QLM3.3.2

NUMBER OF BOOKS AND CHAPTERS IN EDITED VOLUMES/BOOKS PUBLISHED AND PAPERS PUBLISHED IN NATIONAL/ INTERNATIONAL CONFERENCE PROCEEDINGS PER TEACHER DURING LAST FIVE YEARS

3.3.2.1. Total number of books and chapters in edited volumes/books published and papers in national/ international conference proceedings year wise during last five years

Year	2022	2021	2020	2019	2018
Number	01	02	03	04	01

Sl. No.	Year of Publication	Name of the teacher	Title of the book/chapters published	Title of the paper	Title of the proceedings of the conference	Name of the publisher
1	2022	Preeti Nand Kumar	Techniques and Innovation in Engineering Research	Use of Alternative Raw meterial and pulp blending improves the strength properties of Pulp and Paper.		**BPI Publishing House**
2	2021	Dr Dillip Dash	Advances in Data Science and management	Linguistics information for decision making using SVM	Proceedings of ICDSM 2021	Springer
3	2021	Sambit Kumar Mishra, Zdzislaw Polkowski, Samarjeet Borah, **Ritesh Dash**	AI in Manufacturing and Green Technology: Methods and Applications	A Review on Nearest-Neighbor and Support Vector Machine Algorithms and Its Applications		CRC Press,taylor and francis
4	2020	Dr Archana Chowdhury		Migration in multi-population differential evolution for many objective optimization	IEEE World Congress on computational Intelligence (WCCI), 2020	Elsevier
5	2020	G.P. Khuntia, **R. Dash,** S.C. Swain, Prashant Bawaney		A Hybrid Time Series Forecasting Method Based on Supervised Machine Learning Program	Advances in Data Science and Management. Lecture Notes on Data Engineering and Communications Technologies, vol 37. Springer, Singapore	Springer
6	2020	.G.P.Khuntia, R. Dash, S.C. Swain, **Prashant Bawaney**		A Hybrid Time Series Forecasting Method Based on Supervised Machine Learning Program	Advances in Data Science and Management. Lecture Notes on Data Engineering and Communications Technologies, vol 37. Springer, Singapore	Springer

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7	2019	R. Paul, A. K. Giri, R. Dash, A. Dewangan, S. Chandra Swain and Prashant Bawaney		SPV Grid Interconnection with Current Controller Techniques	Innovations in Power and Advanced Computing Technologies (i-PACT), Vellore, India, 2019	doi: 10.1109/i-PACT44901.2019.8960108
8	2019	R. Paul, A. K. Giri, R. Dash, A. Dewangan, S. Chandra Swain and Prashant Bawaney		SPV Grid Interconnection with Current Controller Techniques	Innovations in Power and Advanced Computing Technologies (i-PACT), Vellore, India, 2019	doi: 10.1109/i-PACT44901.2019.8960108
9	2019	R. Paul, A. K. Giri, R. Dash, A. Dewangan, S. Chandra Swain and Prashant Bawaney		SPV Grid Interconnection with Current Controller Techniques	Innovations in Power and Advanced Computing Technologies (i-PACT), Vellore, India, 2019	doi: 10.1109/i-PACT44901.2019.8960108
10	2019	Dr Archana Chowdhury		A Ranking Based Technique to Predict Protein Complexes	IEEE Congress on Evolutionary Computation (CEC)	Elsevier
11	2018	Dr. Archana Chowdhury		Prediction of protein complexes using an evolutionary approach	IEEE Symposium Series on Computational Intelligence (SSCI)	Elsevier

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Year 2022

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Techniques and Innovation in Engineering Research
Vol. 6

Edited by Dr. Figen Balo

B P International

Use of Alternative Raw Materials and Pulp Blending Improves the Strength Properties of Pulp and Paper

Preeti Nand Kumar [a#*]

ABSTRACT

Physical, chemical and morphological characteristics of Ipomoea Carnea were evaluated to determine its suitability for papermaking. Various chemical parameters such as Ash content, cellulose, ethanol–benzene solubility, hollocelulose, lignin and hot water and 1% soda solubility were carried out to find the chemical composition and to find the content resent in the pulp matter. The use of blending of long fibered pulps along with short fibered pulp helps to determine the important aspect of paper making. The morphology and chemical makeup of hard and soft wood varies greatly from one another. Certain elements, such as drainage, wet strength, and press rolls' propensity to stick, are lacking in soft wood. In order to overcome the issues of drainage, and other strength properties blending plays an important role. Pulp blending can be materialized in three distinct ways such as chips blending, pulp blending before beating and pulp blending after beating. The qualities slightly increase physical strength prior to pulp beating. However, beating at 1500 revolutions in a PFI improved the strength characteristics and resulted in an increased pulp yields column. Strength properties of separately cooked pulp blends beaten together showed improvement over the strength properties of pulp obtained from chips blending. Excellent strength properties are obtained when pulps are blended after beating separately.

Keywords: Blending; beating; long fibered; pulping; short fibered.

1. INTRODUCTION

The utilization of non-woody fibers from field crops and agricultural residues is a substitute for woody raw materials for pulp and paper production. Non-woody fibers are primarily employed in several countries to produce specialized papers. In this transformation, non-wood fibers and the blending of fibers may play a significant role as raw materials [1-3]. The primary sources of non-woody raw

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Year 2021

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Lecture Notes on Data Engineering
and Communications Technologies 86

Samarjeet Borah · Sambit Kumar Mishra ·
Brojo Kishore Mishra ·
Valentina Emilia Balas ·
Zdzislaw Polkowski *Editors*

Advances in Data Science and Management

Proceedings of ICDSM 2021

Springer

Linguistic Information for Decision-Making Using SVM

Ritesh Dash, Dillip Ku. Dash, and Radhe Shyam Panda

Abstract Extracting parameters by using linguistic variable which is capable of modelling an electrical signal for power system analysis on the different fault condition has been presented in this paper. Different pattern selection, grammar formulation and representing the signal parameter in terms of linguistic variable are the primitive work carried out in this sponsored research. Half cycle signal data from the fault location has been identified as the researchable area. Using discrete wavelet transformation, the parameters were extracted from the original signal, and by using linguistic variable with the help of machine learning, the classification for the different types of fault has been investigated in detail with MATLAB/Simulink software and Python. The proposed work in this research paper has been tested with different types of fault data for checking the robustness of the controller and its logic.

Keywords SVM · Linguistic variables · Gradient descent

1 Introduction

Electrical power system is highly scattered and nonlinear, and therefore, fault in the transmission line is an usual issue. Out of the different types of electrical transmission line fault, the most common type of fault is line to ground fault, and the most severe type of fault is dead short circuit. Proper identification of electrical fault and its isolation from grid safety point of view is a very critical task [1]. All these mentioned issues can be critically addressed by installing a proper relay which could prevent these problems and lead to minimal amount of loss in the transmission line. In these days, microprocessor-based relays were also used in transmission

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Green Engineering and Technology: Concepts and Applications

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Environmental conservation is an important issue these days for the whole world. Different strategies and technologies are used to save the environment. Technology is the application of knowledge to practical requirements. Green technologies encompass various aspects of technology which help us reduce the human impact on the environment and create ways of sustainable development. Social equability linked to this book series will enlighten the green technology in different ways, aspects, and methods. This technology helps people to understand the use of different resources to fulfill their needs and demands. Some points will be discussed as the combination of involuntary approaches, government incentives, and a comprehensive regulatory framework to encourage the diffusion of green technology. However, least developed countries and developing states of small islands require unique support and measures to promote green technologies.

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Preface

This book prioritizes working towards sustainability of the environment, employing engineering aspects along with green computation and applying various aspects of modern education as well as solutions. Practically, it visualizes specific aspects of artificial intelligence in manufacturing and green technology, covering the implementation of renewable resources enhancing business activities. As the term green technology is focused on preserving the resources and environment along with controlling the negative impact from human activities with sustainable development, obviously the solutions take into account social, economic as well as environmental concerns. The concept of artificial intelligence is used to optimize manufacturing supply chains and enhance energy efficiency, thereby helping companies to anticipate market changes. In this book, implementation has also been emphasized via artificial intelligence in resources with changing technologies where the initiation to process automation has been preserved. In addition to different parameters to measure the efficiency, various characteristics linked to high-end manufacturing activities have been focused. Considering the present situation, the concept of green data center based on storage, management and dissemination of data with control strategies has been placed in this book. It is understood that the concept of green computing, which links to eco-friendly implementation of systems along with resources, is associated with the computing devices in such a way to minimize any adverse impact on the environmental issues in the IT industry. In such situation, along with green technology, the entire environment is looking forward to more energy-efficient mechanisms, managed security services, cloud security solutions at one place by offering equivalent along with cloud management platforms. Similarly focusing on renewable energy—very specific energy which is collected from renewable resources—are commonly wind, sunlight, as well as geothermal heat, which often has a provision in different major areas like generation of electricity, transportation and rural energy services. Also, with the significant role of green computation in the sensor-enabled IoT, smart application enables the sensors in the situation where faster energy depletion is responsible for efficient functioning of the sensors. As such, a specific technique is needed to protect the sensors in IoT. In such cases, meta-heuristic techniques can be the better solution to solve similar types of situations with the near-optimal solutions.

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Editors

Sambit Kumar Mishra has more than 22 years of working experience in different AICTE-approved institutions. He has made more than 29 publications in different peer-reviewed international journals. He is editorial board member of different peer-reviewed indexed journals. Presently, he is associated with Gandhi Institute for Education and Technology, Baniatangi, Bhubaneswar, Odisha, India.

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Samarjeet Borah is currently working as Professor in the Department of Computer Applications, Sikkim Manipal University (SMU), Sikkim, India. Dr. Borah handles various academics, research, and administrative activities. He is also involved in curriculum development activities, board of studies, doctoral research committee, IT infrastructure management, etc. along with various administrative activities under SMU. Dr. Borah is involved with various funded projects in the capacity of Principal Investigator/Co-principal Investigator. The projects are sponsored by agencies like AICTE (Government of India), DST-CSRI (Government of India), Dr. TMA Pai Endowment Fund, etc. He is associated with ACM (CSTA),

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IAENG, and IACSIT. Dr. Borah has organized various national and international conferences in SMU. Some of these events include ISRO Sponsored Training Programme on Remote Sensing and GIS, NCWBCB 2014, NER-WNLP 2014, IC3-2016, IC3-2018, and IC3-2020. He is also associated with various other conferences in the capacity of steering committee member, TPC member, editorial board member, volume editor, and reviewer. Dr. Borah is involved with various book volumes and journals of repute in the capacity of editor/guest editor/reviewer such as *IJHISI*, *IJGHPC*, *IJVCSN*, *IJIPT*, *IJDS*, *IJBM*, *WRITR*, and *IEEE Access*. He is editor-in-chief of the series *Research Notes on Computing and Communication Sciences*, Apple Academic Press (exclusive worldwide distribution by CRC press).

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Migration in Multi-Population Differential Evolution for Many Objective Optimization

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Abstract— The paper proposes a novel extension of many objective optimization using differential evolution (MaODE). MaODE solves a many objective optimization (MaOO) problem by parallel optimization of individual objectives. MaODE involves N populations, each created for an objective to be optimized using MaODE. The only mode of knowledge transfer among populations in MaODE is the modified version of mutation policy of DE, where every member of the population during mutation is influenced by the best members of all the populations under consideration. The present work aims at further increasing the communication between the members of the population by communicating between a superior and an inferior population, using a novel migration strategy. The proposed migration policy enables poor members of an inferior population to evolve with a superior population. Simultaneously, members from the superior population are also transferred to the inferior one to help it improving its performance. Experiments undertaken reveal that the proposed extended version of MaODE significantly outperforms its counterpart and the state-of-the-art techniques.

Keywords—differential evolution; many-objective optimization; individual parallel optimization; multiple population; migration.

I. INTRODUCTION

Many-objective optimization (MaOO) refers to optimization problems, involving four or more conflicting objectives [1]. Over the past decade, popularity of MaOO algorithms have radically increased to solve real world optimization problems, like brain-computer interfacing [2], aerospace engineering [3], extraction of bioactive compound [4], robotics [5] and many more applications. However, there exists vast literature revealing the incapability of evolutionary multi-objective optimization (EMOO) algorithms to solve MaOO problem. The non-dominance criteria used in EMOO to form Pareto fronts fail to maintain sufficient selection pressure for a MaOO problem with four or more objectives. This is due to remarkable growth in the number of Pareto optimal solutions with the increase in the number of objectives beyond three [6], [7].

Researchers are taking keen interest to overcome the impasse of EMOO to solve MaOO problems. Strategies proposed in [8], [9] aim at judicious selection of the significant objectives out of all objectives for a given MaOO
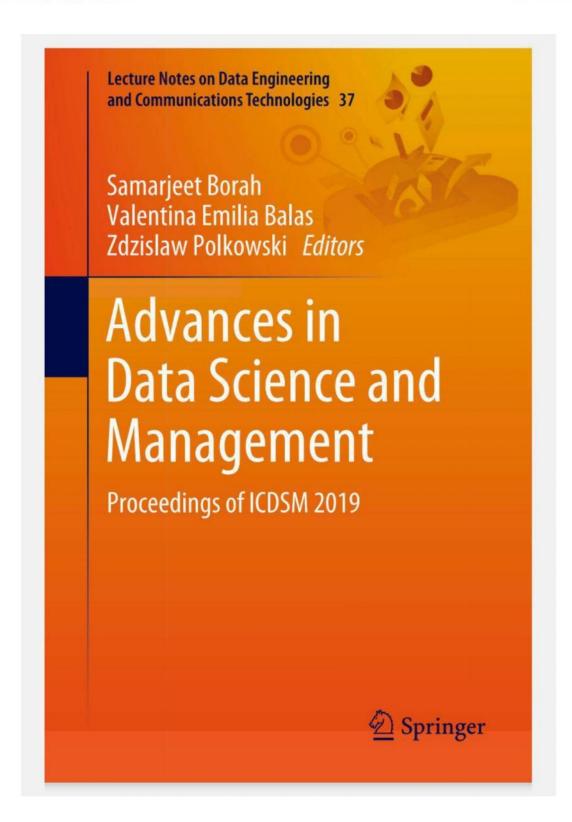
problem. Traces of reference point based MaOO algorithms are found in [10], [11] where decision maker determines the search direction in the preferred regions of the Pareto front. Among the methods, enhancing Pareto optimality criteria, to solve MaOO problems, ε-dominance [12], fuzzy Pareto dominance [13] and subspace dominance comparison [14] need special mentioning. The authors' previous work, referred to as *many-objective optimization using differential evolution* (MaODE) [15], utilizes the implicit parallelism of a population-based evolutionary algorithm (realized with DE) to effectively expedite the convergence of the algorithm.

MaODE solves a MaOO problem in two steps. First, individual N objectives of the given MaOO problem are optimized in parallel by N evolving populations of solutions. Second, the well-performing solutions of all N populations are combined and ranked with respect to individual objectives. The set of equally good solutions with equal *sum of rank* (*SoR*) measures are declared as the solution to the MaOO problem. The scope of knowledge transfer between the populations is provided by modified version of DE/current-to-best/1 mutation policy [16-19] of MaODE. Unlike the traditional DE/current-to-best/1 mutation policy, a target vector belonging to a population $\mathbf{P}^k$ is influenced by the best members of all N populations (instead of the best candidate of $\mathbf{P}^k$ only) to generate its donor vector.

This strategy, however, ignores the average and poor performing members of a population, which if evolved with other populations, may have excelled in their performance. The present work aims at migration of members between different populations to aid an individual to evolve with respect to an objective on which it is most likely to perform well. The migration policy first judiciously selects the communicating pair of populations from N populations. The proposed selection strategy bypasses need of any network topology. The stratagem allows the best population to communicate the worst population, the second best to the second worst, and the third best to the third worst and so on. This communication/migration policy among diverse populations enhances the exploration capability of the MaODE algorithm. The quality of a population is determined based on the median and the interquartile range (IQR) of the objective function values of its members. A population with

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Samarjeet Borah
Valentina Emilia Balas
Zdzislaw Polkowski *Editors*

Advances in Data Science and Management

Proceedings of ICDSM 2019

Springer

A Hybrid Time Series Forecasting Method Based on Supervised Machine Learning Program

Check for updates

Ganesh Prasad Khuntia, Ritesh Dash, Sarat Chandra Swain and Prashant Bawaney

Abstract Clean and inexhaustible source of energy is the requirement of the entire world with respect to the present scenario. Among the different types of energy sources, wind energy is the cleanest energy and inexhaustible source of energy. In order to ensure the production of clean energy, it is required to forecast the level of wind energy from a day ahead. Forecasting of wind energy not only forecasts the level of wind but also predicts the type of wind energy, density, and other important variables. This paper describes the short-term forecasting based on Machine Learning algorithm. This paper compares the different Machine Learning Algorithm and its behavior in predicting or forecasting the day-ahead data for the wind energy system. Machine learning based on Python is formulated in this paper.

Keywords Wind energy · Python · Forecasting · Training set · Testing set

1 Introduction

Power Plant supported Renewable Energy System has dragged the eye of Power researchers, thanks to its scattered expression within the last decade [1, 2]. Massive-scale growth of those sources has created it to satisfy the rise in demand of power. This growth isn't just for an economic or political reason, however additionally for making an appropriate setting for our new generation wherever power is made from clean sources like solar and wind with zero setting pollutions [3–5]. The government

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A Ranking Based Technique to Predict Protein Complexes

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Abstract— Protein complexes play a very important role in biological processes. The identification of the proteins in the protein complex as well as the prediction of protein complexes which are hitherto anonymous will improve the understanding of the protein complexes and related biological processes. Most of the computational methods used to predict protein complexes were based on the principle that proteins inside the complex have more interactions .The protein-protein interaction (PPI) network is thus used to predict protein complexes. The features that affect the interaction of proteins in the protein-protein interaction network are mostly studied for identification of protein complexes. This paper is used to analyze the effect of the characteristic feature related to domains and functions on protein complex prediction. In this paper a ranking approach is applied to the solutions of differential evolution to identify protein complexes. The experimental results show that the proposed method beats the existing methods taking into consideration the typical performance metrics.

Keywords— *protein complex; differential evolution; protein–protein interaction networks; annotation; domain.*

I. INTRODUCTION

A fundamental role is played by protein-protein interactions in biological processes. Proteins mostly perform the biological function by binding together with other proteins to form complexes [1].The understanding of cellular organization and functions can be improved by identifying known protein complexes and predict the unknown complexes from the protein- protein interaction data. Protein complexes can be identified using wet lab experimental technique such as *Tandem affinity purification with mass spectrometry* (TAP-MS) [2]. However due to multiple washing and purification it becomes very difficult to dig out low-affinity protein complexes and also the tag protein used in the experiment may hamper the protein complex formation. The limitations of the wet lab experiments lead to the use of computational methods to predict protein complexes.

The advances in high throughput experiments such as yeast two hybrid [3] have produced huge amount of PPI data of various organisms [4]. This huge amount of PPI data can be used by various computational methods to identify protein complexes. Most of the computational methods model the PPI network as a graph with proteins as nodes and the interactions as the edges of the graph. Apart from identifying protein complexes from PPI network there are several other applications to the graph model of the PPI network [5].

The principle of graph theory is applied to the PPI network as protein complexes are considered as dense sub-graphs in the PPI network [6]. The graph theory approach to predict protein complexes utilize clustering techniques [7].The protein complex identification methods which were based on the topological structures of the PPI network include Markov clustering method (MCL) [8], Cliques (fully connected Sub graphs)[9], Molecular Complex Detection (MCODE) [6].The high throughput experiments produces high false positive and false negative in PPI data which makes the accurate prediction of protein complexes very difficult. It has been observed that the use of information related to expression data and gene ontology improves the prediction of protein complexes by creating more reliable PPI network [10],[11].

In this paper, we propose a method to predict protein complexes based on the criteria of the PPI network, which effect the complex formation. We have used four criteria. The first criterion is based on the similarity of functions of proteins in a complex. It has been observed that proteins present in the same cellular compartment have more possibility to interact than those present in distinct compartments [12]. Furthermore, proteins that share a molecular function or a biological process are also more likely to interact [13]. This shows that the proteins present in a protein complex will exhibit high functional similarity. The second criterion is based on the domain interaction of proteins. The PPI network is the result of interaction of the basic building blocks of proteins called domains [14]. As the proteins present in the complex are linked to each other, they will show domain–domain interaction. The third criterion is based on the compactness of predicted complexes on the basis of true connections of the proteins present in the complex. The fourth and the final criterion is based on the overlap factor of the protein complexes. When protein complexes are identified from a PPI network the uniqueness of the complexes will be ensured if the overlap between the protein complexes is very less. If the degree of overlap between the complexes is not minimized the entire PPI network will be predicted as a complex which is practically not possible. Using the graph theoretic approach

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Prediction of Protein Complexes Using an Evolutionary Approach

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Abstract— A significant role is played by protein complexes in understanding the cellular life. The understanding of the principles behind cellular organization and function will be enhanced if we can predict the protein complexes still undiscovered. Many computational methods have been developed to predict protein complexes and are mostly applied to static protein-protein interaction (PPI) network. The focus of most of the existing methods is on the topological structure of PPI networks and they are based on the assumption that protein complexes are dense subgraphs of PPI network. In this paper, we have used the characteristic features of the proteins such as functional similarity and domain-domain interaction to identify the clusters of protein interaction. Here, a novel method using differential evolution and fuzzy membership induced ranking technique is proposed to identify protein complexes by utilizing functional similarity and domain-domain interaction feature of proteins. Experimental results show that the proposed method outperforms the existing methods with respect to the standard performance metrics.

Keywords—protein–protein interaction networks; protein complex; domain-domain interaction; differential evolution; fuzzy logic.

I. INTRODUCTION

Interaction among proteins plays a central role in various biological processes such as signal transduction, cell cycle and replication. Proteins rarely act as individual units and they often bind together to form complexes to carry out the various biological processes. There are evidences that many proteins are functional only after they are assembled into a protein complex by interacting with member proteins of the complex [1]. Thus to understand the underlying mechanism of most of the cellular functions and to predict the functions of unannotated proteins, correctly identifying the protein complex is very important.

Tandem affinity purification with mass spectrometry (TAP-MS) [2] is a wet lab experimental technique to detect protein complexes. There are several limitations to this method. First, due to the multiple washing and purification steps, low-affinity protein complexes are hard to be extracted. Second, the tag proteins used in the experiments may interfere in the protein complex formation. Last, the TAP-MS experiments are generally time consuming and expensive. Because of the

limitations of the TAP-MS method, computational techniques are being used to uncover protein complexes. The computational detection of protein complexes are based on protein-protein interaction (PPI) data. Here, PPI data is treated as a graph or network where proteins are nodes and interactions are edges between nodes. As protein complexes are usually made up of proteins with common biological functions they are expected to be dense subgraphs in the PPI network [3]. Thus, the problem of computationally detecting the protein complexes can be addressed by identifying the dense subgraphs in PPI networks by using clustering techniques [4].

Some of the methods used to detect the protein complexes by extracting the densely connected subgraphs from the PPI networks include Clique [5], LCMA [6], MCODE [7], CFinder [8] and CMC [9]. All these methods focus on the topological structures of the PPI networks. The presence of high false positive and false negative rates in PPI data obtained from high throughput experiments [10] makes the task of accurately predicting the protein complexes very difficult. Hence additional information such as *gene ontology* (GO) and expression data were used to enhance the confidence of interactions between proteins and later to construct more reliable PPI networks. It has been observed that when various subgraph extraction methods have been employed upon these networks, better prediction performance has been achieved.

In this paper, we propose a new method where the protein complexes are determined by using four criteria, including i) the functional similarity and ii) domain-domain interaction profiles of the proteins in a complex, iii) degree of overlapping between the complexes and iv) the density of the individual complexes. GO annotation driven PPI inference reveals that proteins sharing a common biological process or molecular function have more possibility to interact [12]. Similarly, proteins present in the same cellular section are more likely to interact than the proteins that reside in spatially distant compartments [13]. In other words, proteins perform their biological functions by forming complexes with accurate interaction with each other. It evidently indicates a possibility of high functional similarity of proteins in a real complex.

Domains are the basic building block of proteins. When two proteins interact with each other, it is the domains present