

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

GOMATHI E (43739016)



**DEPARTMENT OF BIOINFORMATICS AND DATASCIENCE
SCHOOL OF BIO AND CHEMICAL ENGINEERING**

SATHYABAMA

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

**Accredited with Grade "A" by NAAC I 12B Status by UGC I
Approved by AICTE**

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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
GOMATHI E (43739016) 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_____

DECLARATION

I, **GOMATHI E** hereby declare that the project entitled “DYNAMIC MATHEMATICAL MODELLING IN BIOINFORMATICS UNLOCKING BIOLOGICAL COMPLEXITY” 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:

Gomathi E

PLACE: CHENNAI

SIGNATURE OF THE CANDIDATE

ACKNOWLEDGEMENT

I am pleased to acknowledge my sincere thanks to the **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.

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1. PROJECT

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 pulmonary fibrosis Geo2R is the source of the geo dataset (GSE 40839)
- After choosing the suitable parameters, the Geo dataset is retrieved.
- Genes that were upregulated genes were copied and paste into the cytoscape network.
- Built a biological network using a BioGrid in cytohubba to analyse the network and identify importance node based various topologies algorithm to determine the The top 10 gens
- Genes must be copied in cluego and contigue cluego parameter such as species ontology and statistical settings.
- Run cluego analysis to identify functional categories or pathways associated with the selected nodes.

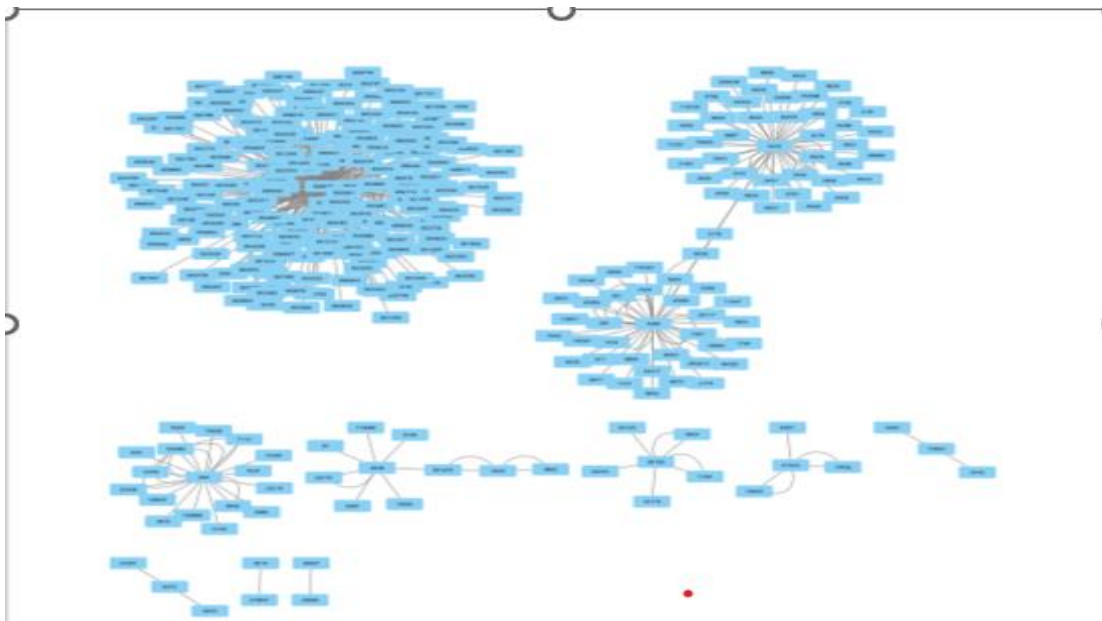


Fig:1 NETWORK OF A TOP 10 UPREGULATED GENES

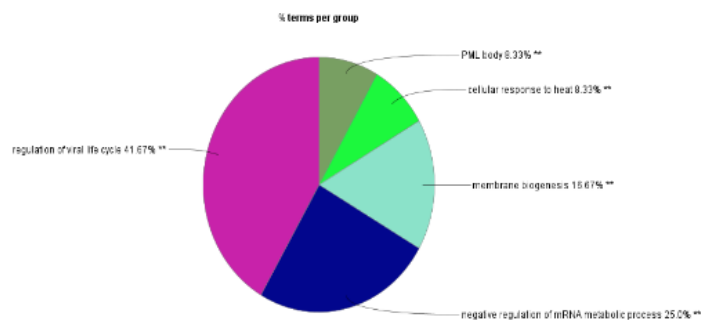


Fig:2 PIE CHART FOR THE TOP 10 GENES

Results for Analysis1									
Cluster #1 Cluster #1 Cluster #1									
ID	Term	Ontology Source	Term PValue	Term PValue Corrected w.t.	Group PValue	Group PValue Corrected w.t.	GO Levels	GO Groups	% Assoc.
GO:0000000	activation of innate immune response	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0, 0, 0, 0]	Group1	4.348
GO:0000001	PML body	GO_CellularComponent	0.000000	0.000000	0.000000	0.000000	[0, 0, 0, 0]	Group1	3.04
GO:0000002	response to interferon-alpha	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group2	15
GO:0000003	response to interferon-alpha	GO_MolecularFunction	0.000000	0.000000	0.000000	0.000000	[0]	Group3	3.009
GO:0000004	response to interferon-alpha	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0, 0, 0, 0]	Group4	6.007
GO:0000005	cellular response to interferon	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group5	3.070
GO:0000006	negative regulation of viral process	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0, 0, 0]	Group6	4.348
GO:0000007	response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group7	18.75
GO:0000008	response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group8	3.009
GO:0000009	regulation of viral genome replication	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0, 0, 0]	Group9	4.348
GO:0000010	response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group10	7.018
GO:0000011	negative regulation of viral genome replication	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0, 0, 0]	Group11	6.007
GO:0000012	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group12	4.274
GO:0000013	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group13	3.797
GO:0000014	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group14	8.971
GO:0000015	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group15	7.143
GO:0000016	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group16	9
GO:0000017	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group17	3.01
GO:0000018	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group18	3.448
GO:0000019	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group19	3.67
GO:0000020	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group20	7.692
GO:0000021	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group21	6.979
GO:0000022	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group22	10.714
GO:0000023	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group23	4.348
GO:0000024	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group24	8.991
GO:0000025	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group25	10.043
GO:0000026	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group26	19
GO:0000027	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group27	3.04
GO:0000028	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group28	3.191
GO:0000029	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group29	3.009
GO:0000030	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group30	3.009
GO:0000031	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group31	4.205
GO:0000032	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group32	10.028
GO:0000033	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group33	3.009
GO:0000034	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group34	4.390
GO:0000035	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group35	4.118
GO:0000036	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group36	6.714
GO:0000037	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group37	3.463
GO:0000038	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group38	7.692
GO:0000039	cellular response to viral	GO_BiologicalProcess	0.000000	0.000000	0.000000	0.000000	[0]	Group39	10.038

Fig:3 TABULAR REPRESENTATION OF FUCTIONAL ANALYSIS

INTERPRETATION:

GEO datasets GSE ID : GSE40839

GENE LIST : 1.CXC10

2.MX1

3.CXCL11

4.IFL127

5.OAS1

6.RSAD2

7.BST2

8.IFLT2

9.RTP4

10.IF1447

TERM	FUNCTIONS	ONTOLOGY SOURCE
Activation of innate immune system	Prevent infections and attack invading pathogens	Biological source
PML body	Involved in multiple genome maintenance pathway DNA repair	Cellular source
Response to interferon alpha	Response on IFN- α depend on dosage	Biological pathway
Ubiquitin like protein binding	Acts on binding site for protein that activate transcription	Molecular process
Defence response to virus	Acts on antigen specific and non-specific reaction in our body	Biological functions
Telomeric DNA binding	This binding protein generate T-loop protect chromosome	Molecular functions

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.

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 MX1 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 MX1 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

Survival :All

Restrict analysis based on cellular content :All

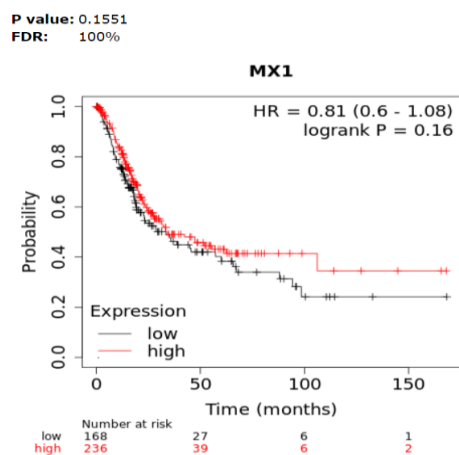


Fig 1- Bladder Carcinoma

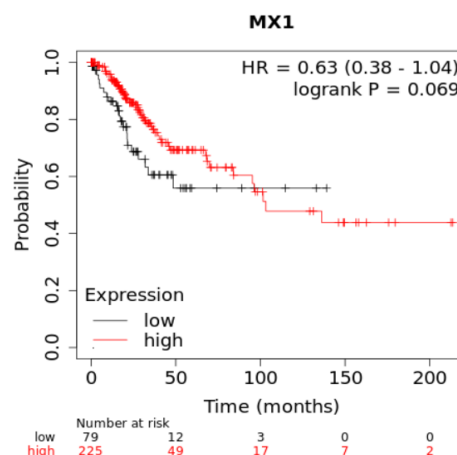


Fig 2 – Breast Cancer

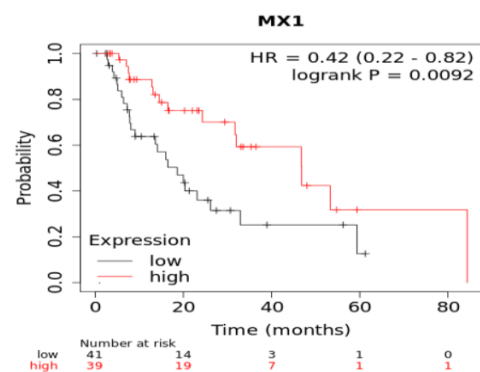


Fig 3 - Cervical Squamous Cell Carcinoma

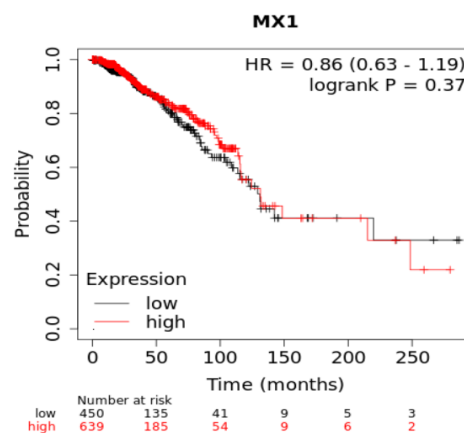


Fig 4 - Esophagal Squamous

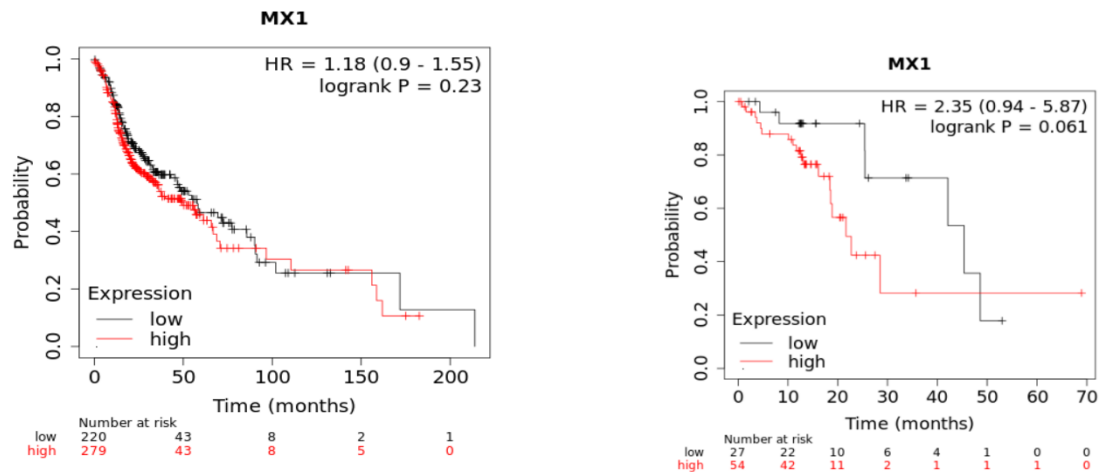


Fig -6 Ovarian Cancer

Fig 5 - Lung Squamous Cell Carcinoma

Interpretation

- KM-plot recognizes **proposed gene symbols MX1** (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: The HR of MX1 in bladder carcinoma is 0.81(0.6-1.08) 50% median survival between groups . it represent the ratio of probabilityfor low expression cohort (33.6)and high expression cohort(34.53)

BREAST CANCER: the HR of MX1 in breast cancer is 0.86(0.6-1.19) 50% median survival between groups . it represent the ratio of probability for low expression cohort (130) and high expression cohort(131)

CERVICAL SQUAMOUS CELL CARCINOMA: The HR of MX1 in bladder carcinoma is 0.42(0.22-0.82) 50% median survival between groups . it represent the ratio of probabilityfor low expression cohort (35)and high expression cohort(42)

ESOPHAGAL SQUAMOUS CELL: The HR of MXI in bladder carcinoma is 0.86(0.63-1.19) 50% median survival between groups . it represent the ratio of probabilityfor low expression cohort (41)and high expression cohort(83)

OVARIAN CANCER: The HR of MXI in bladder carcinoma is 2.35(0.94-5.87) 50% median survival between groups . it represent the ratio of probabilityfor low expression cohort (75)and high expression cohort(108)

LUNG SQUAMOUS CELL CARCINOMA: The HR of MXI in bladder carcinoma is 1.18(0.9-1.55) 50% median survival between groups . it represent the ratio of probabilityfor low expression cohort (21)and high expression cohort(33).

Biomarkers: identifying biological markers for disease Diagnosis and Therapeutic monitoring

INTRODUCTION : The Marker (a) systematically offers five types of therapeutic biomarker, which realized 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 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 rheumatoid arthritis data's were retrieved and literature survey was done

RESULTS:

Biomarker ID	Biomarker Name	Class	Gene Name	Biomarker Type	Representative Drug	Representative Disease
B81WTO	ATP-binding cassette ...	Protein	ABCC11; MR...	P S M R U	Methotrexate	Rheumatoid art..
B8R6QL	Calgranulin B	Protein	S100A9; CA...	P S M R U	Methotrexate	Rheumatoid art..
B5WFQ6	Glucose-6-phosphate ...	Protein	G6PD	P S M R U	Sulfasalazine	Rheumatoid art..
BBZR71	Nucleotide triphosphat...	Protein	NUDT15; MT...	P S M R U	Azathioprine	Rheumatoid art..
BM8H7C	Thiopurine S-methyltr...	Protein	TPMT	P S M R U	Azathioprine	Rheumatoid art..
BHX9K8	Tyrosine-protein kinas...	Protein	BTK; AGMX1...	P S M R U	CC-292	Rheumatoid art..
B2UE6G	Osteopontin	Protein	SPP1; BNSP...	P S M R U	Tocilizumab	Rheumatoid art..
BM7DL8	Interleukin 6	Protein	IL6; IFNB2	P S M R U	Tocilizumab	Rheumatoid art..
BPV52Q	Tumor necrosis factor	Protein	TNF; TNFA; ...	P S M R U	Infliximab	Rheumatoid art..
BR7FV5	Interleukin 6 receptor ...	Protein	IL6R	P S M R U	Tocilizumab	Rheumatoid art..
BF9W7U	Calprotectin	Protein	.	P S M R U	Adalimumab	Rheumatoid art..
BS0NV5	Interleukin 1 beta	Protein	IL1B; IL1F2	P S M R U	P2X7 antagonist	Rheumatoid art..

Fig 1: Biomarker table

INTERPRETATION:

Biomarker ID	Biomarker name	class	Gene name	Biomarker type	Representative drug	Representative disease
BM7DL8	Interleukin 6	protein	IL6,IFNB2	PSMR	tocilizumab	Rheumatoid arthiritis
BPV52Q	Tumor necrosis factor	protein	TNF ,TNFA	PSMR	infliximab	Rheumatoid arthritis

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 Dabrafenib targets screening and binding assessment.

Materials and Methods:

Swiss Target Prediction:

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

PDb: The Protein Databank (PDB) is a file format describing the 3D structure of molecules held in protein data bank. The PDB format accordingly provides for

description and annotations of protein and nucleic acid structures including atomic coordinates, 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.

Swiss Target Prediction: `Swiss target prediction is a online tool to predict the targets of bioactive small molecules in human and other vertebrates. This is useful to understand the molecular mechanism underlying a given phenotype or bioactivity.

Results:

name	-plp1	-plp2	jain	-pmf	dock_score
4DRJ					
44462760	62.67	59.99	-0.51	128.06	75.258
44462760	39.55	52.43	0.25	82.96	73.568
44462760	87.7	75.2	-1.17	82.03	72.217
44462760	57.92	59.25	-1.58	107.68	71.499
44462760	91.48	75.87	-0.56	135.42	71.427
44462760	67.43	61.93	-0.86	128.01	71.11
44462760	69.96	64.76	-0.27	120.87	71.08
44462760	75.08	66.94	-1.43	102.4	70.806
44462760	75.35	68.05	0.18	105.33	70.166
44462760	87.62	71.07	-0.46	138.75	70.035

Fig:1 TABLE OF MOLECULE

name	distance	category	types	from	to
A:LYS121:NZ - 44	2.55404	Hydrogen Bo	Conventional	A:LYS121:N	44462760:F4
A:ASP68:OD2 - 4	3.51419	Halogen	Halogen (Flu	A:ASP68:OD	44462760:F4
A:ASP68:OD2 - 4	4.87041	Electrostatic	Pi-Anion	A:ASP68:OD	44462760
44462760:S1 - A:	4.55795	Other	Pi-Sulfur	44462760:S1	
B:TYR2105 - 444	4.23944	Hydrophobic	Pi-Pi Stacke	B:TYR2105	44462760
44462760 - A:PHE	4.60818	Hydrophobic	Pi-Pi T-shape	44462760	A:PHE77
44462760 - A:LYS	4.92892	Hvdrophobic	Pi-Alkyl	44462760	A:LYS121

Fig:2 TABLE OF NON-BOND

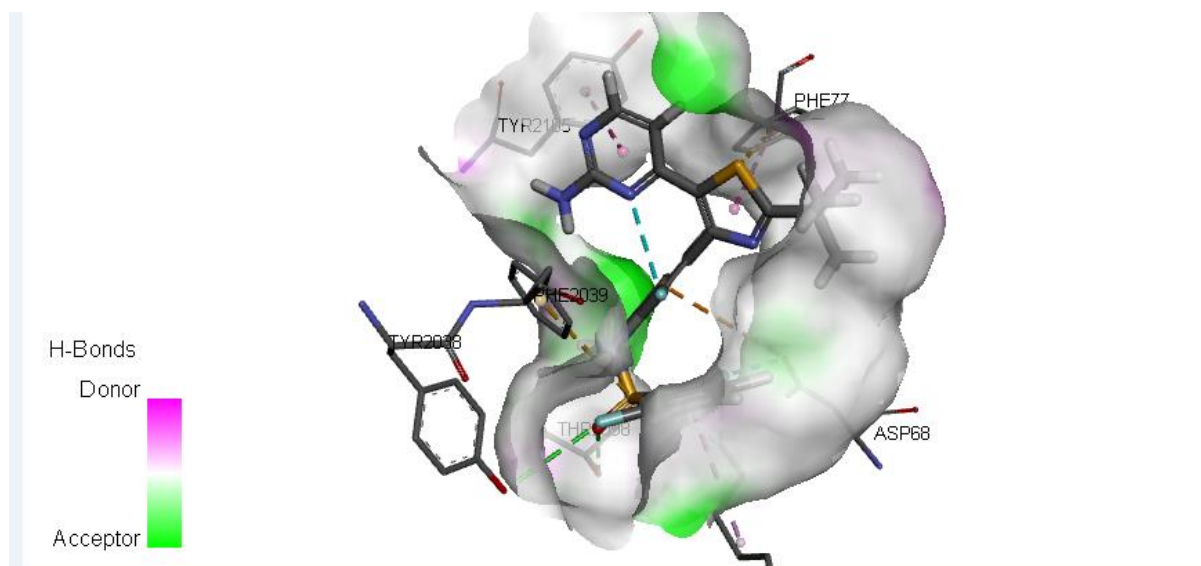


Fig:3 3D STRUCTURE OF 4DRJ

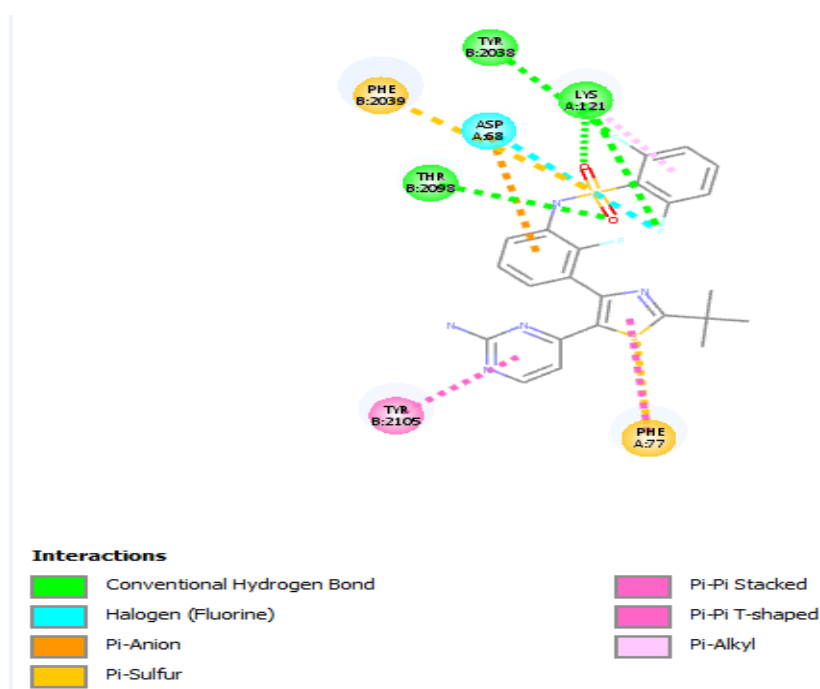


Fig:4 2D STRUCTURE OF 4DRJ

INTERPRETATION:

Dabrafenib is a medication used for the treatment of cancers such as melanoma. It belongs to a class of drugs called BRAF inhibitors. BRAF inhibitors target a specific mutation in the BRAF gene, which is common in certain types of cancer cells. This mutation causes the cells to grow and divide uncontrollably. The relationship between Dabrafenib and 4DRJ in drug discovery lies in understanding how Dabrafenib interacts

with its target protein. The 4DRJ structure in the PDB likely represents the protein target of Dabrafenib or a related protein. By studying the 3D structure of this protein, scientists can gain insights into how Dabrafenib binds to it and inhibits its function.

2. REVIEW ARTICLE

“DYNAMIC MATHEMATICAL MODELLING IN BIOINFORMATICS UNLOCKING BIOLOGICAL COMPLEXITY”

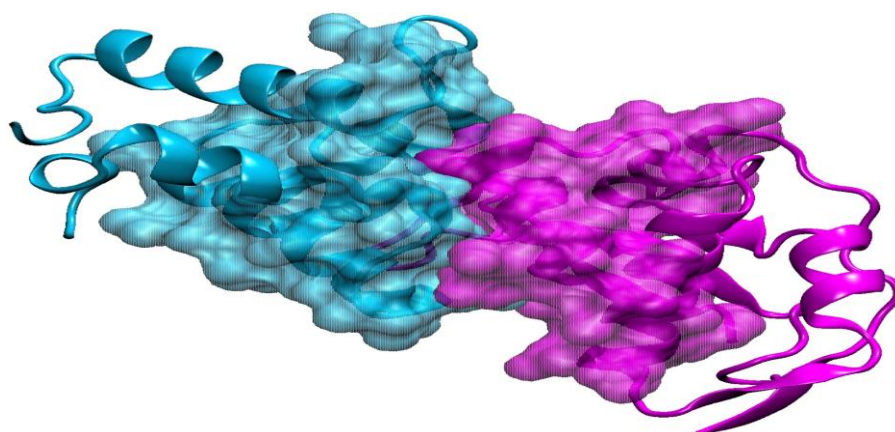
UNDERSTANDING GENE REGULATORY NETWORKS:

Understanding the complexities of gene regulation in organisms requires an understanding of gene regulatory networks, or GRNs. Essentially, GRNs regulate the precise temporal and spatial expression of genes, coordinating cellular functions essential for growth, homeostasis, and response to external stimuli. The transcriptional landscape of an organism is shaped by a complex web of interactions between genes, microRNAs (miRNAs), transcription factors (TFs), and other regulatory molecules that make up these networks. Gene expression patterns are stable and flexible due to the formation of robust regulatory circuits and integration of diverse signaling pathways made possible by the hierarchical structure of GRNs. TFs, proteins that bind to specific DNA sequences within gene promoters to activate or inhibit transcription, are essential for GRN dynamics. Using these methods, GRNs can be reconstructed and studied at different levels of complexity, from single gene regulatory interactions to genome. Broad networks that span multiple biological environments. GRNs are notable for their redundancy and modularity, as individual functional modules act semi-autonomously to control specific biological processes while maintaining resilience to genetic and environmental shocks. Computational biology techniques must be combined with genomic, transcriptomic, and proteomic data to understand the functional significance of GRNs in health and disease to understand the unfolding features and predict cellular responses. In addition, new developments in single-cell technologies provide previously unattainable precision to elucidate the variability and dynamics of GRNs across diverse cell populations, providing insights into disease development, cell fate decisions, and developmental pathways. Ultimately, a thorough understanding of GRN will have a significant impact on many different domains, including synthetic biology, personalized therapies, developmental biology, and regenerative medicine. This opens the door to the development of targeted interventions that modulate gene expression for therapeutic benefits.

PREDICTIVE MODELLING OF PROTEIN PROTEIN INTERACTION

At the intersection of systems biology, bioinformatics, and computational biology, there is a growing field called predictive modeling of protein-protein interactions (PPIs), which aims to understand the complex web of molecular interactions that underpin both disease mechanisms and cellular function. PPIs mediate signal transduction, protein complex formation, enzyme activity modulation, and gene expression regulation, and are essential for nearly every biological process. Accurately predicting and characterizing PPIs is essential to design targeted therapies, aid in drug discovery, and elucidate the molecular basis behind physiological and pathological processes. Predictive models of PPIs integrate disparate data sources and infer biologically meaningful interaction networks by using a wide range of computational approaches such as machine learning algorithms, structural bioinformatics, network analysis, and evolutionary conservation analysis. data, as well as high-throughput experimental datasets such as protein microarray experiments, co-immunoprecipitation coupled to mass spectrometry (co-IP/MS) and yeast two-hybrid assays. Machine learning techniques such as deep learning neural networks, random forests, and support vector machines (SVMs) are often used to train predictive models that can distinguish between interacting and non-interacting protein pairs. These techniques are used to extract patterns and features from large PPI datasets. By focusing on the most illuminating features associated with PPIs, feature selection and dimensionality reduction approaches are often used to reduce the impact of dimensionality and improve the predictive performance of models. Also, using molecular docking simulations and protein three-dimensional structures. Bioinformatics methods predict interaction interfaces and binding interactions between protein pairs, which facilitate the identification of potential drug targets and the development of small-molecule inhibitors. By integrating PPI data into detailed interaction networks using graph theory and network analysis tools, network-based approaches make it possible to identify critical hub proteins and densely coupled protein modules essential for both cellular function and disease pathways. In interacting protein pairs across species, evolutionary conservation analysis prioritizes conserved interactions that have biological value and sheds additional light on the functional implications of PPIs. Noise and biases inherent in high-throughput experimental data, the incompleteness of current interaction databases, and the dynamic nature of PPIs affected by cellular environment and environmental conditions are some of the challenges that persist in predictive modeling

of PPIs despite significant progress in this area. . Furthermore, to verify the physical association between protein partners in a cellular setting, interpretation of predicted interactions requires experimental validation using orthogonal assays such as co-immunoprecipitation, fluorescence resonance energy transfer (FRET), and protein complementation assays. Functional implications of protein interactions in biological systems and building robust PPI networks requires integration of multiple sources from computational predictions, experimental validations, and functional annotations. Going forward, developments in omics technologies such as spatial transcriptomics and single-cell proteomics have the potential to generate high-resolution maps of PPIs within specific cell types and tissue microenvironments, which will facilitate the identification and development of new targets for therapy. Patient-specific precision medicine strategies. In addition, the integration of multi-omics data and the application of interpretable machine learning methods improves the predictability and flexibility of PPI prediction models, accelerates our understanding of complex disease processes, and allows us to identify effective interventions to modify protein interaction networks.



SIMULATING CELLULAR SIGNALLING PATHWAYS

Understanding the complexities of biological systems requires a thorough understanding of complex endeavors such as modeling the cellular signaling cascade. Many functions required for cell survival, growth, proliferation, differentiation and response to external stimuli are coordinated via cellular signaling pathways. These pathways involve a sequence of molecular events set off by extracellular signals that are sensed by cell surface receptors and transmitted to the nucleus or other cellular compartments to elicit specific cellular responses. These signals can be hormones, growth factors, neurotransmitters or environmental cues. The complex web of

signaling molecules that regulate cellular behavior in both health and disease includes transcription factors, second messengers, kinases, phosphatases, and receptors. A powerful tool for discovering underlying mechanisms, predicting biological responses in a variety of conditions, and identifying potential treatments. Targets for intervention are computational simulations of these pathways. The integration of biochemical dynamics, biophysical interactions, and spatial organization is fundamental to the simulation of cellular signaling, as it allows us to capture the spatiotemporal dynamics of signaling events in the context of cells. Representing the chemical interactions and processes that take place within biological signaling networks is a fundamental component of modeling these pathways. These interactions include interactions between ligands and receptors, interactions between proteins, reactions between enzymes and substrates, and post-translational modifications including acetylation, phosphorylation, and ubiquitylation. The rates of these biological reactions are described by mathematical models, often formulated as systems of ordinary or partial differential equations. These models are based on mechanistic models derived from experimental data, principles of mass action kinetics, or enzyme kinetics. These models accurately reflect the dynamics of signaling pathway activation, diffusion, and attenuation, taking into account variables such as fractionation within the cell, protein abundances, diffusion velocity, and enzyme kinetic parameters. Cellular signaling dynamics are significantly shaped by spatial organization in addition to biochemical dynamics. Rather than being homogeneous molecular sacks, cells are complex structures with spatially ordered compartments such as nucleus, cytoplasm, plasma membrane, and organelles. The spatial confinement, membrane localization, and subcellular localization patterns displayed by signaling molecules influence their diffusion properties and interactions. Therefore, spatially detailed models that consider the geometry of cellular compartments, membrane-bound receptors, diffusion barriers, and molecular crowding effects are necessary to simulate biological signaling pathways. The simulation of spatially resolved signaling events and the investigation of how spatial structure affects signaling dynamics and cellular behavior are made possible by computational tools including spatial coherence simulations, reaction-diffusion models, and cellular automata. Furthermore, the inherent unpredictability and randomness in gene expression, cellular responses, and molecular interactions describe cellular signaling as inherently stochastic. Random fluctuations in signaling pathway activity are caused by variations in molecule concentrations, reaction rates,

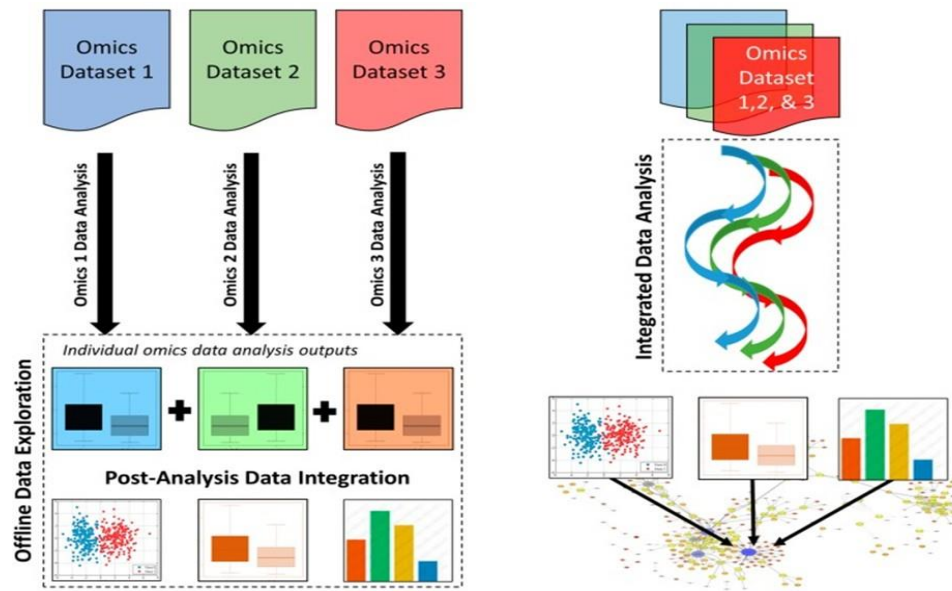
and environmental factors. These fluctuations cause noise in cellular responses and heterogeneity across cells. Modeling of stochasticity in signaling pathways is made possible by stochastic simulation techniques such as the Gillespie algorithm, stochastic differential equations, and Monte Carlo methods. These techniques shed light on the ways in which noise affects signal transduction, decision-making processes, and cellular fate determination.

INTEGRATION OF OMICS DATA FOR SYSTEMS BIOLOGY

By using multiple high-throughput molecular datasets, integration of omics data for systems biology is a multimodal strategy aimed at gaining a more complete understanding of complex biological systems. Omics technologies allow the systematic evaluation of various molecular components in a biological system, providing insights into their structure, function, and

connections. Examples of these technologies are transcriptomics, proteomics, metabolomics, and epigenomics. Integration of multiple omics datasets provides a comprehensive understanding of biological processes by revealing emergent properties undetectable from individual datasets. It also elucidates the interactions between various molecular states. Integration of various data types, each differing in its own data structure, measurement scale, and biological context, is a fundamental component of omics data integration. Essentials. These techniques are widespread and can be adapted to specific research topics and biological systems studied. Examples of these techniques include correlation analysis, co-expression networks, pathway enrichment analysis, machine learning algorithms, and systems biology modelling. In addition, the identification of biomarkers, disease symptoms, molecular pathways and therapeutic targets is possible through omics data integration, stimulating efforts in personalized medicine and translational research. Omics data integration is unraveling the mysteries of complex diseases, understanding mechanisms of therapeutic action and toxicity, and paving the way for personalized precision medicine approaches for individual patients by bridging the gap between genotype and phenotype. However, significant barriers to omics data integration efforts include issues with data heterogeneity, scalability, reproducibility, and interpretability. To address these issues, standardized protocols, robust analytical pipelines, and collaborative structures must be developed to facilitate data validation, sharing, and dissemination. However, the integration of omics data into systems biology promises to transform our understanding of biology, disease, and therapeutic

interventions, ushering in a new era of precision medicine and personalized healthcare, using omics technologies, computational tools, and interdisciplinary collaborations.



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3. MATLAB COURSES

BASIC COURSES

3.1. MATLAB ONRAMP

DESCRIPTION:

The MATLAB Onramp is an interactive introductory tutorial provided by MathWorks, offering users a hands-on learning experience to get started with MATLAB, a widely used programming language and environment for technical computing. Through a series of self-paced modules, users are guided step-by-step to learn MATLAB's syntax, fundamental operations, and essential programming constructs. The Onramp covers key topics such as variables, arrays, loops, conditional statements, and functions, providing a solid foundation in MATLAB programming. Additionally, users learn how to visualize data, import and export files, and perform basic statistical analysis using MATLAB's powerful tools and functions. MATLAB Onramp serves as an accessible entry point for individuals looking to acquire basic MATLAB skills for academic, research, or professional purposes.

WHAT WE LEARNT?

- Introduce users to the basic syntax, functions, and operations of MATLAB.
- Familiarize users with fundamental programming concepts such as variables, arrays, loops, and conditional statements.
- Enable users to create, edit, and run MATLAB code within a user-friendly online environment.
- Teach users how to visualize data, perform basic data analysis, and generate plots using MATLAB's plotting functions.

DURATION:

2 Hours

GRADE:

100%

3.2 SIMULINK ONRAMP

DESCRIPTION:

The Simulink Onramp is an interactive tutorial provided by MathWorks, tailored to introduce users to Simulink, a powerful graphical programming environment for modelling and simulating dynamic systems. Additionally, the Simulink Onramp covers advanced topics such as organizing models using subsystems and creating custom blocks to enhance model clarity and reusability. Ultimately, the Simulink Onramp provides users with the foundational knowledge and skills needed to start using Simulink effectively for a wide range of engineering and scientific applications, empowering them to accelerate their learning curve and apply Simulink to solve real-world problems.

WHAT I LEARNT?

- Understand the capabilities and applications of Simulink for modelling, simulating, and analysing dynamic systems in engineering and science fields.
- Gain proficiency in building and simulating models using Simulink, including connecting blocks, setting block parameters, and running simulations to analyse system behavior.
- Develop skills in organizing models using subsystems and creating custom blocks to encapsulate functionality and improve model clarity and reusability.
- Acquire problem-solving and critical thinking skills by completing hands-on exercises and practical examples that demonstrate the application of Simulink in real-scenarios.

DURATION:

2 Hours

GRADE:

100%

3.3 SIGNAL PROCESSING ONRAMP

DESCRIPTION:

The Signal Processing Onramp is an interactive tutorial provided by MathWorks, designed to introduce users to the fundamentals of signal processing using MATLAB and Signal Processing Toolbox. The Signal Processing Onramp also provides guidance on visualizing signals, interpreting spectral content, and applying signal processing techniques to real-world applications in areas such as audio processing, image processing, and biomedical signal analysis.

WHAT I LEARNT?

- Understand the basic concepts and principles of signal processing, including time-domain and frequency-domain representations of signals, sampling, filtering.
- Learn how to analyze and manipulate signals using MATLAB and Signal Processing Toolbox, including techniques for signal visualization, filtering, spectral analysis, and time-frequency analysis.
- Gain proficiency in using MATLAB and Signal Processing Toolbox functions and commands to perform common signal processing tasks, such as signal denoising, feature extraction, and system identification.
- Develop problem-solving skills and critical thinking by completing hands-on exercises and practical examples that demonstrate the application of signal processing techniques to real-world scenarios, such as image processing, and biomedical signal analysis.

DURATION:

1.5 Hours

GRADE:

100%

3.4 IMAGE PROCESSING ONRAMP

DESCRIPTION:

The Image Processing Onramp is an interactive learning resource provided by MathWorks, aimed at introducing users to the fundamentals of image processing using MATLAB and Image Processing Toolbox. Image Processing Onramp, users acquire the foundational knowledge and skills needed to start using MATLAB and Image Processing Toolbox effectively for image processing tasks, empowering them to tackle a wide range of image analysis challenges in various engineering and scientific domains. It aims to equip users with the skills needed to start using MATLAB and Image Processing Toolbox effectively for image processing.

WHAT I LEARNT?

- Understand the basic concepts and principles of digital image processing, including image representation, enhancement, segmentation, and analysis.
- Learn how to perform common image processing tasks using MATLAB, such as image filtering, edge detection, morphological operations, and feature extraction.
- Gain proficiency in using MATLAB functions and commands for image manipulation and analysis, including image visualization, processing, and measurement.
- Learn about advanced image processing techniques, such as image restoration, image compression, and image segmentation, and how these techniques are used in various applications, including medical imaging, surveillance, and autonomous driving.

DURATION:

2 Hours

GRADE:

100%

3.5 MACHINE LEARNING ONRAMP

DESCRIPTION:

The Machine Learning Onramp course is a comprehensive introductory program designed to familiarize participants with the fundamental concepts and techniques of machine learning. The course begins with an overview of what machine learning is, its applications, and its importance in various industries. An introduction to neural networks and deep learning is provided, covering topics such as feedforward neural networks, convolutional neural networks (CNNs), and recurrent neural networks (RNNs). Teaching techniques for data cleaning, preprocessing, and feature engineering to prepare data for machine learning models.

WHAT I LEARNT?

- Provide participants with a solid understanding of fundamental machine learning concepts, terminology, and methodologies.
- Introduce participants to various machine learning algorithms, including their strengths, weaknesses, and practical applications.
- Teach techniques for data preprocessing, cleaning, and feature engineering to prepare data for use in machine learning models.
- Offering hands-on experience through coding exercises or projects to apply machine learning concepts and algorithms to real-world problems using popular libraries like TensorFlow, Scikit-learn, or PyTorch. Discussing ethical implications, biases, and fairness concerns in machine learning applications.

DURATION:

2 Hours

GRADE:

100%

3.6 DEEP LEARNING ONRAMP

DESCRIPTION:

Deep learning models are based on neural network architectures. Inspired by the human brain, a neural network consists of interconnected nodes or neurons in a layered structure that relate the inputs to the desired outputs. The neurons between the input and output layers of a neural network are referred to as hidden layers. The term “deep” usually refers to the number of hidden layers in the neural network. Deep learning models can have hundreds or even thousands of hidden layers.

WHAT I LEARNT?

- Introduce participants to the core principles of deep learning, including neural network architecture, activation functions, loss functions, and optimization algorithms.
- Familiarize participants with various types of neural network architectures such as FNN, CNN, RNN, and GAN.
- Teach techniques for training deep learning models, including strategies for initializing model parameters, choosing appropriate loss functions, optimizing hyperparameters, and preventing overfitting.
- Provide opportunities for participants to gain practical experience by implementing deep learning models using popular deep learning frameworks such as TensorFlow or PyTorch. This may involve working on coding exercises, projects, or real-world datasets to apply deep learning concepts in practice.

DURATION:

7 Hours

GRADE:

100%

3.7 COMPUTER VISION ONRAMP

DESCRIPTION:

The Computer Vision Onramp course is an introductory program designed to provide learners with a comprehensive understanding of computer vision concepts and techniques. The course usually starts with an overview of what computer vision is, its applications, and its significance in various fields such as healthcare, autonomous vehicles, robotics, etc. These concepts lay the groundwork for understanding more advanced topics. The course covers various image processing techniques like edge detection, image segmentation, and morphological operations. These techniques are essential for preprocessing images before applying more advanced computer vision algorithms.

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.
- Introduce participants to fundamental concepts in computer vision, including image representation, feature extraction, image classification, object detection, image segmentation, and image recognition.

DURATION:

2 Hours

GRADE:

100%

ADVANCE COURSES

3.8 MATLAB FUNDAMENTALS

DESCRIPTION:

"MATLAB fundamentals" refers to the foundational principles and concepts of MATLAB, a high-level programming language and interactive environment developed by MathWorks. These fundamentals encompass the essential knowledge required to understand and use MATLAB effectively for numerical computation, data analysis, visualization, and application development. Familiarize with MATLAB's built-in functions and libraries for numerical computation, linear algebra, and signal processing. Gain proficiency in data visualization techniques, including plotting data, customizing plots, and creating visualizations for analysis and presentation.

WHAT WE LEARNT?

- Learn the basic syntax and programming constructs of MATLAB, including variables, arrays, and control flow statements.
- Understand how to perform mathematical operations, manipulate data structures, and work with matrices and vectors.
- Develop problem-solving skills and computational thinking by solving practical exercises and real-world problems using MATLAB.
- Acquire the foundational knowledge needed to explore more advanced topics in MATLAB, such as image processing, machine learning, and simulation.

DURATION:

16.5 Hours

GRADE:

100%

3.9 MATLAB FOR DATA PROCESSING AND VISUALIZATION

DESCRIPTION:

The "MATLAB for Data Processing and Visualization" course is designed to provide participants with a comprehensive understanding of how to utilize MATLAB, a powerful programming language and computing environment, for handling, analysing, and visualizing data. The course begins with an overview of MATLAB's interface, basic syntax, and fundamental operations. The course covers a range of data analysis techniques available in MATLAB, including descriptive statistics, hypothesis testing, regression analysis, and clustering. Participants learn how to apply these techniques to extract meaningful insights from their data.

WHAT I LEARNT?

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

DURATION:

8 Hours

GRADE:

100%

3.10 MATLAB PROGRAMMING TECHNIQUES

DESCRIPTION:

The MATLAB Programming Techniques course is designed to provide participants with a comprehensive understanding of MATLAB programming concepts and techniques. Throughout the course, students will learn how to efficiently utilize MATLAB for various computational tasks, data analysis, and visualization. Matlab fundamental section covers fundamental concepts like basic MATLAB syntax. Using MATLAB's powerful plotting functions to create various types of plots including 2D and 3D plots, histograms, and scatter plots for data visualization. Techniques for integrating MATLAB with other programming languages (e.g., C/C++, Python) and tools for collaborative development.

WHAT I LEARNT?

- Gaining a solid understanding of the MATLAB programming language, its syntax, and its various features.
- This course helps 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.
- Learning techniques for optimizing MATLAB code to improve performance and efficiency, including vectorization, pre allocation, and parallel computing.

DURATION:

16 Hours

GRADE:

100%

3.11 SOLVING NON-LINEAR EQUATIONS

DESCRIPTION:

In MATLAB, solving nonlinear equations involves finding the values of unknown variables that satisfy a set of equations that cannot be expressed as simple linear relationships. First, you define the equations using symbolic variables or anonymous functions. Then, convert these equations into MATLAB functions. Next, provide an initial guess for the variables involved. MATLAB provides various built-in functions for solving nonlinear equations, such as `'fsolve'`, `'fminunc'`, and `'lsqnonlin'`. Once you have the solution, you can display it and visualize it if needed using MATLAB's plotting capabilities.

WHAT I LEARNT?

- Learn how to accurately formulate nonlinear equations from real-world problems and express them in a format suitable for MATLAB computations.
- Understand different methods available in MATLAB for solving nonlinear equations and learn to select the most appropriate method based on problem characteristics, such as equation complexity, dimensionality, and constraints.
- Learn techniques for verifying the correctness and accuracy of the obtained solutions, including solution visualization and comparison with numerical benchmarks.
- Understand how to integrate optimization techniques into the solution process for nonlinear equations when dealing with optimization problems.

DURATION

3 Hours

GRADE:

100%

3.12 SIGNAL PROCESSING WITH MATLAB

DESCRIPTION:

Signal processing with MATLAB involves the comprehensive analysis, manipulation, and interpretation of signals across various domains such as audio, image, and biomedical data. Users can generate or import signals, visualize them in different domains. MATLAB facilitates the design and implementation of digital filters, spectral analysis methods, and advanced signal processing algorithms. Additionally, it supports signal transformation between time and frequency domains, enabling users to perform Fourier analysis, wavelet transform, and other domain transformations. MATLAB's flexibility extends to signal simulation, modeling, and integration with other toolboxes for comprehensive solutions across domains like communications, image processing, and control systems.

WHAT I LEARNT?

- Acquire skills in visualizing signals using MATLAB's plotting functions, including time-domain waveforms, frequency-domain spectra, and spectrograms.
- Understand how to transform signals between different domains, such as time-domain to frequency-domain transformations using Fourier and wavelet transforms.
- Explore advanced signal processing techniques supported by MATLAB, including adaptive signal processing, time-frequency analysis, and blind source separation.
- Learn how to integrate signal processing with other domains such as communications, image processing, and biomedical engineering using MATLAB's integrated toolboxes.

DURATION:

7.5 Hours

GRADE:

100%

3.13 MACHINE LEARNING WITH MATLAB

DESCRIPTION:

Machine learning teaches computers to do what comes naturally to humans: learn from experience. Machine learning algorithms use computational methods to “learn” information directly from data without relying on a predetermined equation as a model. The algorithms adaptively improve their performance as the number of samples available for learning increases. Machine learning uses two types of techniques: supervised and unsupervised learning.

WHAT I LEARNT?

- Develop a solid understanding of fundamental machine learning concepts, including supervised and unsupervised learning, and reinforcement learning.
- Gain proficiency in using MATLAB's built-in machine learning functions, toolboxes, and libraries for model development, training, and evaluation.
- Learn how to implement and evaluate machine learning models using MATLAB, including techniques for data preprocessing, model selection, and performance evaluation.
- Acquire expertise in deep learning techniques, including convolutional neural networks (CNNs) and recurrent neural networks (RNNs), and learn how to build and train deep learning models using MATLAB.

DURATION:

12 hours

GRADE:

100%

3.14 IMAGE PROCESSING WITH MATLAB

DESCRIPTION:

Image processing with MATLAB involves utilizing MATLAB's comprehensive suite of functions and tools to analyze, manipulate, and enhance digital images. Users can perform tasks such as image acquisition, preprocessing, filtering, feature extraction, and analysis. MATLAB provides a wide range of algorithms and techniques for tasks like noise reduction, edge detection, object recognition, and image segmentation. Additionally, MATLAB offers powerful visualization capabilities for displaying processed images and results.

WHAT I LEARNT?

- Learn to acquire and preprocess images using MATLAB's functions and tools. This involves techniques such as image enhancement, noise reduction, and image registration to prepare images for further analysis.
- Understand and apply various image filtering and restoration techniques available in MATLAB, including spatial domain filters and frequency domain filters to enhance image quality and remove artifacts.
- Gain proficiency in techniques such as edge detection, texture analysis, object detection, and image segmentation to identify regions of interest within images.
- Learn how to visualize and present image processing results effectively using MATLAB's plotting and visualization functions.

DURATION:

11 Hours

GRADE:

100%

3.15 DEEP LEARNING WITH MATLAB

DESCRIPTION:

Deep learning models are based on neural network architectures. Inspired by the human brain, a neural network consists of interconnected nodes or neurons in a layered structure that relate the inputs to the desired outputs. The neurons between the input and output layers of a neural network are referred to as hidden layers. The term “deep” usually refers to the number of hidden layers in the neural network. Deep learning models can have hundreds or even thousands of hidden layers. With "Deep Learning with MATLAB," users can leverage a vast array of built-in algorithms and tools, including convolutional neural networks (CNNs), recurrent neural networks (RNNs), and generative adversarial networks (GANs).

WHAT I LEARNT?

- Gain a foundational understanding of deep learning concepts, including neural network architectures, activation functions, loss functions, and optimization algorithms.
- Develop proficiency in using MATLAB's deep learning functions, toolboxes, and libraries for building, training, and evaluating deep learning models.
- Learn how to implement and train deep learning models using MATLAB, including techniques for data preprocessing, model selection, and hyperparameter tuning.
- Apply deep learning techniques to solve real-world problems in various domains, such as image classification, object detection, natural language processing, and time series analysis.

DURATION:

8 Hours

GRADE:

100%

3.16 OBJECT-ORIENTED PROGRAMMING ONRAMP

DESCRIPTION:

The Object-Oriented Programming (OOP) Onramp is a structured learning program aimed at introducing participants to the principles and practices of object-oriented programming using a specific language or framework, such as Python, Java, or C++. They learn how to design and implement object-oriented solutions to real-world problems, gaining hands-on experience through coding exercises, projects, and interactive tutorials. The onramp emphasizes best practices in software design, including modularization, code reusability, and maintainability. By the end of the onramp, participants are equipped with the foundational knowledge and skills necessary to apply object-oriented programming principles effectively in their programming projects and to continue their learning journey in software development.

WHAT I LEARNT?

- Learn fundamental concepts of object-oriented programming, including classes, objects, inheritance, and polymorphism.
- Gain proficiency in designing and implementing object-oriented solutions to real-world problems.
- Understand best practices in software design, emphasizing modularity, reusability, and maintainability.
- Apply learned skills through coding exercises and projects to build a strong foundation in object-oriented programming.

DURATION:

2 Hours

GRADE:

100%

3.17 APP BUILDING ONRAMP

DESCRIPTION:

The App Building Onramp is a structured learning program designed to equip participants with the skills and knowledge needed to develop mobile or web applications. Throughout the onramp, participants learn key concepts and tools related to app development, such as programming languages (e.g., Java, Swift), development frameworks (e.g., Android Studio, Xcode), user interface design, and application deployment. They engage in hands-on activities, tutorials, and projects to apply their learning and build functional applications from scratch. The onramp covers various aspects of app development, including frontend and backend development, user experience (UX) design, data management, and application testing.

WHAT I LEARN?

- Learn fundamental concepts of app development, including programming languages, frameworks, and design principles.
- Gain hands-on experience in building mobile or web applications from scratch through guided projects.
- Understand the process of app deployment, including testing, debugging, and publishing to app stores or online platforms.
- Develop proficiency in frontend and backend development, user interface design, and application functionality to create functional and user-friendly apps.
-

DURATION:

1 Hour

GRADE:

100%

3.18 REINFORCEMENT LEARNING ONRAMP

DESCRIPTION:

The Reinforcement Learning Onramp is a structured learning program designed to introduce participants to the principles and techniques of reinforcement learning (RL). Throughout the onramp, participants delve into fundamental RL concepts such as Markov decision processes (MDPs), policy iteration, value iteration, and Q-learning. They gain practical experience through hands-on coding exercises, simulations, and projects using programming languages such as Python and frameworks like TensorFlow or PyTorch. The onramp covers a range of RL applications, including game playing, robotics, finance, and autonomous systems. By the end of the onramp, participants are equipped with the foundational knowledge and skills necessary to apply reinforcement learning algorithms effectively in various real-world scenarios.

WHAT I LEARNT?

- Understand fundamental concepts of reinforcement learning, such as Markov decision processes and value functions.
- Gain proficiency in implementing key reinforcement learning algorithms like Q-learning and deep Q-networks.
- Acquire hands-on experience through coding exercises to solve simulated and real-world problems.
- Explore the application of reinforcement learning techniques across various domains such as gaming, robotics, and finance.

DURATION:

2.5 Hours

GRADE:

100%

3.19 STATISTICS ONRAMP

DESCRIPTION:

The Statistics Onramp is a structured learning program designed to introduce participants to fundamental concepts and techniques in statistics. Throughout the onramp, participants engage in guided modules covering topics such as descriptive statistics, probability distributions, hypothesis testing, regression analysis, and data visualization. Hands-on exercises, interactive tutorials, and real-world case studies provide practical experience in applying statistical methods to analyze and interpret data. Participants also learn how to use statistical software such as R or Python with libraries like NumPy, SciPy, or pandas to perform statistical analysis efficiently.

WHAT I LEARNT?

- Develop a solid understanding of fundamental statistical concepts, including measures of central tendency, variability, probability, and hypothesis testing.
- Gain proficiency in applying statistical methods and techniques to analyze data, including descriptive statistics, inferential statistics, regression analysis, and hypothesis testing.
- Learn how to interpret statistical results and effectively communicate findings through data visualization techniques such as histograms, scatter plots, and box plots.
- Acquire hands-on experience through practical exercises and projects, enabling the application of statistical methods to real-world datasets and problems.

DURATION:

1.5 Hours

GRADE:

100%



Course Completion Certificate

Gomathi E

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

MATLAB Onramp

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

DIRECTOR, TRAINING SERVICES

13 November 2023



Course Completion Certificate

Gomathi.E

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

Simulink Onramp

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

DIRECTOR, TRAINING SERVICES

29 February 2024



Course Completion Certificate

Gomathi E

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

Signal Processing with MATLAB

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

DIRECTOR, TRAINING SERVICES

2 April 2024



Course Completion Certificate

Gomathi E

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

Image Processing Onramp

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

DIRECTOR, TRAINING SERVICES

29 March 2024



Course Completion Certificate

Gomathi E

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

Machine Learning Onramp

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

DIRECTOR, TRAINING SERVICES

1 March 2024



Course Completion Certificate

Gomathi E

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

Deep Learning Onramp

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

DIRECTOR, TRAINING SERVICES

10 March 2024



Course Completion Certificate

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Computer Vision Onramp


DIRECTOR, TRAINING SERVICES

4 March 2024



Course Completion Certificate

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MATLAB Fundamentals


DIRECTOR, TRAINING SERVICES

17 November 2023



Course Completion Certificate

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MATLAB for Data Processing and Visualization


DIRECTOR, TRAINING SERVICES

2 April 2024



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MATLAB Programming Techniques


DIRECTOR, TRAINING SERVICES

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Solving Nonlinear Equations with MATLAB


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4 March 2024



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Signal Processing with MATLAB


DIRECTOR, TRAINING SERVICES

2 April 2024



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Machine Learning with MATLAB


DIRECTOR, TRAINING SERVICES

2 April 2024



Course Completion Certificate

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Image Processing with MATLAB


DIRECTOR, TRAINING SERVICES

2 April 2024



Course Completion Certificate

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Deep Learning with MATLAB


DIRECTOR, TRAINING SERVICES

10 March 2024



Course Completion Certificate

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Object-Oriented Programming Onramp


DIRECTOR, TRAINING SERVICES

1 March 2024



Course Completion Certificate

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App Building Onramp


DIRECTOR, TRAINING SERVICES

27 March 2024



Course Completion Certificate

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Reinforcement Learning Onramp


DIRECTOR, TRAINING SERVICES

21 March 2024



Course Completion Certificate

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Statistics Onramp


DIRECTOR, TRAINING SERVICES

1 March 2024

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