

GENE EXPRESSION ANALYSIS

Submitted in partial fulfilment of the required for the award of
Master of Science Degree in Bioinformatics and Data Science By
Lokesh C (43739019)



**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 GANDHISALAI, CHENNAI – 600119

August 2024



SATHYABAMA

INSTITUTE OF SCIENCE AND TECHNOLOGY

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BONAFIDE CERTIFICATE

This is to certify that this Project Report is the bonafide work of
LOKESH C (43739019) who carried out the project entitled “**GENE
EXPRESSION ANALYSIS**”

under my / our supervision from January 2024 to April 2024

Internal Guide

External Guide (if Applicable)

**Head of the Department
Examiner**

Internal Examiner External

Submitted for Viva voce Examination held on _____

DECLARATION

I, **C. LOKESH (43739019)**, hereby declare that the Project Report entitled "GENE EXPRESSION ANALYSIS" done by me under the guidance of **Dr. MAHALAKSHMI** is submitted in partial fulfillment of the requirements for the award of Master of Science degree in Bioinformatics and Data Science

DATE:

C. LOKESH

PLACE: CHENNAI

STUDENT'S SIGNATURE

ACKNOWLEDGEMENT

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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 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.

(C. LOKESH)

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MINI PROJECT

TRANSLATIONAL BIOINFORMATICS

GENE EXPRESSION ANALYSIS

Aim:

Build Network to understand gene interrelationship and regulatory mechanism.

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.

TOOLS TO BE USED:

GENE EXPRESSION OMNIBUS

GEO2R

CYTOSCAPE

CYTOHUBBA

CLUEGO

GENE EXPRESSION OMNIBUS

The Gene Expression Omnibus (GEO) is a publicly available database hosted by the National Center for Biotechnology Information (NCBI), which is part of the United States National Library of Medicine (NLM). It serves as a repository for high-throughput gene expression data, including microarray and next-generation sequencing (NGS) data, as well as other types of functional genomics data.

GEO2R

GEO2R is a web-based tool provided by the Gene Expression Omnibus (GEO) that allows users to analyse gene expression data deposited in GEO datasets. It's designed to perform differential gene expression analysis, which helps identify genes that are differentially expressed between different experimental conditions or biological states.

CYTOSCAPE

Cytoscape is a powerful open-source software platform for visualizing, analyzing, and interpreting complex networks in biological systems. It is widely used by researchers in bioinformatics, systems biology, and computational biology to explore molecular interactions, pathways, and regulatory networks derived from various types of high-throughput data, such as gene expression, protein-protein interactions, and signaling pathways.

CYTOHUBBA

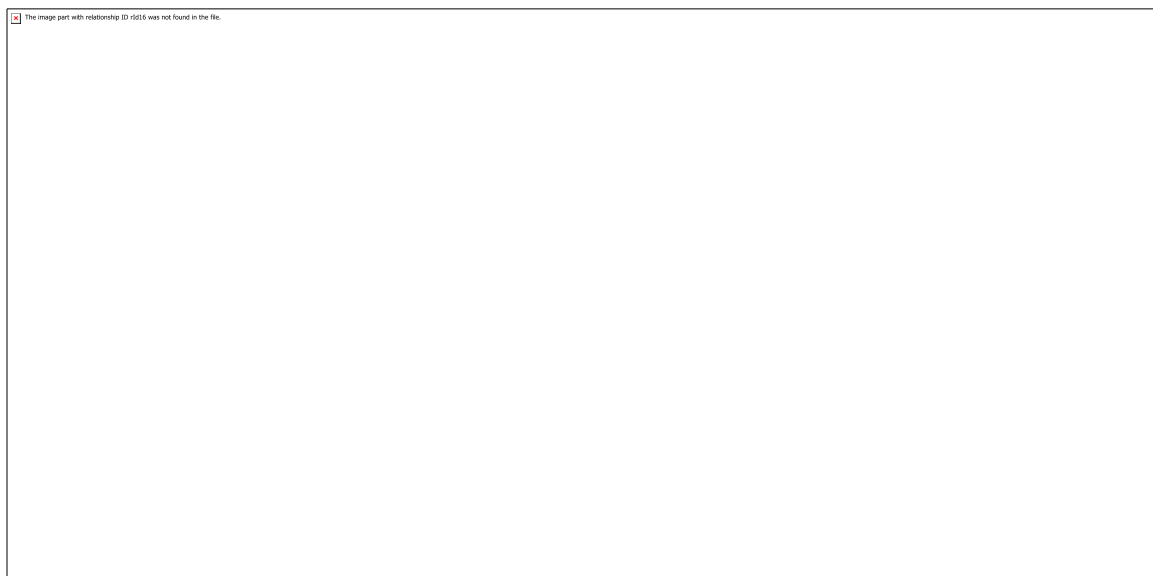
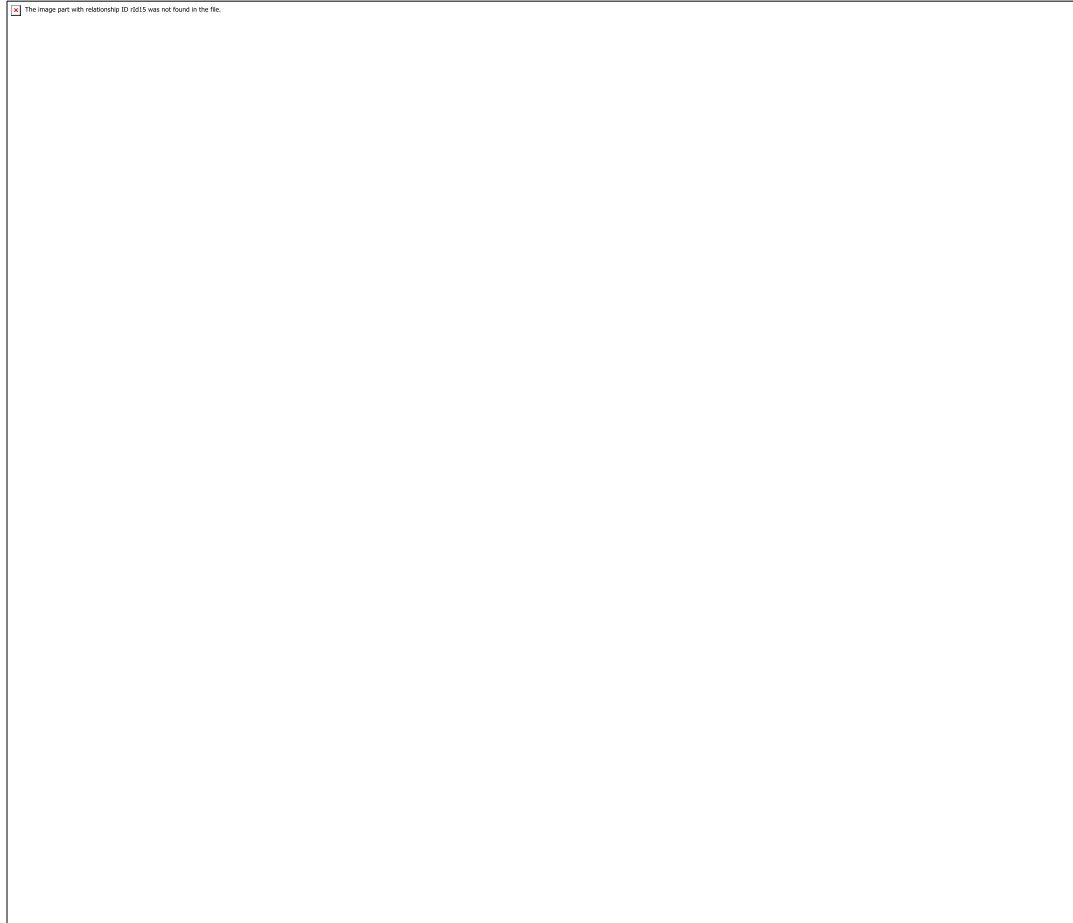
Cytoscape CytoHubba is a plugin that offers various network analysis algorithms for identifying important nodes (e.g., proteins, genes) within biological networks. It focuses on finding nodes that are highly connected or have specific topological features, which can indicate their significance in the network's structure or function. Here's an overview of CytoHubba and its features.

CLUEGO

Clue GO is a Cytoscape plugin designed to analyze and visualize functional enrichment of gene ontology (GO) terms and biological pathways within biological networks. It is commonly used by researchers in bioinformatics and systems biology to

gain insights into the biological significance of gene sets identified through high-throughput experiments, such as gene expression analysis or proteomics Studie .

RESULT:



INTERPRETATION:

GEO datasets GSE ID: GSE40839

GENE LIST: 1 RAD

2 FYV12

3 DA2B

4 JAM-2

5 POTE-15

6 SELM

7 EBNA1BP2

8 CT1.10

9 DIFF6

10 tropomyosin TPM2

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

Cumulative survival probability calculation using KM Plotter

Aim:

Calculate proposed gene S1PR1 cumulative survival probabilities.

Description:

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 logrank 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.

Procedure:

Kaplan Meier plotter home page was accessed using the following hyperlink
<https://kmplot.com/analysis/index.php?p=background>

Proposed gene/protein (o/p of Ex No 1) ---- was submitted in the pan cancer portal

Below listed parameters were opted for analysis

Restriction subtype –All

Split patients by-Auto select best cut off

Survival: Overall survival (os)

Survival: All

Restrict analysis based on cellular content: All

Results:

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Interpretation

KM-plot recognizes proposed gene symbols MX1 (including HUGO Gene Nomenclature Committee approved

Sources for the database include GEO, EGA, TCGA, Metabric, Impact, and PubMed repositories. For more details, please check our publications

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

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

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

ESOPHAGAL SQUAMOUS CELL: The HR of MX1 in bladder carcinoma is 0.86(0.63-1.19) 50% median survival between groups . it represent the ratio of probabilityfor low expression cohort (41)and high expression cohort(83)

OVARIAN CANCER: The HR of MX1 in bladder carcinoma is 2.35(0.94-5.87) 50% median survival between groups . it represent the ratio of probabilityfor low expression cohort (75)and high expression cohort(108)

LUNG SQUAMOUS CELL CARCINOMA: The HR of MX1 in bladder carcinoma is 1.18(0.9-1.55) 50% median survival between groups . it represent the ratio of probabilityfor low expression cohort (21)and high expression cohort(33).

Biomarker Discovery

Aim:

Identify the disease markers related to arthritis and categorize them into pharmacodynamic Biomarker, Monitoring biomarker, safety biomarkers.

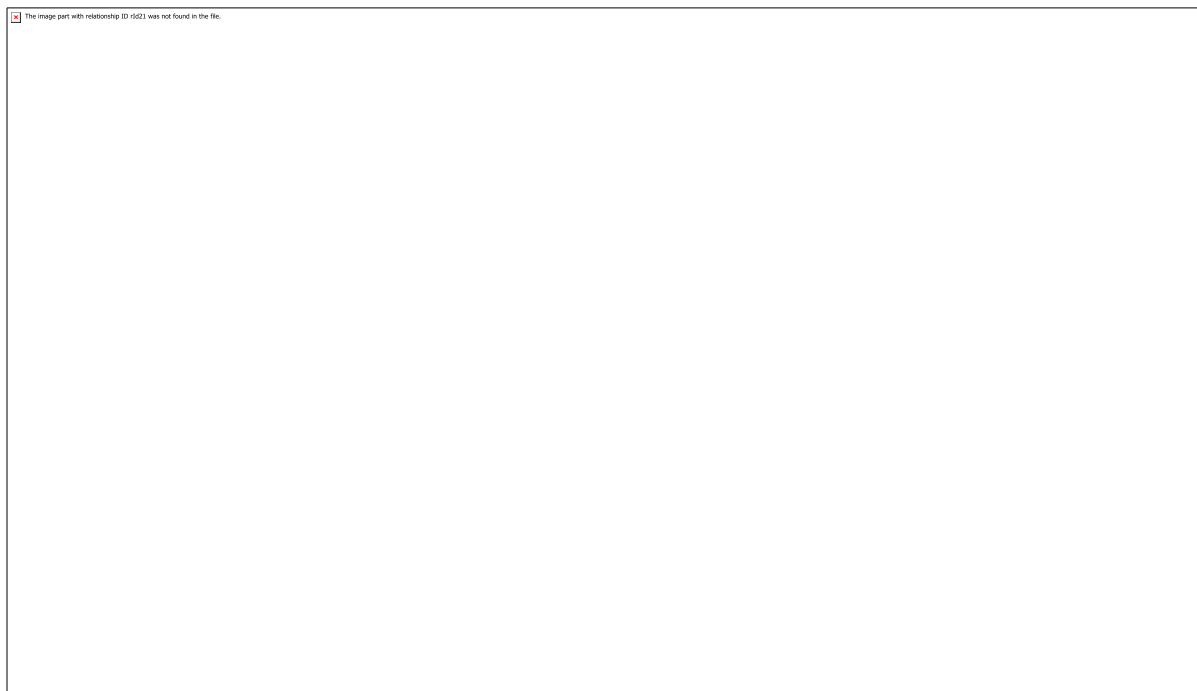
Description about the data resource:

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

Procedure:

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

FIG 3.1



DRUG TARGET PREDICTION:

AIM:

Drug [Acetaminophen](#) targets screening and binding assessment.

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 TargetPrediction 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.

Procedure:

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

RESULT:

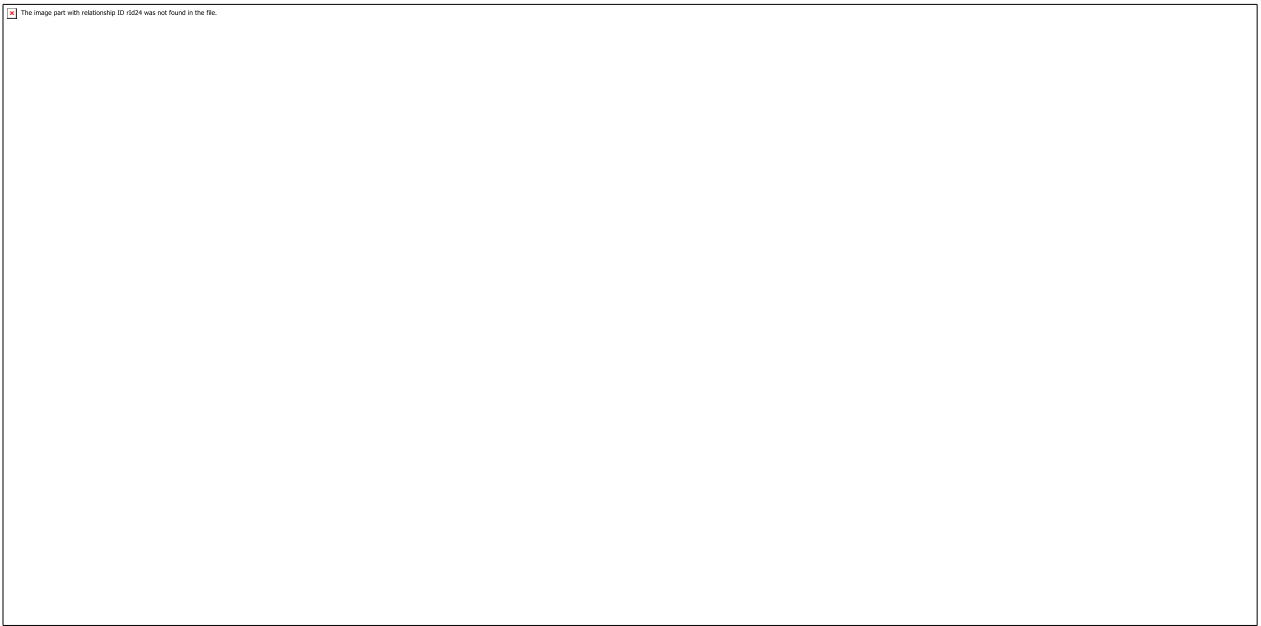


FIG 4.1

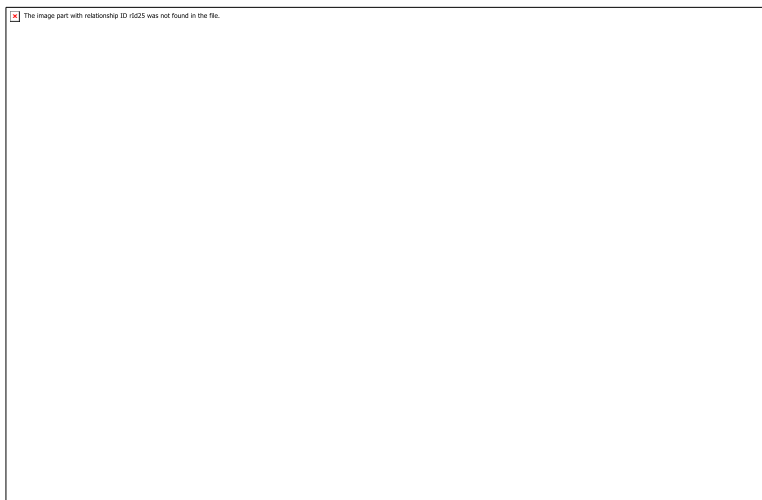


FIG 4.2

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FIG 4.3

INTREPRETATION:

Drug Name :Acetaminophen Cysteine

No. Of TargetsPredicted : 30

Choosen Targets Name : ilex, 6w39, 6f4M, 6gU2, I22i

Choosen Targets Class :classified protein, L350, unclassified protein, lyase
Cytodrome.

Acetaminophen is commonly used to relieve pain and reduce fever, making it effective for conditions such as headaches, muscle aches, arthritis, and cold/flu symptoms. It's also used in some cases for pain relief after surgical procedures.

Regarding biomarkers, acetaminophen can affect liver function tests. Specifically, it can lead to elevated levels of serum transaminases (AST and ALT), indicating potential liver damage or toxicity. Therefore, if a biomarker test shows elevated AST and ALT levels, especially in the context of acetaminophen use, it could suggest hepatotoxicity and the need for further evaluation and management. Additionally, acetaminophen overdose can

lead to severe liver damage, which might be reflected in biomarkers such as serum bilirubin levels and international normalized ratio (INR).

LITERATURE REVIEW

EXPLORING DYNAMICS: BOOLEAN NETWORK GRAPH THEORY AND ODE'S

The last twenty years have seen a revolution in the treatment of human diseases as breakthroughs in systems biology have altered our understanding of microbial populations. Since Newton's time, mathematical modeling has been a key component of nearly all scientific discoveries. The preferred way to describe how molecular species abundances depend on one another is through regulatory networks. The fundamental query, though, is still how cellular phenotypes result from these networks' dynamics. For the main reason, differential equation models in biology do not originate from first principles and suffer from improper parameterization, despite their effectiveness in physics and physical chemistry. Discrete time models built on Boolean networks have been developed in response to these difficulties.



A) FUNDAMENTALS OF BOOLEAN NETWORK MODELING IN GRAPH THEORY:

For a probabilistic Boolean network (PBN), a graph-theoretic design approach is suggested. One well-known mathematical model of intricate network systems, such as gene regulatory networks, is the PBN. Boolean functions represent the manner in which binary states interact in Boolean networks. Probabilistically, Boolean functions are switched in PBNs. This paper proposes a simplified representation of a PBN after providing a brief explanation of its polynomial representation. In this instance, the focus

is on the steady value of the predicted value of the state, which is defined by the minimum feedback vertex set of an interaction graph that expresses the interactions between the states. Input selection and stabilization are addressed using this graphical depiction. A biological example is provided to illustrate the suggested strategy.

Since studying the generic aspects of these models does not require assuming any specific functioning or connectedness of the networks, they can be quite intriguing. In this way, RBNs have been used to investigate possible configurations for the emergence of life. RBNs are a very significant topic to study because they are a generalization of cellular automata. Across multiple research lines conducted by various groups, the tutorial offers the state of the art in RBNs and is aimed at a wide audience. We concentrate on studies conducted inside artificial life because we are unable to use up all.

B) LINKING BOOLEAN NETWORK AND ORDINARY DIFFERENTIAL EQUATION (ODE'S) :

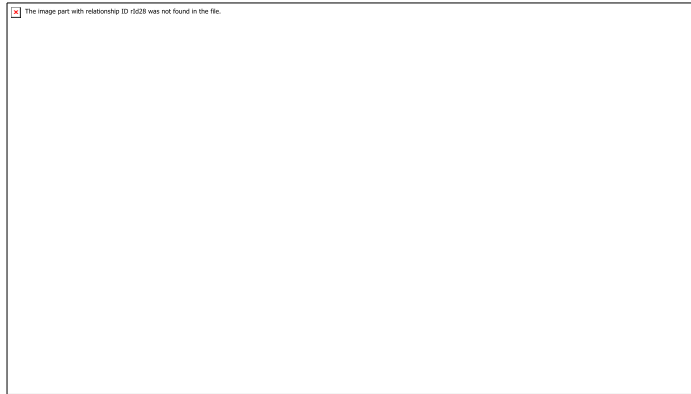
Two alternative methods are used to represent dynamic systems in many domains, including computer science, physics, and biology: Boolean network graph theory and ordinary differential equations (ODEs). The theory of Boolean network graphs deals with discrete dynamical systems, in which each node's state can be either true or false (1 or 0). A system's evolution is dictated by a collection of laws or functions that explain how the states of neighboring nodes affect each node's state. This method works well for simulating asynchronous updates and systems with binary state variables. Conversely, continuous dynamical systems—in which the state variables fluctuate continuously over time—are described by ordinary differential equations, or ODEs.

The rates of change of the variables are connected to their Non-linear systems of differential equations and dynamics Campos, Luis Manuel Braga da CRC Press, 2019 A six-volume set titled Ordinary Differential Equations with Applications to Trajectories and Vibrations includes a second book titled Non-Linear Differential Equations and Dynamical Systems. Collectively, these volumes comprise the fourth installment of the series Mathematics and Physics Applied to Science and Technology. Two chapters (chapters 3 and 4 of the set) make up this second book. Nonlinear differential equations of the first order with variable coefficients are covered in the first chapter. An equation for a first-order differential is equal to a first-order differential in two variables. In addition, differentials with more than two variables and an order greater than one are taken into account. Potential-based vector field representation is one of the applications.

C) DYNAMICAL ANALYSIS OF BIOLOGICAL SYSTEM USING BOOLEAN NETWORKS AND ODE'S:

The constituents of the system become nodes (vertices) and the linkages and interactions between the nodes become edges (links) when a system of interacting components (such as biomolecules) is represented as a network. The edges inside the network are often oriented, signifying the direction of mass transfer or information transmission. Additionally, they can be identified by a positive or negative sign, which signifies activation or inhibition. The biological system's dynamic modeling and structural analysis are based on this network representation. Graph-theoretical metrics like centrality measurements and shortest pathways are used in structural analysis of the network. Continuous or discrete dynamic modeling methodologies are based on the characterization of the molecule abundances by continuous or discrete variables. As emerging techniques, including chaos, dynamical systems, and numerical and symbolic computer systems, blend with and reinforce the classic methods of applied mathematics, there is naturally a great deal of enthusiasm on the research frontier, leading to the establishment of new courses. In order to support the teaching of new courses and address the needs of these advancements, this textbook series was created. TAM's textbooks are appropriate for advanced undergraduate and beginning graduate courses. They are a great addition to the Applied Mathematical Sciences (AMS) collection, which focuses on advanced textbooks and monographs written at the research level.

Preface Examine a differential equation of the first order of the form $x' = f(t, x)$. Throughout elementary school, it's common to feel that Ordinary differential equations, or ODEs, are crucial to the resolution of numerous issues. Because of this, they should be covered in any curriculum that includes science or mathematics. The subject is frequently covered in bits and pieces throughout several courses. In fact, aside from their usage in analytical differential equations courses (where the numerical analyses may be haphazardly applied and inadequately justified), they reappear in the majority of numerical courses, which frequently include a brief crash course that provides an analytical introduction to the subject. Furthermore, some theoretical points seem to be introduced solely to justify.



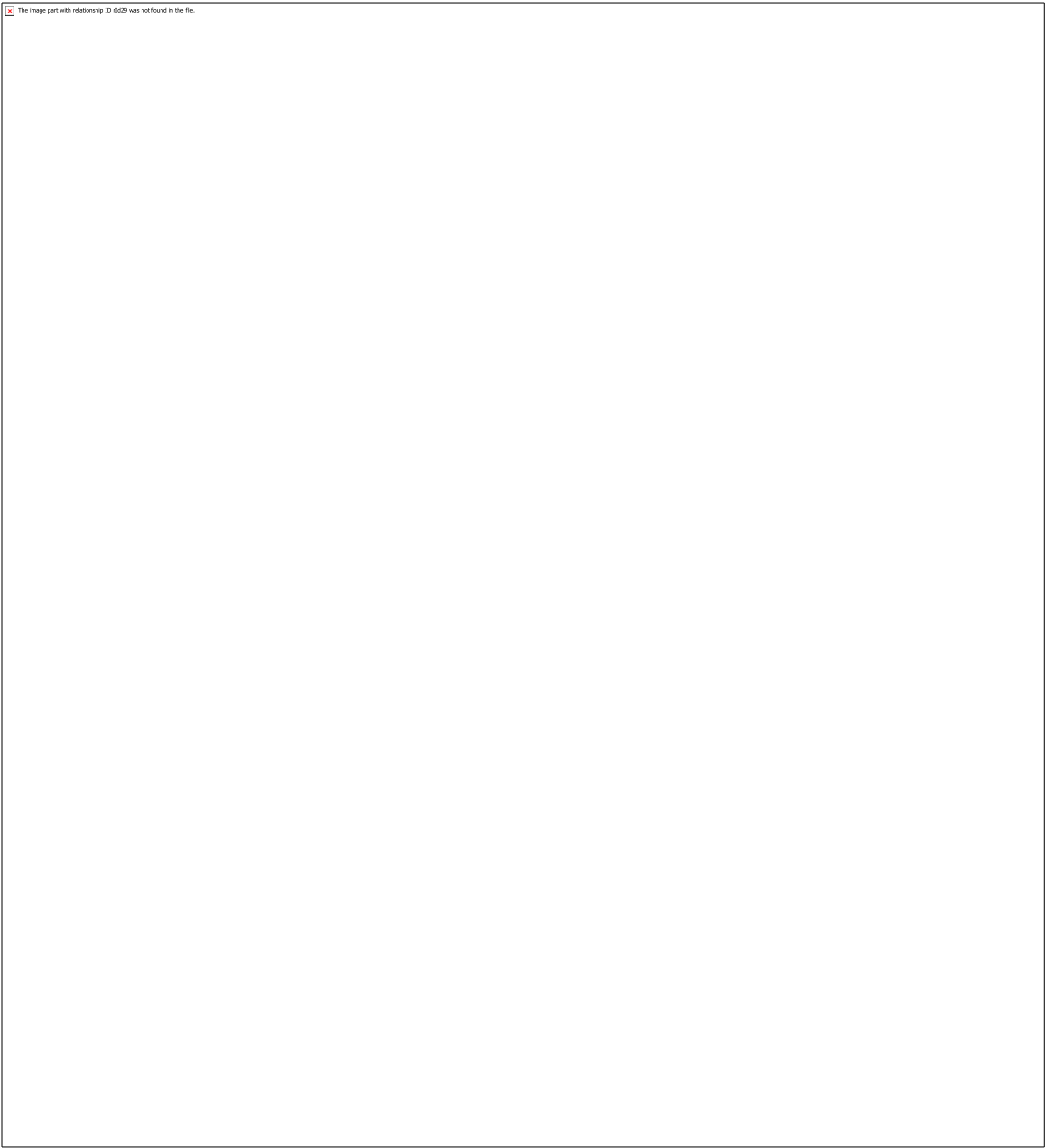
D) APPLICATION AND CHALLENGES IN INTEGRATING BOOLEAN NETWORKS AND ODE'S:

The dynamics of BN are generally linked to complexity since they consist of numerous fundamental components whose behaviors are comparatively simple when compared to the overall system's behaviors. BN are an extension of other pertinent mathematical models that first surfaced as Kauffman networks (KN), which Kauffman proposed in 1969 to model gene regulatory networks, or cellular automata (CA), which were first introduced by Kauffman and were inspired by von Neumann. Wolfram and associates studied CAs to investigate the computational universe. This illustrates how this new paradigm can be used to a variety of scientific fields (mathematics, physics, chemistry, biology, ecology, etc.) and technical fields (computers, artificial intelligence, electronics, circuits, etc.). A leisurely basic differential equations course is an ideal place to get an easy introduction to such concepts. Differential Equations with Applications and Historical Notes, which was specifically prepared for this course, takes great joy in the adventure into the realm of differential equations. An overview of application for ordinary equation John Wiley & Sons Differential equation teaching in the classroom needs to keep up with the times, given the state of industry and technology today. Brannan/Boyce's Differential Equations: An Introduction to Modern Methods and Applications, third edition, is intended for a first-year differential equations course. The mathematics used in Binder Ready Version is congruent with how scientists and engineers utilize it in their daily work. The book highlights a systems approach to the topic and incorporates the use of contemporary science and engineering applications with the usage of modern computing technology. Students are better prepared for the reality of the modern world by emphasizing foundational skills, using technology carefully, and practicing modeling complicated systems.

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Plagiarism Report



MATLABCOURSE

Basedonthe MATLABCertificatethereare17 CourseIhavecompleted

- ✓ AppBuildingOnramp
- ✓ SignalProcessingwithMATLAB
- ✓ ImageProcessingwithMATLAB
- ✓ MATLABProgrammingTechniques
- ✓ MATLABforDataProcessingandVisualization
- ✓ MachineLearningwithMATLAB
- ✓ ImageProcessingOnramp
- ✓ SolvingNonlinearEquationswithMATLAB
- ✓ DeepLearningwithMATLAB
- ✓ StatisticsOnramp
- ✓ MachineLearningOnramp
- ✓ MATLABFundamentals
- ✓ ReinforcementLearningOnramp
- ✓ ComputerVisionOnramp
- ✓ DeepLearningOnramp
- ✓ Object-OrientedProgrammingOnramp
- ✓ MATLABOnramp

AppBuildingOnramp

Through its interactive and self-paced design, the App Building Onramp offers quick video lessons along with practical activities to assist you in learning how to use MATLAB's App Designer to create interactive apps. You will be able

to design, develop, and implement MATLAB apps for a range of uses, from sophisticated data processing procedures to data visualization, after finishing the App Building Onramp.

Grade: 100%

Duration: 1 hr.

SignalProcessingwithMATLAB

Dive into the world of signal processing with MATLAB through our comprehensive Signal Processing Onramp. This interactive course combines theoretical concepts with practical exercises to help you understand and implement various

signal processing techniques using MATLAB. From filtering and spectral analysis to signal visualization, this Onramp will equip you with the skills to analyze and manipulate signals for diverse applications.

Grade: 100%

Duration: 7.5 hrs.

ImageProcessingwithMATLAB

Unlock the power of MATLAB for image processing with our Image Processing Onramp. This hands-

on course is designed to introduce you to the fundamentals of image processing and demonstrate how MATLAB can be used to perform a wide range of image analysis tasks. Through interactive tutorials and real-world examples, you'll learn techniques such as image enhancement, segmentation, and feature extraction, empowering you to manipulate and interpret images effectively.

Grade: 100%

Duration: 11 hrs.

MATLABProgrammingTechniques

Take your MATLAB skills to the next level with our MATLAB Programming Techniques Onramp. This advanced course is tailored for experienced MATLAB users looking to enhance their programming proficiency. From optimization and debugging strategies to advanced data structures and algorithm design, this Onramp covers a wider range of programming techniques to help you write efficient, robust, and maintainable MATLAB.

Grade: 100%

Duration: 16 hrs.

MATLAB for Data Processing and Visualization

It's a great idea to learn MATLAB for data processing and visualization, particularly if you work with numerical data. Here are some things you may learn about data processing and visualization with MATLAB.

These MATLAB skills will enable you to tackle a variety of data processing and visualization jobs, making it an effective tool for data analysis and visualization.

Grade: 100%

Duration: 8 hrs.

Machine Learning with MATLAB

MATLAB is a feature-rich machine learning environment that includes a wealth of built-in tools, functions, and documentation. Gaining knowledge of machine learning in MATLAB will enable you to use a variety of machine learning techniques to solve issues in the real world.

Grade: 100%

Duration: 12 hrs.

ImageProcessingOnramp

With its interactive and self-paced approach, the Image Processing Onramp offers brief video courses together with practical tasks to assist you in comprehending and using MATLAB image processing concepts. You will gain a thorough understanding of image processing principles and methods by finishing the Image Processing Onramp. You will also gain hands-on experience using MATLAB to develop image processing algorithms.

Grade: 100%

Duration: 2 hrs.

SolvingNonlinearEquationswithMATLAB

Unlock the power of MATLAB for solving complex nonlinear equations with the Solving Nonlinear Equations Onramp. This self-paced course is designed to equip you with the skills needed to tackle nonlinear equations efficiently using MATLAB's extensive computational capabilities. Through a series of guided exercises, you'll learn various numerical methods and techniques to find solutions to nonlinear equations in diverse scientific and engineering applications.

Grade: 100%

Duration: 3 hrs.

DeepLearningwithMATLAB

Explore the cutting-edge field of deep learning with MATLAB through our Deep Learning Onramp. This interactive course provides a comprehensive introduction to deep learning concepts and demonstrates how MATLAB can be used to build, train, and deploy deep neural networks. Whether you're new to deep learning or seeking to expand your knowledge, this Onramp will equip you with the skills to tackle complex problems in areas such as image recognition, natural language processing, and more.

Grade: 100%

Duration: 7 hrs.

StatisticsOnramp

Dive into the realm of statistical analysis and data interpretation with the MATLABStatisticsOnramp. This interactive learning experience offers comprehensive coverage of statistical concepts, from basic descriptive statistics to advanced data modeling techniques. By mastering MATLAB's statistical capabilities, you'll be equipped to analyze data, draw meaningful insights, and make informed decisions across various domains.

Grade: 100%

Duration: 3 hrs.

MachineLearningOnramp

Embark on a journey into the exciting world of machine learning with our MachineLearning Onramp. This interactive course provides a hands-on introduction to machine learning concepts and techniques using MATLAB. From classification and regression to clustering and dimensionality reduction, this Onramp covers essential machine learning algorithms and demonstrates how to implement them in MATLAB. By the end of this course, you'll have the skills to build and evaluate machine learning models for a variety of applications.

Grade: 100%

Duration: 2 hrs.

MATLABFundamentals

Learn the essentials of MATLAB programming from scratch with the MATLABFundamentals Onramp. This interactive course is designed for beginners, offering a structured learning path that covers basic MATLAB syntax, data types, control flow, and function writing. Whether you're new to programming or transitioning from another language, this Onramp will lay a solid foundation for your MATLAB journey.

Grade: 100%

Duration: 16 hrs.

Reinforcement Learning Onramp

The Reinforcement Learning Onramp for MATLAB is a thorough introduction course that teaches you how to use MATLAB to build reinforcement learning algorithms and the principles of reinforcement learning.

Grade: 100%

Duration: 2.5 hrs.

Computer Vision Onramp

A great tool for studying computer vision concepts is MATLAB's Computer Vision Onramp. The following is what the Computer Vision Onramp has to offer.

Grade: 100%

Duration: 2 hrs.

Deep Learning Onramp

The Deep Learning Onramp is an interactive, self-paced course that uses MATLAB to teach you how to apply and comprehend deep learning concepts through brief video tutorials and practical activities. After finishing the Deep Learning Onramp, you'll have a firm grasp of the theories and methods behind deep learning in addition to hands-on experience with creating and refining MATLAB deep learning models.

Grade: 100%

Duration: 2 hrs.

Object-Oriented Programming Onramp

Embark on a journey through Object-Oriented Programming (OOP) principles with the MATLAB Object-

Oriented Programming Onramp. This interactive course combines concise video tutorial with hands-on exercises to teach you the fundamentals of OOP in MATLAB. By the end of this Onramp, you'll have a solid understanding of how to leverage OOP concepts to design modular and reusable code in MATLAB.

Grade: 100%

Duration: 2 hrs.

MATLAB Onramp

With a series of practical tasks, the MATLAB Onramp is an interactive lesson that teaches you the fundamentals of MATLAB.

The MATLAB Onramp is an interactive, self-paced learning tool that includes brief video presentations and practical tasks to support comprehension.

Even if you have no prior MATLAB expertise, it's an excellent way to get started with the language.

Grade: A

Duration: 2 hrs.

Skills that I gained from MATLAB

➤ **Programming proficiency** I developed a strong understanding of MATLAB'S Syntax, data structures, and programming logic, enabled me to write Efficient and effective code.

➤ **Data Analysis:** I learned various techniques for importing, cleaning, and Analyzing data, allowed me to extract valuable insights and patterns from

Datasets.

➤ **Visualization:** I gained proficiency in creating insightful visualizations using MATLAB'S plotting functions, enabled me to present data in a clear and Understandable manner.

➤ **Problem Solving:** I honed problem-solving skills by tackling various challenges And projects in MATLAB, equipped real-world problems in scientific and Engine.

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