

Integrated analysis: Gene Expression, Survival, Biomarker, and Drug Target

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

By **R.BRINDHA (43739042)**



**DEPARTMENT OF BIOINFORMATICS AND DATA
SCIENCE**

SCHOOL OF BIO AND CHEMICAL ENGINEERING

SATHYABAMA

INSTITUTE OF SCIENCE AND TECHNOLOGY

(DEEMED TO BE UNIVERSITY)

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BONAFIDE CERTIFICATE

This is to certify that this Project Report is the bonafide work of R.BRINDHA (43739042) who carried out the project entitled “Integrated Analysis: Gene Expression, Survival, Biomarkers, and Drug Target” under Dr. MAHALAKSHMI from January 2024 to April 2024

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DECLARATION

I, R.BRINDHA (**43739042**), hereby declare that the Project Report “Integrated Analysis: Gene Expression, Survival, Biomarkers, and Drug Target” done by me under the guidance of Dr. MAHALAKSHMI is submitted in partial fulfilment of the requirements for the award of Master of Science degree in Bioinformatics and Data Science

DATE:

R.BRINDHA

PLACE: CHENNAI

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 sence of gratitude to my project guide Dr. MAHALAKSHMI Department of Bioinformatics and Data Science for his 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.BRINDHA)

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1. TRANSLATIONAL BIOINFORMATICS

1.1 GENE EXPRESSION ANALYSIS

INTRODUCTION:

A biological network is a method of representing systems as complex sets of binary interactions or relations between various biological entities. A typical graphing representation consists of a set of nodes connected by edges. Cytoscape is a open source software platform for visualizing molecule interactions network and biological pathway and integrating the network with annotations, gene expression profile. Cytohubba predicts and explore the important nodes and edges in given network by several topological algorithms such as Degree, Bottleneck, MCC, DMNC, EPC, Eccentricity, Closeness, Stress, Clustering coefficient and Betweenness.

AIM:

Build a 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 visualising 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 Neighborhood Component, Density of Maximum Neighborhood 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 visualises them into functionally organised networks.

PROCEDURE:

- For the database on ovarian cancer GEO2R is the source of the geo dataset (GSE36895).
- After choosing the suitable parameters, the GEO dataset is retrieved.
- Genes that were upregulated were copied and paste into the cytoscape network.
- Build a biological network using a BioGrid in cytohubba to analyse the network and identify importance node based various topologies algorithm to determine the top 10 genes.
- Genes must be copied in cluego and continue cluego parameter such as species ontology and statistical settings.
- Run cluego analysis to identify functional categories or pathways associated with the selected nodes.

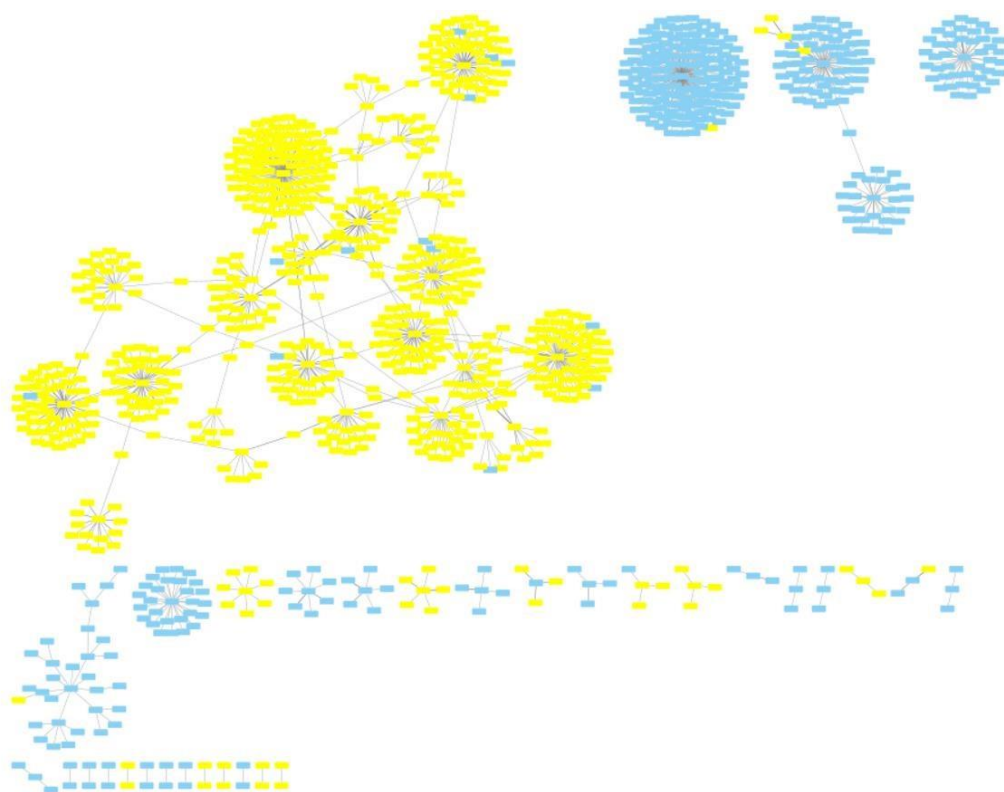


Figure 1: Network pathway of upregulated gene

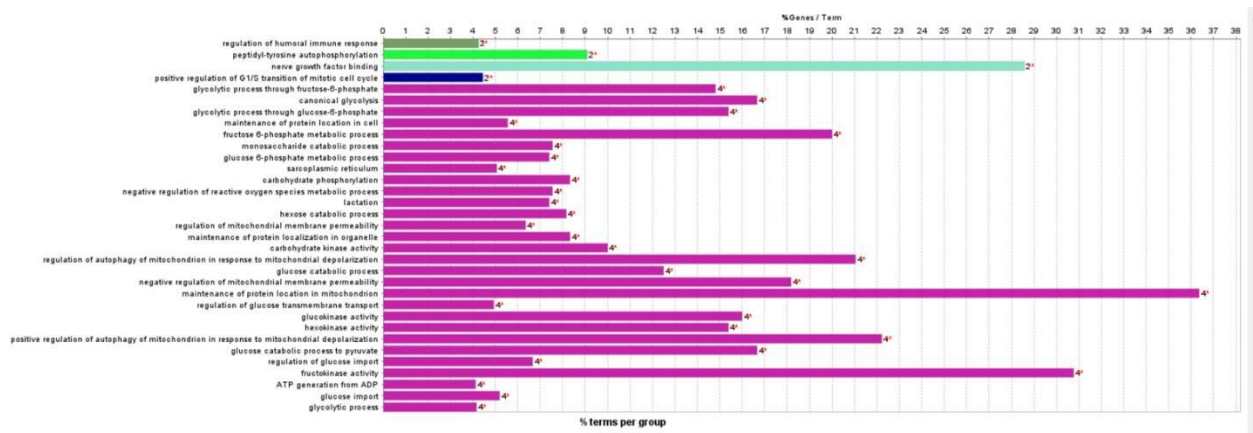


Figure 2: Graph of functional analysis

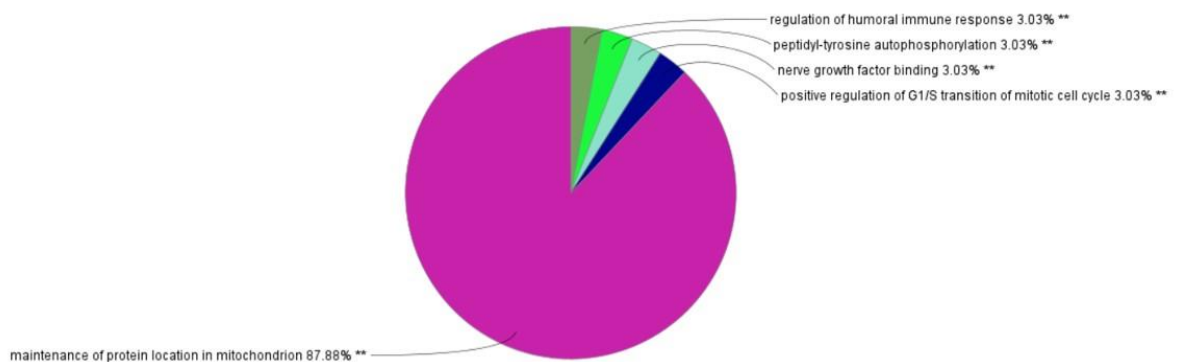


Figure 3: Pie chart of functional analysis

INTERPRETATION:

GEO Dataset GSE ID : GSE36895

Sample no: 54

Platform: GPL570

Type: Expression profiling by array

No of differentially expressed genes: 250

No of upregulated genes: 48

No of downregulated genes: 212

Network features of upregulated genes: nodes- 1082, edges- 1351

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 CPAMD8 cumulative survival probabilities.

INTERPRETATION:

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

- **BLADDER CARCINOMA:**

HR Rate: 1.23(0.89-1.68)

50% of median survival of probability:

Low expression cohort: 38.77

High expression cohort: 26.5

- **BREAST CANCER:**

HR Rate: 0.81(0.59-1.12)

50% of median survival of probability:

Low expression cohort: 122.3

High expression cohort: 148.53

- CERVICAL SQUAMOUS CELL CARCINOMA

HR Rate: 0.69(0.42-1.11)

50% of median survival of probability:

Low expression cohort: 96.27

High expression cohort: 136.2

- ESOPHAGEAL ADENOCARCINOMA:

HR Rate: 1.8(0.92-3.5)

50% of median survival of probability:

Low expression cohort: 46.73

High expression cohort: 14.5

- ESOPHAGEAL SQUAMOUS CELL CARCINOMA:

HR Rate: 0.31(0.11-0.86)

50% of median survival of probability:

Low expression cohort: 25.43

High expression cohort: 48.6

- HEAD NECK SQUAMOUS CELL CARCINOMA:

HR Rate: 1.22(0.9-1.65)

50% of median survival of probability:

Low expression cohort: 68.8

High expression cohort: 48.63

- KIDNEY RENAL CELL CARCINOMA:

HR Rate: 5.37(2.94-9.82)

50% of median survival of probability:

Low expression cohort: 89.47

High expression cohort: 20.8

- LIVER HEPATOCELLULAR CARCINOMA:

HR Rate: 2.14(1.51-3.04)

50% of median survival of probability:

Low expression cohort: 71.03

High expression cohort: 25.6

- LUNG ADENOCARCINOMA:

HR Rate: 1.84(1.34-2.52)

50% of median survival of probability:

Low expression cohort: 59.67

High expression cohort: 40.97

- LUNG SQUAMOUS CELL CARCINOMA:

HR Rate: 0.67(0.51-0.88)

50% of median survival of probability:

Low expression cohort: 35.83

High expression cohort: 63.73

- OVARIAN CANCER:

HR Rate: 0.9(0.68-1.18)

50% of median survival of probability:

Low expression cohort: 45.47

High expression cohort: 44.13

- PANCREATIC DUCTAL ADENOCARCINOMA:

HR Rate: 2.49(1.58-3.93)

50% of median survival of probability:

Low expression cohort: 37.67

High expression cohort: 16.6

- PHEOCHROMOCYTOMAN & PARAGANGLIOMA:

HR Rate: 4.59(0.81-25.91)

50% of median survival of probability:

Low expression cohort: N/A

High expression cohort: N/A

- RECTUM ADENOCARCINOMA:

HR Rate: 0.43(0.19-0.96)

50% of median survival of probability:

Low expression cohort: 36.53

High expression cohort: 43.8

- SARCOMA:

HR Rate: 2.2(1.39-3.47)

50% of median survival of probability:

Low expression cohort: 47.47

High expression cohort: 20.93

- STOMACH ADENOCARCINOMA:

HR Rate: 0.71(0.45-1.03)

50% of median survival of probability:

Low expression cohort: 26.47

High expression cohort: 56.2

- TESTICULAR:

HR Rate: 0(0-Inf)

50% of median survival of probability:

Low expression cohort: N/A

High expression cohort: N/A

- THYMOMA:

HR Rate: 0.12(0.02-0.58)

50% of median survival of probability:

Low expression cohort: N/A

High expression cohort: N/A

- **THYROID CARCINOMA:**

HR Rate: 1.92(0.67-5.54)

50% of median survival of probability:

Low expression cohort: N/A

High expression cohort: N/A

- **UTERINE CORPUS ENDOMETRIAL CARCINOMA:**

HR Rate: 1.76(1.14-2.72)

50% of median survival of probability:

Low expression cohort: 108.37

High expression cohort: 41.37

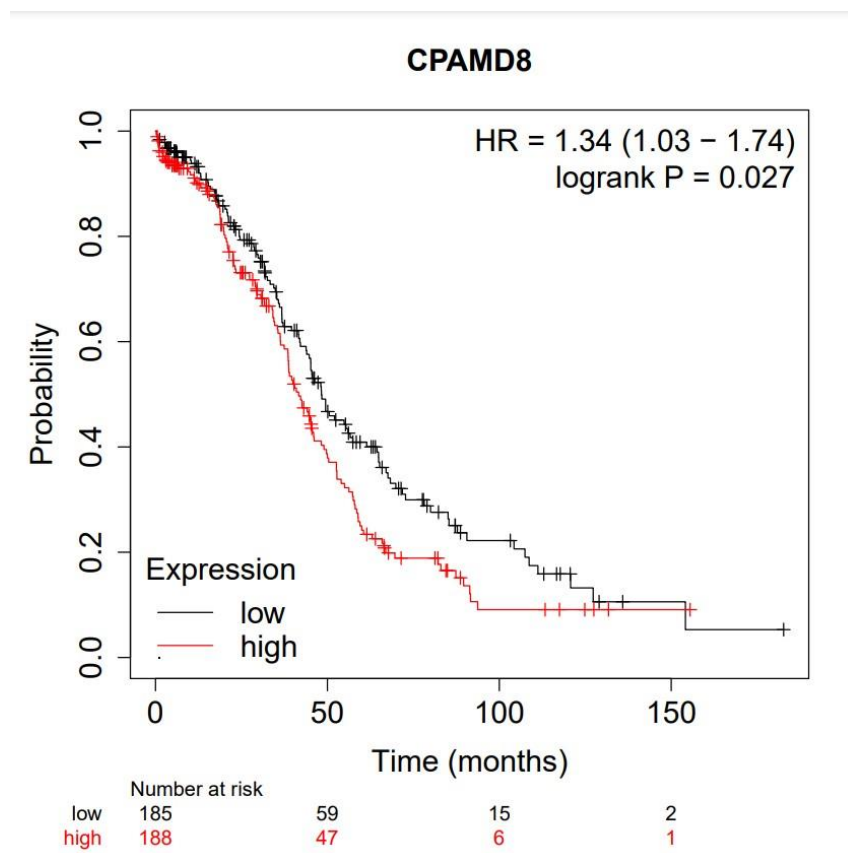


Figure 4 : OVARIAN CANCER

1.3. BIOMARKERS: IDENTIFYING BIOLOGICAL MARKERS FOR DISEASE DIAGNOSIS AND THERAPEUTIC MONITORING

DESCRIPTION:

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

AIM:

Identify the disease markers related to ovarian 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 ovarian cancer data's were retrieved and literature survey was done

INTERPRETATION:

BIOMARKER ID	BIOMARKER NAME	CLASS	GENE NAME	BIOMARKER TYPE	REPRESENTATIVE DRUG	REPRESENTATIVE DISEASE
BAIRLO	NQ01 mRNA	mRNA	Nq01 DIA4 MMORI	PDY SAF PRD	CB-5083	Ovarian cancer

GENERAL INFORMATION OF THE BIOMARKER :

BIOMARKER TYPE AND RELAVANT DATA:

- Predictive biomarker (PRD): 93
- Safety biomarker (SAF): 22
- Pharmacodynamic biomarker (PDY): 3
- Monitoring biomarker (MOI): 5
- Surrogate biomarker (SUR): 1

SAFETY BIOMARKER(SAF):

Application of the Biomarker in Drug Development and Clinical Practice

Drug Status: Approved Drug
Drug Name: Acetaminophen

Drug Status: Approved Drug
Drug Name: Cisplatin

Drug Status: Approved Drug
Drug Name: Gentamicin

Drug Status: Approved Drug
Drug Name: Vancomycin

APPLICATION OF THE BIOMARKER IN DIAGNOSIS AND PROGNOSIS:

DIAGNOSIS:

- Esophageal cancer
- Gastric cancer
- Liver cancer
- Leukemia
- Lymphoma
- Osteosarcoma
- Pancreatic cancer
- Prostate cancer
- Urothelial cancer

PROGNOSIS:

- Colorectal cancer
- Bladder cancer
- Esophageal cancer
- Gastric cancer
- Liver cancer

TISSUE-SPECIFIC EXPRESSION OF THE BIOMARKER:

- Tissue-Specific RNA Expression of this Biomarker in total 32 tissues
- Tissue-Specific Protein Abundance of this Biomarker in total 32 tissues

DISEASE-SPECIFIC EXPRESSION OF THE BIOMARKER:

DISEASE : Ovarian Cancer

TISSUE : Ovarian Tissue

SIGNIFICANT TEST:

Case Vs Healty:	P-Value	log2 FC
	4.08E-0.3	9.58E-0.1
Case Vs Adjacent:	P-Value	log2 FC
	6.28E-0.1	-3.63E-0.1

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.
- **SwissTarget Prediction:** SwissTargetPrediction 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 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 Acetaminophen targets screening and binding assessment.

MATERIAL 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.

PDB: The Protein Data Bank is a repository for the 3-D structural data of large biological molecules, such as proteins and nucleic acid. The PDB format accordingly provides for description and annotation of protein and nucleic acid structures including atomic coordinates, secondary structure assignments, as well as atomic connectivity.

DRUGBANK: DrugBank Online is a comprehensive, free-to-access, online database containing information on drugs and drug targets. As both a bioinformatics and a cheminformatics resource, we combine detailed drug (i.e. chemical, pharmacological and pharmaceutical) data with comprehensive drug target (i.e. sequence, structure, and pathway) information.

PROCEDURE:

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

INTERPRETATION:

DRUG NAME: Acetaminophen

NO.OF. TARGET PREDICTED: 32

CHOOSEN TARGET: 5

HUB GENES SELECTED: CBF-B, HSPA8, PIG61, P34CDC2, NTRK1, G3PD, PARK1, RBBP1, YBR160W, p33

UNIPROT ID	PDB ID	NAME OF THE PROTEIN	RESOLUTION VALUE	CHAIN	DOMAIN
P06493	6GU6	Cyclindependent kinase 1	2.33A ⁰	B	4-287
P29375	5IVB	Lysinspecific demethylase 5A	1.39A ⁰	A	84-174
Q01196	1LJM	Runt-related transcription factor	2.50A ⁰	A	50-178
P24941	1GZ8	Cyclindependent kinase 2	1.30A ⁰	A	4-286

TARGET	COMMON NAME	UNIPROT ID	TARGET CLASS	PROBABILITY
Carbonic anhydrase II	CA2	P00918	Lyase	0.857226280089
Carbonic anhydrase VII	CA7	P43166	Lyase	0.857226280089
Myoglobin	MB	P02144	Unclassified protein	0.857226280089
Cytochrome P450 1A2	CYP1A2	PO5177	Cytochrome P450	0.226173407881
Indoleamine 2,3-dioxygenase	ID01	P14902	Enzyme	0.053517944289

MOLECULE TABLE:

NAME	-PLP1	-PLP2	JAIN	PMF	DOCK SCORE
1LJM	43.58	40.96	0.11	4.69	31.495
1983					
5JFW	60.68	59.22	1.46	76.06	30.098
1983					
5IVB	18.44	21.19	-1.16	106.75	44.051
1983					
1GZ8	15.48	24.36	2.31	0.96	27.323
1983					
6GU6	11.07	13.92	-1.85	40.84	33.054
1983					

NON-BOND TABLE:

NAME	DISTANCE	CATEGORY	TYPE	FROM	TO
1LJM	2.79344	Hydrogen bond	Conventional hydrogen bond	A:ASN1119:ND2	1983:02
A:ASN1119:ND2-1983:02					
5IVB	2.2753				

1983:H14A:HIS483:N E 2		Hydrogen bonding	Conventio n al hydrogen bond	1983:H1 4	A:HIS483: N E2
1GZ8	2.67539	Hydrogen bonding	Conventio n al hydrogen bond	A:ARG1 2 6:NH2	1983:02
A:ARG126:N H2-1983:02					
6GU6	3.07967				1983:02
A:ARG170:N H1-1983:02		Hydrogen bonding	Conventio n al hydrogen bond	A:ARG1 7 0:NH1	

ASN1119 RESIDUE INTERACT WITH 1LJM:

ASN1119 refers to a specific amino acid residue at position 1119 in a protein sequence, whereas 1LJM is likely a protein structure identifier. ASN1119 could potentially interact with residue on the 1LJM protein through any of these mechanisms, such as hydrogen bonding, electrostatic interactions, van der Waals, hydrophobic interaction. ASN1119 is involved in a critical functional site or domain of its respective protein and if 1LJM is involved in a pathway or process related to that function.

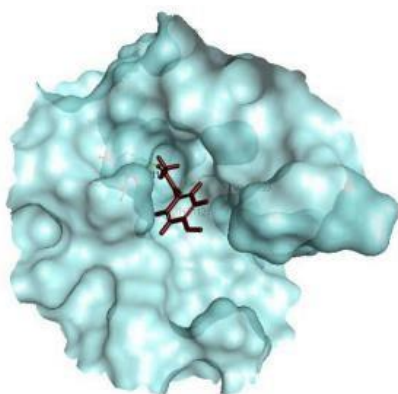


Figure 5.1: 3D STRUCTURE 1LJM

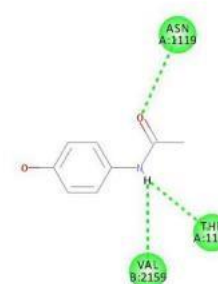


Figure 5.2: 2D STRUCTURE OF 1LJM

LEU746 RESIDUE INTERACT WITH 5JFW:

Protein ligand docking can be used to predict how LEU746 interacts with surrounding amino acids or ligands within the binding site or functional regions of the 5JFW protein. If the interactions involving LEU746 has therapeutic relevance, such as in the case of drug discovery, researchers may explore targeting this interactions to modulate the activity of the 5JFW protein for therapeutic purposes.

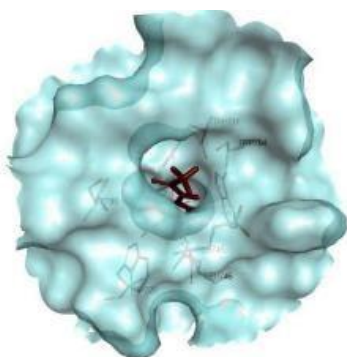


Figure 6.1: 3D STRUCTURE OF 5JFW

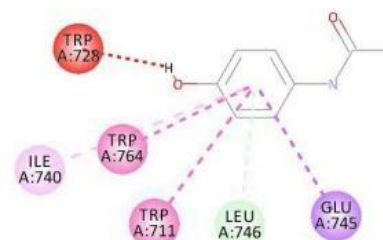


Figure 6.2: 2D STRUCTURE OF 5JFM

HIS483 RESIDUE INTERACT WITH 5IVB:

Protein ligand docking can predict how HIS483 interacts with neighbouring amino acids or any ligands within the proteins binding sites or functional regions. If the interaction involving HIS483 has therapeutic relevance such as drug discovery, researchers might explore targets this interaction to modulate the activity of the 5IVB protein for therapeutic purposes.

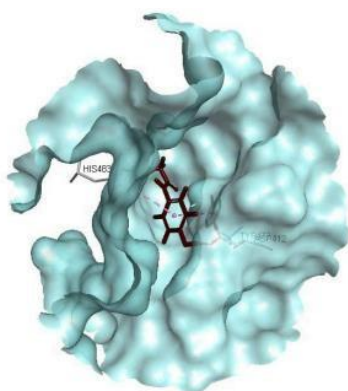


Figure 7.1: 3D STRUCTURE OF 5IVB

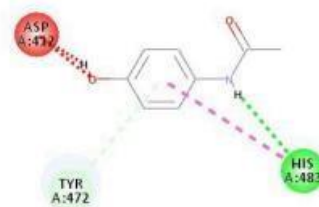


Figure 7.2: 2D STRUCTURE OF 5IVB

ARG126 RESIDUE INTERACT WITH 1GZ8:

Computational techniques such as molecular dynamics simulations or protein ligand docking can predict how ARG126 interact with neighbouring amino acids or ligand. This might involve investigate how mutations or alterations in ARG126 interact in the function of the 1GZ8 protein and its involved in cellular processes or disease pathways.

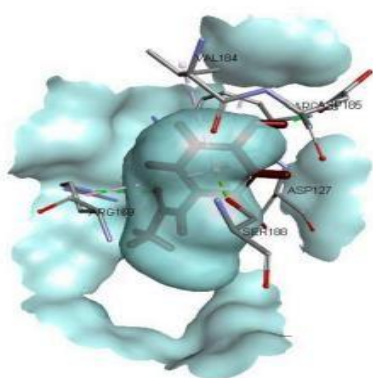


Figure 8.1: 3D STURCTURE OF 1GZ8

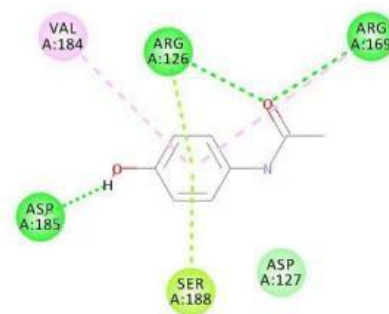


Figure 8.2: 2D STRUCTURE OF 1GZ8

ARG170 RESIDUE INTERACT WITH 6GU6:

Explore the biological implications of the interactions involving ARG170, investigate how mutations or alterations in ARG170 interaction affect the function of the 6GU6 protein and its involvement in cellular processes or disease pathway. If the interaction involving ARG170 has the therapeutic relevance, such as in drug discovery, explore targeting this interaction to modulate the activity of the 6GU6 protein for therapeutic purposes design small molecules or biologics that specifically target the interaction site.

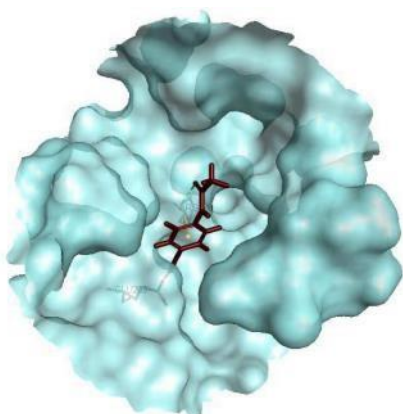


Figure 9.1: 3D STRUCTURE OF 6GU6

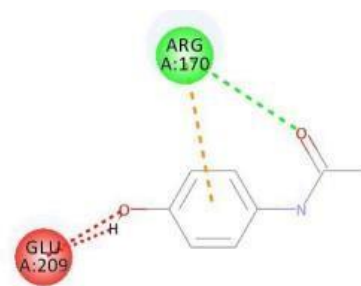


Figure 9.2: 2D STRUCTURE OF 6GU6

3. REVIEW ARTICLE

Brindha Ramachandran

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Heliyon, 2023

Publication

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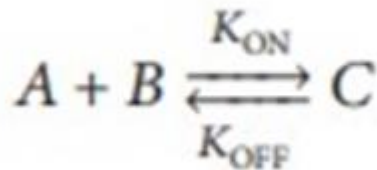
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COMPUTATIONAL MODELING IN BIOINFORMATICS: BRIDGING THEORY AND EXPERIMENT

New developments in high-throughput technology are increasing the demand for more precise systems biology simulations to better understand complicated diseases. The massive amounts of omics data produced by high-throughput experimental techniques are being analyzed using an increasing number of mathematical and computational models. These models aid in the development of new drugs and treatment approaches, improve our understanding of the molecular processes involved, and provide deeper insights into the pathogenic mechanisms of complex diseases. Mathematical modeling of biological systems has become a powerful tool in the search for effective cancer treatments in many different dimensions. High-throughput technology has fueled the evolution of systems biology, demonstrating the basic significance and efficiency of computer modeling. However, while trying to address new biological topics, the development of mathematical modeling tools runs into problems. Boolean networks, Petri nets (PNs), linear programming, and ordinary differential equations (ODEs) are well-known systems modeling techniques. ODE-based approaches capture the dynamic nature of biological processes through interactions between biological molecules. These methods encompass various approaches tailored to specific biological issues and experimental data, including the law of mass action, the Hill function, and Michaelis-Menten kinetics.

Petri nets have garnered attention for modeling gene regulatory networks, metabolic pathways, and signaling pathways. In a Boolean network, nodes represent binary states indicating the activation or inactivation of biological entities. State transitions are governed by Boolean functions, often employing logical operators like AND, OR, and NOT. In a Boolean network with n nodes, there are n Boolean functions ($B_1, B_2, \dots, B_n$) and n Boolean variables ($\sigma_1, \sigma_2, \dots, \sigma_n$). The statuses of all nodes are updated simultaneously in a synchronous pattern, as described by the formula below:



With the following formula, the asynchronous pattern can be expressed:

$$\sigma_i(t+1) = B_i(\sigma_{i_1}(t), \sigma_{i_2}(t), \dots, \sigma_{i_{k_i}}(t))$$

Boolean dynamic modeling of regulatory networks involves network reconstruction, identification of Boolean functions, and system dynamics analysis.

$$\sigma_i^*(t+1) = B_i(\sigma_{i_1}, \sigma_{i_2}, \dots, \sigma_{i_{k_i}}).$$

Linear programming-based approaches contribute to reconstructing gene regulatory networks and metabolic networks and inferring cell-specific signaling networks. Flux balance analysis (FBA), a novel computational approach, aids in genome-scale metabolic network reconstructions. FBA-based methods, leveraging linear programming, effectively address large-scale network optimization problems.

Network reconstruction, Boolean function identification, and system dynamics analysis are all components of the Boolean dynamic modeling of regulatory networks. The current focus areas in systems biology include understanding the 1. Dynamics of cell-cell interactions in tumor progression, 2. conducting systems-level analyses of heterogeneity and the microenvironment, and 3. employing systems biology in clinical trial design. These developments underscore the pivotal role of computational and mathematical modeling in unraveling the complexities of biological systems and advancing therapeutic interventions.

QUANTITATIVE ANALYSIS OF NEXT-GENERATION SEQUENCING DATA:

The significant increase in genomic, transcriptomic, and epigenomic information has spurred the development of comprehensive methods for quantitatively studying how molecules interact within specific cells or tissues. Next-generation sequencing (NGS) techniques have swiftly become widely used in medical applications, spanning from diagnosing genetic conditions and understanding disease networks to discovering drugs and exploring pharmacogenomics. Two methods at the system level include network inference and expression quantitative trait locus (QTL) analysis. These approaches extract valuable insights by combining extensive datasets.

PREDICTIVE MODELING OF RNA STRUCTURE AND FOLDING:

RNA structure prediction methods usually incorporate secondary structure information or only use sequencing data. Due to restricted computational resources, these methods reduce the prediction process to balance accuracy and speed. They frequently employ a coarse-grained model and might ignore some RNA structure and dynamics details that aren't essential for forecasting a structure that is somewhat precise. Effective techniques take into account previous insights from structures identified through experiments, frequently providing statistical directionality towards comparable conformations. Various restrictions and other additional information greatly improve prediction accuracy, as shown in RNA Puzzles tests conducted across the community. The partition function can calculate each possible base pair's probability as well as the likelihood of a structure using folding thermodynamics estimates. Assessing how well the structures predicted by the thermodynamic model alone fit the experimental reactivities of each nucleotide in the sequence, without experimental restrictions, is the goal of the first partition function analysis (the first step). By adding constraints at the nucleotide level, the expected number of structures are modified in the ensuing partition function computation (the fourth step) to better match the experimental data.

The first and second steps include the creation of a series of structures using a model of thermodynamics for RNA folding. A set of roughly 10,000 structures is produced, some of which may not be unique, via the method of partitioning in the first step and random sampling in the second step. The possibility of sampling a structure is determined by its Boltzmann probability of occurrence.

DYNAMIC MODELING OF GENE EXPRESSION DYNAMICS:

Predicting cell behavior under different advancing age settings can be facilitated by modeling gene expression. Numerous approaches, including theoretical information models, Bayesian networks, Boolean networks, and differential equation models, have been developed recently in high-throughput data acquisition to infer Gene Regulatory Networks (GRNs) from transcriptomic data. However, because GRNs are complicated and require inferring many characteristics, modeling gene expression is still difficult. It is frequently impractical to carry out enough experiments to infer a set of within-determined coefficients. Nevertheless, there are a lot of opportunities to comprehend and forecast biological responses under various settings because of gene expression modeling. Researchers employed time-resolved transcriptomic data obtained at 6 intervals (0, 24, 48, 72, 96, and 144 hours) from cells experiencing oncogenic (RAS-OIS) across two biologically identical replicates to statistically characterize the senescence of the transcriptome. They discovered the levels of worldwide gene expression as reported earlier. They have created a virtual screening pathway for tuberculosis and malaria drug discovery. These fifteen experiments in the cascade are designed for specific assays; these include a variety of ADMET properties such as cytotoxicity, solubility in water, permeability, microsomal stability of metabolism, cytochrome inhibition, and cardiac toxicity, as well as whole-cell phenotypic screening. Over the past five years, investments in the fields of artificial intelligence and machine learning have increased dramatically in response to business needs for expedited research and reduced attrition rates.

VIRTUAL SCREENING FOR DRUG DISCOVERY:

They have created a virtual examination pathway for drug discovery against tuberculosis and malaria. This process consists of fifteen models that are customized for specific experiments, which include whole-cell phenotypic screening to different ADMET features like cytotoxicity, solubility in water, permeability, microsomal stability of metabolism, cytochrome inhibition, and cardiac toxicity. Over the last five years, investments in artificial intelligence and machine learning have increased in response to industry demands for faster research and lower attrition rates.. AI/ML applications aim to expedite the identification of new clinical candidates while mitigating the risk of failure, streamlining the drug discovery process.

Virtual screening is vital in the development of drugs, simplifying the search for possible successes and evaluating drugs for subsequent examination, thereby considerably reducing experimental attrition rates. Our AI and machine learning resources include models tailored for whole-cell phenotypic screening against *Mycobacterium tuberculosis* (Mtb) and *Plasmodium falciparum* (Pf), along with numerous ADMET tests like cardiotoxicity, microsomal metabolic stability, and aqueous solubility. We've developed two virtual drug discovery cascades to identify promising antimalarial and antituberculosis compounds, along with their corresponding ADMET characteristics.

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4. MATLAB COURSES

Based on the matlab certificate there are 20 courses I have completed

- Reinforcement Learning Onramp
- Image Processing with MATLAB
- App Building Onramp
- MATLAB Fundamentals
- Solving Nonlinear Equations with MATLAB
- Machine Learning with MATLAB
- Statistics Onramp
- Signal Processing Onramp
- MATLAB Programming techniques
- MATLAB for data Processing and Visualization
- Simulink Onramp
- Wireless Communications Onramp
- MATLAB Onramp
- Image processing Onramp
- Deep Learning Onramp
- Machine Learning Onramp

- Deep Learning with MATLAB
- Computer vision Onramp
- Object-Oriented Programming Onramp
- Signal Processing with MATLAB

DESCRIPTION:

MACHINE LEARNING ONRAMP:

Machine Learning Onramp, is a self-paced tutorial that provides an interactive introduction to practical machine learning methods for classification problems using hands-on exercises with automated assessments and feedback. Topics covered in Machine Learning Onramp include an overview of machine learning and the classification workflow, importing and preprocessing data, engineering features, and building classification models.

WHAT I LEARNT ?

- Participants will gain a solid understanding of the fundamental concepts, techniques, and algorithms used in machine learning. This includes supervised and unsupervised learning methods, data preprocessing techniques, model evaluation, and more.
- With a comprehensive understanding of core concepts such as supervised and unsupervised learning, coupled with proficiency in data preprocessing techniques and model evaluation, individuals gain the confidence to tackle real-world data challenges.

APP BUILDING ONRAMP:

App Building Onramp in MATLAB is an introductory course that teaches you how to create interactive applications in MATLAB using the App Designer tool. The App Designer allows users to build graphical user interfaces (GUIs) for their MATLAB programs, making it easier to interact with code, visualize results, and create more user-friendly applications. It creates the visual layout of an app, using drag-and-drop components like buttons, sliders, drop-down menus, plots, and other interactive elements.

WHAT I LEARNT?

- Many App Building Onramp courses emphasize collaboration and version control using tools like Git. We will learn how to work effectively in a team environment and manage code changes using version control systems.

- The course serves as a stepping stone for individuals who wish to pursue further learning and specialization in specific areas of app development, such as iOS or Android development, game development, or mobile app security.

MATLAB FUNDAMENTALS:

MATLAB Fundamentals is a course designed to provide an in-depth understanding of MATLAB, a high-level programming environment widely used for technical computing, data analysis, algorithm development, and visualization. The course typically covers the core aspects of MATLAB, including its language structure, built-in functions, data manipulation capabilities, and graphical features.

WHAT I LEARNT ?

- Develop proficiency in data analysis and visualization, learning how to import, manipulate, analyze, and present data effectively using MATLAB's powerful tools and functions.
- Modularization and function creation, enabling them to write maintainable and optimized code.
- Depending on the course's depth, participants may also gain exposure to advanced topics such as specialized toolboxes and symbolic computation, expanding their knowledge and skill set.

MATLAB ONRAMP:

MATLAB Onramp is a free, self-paced, online course designed to introduce users to the basics of MATLAB. It provides a hands-on learning experience through interactive exercises, allowing users to quickly build foundational skills in MATLAB programming and data analysis. Explore different data structures in MATLAB, such as arrays, matrices, cell arrays, and structures. Understand how to create and manipulate these data structures.

WHAT I LEARNT ?

- By the end of the course, learners should have a solid understanding of the MATLAB environment, syntax, and basic programming concepts. They will be able to navigate MATLAB confidently and write simple scripts to perform tasks like data analysis, visualization, and basic mathematical computations.
- MATLAB Onramp covers basic data analysis techniques, including manipulation of arrays and matrices, statistical calculations, and visualization of data.
- Completing the MATLAB Onramp serves as a solid foundation for diving into more advanced MATLAB topics and applications. Learners are equipped with the necessary knowledge and skills to explore more complex concepts, such as machine learning, signal processing, and advanced numerical methods.

SIGNAL PROCESSING WITH MATLAB:

Signal processing with MATLAB refers to using MATLAB to analyze, process, and manipulate signals. Signals can be audio, image, video, or other forms of data that vary with time or space. MATLAB provides a robust set of tools and functions specifically designed for signal processing tasks. Understanding the fundamentals of signal processing, such as signals in time and frequency domains, sampling, quantization, and digital representation of signals.

WHAT I LEARNT ?

- Understand how signals are represented in MATLAB, including time-domain and frequency-domain representations.
- Explore different ways to visualize signals, such as plotting time-domain signals, spectrograms, and frequency spectra.
- Understand frequency-domain concepts and apply techniques like the Fast Fourier Transform (FFT) to analyze signal frequency components.

OBJECT-ORIENTED PROGRAMMING ONRAMP:

Object-Oriented Programming Onramp is a course designed to introduce the concepts of object-oriented programming (OOP) using MATLAB. This self-paced, interactive course covers the fundamentals of OOP and demonstrates how to apply these concepts to solve programming problems in MATLAB. Understand the basic concepts of OOP, including objects, classes, methods, properties, and encapsulation. Learn how these concepts help organize and structure code.

WHAT I LEARNT ?

- The Object-Oriented Programming (OOP) course equips with a robust skill set and a deep understanding of software development principles.
- Upon completion, students emerge with the ability to design, implement, and maintain complex software systems using OOP concepts such as encapsulation, inheritance, and polymorphism. They gain proficiency in organizing code efficiently, enhancing reusability, and ensuring scalability.
- Developing problem-solving skills and learn to navigate real-world software development challenges by applying design patterns and leveraging abstraction

SIMULINK ONRAMP:

Simulink Onramp is an introductory course designed to teach the basics of Simulink, a graphical programming environment used for modeling, simulating, and analyzing dynamic systems. Simulink is widely used in engineering and scientific applications, particularly for system modeling and simulation in areas like control systems, signal processing, robotics, and more. The Simulink Onramp course provides a hands-on, interactive learning experience to help users understand the fundamentals of Simulink and how to build basic models.

WHAT I LEARNT ?

- Understand the Simulink workspace and how to create and manage models.
- Adjust parameters in real-time during simulations to explore different system behaviors.
- Manipulate signals with operations like gain, delay, and filtering.

REINFORCEMENT LEARNING ONRAMP:

Reinforcement Learning Onramp is a course designed to introduce the basics of reinforcement learning (RL) using MATLAB and Simulink. Reinforcement learning is a type of machine learning where agents learn to make decisions by interacting with an environment and receiving feedback in the form of rewards or penalties. This course provides a hands-on introduction to the key concepts and tools used in reinforcement learning, guiding learners through the process of building, training, and testing RL agents.

WHAT I LEARNT ?

- Acquiring a comprehensive understanding of the fundamental concepts, principles, and terminology of reinforcement learning, including Markov Decision Processes (MDPs), value functions, policies, and exploration/exploitation tradeoffs.
- Help us to develop problem-solving skills necessary to tackle real-world reinforcement learning problems across diverse domains such as robotics, gaming, finance, healthcare, and more. learnt how to formulate RL problems, choose appropriate algorithms, and evaluate their performance.
- The course will enhance learners' critical thinking abilities as they analyze and evaluate the performance of different RL algorithms in various scenarios.

DEEP LEARNING ONRAMP:

Deep Learning Onramp is an introductory course designed to teach the fundamentals of deep learning using MATLAB. It provides a hands-on approach to learning the basics of deep learning concepts and how to implement them in MATLAB with the Deep Learning Toolbox. The course is typically self-paced and focuses on key elements like neural networks, model training, and practical applications.

WHAT I LEARNT ?

- Many deep learning courses involve hands-on projects where students apply what they've learned to solve real-world problems. Completing these projects
- helps reinforce concepts and build a portfolio of work to showcase to potential employers.
- Completing a Deep Learning Onramp course can serve as a solid foundation for further study or employment in the field of deep learning and artificial intelligence. It can provide a starting point for more advanced courses or projects, or even entry-level positions in industries where deep learning expertise is valued.

MATLAB PROGRAMMING TECHNIQUES:

MATLAB Programming Techniques refer to a set of best practices and advanced methods used to develop robust, efficient, and maintainable MATLAB code. These techniques go beyond basic scripting and aim to help programmers write clean, optimized, and scalable code for various applications. Break down your code into smaller, reusable functions and scripts. This modularity improves code readability, reduces redundancy, and facilitates debugging.

WHAT I LEARNT ?

- Gaining a solid understanding of the MATLAB programming language, its syntax, and its various features.
- This course help us to develop algorithms and implement them in MATLAB for various applications, such as signal processing, image processing, control systems, and more.
- Understanding the importance of documenting their code and results effectively, including writing clear comments and generating reports or presentations.

MATLAB FOR DATA PROCESSING AND VISUALIZATION:

MATLAB for data processing and visualization involves using MATLAB's extensive tools and functions to analyze, transform, and visualize data. This application of MATLAB is popular among researchers, engineers, and data scientists due to its versatility in handling a wide range of data types and its ability to create detailed visualizations. MATLAB allows you to import data from various sources, such as CSV files, Excel spreadsheets, text files, databases, and even web services. You can also export processed data to different formats for sharing or further analysis

WHAT I LEARNT ?

- This help us to learn how to create insightful visualizations of their data using MATLAB's plotting functions, including 2D and 3D plots, histograms, scatter plots,

and more. They will also learn how to customize the appearance of their plots to effectively communicate their findings.

- Many courses include hands-on projects or assignments where participants apply their MATLAB skills to analyze real-world datasets and create meaningful visualizations.
- How to perform basic and advanced data analysis tasks using MATLAB, such as statistical analysis, curve fitting, signal processing, image processing, and machine learning.

IMAGE PROCESSING ONRAMP:

Image Processing Onramp is an introductory course designed to teach the basics of image processing using MATLAB. This course provides a hands-on learning experience through interactive exercises and is suitable for beginners or those with limited experience in image processing. It focuses on key concepts and techniques for manipulating, analyzing, and visualizing images in MATLAB.

WHAT I LEARNT ?

- Completing the Image Processing Onramp course can have numerous outcomes, depending on your goals and aspirations. To gain a solid understanding of the fundamental concepts and techniques used in image processing, equipping you with valuable knowledge applicable across various industries, from healthcare to robotics.
- This course can serve as a stepping stone for further exploration and specialization in fields like computer vision, machine learning, and artificial intelligence.
- Additionally, mastering image processing techniques can enhance your problem-solving skills, allowing you to tackle real-world challenges more effectively.

WIRELESS COMMUNICATION ONRAMP:

In MATLAB, the term "wireless communication onramp" is not a standard or widely recognized term. However, in the context of wireless communication systems and MATLAB, an "onramp" might refer to a set of tools, functions, or resources provided by MATLAB to facilitate the development, simulation, or analysis of wireless communication systems. MATLAB offers various toolboxes and functions for wireless communication system design, simulation, and analysis.

WHAT I LEARNT ?

- Understand basic concepts like modulation, coding, and signal propagation.

- Learn how to generate various types of waveforms used in wireless communication, such as OFDM and QPSK.
- Simulate different types of communication channels, including multipath and fading channels.

IMAGE PROCESSING WITH MATLAB:

Image processing with MATLAB involves the manipulation and analysis of digital images using MATLAB's powerful built-in functions and toolboxes. MATLAB provides a comprehensive environment for performing a wide range of image processing tasks, from basic operations like loading and displaying images to advanced techniques such as image enhancement, segmentation, feature extraction, and pattern recognition.

WHAT I LEARNT?

- Understanding how images are represented in MATLAB, including grayscale, RGB, and other color spaces.
- Applying techniques to improve image quality, such as contrast adjustment, histogram equalization, and filtering for noise reduction.
- Measuring properties of image regions, such as area, centroid, and perimeter, for analysis and object recognition.

SIGNAL PROCESSING ONRAMP:

Signal Processing Onramp is an interactive tutorial provided by MATLAB that serves as an introductory course to the fundamentals of signal processing. It's designed for beginners who want to learn about signal processing concepts and techniques using MATLAB. The Onramp starts with an overview of what signal processing is and its importance in various fields such as telecommunications, audio processing, and biomedical engineering. It covers fundamental concepts such as signals (continuous and discrete), systems, and basic operations like convolution and correlation.

WHAT I LEARNT ?

- Participants gain a strong foundational understanding of signal processing concepts and techniques, including time-domain and frequency-domain analysis, filtering, convolution, and spectral analysis.
- Implementing signal processing algorithms and techniques using MATLAB's tools and functions. They learn how to manipulate and analyze signals effectively, perform filtering operations, and conduct spectral analysis.

STATISTICAL ONRAMP:

The Statistics Onramp is an interactive learning module provided by MATLAB that serves as a beginner-level course covering the fundamentals of statistics using MATLAB's tools and functions. It's designed for individuals who want to learn about statistical concepts and their practical application in data analysis. The Onramp begins with an introduction to basic statistical concepts, such as descriptive statistics (mean, median, mode), variability (standard deviation, variance), and probability distributions.

WHAT I LEARNT ?

- Participants gain a strong foundational understanding of statistical concepts, including descriptive statistics, probability distributions, hypothesis testing, and regression analysis.
- Practical skills in using MATLAB for statistical analysis, learning how to perform various statistical tests, calculations, and visualizations efficiently.
- Interpreting data using statistical methods, enabling them to draw meaningful conclusions and make informed decisions based on data insights.

SOLVING NON-LINEAR EQUATIONS WITH MATLAB:

Solving nonlinear equations with MATLAB involves utilizing a variety of numerical methods and optimization algorithms to find solutions to equations that cannot be solved analytically. MATLAB provides a rich set of built-in functions and toolboxes specifically designed for this purpose, making it a powerful platform for tackling nonlinear equations encountered in various fields of science, engineering, and mathematics.

WHAT I LEARNT ?

- Participants become proficient in using a variety of numerical methods and algorithms for solving nonlinear equations, such as iterative methods, optimization techniques, and root-finding algorithms.
- Advanced MATLAB programming skills, learning how to implement and apply numerical methods to solve nonlinear equations efficiently.
- Participants acquire practical experience in solving a diverse range of nonlinear equation problems encountered in various fields, such as engineering, science, finance, and economics.

MACHINE LEARNING WITH MATLAB:

Machine learning with MATLAB offers a comprehensive platform for developing, implementing, and deploying machine learning models across a wide range of applications. MATLAB provides an extensive set of built-in functions, toolboxes, and resources specifically tailored for machine learning tasks, making it an ideal environment for both beginners and experienced practitioners in the field. MATLAB provides resources for newcomers to learn about machine learning concepts, including supervised learning, unsupervised learning, and reinforcement learning. Beginners can grasp fundamental concepts such as classification, regression, clustering, and dimensionality reduction through interactive tutorials, examples, and documentation.

WHAT I LEARNT ?

- Help us to Gain proficiency in utilizing MATLAB, a versatile computational tool, to develop, train, and deploy machine learning models for various realworld applications.
- With hands-on experience in data preprocessing, feature selection, model evaluation, and algorithm implementation, participants are equipped to tackle complex problems and make informed decisions in data-driven environments.
- Furthermore, acquiring the ability to interpret and communicate the results of machine learning models effectively, empowering them to contribute meaningfully to projects and initiatives across diverse industries.

DEEP LEARNING WITH MATLAB:

Deep learning with MATLAB provides a powerful and comprehensive environment for developing, implementing, and deploying deep neural network models for a wide range of applications. MATLAB offers an extensive set of built-in functions, toolboxes, and resources specifically tailored for deep learning tasks, making it an ideal platform for both beginners and experienced practitioners in the field. MATLAB offers resources for newcomers to learn about deep learning concepts, including neural networks, convolutional neural networks (CNNs), recurrent neural networks (RNNs), generative adversarial networks (GANs), and deep reinforcement learning. Beginners can grasp fundamental concepts such as network architectures, training algorithms, and optimization techniques through interactive tutorials, examples, and documentation.

WHAT I LEARNT ?

- By harnessing deep learning algorithms within MATLAB's framework, researchers and practitioners have achieved remarkable outcomes. One notable area of impact is in image recognition and classification, where convolutional neural network (CNNs) have demonstrated unprecedented accuracy in identifying objects within complex visual scenes
- Deep learning with MATLAB has revolutionized medical image analysis, facilitating the detection of anomalies in MRI scans, X-rays, and histopathology slides. Researchers can leverage MATLAB's deep learning tools to create customized

architectures tailored to specific medical imaging tasks, ultimately enhancing diagnostic accuracy and patient care.

COMPUTER VISION ONRAMP:

The Computer Vision Onramp is an interactive tutorial provided by MATLAB, offering an entry-level course on the fundamental concepts and techniques of computer vision. Designed for beginners, this Onramp equips learners with the foundational knowledge needed to understand and apply computer vision algorithms using MATLAB's tools and functions. The Onramp begins with an overview of computer vision, explaining its significance, applications, and key concepts such as image representation, feature extraction, and object detection.

WHAT I LEARNT ?

- Upon completing the Computer Vision Onramp course, participants emerge with a robust understanding of the fundamental principles and techniques underlying computer vision.
- Armed with this knowledge, we gain the ability to process and analyze images effectively, extracting meaningful information and insights.
- To become proficient in employing various image processing techniques, feature extraction methods, and object detection algorithms to tackle real-world challenges.