Data Availability Statement: All codes and the datasets are available at https://github.com/Korosh137/MDEA.git (accessed on) or upon request to K.M.

Modified Diffusion Entropy Analysis (MDEA)

In the MDEA technique, the first step is to project the data of each channel onto the interval [0,1] by normalizing each time series by the total time interval of the dataset. This enables the processing of each time series to be directly compared. The data profile over the unit interval is then divided into parallel stripes (Figure A1a, ECG data). (The inset in the figure displays what the events would look like when the stripe size is 0.1. Note that a slowly varying feature of the data trace would have relatively few events well-spaced in time. However, a sharply peaked feature would have a large number of closely spaced events.) Next, the events are extracted by defining them as unit amplitude pulses if the signal at that time is in a different stripe with respect to its previous value (Figure A1b) and zero if it remains in the same stripe. Using the time series of the extracted events, we create a diffusion trajectory (Figure A1c), i.e., the cumulative sum of the events in Figure A1b. The statistics of a single diffusion trajectory (blue curve in Figure A1c) are determined by selecting a window size w and partitioning the diffusion trajectory into many pieces, each starting from an event. By initiating all the segments from an event, they can all be shifted to start from a common origin (Figure A1d). Finally, we evaluate the ensemble distribution of histograms at a given time (Figure A1e) because the events are statistically independent.

To make the statistics of the single time-series diffusion trajectory correspond to that performed in the MDEA processing of the data, we pick a window size τ and slice the empirical signal into many pieces, each of length $w = \tau$ and start from an event (panel d). By shifting all the slices to start from this origin, we evaluate the distribution of trajectories at time τ (panel e). Denoting the probability density function for different window sizes as $P(x, \tau)$, we can define the SW entropy as follows:

$$S(\tau) = -\int dx P(x,\tau) \log_2 P(x,\tau) \quad \text{(A1)}$$

Assuming that $P(x, \tau)$ is the probability density function corresponding to window size τ, we can define the diffusion entropy using the SW entropy as being the information contained in the time series. Using the scaling probability density function, without knowing the $F(.)$ function, the deviation of the SW entropy from its reference state defined by the unknown function is

$$\Delta S(\tau) \equiv S(\tau) - S_{ref} = \delta \ln \tau \quad \text{(A2)}$$

Consequently, if a graph of the SW entropy for an empirical process versus the logarithm of the time yields a curve with a positive slope, which we interpret to be the scaling index δ.

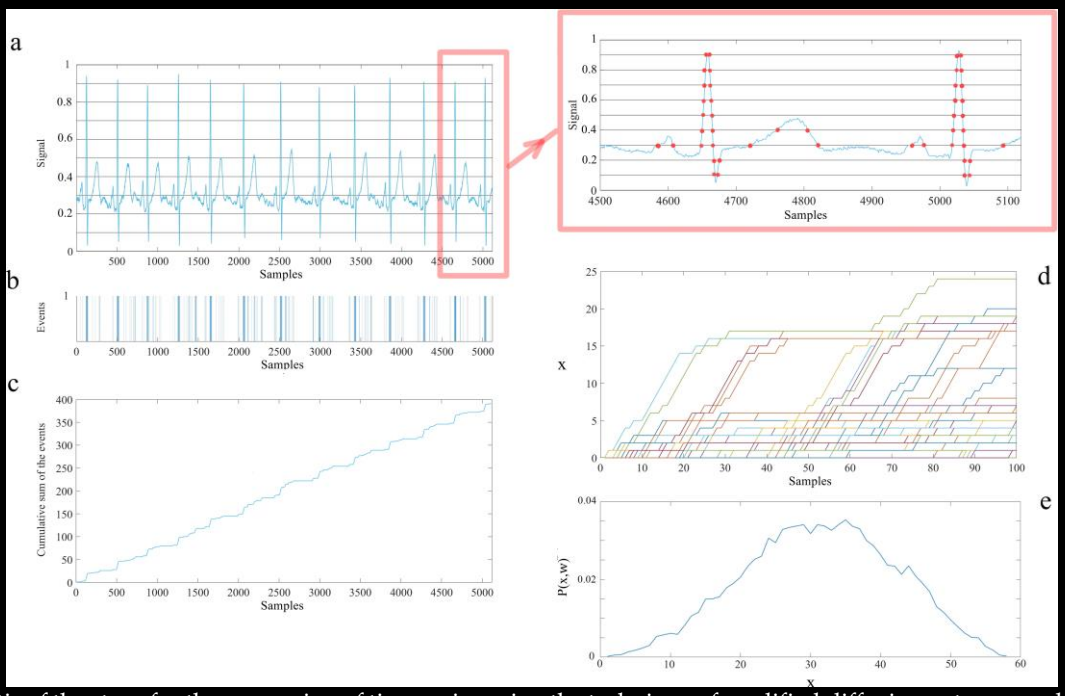

Figure A1. A schematic of the steps for the processing of time series using the technique of modified diffusion entropy analysis. Panel (**a**): The blue curve is the heart rate signal which is projected onto the interval [0, 1] and then divided to the stripe size of 0.1, which is magnified in the inset. Note that sharply peaked features in the ECG have a cluster of events in (**b**), whereas a sloping feature has well-spaced events; see the inset for a visual verification of this explanation. The horizontal lines define the stripes. Panel (**b**): The events (represented as distinct separated unit amplitude pulses) are extracted from the passage of the continuous blue curve from one stripe to others. Panel (**c**): The diffusion trajectory made by the cumulative summation of the events of panel (**b**). The vertical lines show a selected set of windows with a size of 100 that sliced the diffusion trajectory. Panel (**d**): The partitioned trajectories of panel (**c**) shifted to initiate each trajectory from a common origin and terminate each after a time w, the length of the window. Panel (**e**): The histogram of the position of the trajectories at the end of the windows (to create this histogram we used 60 s of data and a stripe size of 0.01). Taken from [1] with permission.

1. Mahmoodi, K.; Kerick, S.E.; Grigolini, P.; Franaszczuk, P.J.; West, B.J. Complexity synchronization: A measure of interaction between the brain, heart and lungs. Sci. Rep. 2023, 13, 11433.
2. West, B.J.; Grigolini, P.; Kerick, S.E.; Franaszczuk, P.J; Mahmoodi, K. Complexity synchronization of organ networks. Entropy. 2023 28;25(10):1393.