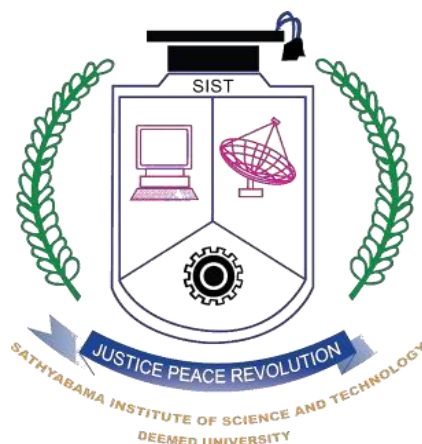


INTEGRATED ANALYSIS: GENE EXPRESSION, SURVIVAL, BIOMARKERS AND DRUG TARGETS

Submitted in partial fulfilment of the required for the award of
Master of Science Degree in Bioinformatics and Data Science by
M SANGEERTHANA (43739020)



DEPARTMENT OF BIOINFORMATICS AND DATA SCIENCE

SCHOOL OF BIO AND CHEMICAL ENGINEERING

SATHYABAMA

INSTITUTE OF SCIENCE AND TECHNOLOGY
(DEEMED TO BE UNIVERSITY)

Accredited with Grade “A++” by NAAC JEPPIAAR
NAGAR, RAJIV GANDHI SALAI, CHENNAI – 600119

APRIL 2024



SATHYABAMA

INSTITUTE OF SCIENCE AND TECHNOLOGY
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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 **SANGEERTHANA M (43739020)** 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, **SANGEERTHANA M** 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 Master of Science degree in Bioinformatics and Data Science.

DATE:

SANGEERTHANA M

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. MAHALAKSHMI Department of Bioinformatics and Data Science for his valuable guidance, suggestions, and constant encouragement that paved way for the successful completion of my project work.

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

(SANGEERTHANA M)

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

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

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

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

PROCEDURE:

- For the database and disease Liver Tumor Geo2R is the source of the geo dataset (GSE107170)
- 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 Bio Grid 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 continue cluego parameter such as species ontology and statistical settings.
- Run cluego analysis to identify functional categories or pathways associated with the selected nodes.

RESULTS:

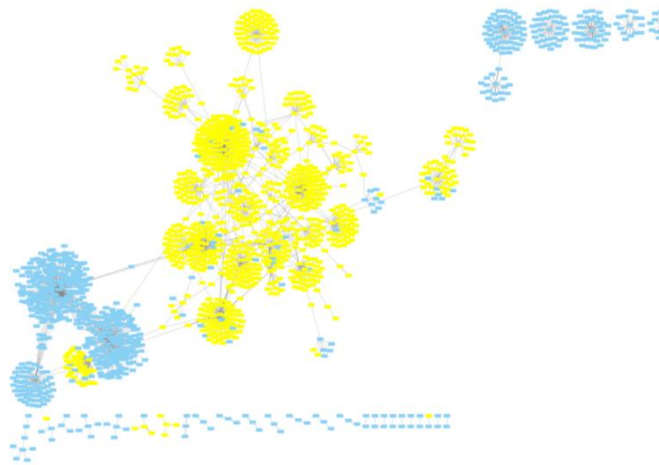


Fig 1: Network Pathway of Upregulated Genes

Results for Analysis0

ClueGO Results (Cluster #1) Cluster #1 ClueGO Log

Hide Labels

ID	Term	Ontology Source	Term PValue
☒ GO:007...	plasma lipoprotein particle organization	GO_BiologicalProcess-EBI-U...	8.9 E-4
☒ GO:190...	positive regulation of phospholipid metabolic process	GO_BiologicalProcess-EBI-U...	3.3 E-5
☒ GO:001...	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	GO_MolecularFunction-EBI-U...	5.7 E-4
☐ GO:003...	primary alcohol metabolic process	GO_BiologicalProcess-EBI-U...	7.4 E-5
☐ GO:004...	doxorubicin metabolic process	GO_BiologicalProcess-EBI-U...	6.1 E-6
☐ GO:004...	daunorubicin metabolic process	GO_BiologicalProcess-EBI-U...	4.2 E-6
☒ GO:000...	alditol:NADP+ 1-oxidoreductase activity	GO_MolecularFunction-EBI-U...	8.4 E-10
☐ GO:007...	positive regulation of biomineral tissue development	GO_BiologicalProcess-EBI-U...	3.1 E-6
☐ GO:001...	transmembrane receptor protein kinase activity	GO_MolecularFunction-EBI-U...	8.1 E-6
☐ GO:190...	protein kinase complex	GO_CellularComponent-EBI-U...	1.2 E-5
☐ GO:009...	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	GO_BiologicalProcess-EBI-U...	1.0 E-4
☐ GO:001...	peptidyl-threonine phosphorylation	GO_BiologicalProcess-EBI-U...	8.5 E-6

Fig 2: Table of Functional Analysis

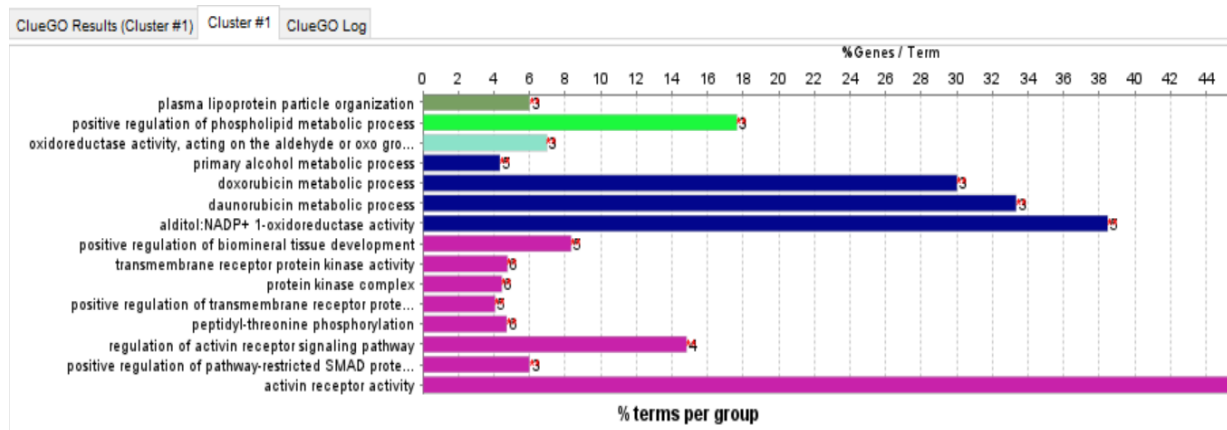


Fig 3 – Graph of functional analysis

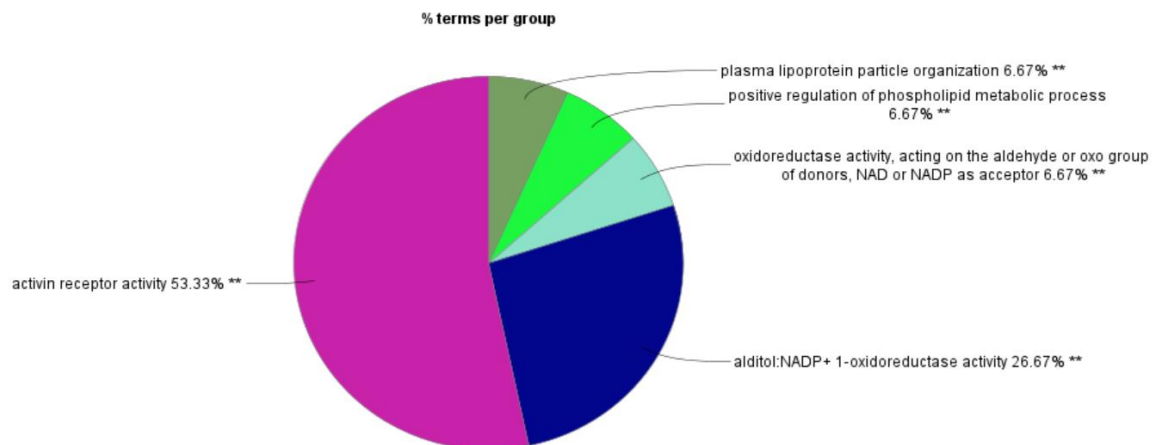


Fig 4: Pie Chart of functional analysis

INTERPRETATION:

Geo Dataset GSE Id: GSE107170

Upregulated Gene

- AKR1B10
- CRNDE
- SULTIC2
- GPC3
- NMRAL1P1
- MAGEA1
- ZIC2
- ROBO1
- SULT1C2
- ZNF595

CLUEGO

TERM	FUNCTION	ONTOLOGY
Plasma lipoprotein particle organization 6.67%	Delivery and smooth transportation of triglyceral fatty acid and cholesterol from cell	Biological process
Positive regulation of phospholipid metabolic process 6.67%	The fatty acid may influence metabolism of altering the biosynthesis of prestaglandins	Biological process
Oxidoreductase activity acting on the aldehyde or oxo group of donors NAD or NADP as acceptor 6.67%	Enzyme that catalyze the transfer of electron from one molecule	Molecular function
Alidotol : NADP +1-oxireductase activity 26.67%	Catalyze the reduced nicotinamide adenine (NADPH)variety of carbonyl compounds	Biological function

Activin receptor activity 53.33%	Plays a critical role in glucose stimulated insulin secretion and glucose homeostatic control of pancreatic endocrine	Biological function
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Cumulative survival probability calculation using KM Plotter

Introduction:

KM-plotter is the most sophisticated online survival analysis tool, performing all calculations in real time (not loading pre-calculated images). The background database is manually curated. Gene expression data and relapse free and overall survival information are downloaded from GEO, EGA and TCGA. The database is handled by a PostgreSQL server, which integrates gene expression and clinical data simultaneously. To analyze the prognostic value of a particular gene, the patient samples are split into two groups according to various quantile expressions of the proposed biomarker. The two patient cohorts are compared by a Kaplan-Meier survival plot, and the hazard ratio with 95% confidence intervals and log rank P value are calculated. Databases and clinical data are supervised and extended regularly.

To avoid missing correlations due to the use of a specific cutoff, all available cutoff values between the lower and upper quartiles of expression are used for the selected gene, and false discovery rate (FDR) using the Benjamini-Hochberg method is computed to correct for multiple hypothesis testing. The cutoff value with the highest significance (lowest FDR) is determined. In case of multiple cutoff values with identical significance, the cutoff with the highest hazard (HR) rate is selected for the final analysis.

Aim

Calculate Proposed gene GPC3 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.

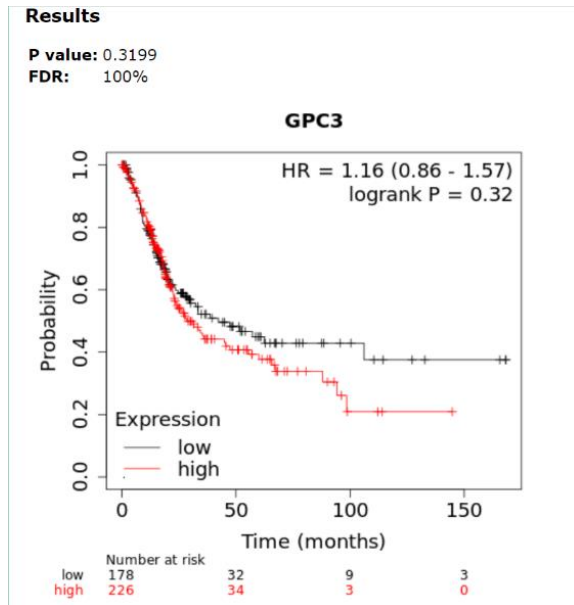


Fig 1: Bladder Carcinoma

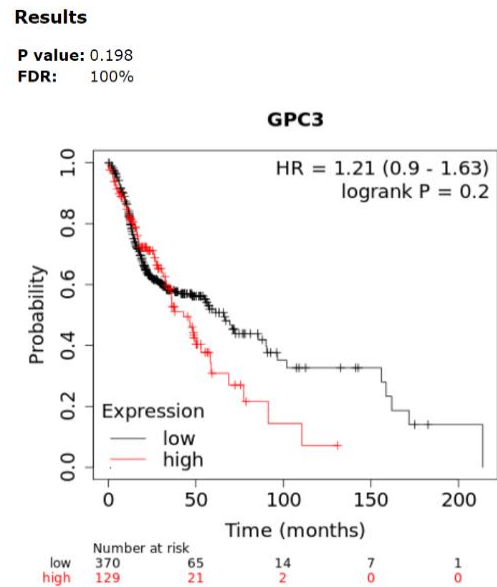


Fig 2: Breast Cancer

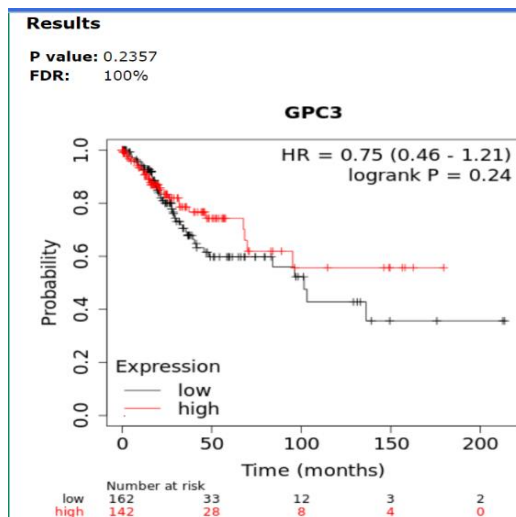


Fig 3: Cervical squamous cell carcinoma

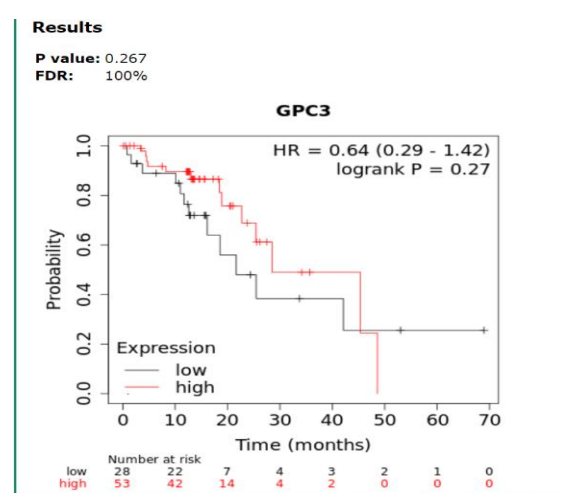


Fig 4: Esophageal Adenocarcinoma

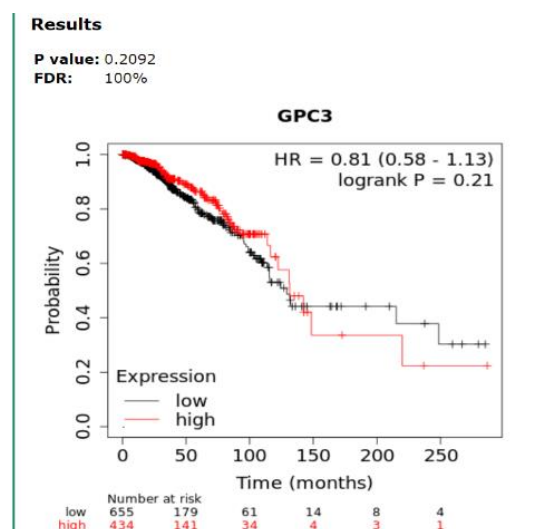


Fig 5: Head-neck squamous cell carcinoma

Interpretation

- KM-plot recognizes proposed gene symbols GPC3 (including HUGO Gene Nomenclature Committee approved).
- Sources for the database include GEO, EGA, TCGA, Metabric, Impact, and PubMed repositories. For more details, please check our publications.
- **Bladder carcinoma**
 - HR Rate: 1.16(0.86-1.57)
 - 50% of median survival of probability
 - Low expression cohort: 42.33
 - High expression cohort: 28.63
- **Breast cancer**
 - HR Rate: 1.21(0.9-1.63)
 - 50% of median survival of probability
 - Low expression cohort: 129.1
 - High expression cohort: 131.37
- **Cervical squamous cell carcinoma**
 - HR Rate: 0.75(0.46-1.21)
 - 50% of median survival of probability
 - Low expression cohort: 29.3
 - High expression cohort: 46.47
- **Esophageal Adenocarcinoma**
 - HR Rate: 0.64(0.29-1.42)
 - 50% of median survival of probability
 - Low expression cohort: 32.9
 - High expression cohort: 261.3
- **Head-neck squamous cell carcinoma**
 - HR Rate: 0.81(0.58-1.13)
 - 50% of median survival of probability
 - Low expression cohort: 26.17
 - High expression cohort: 28.5

Biomarkers: identifying biological markers for disease

Diagnosis and therapeutic monitoring

Introduction:

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

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

Procedure:

- The marker database was retrieved using the following link <http://themarkr.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
BHPV45	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	Iplimumab	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..
B6XA7P	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

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 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:

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

PDB: The Protein Databank (PDB) is a file format describing the 3D structure of molecules held in protein data bank. The PDB format accordingly provides for description and annotations of protein and nucleic acid structures including atomic co-ordinates, secondary structure assignments as well atomic connectivity.

Drug Bank: Drug bank database is a comprehensive freely accessible online database containing information on drugs and drug targets. This database is a unique bioinformatics and cheminformatics resource that combines detail drug

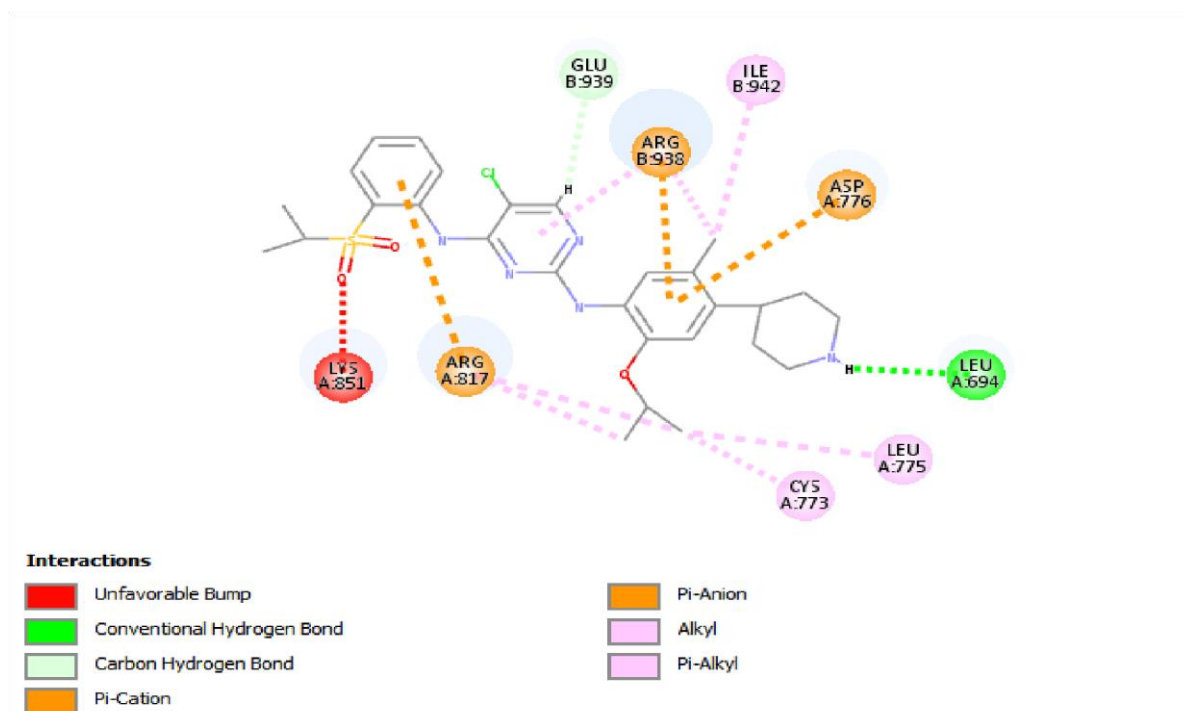


Fig 1: 2D structure of 5CNN Protein

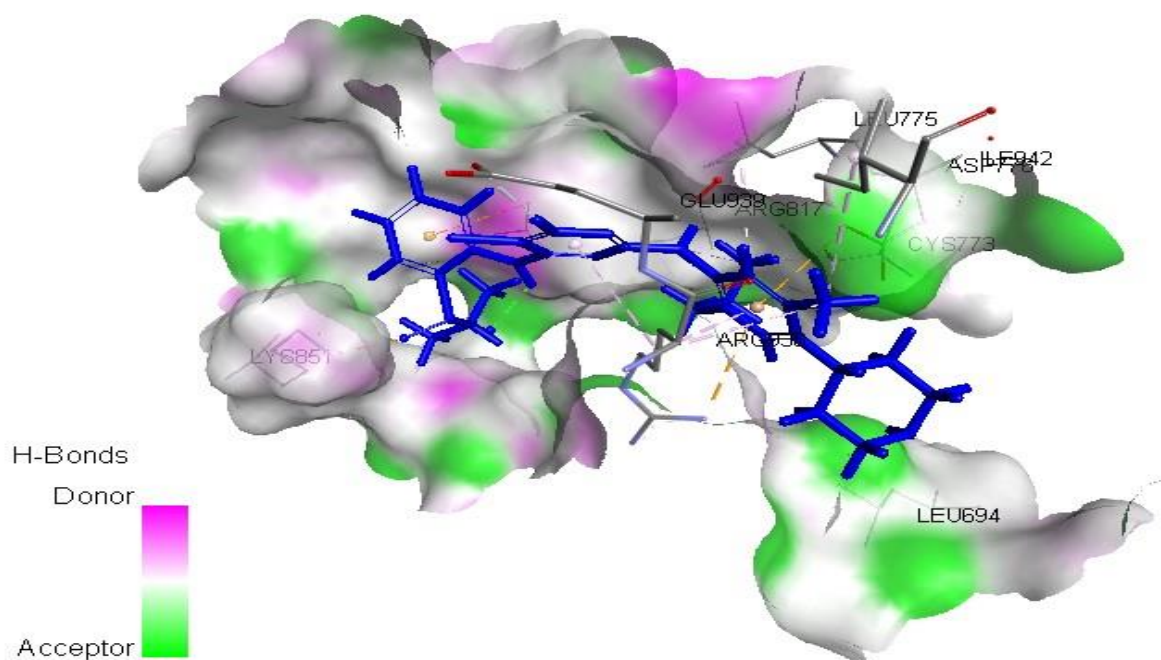


Fig 2: 3D Structure of 5CNN Protein

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 1: 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 Charge	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 2: Table of non-bond

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 signaling 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.

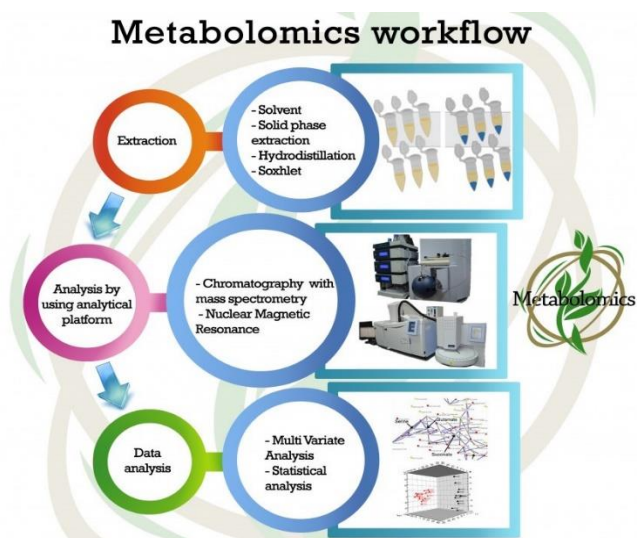
2. REVIEW ARTICLE

METABOLOMICS EXPLORED: A JOURNEY INTO CELLULAR CHEMISTRY

Metabolomics Explored: A Journey into Cellular Chemistry

"A Journey into Cellular Chemistry" sounds like an attractive title for a book or article exploring the intricacies of cellular metabolism. Metabolomics is a growing field of research devoted to the detailed study of small molecules inside cells. Tissues and organisms, in such a work, are involved in a variety of biology. Readers can expect to take a journey through the vast landscape of metabolism, from energy production to signaling pathways, providing insights into how cells function and respond to internal and external stimuli through these techniques to identify and quantify metabolites associated with health, disease, and environmental influences. Researchers can unravel the fingerprints of change, and "metabolism research" will draw attention to applications of metabolism in fields ranging from medicine and pharmacology to agriculture and environmental science. For example, metabolomics has the potential to revolutionize personalized medicine by providing insights into individual metabolic profiles and guiding tailored treatment strategies. Throughout the journey, readers will encounter the complexities of metabolic networks, the dynamics of metabolic regulation, and the interplay between metabolites and cellular functions. It's a journey that underscores the interconnectedness of biochemical pathways and the delicate balance required for life to thrive. Ultimately, "The Study of Metabolism" gives readers a deeper appreciation for the elegance and complexity of cellular chemistry, which explains the fundamental processes that sustain life at its most fundamental level.

Metabolomics Workflow: For sample preparation to data analysis



Metabolomics workflow involves a meticulous process from sample preparation to data analysis, critical to understanding metabolic profiles associated with various biological states or conditions. First, sample collection is performed meticulously, ensuring representative samples from the biological system of interest, such as blood, urine, or tissue. Then, these samples undergo rigorous preparation procedures to extract metabolites while

minimizing degradation or alteration. This often involves techniques such as solvent extraction, filtration, and optimization of the stability and detection of metabolites. Following sample preparation, advanced analytical techniques are used to analyze metabolites in detail. Mass spectrometry (MS) and nuclear magnetic resonance (NMR) spectroscopy are common platforms used to identify and quantify metabolites. These techniques offer high sensitivity and resolution, allowing detection of a wide range of metabolites present in complex biological samples. Once the raw data is received, it undergoes extensive pre-processing to ensure data quality and consistency. Steps such as noise reduction, baseline correction, and peak alignment can improve the accuracy and reliability of subsequent analyses. Statistical methods are used to analyze the processed data, with the aim of finding significant differences in metabolite levels between experimental groups or conditions. Multivariate analysis techniques such as principal component analysis (PCA) and orthogonal partial least squares discriminant analysis (OPLS-DA) are often used to discover patterns and relationships within the data, helping to identify biomarkers or metabolic signatures associated with specific phenotypes or treatments. Furthermore, pathway analysis tools are used to elucidate the biological relevance of identified metabolites, mapping them into metabolic pathways and networks that provide valuable insights into the underlying biochemical processes affected by experimental conditions or interventions. In addition, integration with other omics data, such as genomics and proteomics, allows a comprehensive understanding of biological systems and their response to perturbations. In conclusion, metabolomics workflow

consists of interconnected steps, from sample preparation to data analysis. Important for unraveling complex metabolic dynamics within biological systems. By leveraging advanced analytical techniques and bioinformatics tools, metabolomics enables discovery of biomarkers, elucidation of metabolic pathways and deeper insights into physiological and pathological processes, ultimately contributing to advances in biomedical research and personalized medicine.

Metabolomics in Agriculture: Improving Crop Yield and Quality

Metabolomics, an emerging field at the intersection of biology, chemistry and data science, is poised to revolutionize agriculture by providing unprecedented insights into the molecular mechanisms governing plant growth, development and stress responses. Through the exhaustive analysis of small molecules (metabolites) in a biological system, metabolomics provides a comprehensive snapshot of its physiological state. In the context of agriculture, this approach has enormous potential to improve crop productivity and resilience in the face of increasing challenges such as climate change, pest infestations and soil degradation. By describing the metabolism of crop plants under different environmental conditions and management practices, researchers can elucidate complex metabolic networks underlying key agronomic traits. This knowledge serves as a blueprint for tailoring cultivation strategies to maximize yield, quality and resource use efficiency while minimizing environmental impacts. Furthermore, metabolomics enables the discovery of novel biological compounds with applications in plant breeding, crop protection and post-harvest management, thereby expanding farmers' toolkit for sustainable agriculture. By leveraging advanced analytical platforms and bioinformatics tools, metabolomics helps identify biomarkers indicative of plant health, nutrient status and stress tolerance, empowering farmers with actionable insights for timely intervention and decision-making. Integrating metabolomics into a precision agriculture framework promises to usher in a new era of data-driven agricultural practices tailored to the individual needs of each field and crop, thereby optimizing resource allocation and improving overall agricultural sustainability. Through collaborative efforts between researchers, breeders, farmers and policy makers, metabolomics has the potential to ensure food security, environmental protection and economic prosperity across the entire agri-food value chain, from seed to table. Metabolomics, a rapidly advancing field, holds significant promise for revolutionizing agriculture by increasing crop yields and quality. By analyzing metabolites within plants in detail, metabolomics provides unparalleled insights

into their biochemical processes and interactions with the environment. With sophisticated techniques such as mass spectrometry and nuclear magnetic resonance spectroscopy, researchers can detect and quantify a wide array of metabolites, including sugars, amino acids and secondary metabolites important for plant growth and defense. This comprehensive understanding allows for targeted interventions to improve agricultural practices. Metabolomics helps identify metabolic pathways associated with desirable traits such as drought tolerance, disease resistance, and nutrient utilization efficiency. By understanding the metabolic signatures of high-yielding and resilient crops, breeders can accelerate the development of superior varieties through marker-assisted selection and genetic engineering. Furthermore, metabolomics enables real-time monitoring of plant responses to environmental stresses and agronomic treatments, empowering farmers to implement timely interventions to reduce yield losses and improve product quality. By harnessing the power of metabolism, agriculture can take a transformative journey towards sustainability, resilience and food security in the face of mounting global challenges.

Metabolomics and Toxicology: Assessing Chemical Exposure

Metabolomics plays an important role in toxicology by providing a comprehensive assessment of chemical exposure and its effects on biological systems. At the heart of this approach is the analysis of small molecule metabolites present in biological samples such as blood, urine or tissue that reflect the metabolic response to chemical exposure. A workflow typically involves several key steps. First, samples are collected from exposed individuals or test specimens and prepared for analysis. This may involve various extraction methods to isolate metabolites from the biological matrix. Then, advanced analytical techniques such as mass spectrometry (MS) and nuclear magnetic resonance (NMR) spectroscopy are used to identify and quantify a wide range of metabolites in the samples. Once the data is obtained, sophisticated bioinformatics tools and statistical analyzes are used to process and interpret the results. This includes data normalization to account for variations in sample preparation and instrument performance, and statistical tests to identify metabolites that are significantly altered following chemical exposure. Multivariate analysis methods such as Principal Component Analysis (PCA) and Partial Least Squares Discriminant Analysis (PLS-DA) are often used to discern patterns and groups within the data, helping to identify biomarkers indicative of exposure or toxicity. Furthermore, pathway analysis tools are used to map identified metabolites

onto biochemical pathways, providing insights into the underlying biological mechanisms affected by chemical exposure. This not only helps to understand toxicological effects at a molecular level, but also to identify potential targets for intervention or biologic development. Overall, metabolomics in toxicology provides a holistic view of chemical exposure and its effects on biological systems, enabling early detection of toxicity, elucidation of underlying mechanisms, and identification of biomarkers to inform risk assessment and regulatory decisions. This integrated approach holds great promise for improving our understanding of chemical safety and protecting public health.

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2. Yang Chen,En-Min Li and Li-Yan Xu Metabolomics Analysis: A Bioinformatics Workflow 2018;122:1302-1315
3. T Bongiovanni ¹, R Pintus, A Dessì, A Noto, S Sardo, G Finco, G Corsello, V FanoS metabolomics applied to sports 14,623-641(2015)
Fatemeh Dehghani, Saeed Yousefinejad 14,133-144(2017)

ORIGINALITY REPORT

6%	%	6%	%
SIMILARITY INDEX	INTERNET SOURCES	PUBLICATIONS	STUDENT PAPERS

PRIMARY SOURCES

-  Zhen Lu, Shuang Wang, Chenglong Ji, Xiujuan Shan, Huifeng Wu. "Evaluation of metal pollution-induced biological effects in Chinese shrimp Fenneropenaeus chinensis by NMR-based metabolomics", Marine Pollution Bulletin, 2020
Publication 3%
-
-  Lingping Hu, Hongwei Zhang, Zhiheng Hu, Yaoxian Chin, Xiaomei Zhang, Jianchu Chen, Yaqin Hu. "Comparative proteomics analysis of three commercial tuna species through SWATH-MS based mass spectrometry and chemometrics", Food Control, 2022
Publication 1%
-
-  Mahbobeh Latifimehr, Ali Asghar Rastegari, Zahra Zamani, Pezhman Fard Esfahani, Leila Nazari. "The Investigation of Metabonomic Pathways of Serum of Iranian Women with Recurrent Miscarriage Using 1H NMR", BioMed Research International, 2021
Publication 1%
-

4.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

ADVANCE 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 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 modeling 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 modeling, 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 analyze 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, 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 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 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. 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

Sangeerthana M

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

MATLAB Onramp


DIRECTOR, TRAINING SERVICES

13 November 2023



Course Completion Certificate

Sangeerthana.M

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

Simulink onramp


DIRECTOR, TRAINING SERVICES

29 February 2024

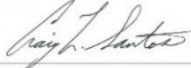


Course Completion Certificate

Sangeerthana M

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

Signal Processing with MATLAB


DIRECTOR, TRAINING SERVICES

31 March 2024



Course Completion Certificate

Sangeerthana M

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

Image Processing Onramp


DIRECTOR, TRAINING SERVICES

7 March 2024



Course Completion Certificate

Sangeerthana M

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

Machine Learning Onramp


DIRECTOR, TRAINING SERVICES

28 December 2023



Course Completion Certificate

Sangeerthana M

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

Deep Learning Onramp


DIRECTOR, TRAINING SERVICES

29 December 2023



Course Completion Certificate

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Computer Vision Onramp



DIRECTOR, TRAINING SERVICES

29 December 2023



Course Completion Certificate

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MATLAB Fundamentals



DIRECTOR, TRAINING SERVICES

6 January 2024



Course Completion Certificate

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MATLAB for Data Processing and Visualization



DIRECTOR, TRAINING SERVICES

31 March 2024



Course Completion Certificate

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MATLAB Programming Techniques



DIRECTOR, TRAINING SERVICES

22 February 2024



Course Completion Certificate

Sangeerthana M

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

Solving Nonlinear Equations with MATLAB


DIRECTOR, TRAINING SERVICES

31 March 2024



Course Completion Certificate

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

Signal Processing with MATLAB


DIRECTOR, TRAINING SERVICES

31 March 2024



Course Completion Certificate

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Machine Learning with MATLAB


DIRECTOR, TRAINING SERVICES

6 January 2024



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Image Processing with MATLAB


DIRECTOR, TRAINING SERVICES

31 March 2024



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Deep Learning with MATLAB


DIRECTOR, TRAINING SERVICES

29 December 2023



Course Completion Certificate

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Object-Oriented Programming Onramp


DIRECTOR, TRAINING SERVICES

7 March 2024



Course Completion Certificate

Sangeerthana.M

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

App Building Onramp


DIRECTOR, TRAINING SERVICES

27 March 2024



Course Completion Certificate

Sangeerthana M

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

Reinforcement Learning Onramp


DIRECTOR, TRAINING SERVICES

28 December 2023



Course Completion Certificate

Sangeerthana M

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

Statistics Onramp

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

DIRECTOR, TRAINING SERVICES

5 March 2024