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Assessment of complexity and dynamical coupling between complex systems using Entropy Rate and Mutual Information Rate Measures: simulations and application to physiological data

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The human organism has been recently described, according to the "Network Physiology" approach, as a complex integrated network composed of multi-component organ systems continuously interacting through various feedback mechanisms to provide homeostatic balance and to react to external stimuli or intrinsic physiological alterations [1]. The dynamical behaviour of a complex system and its pairwise interactions with another system can be respectively evaluated using information-theoretic measures of Entropy Rate (ER) and Mutual Information Rate (MIR). In particular, ER has been widely employed to assess the complexity of a random process, related to nonregularity and unpredictability of its dynamics [2]. On the other hand, MIR is a dynamic measure of the non-directed symmetric interrelationships between coupled systems, and can be expressed as the sum of the individual ERs of the two processes minus their joint entropy rate [3]. Thanks to their suitability for describing short-length data with strong stochastic and noisy components, such measures are of great interest for the practical analysis of physiological time series [2,3].

In this work, after defining the theoretical formulation of ER and MIR dynamical measures, different approaches for their estimation are compared: a linear model-based estimator relying on Gaussian data, two model-free estimators based on discretization of the variables carried out either via uniform quantization through binning or rank ordering through permutations, and a model-free estimator based on direct computation of the differential entropy via k-nearest neighbor searches. The various estimators are first validated and compared on simulated univariate and coupled dynamic systems, including linear autoregressive or mixed non-linear deterministic and linear stochastic dynamics processes. Then, the framework is applied to different datasets of real-world time series describing the dynamics of coupled biomedical physiological systems, including physiological variability series descriptive of cardiovascular and cardiorespiratory interactions assessed at rest and during physiological stress or during controlled breathing conditions.

Our results evidence that statistically significant and physiologically meaningful patterns of the ER and MIR measures can be achieved in the analyzed datasets with a proper selection of the estimation parameters. Simple and fast approaches based on linear parametric or permutation-based model-free estimators allow efficient discrimination of changes in the short-term evolution of complex dynamic systems, while computationally expensive nearest-neighbour method achieves more reliable results in presence of non-linear dynamics [2,3].

References

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