Topological modelling of complex time-dependent systems

Matteo Rucco[1], Marco Piangerelli[1], Emanuela Merelli[1], Rocio Gonzalez-Diaz[2], Nieves Atienza[2], and Maria-Jose-Jimenez[2]

[1] JSchool of Science and Technology, Computer Science Division,University of Camerino, Italy
[2] Depto. Matematica Aplicada I, E.T.S.I. Informatica, Universidad de Sevilla, Spain

Complex time-dependent dynamical systems are generally composed by a huge number of heterogeneous interacting components, and the time-dependent behaviour of the whole system (global) is not just the linear composition of the behaviours of the components (local). Thus, a model of a complex dynamical system can be obtained only by entangling the local and the global behaviours. Among the others, we claim that topology is the right tool for obtaining simultaneously both local and global information. Topology is the branch of mathematics that allows to study shapes and maps among them. Topological data analysis techniques are used for completing the data produced by a complex systems to higher dimensional structures, the so-called simplicial complexes. Simplicial complexes allow to identify new n-ary relations among data that otherwise cannot be pinpointed out. More formally and commonly, a complex network is used for dealing with classical 2-bodies problem, even in case of a system formed by a huge number of interacting components. Simplicial complexes are used for extending the 2-bodies problem to the n-bodies problem, e.g. a 2-dimensional simplicial complex is a filled triangle and it represents the simultaneous interaction of 3 entities. This interaction can be observed if and only if the shape of the triangle is preserved, it means that the triangle can not be decomposed to a collection of 3 edges. A possible global description of a simplicial complex is obtained by homology. Roughly speaking, homology is an algebraic machinery that describes a simplicial complex by counting the number of n-d holes, and in a combinatorial setting we deal with persistent homology instead of classical homology. In order to extract new insights from persistent homology new statistics have been defined, one among the other is known as persistent entropy. There are several techniques for building simplicial complexes from data and for computing persistent homology, in this work we refer to the Clique Weight Rank Persistent Homology. CWRPH starts from a network representation of the complex systems and it completes the networks to the simplicial complexes by using the clique complexes, then it computes persistent homology. The first novelty of our work is a stability theorem for comparing the persistent entropy computed over a collection of time-dependent clique complexes. The second novelty is that we take into account also co-homoloy theory. Co-homology is dual to homology and it provides a local description of simplicial complexes. Briefly, co-homology helps to identify the most important simplices: the removal of these simplices changes dramatically the homology of the whole systems and subsequently the persistent entropy. From a modelling point of view this corresponds to identify the most important set of components of the complex systems and their higher dimensional relationships.We apply the two novelties for modelling two case studies: the immune system and the epilepsy.