

Editorial

Petra Perner

Institute of Computer Vision and Applied Computer Sciences, IBAI, Germany

This issue deals with two innovative topics: the computerized optimization of Telemedicine process [1] and a computerized knowledge representation of the landscape of RNA folding structures [2].

In the first paper discrete event models are used to model the logistics and medical diagnosis in a Telemedicine process that is characterized by a dynamic chain of interaction between the patient, the medical doctor, and the laboratory's. The amount of logistics involved in telemedicine process is estimated in order to find the optimum scheduling of medical procedure. This should result in an efficient diagnosis, treatment for patients, and for medical staff to save time, energy and to respect the environment. A new Markov chain model, based on a Petri net support, is proposed for modeling causal relations between the factors that determines the necessity and opportunity of using telemedicine diagnostic procedures, for estimating the probability of both their occurrence and impact on human health. Markov chain models and Petri nets have been chosen since they can model the dynamic nature of the knowledge involved in such a Telemedicine process. Performance metrics for the different diagnosis models of data flow were also defined and lead to an optimal selection the right diagnosis model.

The description of RNA folding landscape by Basin Hopping Graph (BHG) as described in the second paper gives a new knowledge representation of these types of molecules. RNA folding is the process by which a linear ribonucleic acid (RNA) molecule acquires secondary structure through intra-molecular interactions. The folded domains of RNA molecules are often the sites of specific interactions with proteins in forming RNA protein (ribonucleoprotein) complexes. The Basin Hopping Graph is a novel model for the representation and description of the RNA folding structure.

The paper gives the computing algorithm of barrier tree based on the BHG, the experimental results in Rfam13.0 and PseudoBase indicate that the algorithm is more effective, as the algorithm deals with innovative types of pseudoknots in RNA folding structure, and analyze their possible transitions between types of pseudoknots. The proposed knowledge representation will be the basis for more advanced reasoning processes over RNA molecules.

Leipzig, March 2020

Petra Perner

References

1. Calin Cuifudean, Modeling the Risks of Telemedicine Diagnosis, TRANSACTIONS ON MASS-DATA ANALYSIS OF IMAGES AND SIGNALS Volume 10, Number 1, September 2019, p. 3-18, P-ISSN1868-6451, E-ISSN 2509-9353.
2. Zhendong Liu, Gang Li, and Patrick Wang, The Computing Algorithm of Barrier Tree Based on the Basin Hopping Graph in RNA Structure, TRANSACTIONS ON MASS-DATA ANALYSIS OF IMAGES AND SIGNALS, Volume 10, Number 1, September 2019, p. 19-29, P-ISSN1868-6451, E-ISSN 2509-9353.