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Reconstruction and Analysis of Cancer specific Gene Regulatory Networks from Gene Expression Profiles

Khalid Raza^{1*} and Rajni Jaiswal²

¹Department of Computer Science, Jamia Millia Islamia (Central University),

New Delhi-110025, India.

²Department of Computer Science, Jamia Hamdard, New Delhi-110062, India

ABSTRACT

The main goal of Systems Biology research is to reconstruct biological networks for its topological analysis so that reconstructed networks can be used for the identification of various kinds of disease. The availability of high-throughput data generated by microarray experiments fuelled researchers to use whole-genome gene expression profiles to understand cancer and to reconstruct key cancer-specific gene regulatory network. Now, the researchers are taking a keen interest in the development of algorithm for the reconstruction of gene regulatory network from whole genome expression profiles. In this study, a cancer-specific gene regulatory network (prostate cancer) has been constructed using a simple and novel statistics based approach. First, significant genes differentially expressing them self in the disease condition has been identified using a two-stage filtering approach t-test and fold-change measure. Next, regulatory relationships between the identified genes has been computed using Pearson correlation coefficient. The obtained results has been validated with the available databases and literatures. We obtained a cancer-specific regulatory network of 29 genes with a total of 55 regulatory relations in which some of the genes has been identified as hub genes that can act as drug target for the cancer diagnosis.

KEYWORDS

Gene regulatory network, microarray analysis, prostate cancer, differentially expressed genes

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Application of three graph Laplacian based semisupervised learning methods to protein function prediction problem

Loc Tran

University of Minnesota

Abstract:

Protein function prediction is the important problem in modern biology. In this paper, the un-normalized, symmetric normalized, and random walk graph Laplacian based semi-supervised learning methods will be applied to the integrated network combined from multiple networks to predict the functions of all yeast proteins in these multiple networks. These multiple networks are network created from Pfam domain structure, co-participation in a protein complex, protein-protein interaction network, genetic interaction network, and network created from cell cycle gene expression measurements. Multiple networks are combined with fixed weights instead of using convex optimization to determine the combination weights due to high time complexity of convex optimization method. This simple combination method will not affect the accuracy performance measures of the three semi-supervised learning methods. Experiment results show that the un-normalized and symmetric normalized graph Laplacian based methods perform slightly better than random walk graph Laplacian based method for integrated network. Moreover, the accuracy performance measures of these three semi-supervised learning methods for integrated network are much better than the best accuracy performance measures of these three methods for the individual network.

Keywords:

semi-supervised learning, graph Laplacian, yeast, protein, function

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Anti-Synchronizing Backstepping Control Design for Arneodo Chaotic System

Sundarapandian Vaidyanathan¹

¹Research and Development Centre, Vel Tech Dr. RR & Dr. SR Technical University

Avadi, Chennai-600 062, Tamil Nadu, INDIA

ABSTRACT

In this paper, we derive new results for backstepping controller design for the anti-synchronization of Arneodo chaotic system (1980). Backstepping control is a recursive procedure that combines the choice of a Lyapunov function with the design of a feedback controller. In anti-synchronization of chaotic systems, the states of the synchronized systems have the same absolute values, but opposite signs. First, we derive an active backstepping controller for the anti-synchronization of identical Arneodo chaotic systems. Next, we derive an adaptive backstepping controller for the anti-synchronization of identical Arneodo chaotic system, when the system parameters are unknown. The anti-synchronization results for Arneodo chaotic systems have been proved using Lyapunov stability theory. Numerical simulations have been shown to illustrate the backstepping controllers derived in this paper for Arneodo chaotic system.

KEYWORDS

Backstepping Control; Chaos; Anti-Synchronization; Arneodo System

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An Efficient PSO Optimized Integration Weight Estimation Using D-prime Statistics for A Multibiometric System

S. M. Anzar¹ and P. S. Sathidevi²

**¹Department of Electronics & Communication Engineering, National Institute of Technology,
Calicut, India, 673601**

**²Department of Electronics & Communication Engineering, National Institute of Technology,
Calicut, India, 673601**

ABSTRACT

The efficiency of a multibiometric system can be improved by weighting the scores obtained from the degraded modalities in an appropriate manner. In this paper, we propose an efficient PSO (Particle Swarm Optimization) based integration weight optimization scheme using d-prime statistics to determine the optimal weight factors for the complementary modalities, under different noise conditions. Instead of treating the weight estimation process from an algebraic point of view, an attempt is made to consider the same from the principles of linear programming techniques. The performance of the proposed method is analysed in the context of fingerprint and voice biometrics using sum rule of fusion. The d-prime statistics of fingerprint and voice modalities are measured and the integration weights are computed as the ratio of these two statistics. The computed d-prime ratio is then optimized against the recognition accuracy. The optimizing parameter is estimated in the training/validation phase using Leave-One-Out Cross Validation (LOOCV) technique. Experimental studies show that the proposed method improves recognition rate under normal operating conditions and reduces the FAR (False Acceptance Rate) considerably even at extreme low SNR (Signal to Noise Ratio) conditions. The proposed biometric solution can be easily integrated into any multibiometric system with score level fusion. Moreover, it finds extremely useful in applications where there are less number of available training samples.

KEYWORDS

Multibiometric System, Integration Weight, d-prime Statistics, Particle Swarm Optimization, Robustness

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Gene Expression Mining for Predicting Survivability of Patients in Earlystages of Lung Cancer

Shoon Lei Win, Zaw Zaw Htike, Faridah Yusof, Ibrahim A. Noorbatcha

Faculty of Engineering, IIUM, Kuala Lumpur, Malaysia

ABSTRACT

After numerous breakthroughs in medicine, microbiology, and pathology in the past century, lung cancer still remains as a leading cause of cancer-related death even in the developed countries. Lung cancer accounts roughly for 30% of all cancer-related deaths in the world. Diagnosis and treatments are still based on traditional histopathology. It is of paramount importance to predict the survivability of patients in early stages of lung cancer so that specific treatments can be sought. Nonetheless, histopathology has been shown by previous studies to be inadequate in predicting lung cancer development and clinical outcome. The microarray technology allows researchers to examine the expression of thousands of genes simultaneously. This paper describes a state-of-the-art machine learning based approach called averaged one-dependence estimators with subsumption resolution to tackle the problem of predicting whether a patient in early stages of lung cancer will survive by mining DNA microarray gene expression data. To lower the computational complexity, we employ an entropy-based gene selection approach to select relevant genes that are directly responsible for lung cancer survivability prognosis. The proposed system has achieved an average accuracy of 92.31% in predicting lung cancer survivability over 2 independent datasets. The experimental results provide confirmation that gene expression mining can be used to predict survivability of patients in early stages of lung cancer.

KEYWORDS

Lung cancer, survivability prediction; microarray gene expression

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Adaptive Control and Synchronization of a Generalized Lotka-Volterra System

Sundarapandian Vaidyanathan¹

¹Research and Development Centre, Vel Tech Dr. RR & Dr. SR Technical University

Avadi, Chennai-600 062, Tamil Nadu, INDIA

ABSTRACT

The Lotka-Volterra equations are a system of equations proposed to provide a simplified model of two-species predator-prey population dynamics. In this paper, we investigate the problem of adaptive chaos control and synchronization of a generalized Lotka-Volterra system discovered by Samardzija and Greller (1988). The Samardzija-Greller model is a two-predator, one-prey generalization of the Lotka-Volterra system. First, adaptive control laws are designed to stabilize the generalized Lotka-Volterra system to its unstable equilibrium point at the origin based on the adaptive control theory and Lyapunov stability theory. Then adaptive control laws are derived to achieve global chaos synchronization of identical generalized Lotka-Volterra systems with unknown parameters. Numerical simulations are shown to validate and demonstrate the effectiveness of the proposed adaptive control and synchronization schemes for the generalized Lotka-Volterra system.

KEYWORDS

Adaptive Control, Stabilization, Chaos Synchronization, Generalized Lotka-Volterra Chaotic System

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Improvement of the Fingerprint Recognition Process

Farah Dhib Tatar¹ And Mohsen Machhout²

¹Department of Electrical Engineering, National School of the Studies of Engineer of Tunis, Tunisia

²Faculty of Sciences of Monastir, Monastir, Tunisia

ABSTRACT

The increased development of IT tools and social communication networks has significantly increased the need for people to be identified with reliable and secure tools hence the importance of using biometric technology. Biometrics is an emerging field where technology improves our ability to identify a person. The advantage of biometric identification is that each individual has its own physical characteristics that cannot be changed, lost or stolen. The use of fingerprinting is today one of the most reliable technologies on the market to authenticate an individual. This technology is simple to use and easy to implement. The techniques of fingerprint recognition are numerous and diversified, they are generally based on generic algorithms and tools for filtering images.

This article proposes a fingerprint recognition chain by highlighting improved processing tools to facilitate data retrieval. The results are retrieved and validated using Matlab.

KEYWORDS

Fingerprint, Biometrics, Images Processing, Minutiae, Matlab

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Survey on Modelling Methods Applicable to Gene Regulatory Network

Chanda Panse¹ and Dr. Manali Kshirsagar¹

¹Department of Computer Technology, Yeshwantrao Chavan College of Engineering, Nagpur, India

¹Department of Computer Technology, Yeshwantrao Chavan College of Engineering, Nagpur, India

ABSTRACT

Gene Regulatory Network (GRN) plays an important role in knowing insight of cellular life cycle. It gives information about at which different environmental conditions genes of particular interest get over expressed or under expressed. Modelling of GRN is nothing but finding interactive relationships between genes. Interaction can be positive or negative. For inference of GRN, time series data provided by Microarray technology is used. Key factors to be considered while constructing GRN are scalability, robustness, reliability and maximum detection of true positive interactions between genes. This paper gives detailed technical review of existing methods applied for building of GRN along with scope for future work.

KEYWORDS

Gene Regulatory Network, Microarray, robustness, scalability, reliability

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Sliding Mode Controller Design for The Global Chaos Synchronization of Rucklidge Chaotic Systems

Sundarapandian Vaidyanathan¹

¹Research and Development Centre, Vel Tech Dr. RR & Dr. SR Technical University Avadi,
Chennai-600 062, Tamil Nadu, INDIA

ABSTRACT

This paper describes the design of sliding mode controller for the global chaos synchronization of identical Rucklidge chaotic systems (Rucklidge, 1992). Rucklidge chaotic system is one of the paradigms of threedimensional chaotic systems. The stability results derived in this paper for the complete synchronization of the identical Rucklidge chaotic systems via sliding mode control are established using Lyapunov stability theory. Since the Lyapunov exponents are not required for these calculations, the sliding mode control method is very effective and convenient to achieve global chaos synchronization of Rucklidge chaotic systems. Numerical simulations are presented to demonstrate the effectiveness of to the synchronization schemes derived in this paper for the identical Rucklidge chaotic systems.

KEYWORDS

Sliding Mode Control, Chaos Synchronization, Chaotic Systems, Rucklidge Systems..

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A Survey on Recent Trends in Human-Computer Interaction

Srinivas Koppu¹, V. Madhu Viswanatham² and Kamalakannan J¹

¹ **School of Information Technology and Engineering, VIT University, Vellore, India,**

² **School of computing Science and Engineering VIT University, Vellore, India**

ABSTRACT

This paper identifies the different kinds of methods, which helps human to communicate with computer. Traditionally the user interacting with computer via command line or GUI or common hand-held devices such as mouse and keyboard which is not feasible for a handicapped or a blind or a mute people. In order to interact with computer, the good interface required, the interface is sub part of human computer Interaction (HCI). HCI not only software design, it also concentrates on design of hardware devices. Describe the interaction between Brain and Computer based on EEG patterns. Brain generates EEG signal Based upon that system has to act and it has to perform tasks like human in real world. Thus the research work that is proposed would be to build a human to computer interaction through EEG signal. The system that allow the user to interact directly brain to computer based EEG signal and no need to use any input device to interact with any type of systems such as computer , TV's. This way the computer system can reduce the man work needed to feed information into the system by a large extent.

KEYWORDS

EEG signal, Brain Computer Interface (BCI), Human Computer Interaction (HCI), Speech Recognizer, Neural Networks, Cognitive Science.

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