

Shrimati Indira Gandhi College
(Nationally Re-accredited at 'A' Grade by NAAC)

Tiruchirappalli-2



SIGARIA

RESEARCH JOURNAL

SHRIMATI INDIRA GANDHI COLLEGE

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SHRI.S. KUNJITHAPATHAM, B.Com, B.L
SECRETARY



Our College is one of the premier institutions with research Activity in Two disciplines. Our faculties contribute original research articles to National and International Journals apart from publishing books, some of them have been prescribed as Text Books.

In order to encourage our faculty from all disciplines to do more Research and Publish more papers, the college has decided to bring out a "JOURNAL" named "**SIGARIA**" from this year. This journal will contain abstract of all papers published by faculty belonging to various disciplines. This is an effort to motivate other faculty to also publish articles in journals. This journal is aimed at disseminating research work done by faculty to all departments of the college. The 2010 Journal will be published in July 2010, which will contain all the papers from all our teachers.

I acknowledge the idea and effort taken by the Principal and the Editorial Board, in bringing out this Research volume.



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PRINCIPAL

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FOREWORD

I am happy to see the rolling out of the first copy of SHRIMATI INDIRA GANDHI COLLEGE RESEARCH journal named SIGARIA. Though it is a volume compiling abstracts of Research papers of the Staff of the College published in various Journals, it provides a comprehensive publication facilitating staff members to know the outcome of Research in the college. This volume compiles the paper published by staff members during the period July 2009-june 2010. Next volume will have the papers of 2010-11. I congratulate the Editorial Board for bringing out the Research publication. It is yet another milestone in the journey of Shrimati Indira Gandhi College.

PRINCIPAL

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Department of Bank Management

- **Dr. M. Chandrasekaran, and Ms. K. Sujatha** –“Job Satisfaction among College Teachers with special reference to different categories of Self-financing Arts and Science Colleges in Tiruchirappalli District”, Cauvery Research Journal, Vol. 3(1&2), Jul 09 - Jan 10.

Abstract:

The study was focused on finding out the satisfaction level of the college teachers at various ownership levels as this factor reflects on the overall development of the students. The satisfaction level differed at different categories.

P.G & Research Department of Computer Science

- **Dr. K. Meena, Dr. K.R.Subramanaian, and Ms. M. Gomathy-** “Intelligent Separation of Mixed Speech Signal using Fourier Spectra and Back Propagation Algorithm”, Noble Journals – International Journal of speech processing, http://noblejournals.com/about_us.php, Vol. 3(1), July 2009, Page No. 15-25.

Abstract:

A Methodology for separation of multiple audio signals recorded as a mixed signal via a single channel has been presented in this paper. The mixed signal is sampled at 8KHz. Frames of 25ms and overlapping frame of 15ms is obtained from the signal. The algorithms of the power spectra of the frames are determined. From the spectra, the a posteriori probabilities of pairs of spectra are determined. The probabilities are used to obtain Fourier spectra for each individual signal in each frame. A back-propagation algorithm (BPA) is used to learn the signal patterns. Individual Signals are obtained using the outputs of Fourier spectra and the BPA. The separation of the signals is appreciable.

Department of Information Technology & B.C.A

- **Dr. K. Meena, Ms. K. Menaka, Mr. T.V. Sundar, and Dr. K.R. Subramanian** - "A Statistical Method for Verification of Rareness in DNA Sequence using Sequence encoding", Online Journal of Bio-Informatics, ISSN 1443-2250, <http://onljvetres.com/bioinfo.htm>, Vol. 10(1), Page No.74-81, 2009.

Abstract:

A Statistical method for verification of rareness in DNA sequences using sequence encoding. Online J Bioinformatics, 10(1): 74-81, 2009. Consensus sequence among a family of related sequences is the sequence that shows the characteristics common to most members of the family. Consensus sequences are important in various DNA Sequencing analysis and applications and are a convenient way in characterizing a family of molecules. Rareness or anomaly detection followed by in depth analyzes in such sequences may reveal significant information regarding the structural, functional and biochemical pathways of the genes which are of much importance to biologists. This paper describes a new method of encoding the DNA sequences for sequence analyses and subsequent application of a statistical method called Analysis of Variance to verify the nature of consensus among the family of given related sequences. The verification for the existence of consensus or rareness is judged based upon the calculation of the variation within the sequence data upon the calculation of the variation within the sequences data and the group of sequence. For an illustration, some DNA consensus sequences corresponding to human repetitive elements submitted to Repbase have been used.

P.G Department of Computer Applications

- **Dr. K. Meena, Mr. M. Duraraj, and Dr. K. R. Subramanian-** “Data Mining Algorithm used in a Mobile Computing Environment”, College Science in India www.collegescienceinindia.com, ISSN: 1939 2648, Vol. 3(1), Page No. 1-11, Feb 2009.

Abstract:

Efficient Data mining Techniques are required to discover useful Information and knowledge. This is due to the effective involvement of computers and the improvement in Database technology which has provided large data. The Mobile Data Allocation scheme is proposed such that the data are replicated statically for traditional database for which the moving patterns. Of Mobile user o mine the results and improve the Mobile system are used. A simulation Square Mess is prescribed as a probabilistic model to secure the routes to the various serving nodes of the mobile system.

An algorithm for incremental Mining of moving patterns is introduced for finding a Sub algorithm to find the Maximal moving sequences. Data Allocations schemes have been devised to utilize the knowledge of user moving patterns for proper Allocation of both personal and shared data. Hence the efficient Location Management and questions strategy would lead to beneficial output through a mobile computing system.

- **Dr. K. Meena and Dr. M. Manimekalai-** Prediction of Amino acid levels In Protein Sequences Using Artificial Neural Networks”, Journal of Advanced Research in Computer Engineering, ISSN: 0974-4320 <http://serialsjournals.com/>, (Peer Reviewed) Volume (3) Page No.19 – 21, 2009.

Abstract:

A Mathematical Method for Artificial Neural Network offers an original, broad and integrated approach that explains each tool in a manner that is independent of specific ANN systems. Artificial Neural Networks are abstract mathematical models of brain structure and functions. They are nothing but a mathematical model that relies on varying the strength of connections between the internal processing elements to interpret data. They can be applied to

many pattern classification problems. In this paper, it has been used predict the level of amino acid in protein sequences.

- **Dr. K. Meena, and Dr. M.Manimekalai-** “Evaluation of the Dynamic Programming Method used for Protein Secondary structure prediction”, Pacific-Asian Journal of Mathematics, ISSN: 0973-5240, <http://serialsjournals.com/>, (Peer Reviewed) Vol. 3(1-2) Page No. 187-194, Jan-Dec 2009.

Abstract:

Bioinformatics continuously improve methods predicting simplified aspects of structure. Particularly, the field of secondary structure has achieved a break – through by combining algorithms of artificial intelligence with evolutionary information. Due to their remarkable success. Secondary structure predictions have become the working horse for numerous methods aiming at predicting protein structure and function. The explosive accumulation of protein sequence in the wake of larger scale sequencing projects is in stark contrast to the much slower experimental determination of protein structure. Hence improved methods of structure prediction from protein sequence are needed. In this paper a methods which substantially increases the accuracy and quality of secondary structure prediction has been explained and evaluated which is nothing but Dynamic Programming. Dynamic Programming is a Statistical approach for secondary structure prediction based on information theory and simultaneously taking in to consideration pair wise residue types and conformational states. The prediction of residue secondary structure by one residue window sliding makes ambiguity in state prediction. This can be overcome by using Dynamic Programming concepts where in the path with maximum score is found. This Article comprises the detailed description of Dynamic Programming concepts and evaluation of the same.

- **Dr. K. Meena and Dr. M. Manimekalai-** “Prediction of Protein and Amino Acid Contents in seeds of Food Legumes using Fuzzy k-Nearest Neighbor Algorithm”, International Journal of Fuzzy Systems & Rough Systems, (Peer Reviewed) <http://serialsjournals.com/>, ISSN : 0974-858X , Vol. 2(2), July-Dec 2009, Page No.73-77.

Abstract:

The relationship between Protein Amino Acid sequence and secondary structure is complex, reflecting the intricate Thermodynamic and kinetic of protein folding. The accuracy to protein secondary structure prediction has been improving steadily towards the 88% estimated theoretical limit. There are two types of prediction algorithms: Single- sequence prediction algorithm imply that information about other (homologous) proteins is not available, while algorithms of the second type imply that information about homologous proteins is available, and use it intensively. The single sequence algorithms could make an important contribution to studies of proteins with no detected homologous however the accuracy of protein secondary structure prediction from a single-sequence is not high as when the additional evolutionary information is present. Food legumes are considered as the major source dietary proteins among the plant species. In this paper a new approach for predicting the secondary structure of proteins of soybeans using fuzzy K-nearest neighbor algorithm has been proposed and it has been compared with artificial Neural Network method. (Back Propagation Algorithm)

● **Dr. K. Meena and Dr. M. Manimekalai-** “Protein Structure Prediction in Soya beans using Neural Networks”, CIIT International Journal of Artificial Intelligence Systems & Machine Learning, Print: ISSN 0974 – 9667 & Online: ISSN 0974 – 9543, Feb 2010.

Abstract:

Protein is definite kind of biological macromolecules that is present in all biological organism. Amino acids are the building blocks of proteins. They are primary structure, secondary structure, tertiary structure and quaternary structure. Most of the existing algorithms for predicting the content of the protein secondary structure elements have been based on the conventional amino acid composition, where no sequence coupling effects are taken into consideration. Prediction of three dimensional structure, secondary structure, and functional sites of protein from primary structure are the three major problems in structural bioinformatics. More than a few different approaches have been previously used in these kind of prediction among which, artificial neural network have been of great interest due to their capability of learning observations and prediction of the structures for non classified instances.

This paper proposes a technique for prediction of protein structure in soyabeans using neural networks. This paper uses RBFNN in order to predict the secondary structure. In our approach, genetic encoding scheme is used to generate the centers and widths of radial basis function. The neural network architecture used in our approach is a feed forward and fully connected neural network whose Gaussian centers are optimized from data Bank (PDB).

Department of Mathematics

- **Dr. M.A. Goapalan, Ms. V. Pandichelvi, and Dr. S. Vidhyalakshmi** - "Integral Solutions of Non-Homogeneous Biquadratic Equations with six unknowns $x^2 + y + y^2 = (z + w)(u^3 + v^3)$ ", International Journal of Mathematical Science- Serials Publications, peer-reviewed, ISSN : 0972-754X, <http://serialsjournals.com/>, Vol. 9(1-2), Page No. 127-131, Jan-Jun 2010.

Abstract:

We present two different patterns of non-zero integral solutions for the biquadratic equation with six unknowns $x^2 + y + y^2 = (z + w)(u^3 + v^3)$. A few relations among the solutions and special polygonal numbers are also presented.

- **Dr. M.A. Gopalan, Dr. S. Vidhyalakshmi, Ms. S. Devibala**- "Ternary Quadratic Diophantine Equation $24^{n+3}(x^3 + y^3) = z^4$ ", Impact journal of science and Technology, ISSN: 0973-8290, Vol.4(1), Jan-Mar 2010.

Abstract:

The quadratic equation with three unknowns given by $24^{n+3}(x^3 + y^3) = z^4$, $n > 0$ analyzed for its integral solutions. A few interesting properties among the solutions are presented.

- **Dr. M.A. Gopalan, Dr. S. Vidhyalakshmi, and Ms. S. Devibala**- Observation on the Quadratic Equation with Four Unknowns $xy=2(z+w)$, International Journal of mathematical Science, peer-reviewed, ISSN: 0972-754X, <http://serialsjournals.com/>, Vol. 9(1-2), Page No.161-166, Jan-Jun 2010.

Abstract:

We obtain infinitely many non-zero integer quadruples (x,y,z,w) satisfying the non-homogeneous quadratic equation in four unknowns $xy=2(z+w)$, A few interesting relations between the solutions, special polygonal and pyramidal numbers are presented.

● **Dr. M.A. Gopalan, Dr. S. Vidhyalakshmi, and Ms. S. Devibala**- "Integral Solutions of $x^2 + xy + y^2 = z^3$ ", Impact Journal of Science & Technology, ISSN: 0973-8290, Vol. 3(3), Page No. 29-37, Jul- Sep 2009.

Abstract:

Patterns of non-trivial parametric integral solutions of the ternary cubic Diophantine equation $x^2 + xy + y^2 = z^3$ are obtained. Verities of relations among the solutions are given.

AREAS FOR RESEARCH

COMMERCE

- ❌ Artificial Neural Networks
- ❌ Data mining
- ❌ Bio Informatics
- ❌ Image Processing and Pattern Recognition
- ❌ Computer Applications using Discrete Mathematical Tools
- ❌ Computer Applications using Numerical and Statistical methods
- ❌ Marketing
- ❌ Inventory Management
- ❌ Finance Management
- ❌ Effective Management & Administration

MICROBIOLOGY

- ❌ Agricultural Microbiology
- ❌ Mycology
- ❌ Environmental Microbiology

BIOCHEMISTRY

- ❌ Biomolecules, Biotechnology
- ❌ Immunology Endocrinology Enzymes / Cancer Biology
- ❌ Techniques , Molecular Biology
- ❌ Clinical Biochemistry , Food & Nutrition

TAMIL

- ❌ Mozhiyiyal
- ❌ Ariviyal Tamil
- ❌ Sangam Literature
- ❌ Bhakthi Literature

MATHEMATICS

- ❌ Number Theory
- ❌ Fluid Dynamics
- ❌ Applied Mathematics
- ❌ Applications of Computer Science in Mathematics

MANAGEMENT STUDIES

- ❌ Pay on perquisites
- ❌ Employability skills in Arts & Science
- ❌ Women Role in IT sector

SOCIAL WORK

- ❌ Community Development
- ❌ Medical and Psychiatry
- ❌ Human Resource Management