

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

YUVASHREE.M (43739022)



**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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DEPARTMENT OF BIOINFORMATICS AND DATA SCIENCE

BONAFIDE CERTIFICATE

This is to certify that this Project Report is the Bonafide work of **M.YUVASHREE (43739022)** 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 M YUVASHREE (43739022) 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 fulfilment of the requirements for the award of Master of Science degree in Bioinformatics and Data Science.

DATE:

YUVASHREE.M

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. JEMMY CHRISTY 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.

(YUVASHREE.M)

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1. TRANSLATIONAL BIOINFORMATICS

1.1 GENE 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 and disease Liver Tumor Geo2R is the source of the geo dataset ()
- 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 Bio Grid in cyto hubba to analyse the network and identify importance node based various topologies algorithm to determine the top 10 gens
- Genes must be copied in clue go and continue clue go param3eter such as species ontology and statistical settings.
- Run clue go analysis to identify functional categories or pathways associated with the selected nodes.

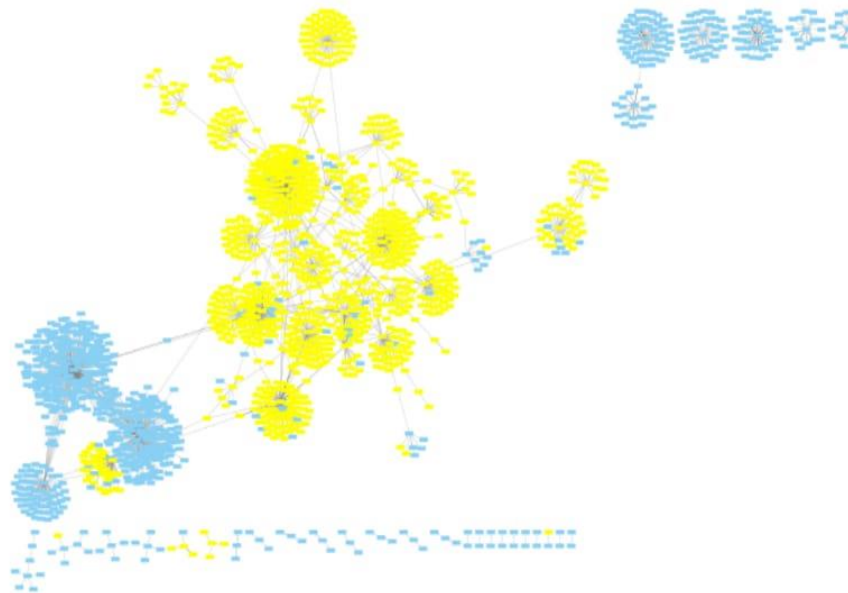


Fig 1.1: Network Pathway of Upregulated Genes

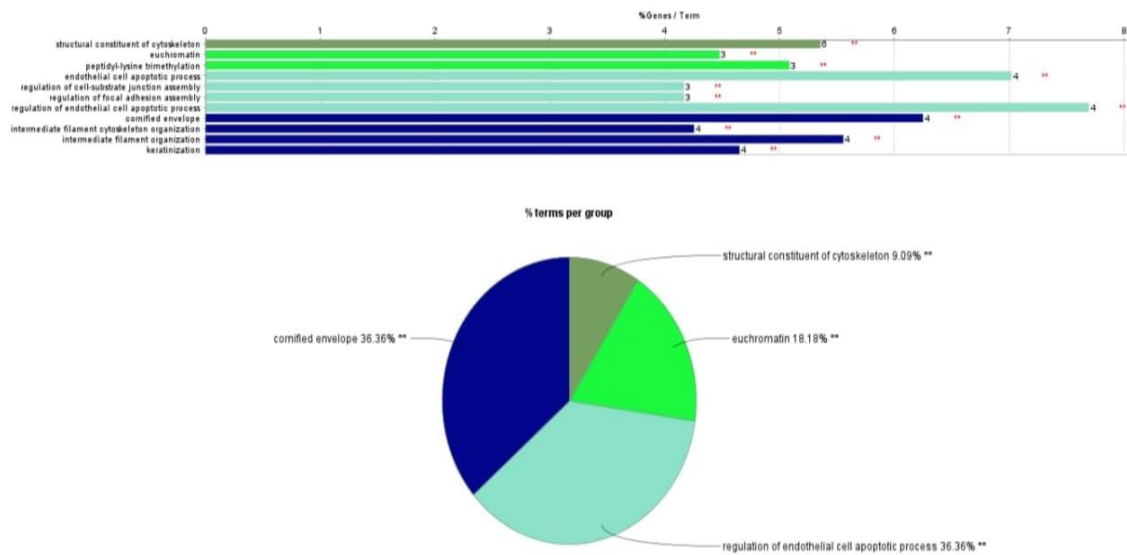


Fig 1.2 – Graph of functional analysis and Pie Chart of functional analysis

INTERPRETATION:

Geo Dataset GSE Id: GSE153434

Sample no : 10

Type :Expression profiling by array

No of differentially expressed genes: 251

No of upregulated genes: 71

No of downregulated genes: 180

Top 10 Upregulated Gene: FAM20C, MTHFD2, ELL2, DEPP1, SLC39A14, MT1X, GLRX, NNMT, ITGB3, CLMP

Filter node: ID [9606]

CLUEGO

TERM	FUNCTION	ONTOLOGY
Structural constituent of cytoskeleton 9.09%	Actin filaments, microtubules, and intermediate filaments are primary structural constituents of the cytoskeleton. Actin filaments support cell shape and movement, microtubules serve as tracks for intracellular transport, and intermediate filaments provide mechanical strength.	Biological
Euchromatin 18.18%	Euchromatin is one of the two main types of chromatin, the material that makes up chromosomes within the cell nucleus. It is less condensed than heterochromatin and appears lighter under a microscope during interphase.	Biological
Regulation of endothelial cell apoptic process 36.36%	The regulation of endothelial cell apoptosis is a critical process involved in various physiological and pathological conditions, including development, tissue homeostasis, and diseases such as cancer and cardiovascular disorders.	Biological
Cornified envelope 36.36%	The cornified envelope is a structure formed during the terminal differentiation of keratinocytes, the predominant cell type .	

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 **FAM20C** cumulative survival probabilities

Materials And Methods:

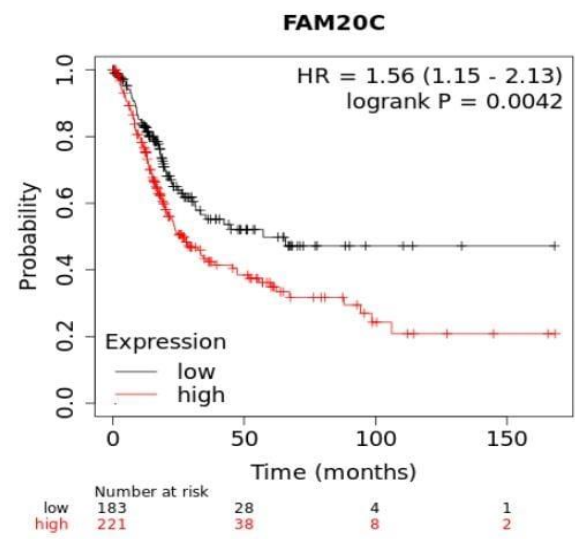
KM-PLOTTER: KM-plotter is the most sophisticated online survival analysis, performing all calculations in real time (not loading pre-calculated images). The background database is manually curated. Gene expression data and relapse-free and overall survival information are downloaded from GEO, EGA and 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) **FAM20C** 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: 0.0042
FDR: over 50%



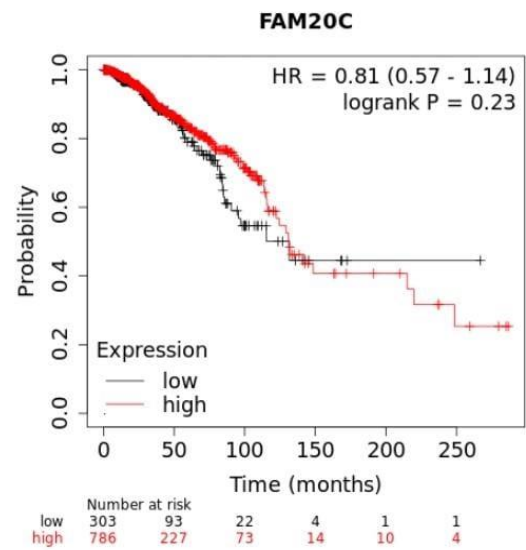
Median survival

Low expression cohort (months)	High expression cohort (months)
57.27	26.5

Fig 2.1: Bladder Carcinoma

Results

P value: 0.2255
FDR: 100%



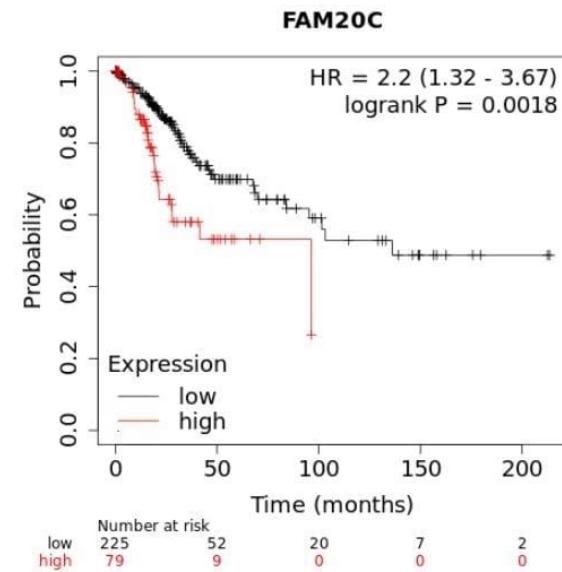
Median survival

Low expression cohort (months)	High expression cohort (months)
131.5	131.37

Fig 2.2: Breast Cancer

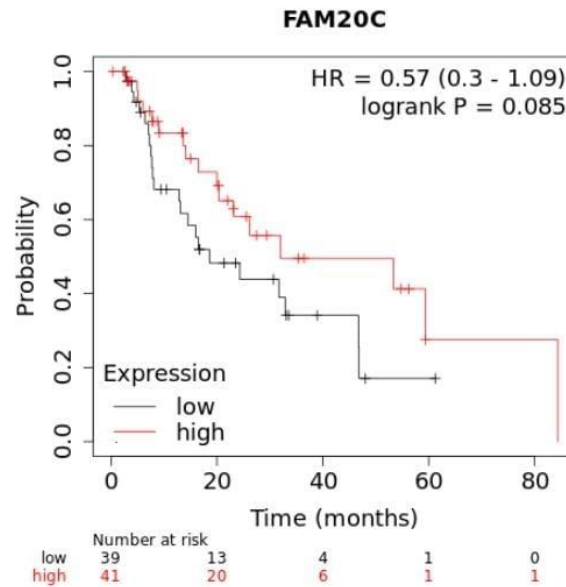
Results

P value: 0.0018
FDR: 20%



Results

P value: 0.0853
FDR: 100%



Median survival

Low expression cohort (months)	High expression cohort (months)
18.6	32

Median survival

Low expression cohort (months)	High expression cohort (months)
136.2	96.27

Fig 2.3: Cervical squamous cell carcinoma

Fig 2.4: Esophageal Adenocarcinoma

Interpretation

- KM-plot recognizes **proposed gene symbols FAM20C** (including HUGO Gene Nomenclature Committee approved)
- Sources for the database include GEO, EGA, TCGA, Metabric, Impact, and PubMed repositories. For more details, please check our publications
- **Bladder carcinoma:**
HR Rate: 1.56(1.15-2.13)
50% of median survival of probability:
Low expression cohort: 57.27

High expression cohort: 26.5

- **Breast cancer**

HR Rate: 0.81(0.57-1.14)

50% of median survival of probability:

Low expression cohort: 131.5

High expression cohort: 131.37

- **Cervical squamous cell carcinoma**

HR Rate: 2.2(1.32-3.67)

50% of median survival of probability:

Low expression cohort: 18.6

High expression cohort: 32

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 Lung 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 Lung cancer data's were retrieved and literature survey was done

RESULTS:

INTERPRETATION:

BIOMARKER ID	BIOMARKER NAME	CLASS	GENE NAME	BIOMARKER TYPE	REPRESENTATIVE	
					DRUG	DISEASE
BM7DL8	Interleukin 6	Protein	IL6;FNB2	. PDY . SAF . MOI . PRT	Tocilizumab	Rheumatoid arthritis

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.

Swiss Target Prediction 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 Swiss Target Prediction, we have statistically quantify 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 Hydroxychloroquine 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 organizations 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 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 chemi-informatics resource that combines detail 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. Swiss target 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: Hydroxychloroquine

TARGETS: PIG61, PLK1, DHTR, RIPK7, DER, FAK, MSTD, UBC,YLR293C, DCBIL

CHOSEN TARGET : PLK1

UNIPORT ID	NAME	PROTEIN NAME
P53350	PLK1-HUMAN	SERINE THREONINE-OROTEN KINASE

NAME	-plp1	-plp2	jain	-pmf	Dock-score
IUMW					
3652	58.83	55.85	-1.77	43.72	44.758
3652	59.42	56.23	-1.46	58.88	43.049
3652	63.12	57.81	-0.99	41.81	41.177
3652	76.13	68.91	-1.26	30.61	40.872
3652	50.06	46.82	-2.55	35.98	39.927
3652	64.91	57.67	-1.88	38.15	39.594
3652	63.96	57.01	-1.96	35.55	39.535
3652	70.62	68.23	-1.51	36.06	38.846
3652	63.08	60.43	-1.76	50.71	38.548

3652	53.07	52.87	-2.77	61.64	38.475
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Fig 3.1- Table of Molecules

NAME	DISTANCE	CATEGORY	TYPES	FROM	TO
3652:H31-B:TYR421:0112	2.75974	HYDROGEN BOND	CONVENTIONAL HYDROGEN	3652:HB1	B:TYR42
A:GLY448:CA-3652:02	2.81907	HYDROGEN BOND	CONVENTIONAL HYDROGEN	A:GLY 448:CA	3652:07
3652:H31-c:0113	4.36043	HYDROPHOBIC	Pi-Alkyl	B:TYR421:011	3625:C15
3652-B:LYS474	4.25298	HYDROPHOBIC	Pi-Alkyl	B:3652-121	B:LYS474
3652:C15-B:LE3651:03	3.72046	HYDROGEN BOND	CARBON HYDROGEN	A:GLY448:CA	3652:02

Fig 3.2: Table of Non – Bond

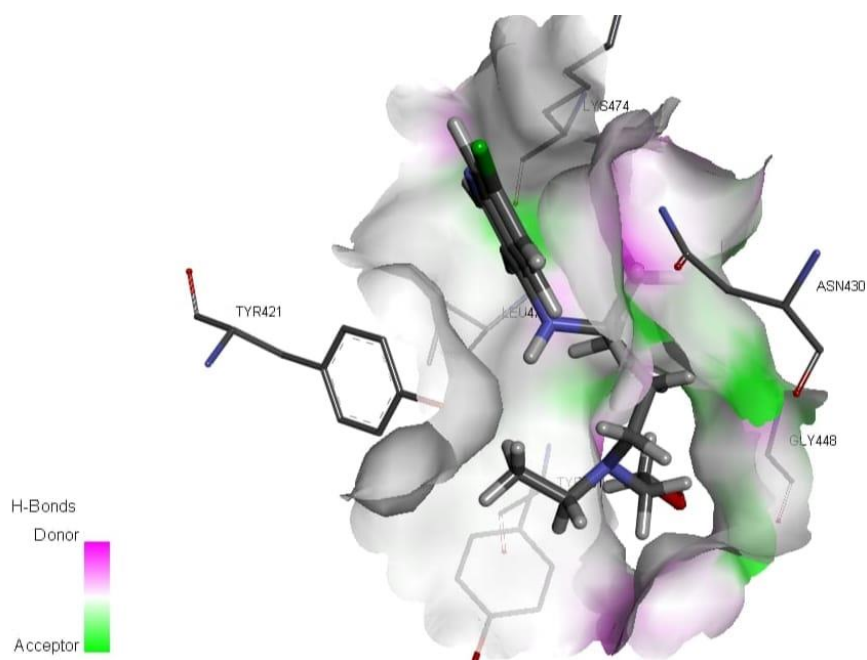


Fig 3.3: 3D STRUCTURE

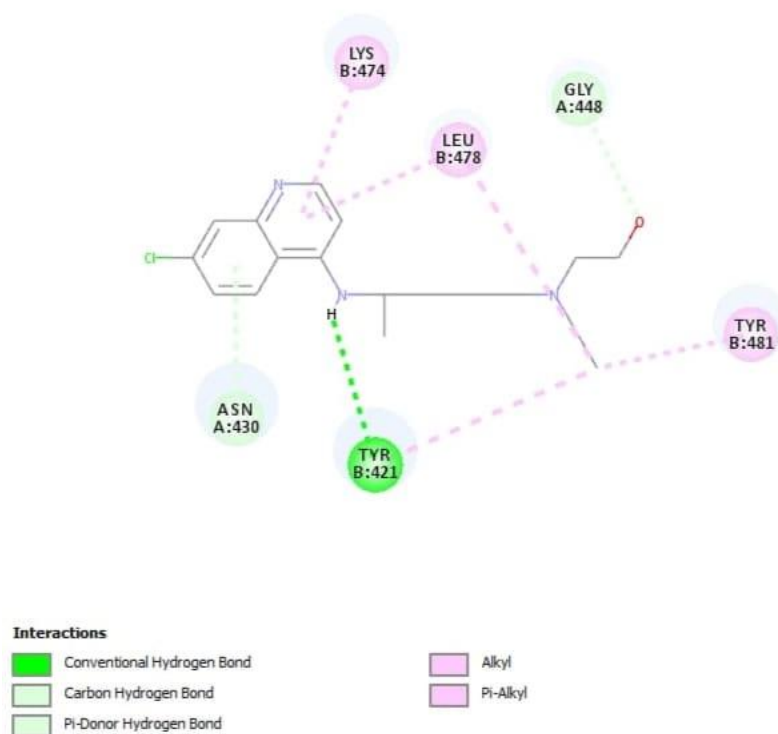


FIG 3.4: 2D STRUCTURE

INTERPRETATION:

3652:H31-B:TYR421:011-If "3652:H31-B:TYR421:011 Represent specific molecules, proteins, genes, or other biological entities, understanding their interaction would depend on their respective functions, structures, and biochemical properties. In this scenario represents a specific molecular entity, possible protein with TYR421 indicating a tyrosine residue modified by the addition of hydroxyl group.

A:GLY448:CA-3652:02-interactions between biomolecules can involve various mechanisms, including binding, signalling, enzymatic reactions, and structural changes, among others. Determining the nature and implications of an interaction typically requires experimental studies or computational analyses

3652:H31-c:0113: The interaction between 3652:H31-c:0113 and Hydroxychloroquine is crucial in drug discovery for evaluating potential therapeutic effects, understanding drug mechanisms, and optimizing candidate compounds. Experimental and computational approaches elucidate their binding affinity and functional impact, guiding the development of novel pharmaceutical interventions.

3652-B:LYS474:In drug discovery, understanding the interaction between 3652:H31-c:0113 and Hydroxychloroquine is pivotal for evaluating compound efficacy and guiding therapeutic development. Experimental and computational methods assess their binding affinity and functional impact, informing the optimization of drug candidates. Meanwhile, IUME's role in drug discovery extends to its potential as a target or modulator, crucial for identifying novel therapeutic avenues and predicting compound effects, thus contributing significantly to the development of effective pharmaceutical interventions through comprehensive investigation and analysis across various stages of drug development.

3652:C15-B:LE3651:03:The cellular enzyme is involved. catalyse biochemical reactions essential for cellular functions. They facilitate substrate conversion into products, regulating metabolic pathways, signal transduction, and macromolecule synthesis. Enzyme activity relies on precise structural arrangements and optimal environmental conditions, ensuring efficient and specific substrate recognition and catalysis within the cellular milieu

2. PLAGARISM REORT

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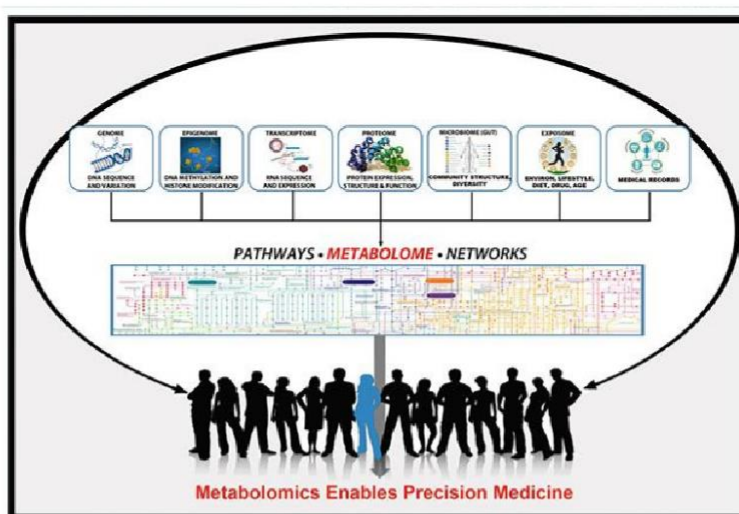
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UNVEILING METABOLOMICS

EXPLORING THE DYNAMICS OF CELLULAR METABOLISM

INTRODUCTION

- The dynamic nature of cellular metabolism means that the physiological program of the cell is constantly modified. Metabolic regulation occurs at all biological levels, including post-transcriptional, post-translational, and allosteric.
- This regulatory information is expressed by the metabolome, although in a convoluted manner. To enable dynamic metabolic characterization at high resolution and to decipher such complex information, several approaches are needed. Live-cell metabolomics is a powerful tool for studying the dynamics of metabolic reactions.
- In these reactions, nutrients are converted into building blocks for cellular functions and energy. Understanding the rhythms of cellular metabolism is crucial for many fields, including biochemistry, physiology, medicine, and biotechnology.



TECHNIQUES AND INTRODUCTION TECHNOLOGIES IN METABOLOMICS

The study of small compounds, or metabolites, that are found in biological systems is known as metabolomics. It seeks to comprehend the regulation of metabolic pathways in order to provide insights into a range of physiological and pathological processes.

- **Mass Spectrometry (MS):**

Liquid Chromatography-Mass Spectrometry (LC-MS): This potent technology allows for the identification and quantification of metabolites in complicated samples by combining mass spectrometry detection with liquid chromatography separation.

- **Gas Chromatography-Mass Spectrometry (GC-MS):**

Another popular method that offers great sensitivity and repeatability is GC-MS, which divides metabolites according to their volatility before examining them using mass spectrometry.

- **Nuclear Magnetic Resonance (NMR):**

With the use of non-destructive NMR spectroscopy, metabolites in biological samples can be identified based on their distinct chemical characteristics, yielding quantitative and structural details on the metabolites.

- **High-Performance Liquid Chromatography (HPLC):**

Using a liquid mobile phase and a solid stationary phase, HPLC separates metabolites according to their chemical characteristics. UV or fluorescence detection is frequently used in conjunction with HPLC to quantify metabolites.

- **Capillary Electrophoresis (CE):**

CE offers high separation efficiency by employing an electric field to separate metabolites according to their size and charge.

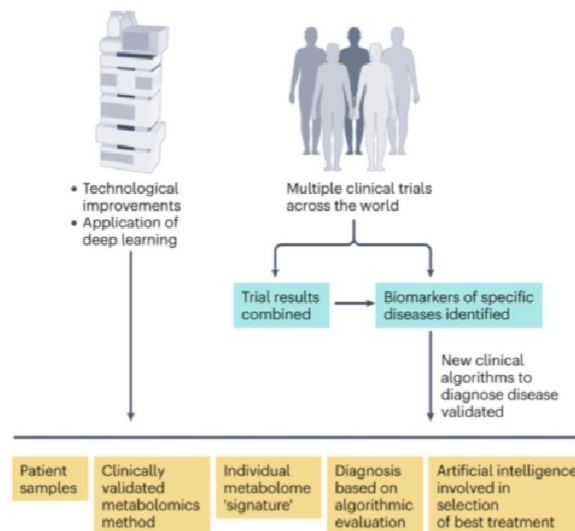
METABOLOMICS IN PRECISION MEDICINE

- ⇒ Precision medicine has shown that metabolomics is a useful tool because it provides information on individual differences in metabolic profiles and how these variations affect disease diagnosis, prognosis, and treatment. This is a conversation on personalized disease diagnosis in precision medicine using metabolomics. Identification of metabolic markers linked to certain diseases or disease subtypes is made possible by metabolomic profiling. These signatures can be utilized to track the course of the disease and the effectiveness of treatment, in addition to providing a more precise and timely diagnosis.
- ⇒ Approval of patient demographics, By helping to classify patient populations according to their metabolic profiles, metabolomics can support the development of more specialized and successful treatment plans. Clinical professionals can make well-informed decisions about therapy selection and dosage by using predictive and

metabolic biomarkers, which have the ability to predict an individual's reaction to medications or therapies.

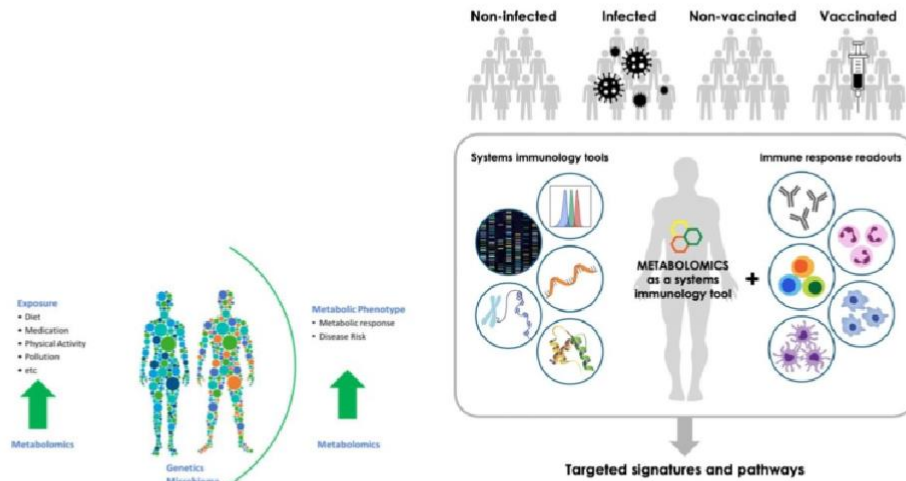
- ⇒ Tracking the response of treatment, Through the recording of changes in metabolite levels and metabolic pathways, metabolic profiling makes it possible to evaluate treatment response in real time. Determining the Therapeutic Targets Through metabolomics, important compounds linked to the etiology of disease can be identified as well as dysregulated metabolic pathways. dietary Interventions and Lifestyle Modifications: Based on unique metabolic phenotypes, Metabolomics can guide customized nutritional interventions and lifestyle changes.

TRANSLATING METABOLOMICS DISCOVERIES INTO CLINICAL APPLICATION



- ⇒ A complex process, "translating metabolomics discoveries into clinical applications" aims to use knowledge of metabolites in biological systems to better treat patients. First, using metabolomics methods like nuclear magnetic resonance spectroscopy and mass spectrometry, researchers find possible biomarkers. To establish their therapeutic relevance, these biomarkers—which are suggestive of a range of illnesses or ailments—go through a rigorous validation process in sizable patient cohorts. Then, in comparison to current markers, their usefulness is evaluated in diagnostic, prognostic, or therapeutic monitoring scenarios. Personalized treatment plans or early disease identification are made possible by the development of diagnostic assays utilizing validated biomarkers that have demonstrated clinical use and are intended for routine use in clinical laboratories. Their efficacy and dependability are continuously monitored and improved in actual clinical settings.
- ⇒ By giving physicians useful tools for more precise diagnosis, prognosis, and therapy decision-making catered to each patient's needs, metabolomics advances precision medicine through this approach.

METABOLOMICS AND PERSONALIZED HEALTH MANAGEMENT



- ⇒ A potent omics technique called metabolomics has great potential to advance individualized health care. Metabolomics provides a greater understanding of illness causes, early identification, and customized therapies based on the whole metabolic signatures of individual patients. This method has the potential to revolutionize a number of medical fields, such as prognosis, precision medicine, and treatment monitoring.
- ⇒ Metabolomics provides a comprehensive picture of an individual's metabolic status in individualized health management, taking into account both hereditary and environmental factors. Metabolomics uses sophisticated analytical methods like nuclear magnetic resonance spectroscopy and mass spectrometry to find complex metabolic fingerprints linked to both health and disease. As biomarkers, these fingerprints help with disease classification, treatment response prediction, and therapeutic efficacy monitoring.
- ⇒ Moreover, metabolomics enhances our comprehension of intricate biological systems by collaborating with other omics fields like proteomics and genomics. A more thorough definition of disease phenotypes is made possible by the integration of multi-omics data, which also makes it easier to construct patient-specific targeted therapies.
- ⇒ The application of metabolomics to customized health management has enormous promise, but there are still obstacles to overcome, such as standardizing procedures and interpreting and analyses data. It will take cooperation between scientists, medical professionals, and legislators to get beyond these obstacles and fully utilize metabolomics for therapeutic purposes.

Yuvashree M

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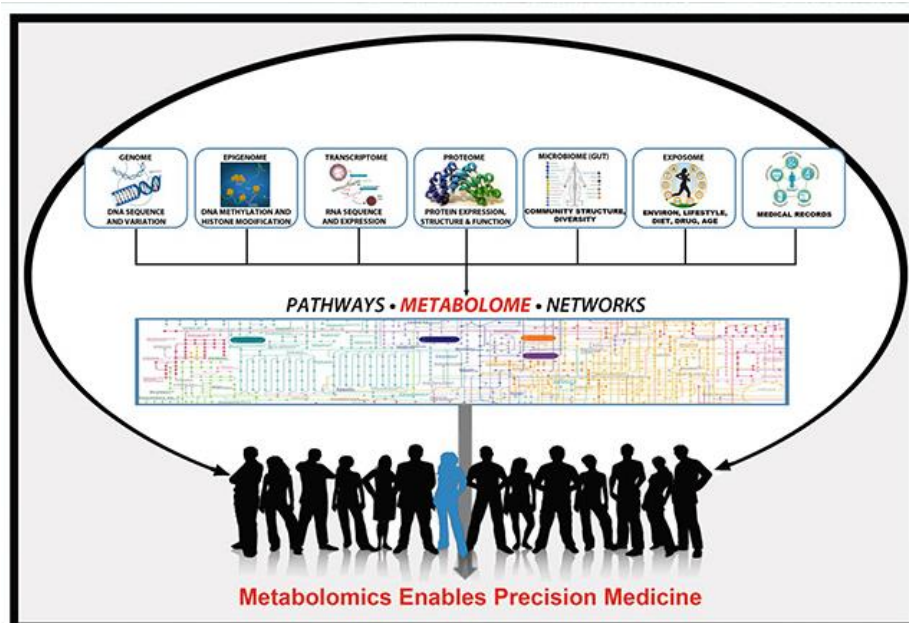
2.1 REVIEW ARTICLE

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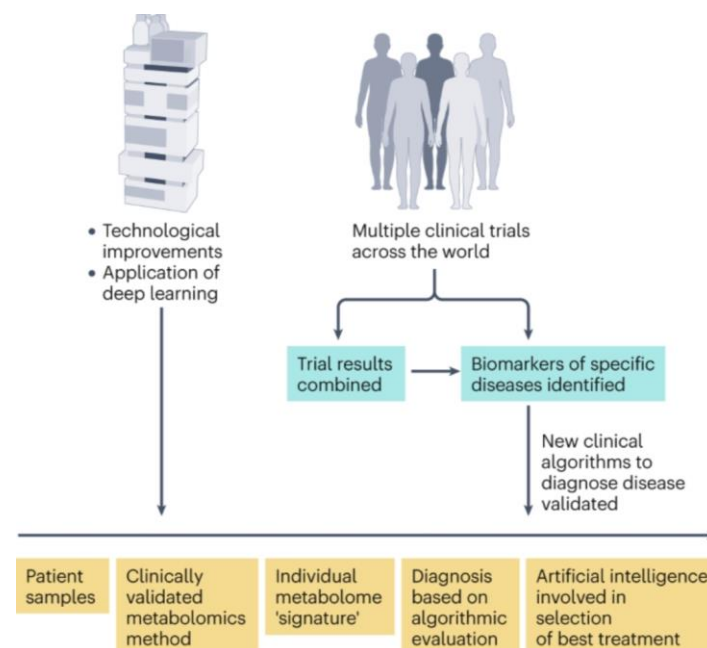
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- ⇒ Precision medicine has shown that metabolomics is a useful tool because it provides information on individual differences in metabolic profiles and how these variations affect disease diagnosis, prognosis, and treatment. This is a conversation on personalized disease diagnosis in precision medicine using metabolomics. Identification of metabolic markers linked to certain diseases or disease subtypes is made possible by metabolomic profiling. These signatures can be utilized to track the course of the disease and the effectiveness of treatment, in addition to providing a more precise and timely diagnosis.
- ⇒ Approval of patient demographics, By helping to classify patient populations according to their metabolic profiles, metabolomics can support the development of more specialized and successful treatment plans. Clinical professionals can make well-informed decisions about therapy selection and dosage by using predictive and metabolic biomarkers, which have the ability to predict an individual's reaction to medications or therapies.

⇒ Tracking the response of treatment, Through the recording of changes in metabolite levels and metabolic pathways, metabolic profiling makes it possible to evaluate treatment response in real time. Determining the Therapeutic Targets Through metabolomics, important compounds linked to the ethology of disease can be identified as well as dysregulated metabolic pathways. dietary Interventions and Lifestyle Modifications: Based on unique metabolic phenotypes, Metabolomics can guide customized nutritional interventions and lifestyle changes.

TRANSLATING METABOLOMICS DISCOVERIES INTO CLINICAL APPLICATION

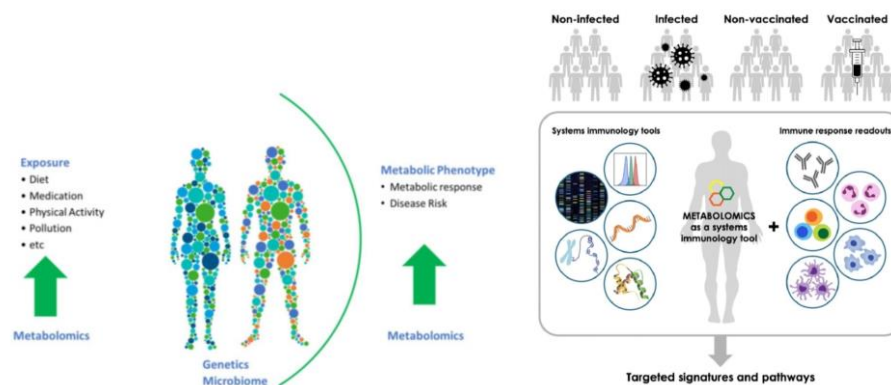


⇒ A complex process, "translating metabolomics discoveries into clinical applications" aims to use knowledge of metabolites in biological systems to better treat patients. First, using metabolomics methods like nuclear magnetic resonance spectroscopy and mass spectrometry, researchers find possible biomarkers. To establish their therapeutic relevance, these biomarkers—which are suggestive of a range of illnesses or ailments—go through a rigorous validation process in sizable patient cohorts. Then, in comparison to current markers, their usefulness is evaluated in diagnostic, prognostic, or therapeutic monitoring scenarios. Personalized treatment plans or early disease identification are made possible by the development of diagnostic

assays utilizing validated biomarkers that have demonstrated clinical use and are intended for routine use in clinical laboratories. Their efficacy and dependability are continuously monitored and improved in actual clinical settings.

- ⇒ By giving physicians useful tools for more precise diagnosis, prognosis, and therapy decision-making catered to each patient's needs, metabolomics advances precision medicine through this approach.

METABOLOMICS AND PERSONALIZED HEALTH MANAGEMENT



- ⇒ A potent omics technique called metabolomics has great potential to advance individualized health care. Metabolomics provides a greater understanding of illness causes, early identification, and customized therapies based on the whole metabolic signatures of individual patients. This method has the potential to revolutionize a number of medical fields, such as prognosis, precision medicine, and treatment monitoring.
- ⇒ Metabolomics provides a comprehensive picture of an individual's metabolic status in individualized health management, taking into account both hereditary and environmental factors. Metabolomics uses sophisticated analytical methods like nuclear magnetic resonance spectroscopy and mass spectrometry to find complex metabolic fingerprints linked to both health and disease. As biomarkers, these fingerprints help with disease classification, treatment response prediction, and therapeutic efficacy monitoring.
- ⇒ Moreover, metabolomics enhances our comprehension of intricate biological systems by collaborating with other omics fields like proteomics and genomics. A more thorough definition of disease phenotypes is made possible by the integration of multi-omics data, which also makes it easier to construct patient-specific targeted therapies.

⇒ The application of metabolomics to customized health management has enormous promise, but there are still obstacles to overcome, such as standardizing procedures and interpreting and analyses data. It will take cooperation between scientists, medical professionals, and legislators to get beyond these obstacles and fully utilize metabolomics for therapeutic purposes.

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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 provides a comprehensive introduction to MATLAB, covering key concepts like basic syntax, data manipulation, and plotting. It's a self-paced course with interactive modules and hands-on exercises, making it suitable for beginners and those needing a refresher. I gained fundamental MATLAB skills essential for various fields, from engineering to data science.

2.RENIFORCEMENT LEARNING ONRAMP

DESCRIPTION:

Reinforcement Learning OnRamp is an educational platform focusing on teaching the essentials of reinforcement learning. It offers interactive tutorials, practical exercises, and real-world examples to facilitate understanding. With a hands-on approach, users can explore algorithms like Q-learning and deep reinforcement learning in simulated environments. This platform equips learners with the skills to tackle challenges in autonomous systems and robotics.

3.OBJECT-ORINENTED PROGRAMMING ONRAMP

DESCRIPTION:

Object-Oriented Programming OnRamp is an educational platform focused on teaching the principles and practices of object-oriented programming (OOP). It offers interactive tutorials, hands-on exercises, and real-world examples covering concepts like classes, objects, inheritance, and polymorphism. From this course I was able to know how to design and implement robust, modular software solutions using OOP principles. With its structured curriculum and practical approach, Object-Oriented Programming OnRamp equips with essential skills for software development in various domains.

4.MACHINE LEARNING ONRAMP

DESCRIPTION:

Machine Learning OnRamp is an educational platform designed to introduce to the fundamentals of machine learning. It offers interactive tutorials, hands-on exercises,

and real-world examples covering topics like supervised and unsupervised learning, classification, and regression. On this course i explored popular algorithms such as decision trees, support vector machines, and neural networks.

5.COMPUTER VISION ONRAMP

DESCRIPTION:

Computer Vision OnRamp is an educational platform dedicated to teaching the principles and applications of computer vision. It offers interactive tutorials, hands-on exercises, and real-world examples covering topics such as image classification, object detection, and image segmentation. On this course I gained knowledge on algorithms like convolutional neural networks (CNNs) and deep learning architectures tailored for visual data analysis. With its structured curriculum and practical approach, Computer Vision OnRamp equips with the skills to develop innovative solutions in fields like autonomous vehicles, healthcare, and surveillance.

6.MATLAB FUNDAMENTALS

DESCRIPTION:

MATLAB Fundamentals covers essential concepts including data types, arrays, control flow, and functions through interactive tutorials and practical exercises. Participants learn to manipulate data, create plots, and automate tasks, enhancing their proficiency in MATLAB programming. By mastering these fundamentals, I acquire the skills necessary for various fields, from engineering to finance, empowering to solve diverse computational problems efficiently.

7.SIMULINK ONRAMP

DESCRIPTION:

Simulink is the A user-friendly introduction to Simulink, a potent tool for modelling, simulating, and evaluating dynamic systems, is provided by Onramp. I examine fundamental ideas like block diagrams, simulation, and model-based design through engaging classes and practical projects. The fundamental abilities required to design and model dynamic systems in a variety of fields, including as signal processing and control systems.

8.MATLAB FOR DATA PROCESSING AND VISUALIZATION

DESCRIPTION:

Matlab is a powerful tool for data processing and visualization, offering a wide range of functions and libraries. Its intuitive interface facilitates efficient manipulation and analysis of datasets of various sizes and formats. From this course I gained knowledge on visualizations, including plots, charts, and graphs, to explore and communicate their findings effectively. From preprocessing to presentation, Matlab streamlines the entire data analysis pipeline.

9.MACHINE LEARNING WITH MATLAB

DESCRIPTION:

Matlab's machine learning toolbox provides a powerful environment for data analysis and modeling. Leveraging a wide array of algorithms, users can tackle classification, regression, clustering, and more. Its intuitive interface streamlines data preprocessing, model training, and evaluation. Additionally, Matlab's extensive visualization capabilities aid in understanding and interpreting results effectively. With robust documentation and community support, Matlab is a versatile tool for machine learning tasks."

10.DEEP LEARNING WITH MATLAB

DESCRIPTION:

Deep Learning Onramp is a comprehensive MATLAB course introducing neural networks, CNNs, and RNNs through interactive modules and practical exercises. Participants gain proficiency in image classification, object detection, and sequence prediction, crucial for real-world applications. From this I learned, fostering a deeper understanding of deep learning concepts. By the course's conclusion, learners are equipped with essential skills to tackle complex problems in computer vision, natural language processing, and autonomous systems.

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:

Image Processing OnRamp is an educational platform dedicated to teaching the principles and techniques of digital image processing. It provides interactive tutorials, practical exercises, and real-world examples to aid comprehension. I learned about topics like image enhancement, segmentation, and feature extraction. With hands-on activities, this platform equips I gained on skills applicable in fields such as computer vision and medical imaging.

13.MATLAB PROGRAMMING TECHNIQUES

DESCRIPTION:

Matlab programming techniques encompass a diverse array of strategies for efficient code development and optimization. From this I gained an knowledge on Leveraging built-in functions, vectorization, and parallel computing, users can enhance code performance and scalability.

14.statistic onramp

DESCRIPTION:

Statistics OnRamp is an online platform offering interactive lessons and resources for introductory statistics. From this I gained knowledgr on probability, data analysis, and statistical inference. I was able to access tutorials, exercises, and quizzes to reinforce learning.. With its user-friendly interface and comprehensive content, Statistics OnRamp provides a solid foundation in statistical concepts.

15.SOLVING NONLINEAR EQUATION WITH MATLAB

DESCRIPTION:

Solving Nonlinear Equations with MATLAB involves utilizing powerful numerical methods to find solutions to equations that cannot be solved analytically. MATLAB offers various functions and techniques such as `fsolve`, `fzero`, and symbolic toolbox

for solving nonlinear equations efficiently. Through code examples, tutorials, and documentation, MATLAB empowers users to tackle a wide range of nonlinear equations encountered in engineering, physics, and mathematics. Mastery of these methods equips users with the ability to model and solve complex real-world problems effectively, enhancing their problem-solving skills in diverse fields.

16.SIGNAL PROCESSING WITH MATLAB

DESCRIPTION:

The Signal Processing Onramp provides a foundational understanding of signal processing concepts. It covers topics such as time-domain and frequency-domain analysis, filtering, and signal modulation. I gained knowledge through interactive modules and practical exercises.

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

MATLAB CERTIFICATES



Course Completion Certificate

Yuvashree M

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

MATLAB Onramp

DIRECTOR, TRAINING SERVICES

15 November 2023



Course Completion Certificate

Yuvashree M

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Simulink Onramp

DIRECTOR, TRAINING SERVICES

31 March 2024



Course Completion Certificate

Yuvashree M

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Solving Nonlinear Equations with MATLAB


DIRECTOR, TRAINING SERVICES

5 March 2024



Course Completion Certificate

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Deep Learning Onramp


DIRECTOR, TRAINING SERVICES

22 February 2024



Course Completion Certificate

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MATLAB Fundamentals


DIRECTOR, TRAINING SERVICES

22 February 2024



Course Completion Certificate

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Machine Learning with MATLAB


DIRECTOR, TRAINING SERVICES

7 March 2024



Course Completion Certificate

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MATLAB for Data Processing and Visualization



DIRECTOR, TRAINING SERVICES

17 February 2024



Course Completion Certificate

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MATLAB Programming Techniques



DIRECTOR, TRAINING SERVICES

22 February 2024



Course Completion Certificate

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Statistics Onramp

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

DIRECTOR, TRAINING SERVICES

2 March 2024



Course Completion Certificate

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Reinforcement Learning Onramp

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

DIRECTOR, TRAINING SERVICES

17 December 2023



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Image Processing Onramp


DIRECTOR, TRAINING SERVICES

5 March 2024



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Machine Learning Onramp


DIRECTOR, TRAINING SERVICES

15 December 2023



Course Completion Certificate

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Computer Vision Onramp

A handwritten signature in black ink, appearing to read "Rajesh Santosh".

DIRECTOR, TRAINING SERVICES

16 December 2023



Course Completion Certificate

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

Object-Oriented Programming Onramp

A handwritten signature in black ink, appearing to read "Rajesh Santosh".

DIRECTOR, TRAINING SERVICES

17 December 2023



Course Completion Certificate

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Signal Processing Onramp


DIRECTOR, TRAINING SERVICES

7 March 2024



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Signal Processing with MATLAB


DIRECTOR, TRAINING SERVICES

2 March 2024



Course Completion Certificate

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Image Processing with MATLAB


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Deep Learning with MATLAB


DIRECTOR, TRAINING SERVICES

12 February 2024