and are based on two input parameters: the sequence length  $m$  and the tolerance level  $r$ . The output of these algorithms provides a likelihood measure that two sequences within tolerance level  $r$  remain close at the next point. The smallest values of entropy correspond to perfectly regular sequences. AE and SE increase as  $r$  decreases, because the criterion for sequence matching becomes more stringent [3].

The MSE algorithm introduces an idea of using AE and SE measures for changing scale,  $\tau$ , where  $\tau = 1, 2, \dots$ . Coarse-grained sequences are reconstructed as follows: The original sequence of length  $N$  is divided into segments of length  $\tau$ , and the mean value is calculated for each segment creating coarse-grained sequences of length  $N/\tau$ . This is basically similar to smoothing and decimation of the original sequences. Therefore variation, expressed here as a standard deviation (SD), will decrease at each increase of  $\tau$  according to the statistical properties of the original time series. However, in the MSE approach the same  $r$  value [4] is used for different scales. Therefore, the changes in MSE on each scale will depend on both the regularity and variation of the coarse-grained sequences. The fundamental difference between these entropy measures and variation is due to the fact that AE and SE are sensitive to the order of samples in the sequence, but variation is not. Therefore, the outcome of the MSE algorithm does not allow one to make a clear conclusion as to what extent this separation is based on the affected regularity or variation.

We provide simulations on white noise and  $1/f$  noise as it was performed in [1]. Figure 1(a) shows an outcome of the proposed MSE algorithm, and it is identical to the data presented by the authors. Additional information is provided on how variation (SD) changes with the scale [Fig. 1(b)]. Figure 1(b) shows that the scale-related changes in SD for  $1/f$  noise are much smaller than for white noise. Expectedly, it also means that  $r$  increases for white noise as the scale increases, which in turn should lead to changes in entropy values. To demonstrate the effect of variation at each scale, we performed the MSE algorithm with  $r$  calculated for SD at each scale [Fig. 1(c)]. The reason for the discrepancy between

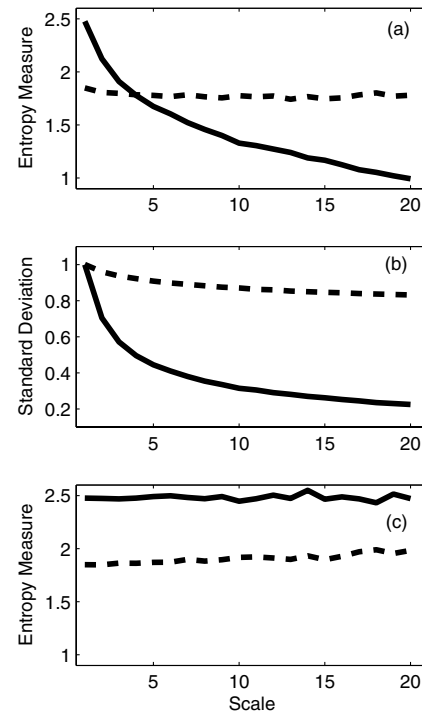


FIG. 1. (a) MSE analysis of white noise (solid line) and  $1/f$  noise (dashed line),  $r$  is fixed for all scales. (b) Standard deviations (as a measure of variation) at each scale for the processes presented in (a). (c) The same as in (a) but now  $r$  is calculated for each scale separately.

Figs. 1(a) and 1(c) is that in the modified MSE approach  $r$  is adjusted according to the changes in variation.

Vadim V. Nikulin and Tom Brismar  
Karolinska Institutet  
Department of Clinical Neuroscience  
Clinical Neurophysiology  
Karolinska University Hospital, R2:01  
SE-17176 Stockholm, Sweden

Received 6 June 2003; published 27 February 2004

DOI: 10.1103/PhysRevLett.92.089803

PACS numbers: 87.80.Tq, 05.45.Tp

- [1] M. Costa, A. L. Goldberger, and C.-K. Peng, *Phys. Rev. Lett.* **89**, 068102 (2002).
- [2] S. M. Pincus, *Proc. Natl. Acad. Sci. U.S.A.* **88**, 2297 (1991).
- [3] J. S. Richman and J. R. Moorman, *Am. J. Physiol. Heart Circ. Physiol.* **278**, H2039 (2000).
- [4] For demonstration purposes, sample entropy is used as in Ref. [1]. Parameters are  $r = 0.15 \times \text{SD}$  and  $m = 2$ ,  $N = 30\,000$  (SD is calculated for the original sequences). To facilitate comparison between different data sets, original sequences were normalized to have  $\text{SD} = 1$ .