

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

RAKSHANA R (43739008)



**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 | 12B Status by UGC | 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 **RAKSHANA R (43739008)** who carried out the project entitled “Integrated Analysis: Gene Expression, Survival, Biomarkers, and Drug Targets” under my / our supervision from January 2024 to April 2024.

Internal Guide

External Guide (if Applicable)

Head of the Department

Submitted for Viva voce Examination held on _____

Internal Examiner

External Examiner

DECLARATION

I, **RAKSHANA R** hereby declare that the project entitled “Integrated Analysis: Gene Expression, Survival, Biomarkers, and Drug Targets” done by me under the guidance of **DR. Jemmy Christy** is submitted in partial fulfilment of the requirements for the award of a Master of Science degree in Bioinformatics and Data Science.

DATE:

RAKSHANA R

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.

I would like to express my sincere and deep sense of gratitude to my project guide

DR. SWETHA SUNKAR Department of Bioinformatics and Data Science for his valuable guidance, suggestions, and constant encouragement that paved the 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.

(RAKSHANA R)

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1. PROJECT

1.1 GENE EXPRESSION ANALYSIS

Introduction: A Biological network represents systems as complex sets of binary interactions or relations between various biological systems and can reveal informative patterns within the systems. Cytoscape is an open-source software platform for visualizing molecule interaction networks and biological pathways and integrating the network with annotations, and gene expression profiles. Cytohubba predicts and explores the important nodes and edges in a given network by several topological algorithms such as degree, bottleneck, MCC, DMNC, MNC, EPC, Eccentricity, Closeness, Stress, Clustering co-efficient and betweenness.

Aim: Build a Network to understand gene interrelationships and regulatory mechanisms.

Materials and Methods:

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

Cytoscape: Cytoscape is an open-source software platform for visualizing molecule interactions network and biological pathways and integrating the network with annotations, and gene expression profiles.

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 visualizing them into functionally organized networks.

Procedure:

- For the database and disease Lung Cancer Geo2R is the source of the geo dataset (GSE19804)
- After choosing the suitable parameters, the Geo dataset is retrieved.
- Genes that were upregulated genes were copied and pasted into the cystoscape network.
- Built a biological network using a BioGrid in cytohubba to analyze the network and identify importance node-based various topologies algorithms to determine the top 10 genes
- Genes must be copied in cluego and continue cluego parameters such as species ontology and statistical settings.
- Run cluego analysis to identify functional categories or pathways associated with the selected nodes.

Results:

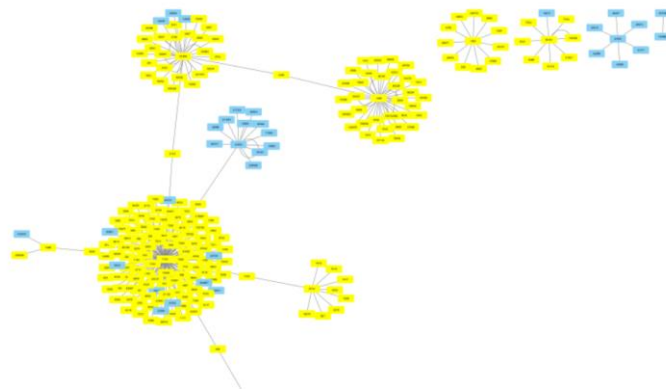


Fig 1- Network Pathway of Top-Upregulated Genes

Results for Analysis0			
ClueGO Results (Cluster #1) Cluster #1 ClueGO Log			
ID	Term	Ontology Source	Term PValue
☒ GO:000...	inner cell mass cell proliferation	GO_BiologicalProcess-EBI-U...	1.9 E-5
☒ GO:001...	peptidyl-threonine phosphorylation	GO_BiologicalProcess-EBI-U...	9.9 E-6
☒ GO:004...	mitotic G2/M transition checkpoint	GO_BiologicalProcess-EBI-U...	1.2 E-3
☒ GO:000...	endoderm development	GO_BiologicalProcess-EBI-U...	4.5 E-4
☐ GO:003...	endodermal cell differentiation	GO_BiologicalProcess-EBI-U...	1.1 E-3
☒ GO:004...	regulation of fibroblast proliferation	GO_BiologicalProcess-EBI-U...	1.9 E-6
☐ GO:004...	positive regulation of fibroblast proliferation	GO_BiologicalProcess-EBI-U...	8.1 E-5
☐ GO:190...	positive regulation of neuron death	GO_BiologicalProcess-EBI-U...	4.9 E-4
☐ GO:190...	regulation of oxidative stress-induced cell death	GO_BiologicalProcess-EBI-U...	2.9 E-4
☐ GO:004...	regulation of neurotransmitter secretion	GO_BiologicalProcess-EBI-U...	5.9 E-4
☒ GO:190...	cellular response to amyloid-beta	GO_BiologicalProcess-EBI-U...	2.5 E-5

Fig 2- Tabular Representation of Functional Analysis

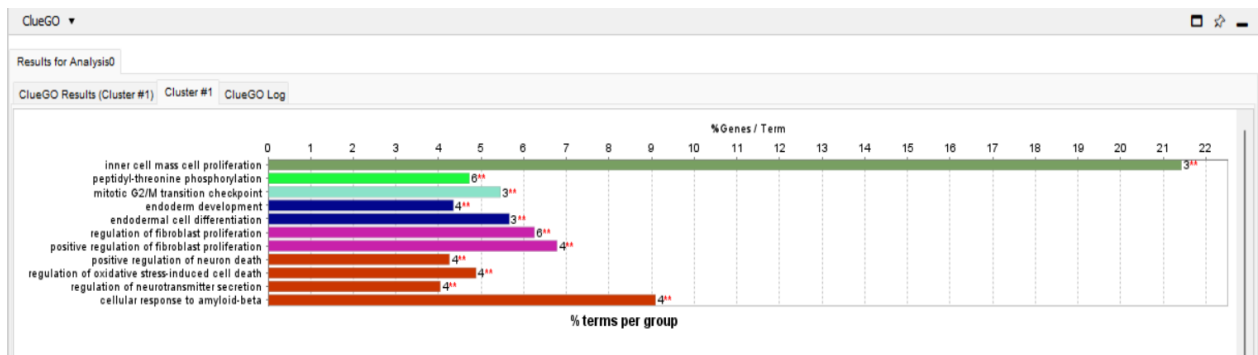


Fig 3- Graph For the Functional Analysis

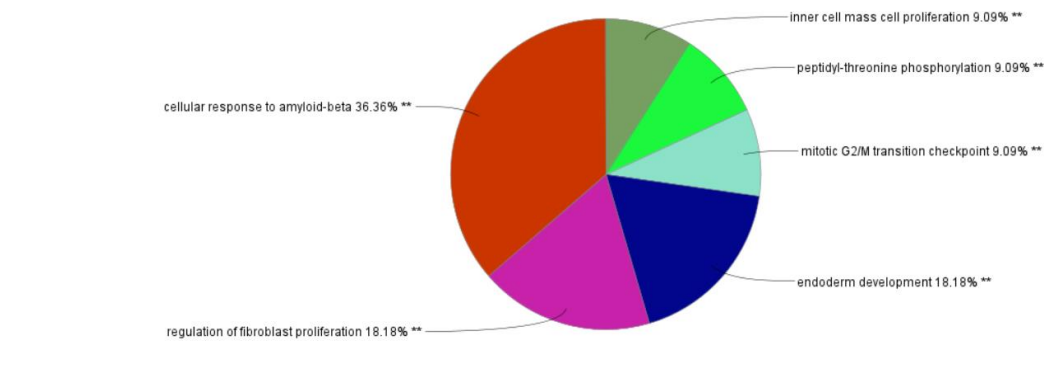


Fig 4- Functional Analysis Pie Chart

Interpretation:

Geo Dataset GSE Id: Gse19804

Upregulated Genes:

- COL10A1
- HS6ST2

- CTHRC1
- CST1
- TOP2A
- PROM2
- GCNT3
- XDH
- COL11A1
- ABCC3

Filter Node: ID [9606]

CLUEGO:

TERM	FUNCTION	ONTOLOGY
Inner mass cell proliferation	The inner cell mass or embryoblast early development of an embryo	Biological
Peptidine threonine phosphorylation	It plays a major role in cellular signalling pathways in the regulatory process	Biological
Mitotic G2/in transition checkpoint regulation of fibroblast proliferation	It is a critical regulatory mechanism in the cell cycle's proper progression from G2 phase to mitosis	Biological
Endoderm Development	It is a crucial process during embryogenesis in animals including humans.	Biological
Cellular Response to amyloid-beta	It serves the function of protecting the brain from its toxic effects	Biological

1.2 Cumulative survival probability calculation using KM Plotter

Introduction: KM-plotter is the most sophisticated online survival analysis tool, performing all calculations in real time. The background database is manually curated. Gene expression data, 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 the 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 CST1 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>.
- Top listed mRNA/protein biomarkers relevant to the data were retrieved & literature survey was done.

Results:

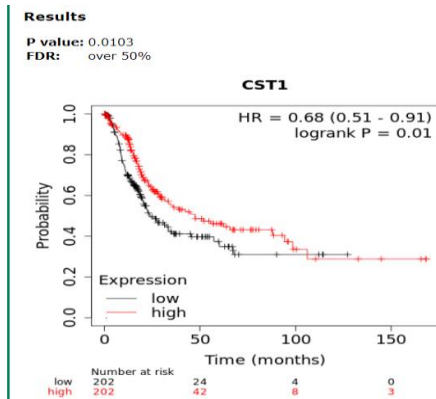


Fig 1- Breast Cancer

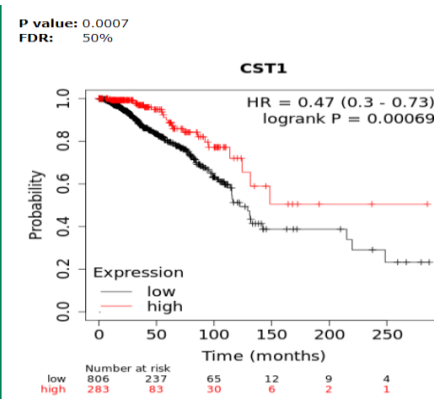


Fig 2- Esophageal Adenocarcinoma

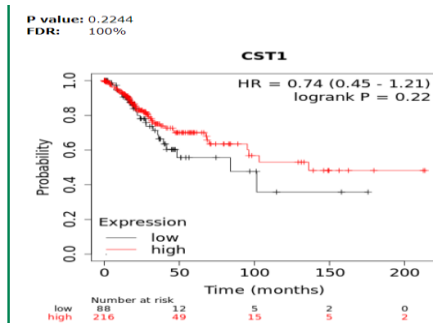


Fig 3- Esophageal squamous cell
Carcinoma

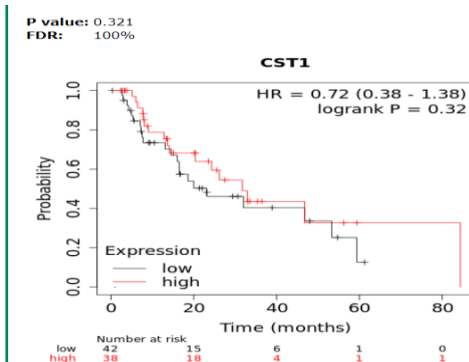


Fig 4- Head neck squamous cell
carcinoma

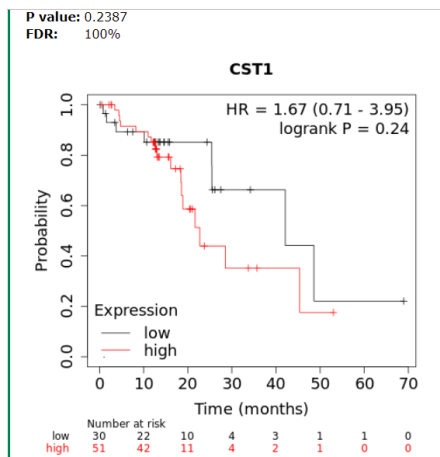


Fig 4- Kidney renal clear cell
carcinoma

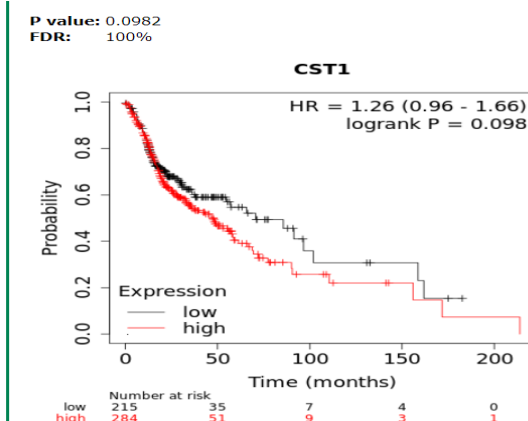


Fig 5- Liver hepatocellular Carcinoma

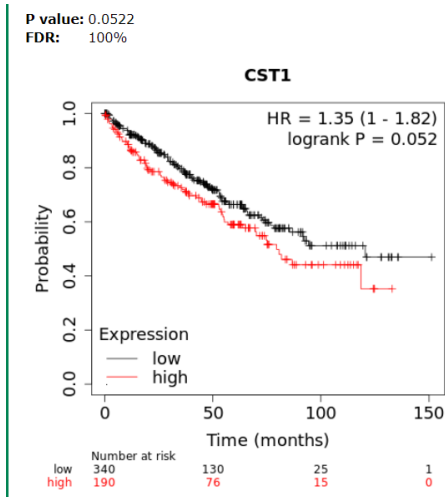


Fig 6- Lung Adenocarcinoma

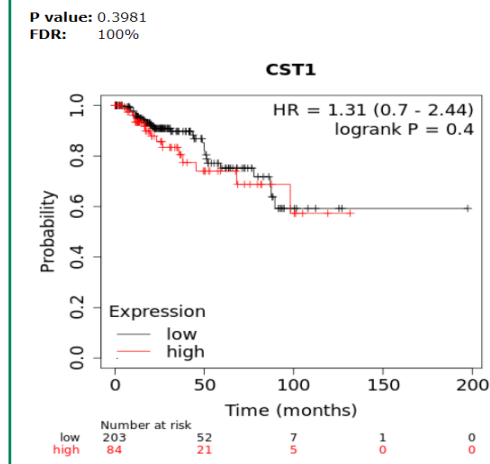


Fig 7- Lung Squamous Cell
Carcinoma

Interpretation

- Km plot recognize proposed gene symbols CST1(including Gene nomenclature communities Approved)
- Sources for the database include GEO, ECGA, TCGA, metabolomic Impact, and PubMed representation.
- Hazard ratio: The HR is a commonly used measure to quantify the difference in survival between groups.
- Breast Cancer:
 - HR Rate: 0.68(0.51-0.91)
 - 50% of median survival of probability.
 - Low Expression cohort: 23
 - High Expression cohort:43
- Esophageal Adenocarcinoma
 - HR Rate: 0.47(0.3-0.73)
 - 50% of median survival probability
 - Low Expression cohort: 23
 - High Expression cohort:31
- Esophageal squamous cell carcinoma
 - HR Rate: 0.74(0.45-1.21)
 - 50% of median survival probability
 - Low Expression cohort: 42

High Expression cohort:22

- Head Neck squamous cell carcinoma
HR Rate: 0.72(0.38-1.38)
50% of median survival probability
Low Expression cohort: 120
High Expression cohort:79
- Kidney renal Clear cell carcinoma
HR Rate: 1.67 (0.71-3.95)
50% of the median survival probability
Low Expression cohort: 120
High Expression cohort:70
- Liver hepatocellular Carcinoma
HR Rate: 1.26(0.96-1.66)
50% of median survival probability
Low Expression cohort: 54
High Expression cohort:70
- Lung Adeno carcinoma:
HR Rate: 1.35(1-1.82)
50% of median survival probability
Low Expression cohort: 35
High Expression cohort:61
- Lung Squamous cell Carcinoma
HR Rate: 1.31(0.7-2.44)
50% of the median survival probability
Low Expression cohort: 45
High Expression cohort:44

1.3 Biomarkers: identifying biological markers for disease

Diagnosis and therapeutic monitoring

Introduction: TheMarker systematically offers five types of therapeutic biomarkers, which realize the collective consideration among different drug discovery stages, comprehensively describe the therapeutic biomarker for the largest number of drugs among existing knowledge bases, and extensively cover 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 Lung Cancer and categorize them into pharmacodynamic Biomarker, Monitoring biomarkers, safety biomarkers

Procedure:

- The marker database was retrieved using the following link <http://themarker.idrblab.cn/about>
- Top listed mRNA/protein Biomarker relevant to the Lung Cancer data were retrieved and a literature survey was done

Results:

Biomarker ID	Biomarker Name	Class	Gene Name	Biomarker Type	Representative Drug	Representative Disease
B6XD8U	Inhibin beta B chain	Protein	INHBB	P S M R U	Chemotherapy	Hodgkin lymph...
B4WF3E	DNA topoisomerase I	Protein	TOP1	P S M R U	LMP400	Lymphoma
BHFV45	Gamma-Histone H2AX	Protein	H2AX; H2AFX	P S M R U	LMP400	Lymphoma
B6V0WU	Lymphocyte activation...	Protein	TNFRSF8; C...	P S M R U	Brentuximab v...	Mature T-cell ly..
BAJ5T6	ALK tyrosine kinase r...	Protein	ALK	P S M R U	Lorlatinib	Lung cancer
BUMT52	Interleukin 2 receptor ...	Protein	IL2RA	P S M R U	Ipilimumab	Melanoma
B6CUE3	Interleukin 10	Protein	IL10	P S M R U	Compound 3	B cell lymphoma
BT9QP3	UGT1A1	Gene	UGT1A	P S M R U	Belinostat	Mature T-cell ly..
B8XA7P	EZH2	Gene	EZH1; ENX-...	P S M R U	Tazemetostat	Follicular lymph..
B6JV2A	Serine	Compound	.	P S M R U	SHIN2	Mature T-cell ly..

Fig 1 – Biomarker Table

Interpretation:

Biomarker ID	Biomarker name	Class	Gene Name	Biomarker Type	Representative	
					Drug	Disease
B6CUE3	Interleukin 10	Protein	IL10	PSM	Anti-PD/PD L1 therapy	Lung cancer

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

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

Swiss Target Prediction: Swiss Target Prediction is an online tool to predict the macromolecular targets (proteins from humans, mice, and rats) 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 quantified that two similar bioactive molecules are likely to share their protein targets. Therefore, for a query molecule, we identify the most similar molecules among a set of about 370'000 actives on known targets. The predicted targets are those having the actives displaying the highest similarity with the query molecule.

Aim:

Drug Ceritinib targets screening and binding assessment.

Materials and Methods:

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

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

PDB: The Protein Databank (PDB) is a file format describing the 3D structure of molecules held in the 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: A drug bank database is a comprehensive, freely accessible online database containing information on drugs and drug targets. This database is a unique bioinformatics and chemo-informatics resource that combines detailed drugs.

Results:

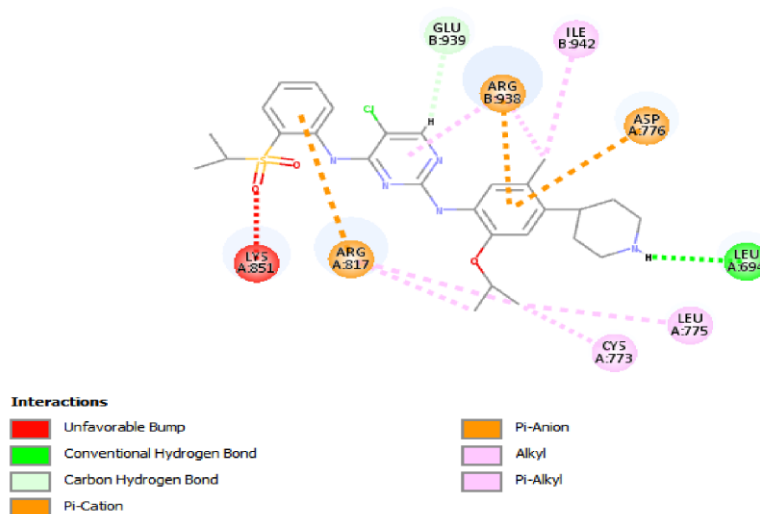


Fig 1 – 2D structure of 5CNN Protein

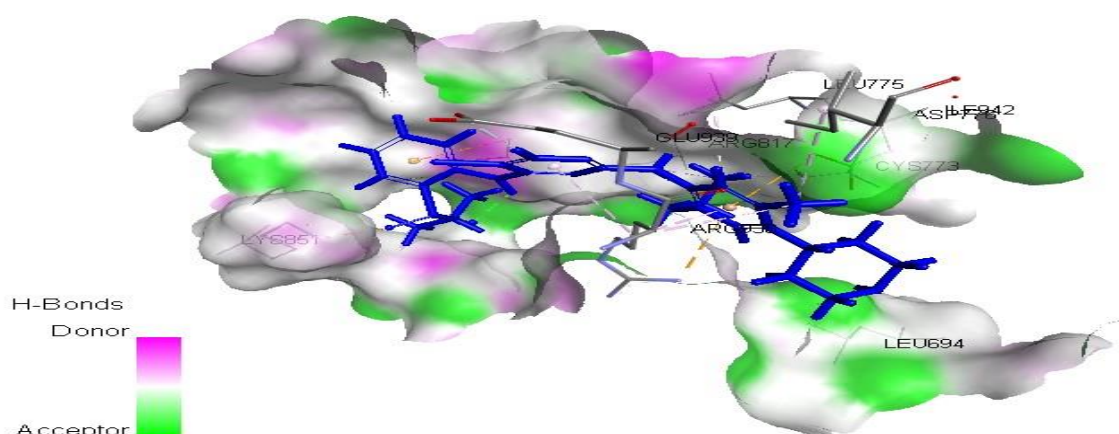


Fig 2 – 3D structure of 5CNN Protein

Interpretation:

NAME	-PLP1	-PLP2	JAIN	-PMF	DOCK_SCORE
5CNN					
57379345	69.01	63.22	-1.01	79.23	79.933
57379345	62.78	67.13	-0.81	41.03	73.834
57379345	74.07	70.32	-0.37	69.12	72.013
57379345	74.28	67.16	-1.17	67.29	71.364
57379345	83.82	70.22	-2.01	78.87	70.941
57379345	64.79	58.42	-2.36	74.72	69.463
57379345	14.35	23.82	-2.07	63.18	68.434
57379345	66.88	61.45	-2.31	79.65	68.336
57379345	76.94	69.87	-2.1	103.16	67.765
57379345	76.85	68.49	-1.55	71.22	67.66

Fig 3 – Table of Molecules

NAME	DISTANCE	CATEGORY	TYPES	FROM	TO
A:ARG681:NH2	2.53008	Hydrogen Bond;	Salt Bridge	A:ARG681:NH2	A:GLU687:OE1
A:ARG681:NH1	4.90498	Electrostatic	Attractive Charg	A:ARG681:NH1	A:GLU687:OE2
A:ALA678:N - A:	3.03083	Hydrogen Bond	Conventional Hy	A:ALA678:N	A:ASN676:OD1
A:GLY695:CA - I	3.59984	Hydrogen Bond	Carbon Hydroge	A:GLY695:CA	B:ASP806:OD2
A:ARG817:NH1	3.94849	Electrostatic	Pi-Cation	A:ARG817:NH1	A:TRP856
A:ARG817:NH1	3.19826	Hydrogen Bond;	Pi-Cation;Pi-Dor	A:ARG817:NH1	A:TRP856
A:GLU805:OE2	4.90704	Electrostatic	Pi-Anion	A:GLU805:OE2	A:HIS869
A:TYR777:OH -	4.03422	Hydrogen Bond	Pi-Donor Hydrog	A:TYR777:OH	A:HIS781
A:LYS690:CD - A	3.62988	Hydrophobic	Pi-Sigma	A:LYS690:CD	A:TYR703
A:CYS757:SG -	4.82651	Other	Pi-Sulfur	A:CYS757:SG	A:PHE688
A:HIS781 - A:TY	4.17918	Hydrophobic	Pi-Pi Stacked	A:HIS781	A:TYR777
A:ASP831:C,O;F	4.00424	Hydrophobic	Amide-Pi Stacked	A:ASP831:C,O;F	A:HIS811
A:LEU680 - A:LE	5.43054	Hydrophobic	Alkyl	A:LEU680	A:LEU753
A:PHE688 - A:IL	5.26656	Hydrophobic	Pi-Alkyl	A:PHE688	A:ILE720

Fig 4 – Table of non-Bond

Protein and Drug relationship

Ceritinib is a medication used in the treatment of certain types of cancer, particularly non-small cell lung cancer (NSCLC). It works by inhibiting a protein called anaplastic lymphoma kinase (ALK), which is often abnormal in NSCLC. This abnormality can lead to uncontrolled growth of cancer cells. regarding 5CNN, it appears to be a gene identifier or code, possibly related to cancer research. ceritinib is known to target ALK-positive NSCLC, so if there's a genetic mutation associated with NSCLC that corresponds to the 5CNN code.

Protein Significance

EGFR, or Epidermal Growth Factor Receptor, is a protein found on the surface of cells. It's involved in signalling pathways that regulate cell growth, proliferation, and survival. In cancer, particularly non-small cell lung cancer (NSCLC), mutations or overexpression of the EGFR gene can lead to uncontrolled cell growth and the development of tumors. EGFR inhibitors are a class of drugs used in cancer treatment that target the EGFR protein. They work by blocking the activity of EGFR, thereby inhibiting the growth and spread of cancer cells.

2. REVIEW ARTICLE

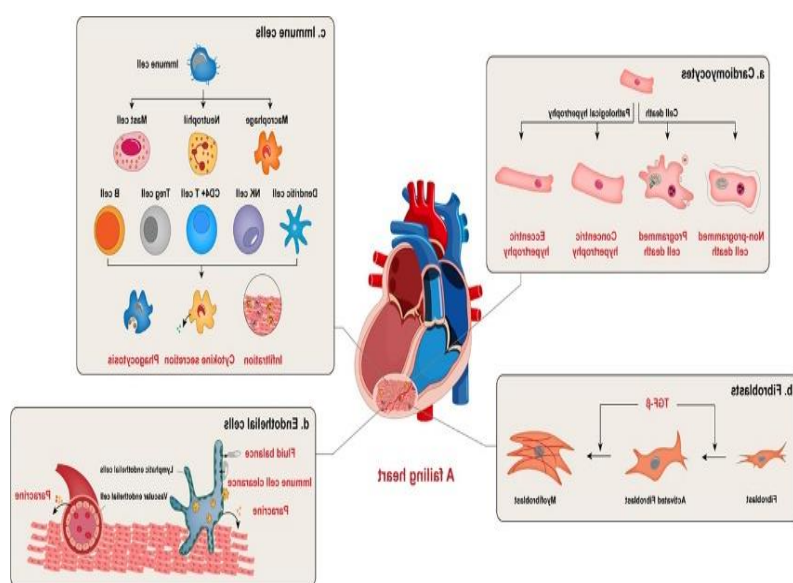
2.1 "From Bench to Bedside: Translating Cellular Signalling Discoveries into Therapeutic Strategies in Cardiovascular Disease"

Translating Cellular Signalling Discoveries into Therapeutic Strategies

The process of translating discoveries about cellular signalling into therapeutic approaches is complex and combines basic science with clinical systems to develop new solutions for various diseases. Key physiological processes are governed by cellular signalling pathways that are commonly dysregulated in various disease states such as cancer, cardiovascular disease, neurodegenerative diseases, and autoimmune diseases. Therefore, an important first step toward therapeutic intervention is to identify the molecular mechanisms that generate differential signalling and identify drug targets within these pathways. This process often begins with basic research projects that use a combination of systems biology, genetics, and biochemical techniques to try to understand the structure, function, and regulation of downstream effectors, receptors, and signalling molecules. The discovery of novel signalling components and their discovery is accelerated by high-throughput screening assays, omics technologies, and computational modeling. This leads to important insights into disease mechanisms and potential therapeutic targets. After candidate targets are identified, the process moves to drug discovery and development. Medicinal chemistry, thoughtful drug design, and preclinical testing are used to increase the safety, efficacy, and selectivity of medical agents. At this stage, novel small molecule inhibitors, monoclonal antibodies, gene therapies, and other approaches that alter the activity of specific signalling proteins or pathways linked to the cause of the disease are often designed and synthesized. At the same time, biomarkers and diagnostic assays can be developed to classify patients according to their molecular profiles. This will allow for more individualized treatment plans and facilitate patient selection and clinical trial design. To improve therapeutic outcomes and reduce side effects, translational research efforts are focused on identifying prognostic biomarkers, and improving therapeutic regimens, and countermeasures. Ultimately, the successful translation of discoveries about cellular signalling into clinical practice requires interdisciplinary collaboration between basic scientists, clinicians, pharmacologists,

regulatory bodies, and industry partners. Strong infrastructure and financial support are essential to enable knowledge sharing, technology transfer, and commercialization of novel therapies. In general, the process of translating discoveries about cellular signalling into effective therapeutic approaches is dynamic and repeatable, spanning from bench to bedside, with the ultimate goal of improving human health and patient outcomes.

Targeting Signalling Pathways: Strategies for Drug Development



A cornerstone of contemporary pharmacology is targeting signalling pathways for drug discovery, presenting a potential strategy for treating various disorders by altering important biological functions. Important cellular processes such as differentiation, proliferation,

survival, and metabolism are governed by signalling pathways, and disruption of these pathways has been linked to many diseases, including cancer, inflammatory diseases, metabolic abnormalities, and neurological disorders. Consequently, a key strategy in drug discovery and development is to find drug targets within these pathways and develop therapeutics that specifically alter their activity. A thorough knowledge of the molecular mechanisms underlying pathway activation, propagation, and downstream effects is usually the first step in this endeavor. These mechanisms are elucidated using a combination of systems biology, genetics, and biochemical techniques. Prioritizing candidate compounds with the most promise for therapy is possible through rapid target discovery and validation provided by high-throughput screening assays, omics technologies, and computational modeling. Once identified, these targets form the basis for logical drug design, in which targeted therapies involving nucleic acid-based drugs, small molecule inhibitors, monoclonal antibodies, or other methods are developed to directly interfere with target protein function or interfere with critical signalling

relationships. To maximize therapeutic efficacy while minimizing toxicity and off-target effects, the affinity, selectivity and pharmacokinetic properties of lead compounds can be optimized through fragment-based methods, virtual screening and structure-based drug design. Pharmacological studies simultaneously evaluate the pharmacological properties, safety and tolerability of proposed drugs, providing important information about their efficacy and mode of action. They advance through preclinical research in human subjects. This prepares the way for the later stages of the clinical trial. The objectives of these late-phase trials are to assess the long-term safety and tolerability of investigational drugs, to compare their efficacy with standard-of-care therapies, and to determine the therapeutic utility of these drugs in large patient groups. Regulatory bodies are essential to the drug development process because they assess the quality, safety, and efficacy of novel therapies and meet the stringent requirements that must be met before they are approved and placed on the market. In addition, patient advocacy and participation groups provide insight into the clinical needs of specific infections that help prioritize research programs and develop new treatment strategies.

Precision Medicine: Tailoring Therapies Based on Signalling Profiles

An innovative approach to health care, precision medicine involves personalizing medical procedures and treatment for each patient according to their specific genetic, environmental, and lifestyle variables. The primary goal of precision medicine is to maximize therapeutic efficacy while minimizing side effects, resulting in personalized and focused treatments. The basis of this strategy is the knowledge that different individuals can respond differently to the same treatment due to genetic variations and other factors. By examining these variants, researchers and clinicians can identify certain biomarkers and signalling profiles associated with diseases and treatment outcomes. An array of cellular pathways and chemical interactions that form signalling profiles is essential in defining how cells respond to drugs and other external stimuli. By understanding these signalling profiles, it is possible to develop targeted drugs that inhibit specific disease-related pathways, resulting in more efficient therapies with fewer adverse effects. Personalized medicine has great potential to replace a one-size-fits-all strategy in many medical specialties, including neurology, cardiology, oncology, and infectious diseases. Cancer treatment regimen. Historically, the location and stage of the tumor determined the course of cancer treatment rather than the precise genetic characteristics of the

cancer cells. Oncologists can now identify genetic abnormalities and other indicators that drive the development of cancer, thanks to advances in genome sequencing and molecular profiling. For example, changes in genes such as EGFR (epidermal growth factor). This unique strategy has resulted in significant gains in patient outcomes such as increased response rates, prolonged progression-free survival, and improved quality of life. Precision medicine is making advances not only in oncology but also in cardiology. Cardiovascular disorders (CVDs). Heart failure, arrhythmia, coronary artery disease and other disorders affecting the heart and blood vessels are all considered cardiovascular diseases. Treatments for CVD generally focus on controlling symptoms and reducing risk factors such as high blood pressure and cholesterol. But thanks to advances in molecular profiling and genetic testing, scientists are finding genetic variants linked to higher risk of CVD and better drug response. Before precision medicine can be used, several hurdles must be overcome, such as the need for comprehensive genomic data, integration of multi-omics data, and ethical concerns about patient privacy and consent. Some healthcare settings may lack access to the sophisticated infrastructure and computational resources needed to generate and analyze genomic data. Furthermore, integration of data from different sources, such as transcriptomics, proteomics, metabolomics, and genomes, poses technical challenges for data standardization and interpretation. Furthermore, to guarantee the ethical use of private medical records, it is necessary to carefully address issues related to patient confidentiality, authentication, and information exchange. Despite these obstacles, precision medicine has a bright future due to continuous technological improvements, data analysis and collaboration. Research projects. Precision medicine holds great promise to transform health care delivery and improve patient outcomes as genomic sequencing becomes more accessible and affordable. Precision medicine harnesses the power of molecular data and signal properties to provide a revolutionary, completely personalized, predictive and preventive approach to health care.

Therapeutic Resistance: Challenges and Strategies in Targeted Therapy

Targeted therapy faces a major hurdle in the form of therapeutic resistance, which can compromise treatment efficacy and limit clinical outcomes in many diseases, such as autoimmune disorders, cancer, and infectious diseases. Targeted therapies exploit certain genetic variants or vulnerabilities in diseased cells to selectively inhibit key signaling pathways or molecular targets associated with disease progression. Despite early efficacy, the establishment of resistance mechanisms often leads to treatment failure and disease relapse, so the development of novel therapies to overcome or overcome resistance is essential. Treatment resistance is caused by various mechanisms such as tumor heterogeneity, clonal evolution, epigenetic changes and genetic changes. Genetic mutations can cause resistance by interfering with drug-target interactions, altering downstream signaling cascades, or triggering compensatory processes that circumvent therapeutic inhibition. Gene expression patterns and increase resistance. By favoring subpopulations of cancer cells with inherited or acquired resistance mutations, clonal evolution and tumor heterogeneity contribute to resistance by generating drug-resistant clones that accelerate disease course. Furthermore, through paracrine signaling, immune evasion, and metabolic reprogramming, the tumor microenvironment—composed of stromal cells, immune cells, and extracellular matrix components—plays an important role in promoting treatment resistance. A variety of strategies are needed to combat treatment resistance, including the development of next-generation targeted drugs, combination therapies, biomarker-driven treatment programs, and patient-specific precision medicine techniques. Next-generation targeted therapies seek to overcome resistance by focusing on alternative signalling pathways, using artificial lethality, or modifying immune responses to enhance antitumor immunity. Combination therapies work together to avoid the establishment of resistance by targeting multiple nodes in the disease pathway and combining targeted drugs with immunotherapy, conventional chemotherapy, or other targeted agents. Biomarker-driven therapeutic strategies use transcriptomic analysis, gene profiling, and other molecular diagnostic techniques to identify predictive biomarkers of response or resistance. This allows patients to be stratified into appropriate treatment regimens and to identify patients who may benefit from targeted therapy. Through integration of clinical phenotypes, patient-specific

characteristics, and multi-omics data, precision medicine approaches improve therapeutic outcomes while reducing the likelihood of resistance. Development of rational drug design techniques such as fragment-based, structure-based and computer-aided drug design facilitates the development of small-molecule inhibitors with better pharmacological properties, resistance profiles and target specificity. Furthermore, developments in systems biology, functional genetics and high-throughput screening make it possible to identify new drug targets and understand the complex signalling networks linked to treatment resistance, providing important new information for developing creative therapeutic approaches. In summary, various molecular and cellular pathways that confer adaptive advantages to diseased cells are responsible for the development of therapeutic resistance, which poses a significant challenge for targeted therapy. To overcome treatment resistance, a thorough understanding of the underlying biology must be combined with the development of new therapeutic approaches that specifically target the broad spectrum of resistance mechanisms present in various disease states. Using advances in precision medicine, biomarker-driven treatment approaches, and logical drug design can reduce treatment resistance and improve clinical outcomes for patients receiving targeted therapies.

Clinical Applications: Signalling Biomarkers and Disease Monitoring

Clinical signaling biomarker applications for disease monitoring include a wide range of methods for diagnosis, prognostication, and guidance of therapeutic intervention in oncology, cardiology, neurology, and infectious diseases. Signaling biomarkers provide important information about the origin, course, and response to treatment of diseases. They include proteins, nucleic acids, metabolites, and other molecular entities involved in cellular signaling pathways. These biomarkers serve as proxy indicators of disease activity, severity, and therapeutic efficacy because they represent differential signaling events within diseased cells as a result of genetic alterations, epigenetic changes, dysregulated protein expression, or disrupted signaling cascades.

Oncogenes, tumor suppressor genes, and activated signaling pathways (EGFR, PI3K/AKT/mTOR, MAPK, etc.) are examples of signaling biomarkers that are frequently used in oncology for cancer diagnosis, patient staging, and treatment selection. These biomarkers also inform the use of targeted therapies,

immunotherapies, and combination regimens that are personalized to each patient's molecular profile. Furthermore, non-invasive monitoring of tumor dynamics and treatment response can be achieved by liquid biopsy-based techniques using circulating tumor cells (CTCs), cell-free DNA (cfDNA), and extracellular vesicles (EVs). These techniques allow real-time assessment of disease progression and identification of minimal residual disease (MRD) or relapse. Cardiology uses biomarkers such as brain natriuretic peptide (BNP), C-reactive protein (CRP), and cardiac troponins to diagnose acute coronary syndromes, heart failure exacerbations, and infective myocarditis. These Biomarkers Are Signs of Myocardial Injury, Heart Failure, and Inflammation Neurologists use biomarkers such as tau protein, amyloid-beta, and neurofilament light chain (NFL) to monitor and diagnose neurodegenerative diseases such as multiple sclerosis, Parkinson's disease, and Alzheimer's disease. These biomarkers facilitate early diagnosis, patient stratification, and development of disease-modifying therapies targeting underlying molecular mechanisms by shedding light on disease pathophysiology, neuronal injury, and disease progression. Viral infections such as HIV, hepatitis and respiratory viruses are diagnosed, monitored and treated using biomarkers such as viral RNA, viral antigens and host immune response markers (eg cytokines, chemokines) in infectious diseases. These biomarkers enable rapid identification of viral infections, assessment of disease severity, and monitoring of treatment response. They assist in the selection of antiviral treatments and inform public health initiatives aimed at preventing the spread of disease. In general, signalling biomarkers are essential for monitoring disease in various clinical settings, providing insightful information about diagnosis, prognosis, and treatment, which improves patient care and leads to better clinical outcomes. New technologies such as mass spectrometry, multiplex immunoassays, and next-generation sequencing offer unprecedented possibilities to identify novel biomarkers, understand disease mechanisms, and develop personalized clinical strategies based on specific patient molecular profiles. Furthermore, the integration of multi-omics data and the development of predictive models for disease diagnosis, prognosis and treatment response prediction are made possible by developments in data analytics, artificial intelligence and machine learning. These advances mark the beginning of a new era in precision medicine that has the potential to completely transform clinical practice and improve patient care. Nevertheless, there are still challenges in standardizing test procedures, validating biomarker performance in patient populations, and

incorporating biomarker data into clinical decision-making processes to transform biomarker findings into clinically useful tools. To overcome these barriers, researchers, clinicians, regulatory bodies, and industry must collaborate to advance biomarker development, validation, and clinical practice application to improve patient outcomes and personalized care paradigm

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3. MATLAB COURSES

Based on the MATLAB Certificate there are 19 Courses I have completed

- **Basic Courses**

- ✓ MATLAB Onramp
- ✓ Simulink Onramp
- ✓ Signal Processing Onramp
- ✓ Image Processing Onramp
- ✓ Machine Learning Onramp
- ✓ Deep Learning Onramp
- ✓ Computer Vision Onramp

- **Advanced Courses**

- ✓ MATLAB Fundamentals
- ✓ MATLAB for Data Processing and Visualization
- ✓ MATLAB Programming Techniques
- ✓ Solving Nonlinear Equations with MATLAB
- ✓ Signal Processing with MATLAB
- ✓ Machine Learning with MATLAB
- ✓ Image Processing with MATLAB
- ✓ Deep Learning with MATLAB
- ✓ Object - Oriented Programming
- ✓ App Building Onramp
- ✓ Reinforcement Learning Onramp
- ✓ Statistics Onramp

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 DID I LEARN?

- 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 DID I LEARN?

- Understand the capabilities and applications of Simulink for modeling, simulating, and analyzing 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 analyze system behaviour.
- 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 guides 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 DID I LEARN?

- Understand the basic concepts and principles of signal processing, including time-domain and frequency-domain representations of signals, sampling, and 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 DID I LEARN?

- 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 DID I LEARN?

- 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 DID I LEARN?

- 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 in MATLAB is a structured learning program designed to equip participants with essential skills and knowledge in computer vision using MATLAB. Throughout the onramp, participants engage in guided learning modules that cover fundamental concepts such as image representation, feature extraction, and object detection. They gain hands-on experience implementing computer vision algorithms using MATLAB's powerful Computer Vision Toolbox, learning techniques for image processing, feature detection, and object tracking. Practical exercises and projects allow participants to apply their newly acquired skills to real-world scenarios, reinforcing their understanding.

WHAT DID I LEARN?

- Understand fundamental computer vision concepts such as image representation and feature extraction.
- Learn to implement computer vision algorithms using MATLAB's Computer Vision Toolbox.
- Gain proficiency in image processing techniques for tasks like filtering and feature detection.
- Apply learned skills to practical projects, reinforcing understanding through hands-on experience.

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 DID I LEARN?

- 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, analyzing, 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 DID I LEARN?

- 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 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.

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. The 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 DID I LEARN?

- 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 DID I LEARN?

- 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 DID I LEARN?

- 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 DID I LEARN?

- 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 DID I LEARN?

- 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 DID I LEARN?

- 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 DID I LEARN?

- 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 DID 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 DID I LEARN?

- 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 DID I LEARN?

- 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

Rakshana R

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

MATLAB Onramp



DIRECTOR, TRAINING SERVICES

14 November 2023



Course Completion Certificate

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Simulink Onramp



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29 February 2024



Course Completion Certificate

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Signal Processing Onramp


DIRECTOR, TRAINING SERVICES

7 March 2024



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Machine Learning Onramp


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Deep Learning Onramp


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Computer Vision Onramp


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MATLAB Fundamentals


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2 December 2023



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MATLAB for Data Processing and Visualization


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MATLAB Programming Techniques


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30 March 2024



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Solving Nonlinear Equations with MATLAB


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Signal Processing with MATLAB


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7 March 2024



Course Completion Certificate

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Machine Learning with MATLAB


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Course Completion Certificate

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Image Processing with MATLAB

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

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30 March 2024



Course Completion Certificate

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Deep Learning with MATLAB

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

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Object-Oriented Programming Onramp


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App Building Onramp


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Reinforcement Learning Onramp


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Statistics Onramp


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1 March 2024