Mutual Information Rate Decomposition as a Tool to Investigate Coupled Dynamical Systems: Estimation Approaches, Simulations and Application to Physiological Signals

The use of information-theoretic measures applied to bivariate time series is becoming more and more popular for the characterization of coupled dynamical systems. In this context, the mutual information rate (MIR) is a long-known measure of the interaction between two random processes mapping the evolution over time of coupled systems. However, while this measure can be reliably computed from bivariate linear models fitting the observed time series, it is much harder to quantify if the model assumptions need to be relaxed for the study of nonlinear coupled dynamics.

In this work, we present a framework for the computation of the MIR between two random processes X and Y, expressed equivalently as the sum of the individual entropy rates of X and Y minus their joint entropy rate, or as the sum of the transfer entropies from X to Y and from Y to X plus the instantaneous information shared by the processes at zero lag. After defining the theoretical formulation of the framework, different approaches for the estimation of each dynamic measure composing the MIR are provided: the linear model-based estimator relying on Gaussian data; two model-free estimators based on discretization, performed via uniform quantization through binning or rank ordering through permutations; a model-free estimator based on direct computation of the differential entropy via k-nearest neighbor searches.

The four estimators are first extensively validated and compared on simulations of coupled dynamic systems, including linear vector autoregressive processes and nonlinear chaotic maps (coupled logistic and Henon maps, Roessler-Lorenz system). Then, the framework is applied to different datasets of real-world time series describing the dynamics of coupled biomedical physiological systems, including blood oxygen level dependent signals mapping resting-state brain hemodynamics and physiological variability series descriptive of cardiovascular, cardiorespiratory, and cerebrovascular interactions assessed at rest and during physiological stress. Both in simulated and physiological systems, the significance of the MIR and each of its constituent terms is assessed by means of surrogate data analysis, to validate statistically the presence of coupled dynamics and to determine which MIR terms determine the coupling.

Our results show that, with careful selection of the estimation parameters, statistically significant and physiologically meaningful patterns of the MIR and of its components can be achieved in the analyzed datasets. While the model-free estimators elicit specific coupling patterns in chaotic dynamics, the linear estimator highlights comparable trends in most of the analyses of physiological time series.

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