

Integrated Analysis: Gene Expression, Survival, Biomarkers, and Drug Targets

Submitted in partial fulfilment of the required for the award of
Master of Science Degree in Bioinformatics and Data Science

BY

ANUSHA.R(43739023)



**DEPARTMENT OF BIOINFORMATICS AND DATA SCIENCE
SCHOOL OF BIO AND CHEMICAL ENGINEERING**

SATHYABAMA

**INSTITUTE OF SCIENCE AND TECHNOLOGY
(DEEMED TO BE UNIVERSITY)**

**Accredited with Grade “A++” by NAAC | 12B Status by UGC |
Approved by AICTE**

JEPPIAAR NAGAR, RAJIV GANDHI SALAI, CHENNAI - 600 119

April – 2024



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www.sathyabama.ac.in

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BONAFIDE CERTIFICATE

This is to certify that this Project Report is the Bonafide work of R. ANUSHA (43739023) who carried out the project entitled "Integrated Analysis: Gene Expression, Survival, Biomarkers, and Drug Targets" under my / our supervision from January 2024 to April 2024.

Internal Guide

External Guide (if Applicable)

Head of the Department

Submitted for Viva voce Examination held on_____

Internal Examiner

External Examiner

DECLARATION

I R. ANUSHA (43739023) hereby declare that the Project Report entitled “**Integrated Analysis: Gene Expression, Survival, Biomarkers, and Drug Targets**” done by me under the guidance of DR. Jemmy Christy is submitted in partial fulfillment of the requirements for the award of Master of Science degree in Bioinformatics and Data Science.

DATE:

ANUSHA R

PLACE:

SIGNATURE OF THE CANDIDATE

ACKNOWLEDGEMENT

I am pleased to acknowledge my sincere thanks to Board of Management of SATHYABAMA for their kind encouragement in doing this project and for completing it successfully. I am grateful to them.

I convey my thanks to Dr. REKHA CHAKRAVARTHI M.E., Ph.D. Dean of Arts and science for providing me necessary support and details at the right time during the progressive reviews.

I would like to express my sincere and deep sense of gratitude to my Project Guide Ms. MANISHA Department of Bioinformatics and Data Science for her valuable guidance, suggestions and constant encouragement paved way for the successful completion of my project work.

I wish to express my thanks to all Teaching and Non-teaching staff members of the Department of Bioinformatics and Data Science who were helpful in many ways for the completion of the project.

(R. ANUSHA)

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1.TRANSLATIONAL BIOINFORMATICS

1.1GENE EXPRESSION ANALYSIS

INTRODUCTION:

A Biological network represents systems as complex set of binary interactions or relation between various biological systems and can reveal informative patterns within the systems. Cytoscape is a open source software platforms for visualizing molecule interactions network and biological pathway and integrating the network with annotations, gene expression profile. Cytohubba predict and explore the important nodes and edges in given network by several topological algorithm such as degree, bottleneck, MCC, DMNC, MNC, EPC, Eccentricity, Closeness, Stress, Clustering co-efficient and betweenness.

AIM:

Build Network to understand gene interrelationship and regulatory mechanism.

MATERIALS AND METHODS:

GEO2R is an interactive web tool that allows users to compare two or more groups of samples in a GEO series in order to identify genes that are differentially expressed across experimental conditions.

CYTOSCAPE: Cytoscape is a open source software platforms for visualizing molecule interactions network and biological pathway and integrating the network with annotations, gene expression profile.

CYTOHUBBA: CytoHubba provides 11 topological analysis methods including Degree, Edge Percolated Component, Maximum Neighbourhood Component, Density of Maximum Neighbourhood Component, Maximal Clique Centrality and six centralities (Bottleneck, Eccentricity, Closeness, Radiality, Betweenness, and Stress) based on shortest paths.

CLUEGO: ClueGO is a Cytoscape App that facilitates the biological interpretation of large lists of genes and proteins by selecting representative Gene Ontology terms and pathways from multiple ontologies and visualizes them into functionally organized networks.

PROCEDURE:

- For the database on lung adenocarcinoma Geo2R is the source of the geo dataset (GSE118370).
- After choosing the suitable parameters, the Geodataset is retrieved.
- Genes that were upregulated genes were copied and paste into the cytoscape network.
- Built a biological network using a BioGrid in cytohubba to analyse the network and identify importance node based various topologies algorithm to determine the the top 10 gens
- Genes must be copied in cluego and contigue cluego parameter such as species ontology and statistical settings.
- Run cluego analysis to identify functional categories or pathways associated with the selected nodes.

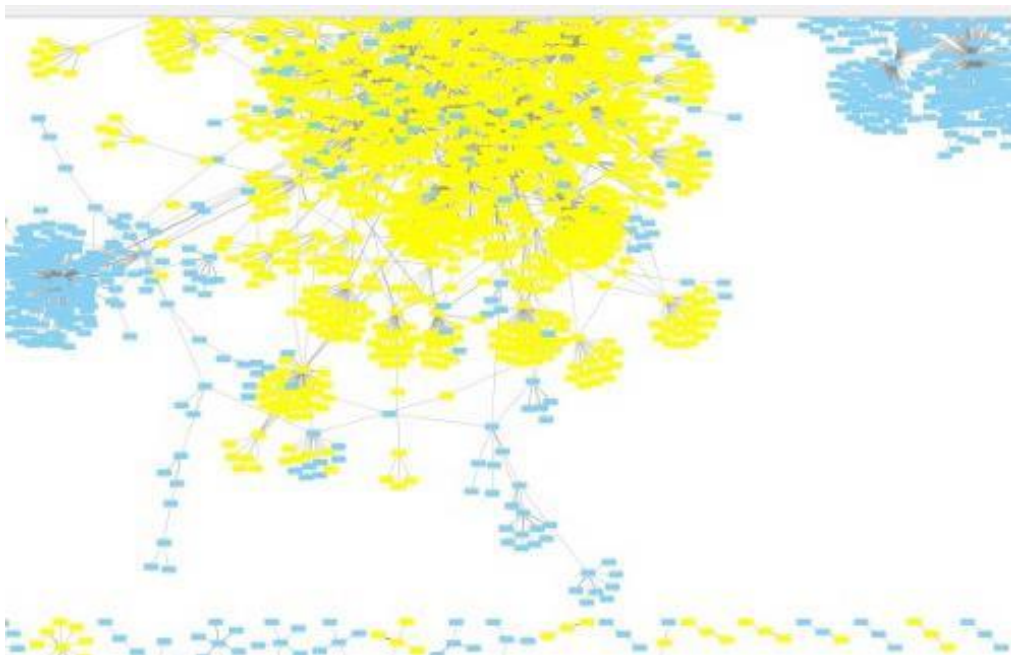


Fig 1: Network Pathway of Upregulated Genes



Fig 2: Graph of functional analysis

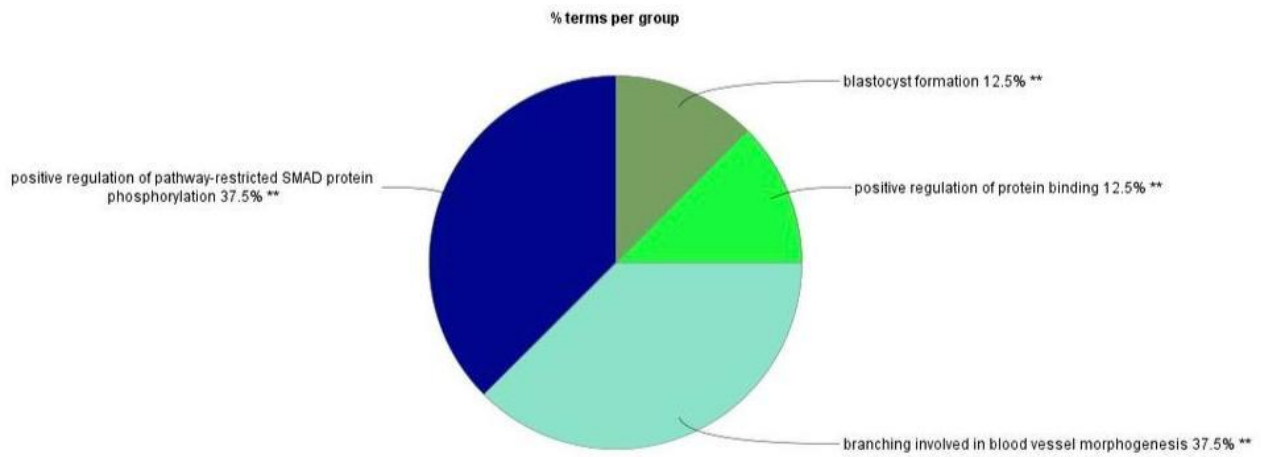


Fig 3: Pie Chart of functional analysis

INTERPRETATION:

Geo Dataset GSE Id: GSE118370

Sample no: 12 samples

Platform: GPL570

Type: Expression profiling by array

No of differentially expressed genes: 251

No of upregulated genes: 129

No of down regulated genes: 122

Network features of up regulated genes: nodes-3597, edges-5686

TERM	FUNCTION	ONTOLOGY
Blastocyst formation 12.5%	Blastocyst formation, occurring at 12.5% function, may suggest impaired embryonic development. In the context of lung adenocarcinoma, this could potentially reflect disruptions in cellular differentiation pathways or genetic predispositions affecting both embryogenesis and cancer progression. Further research is needed to elucidate the precise mechanistic links between blastocyst formation and lung adenocarcinoma.	Biological
Positive regulation of protein binding 12.5%	It indicate a partial dysfunction in cellular signaling pathways crucial for protein interactions. In the context of lung adenocarcinoma, this dysregulation could contribute to aberrant protein-protein interactions, potentially influencing oncogenic processes such as cell proliferation or metastasis. Further investigation is necessary to delineate the specific proteins involved and their impact on lung adenocarcinoma progression.	Biological
Branching involved in blood vessel morphogenesis 37.5%	In lung adenocarcinoma, compromised vessel branching could hinder adequate oxygen and nutrient supply to tumors, promoting hypoxia and	Biological

	metastatic dissemination. Understanding the mechanisms underlying branching defects could offer insights into tumor angiogenesis and potential therapeutic targets.	
Positive regulation of pathway-restricted SMAD protein phosphorylation 37.5%	Increased positive regulation of pathway-restricted SMAD protein phosphorylation (37.5%) in lung adenocarcinoma may potentiate TGF-β signaling, promoting tumor invasiveness and immune evasion, highlighting its role as a potential therapeutic target.	Biological

1.2 Cumulative survival probability calculation using KM Plotter

Introduction:

KM-plotter is the most sophisticated online survival analysis tool, performing all calculations in real time (not loading pre-calculated images). The background database is manually curated. Gene expression data and relapse free and overall survival information are downloaded from GEO, EGA and TCGA. The database is handled by a PostgreSQL server, which integrates gene expression and clinical data simultaneously. To analyze the prognostic value of a particular gene, the patient samples are split into two groups according to various quantile expressions of the proposed biomarker. The two patient cohorts are compared by a Kaplan-Meier survival plot, and the hazard ratio with 95% confidence intervals and log rank P value are calculated. Databases and clinical data are supervised and extended regularly. To avoid missing correlations due to the use of a specific cutoff, all available cutoff values between the lower and upper quartiles of expression are used for the selected gene, and false discovery rate (FDR) using the Benjamini-Hochberg method is computed to correct for multiple hypothesis testing. The cutoff value with the highest significance (lowest FDR) is determined. In case of multiple cutoff values with identical significance, the cutoff with the highest hazard (HR) rate is selected for the final analysis.

Aim

Calculate Proposed gene CDH5 cumulative survival probabilities

Materials And Methods:

KM-PLOTTER: KM-plotter is the most sophisticated online survival analysis, performing all calculations in real time (not loading pre-calculated images). The background database is manually curated. Gene expression data and relapse-free and overall survival information are downloaded from GEO, EGA and TCGA.

Procedure:

- Kaplan Meier plotter home page was accessed using the following hyperlink <https://kmplot.com/analysis/index.php?p=background>
- Proposed gene/protein (o/p of Ex No 1) CDH5 was submitted in the pan cancer portal
- Below listed parameters were opted for analysis
- Restriction subtype –All
- Split patients by-Auto select best cut off
- Survival:Overall survival(os)

- Survival: All

Results

P value: 0.0883

FDR: 100%

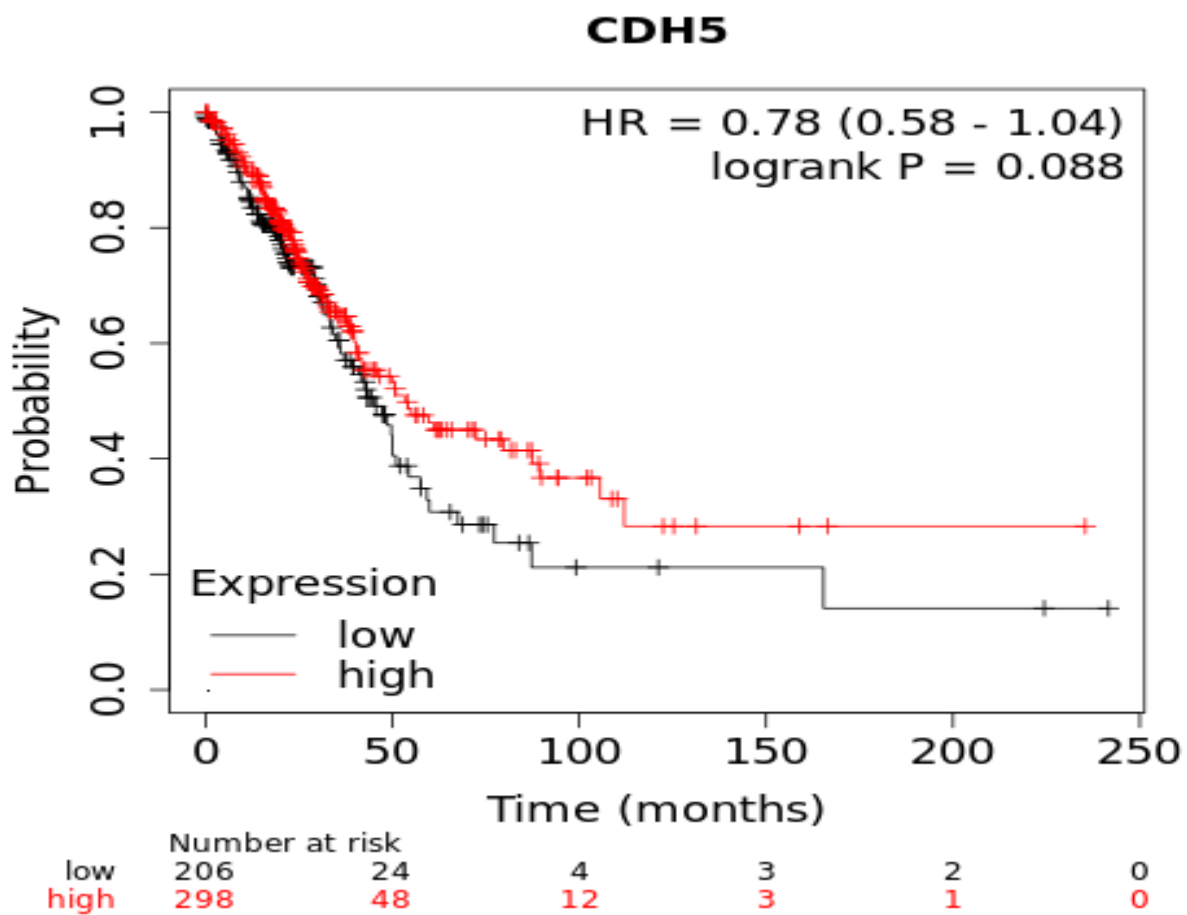


Fig 1: Lung adenocarcinoma

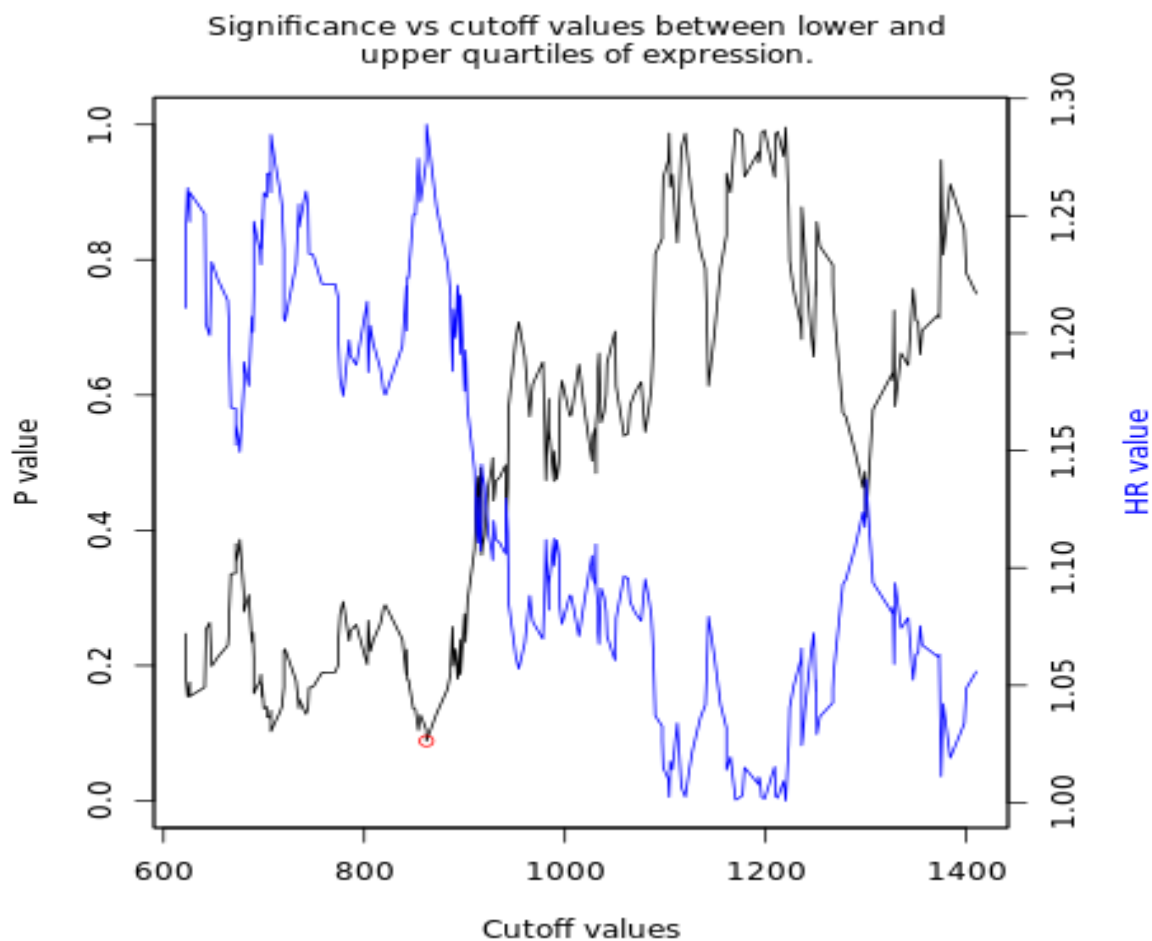


FIG 2: Auto cutoff plot

Interpretation

- KM-plot recognizes proposed gene symbols CDH5 (including HUGO Gene Nomenclature Committee approved).
- Sources for the database include GEO, EGA, TCGA, Metabric, Impact, and PubMed repositories.
- Bladder carcinoma:

HR Rate: 1.4(0.81-1.89)

50% of median survival of probability:

Low expression cohort: 6.23

High expression cohort: 27.83

☐ Breast cancer

HR Rate: 0.76(0.54-1.06)

50% of median survival of probability:

Low expression cohort: 124.53

High expression cohort: 131.97

□ Cervical squamous cell carcinoma

HR Rate: 0.75(0.46-1.21)

50% of median survival of probability:

Low expression cohort: 29.3

High expression cohort: 46.47

□ Esophageal Adenocarcinoma

HR Rate: 0.64(0.29-1.42)

50% of median survival of probability:

Low expression cohort: 32.9

High expression cohort: 261.3

□ Head-neck squamous cell carcinoma

HR Rate: 0.81(0.58-1.13)

50% of median survival of probability:

Low expression cohort: 26.17

High expression cohort: 28.5

1.3 Biomarkers: identifying biological markers for disease

Diagnosis and therapeutic monitoring

Introduction:

The Marker systematically offers five types of therapeutic biomarker, which realized the collective consideration among different drug discovery stages, comprehensively describes the therapeutic biomarker for the largest number of drugs among existing knowledge bases, and extensively covers the largest classes of disease among available databases. Due to the rapid advances in AI technology, the comprehensive data collected by The Marker were expected to have great implication and impact on the clinical development and clinical practice of drugs.

Aim:

Identify the disease markers related to breast cancer and categorize them into pharmacodynamic Biomarker Monitoring biomarker safety biomarkers.

Procedure:

- The marker database was retrieved using following link <http://themarker.idrblab.cn/about>.
- Top listed Mrna/protein Biomarker relevant to the breast cancer data's were retrieved and literature survey was done.

RESULTS:

INTERPRETATION:

BIOMARKER ID	BIOMARKER NAME	CLASS	GENE NAME	BIOMARKER TYPE	REPRESENTATIVE DRUG
B3HTD6	C-Reactive protein	protein	CRP, PTX1	PDY, SAF, MOI, PRD	Trastuzumab

1.4 Drug-Target Interaction Prediction: Approaches for predicting interactions specific to patient treatment and drug design

Introduction:

Drug targets are specific molecules or biological structures involved in disease pathways that can be modulated by drugs to produce a therapeutic effect. Selecting the right drug target is crucial for the development of effective and safe medications.

Swiss Target Prediction: Swiss Target Prediction is an online tool to predict the macromolecular targets (proteins from human, mouse and rat) of bioactive small molecules. This is useful to understand the molecular mechanisms underlying a given phenotype or bioactivity, to rationalize possible side-effects, to predict off-targets and to assess the possibility of repurposing therapeutically-relevant compounds. SwissTargetPrediction is based on the so-called 'similarity principle', which generally states that two similar molecules are prone to have similar properties. In the context of SwissTargetPrediction, we have statistically quantified that two similar bioactive molecules are likely to share their protein targets. Therefore, for a query molecule, we identify the most similar molecules among a set of about 370,000 actives on known targets. The predicted targets are those having the actives displaying the highest similarity with the query molecule.

Aim:

Drug Benzalkonium targets screening and binding assessment.

Materials and Methods:

Swiss Target Prediction:

UniProt: UniProt is a freely accessible database of protein sequence and functional information, many entries being derived from genome sequencing projects. It contains a large amount of information about the biological function of proteins derived from the research literature. It is maintained by the UniProt consortium, which consists of several European bioinformatics organisations and a foundation from Washington, DC, USA.

PDB: The Protein Databank (PDB) is a file format describing the 3D structure of molecules held in protein data bank. The PDB format accordingly provides for description and annotations of protein and nucleic acid structures including atomic co-ordinates, secondary structure assignments as well as atomic connectivity. **Drug Bank:** Drug bank database is a comprehensive, freely accessible online database containing information on drugs and drug targets. This database is a unique bioinformatics and cheminformatics resource that combines detailed drug

Procedure:

1. Disease/Disorder breast cancer associated FDA approved drugs was chosen and smiled notation was retrieved from Pubchem using following link <https://pubchem.ncbi.nlm.nih.gov/>
2. Swisstarget home page was accessed using following link <http://www.swisstargetprediction.ch/index.php>
3. Predicted the targets (Top five) and drug interaction was analyzed using discovery studio Receptor ligand interaction module

INTERPRETATION:

DRUG NAME: Benzalkonium

NO OF TARGET PREDICTED:75

CHOOSEN TARGET:1

HUB GENES SELECTED: PIGG1, GON-10, CSNK2A1, GSK313, NFK133, DHTR, KIAA0901, L00000587, CA3, LIAG.

UNIPROT ID	ENTRY NAME	PROTEIN NAME	GENE NAME	ORGANISM
Q9UBN7	HDAC6-HUMAN	Histone deacetylase 6	KIAA0901	Homo sapiens (human)

name	-PLP1	-PLP2	jain	_pMF	DOCK_SCORE
244	36.59	42.01	0.02	7.67	20.012
244	36.16	41.54	0.07	5.98	20.025
244	36.16	41.54	0.07	5.98	20.025
244	36.39	41.43	-0.17	6.85	20.028
244	36.39	41.43	-0.17	6.85	20.028
244	32.19	37.81	-0.15	5.68	20.102
244	31.79	37.21	0.17	6.14	20.22
244	31.14	36.9	-0.19	5.12	20.226
244	31.14	36.9	-0.19	5.12	20.226
244	31.14	36.9	-0.19	5.12	20.226

Fig 1- Table of Molecules

name	distance	category	type	from	to
244:H16 - A: GLY100:O	2.25848	Hydrogen Bond	Conventional Hydrogen Bond	244:H16	A: GLY100:O
A: GLN96:CA - 244: O1	3.24463	Hydrogen Bond	Carbon Hydrogen Bond	A: GLN96:CA	244: O1
A: GLU101:O - 244	2.89289	Other	Pi-Lone Pair	A: GLU101:O	244
A: HIS107 - 244	4.54152	Hydrophobic	Pi-Pi T-shaped	A: HIS107	244

Fig 2: Table of Non-Bond

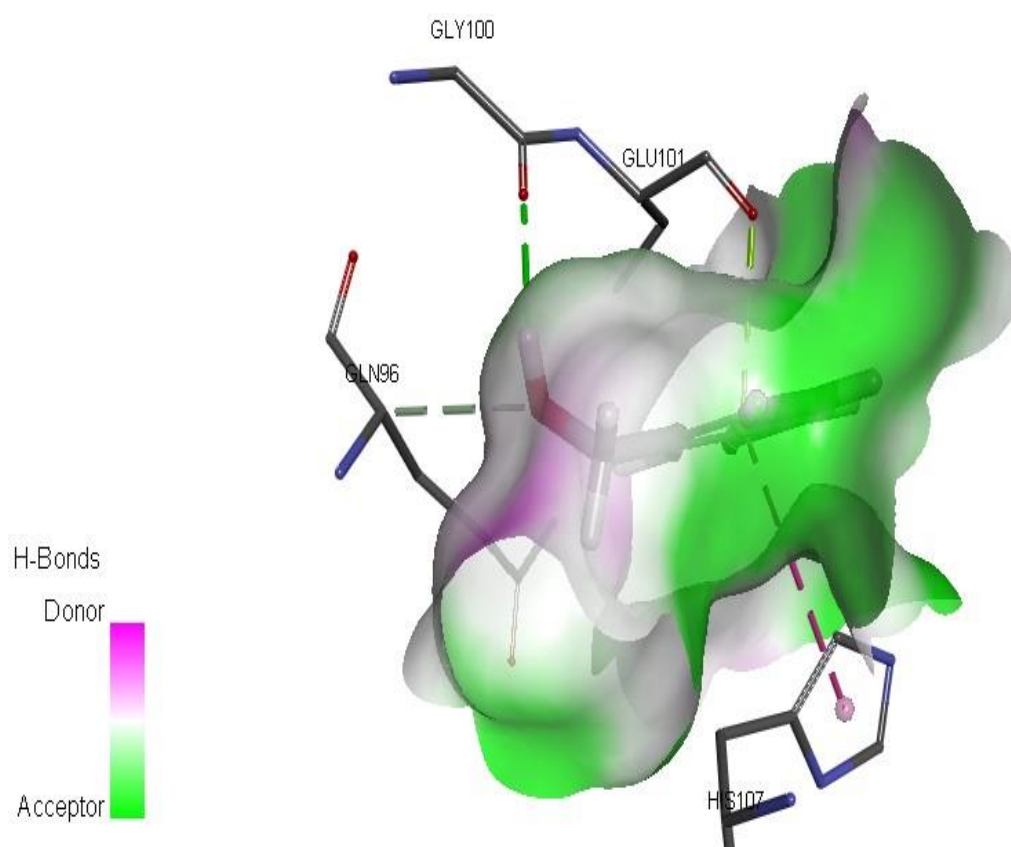


Fig 3:3D structure

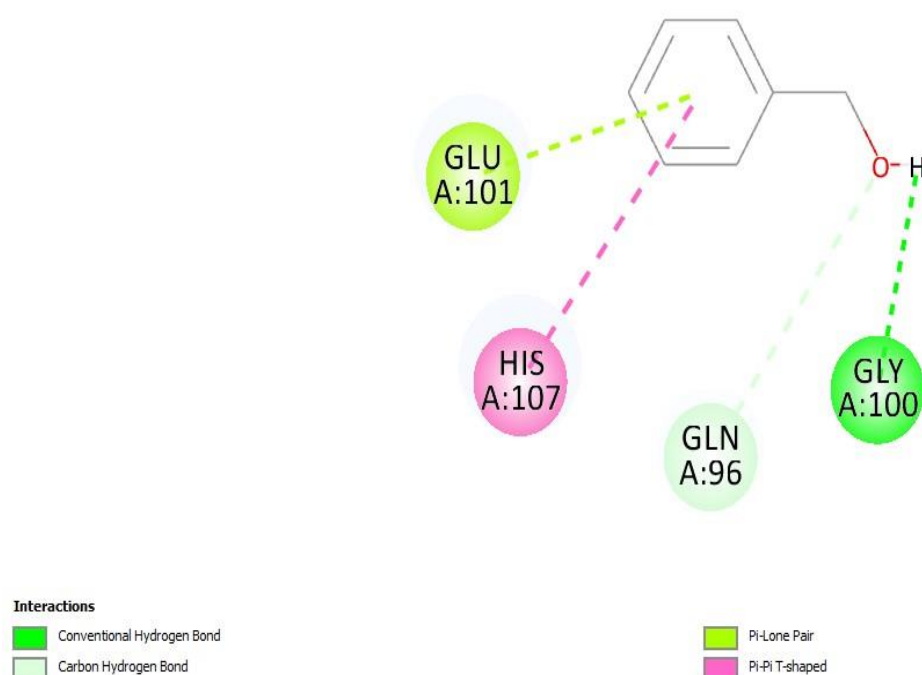


Fig 4: 2D Structure

244:H16 - A:GLY100: The relation "244:H16 - A:GLY100:O" possibly denotes a specific molecular interaction or structural motif involving a glycine residue at position 100 within a protein. In drug discovery related to the gene KIAA0901, understanding this interaction could provide insights into the protein's function, potentially aiding in the design of targeted therapies. Investigating how this interaction influences KIAA0901's role in cellular pathways associated with disease progression may unveil novel therapeutic strategies for diseases linked to KIAA0901 dysregulation.

A:GLN96:CA - 244: likely refers to a specific atomic interaction between a glutamine residue at position 96 in a protein and an oxygen atom at site 1 of a molecule with the identifier "244." Understanding this interaction in the context of the gene KIAA0901 could provide crucial insights into its protein structure and function, aiding in the identification of potential drug targets or the design of therapeutic compounds. Targeting this interaction may lead to the development of novel drugs that modulate KIAA0901 activity, offering new avenues for therapeutic intervention in diseases associated with KIAA0901 dysfunction.

A:GLU101:O – 244: suggests a specific atomic interaction between an oxygen atom of glutamate at position 101 in a protein and another molecule labeled "244." Understanding this interaction within the context of the gene KIAA0901 could provide insights into the protein's structure and function, potentially guiding drug discovery efforts. Targeting this interaction may lead to the development of

therapeutics that modulate KIAA0901 activity, offering new avenues for treating diseases associated with KIAA0901 dysregulation, such as cancer or neurological disorders.

A:HIS107 – 244: suggests a specific atomic interaction involving a histidine residue at position 107 in a protein and another molecule labeled "244." Understanding this interaction within the context of the gene KIAA0901 could elucidate its structural and functional significance, potentially informing drug discovery efforts. Targeting this interaction might offer opportunities to modulate KIAA0901 activity, presenting novel strategies for therapeutic intervention in diseases linked to KIAA0901 dysfunction, such as cancer or neurological disorders. Further exploration of this interaction could uncover promising avenues for developing targeted therapies aimed at restoring normal KIAA0901 function.

2.PLAGIARISM REPORT

Anusha Ravi
by OfficialTurnitin

Submission date: 28-Apr-2024 07:19PM (UTC+0900)

Submission ID: 2364094060

File name: plagrisim-final-anusha.docx (172.07K)

Word count: 926

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UNRAVELLING COMPLEXITY

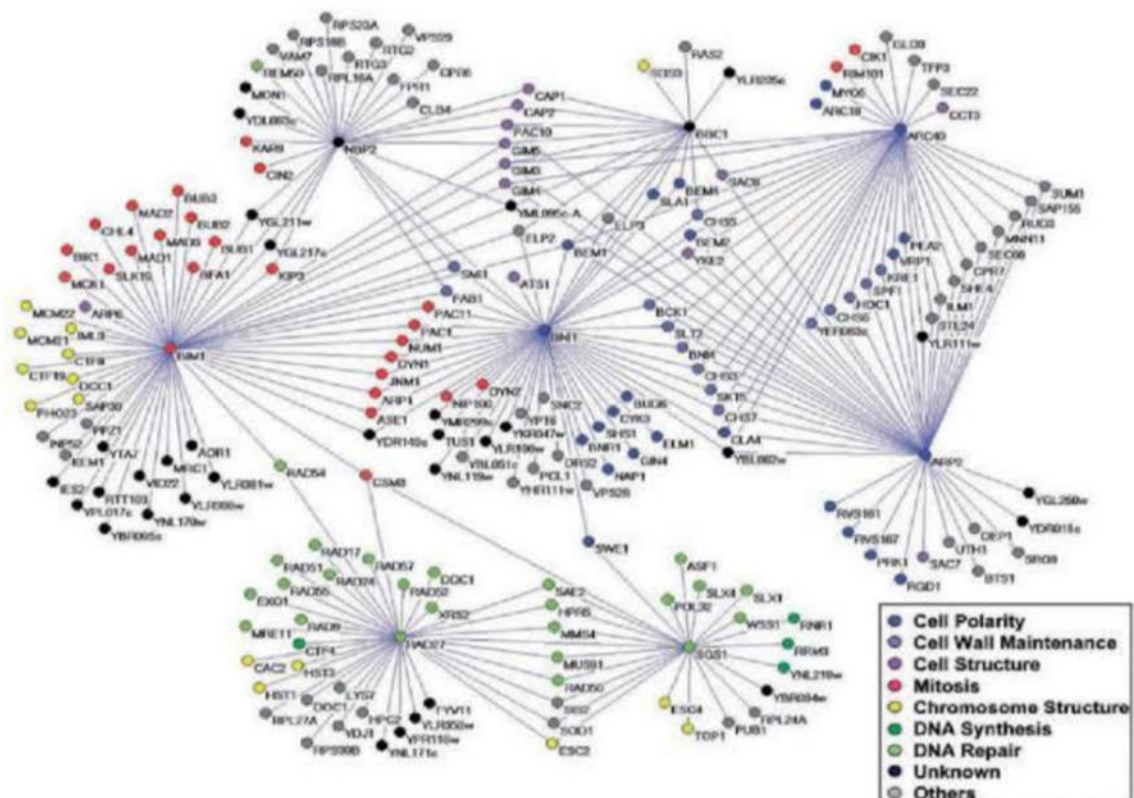
EXPLORING NETWORK ANALYSIS IN BIOLOGICAL SYSTEM

INTRODUCTION

Network analysis has emerged as a fundamental tool in unraveling the complexity of biological systems. From molecular interactions to ecosystem dynamics, biological networks provide a comprehensive framework for studying the intricate relationships within living organisms. This article explores the application of network analysis across scales, highlighting its significance in understanding biological phenomena. By examining molecular interactions, metabolic pathways, cellular signaling, ecological relationships, and brain connectivity, we can gain deeper insights into the organization, function, and dynamics of biological systems. Through network analysis, researchers can identify key components, detect patterns, and predict behaviors, ultimately advancing our understanding of biology.

APPLICATIONS OF NETWORK ANALYSIS IN TRANSCRIPTIONAL REGULATORY NETWORKS

Analysing network in transcriptional regulatory networks (GRNS) offers diverse applications in understanding gene expression dynamics and regulatory mechanism. It helps identify regulatory modules, comprising co-regulated genes, and characterizes key regulators like transcription factor or miRNAs. By integrating gene expression data, analysis predicts gene function and infers regulatory interactions, aiding in the reconstruction of GRNS. It also elucidates disease mechanisms by uncovering dysregulated pathways and potential drug targets for various disease. Overall, network analysis in GRNS enhances our understanding of gene regulation, cellular processes, and disease pathways, facilitating the development of precision medicine approaches. Through network topology analysis, important regulators coordinating gene expression are found, and functional modules within the network are revealed by clustering techniques. Understanding of gene roles is improved by predicting gene activities based on connection patterns. The use of dynamic modeling approaches clarifies temporal patterns and stimulus reactions. Network analysis also helps identify genes linked to disease and reveals the molecular causes of various disorders. These methods greatly advance the fields of biological and biomedical research by providing deeper insights into the dynamics of gene regulation through computer studies and experimental confirmation.

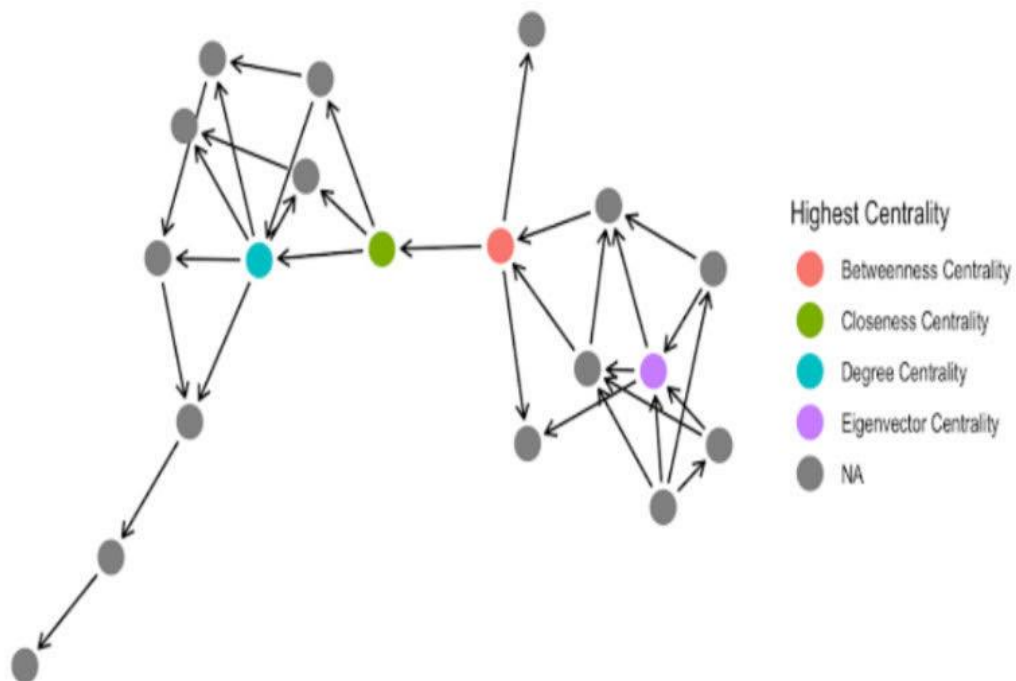


FUNDAMENTALS OF NETWORK THEORY AND ANALYSIS

The principles of network theory and analysis are essential resources for understanding the complexities of interconnected systems in a variety of fields, such as computer science, biology, and sociology. Fundamentally, network theory views complex systems as networks made up of edges that indicate connections or interactions between nodes, which stand for distinct entities. Measures of network topology, such as degree distribution and centrality metrics like degree, betweenness, and closeness centrality, are essential to network analysis. These metrics shed light on the nodes' significance and connectedness within the network. High centrality nodes, for example, are frequently important hubs or influencers in the network. Moreover, the identification of modular structures in networks is largely dependent on community detection techniques. These algorithms divide the network into cohesive node groupings called communities or modules. These communities or modules are generally thought of as closely linked clusters of nodes with comparable roles or qualities, or as functional units. It is crucial to comprehend these modular structures in order to decipher the organizing principles that underlie complex systems. By modeling the temporal evolution of networks and forecasting their behavior under various scenarios, dynamic modeling techniques enhance network analysis even further. Simple, deterministic techniques like Boolean networks and more complex, stochastic models like dynamic Bayesian networks are examples of these concepts. Through the dynamic interplay between nodes and edges throughout time, these models allow researchers to predict traits that arise in the network and how it will react to perturbations. This multidisciplinary paradigm cuts across

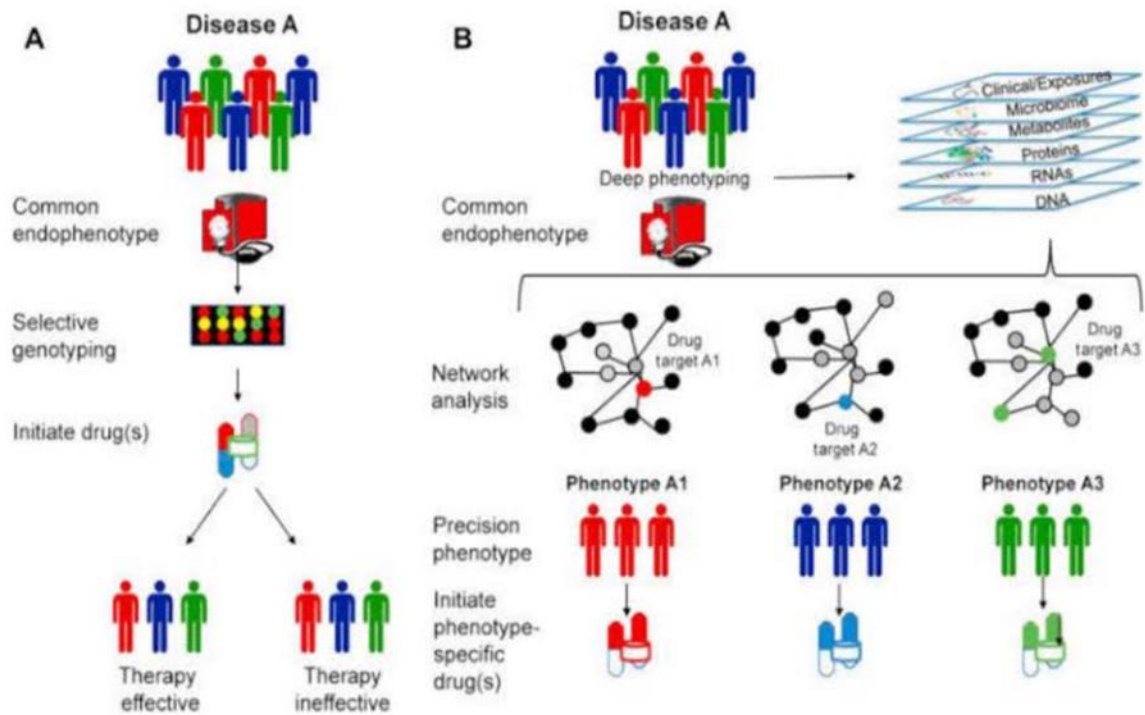
academic lines and provides insightful analysis of a wide range of phenomena, including social networks, genetic regulatory networks, and technology infrastructures. Researchers can advance their understanding of the fundamental dynamics and structure of complex systems by utilizing the concepts of network theory and analysis. This can lead to novel discoveries in a variety of domains, including social dynamics, network security, and disease biology. In the end, knowing these foundations enables researchers to drive innovation in a wide range of fields and negotiate the complexity of interrelated systems.

Variability of Centrality Measures



NETWORK MEDICINE: UNDERSTANDING DISEASE NETWORKS

Network medicine is an interdisciplinary approach that applies network analysis principles to understand the complex interactions underlying disease. By representing diseases as networks of interconnected molecular components, such as genes, proteins, and pathways, network medicine aims to elucidate the underlying mechanisms, identify novel biomarkers, and discover therapeutic targets. This approach considers diseases not as isolated entities but as manifestations of perturbations within interconnected biological networks. By analyzing disease networks, researchers can uncover disease subtypes, identify key driver genes or pathways, and predict disease progression and treatment responses. Network medicine holds promise for personalized medicine by providing insights into the molecular mechanisms driving individual variations in disease susceptibility, progression, and treatment outcomes.



EMERGING TRENDS AND CHALLENGES IN NETWORK ANALYSIS

Emerging trends and challenges in network analysis reflect the evolving landscape of complex systems research. With the proliferation of data, scalability has emerged as a critical challenge, necessitating the development of efficient algorithms and computational frameworks to analyze large-scale networks effectively. Additionally, the rise of multilayer and multiplex networks presents new challenges in capturing

and analyzing interconnected layers of interactions, requiring innovative approaches to model and visualize these complex structures. Dynamic networks, which evolve over time, pose another challenge in understanding temporal dependencies and predicting system behavior. In fields like neuroscience, the integration of network analysis with temporal data offers new insights into brain dynamics but also requires sophisticated modeling techniques. Ethical considerations, including data privacy and algorithmic fairness, are also becoming increasingly important, prompting the need for transparent and responsible practices in network analysis research. Moreover, interdisciplinary collaboration is essential for addressing these challenges and leveraging network analysis to tackle real-world problems effectively. By embracing these emerging trends and addressing associated challenges, network analysis continues to advance our understanding of complex systems and drive innovation across disciplines.

Anusha Ravi

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2.1 REVIEW ARTICLE

UNRAVELLING COMPLEXITY

EXPLORING NETWORK ANALYSIS IN BIOLOGICAL SYSTEM

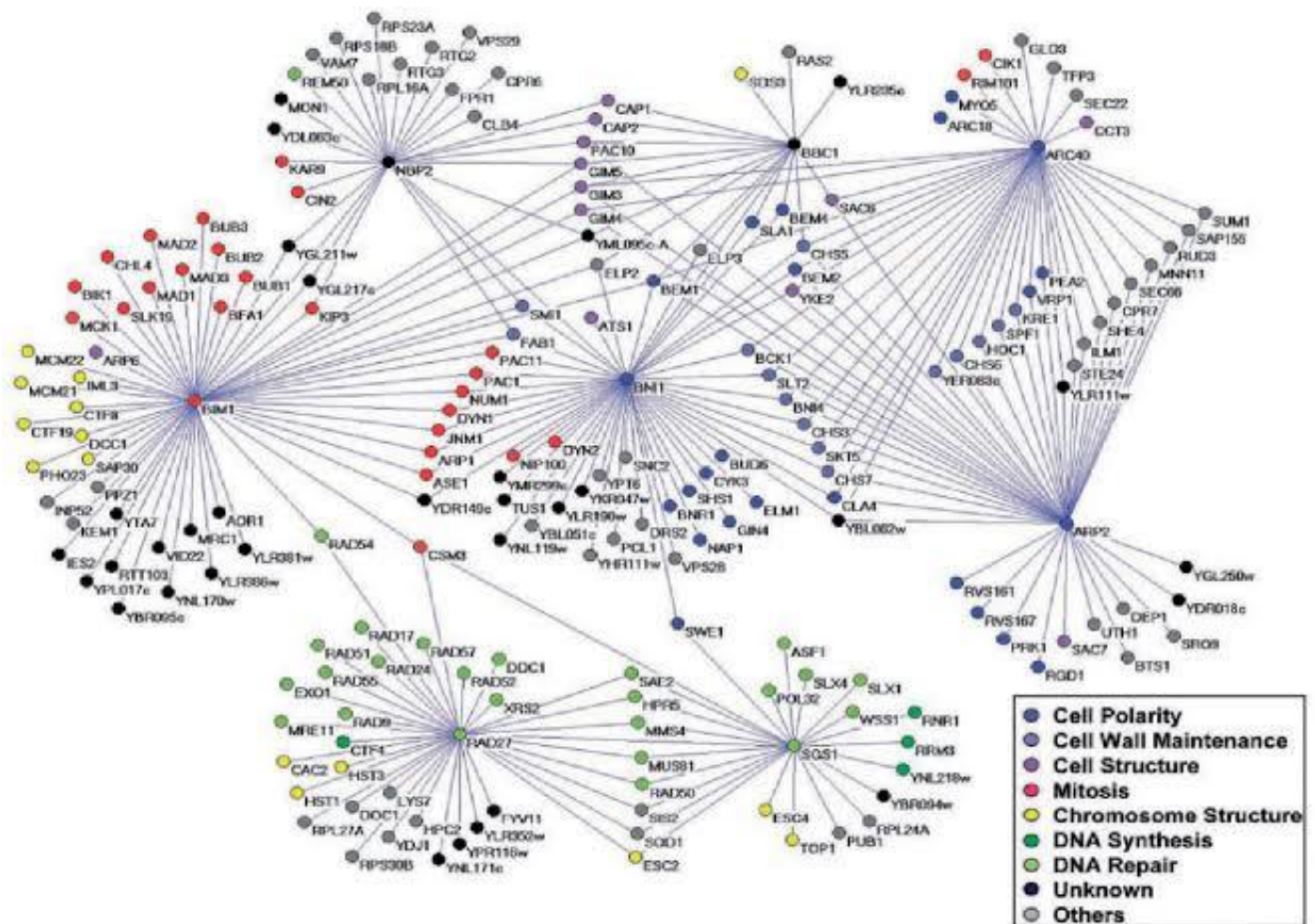
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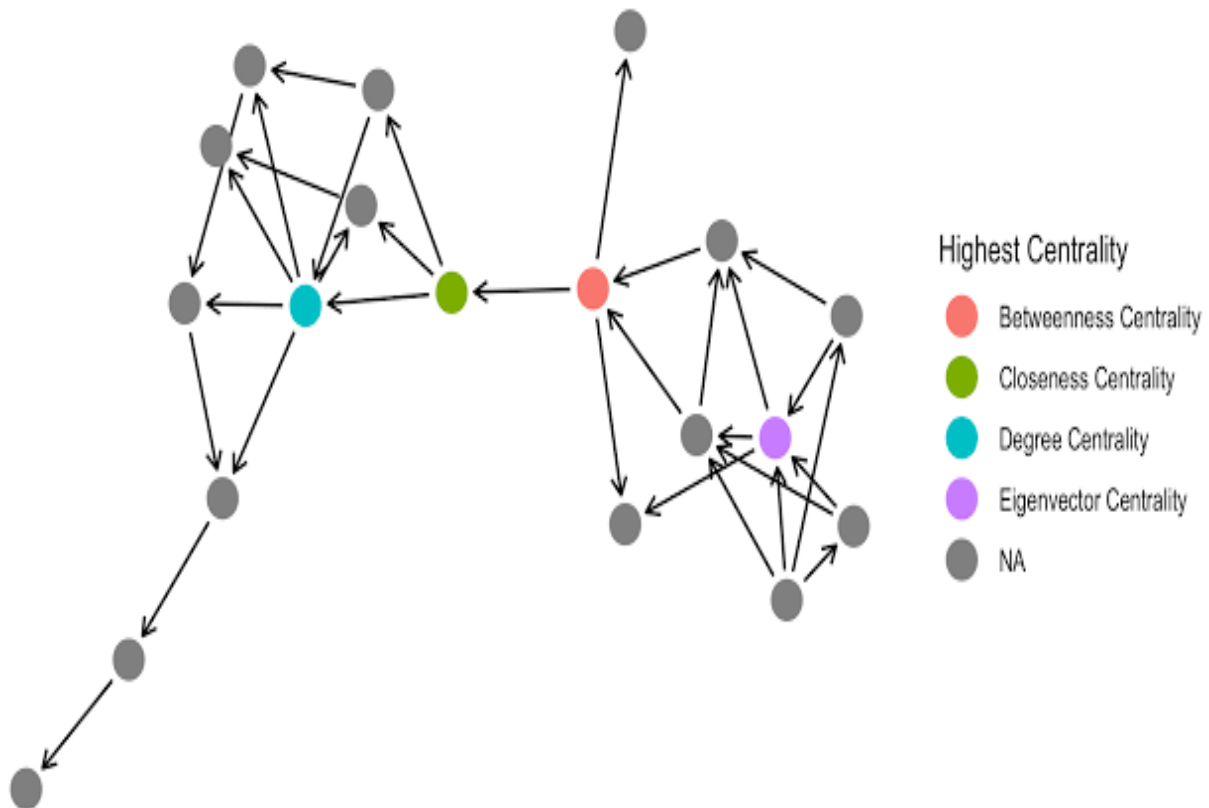
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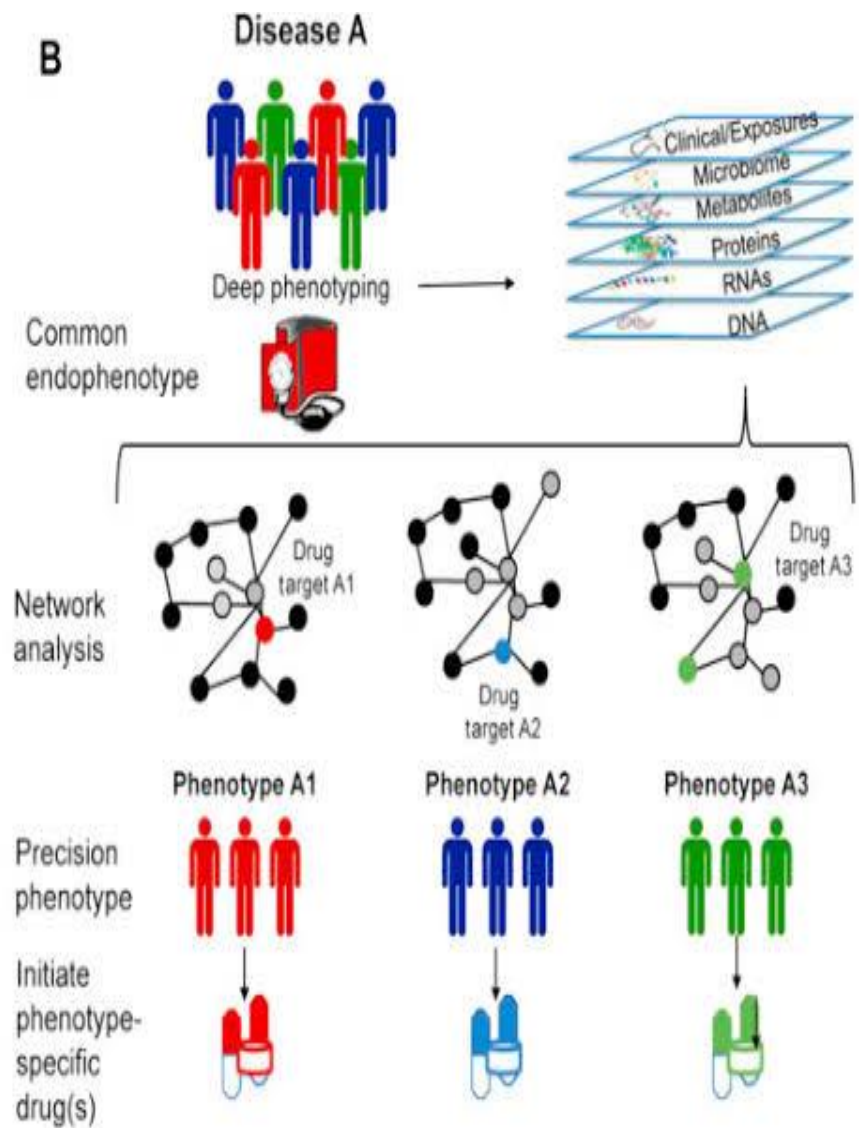
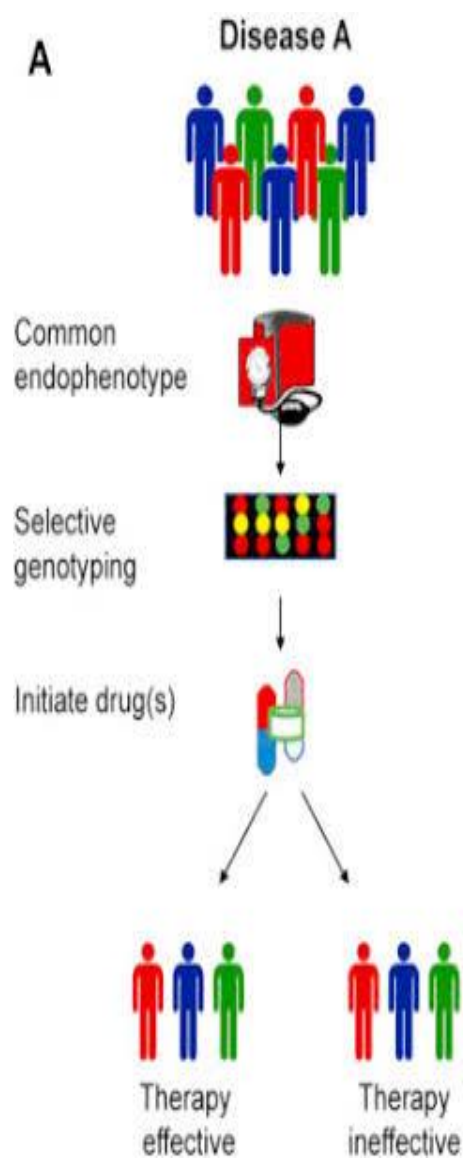
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Network medicine is an interdisciplinary approach that applies network analysis principles to understand the complex interactions underlying disease. By representing diseases as networks of interconnected molecular components, such as genes, proteins, and pathways, network medicine aims to elucidate the underlying mechanisms, identify novel biomarkers, and discover therapeutic targets. This approach considers diseases not as isolated entities but as manifestations of perturbations within interconnected biological networks. By analyzing disease networks, researchers can uncover disease subtypes, identify key driver genes or pathways, and predict disease progression and treatment responses. Network medicine holds promise for personalized medicine by providing insights into the molecular mechanisms driving individual variations in disease susceptibility, progression, and treatment outcomes.



EMERGING TRENDS AND CHALLENGES IN NETWORK ANALYSIS

Emerging trends and challenges in network analysis reflect the evolving landscape of complex systems research. With the proliferation of data, scalability has emerged as a critical challenge, necessitating the development of efficient algorithms and computational frameworks to analyze large-scale networks effectively. Additionally, the rise of multilayer and multiplex networks presents new challenges in capturing and analyzing interconnected layers of interactions, requiring innovative approaches to model and visualize these complex structures. Dynamic networks, which evolve over time, pose another challenge in understanding temporal dependencies and predicting system behavior. In fields like neuroscience, the integration of network analysis with temporal data offers new insights into brain dynamics but also requires sophisticated modeling techniques. Ethical considerations, including data privacy and algorithmic fairness, are also becoming increasingly important, prompting the need for transparent and responsible practices in network analysis research. Moreover, interdisciplinary collaboration is essential for addressing these challenges and leveraging network analysis to tackle real-world problems effectively. By embracing these emerging trends and addressing associated challenges, network analysis continues to advance our understanding of complex systems and drive innovation across disciplines.

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3.MATLAB COURSE

Based on the Matlab Certificate there are 18 Course I have completed

- ✓ Signal Processing with MATLAB
- ✓ Image Processing with MATLAB
- ✓ MATLAB Programming Techniques
- ✓ MATLAB for Data Processing and Visualization
- ✓ Machine Learning with MATLAB
- ✓ Image Processing Onramp
- ✓ Solving Nonlinear Equations with MATLAB
- ✓ Deep Learning with MATLAB
- ✓ Statistics Onramp
- ✓ Wireless Communications Onramp
- ✓ MATLAB Fundamentals
- ✓ Reinforcement Learning Onramp
- ✓ Computer Vision Onramp
- ✓ Deep Learning Onramp
- ✓ Object-Oriented Programming Onramp
- ✓ Machine Learning Onramp
- ✓ Simulink Onramp
- ✓ MATLAB Onramp

1.MATLAB Onramp

DESCRIPTION:

MATLAB Onramp is an interactive tutorial designed to introduce beginners to MATLAB, a high-level programming language used in technical computing and data analysis. It covers fundamental concepts such as variables, arrays, plotting, and programming logic through hands-on exercises and quizzes. By completing MATLAB Onramp, I gain essential skills to start utilizing MATLAB for various scientific and engineering tasks.

2.REINFORCEMENT LEARNING ONRAMP

DESCRIPTION:

Reinforcement Learning Onramp offers a comprehensive introduction to reinforcement learning (RL), a subset of machine learning focused on decision making. Participants learn key RL concepts such as Markov decision processes, policy optimization, and Q-learning through practical examples and exercises. By completing the Onramp, I acquire the foundational knowledge needed to apply RL algorithms to solve complex decision-making problems in various domains.

3.OBJECT-ORIENTED PROGRAMMING ONRAMP

DESCRIPTION:

The Object-Oriented Programming (OOP) Onramp provides a structured introduction to OOP concepts, such as classes, objects, inheritance, and polymorphism. Through interactive lessons and coding exercises, I learn how to design and implement robust software solutions using OOP principles. By mastering OOP fundamentals, I develop the skills necessary to build modular, maintainable, and scalable programs in languages like Java, Python, and C++.

4.MACHINE LEARNING ONRAMP

DESCRIPTION:

The Machine Learning Onramp offers a beginner-friendly exploration of machine learning techniques and algorithms. I learn essential concepts like supervised and unsupervised learning, model evaluation, and feature selection through hands-on exercises and real-world examples. By completing the Onramp, I gain the foundational knowledge needed to start building and deploying machine learning models for various applications.

5.COMPUTER VISION ONRAMP

DESCRIPTION:

The Computer Vision Onramp provides a structured introduction to the field of computer vision, covering topics such as image processing, object detection, and deep learning for visual recognition. Through practical exercises and projects, I learn how to extract meaningful information from images and videos using state-of-the-art techniques. By completing the Onramp, I gain the foundational skills necessary to tackle real-world computer vision tasks across industries such as healthcare, automotive, and robotics.

6.MATLAB FUNDAMENTALS

DESCRIPTION:

MATLAB Fundamentals offers a foundational understanding of MATLAB, focusing on its syntax, data types, and basic operations. I learn to write scripts and functions, manipulate matrices, and visualize data using built-in plotting functions. By mastering these fundamentals, I gain the proficiency needed to start programming in MATLAB for various scientific and engineering applications

7.SIMULINK ONRAMP

DESCRIPTION:

The Simulink Onramp introduces participants to Simulink, a graphical programming environment for modeling, simulating, and analyzing dynamic systems. Through interactive tutorials, I learn to build and simulate models using blocks representing system components. By completing the Onramp, I gain proficiency in using Simulink to design and simulate complex systems across industries such as automotive, aerospace, and control systems.

8.MATLAB FOR DATA PROCESSING AND VISUALIZATION

DESCRIPTION:

MATLAB for Data Processing and Visualization teaches how to leverage MATLAB for efficient data analysis and visualization tasks. I learn techniques for importing, cleaning, and analyzing data, as well as creating insightful visualizations using MATLAB's powerful plotting capabilities. By completing this course, I gain essential skills to extract valuable insights from data and present findings effectively.

9.MACHINE LEARNING WITH MATLAB

DESCRIPTION:

Machine Learning with MATLAB provides a comprehensive introduction to machine learning techniques and algorithms using MATLAB's powerful toolbox. I learn to preprocess data, train and evaluate machine learning models, and deploy them for practical applications. By completing this course, I gain the skills necessary to tackle real-world machine learning challenges using MATLAB.

10.DEEP LEARNING WITH MATLAB

DESCRIPTION:

"Deep Learning with MATLAB" offers an immersive journey into deep learning concepts and applications using MATLAB's Deep Learning Toolbox. I delve into neural network architectures, training strategies, and deployment techniques for tasks like image classification and object detection. By completing this course, I gain proficiency in leveraging MATLAB for building and deploying deep learning models in various domains.

11.DEEP LEARNING ONRAMP

DESCRIPTION:

The Deep Learning Onramp provides a foundational understanding of deep learning principles and techniques using MATLAB. I learn to design, train, and deploy deep neural networks for tasks such as image classification and sequence prediction. By completing the Onramp, I gain essential skills to start applying deep learning to solve real-world problems efficiently.

12.IMAGE PROCESSING ONRAMP

DESCRIPTION:

The Image Processing Onramp offers a structured introduction to image processing techniques using MATLAB. I learn to enhance, analyze, and manipulate digital images through hands-on exercises and projects. By completing the Onramp, I gain the foundational knowledge needed to process and analyze images for various applications in fields such as healthcare, remote sensing, and computer vision.

13.MATLAB PROGRAMMING TECHNIQUES

DESCRIPTION:

"MATLAB Programming Techniques" explores advanced programming concepts and best practices for efficient MATLAB coding. I learn techniques for optimizing code performance, debugging, and modularizing code for maintainability. By completing this course, it enhance my proficiency in MATLAB programming and develop skills to tackle complex computational tasks effectively.

14.statistic onramp

DESCRIPTION:

The Statistics Onramp provides a foundational understanding of statistical concepts and techniques using MATLAB. I learn to analyze data, perform hypothesis testing, and conduct various statistical tests through interactive tutorials. By completing the Onramp, I gain essential skills to interpret and draw meaningful insights from data using statistical methods.

15.SOLVING NONLINEAR EQUATION WITH MATLAB

DESCRIPTION:

"Solving Nonlinear Equations with MATLAB" equips participants with techniques to find numerical solutions to nonlinear equations. Through practical examples and exercises, I learn methods like Newton-Raphson and secant methods for root finding. By completing this course, I gain proficiency in using MATLAB for solving a wide range of nonlinear equations efficiently.

16.SIGNAL PROCESSING WITH MATLAB

DESCRIPTION:

"Signal Processing with MATLAB" introduces fundamental concepts and techniques for analyzing and manipulating signals. I learn to apply digital filters, perform spectral analysis, and implement signal processing algorithms using MATLAB's toolbox. By completing this course, I develop the skills

needed to process and analyze various types of signals encountered in fields such as telecommunications, audio processing, and biomedical engineering.

17.SIGNAL PROCESSING ONRAMP

DESCRIPTION:

The Signal Processing Onramp provides a structured introduction to signal processing concepts and techniques using MATLAB. I learn to analyze, filter, and visualize signals through interactive tutorials and exercises. By completing the Onramp, I gain essential skills to process and interpret various types of signals encountered in fields such as communications, audio processing, and biomedical engineering.

18.IMAGE PROCESSING WITH MATLAB

DESCRIPTION:

"Image Processing with MATLAB" offers a comprehensive exploration of techniques for analyzing and manipulating digital images. I learn to perform tasks like image enhancement, segmentation, and feature extraction using MATLAB's toolbox. By completing this course, I gain proficiency in utilizing MATLAB for a wide range of image processing applications in fields such as medicine, surveillance, and remote sensing.

SKILLS THAT I GAINED FROM THE MATLAB:

- **Programming Proficiency:** I developed a strong understanding of MATLAB's syntax, data structures, and programming logic, enabled me to write efficient and effective code.
- **Data Analysis:** I learned various techniques for importing, cleaning, and analyzing data, allowed me to extract valuable insights and patterns from datasets.

- Visualization: I gained proficiency in creating insightful visualizations using MATLAB's plotting functions, enabled me to present data in a clear and understandable manner.
- Problem Solving: I honed problem-solving skills by tackling various challenges and projects in MATLAB, equipped me to tackle real-world problems in scientific and engineering domains.

3.1 MATLAB CERTIFICATES



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

MATLAB Onramp



DIRECTOR, TRAINING SERVICES

13 November 2023



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

Reinforcement Learning Onramp



DIRECTOR, TRAINING SERVICES

17 December 2023



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

Object-Oriented Programming Onramp



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Anusha R

has successfully completed **100%** of the self-paced training course

Machine Learning Onramp



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Anusha R

has successfully completed **100%** of the self-paced training course

Computer Vision Onramp



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Anusha R

has successfully completed **100%** of the self-paced training course

MATLAB Fundamentals


DIRECTOR, TRAINING SERVICES

4 February 2024



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

Simulink Onramp


DIRECTOR, TRAINING SERVICES

28 March 2024



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

MATLAB for Data Processing and Visualization



DIRECTOR, TRAINING SERVICES

2 February 2024



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

Machine Learning with MATLAB



DIRECTOR, TRAINING SERVICES

12 February 2024



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

Deep Learning with MATLAB



Craig L. Santos

DIRECTOR, TRAINING SERVICES

9 February 2024



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

Deep Learning Onramp



Craig L. Santos

DIRECTOR, TRAINING SERVICES

12 February 2024



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

Image Processing Onramp



A handwritten signature in black ink, reading "Ray L. Santos".

DIRECTOR, TRAINING SERVICES

5 March 2024



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

MATLAB Programming Techniques



A handwritten signature in black ink, reading "Ray L. Santos".

DIRECTOR, TRAINING SERVICES

17 February 2024



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

Statistics Onramp



A handwritten signature in black ink, reading "Rajesh Santos", positioned above a horizontal line.

DIRECTOR, TRAINING SERVICES

1 March 2024



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

Solving Nonlinear Equations with MATLAB



A handwritten signature in black ink, reading "Rajesh Santos", positioned above a horizontal line.

DIRECTOR, TRAINING SERVICES

5 March 2024



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

Signal Processing with MATLAB



DIRECTOR, TRAINING SERVICES

6 April 2024



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

Signal Processing Onramp



DIRECTOR, TRAINING SERVICES

7 March 2024



Course Completion Certificate

Anusha R

has successfully completed **100%** of the self-paced training course

Image Processing with MATLAB



Craig L. Santos

DIRECTOR, TRAINING SERVICES

5 April 2024