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2/2

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Table of Contents

Title	Page.No
Parallel Hierarchical Subspace Clustering for Segmenting Large Text Corpuses ***S. Karthick, S. Mercy Shalinie, S. Umabharathi, S. Kavya Saroja***	1
Survey on: Home Automation Systems ***Pratik Waghmare, Mayur Chandgude, Prafull Chaure, Abhay Chaudhari***	7
Attacks and mitigation techniques on mobile ad hoc network- A survey ***Sagarika Kar Chowdhury, Mainak Sen***	11
Performance of CSS Cognitive Radio Networks under Primary User Emulation Attack ***Rajesh D. Kadu, Dr. Pravin P. Karde, Dr. V. M. Thakare***	19
Computational Modelling of Bio signal-based Occupancy Sensing System using Doppler Radar ***Preethi K Mane, Dr. K Narasimha Rao***	25
Flexible capacitive based printed sensor using different dielectrics for real time applications ***Vithyasaahar Sethumadhavan, Snehal Saraf, Ajit Chaudhari, Ravindra Gaikwad***	32
Cost Estimation and Analysis of Computing Models in Education ***Ms Zaibunnisa Malik, Ms Zainab Delawala, Ms Aarfah Ahmad***	37
Ontology Based information extraction from Resume ***Mhapasekar Darshan Prakash***	43
An Improved Digital Watermarking Technique Based on 5-DWT,FFT & SVD ***Ninny Mittal, Anand Singh Bisen, Rohit Gupta***	48
Design of Error Normalized LMS Adaptive filter for EEG signal with Eye Blink & PLI Artefacts ***N.Sruthi Sudha, Rama Kotireddy Dodda***	54
FPGA Reconfiguration using UART and SPI Flash ***Pranav S Mutha , Yogita M Vaidya***	59
Advanced Standard Encryption (AES) implementation on FPGA with hardware in loop ***Sheetal U. Jonwal, Pratibha P. Shingare***	64

Optimized Driver Safety through Driver Fatigue Detection Methods 68
Omar Wathiq , Bhavna D. Ambudkar

Single Band Planar Monopole Antenna with A-shaped EBG 74
Shridhar Desai , Nilesh B. Nagrale , Mahesh Kadam

Easy Village 78
Aswini C, Jithin K C, Hasna A, Arun S, Dharanya K M, Nitha T M

Modelling and Simulation of Photovoltaic Module for Micro inverter Application 82
Manthan Patel, Hinal Surati, Jay Patel

Electrical energy audit in a Uka Tarsadia University - A case study 86
Urmil Desai ,jaynesh patel,jay patel,ankur rana,darshan patel

Efficient Algorithm and Study of QoS-Aware Mobile Ad Hoc Network Methods 90
Aparna Junnarkar, A.B. Bagwan

Microstrip Patch Antennas for Wireless Communication: A Review 96
Mandar P. Joshi, Vitthal J. Gond

Load Balancing in Cloud Computing: Methodological Survey on different types of algorithm 100
Jaimeel Shah,Dr Sharnil Pandya,Dr Narayan Joshi,Dr Ketan Kotecha,Dr D.B.Choksi

Cognitive Examination for the Early Diagnosis of Alzheimer's Disease 108
Sandeep C S, Sukesh Kumar A, Susanth M J

Enhancement of Security by using Greedy Approach and Encryption in Mobile Ad Hoc Network 113
Abhishek Agrawal, Abhilash Sonker

Design and Implementation of SRAM Macro Unit 119
Surya Narayan Panda, Somanath Padhi, Vedula Phanindra, Umakanta Nanda Sushant Kumar Pattnaik, Debasish Nayak

A Comparative Analysis of Feature Selection Stability Measures 124
Mohana Chelvan P, Perumal K

Comparative Analysis of Different Approaches to Solve The Job Assignment Problem 129
Mohit Manoj Vinchoo, Rugved Vivek Deolekar

Wireless Power Transfer System for Biomedical Application: A Review 135
D.B.Ahire, Dr.Vitthal J.Gond

Design of auto-performance optimization tool for Diesel engine 141
Abhishek Kumar, Anjay Prasad, Vishal Halale, Bipin Hingu, Kowsalya M

Detecting Movements and Predicting the Future Path of a Moving Object in Wireless Sensor Network 146
sonal M Gupta, Sachin Deshpande

Intelligent Knowledge Sharing for Agricultural Information 153
Chetana J. Kolte, Avinash Shrivas

Multiple Image watermarking using LWT, DCT and Arnold transformation 158
Chandan Preet , Rajesh Kumar Aggarwal

Eye-Writer Using Real Time Operating System 163
Abhijeet P. Desai , Sanjna S. Repal

Trust based Mobile Ad-hoc Networks 166
Sonam Choubey, Krishna Kumar Joshi

Improved Routing Security using Intrusion Detection System in Mobile Ad Hoc Network 172
Hemlata Kaurav, Krishna Kumar Joshi

Standards Elimination Parser using Natural Language Processing 177
Chaitanya Lele, Himanshu Telkikar, Sumod Shinde, Rugved Vivek Deolekar

Analysis of Diseases in Fruits using Image Processing Techniques 183
Kawaljit kaur, Chetan Marwaha

Wireless Sensor Network for Real Time Monitoring and Controlling of Railway Accidents 190
Apurva Potdar, Sagar Shinde, Pooja Nikam, Monika Kurumkar

Recognition Of Cursive English Handwritten Characters 199
Pritam Dhande,
Reena Kharat

A new neural network based algorithm for identifying handwritten mathematical equations 204
Sagar shinde, R. B. Waghulade, D. S. Bormane

Efficiency Analysis of Quadratic Buck Converter for LED Lamp Driver Applications 210
Ravindranath Tagore Yadlapalli, Anuradha Kotapati

Mathematical modeling of bevel gear for gate valve application
Avishkar Ramchandra Bhoskar, Sanjay D. Yadav

Designing and Analysis of an Efficient and Accurate Approach for Image Segmentation 220
Arpit Kushwah, Manish Dixit

Achievements and Perspectives of GaN based Light Emitting Diodes: A Critical Review 224
Shameem Ahmad, Mohd Adil Raushan, M.J. Siddiqui

GaAs based charge plasma transistor for parameters performance enhancement 230
Pooja Rani, Shweta Meena

Estimation of Crowd Density by Counting Objects 235
Charul Singh, Mandar Sohani

Analysis of multilayered SAW based gas sensor 239
Akriti Gupta, Pradeep Kumar, Sujata Pandey

Rectifier performance affected by time delays improves with fuzzy preview control 243
Gundavarapu V Nagesh Kumar, Kavirayani Srikanth

Forecasting Air Quality Index using Regression Models: A Case Study on Delhi and Houston 248
Sankar Ganesh S, Sri Harsha Modali, Soumith Reddy Palreddy, Arulmozhivarman P

Novel symmetric and asymmetric topology of multilevel inverter with reduced number of switches 255
Kelam Bala Muralidhar Reddy, Swapnajit Pattnaik

An approach for Analysis and Identification of Raga of Flute Music using Spectrogram 261
Anoop M N, Deepak T S, Shreekanth T

Energy Efficient Hierarchical Routing Protocols and Simulation Environment for Wireless Sensor Networks 267
Praveen Singh Rawat, Vishal Kumar

An Energy Optimized Path Selection and Dynamic cluster head selection for Wireless Mesh Network 272
Bhawna Gangwar, J.D. Bhosale, Neha Gangwar

A survey on Location Management in LTE network 278
Abantika Choudhury, Abhijit Sharma, Uma Bhattacharya

Design and Study of Waveguide using HFSS-High Frequency Structural Simulator 284
Naga Sai Sharath Saindla, Arun Kumar Yellola, Samya Sabavath, Neelan Kumar Uppari, Mudasar Basha
Initial analysis of brain EEG signal for mental state detection of human being 287
Nisha Vishnupant Kimmatkar, B. Vijaya Babu
Efficient Implementation of GLCM based Texture Feature Computation using CUDA Platform 296
Asad Parvez, Anuradha C. Phadke
Mimicking Voice Recognition Using MFCC-GMM Framework 301
Unnikrishnan V M, Rajeev Rajan
Identifying Design Patterns for Risk Management System using Big Data Analytics 305
D Kannan , B. Dojohn Loyd
Implementation of a Real Time Communication System for Deaf People Using Internet Of Things 313
Piyush Patil,Jayesh Prajapat
Environment Sniffing Smart Portable Assistive Device For Visually Impaired Individuals 317
Piyush Patil,Akshay Sonawane
Smart IoT Based System For Vehicle Noise And Pollution Monitoring 322
Piyush Patil
Providing Smart Agricultural Solutions/Techniques By Using Iot Based Toolkit 327
Piyush Patil,Vivek Sachapara
Enhanced System For Selfish Node Revival Based On Watchdog Mechanism 332
Afsal Meeran, Praveen A.N, Ratheesh T.K
Forecasting Air Quality Index based on Mamdani fuzzy inference system 338
Sankar Ganesh S , N Bhargav Reddy , Arulmozhivarman P
An Optimal Color Image Edge Detection Approach 342
Dibya Jyoti Bora
High Spatial Resolution Hyperspectral Image using Fusion Technique 348
Suchitha K, Premananda B.S., Arvind Kumar Singh

Bliss Bot for Pharmaceutical Inspection 354
G. Rohith Reddy, D. Rushali, T. Sai Jahnavi, B. Anil Kumar

A Novel Secure Authentication Approach for Wireless Communication using Chaotic Maps 360
B. Madhuravani, DSR Murthy

Impact of ERB and Bark scales on Perceptual Distortion based Near-end Speech Enhancement 364
Nikhil G.V, Keerthi A.M, Premananda B.S

Design of Multiband antenna with U shaped strip and L shaped strips for WLAN / Bluetooth /WiMAX/HYPERLAN Applications. 371
P.N.Tajane & P.L.Zade

Healthcare Monitoring System using IoT 374
Swaleha Shaikh, Vidya Chitre

Full duplex Millimeter-Wave Radio-Over- Fiber System using Optical Heterodyning and Self-Homodyning 378
Joseph Zacharias, Anju Krishnan R, Josy Joy, Saritha Elizabeth, Vijayakumar Narayanan

Data Security Using SVD Based Digital Watermarking Technique 382
Alifa D'Silva, Nayana Shenvi

Authenticating Messages in Wireless Sensor Networks 387
Jeba Sangeetha Nadar, Jayashri Mittal

Advanced Material Synthesis and its Characterization Towards Applications of Organic Electronics 393
Sreemoyee Chatterjee, Suprovab Mandal

Synthesis of a Perylene-Diimide Derivative: Small Organic Molecule and Its Characterization towards Organic Electronics Application 400
Sreemoyee Chatterjee, Suprovab Mandal

FPGA Implementation of Mouse Interface 407
V.Pravalika, P.Bhavya Reddy, G.John, B.Anil Kumar, K.Madhava Rao

Design of Semi-orthogonal Wavelet for Human Ear Recognition 413
Sakshi, Manish Kr. Saini, J.S. Saini

Low Leakage Write-Enhanced Robust 11T SRAM Cell with Fully Half-Select-Free Operation 419
Sayeed Ahmad, Naushad Alam, Mohd. Hasan

A Novel Stream Cipher using Pesudo Random Binary Sequence Generator for Medical Image Encryption 425
P.Vidhya Saraswathi,M.Venkatesulu

A review on Energy Efficient Data Centric Routing Protocol for WSN
Agrawal Ashish, Ankita Desai, Achyut Sakadasariya 430

Automatic Dialect Recognition Using Feature Fusion 435
Sreeraj V V, Rajeev Rajan

Multi-Modal Biometric Security with Multi-Algorithm 440
Fathima N, Smitha Satheesh

Preventing Shoulder Surfing Attack Using Touch Screen Based PIN Authentication Method in Invisible Form 444
Siddhesh Vaidya, Sayali Kadam, Varsha Bhosale

Development Of a Modular and Optimum Multisensor Integration Platform for Navigation 450
S.Sajithra Varun, R.Nagaraj

Comparison of L, LC & LCL filter for grid connected converter 455
Utsav P. Yagnik, Mehul D. Solanki

Classical Review of Frequency Response Analysis of Transformer 459
Yagnik V. Ajudiya

A Novel Seven Segment Digital Clock Implementation On FPGA
Nikhil Kumar Vuthuri, Vijaya Mahewar, Gowtham yeddluri, Eshwar sai Movva, Vandana.ch 465

FPGA based Traffic Light Controller
S. Venkata Kishore, Vasavi Sreeja, Vibhuti Gupta, V.Videesha, I. B. K. Raju, K. Madhava Rao 469

Automated Secern Robot 476
P. Santosh Reddy, Ch. Praveena Kumari, Ch. Sai Supraja, K. Prabhakara Rao

Energy Conservation through Energy Audit 481
Vivek Jadhav, Rushikesh Jadhav, Pramod Magar, Sandip Kharat, S. U. Bagwan

An Efficient & Effective Feature Subset Selection for High Dimensional Data 486
Swapnil Ramesh Kumbhar, Siddheshwar Vilas Patil

Pearson Correlation Coefficient Analysis (PCCA) on Adenoma Carcinoma Cancer 492
Mujahid Adnan KR, Chandrasegar Thirumalai

Analysis of Global Warming in India over Maximum Temperature using Pearson and Machine Learning 496
Chandrasegar Thirumalai, Gajavelli Saikrishna, C Suprabath Raju, Senthilkumar M

Implementation of Image Fusion Based on Wavelet Domain using FPGA 500
Manasa Pemmaraju, Sai Chand Mashetty, Srinivas Aruva,Mohanshankar Saduvelly, Bharat Babu Edara

Voice controlled Humanoid Robot with artificial vision 505
U Bharath Sai, K Sivanagamani, B Satish, M Ranga Rao

Design and Implementation of Smart Solar LED Street Light 509
Viraj Bhosale, Maheshkumar Bhairi, Manohar Edake, Bhaskar Madgundi Shubhangi Kangle

Performance of Branch Predictors of a CPU 513
Atul Oak, R.D. Daruwala

An approach of Knowledge representation with dhAtu-roop using Paninian framework of Sanskrit Grammar
Bhavin Panchal, Vishvajit Bakrola, Dipak Dabhi

Detection of Leukemia and its Types using Image Processing and Machine Learning 522
Preeti Jagadev, H.G.Virani

Species Recognition Using Audio Processing Algorithm 527
Rahulkumar P. Tivarekar, Hassanali G. Virani

A Novel Study on Color Image Denoising and Comparison of Various State-of-the-art Methods 533
Sidheswar Routray, Arun Kumar Ray, Chandrabhanu Mishra

Study of Back-Propagation and Self Organizing Maps for Robotic Motion Control: A Survey 537
Sonali B.Wankhede

Study and Implementation of IOT based Smart Healthcare System 541
Naina Gupta, Hera Saeed, Sanjana Jha, ManishaChahande, Sujata Pandey

Implementation of Re-encryption Based Security Mechanism to Authenticate Shared Access in Cloud Computing 547
Neha Mahakalkar, Vaishali Sahare

Traffic Information Verification Techniques in VANET: A Review
Bhumika Patel, Fenil Khatiwala, Vijay Reshamwala 551
Mitigating Techniques of Black Hole Attack in MANET: A Review
Monika Mistry, Purvi Tandel, Vijay Reshamwala 554
TURBO Coded OFDM Performance analysis For Digital Video Broadcasting
G.Rajeswara Rao, G.Sasibhushan Rao 558
An Improved Digital Watermarking Technique Based on 5-DWT,FFT & SVD 561
Ninny Mittal, Anand Singh Bisen, Rohit Gupta
An Improved Image Steganography based on 2-DWT-FFT-SVD on YCBCR Color Space 567
Sunil Kumar Yadav, Manish Dixit
Search for Secure Data Transmission in MANET : A Review
Tosha Naik, Fenil Khatiwala, Achyut Sakadasariya 573
AODV modification to address link breakage issue : A Review
Yashi Choksi, Purvi Tandel, Trushna Khatri 576
Normalization Using Improvised K-Means Applied in Diagnosing Thyroid Disease with ANN 579
Kunal Mahurkar, D. P. Gaikwad
An Efficient Channel Selection based on Task Classification
A.Karthika 584
Design of Y shape gas carburetor for homogeneous mixture
Prashant Anil Rokade, Sanjay D. Yadav
Novel ABC Based Training Algorithm for Ovarian Cancer Detection Using Neural Network 594
Aditya Singh, Divya Kumar
Smart Energy Meter Using Arduino and GSM
Sneha Chaudhari, Purvang Rathod, Ashfaque Shaikh, Darshan Vora, Jignesha Ahir 598
Design of Split Ring Resonator Embedded Metamaterial Monopole Antenna for Short Range Communication 602
Dalfiah.J, Dabu Karuppasamy
Design & development of IVN(In vehicle network) proto concept for vehicle parameter monitoring & control 607
Mayur A Bhosekar, V.V.Khatavkar

Intrusion Detection System using Hybrid Fuzzy Genetic Algorithm 613
Sumalatha Potteti, Namita Parati

A New Algorithm Combining Substitution and Transposition Cipher Techniques for Secure Communication 619
Umang Bhargava, Aparna Sharma, Raghav Chawla, Prateek Thakral

Implementation of Unimodal to Multimodal Biometric Feature Level Fusion of Combining Face Iris and Ear in Multi-Modal Biometric System 625
Shradha D.Jamdar, Yogesh Golhar

Color Image Dual Watermarking using DCT and DWT Combine Approach 630
Dimple Bansal, Manish Mathuria

Analysis of GSM Air interface using DVB-T Receiver and GNU Radio 635
Kinjal Aggrawal, Mansi Kamani, Khyati Vachhani

Arduino based Smart Electronic Voting Machine 641
V. Kiruthika Priya,V. Vimaladevi, B. Pandimeenal, T. Dhivya

Hydroponics Farming 645
Rahul Nalwade, Tushar Mote

Detection of Object in Motion Using Improvised Background Subtraction Algorithm 651
Prerna Dewan, Rakesh Kumar

An Improved Linux Firewall Using a Hybrid Frame of Netfilter 657
Nivedita, Rakesh Kumar

Performance Analysis of Energy Efficient Algorithm for MIMO Based CRN with Antenna Selection and Maximal Ratio Combining 663
Ashwani Singh, Hariharan S

Process Design Kits for RF Analog & Mixed Signal Design Methodologies enabling Silicon Success 669
Mayank Chakraverty, Krishna Arla Prabhu, Harisankar PS

Improving Replication Results through Directory Server Data Replication 677
Raksha Patil, Madhuri Zawar

Survey on Design challenges and Analysis of service Architecture of DRM 682
T.S.Srinivas, V.B.Narasimha, M.E.Puroshothammam

Analysis of Scheduler Settings on the Performance of Multi-core Processors 687
Sunita Dhotre, Suhas Patil, Pooja Patil, Rucha Jamale

Temperature and Heart Beat Monitoring System Using IOT 692
G. Vijay Kumar, A.Bharadwaja, N.Nikhil Sai

Parallelization of Graph Labeling Problem in Multicore using OpenMP 696
R.Muthuselvi, M.Muneeswari, K.Sudha, V.Vasantha

Evolution and Prediction of Radical Multi-Dimensional E-Learning System with Cluster based Data Mining Techniques 701
N.V. Krishna Rao, N Mangathayaru, M. Sreenivasa Rao

Experimental Studies on Realization of Underwater Optical Communication Link 708
Amardeep Kumar, Ramavath prasad Naik, U. Shripathi acharya

Intelligent Security Lock 713
Varad Pandit, Prathamesh Majgaonkar, Pratik Meher, Shashank Sapaliga, Sachin Bojewar

Implementation of Devanagri Character Recognition System Through Pattern Recognition Techniques 717
Snehal R. Pachpande, Anagha N. Chaudhari

Backbone-Based Interflow Network Coding and Compression in VANETs 723
Glymalakshmy G, Latha R Nair

Crime Identification using FP-Growth and Multi Objective Particle Swarm Optimization 727
Shivangee Agrawal, Vikas Sejwar

Parallel Decision Tree with Map Reduce Model for Big Data Analytics 735
Arati Koli, Swati Shinde

Modelling of a GaAs based Infrared LED with high efficiency and minimal computation time 740
Joyjit Chatterjee

Automatic Plant Monitoring System 744
K. Krishna Kishore, M. H. Sai Kumar, M. B. S. Murthy

Design and Analysis for Improving Reliability and Accuracy of Big-Data based Peripheral Control through IoT 749
M. Sandhya Rani, B Geeta Vani

Facial Expression Controlled Robot 754
A. Sri Yasaswini, B.Akshitha, R Sai Suchitra, M Ranga Rao

EEG Signal Artifact Removal Using ORICA Algorithm 758

Deepak Bansal, R.K. Sharma

DWT based Epileptic Seizure Detection from EEG signal using k-NN classifier 762

Harender, R.K. Sharma

Visual Quality Restoration & Enhancement of Underwater Images Using HSV Filter Analysis 766

Shailendra Kumar Dewangan

Mapping of terms between Healthcare Providers and Patients 773

Judah Benhur Varma, K. Deeba

Implementation Of Biometric Smart Card Using Multi Biometrics 777

R.Tamezheneal, S.Sumathi

Classification and Detection of Ovarian Cysts in Ultrasound Images 783

G Vasavi, S Jyothi

Low-pass Filtering in CSD space and Sparsity based Denoising 788

Haritha G, Manju Manuel

Design of Highly Nonlinear Photonic Crystal Fiber for Supercontinuum Generation 793

Neethu S Thankan, Joyce George

Blur type inconsistency based image tampering detection 798

Amrutha S, Manju Manuel

Reconfigurable Digital FIR Filter Bank for Hearing Aids Using Minimax Algorithm 803

Reshma A S, Manju Manuel

On an Effort to Enhance Lifetime of A Regression based Clustered Network using Candidate Selection 809

K Lakshmi Joshitha, A Gangasri

Design of a Low-voltage Low Power Dynamic Latch Comparator for A 1.2-V 0.4-mW CT Delta Sigma Modulator With 41-dBm SNDR 815

Tuhinansu Pradhan, Amit Bakshi

FPGA Implementation of Min-Sum Algorithm for LDPC Decoder 821

Sreemohan P V, Nelsa Sebastian

Strengthening Password Security through Honeyword and HoneyEncryption Technique 827

Vasundhara R.Pagar, Rohini G.Pise

Comparative analysis of various Channel Estimations under different Modulation Schemes 832
Indu Chandran, M.Raju, K.Ashoka Reddy
Design and Implementation of FIR Filter with modified Product Accumulation Block using Booth Multiplier 838
Nisha Chaudhary, Shewta Meena
T- shape Microstrip Patch Antenna for WiMAX Applications
G.Krishna Reddy, Vikram S. Kamadal, D.Punniamoorthy, G. Venu Gopal, K. Poornachary 842
Bankruptcy Prediction Model Using Random Forest
Rachana Ramesh, Shreya Joshi, Shagufta Tahsildar
Automatic ration material dispensing system using GSM and RFID technology 852
Aishwarya M, Ananya K Nayaka, Chandana B S, Divyashree N, Padmashree S
Dielectric Pocket Ge-source Double Gate Junctionless MOSFET with improved OFF- Current and Subthreshold Characteristics 857
Neelam Kumari, Shweta Meena
Detection of Heart Conditions using HRV Processor in MATLAB Simulink 861
Anshul Malik, R.K. Sharma
Study of R Peaks using HRV Processor in MATLAB Simulink 865
Himanshu Chhabra, R.K. Sharma
Cost Aware Test Suite Reduction Algorithm for Regression Testing 869
C.P.Indumathi, S.Madhumathi
Dynamic Load Balancing Strategy in Software-Defined Networking 875
Saket Bhelekar, Mrdvika Iyer, Gargee Mehta, Sheetal Chaudhari
Face Recognition and Detection using Neural Networks 879
Vinita Bhandiwad, Bhanu Tekwani
Transformation of SQL system to NoSQL system and performing Data Analytics using SVM 883
Sanket Ghule, Ramkrishna Vadali
Solar PV based resonant inverter for induction cooker 888
Farheen Naaz Ansari , K Subramanian
FPGA Implementation of Encoder and Decoder for Golay Code 892
Allan Jose, Sujithamol S

A Robust Technique for Splicing Detection in Tampered Blurred Images 897
Ambili B, Nimmy George

Fixed Latency Serial Transceiver with Single Bit Error Correction on FPGA 902
Aiswarya A.S, Anu George

Automatic Recognition of Facial Expression Using Features of Salient Patches with SVM And ANN classifier 908
Varanya P V, Anu George

Smart Luggage 914
P. Sai Vamsi, V. Madhava Sarma, S.V.Y.S. Samraj, S.R. Deepika, N. Neha, K. Prabhakara Rao

Opportunistic Subcarrier Allocation scheme for FFR-aided LTE networks 919
K.Srinivasa Rao, N.Roopa Vathi

Design and Implementation of different types of Full adders in ALU and leakage minimization 924
Sushant Kumar Pattnaik, Umakanta nanda, Debasish Nayak, Soumya R.Mohapatra, Aditya B. Nayak, Anwesha Mallick

Feature Selection Based Intrusion Detection System Using the Combination of DBSCAN, K-Mean++ and SMO algorithms 928
Vandana Shakya , Rajni Ranjan Singh Makwana

A Survey: On Data Deduplication for Efficiently Utilizing Cloud Storage for Big Data Backups 933
Anand Bhalerao, Ambika Pawar

Implementation on an approach for Mining of Datasets using APRIORI Hybrid Algorithm 939
Kajal R. Thakre, RanjanaShende

A Model for Forecasting Dengue Disease Using Genetic based Weighted FP-Growth 944
Vandana Rajput, Amit Manjhvar

A Compact Four Element UWB MIMO Antenna 949
P Naveen Kumar Reddy, S Anuradha

Random Dopant Induced Threshold Voltage Variation Analysis of Asymetric Spacer FinFETs 953
Navdeep Gehlawat, Gaurav Saini

An Assessment Framework of SIAM/ARAI Fuel Efficiency using Semi-Supervised and Similarity Methods 957
Chandrasegar Thirumalai, Kolisetty Sidhardha, Kalyan Kumar D, Devireddy Vinod Kumar Reddy
Study of Self-Heating Effects on Fully Depleted SOI MOSFETs with BOX layer Engineering 962
Sudhanshu kumar pandey , Gaurav saini
Simulation Study of Permanent Magnet Synchronous Generator (PMSG) connected to Variable speed Wind Energy Conversion System (WECS) 966
Anjana Jain, Shashwat Trivedi, Paras Sharma, Shyam Gopal Reddy, R. Chaitanya, Dr. Shankar. S
IOT based wearable biomedical monitoring system 971
Supriya Kale, Satendra Mane, Pravin Patil
Online User Behavior: A Decade's Perspective 977
Dhanashree Deshpande, Shrinivas Deshpande
Impact of Modifiable and Non-Modifiable Risk Factors on the Prediction of Stroke Disease 985
Priya Govindarajan, Ravichandran KS, Sundararajan S, Sreeja S
Performance Evaluation of Different Routing Protocols For 802.11b and 802.11n 990
Prerana Dhanaraj Mahajan, Shraddha Panbude
Prediction of Diabetes Disease using Control Chart and Cost Optimization-Based Decision 996
Chandrasegar Thirumalai, K Vamsi Krishna, G V SaiSharan, Kota Jayadev Senapathi
Calculating the User-item Similarity using Pearson's and Cosine Correlation 1000
Dharaneeshwaran N, Srinivasan A, Nithya S, Senthilkumar M
Detection of Colorectal Carcinoma Cell using Cantilever based MEMS Bio-Sensor 1005
Syed.shameem, P.S.srinivas babu
FPGA Implementation of Image Enhancement Technique for Automatic Vehicles Number Plate Detection 1010
Rahul Shandilya, RK Sharma
Low Power Positive-Edge Triggered D-type flip-flop 1018
Rahul Shandilya, RK Sharma

Dynamic Analysis of Luo Converter With All Parasitics 1024
Deepa.K, MD.Fayaz Baig, P.Mohith, A.V. Abhinav

Real Time Detection and Reporting of Vehicle Collision 1029
Parag Parmar, Ashok Sapkal

Sigma Delta Analog to Digital Converter: Design and Implementation with reduction in Power Consumption 1035
Neha Gandhi, Sushma Shelke

Implementation of One Cycle Control for a Stand Alone System 1040
V. Sailaja, K. Deepa, Aniket Sahare, E. Pranaynath Reddy, G. Krishna Sai Reddy

Examination of Sea-Surface Temperature, Salinity and Water Level Predicted by Coastal Ocean Models utilizing Box-Plot Method 1044
Chandrasegar Thirumalai, L. Alice Auxilia, K. Sowmiya, E. Kavitha

Far Field Prediction of a PCB Using Simulation and Validation 1048
Gokarna Patil,Pratibha Shingare, Rajesh H, Sunil Dandge, R S Mahajan

Data analysis using Box and Whisker plot for Functional Point
Divagar K, Deepchandar E, Kavin K, Kumaran U

Prediction of Benign and Malignant Tumor 1057
Kriti Sharma, Apoorva Rani, Brahimini Muktha, Chandrasegar T

Design and Analysis of Meanderline PIFA Antenna with MIMO System for Mobile Handheld Device 1061
Jayendra Rahul Toro, Yogesh Kumar Choukiker

An Experimental Investigations on Classifiers for Brain Computer Interface (BCI) based Authentication 1066
E.Grace Mary Kanaga, Muthu Kumaran, M.Hema, R.Gowri Manohari, Tina Anu Thomas

Data analysis using Box and Whisker plot for Stationary shop analysis 1072
Vignesh V, Dinakaran K, Pavithra D, Chandrasegar Thirumalai

Analyzing Complexity Nature Inspired optimization Algorithms using Halstead Metrics 1077
Madhan M, Anbuarasan T, Dhivakar I, Chandrasegar Thirumalai

Data analysis using Box plot and Control Chart for Air Quality 1082
Praveen V, Delhi Narendran T, Pavithran R, Chandrasegar Thirumalai

Analyzing User Knowledge by Pearson and Spearman Method 1086
P Yuvaraj, R Anirudh, Sharmila J, Chandrasegar Thirumalai

Analysis of Age, Astigmatic and Tear Protection Rate in Contact Lenses Selection 1090
Jagadish D, Vasanth Kumar J, Kumaran U, Chandrasegar Thirumalai

Remote sensing HSI Classification and estimation of mimetite mineral spectral signatures from ISRO,India 1095
Shanti Swamy, S.M.Asutkar, G.M.Asutkar

Bare-Metal Agent Architecture for Target Communication Framework 1100
Shashanka Navada, Arun M, Srimukhee Balasubramanian

SFCW Ground Penetrating Radar for soil profile measurement simulation mode user interface 1106
Poonam Prabhakar Dive, Anil Kulkarni, Rama Rao, Ajay Khandare, Shraddha Panbude

Software Complexity Analysis Using Halstead Metrics 1109
Hariprasad T, Seenu K, Vidhyagaran G, Chandrasegar Thirumalai

Heuristic Prediction of Rainfall Using Machine Learning Techniques 1114
Chandrasegar Thirumalai, M Lakshmi Deepak, K Sri Harsha , K Chaitanya Krishna

Calculating the Heart Disease in Switzerland using Pearson's Correlation 1118
Kalyanasundaram R, Tamizhselvan BR, Ajay Prasanth, Kumaran U

Evaluation of McCabe's Cyclomatic Complexity Metrics for Secured Medical Image 1122
V Shanthi, G Krishna Chaithanya, Jeevana P, Chandrasegar Thirumalai

Analyzing the Linked List complexity using Correlation methods 1127
K Sravani, D Pavithra, S Dhanya, Chandrasegar Thirumalai

Nature Inspired Algorithm 1131
Ajay Adithyan T, Gururaj B, Vasudha Sharma, Chandrasegar Thirumalai

Relation Classification from Unstructured Medical Text using Feature Based Machine Learning Approach 1135
Saumaya Gupta, Amit Kumar Manjhvar

Analysis on Diabetes Patients Using Pearson, Cost Optimization, Control Chart 1139
Poovarasan R, Yuvashree K, Keerthi S, Chandrasegar Thirumalai, IEEE Member

Quantitative Performance Analysis of Face Recognition System 1143
S.Srilatha, A.R.Pallavi, R.Uma, Srinivas Koppu

Analysis of LOC attributes using code analyzer and Correlation methods 1147
Ganguri Srilatha, Pathi Sreshta, R Madhumathi, Chandrasegar Thirumalai

Analyzing Correlation Coefficient using Software Metrics 1151
Ujera, Sudha R, Ragavi V, Chandrasegar Thirumalai

Application of High Utility mining for Pattern Prediction 1154
SHASHIKALA KAKARADDI (PATIL) , Sachin Bojewar

Digital Image Compression Hybrid Technique based on Block Truncation coding and Discrete Cosine Transform 1159
Nehal Markandeya, Sonali Patil

Improved Rendezvous Nodes based LEACH using Multiplexing of Sensed Data 1163
Isha Mahajan, Sanjeev Mahajan, R.C Gangwar

easy Connect(eC) 1169
Anusha Chare, Krutika Dhakate, Neeraj Joshi, Arun M, Hariharasudhan V

A DETAILED STUDY ON MACHINE LEARNING TECHNIQUES FOR DATA MINING 1175
Sivaramakrishnan R Guruvayur, Suchithra R

A Model for Forecasting Dengue Disease Using Genetic based Weighted FP-Growth

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***Abstract*— In few years, Data Mining is a big and motivating research area in medical & healthcare department. It is helpful to find profitable and successful systematic method in wellbeing data. It is helpful to forecast the different diseases like-Dengue fever, Cancer, Diabetes, heart disease etc. A big agreement of reading former conceded out on disease detection using an optimization technique to palliate the drawbacks of conventional approaches. In our paper, we have to design a novel model for forecast the dengue disease. Here, we use genetic algorithm to calculate the actual weight of attributes afterwards applied the FP-Growth with actual weight. Theoretical study and experiments have displayed that the modified approach is able to detect the virtual significance of attributes in requisites of their weights. This model are deliberate and the parameters are set to get optimal forcast performance. At last, the outcome displays that the model produces the better prediction.**

***Keywords*— Data Mining (DM) , Dengue Fever, Medical Data Mining, Genetic Algorithms (GA), Weighted FP-Growth.**

I. INTRODUCTION

At this time, Data Mining (DM) is well-suited technology in every field. Data mining is a step of KDD process which is used for extract the useful information or pattern from huge amount of data. Now days, DM is also applicable and most emerging research area in health and medicinal sector. In medical area, Data mining gives a few points of interest, for example, identification of disease, treatment at lower cost, recognize reason of sickness etc. The convenience of gigantic measures of medicinal data immediate the necessity for effective data analysis devices to remove helpful learning. Specialists have for a long while been concerned with applying true and DM tools to enhance data examination on extensive data sets. Disease forecast is also most applicable area where DM tools are demonstrating fruitful outcomes. As of late, researchers have been examining the impact of hybridizing beyond strategy demonstrating upgraded brings about the determination of dengue disease. Nonetheless, DM approaches to distinguish a reasonable treatment for dengue sickness patients has gotten less consideration [1].

More than the very last 15 years, DF has spread more rapidly and over a wider range. Millions of dengue suitcases are diagnosed every year, and about 20,000 patients die from the disease annually. Still, the malady are generally considered difficult issue in the pasture of illness avoidance and control[2].

Dengue fever (DF) is an influenza-like sickness increase by the chomp of a tainted mosquito which is speedy rising as a noteworthy medical issue. DF is a sickness brought on by dengue contamination and is otherwise called break bone fever is broaden by Aedes mosquito. Bleeding , Lower blood platelets, Low circulatory strain, Metallic feel in mouth, Headache, Joint pain, Rashes are some sign of dengue disease. Dengue is categorized as two classes, i.e., class 1 and class 2. Initial one is conventional dengue called dengue fever as well as the other is dengue hemorrhagic fever. DF is a deadly acute mosquito-born transmittable infection produced by the dengue germs. Dengue ferment is a state of high temperature of sickness brought around by the Single-stranded RNA flavivirus. Dengue might be misdiagnosed as different diseases: flu, typhoid, zika, jungle fever. At hand , Particular pharmaceutical or antibiotic accessible to treat it are not available. Dengue fever happens in form of cycles and this cycle is available inside the body of a tainted individual for two weeks or under two weeks[3].

Although recently there have a few studies on dengue prediction model, unfortunately on our observation some of those models still have constraint in requisites of parameter and accuracy. So far , we needed more discussion about the reasonable model to forecast the future dengue outbreak. From the research displays that this approach may resolve the complexity of finding a suitable parameter and it promise to predict accurately and rapidly.

This paper proposes the model with genetic algorithm and weighted FP-growth for foreseeing dengue disease precisely. The remaining part of the paper, we can define as; Section II portrays medical data mining. Section III runs some background of related work. Proposed methodology covered in Section IV. Section V talks about the experimental outcomes and analysis. At long last, conclude the paper and further scopes are condensed in Section VI.

II. MEDICINAL DATA MINING

2.1. Issues in Medicinal Data Mining

Medicinal data Mining is to be notable along with the most difficult fields of Data Mining. As present is a nonstop increment in the quantity of patients because of different diseases, the best test lies in early diagnosis and foreseeing of diseases with high order exactness. In clarification, Data mining can deal with this issue [4].

2.1.1 Data Related Problems

With the rapid growth of database technology, information technology has penetrated into various fields, including medicine Many large and medium-sized hospitals have set up HIS own hospital information system (HIS), with the application and development of HIS, amount of data in the database rapidly expand, the database scale expands gradually, increasing complexity[5].

There was a time when online clinical data of health related were not easily available. As data size goes on increasing, although, restriction in computational abilities that prohibit the employ of practical application in mathematical models. Currently all medical data and of all the types are not only for analysis but resources for computation are also available that supports variety of sophisticated methods. Much software which was introduced earlier is not relevant for analyzing the clinical data in describing the treatment required by patient by diagnosing the problem. Data from health industries arises in the unstructured form so it is obligatory to covert them in structured form and reduces its size into nominal value with possible solution[6].

IV. LITERATURE SURVEY

Nirbhay Mathur et. al (2016) he proposed model is limited model for dengue rates, in spite of the reality the model can find the right position for the vulnerability map. Alongside the forecast demonstrating on data utilizing centroid model and distribution model based on K-means and Expectation Maximization (EM) algorithms individually.The outcomes are approved for a small local region (Petaling region of Selangor state) in Malaysia and they indicated defenselessness hotspot in imagining the dengue occurrences. Subsequently, the proposed technique can confine the way of dengue frequency which can further be used for vector disease controlled process[7].

Shiladitya Saha and Sankhadip Saha (2016) design an astute processing models utilizing multilayer perceptron and SVM for categorizing real and native cases of dengue. For decision taking, Dempster-Shafer based classifier combination methodology is connected here to frame a board of forecast machine for better result. Comes about demonstrate that DS hypothesis gives as best as 96.02% with 4 MLPs and 3 SVMs while that of chose elements utilizing Fishers Score gives 96.56% accuracy[8].

Dini Rahmawati and Yo-Ping Huang (2016) determined the best kernel to categorize the combined data of climatology and statistical dengue fever to build an optimal model that can be efficiently applied to forecast the future outbreak and detection of future event of dengue fever. The C-SVM kernel base is acclimated categorize the object in dataset by using RBF and linear kernels giving significant different results in performance before and after optimizing parameters[9].

Shaufiah and Boby Siswanto (2016) display the research is to see the distinction between the outcomes of Dengue Hemorrhagic Fever (DHF) and Typhoid Fever (TF) on blood test. Consequences of the analysis will determine what parameters that indicate a patient suffering from DHF or TF. The procedure is done by applying the notion of Association rules mining algorithms using IST-EFP algorithm combined with fp-growth algorithm. Performed dimensional reduction on dataset by using IST-EFP algorithm. ARM uses reduced dataset generated by IST-EFP algorithm will still have a meaning that does not change as they should. [10].

Sandip R. Shinde, Poonam S. Bhadikar (2016) proposed approach preface a representation that seeks for the improved concert of the classifier in provisions of accuracy of classification model, number of features to build the model etc. The idea behind of this paper to compare the two different strategies to achieve improved performance. Information gain works for select the attribute subset. This approach is compared with Genetic algorithm based method to discover optimal group of features that adds more to the classification. Then these attributes are given as input to MLP NN by back propagation algorithm[11].

Shermon S. Mathulamuthu et. al (2016) builds a dengue incidence prediction model to avoid epidemic using climate models in real time. DM techniques such as clustering and multiple regression are acclimated representation the data for get the best fitting regression curve. In the later stage, a real time adaptive computation software will be developed that could forecast the dengue incidences immediately. This research is mostly centered on DM techniques and its application in big data machine learning. Particularly in these studies, big data are being processed in machine learning using R-computational software[12].

Wahjoe Tjatur, Shiori Sasaki, Yasushi Kiyoki (2015) presented an ecological context dependent analysis for predicting next situation and determine suitable prevention. This finding is important for implementing specific strategy in specific situation and develop new prediction system by mete-level knowledge base. However, this structure ought to be improved to increase the exactness of prediction by adding more features in ecological context or another context related with creature life cycle[13].

Yoon Ling et. al (2014) generate a prediction risk map. They utilized Boosted Regression Trees (BRT) to represent nonlinearities and connections between the components with high prescient correctnesses. This model with a cross-approved execution score (Area Under the Receiver Operator Characteristic Curve, ROC AUC) of 0.81 demonstrated that the largest part of fundamental land utilize variables are human settlements (show significance of 39.2%), trailed by water bodies (16.1%), blended agriculture (8.7%), open land (7.5%) and dismissed meadow (6.7%).Our observations possibly a necessary quality for humanizing surveillance and control interventions for dengue[14].

Chien-Hua Wang, Sheng-Hsing Liu and Chin-Tzong (2012) proposed fuzzy partition technique and choose membership function (MF) of significant estimations of every transaction thing. Additionally, from managers they can mirror the consequence of things as linguistic terms, which are changed as fuzzy sets of weights. Next, fuzzy weighted FP growth is utilized to finish the procedure of data mining. The strategy above is relied upon to enhance Apriori algorithm for its better productivity of the entire association rules[15].

V. PROPOSED METHODOLOGY

A. Genetic Algorithm

A genetic algorithm (or GA) is a heuristic search optimization method used in soft computing to discover true or estimated results and search problems. Genetic algorithms are a specific class of metamorphic algorithms that is inspired by nature of science for example , adaptation, selection, crossover (also called recombination) and mutation. A GA is a seeking heuristic strategy, motivated by the laws of genetics, which is helpful to resolves the complex problems. It work on two essential factor first one is endurance of fittest and another is genetic diversity. In this process, firstly generate the random solutions of every one member population. Each individual comprises set of characterstics of its chromosomes. Then, by using of genetic operator on chromosomes produce a next population of individuals[16]. It is done to find best solution to given criteria. This can be finding by using fitness function.

B. FP-Growth

The FP-Growth Algorithm is an effective and versatile strategy for discovering the total frequently occurs rules via sample fragment growth, utilizing an amplified prefix-tree structure for putting away dense and critical information about frequent patterns named frequent-pattern tree (FP-tree)[17].

1) WEIGHTED _FPGROWTH

Weighted_FP-Growth is an updated algorithm considers a weight as a parameter to finding the meaning of an attribute. The importance is a general parameter whose value fluctuates from individual to individual. In this altered adaptation we generates actual weight values (from 0.0 to 1.0) using genetic strategy for MATLAB. The working rule of Weighted_FP Growth actualizes an idea of building Frequent-Pattern tree by pruning those attributes/ items from the database whose weights are below the minimum weight threshold and afterward embeddings the remaining items to the tree and furthermore having more support count than the minimum threshold value. We have design the updated version in MATLAB using a few alterations in the already developed version of FP growth[18].

PROPOSED ALGORITHM:

Input : A medical dataset D in encoded form of binary values.
Output: A record of genetic based weighted association rules.

Strategy:

```
Step 1. Select the Dataset (on the basis of symptoms).
Step 2. Apply Genetic Algorithm

1) Initialize the randomly generated Population and estimate
   the fitness value of each individual.
2) Iteration for finding fitness function
      a) Select 2 – members from inhabitants through probability
         relative to their fitness value.
      b) Assign crossover by 80% `population possibility up to
         crossover rate using tournament selection.
      c) Calculate the fitness cost of offspring.
      d) Apply Mutation with 30% population possibility up to
         mutation rate and assess the strength for finding
         mutates values of offspring.
      e) Repeat (a) to (e) until enough members are generated
         to form the next generation.
      f) Sort the population according to fitness function.
      g) Select the truncate population.
3) Repeat step (2) & (3) until stopping criteria is met.

Step 3. According to fitness function and values of attributes,
we calculate the weights.
Step 4. Select those attributes whose satisfied the
min_threshold weight which is initially set.
Step 5. Apply weighted FP-growth[19].
Step 6. Generate the rules.
```

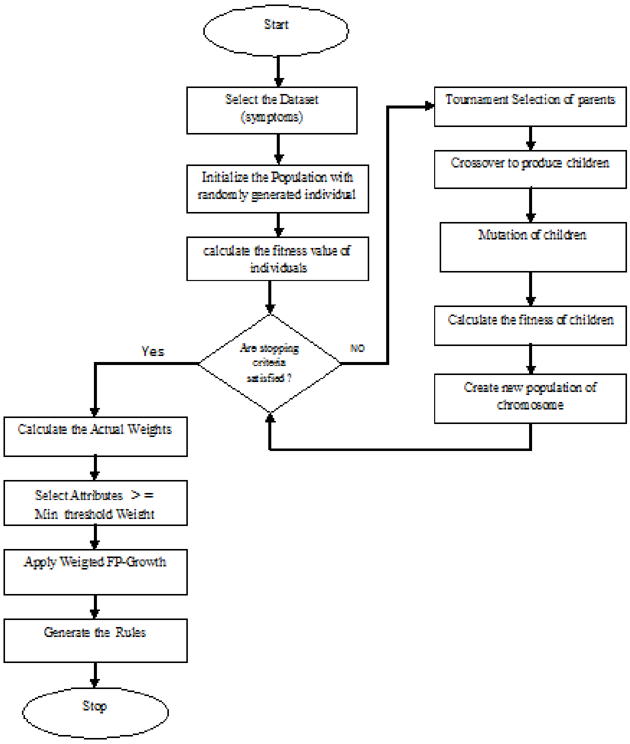

Fig.1. Flowchart of Proposed Methodology

VI. EXPERIMENTAL RESULT AND ANALYSIS

After examine existing method, we have develop a novel model used for better prediction. It generates a FP- tree (in Fig. 2) with values of support and weight that are greater than minimum support and minimum weight values.

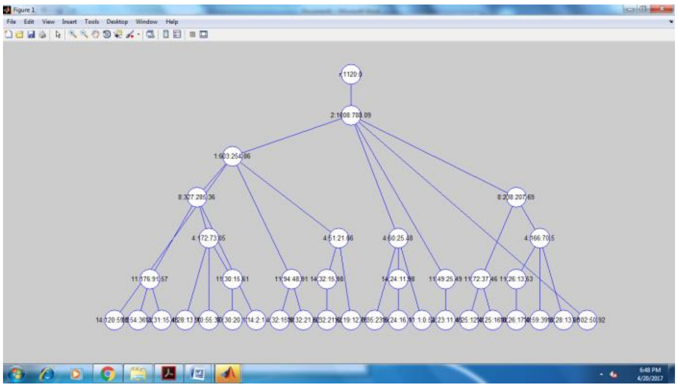

Fig.2. Generated Tree (Results)

In Fig.3, we shows the comparison graph between existing approach and proposed approach. We match up to the weights at different-different attributes.

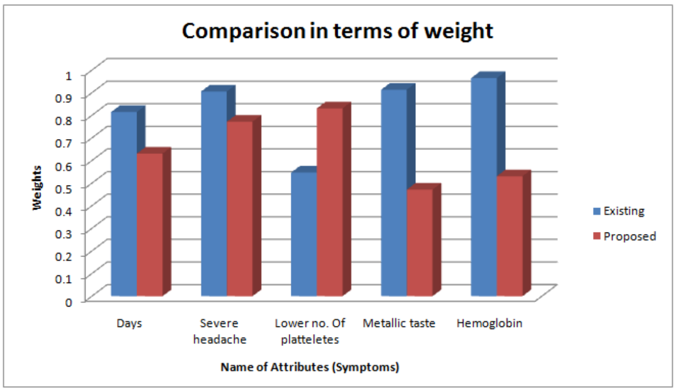

Fig.3. Comparison graph between existing method and proposed approach

In Fig.4, We examine the performance of our projected method with weighted FP- growth algorithm as far as time overcome with test dataset. It observed that an elapsed time are reduced by the proposed approach.

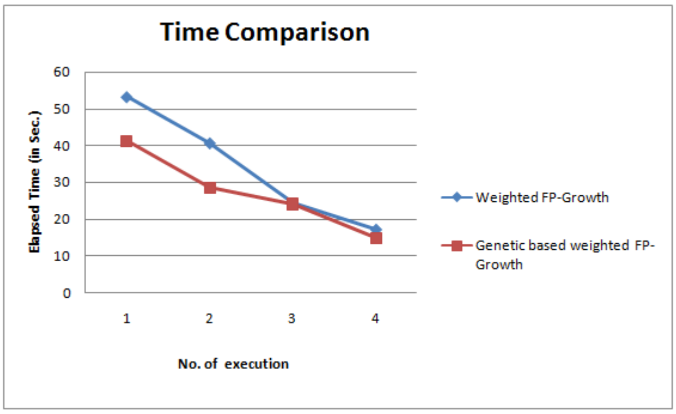

Fig.4. Time Comparison Line Graph

After execution our proposed approach, We have observed generated total patterns are less than in compare to existing approach at different-different support values (in Fig.5).

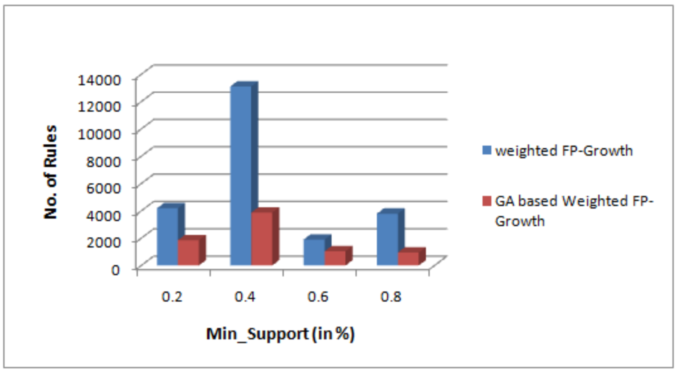

Fig.5. No. of rules generated with different min_support values

VII. CONCLUSION

The main purpose of this research paper was propose the design a model and outline our preliminary results. From these results, we conclude that the approach which is genetic algorithm based for the determination of actual weight in weighted FP-growth. It may possibly be a very promising approach for forecasting dengue disease. However this preliminary experiment not represents the real dataset since the created synthetic dataset was used. The outcome displays that this approach produces the better prediction compared to weighted FP-Growth.

Therefore, in the prospect we will include the real data using different architectures with an another optimization techniques on other parameters to define the best architecture for early prediction.

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