

Comment on “Network analysis of human heartbeat dynamics” [Appl. Phys. Lett. 96, 073703 (2010)]

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Comment on “Network analysis of human heartbeat dynamics” [Appl. Phys. Lett. 96, 073703 (2010)]

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In a recent paper,¹ Zhi-Gang Shao constructed the associated networks of time series of human heartbeat interval based on the visibility algorithm,² and analyzed the statistical properties of associated networks of human heartbeat dynamics. With the filtered data of five healthy subjects and five patients with congestive heart failure (CHF) in Ref. 4, the author claimed that the assortative coefficient³ of associated networks can be used to distinguish the healthy subjects from the CHF patients, which, however, fails working as the indicator as we present below in this comment with larger data sets.

The databases⁴ used in Ref. 1 are MIT-BIH normal sinus rhythm database⁵ (nsrdb, including 18 healthy subjects) and BIDMC CHF Database⁶ (chfdb, including 15 CHF subjects). Not limited to the data of five healthy subjects and five CHF patients studied in Ref. 1 of these two databases, first we get

the original heartbeat time series of 15 healthy subjects and 15 CHF patients using the WFDB softpackage,⁴ and also use the NGUESS software⁴ to remove the outliers and obtain the “filtered” time series from the nsrdb and chfdb, including all the data of Ref. 1. Then, we generate the associated networks with the visibility algorithm² and calculate their assortative coefficients.³ The length of the time series is set to be 10 000. As shown in Fig. 1, the associated networks of healthy and CHF heartbeat interval do not show very clear difference of their assortativity mixing, and even in the case of the filtered data as those of Ref. 1, the assortative coefficients of such associated networks generated by the healthy and CHF data are more difficult to distinguish.

Note that the length of time series is an important factor to affect the connectivity structures of generated associated networks with the visibility algorithm, whose assortative

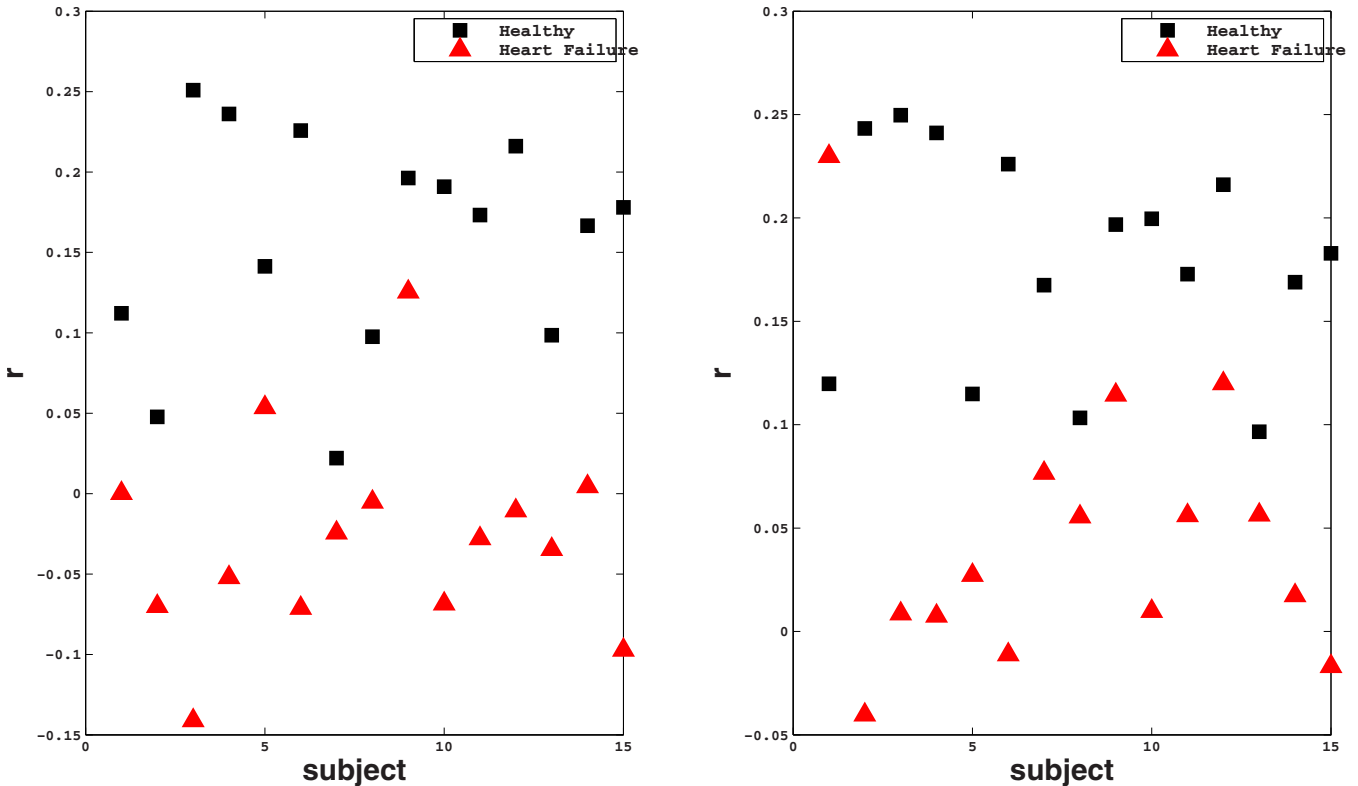


FIG. 1. (Color online) The assortative coefficient r of the associated networks for (left) the original time series of the heartbeat interval and (right) the “filtered” time series from the nsrdb and the chfdb. The length of each time series is 10 000.

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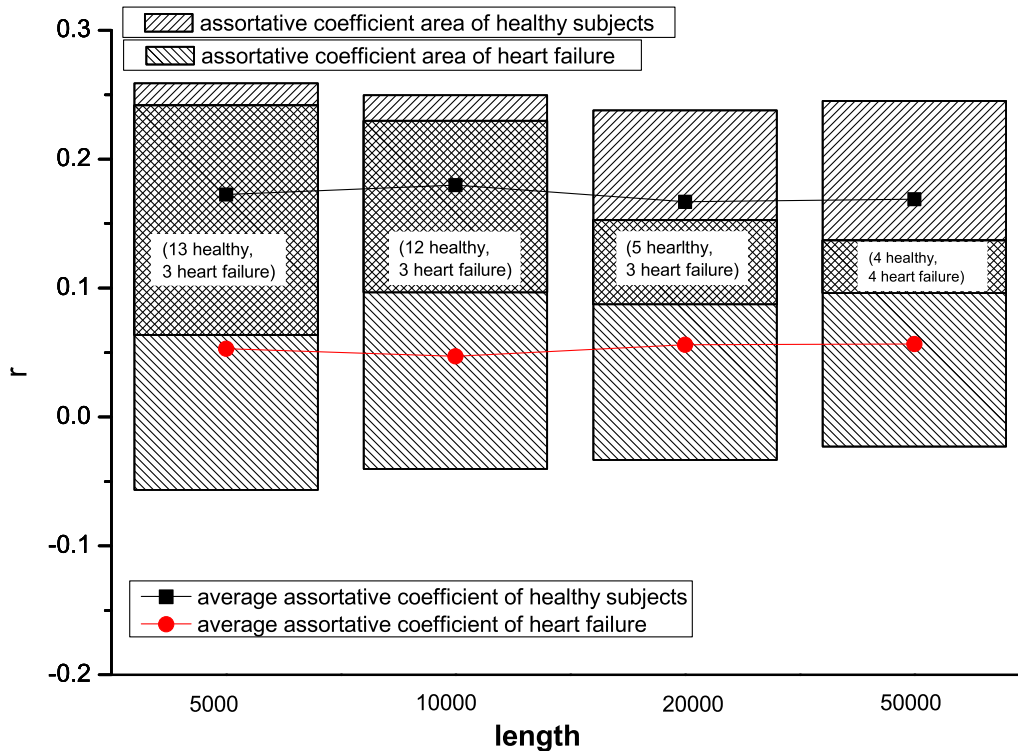


FIG. 2. (Color online) The assortative coefficient r of the associated networks constructed from the “filtered” time series of 15 healthy subjects and 15 CHF subjects in Fig. 1 with the time series length of 5000, 10 000, 20 000, and 50 000, respectively.

degree-mixing patterns may differ significantly. We further calculate the assortativity coefficients of heartbeat networks generated by the filtered time series of the fifteen healthy subjects and the fifteen CHF subjects with the length of 5000, 10 000, 20 000, and 50 000, respectively, and observe the distributions of the assortativity coefficients in the cases of such four lengths. As shown in Fig. 2, the distributed areas of assortativity coefficients of the healthy subjects’ networks all overlap with those of the CHF subjects’ networks, while in the case of length of 50 000, the overlap area between the healthy subjects and the CHF subjects is the smallest among all investigated four lengths. Besides, there are totally 13, 12, 5, and 4 healthy subjects and 3, 3, 3, and 4 CHF subjects in the corresponding overlap areas when the time series length is 5000, 10 000, 20 000, and 50 000, respectively.

Therefore, we do not agree with the conclusion in Ref. 1 that the assortative coefficient of associated networks could distinguish between healthy subjects and patients with congestive heart failure without claiming the dependence of the sampled length of time series, on the contrary, with the illus-

trations in this comment we conclude that the assortative coefficients of such associated heartbeat networks fail working as an effective indicator to identify healthy subjects from patients with congestive heart failure at large.

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