

ERRATUM

Erratum to: Testing pattern synchronization in coupled systems through different entropy-based measures

Peng Li · Chengyu Liu · Xinpei Wang ·
 Liping Li · Lei Yang · Yongcai Chen ·
 Changchun Liu

Published online: 3 April 2013
 © International Federation for Medical and Biological Engineering 2013

Erratum to: Med Biol Eng Comput DOI 10.1007/s11517-012-1028-z

Owing to a clerical error, the distance between two vectors was defined incorrectly for multivariate multiscale sample entropy (MMSE) in Table 1. The results and conclusion of our simulation was, however, unaffected because our simulation applied the correct definition, which is given below. For clarity, we give below the whole description of MMSE as in Table 1. The place where the mistake came in is shown in bold. We apologize for this oversight and for any confusion that it has caused.

For p -variate normalized sequences $\{y_{k,j} : k = 1, 2, \dots, p; j = 1, 2, \dots, N\}$ and a scale factor ε ($1 \leq \varepsilon \leq E$), coarse grain each series by $x_{k,i}^\varepsilon = \frac{1}{\varepsilon} \sum_{i=(j-1)\varepsilon+1}^{j\varepsilon} y_{k,j}$, $1 \leq j \leq \lfloor \frac{N}{\varepsilon} \rfloor$. Form $X_m^\varepsilon(i) = \{x_{1,i}^\varepsilon, x_{1,i+\tau_1}^\varepsilon, \dots, x_{1,i+(m_1-1)\tau_1}^\varepsilon, x_{2,i}^\varepsilon, x_{2,i+\tau_2}^\varepsilon, \dots, x_{2,i+(m_2-1)\tau_2}^\varepsilon, \dots, x_{p,i}^\varepsilon, x_{p,i+\tau_p}^\varepsilon, \dots, x_{p,i+(m_p-1)\tau_p}^\varepsilon\} = \{z_i^\varepsilon, z_{i+1}^\varepsilon, \dots, z_{i+m-1}^\varepsilon\}$ for each ε , where $\mathbf{M} = \{m_1, m_2, \dots, m_p\}$ and $\boldsymbol{\tau} = \{\tau_1, \tau_2, \dots, \tau_p\}$ is the embedding

vector and the time lag vector, respectively, $m = \sum_{k=1}^p m_k$, $i = 1, 2, \dots, N^\varepsilon - n$, $n = \max\{\mathbf{M}\} \times \max\{\boldsymbol{\tau}\}$ and $N^\varepsilon = \lfloor \frac{N}{\varepsilon} \rfloor$ which is the sequence length at scale ε . **The distance between two vectors is defined as:**

$$d\{X_m^\varepsilon(i), X_m^\varepsilon(j)\} = \mathbf{max}_{l=1}^m \left\{ \left| z_{i+l-1}^\varepsilon - z_{j+l-1}^\varepsilon \right| \right\}.$$

Denote $B_i^{\varepsilon,m}(r)$ the average number of j that $d[X_m^\varepsilon(i), X_m^\varepsilon(j)] \leq r, j \neq i$. Extend the dimensionality of the embedding vector from m_k to $m_k + 1$ and thus $p \times (N^\varepsilon - n)$ vectors $X_{m+1}^\varepsilon(i)$ are obtained and calculate $B_i^{\varepsilon,m+1}(r)$ as the average number of j that $d[X_{m+1}^\varepsilon(i), X_{m+1}^\varepsilon(j)] \leq r, j \neq i$. Then MMSE is defined by:

$$\text{MMSE}(\mathbf{M}, \boldsymbol{\tau}, r, \varepsilon) = -\ln \left(\left(\frac{1}{p(N^\varepsilon - n)} \sum_{i=1}^{p(N^\varepsilon - n)} B_i^{\varepsilon,m+1}(r) \right) / \left(\frac{1}{N^\varepsilon - n} \sum_{i=1}^{N^\varepsilon - n} B_i^{\varepsilon,m}(r) \right) \right).$$

The online version of the original article can be found under doi:10.1007/s11517-012-1028-z.

P. Li · C. Liu · X. Wang · L. Yang · Y. Chen · C. Liu (✉)
 School of Control Science and Engineering, Shandong
 University, 17923 Jingshi Road, Jinan 250061,
 People's Republic of China
 e-mail: lskyp@mail.sdu.edu.cn; changchunliu@sdu.edu.cn

L. Li
 Biomedical Engineering, College of Science and Technology,
 Shandong University of Traditional Chinese Medicine,
 Daxue Road, Jinan 250355, People's Republic of China