Biological networks are formal models that store data and encode molecular interactions in a cell. They help to characterize biological entities and their interaction patterns. One type of biological network is the metabolic network which represent the set of metabolic pathways. Metabolic pathways are a series of chemical reactions, in which the product from one reaction serves as the input to another reaction. Many pathways remain incompletely characterized, and in some of them not all enzyme components have been identified. As well, many other biological network interactions have not been completely identified. Thus, better models to predict metabolic pathways and biological networks are one of the major challenges of computational biology. Machine learning is an area of computer science where models can be developed to predict behaviors based on “learned” data. Machine learning methods, such as Artificial Neural Network (AAN), Bayesian Networks (BN), Support Vector Machine (SVM) and Kernel Methods (KM), have been used in bioinformatics to predict biological networks.

In this talk, we firstly describe some of the biological network representation, machine learning methods and their applications. Secondly, we introduce a new method, as a combination of kernels and SVM methods, to predict metabolic networks. This method is based on a new kernel framework, called Pairwise Rational Kernels (PRKs), which manipulates pairs of sequence data, as pairwise combinations of rational kernels. Thus, sequence data related to the metabolic networks are represented as automata and finite-state transducers, to obtain rational kernels. Using SVMs and PRKs, new interactions of the metabolic network can be predicted. These methods can also be used to predict other biological interactions, as well as other networks where pair of sequence (or text) data are involved, e.g., social networks.

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