

PROFESSIONAL TRAINING REPORT

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Submitted in partial fulfillment of the requirements for the award of
Master of Science Degree in Bioinformatics and Data Science

By

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SATHYABAMA

**INSTITUTE OF SCIENCE AND TECHNOLOGY
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BONAFIDE CERTIFICATE

This is to certify that professional training report is the bonafide, work of ABITHA S (43739039). Who underwent the professional training from September 2024 to November 2024

INTERNAL GUIDE

EXTERNAL GUIDE (If Applicable)

HEAD OF THE DEPARTMENT

Submitted for viva Examination held on:

INTERNAL EXAMINER

EXTERNAL EXAMINER

DECLARATION

I ABITHA S (43739039) hereby declare that the Internship report entitled "DEEP LEARNING" done by me under the guidance of Mrs.R. SUDHA, at SATHYABAMA INSTITUTE OF SCIENCE AND TECHNOLOGY is submitted in partial fulfillment of the requirements for the award of Master of Science degrees in Bioinformatics and Data Science.

DATE:

ABITHA S

PLACE:

SIGNATURE OF THE CANDIDATE

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DEEP LEARNING INTERNSHIP REPORT

CHAPTER:1

1.1 ABSTRACT

This report explores the complex realm of deep learning neural networks, examining how they're applied, improved, and their potential impact across various fields. By combining theoretical exploration, hands-on experiments, and real-world examples, this study seeks to provide a thorough understanding of deep learning neural networks and their role in shaping the future of artificial intelligence. In my investigation of deep learning neural networks, I aim to grasp their practical uses and their influence on different domains. Through theoretical study, practical experimentation, and real-life instances, I intend to share insights into deep learning and its impact on the development of artificial intelligence.

CHAPTER:2

2.1 INTRODUCTION

Deep learning is based on the branch of machine learning, which is a subset of artificial intelligence. Since neural networks imitate the human brain and so deep learning will do. In deep learning, nothing is programmed explicitly. Basically, it is a machine learning class that makes use of numerous nonlinear processing units so as to perform feature extraction as well as transformation. The output from each preceding layer is taken as input by each one of the successive layers. Deep learning models are capable enough to focus on the accurate features themselves by requiring a little guidance from the programmer and are very helpful in solving out the problem of dimensionality. Deep learning algorithms are used, especially when we have a huge no of inputs and outputs. Since deep learning has been evolved by the machine learning, which itself is a subset of artificial intelligence and as the idea behind the artificial intelligence is to mimic the human behavior

"The idea of deep learning to build such algorithm that can mimic the brain". Deep learning is implemented with the help of Neural Networks, and the idea behind the motivation of Neural Network is the biological neurons, which is nothing but a brain cell.

CHAPTER:3

3.1 OBJECTIVE

As a student learning deep learning, my primary objective is to develop a comprehensive understanding of the principles, techniques, and applications of deep learning in artificial intelligence. Specifically, I aim to:

1. Grasp the fundamental concepts underlying neural networks, including their architectures, activation functions, and training algorithms.
2. Explore a diverse range of deep learning applications, including image recognition, natural language processing, and reinforcement learning, through hands-on projects and case studies.
3. Collaborate with peers and mentors to tackle challenging problems and engage in discussions to deepen my understanding of advanced topics in deep learning research.
4. Develop critical thinking and problem-solving skills by independently investigating and experimenting with novel techniques and approaches in deep learning.
5. Build a portfolio of projects and research work that demonstrates my proficiency and expertise in deep learning.
6. Stay updated on the latest developments and advancements in deep learning through continuous learning, participation in seminars, workshops, and online communities, and by actively following research publications and industry trends.
7. Overall, my objective is to emerge from my deep learning studies with a strong foundation of theoretical knowledge, practical skills, and a passion for leveraging deep learning to tackle real-world challenges and contribute to advancements in artificial intelligence.

3.2 SCOPE OF DL

Deep learning (DL) offers several advantages over traditional machine learning (ML) techniques and contributes significantly to the broader field of artificial intelligence (AI) in the following ways:

1. **Automated Feature Extraction:** In traditional ML, feature engineering is a crucial step where domain knowledge is used to manually extract relevant features from raw data.
2. **Handling Complex Data:** DL excels in processing and learning from large volumes of complex data, such as images, text, and audio. Deep neural networks can capture intricate patterns and relationships within high-dimensional data, enabling more accurate and robust predictions compared to traditional ML algorithms.
3. **Improved Accuracy and Performance:** DL models, especially deep neural networks with multiple layers, have demonstrated superior performance in various tasks, including image recognition, natural language processing, and speech recognition.
4. **Scalability:** DL algorithms are highly scalable and can handle large-scale datasets and complex models efficiently, thanks to advancements in hardware (e.g., GPUs, TPUs) and software frameworks.
5. **Transfer Learning and Fine-tuning:** DL facilitates transfer learning, where pre-trained models trained on large datasets can be fine-tuned on smaller, domain-specific datasets to adapt to new tasks.
6. **Advancements in AI Research:** DL has significantly advanced the field of AI by enabling breakthroughs in areas such as computer vision, natural language understanding, and autonomous systems.

In summary, deep learning offers several benefits over traditional machine learning techniques and plays a crucial role in advancing the broader field of artificial intelligence. Its ability to automatically learn hierarchical representations of data, handle complex datasets, achieve high accuracy and scalability, and facilitate transfer learning makes deep learning a powerful tool for solving a wide range of AI problems

CHAPTER:4

EXPERIMENTAL, METHODS AND ALGORITHMS USED IN DL

4.1 The Importance of layers in DL

In deep learning, layers are like building blocks that help neural networks understand and work with data. Each layer has a specific job: the input layer gets the raw data, hidden layers transform it in different ways, and the output layer gives us the final result. For example, if we're working with pictures, convolutional layers help find important features, like edges or shapes, while recurrent layers handle things like sequences or patterns in text. Finally, the output layer gives us the answer we're looking for, whether it's guessing what's in a picture or predicting a number. By using these layers together, neural networks can learn from tricky data and make smart decisions.

Here's an overview of some common layers I have learnt during my internship in deep learning:

1. **Input Layer:** The input layer receives the raw data and passes it to the subsequent layers for processing. Each neuron in this layer represents a feature of the input data.
2. **Hidden Layers:** Hidden layers are intermediary layers between the input and output layers. They perform transformations on the input data through a series of weighted connections and activation functions. Multiple hidden layers allow the network to learn complex patterns and representations.
3. **Convolutional Layers (Convolutional Neural Networks - CNNs):** Convolutional layers are specialized layers designed for processing grid-like data, such as images. They consist of filters (kernels) that slide over the input data, extracting spatial features through convolution operations. Convolutional layers are crucial for tasks like image recognition and object detection.

4. **Pooling Layers:** Pooling layers are often used alongside convolutional layers to reduce the spatial dimensions of the feature maps, thus decreasing computation and controlling overfitting.
5. **Recurrent Layers (Recurrent Neural Networks - RNNs):** Recurrent layers are designed to process sequential data, such as time series or natural language. They maintain an internal state (hidden state) that captures temporal dependencies across sequential inputs. Long Short-Term Memory (LSTM) and Gated Recurrent Unit (GRU) are popular recurrent layer architectures that address the vanishing gradient problem.
6. **Dense Layers (Fully Connected Layers):** Dense layers are traditional feedforward layers where each neuron is connected to every neuron in the previous and subsequent layers. They perform linear transformations on the input data, followed by activation functions, and are commonly used in the final layers of neural networks for classification or regression tasks.
7. **Batch Normalization Layers:** Batch normalization layers are inserted into neural networks to normalize the activations of each layer.
8. **Dropout Layers:** Dropout layers are used to prevent overfitting by randomly deactivating a fraction of neurons during training, forcing the network to learn redundant representations and improving generalization performance.

Understanding and effectively utilizing these layers are essential for designing and training deep learning models tailored to specific tasks and datasets. Each layer type contributes unique capabilities to the network architecture, allowing for flexibility and adaptability across various domains and applications.

CHAPTER:5

The algorithms used in DL

In deep learning, optimization techniques are crucial for training neural networks to understand patterns in data accurately. Backpropagation is a fundamental algorithm where we figure out how to adjust network parameters to minimize errors. Stochastic Gradient Descent (SGD) helps speed up training by adjusting parameters based on smaller chunks of data instead of the whole set. By using these techniques alongside different layers in neural networks, we can train them to recognize images, understand language, and do many other tasks well. This helps advance deep learning in various fields

Types of Algorithms used in Deep Learning

1. Convolutional Neural Networks (CNNs)
2. Long Short Term_Memory Networks (LSTMs)
3. Recurrent Neural Networks (RNNs)
4. Generative Adversarial Networks (GANs)
5. Radial Basis Function Networks (RBFNs)
6. Multilayer Perceptron (MLPs)
7. Self Organizing Maps (SOMs)
8. Deep Belief Networks (DBNs)
9. Restricted Boltzmann Machines(RBMs)
10. Autoencoders

Deep learning algorithms work with almost any kind of data and require large amounts of computing power and information to solve complicated issues. I have listed some of the algorithm, I have covered during my learning,

5.1 Convolutional Neural Networks (CNNs)

Convolutional Neural Networks (CNNs) are a pivotal class of deep neural networks designed specifically for processing grid-like data, notably images, revolutionizing computer vision tasks. Utilizing convolutional layers, CNNs extract features through filters applied across input data, capturing intricate patterns such as edges and textures. Subsequent pooling layers feature maps, reducing spatial dimensions while retaining crucial information. Activation functions introduce non-linearity, enhancing the network's capacity to model complex relationships. Fully connected layers further process extracted features for classification or regression tasks. CNNs are trained via backpropagation and optimization algorithms, adjusting weights and biases to minimize a defined loss function. Transfer learning, leveraging pre-trained models, accelerates training and enhances performance. With their hierarchical structure and automatic feature learning capabilities, CNNs have become indispensable in tasks such as image recognition, object detection, and classification, advancing artificial intelligence's capabilities in understanding and interpreting visual data.

5.2 Long Short Term Memory Networks (LSTMs)

Long Short-Term Memory Networks (LSTMs) are a type of recurrent neural network (RNN) designed to address the vanishing gradient problem and capture long-term dependencies in sequential data. Unlike traditional RNNs, LSTMs have a more complex architecture consisting of memory cells, input gates, forget gates, and output gates, allowing them to selectively retain or forget information over multiple time steps. This architecture enables LSTMs to effectively capture and remember relevant information from past inputs while filtering out noise and irrelevant information, making them particularly well-suited for tasks such as speech recognition, natural language processing, and time series prediction. LSTMs have become a cornerstone of deep learning applications involving sequential data due to their ability to handle long-range dependencies and mitigate the challenges associated with training recurrent neural networks on sequences of varying lengths.

5.3 Recurrent Neural Networks (RNNs)

Recurrent Neural Networks (RNNs) are a class of artificial neural networks designed to effectively model sequential data by incorporating feedback loops within the network architecture. Unlike traditional feedforward neural networks, RNNs possess connections that allow information to persist over time, enabling them to capture temporal dependencies in sequential data. This unique architecture makes RNNs well-suited for tasks such as natural language processing, time series analysis, speech recognition, and handwriting recognition. One key feature of RNNs is their ability to process input sequences of variable length and produce output sequences of varying lengths, making them flexible and adaptable to a wide range of applications. However, traditional RNNs suffer from the vanishing gradient problem, which limits their ability to capture long-term dependencies in sequences. To address this issue, variants of RNNs, such as Long Short-Term Memory (LSTM) networks and Gated Recurrent Units (GRUs), have been developed, incorporating specialized mechanisms to better preserve and update information over long sequences. These advancements have significantly enhanced the effectiveness of RNNs in modeling sequential data and have led to their widespread adoption in various domains.

5.4 Generative Adversarial Networks (GANs)

GANs consist of two neural networks, the generator and the discriminator, which are trained simultaneously through a competitive process. The generator learns to generate realistic data samples, such as images or audio, from random noise, while the discriminator learns to distinguish between real and fake samples. Through adversarial training, the generator gradually improves its ability to generate convincing samples, while the discriminator becomes more adept at detecting fake ones. GANs have demonstrated remarkable success in generating high-quality, realistic data samples across various domains, including image synthesis, video generation, and text generation. However, training GANs can be challenging due to issues such as mode collapse, instability, and convergence difficulties, which require careful design and optimization strategies. Despite

these challenges, GANs have become a powerful tool for creative applications in art, entertainment, and data generation, driving innovations in AI research and applications.

5.5 Multilayer Perceptron's (MLPs)

Multilayer Perceptron (MLPs) represent a class of feedforward artificial neural networks characterized by multiple layers of interconnected neurons, including an input layer, one or more hidden layers, and an output layer. MLPs serve as universal function approximators, capable of learning complex nonlinear relationships within data. Each neuron in an MLP applies a nonlinear activation function to the weighted sum of its inputs, enabling the network to model intricate patterns and features within the data. Training an MLP involves adjusting the weights and biases of the network using optimization algorithms such as gradient descent and backpropagation, which minimize the error between the predicted and actual outputs during the training process. MLPs have been successfully applied in various domains, including classification, regression, and pattern recognition tasks, and they continue to be widely used in machine learning and artificial intelligence applications.

5.7 Restricted Boltzmann Machines (RBM)

Restricted Boltzmann Machines (RBMs) are unsupervised deep learning models that serve as building blocks for more complex neural networks. They consist of a layer of visible units representing input data and a layer of hidden units that capture higher-level features through a process of probabilistic inference. RBMs learn to reconstruct input data by adjusting the weights between visible and hidden units using a training algorithm called Contrastive Divergence. They are particularly effective in modeling complex data distributions and extracting meaningful features from high-dimensional input spaces. RBMs have found applications in various domains, including dimensionality reduction, collaborative filtering, and feature learning in deep neural networks. Their ability to capture intricate patterns and relationships within data makes them valuable tools in the arsenal of deep learning techniques.

5.8 Autoencoders

Autoencoders are a type of neural network architecture widely used in unsupervised learning tasks within the realm of deep learning. Operating on an encoder-decoder framework, they aim to reconstruct input data by first compressing it into a latent space representation (encoding) and then reconstructing it back to its original form (decoding). The network learns to minimize the reconstruction error, effectively capturing the most salient features of the input data. Autoencoders have diverse applications, including data denoising, dimensionality reduction, and anomaly detection. Variants such as denoising autoencoders, variational autoencoders, and sparse autoencoders offer specialized capabilities, making autoencoders versatile tools for learning efficient representations of complex data structures.

CHAPTER:6

6.1 APPLICATIONS

1. Image Recognition and Classification: Deep learning models, especially convolutional neural networks (CNNs), are widely used for tasks such as object detection, facial recognition, medical image analysis, and autonomous driving.
2. Natural Language Processing (NLP): Deep learning techniques, including recurrent neural networks (RNNs) and transformers, are used for tasks such as language translation, sentiment analysis, text summarization, and chatbots.
3. Speech Recognition and Generation: Deep learning models, such as recurrent neural networks (RNNs) and convolutional neural networks (CNNs), are employed in speech recognition systems like virtual assistants (e.g., Siri, Alexa) and speech synthesis systems (e.g., text-to-speech).
4. Recommendation Systems: Deep learning algorithms, particularly neural collaborative filtering and deep autoencoders, are used in recommendation systems for, streaming services, and social media platforms.
5. Healthcare: Deep learning is utilized in medical imaging for tasks like disease diagnosis, tumor detection, and medical image segmentation. It's also used in genomics, drug discovery, personalized medicine, and health monitoring.
6. Autonomous Vehicles: Deep learning plays a crucial role in autonomous vehicles for tasks such as object detection, lane detection, pedestrian detection, and decision-making based on sensor data (lidar, radar, cameras).
7. Finance: Deep learning is used in finance for tasks like fraud detection, risk assessment, algorithmic trading, credit scoring, and customer relationship management.

8. Gaming: Deep learning techniques, such as reinforcement learning, are used in game AI for tasks like game strategy optimization, opponent modeling, and game environment simulation.
9. Manufacturing and Industry: Deep learning is applied in manufacturing for predictive maintenance, quality control, anomaly detection, and process optimization.
10. Agriculture: Deep learning is used in agriculture for tasks like crop monitoring, yield prediction, disease detection in plants, and precision agriculture.

These applications demonstrate the versatility and effectiveness of deep learning across a wide range of domains, contributing to advancements and innovations in various fields.

CHAPTER:7

7.1 LEARNING OUTCOME

1. **Hands-on Skill Development:** Through practical application, I acquired valuable skills in implementing deep learning techniques using frameworks like TensorFlow and PyTorch, mastering data preprocessing, model training, and evaluation.
2. **Deepened Conceptual Understanding:** The internship deepened my understanding of core concepts such as neural network architectures, activation functions, and optimization algorithms.
3. **Effective Problem-Solving:** I honed my problem-solving abilities by tackling complex challenges in deep learning, from selecting appropriate model architectures to optimizing hyperparameters and enhancing model performance.
4. **Real-World Application:** By working on real-world datasets and projects, I gained practical insights into the application of deep learning across diverse domains like image recognition, natural language processing, and time series analysis.
5. **Enhanced Collaboration and Communication:** Collaborating with peers and mentors, I improved my teamwork and communication skills, effectively conveying ideas and presenting findings with confidence.
6. **Embracing Continuous Learning:** The internship instilled in me a commitment to continuous learning and staying updated with the latest advancements in deep learning, ensuring adaptability and readiness for future challenges.
7. **Preparation for Career Success:** Armed with a portfolio of projects and industry experience, I feel well-prepared to pursue career opportunities in artificial intelligence, machine learning, data science, or research, confident in my ability to make meaningful contributions to the field.

7.2 SUMMARY AND CONCLUSION

Deep learning continues to gain popularity owing to its highly accurate results, ability to make predictions on unstructured datasets, and provide useful insights about the datasets. While often confused with machine learning and artificial intelligence, it is specifically based on artificial neural networks. And although its use in business is still at a nascent stage, it holds much promise as it is already transforming several industries. It's likely that deep learning will continue to evolve and have a significant impact on our society in the future. The deep learning internship proved to be a valuable and fulfilling journey, empowering me with essential skills, expertise, and assurance to embark on a career in this dynamic and swiftly evolving domain. It laid a strong groundwork for ongoing development and advancement, and I am appreciative of the chance to have contributed to and benefited from this enriching opportunity.



DEEP LEARNING COURSE COMPLITON CERTIFICATE

MINI PROJECT

"Integrated Analysis of Gene Expression Profiles in Osteoporosis: Identification of Hub Genes, Biomarkers, and Drug Targets Through Computational Approaches"

CHAPTER:1

1.1 ABSTRACT

Osteoporosis, characterized by reduced bone mineral density and increased fracture risk, is a prevalent skeletal disorder with significant public health implications. In this study, we conducted a comprehensive analysis of gene expression profiles associated with osteoporosis to identify potential biomarkers, hub genes, and drug targets using computational approaches. Gene expression data from osteoporotic and healthy control samples were obtained from public repositories and analyzed using bioinformatics tools. Differential expression analysis revealed a set of dysregulated genes associated with osteoporosis pathogenesis. Weighted gene co-expression network analysis (WGCNA) identified modules of co-expressed genes, from which hub genes were extracted based on their connectivity within the network. Functional enrichment analysis of hub genes revealed biological processes and pathways implicated in osteoporosis, providing insights into underlying molecular mechanisms. Additionally, drug target prediction and drug repurposing were performed using molecular docking studies to identify potential therapeutic agents for osteoporosis treatment. Our findings highlight candidate biomarkers and drug targets for further experimental validation and therapeutic development, demonstrating the utility of computational approaches in unraveling the complexities of osteoporosis and facilitating drug discovery efforts.

1.2 Background of Study

As someone deeply intrigued by osteoporosis, I find it fascinating to explore this common skeletal disorder characterized by reduced bone density and increased fracture risk, impacting millions worldwide. Recognizing the multifaceted nature of its causes, including genetic, hormonal, environmental, and lifestyle factors, underscores the complexity of osteoporosis. Leveraging advanced gene expression analysis techniques, such as microarray and RNA sequencing, offers valuable insights into the molecular underpinnings of this condition. By delving into computational methods like weighted gene co-expression network analysis (WGCNA) and functional enrichment analysis, I aim to uncover pivotal hub genes and potential biomarkers, shedding light on key regulatory pathways. Moreover, I'm excited to employ in silico drug discovery approaches, including drug target prediction and repurposing studies, to identify novel therapeutic avenues for osteoporosis treatment. Through this research, I endeavor to deepen our understanding of osteoporosis pathophysiology and contribute to the development of effective therapeutic interventions for this prevalent skeletal disorder.

1.3 LITERATURE SURVEY

I embarked on a journey through the extensive literature surrounding this complex skeletal disorder. My exploration covered several key areas:

1. Understanding the Global Impact: Delving into epidemiological studies, I gained insight into the widespread prevalence of osteoporosis and its profound impact on individuals and healthcare systems worldwide.
2. Exploring Genetic Influences: Recognizing the importance of genetics in osteoporosis, I delved into genome-wide association studies (GWAS) and genetic variant analyses to uncover the genetic factors contributing to bone mineral density (BMD) and fracture risk.

3. Embracing Omics Technologies: Immersing myself in the realm of omics technologies, including microarray and RNA sequencing (RNA-seq), I uncovered the intricate gene expression patterns associated with osteoporosis, revealing potential biomarkers and molecular pathways involved in disease progression.
4. Uncovering Hub Genes and Biomarkers: Through computational analyses like weighted gene co-expression network analysis, I identified hub genes and biomarkers that serve as crucial regulatory nodes in the complex network of gene associated with osteoporosis, providing valuable insights into its underlying molecular mechanisms.
5. Pursuing Drug Discovery Avenues: With a keen interest in therapeutic interventions, I explored in silico drug discovery methods, including drug target prediction and repurposing studies, to uncover novel treatment options and repurpose existing drugs for osteoporosis management, contributing to the advancement of therapeutic strategies in the field.

By immersing myself in the literature surrounding osteoporosis, I aimed to gain a comprehensive understanding of the disease and its complexities, laying the groundwork for the analyses and interpretations conducted in this study.

CHAPTER:2

2.1 AIM AND SCOPE THE INVESTIGATION

The aim of this project is to leverage computational methods to analyze gene expression profiles associated with osteoporosis, identify hub genes and potential biomarkers, elucidate underlying molecular mechanisms, and explore drug targets and repurposing opportunities.

1. **Data Collection and Preprocessing:** We will gather publicly available gene expression data sets associated with osteoporosis from repositories such as GEO and Array Express. These data sets will undergo rigorous preprocessing steps to ensure data quality and consistency.
2. **Differential Expression Analysis:** Using bioinformatics tools, we will perform differential expression analysis to identify genes that are differentially expressed between osteoporotic and healthy control samples, providing insights into dysregulated molecular pathways in osteoporosis.
3. **Weighted Gene Co-Expression Network Analysis (WGCNA):** Employing WGCNA, we will construct gene co-expression networks and identify modules of co-expressed genes associated with osteoporosis. Hub genes within these modules will be prioritized as potential biomarkers and key regulators of osteoporosis pathophysiology.
4. **Functional Enrichment Analysis:** Functional enrichment analysis will be conducted to elucidate the biological processes and pathways enriched among differentially expressed genes and hub genes, providing mechanistic insights into osteoporosis development and progression.
5. **Drug Target Prediction and Repurposing:** In silico drug discovery approaches, including drug target prediction and drug repurposing studies using molecular docking techniques, will be employed to identify potential therapeutic targets and repurpose existing drugs for osteoporosis treatment.

CHAPTER:3

EXPERIMENTAL MATERIALS AND METHODS

3.1 Data Collection:

The Gene Expression Omnibus (GEO) [18], an online public database made available by National Center for Biotechnology Information (NCBI) in 2000, is currently one of the most comprehensive gene expression databases. The mRNA expression profile microarray data were obtained from the GEO dataset: [GSE7158](#) series included 12 OP (low bone density) samples and 14 NC (high bone density) samples

3.2 My Approach to PPI Network Construction:

The geo2r analysis was performed and the statistical methods are applied to filter the upregulated genes and downregulated genes by filtering fold change value greater than 1 and P value less than or equal to 0.05, the top 10 genes are considered (fig.2). I took only the upregulated genes and began by sourcing protein-protein interaction data relevant to osteoporosis from reliable databases like STRING or Bio GRID. (Fig.2)

Using Cytoscape, a versatile bioinformatics tool, I imported the PPI data and visually represented the network, with nodes representing proteins and edges denoting their interactions.

3.3 Identification of Hub Genes through CytoHubba:

Leveraging the CytoHubba plugin within Cytoscape, I applied various centrality algorithms, such as Degree and Betweenness, to pinpoint hub genes within the PPI network. Based on centrality scores computed by CytoHubba algorithms, I meticulously curated a list of hub genes **CDC5L, CUL1, CXCL10, EIF2AK2, POLR2B, PTEN, DHFR, STAT1, and TBP**, focusing on those exhibiting the highest connectivity and influence within the network. To ascertain the biological significance of identified hub genes, I conducted functional annotations and enrichment analyses, shedding light on their potential roles in osteoporosis pathophysiology. I meticulously cross-referenced the identified hub genes with existing literature and databases, ensuring their relevance to osteoporosis and bone metabolism and validating their candidacy as potential biomarkers and therapeutic targets

3.4 RESULT

DEGs between low bone mineral density (OP) and high bone mineral density (NC)

I used the parameter value of $p < 0.05$, $|\log(2) \text{ FC}| > 1.5$ to preprocess data sets [GSE7158](#) and I identified 600 up-regulated and 565 down-regulated genes. The volcano diagram for all genes and the expression heatmap of the top 10 DEGs (Fig.2). The No. of Nodes and Edges are found to be 156 and 75.

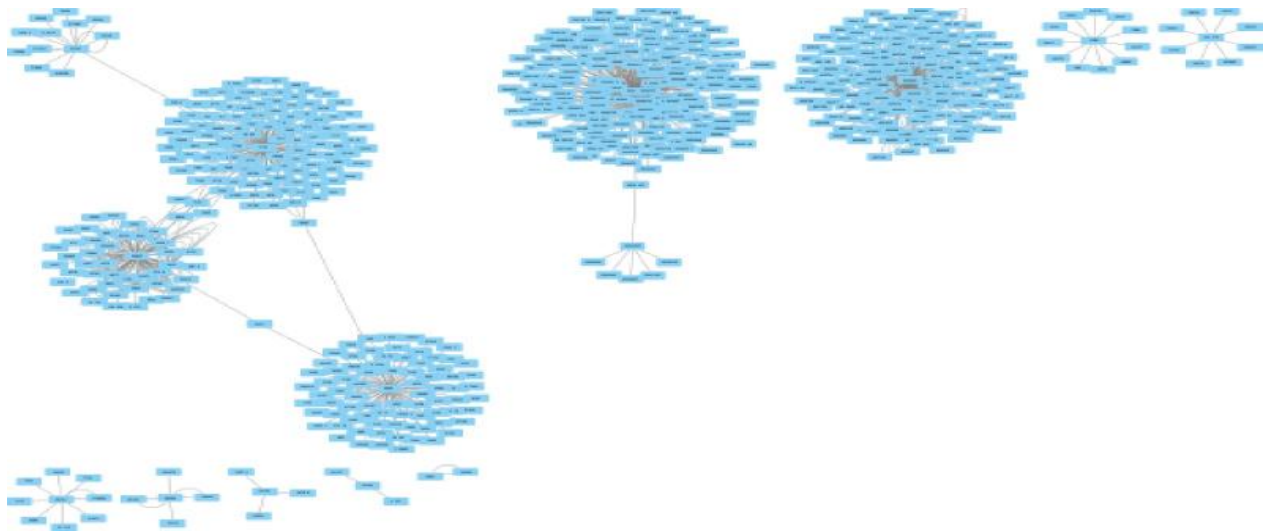
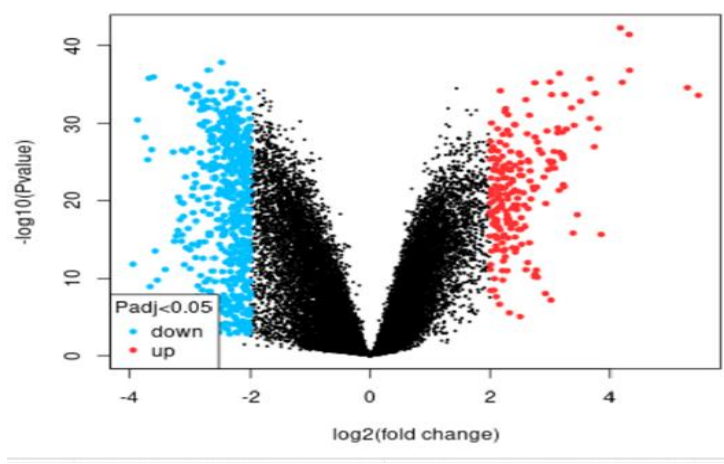


Fig.1: DIFFERENTIAL GENE EXPRESSION NETWORK FROM CYTOSCAPE



GSE7158; Normal vs diseased

Fig:2 VALCANO PLOT FROM GEO2R ANALYSIS

CHAPTER:4

4.1 Identification of Biomarker:

- Hub Gene Selection: After thorough analysis of the protein-protein interaction (PPI) network, DHFR emerged as a promising candidate with high centrality and relevance to osteoporosis. This gene was selected as a potential biomarker due to its critical role in the disease pathway and its potential utility in diagnostic or therapeutic applications.
- Biomarker Validation: Extensive literature review and validation studies were conducted to corroborate the significance of the selected gene as a biomarker for osteoporosis. Its association with the disease phenotype and its potential as a diagnostic or prognostic marker were carefully evaluated to ensure its suitability for further investigation.

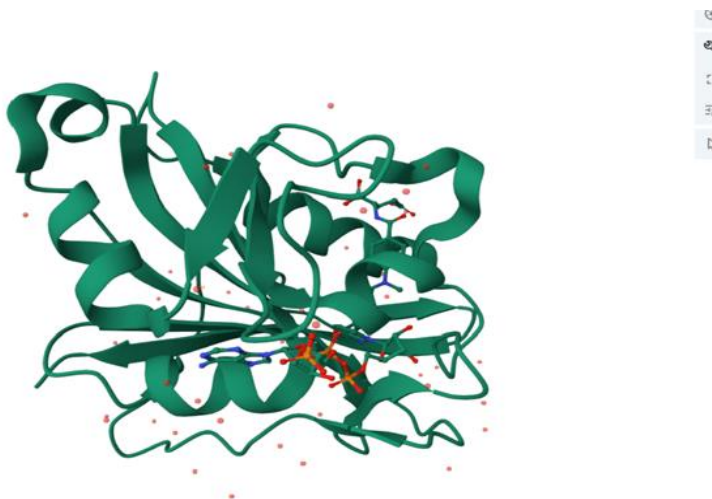


Fig.3: THE DRUG ALONG WITH THE BIOMARKER(DHFR) COMPLEX

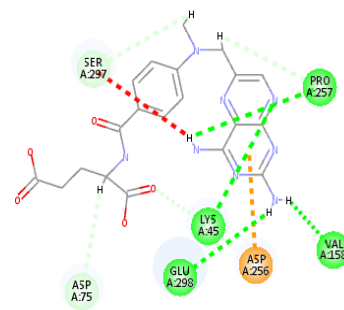
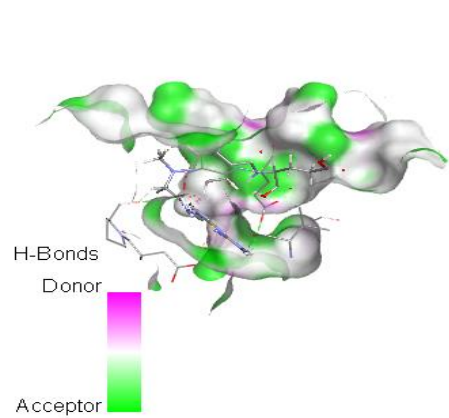
4.2 Drug Target Exploration:

- Biomarker-Associated Drug Search: Leveraging bioinformatics tools and databases, we conducted a comprehensive search for drugs targeting the identified biomarker. Specifically, we explored drug databases such as the Protein Data Bank (PDB) to identify small molecules or ligands known to interact with the biomarker protein.
- Drug Selection Criteria: Criteria such as binding affinity, specificity, and availability of structural information were considered in the selection of the drug for molecular docking studies. Emphasis was placed on drugs with documented therapeutic relevance to osteoporosis or related bone disorders.

4.3 Molecular Docking Studies:

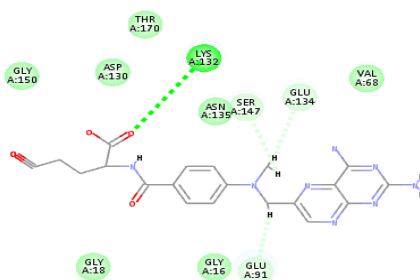
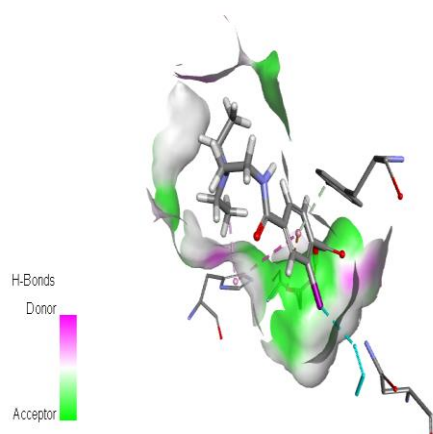
- Structural Retrieval: The three-dimensional structures of both the selected drug and the biomarker protein were retrieved from relevant databases, such as PubChem for the drug and the Protein Data Bank (PDB) for the biomarker protein.
- Docking Protocol: Molecular docking simulations were performed using discovery studios tools to predict the binding interactions between the drug and the biomarker protein. Various docking algorithms and scoring functions were employed to assess the stability and strength of the predicted drug-protein complexes.
- Analysis and Interpretation: The docking results were analyzed to identify potential binding sites, hydrogen bonds, and other interactions between the drug and the biomarker protein. The predicted binding affinity and binding mode provided valuable insights into the feasibility and efficacy of the drug as a potential therapeutic agent for osteoporosis.

THE MOLECULAR DOCKING RESULTS ARE GIVEN BELOW (Fig:3):



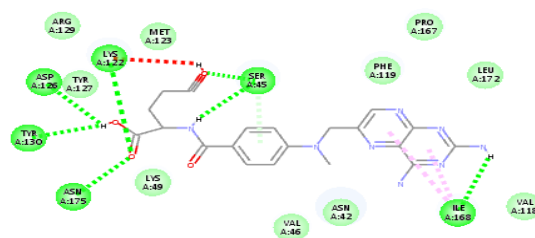
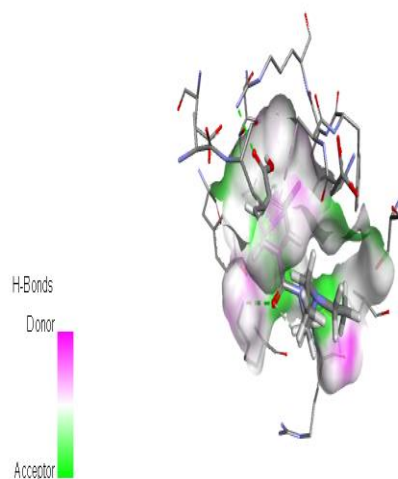
Interactions

- Conventional Hydrogen Bond
- Carbon Hydrogen Bond
- Unfavorable Donor-Donor
- Pi-Anion



Interactions

- van der Waals
- Conventional Hydrogen Bond
- Carbon Hydrogen Bond



Interactions

- van der Waals
- Conventional Hydrogen Bond
- Carbon Hydrogen Bond
- Unfavorable Donor-Donor
- Pi-Donor Hydrogen Bond
- Pi-Alkyl

CHAPTER:5

RESULT

The drug Methotrexate was studied in SwissTarget and over 100 targets were predicted upon which 5 alone with high probability is selected and studied in Cytoscape and Cytohubba and the hub genes are found to be AOS1, CHK1, Lag, PART and SFN, As we dock the drug Methotrexate with these hub genes, the drug interacts with AOS1, CHK1 and SFN and their interaction and their significance are studied.

INTERPRETATION

The domain region of 346 in the A chain of AOS1(Sumo E1 activating enzyme) is reacting with the drug Methotrexate that has a dock core of 65.367 on the residue Arginine 182. It is a key residue on the active site of SAE1, understanding the interaction involving arginine 182 is crucial that the modification or inhibitors designed to interact with this residue could potentially disturb with the enzyme's function, offering therapeutic opportunities for the conditions influenced by abnormal SUMOLYLATION.

The domain region of 276 in A chain of CHK1(checkpoint Kinase1) is reacting with the drug with dock score of 68.63 at the residue Lysin 132, It is a vital protein in cell cycle regulation and DNA damage responses. Modifying or targeting lysine 132 could influence the protein's structure, function or interactions, offering therapeutic opportunities for conditions related to the DNA synthesis and halt's target protein's activity. The significance pf Methotrexate lies on DNA damage response pathways, cancer calls with impaired CHK1function may be more susceptible to Methotrexate induced cell death.

The domain region of 168 in the A chain of SFN reacts with the drug Methotrexate and it has a dock score of 88.966 from the residue serine 45. In the drug design targeting SNF, the role of serine 45 is essential. Modifications inhibitors designed to interact with this residue could potentially modulate the channel's offering therapeutic opportunities for conditions influenced by aberrant sodium channel function, such as epilepsy or pain

disorder. the drug Methotrexate a chemotherapy drug, inhibits DNA synthesis and cell proliferation. The SNF function in cell cycle regulation may affect cancer cell's response to Methotrexate.

CONCLUSION

In conclusion, this study represents a comprehensive exploration of computational methods for the identification of biomarkers, drug targets, and potential therapeutic agents for osteoporosis. Through the integration of network analysis, biomarker identification, and molecular docking studies, we have made significant strides towards understanding the molecular mechanisms underlying osteoporosis and identifying novel avenues for therapeutic intervention.

The identification of a promising biomarker and associated drug targets offers promising prospects for the development of personalized diagnostics and targeted therapies for osteoporosis. While further experimental validation is warranted, the insights gained from this study pave the way for future research efforts aimed at addressing the unmet clinical needs in osteoporosis management. Overall, this project underscores the potential of computational approaches in accelerating drug discovery and personalized medicine in the field of skeletal disorders, with implications for improving patient outcomes and quality of life in osteoporosis and related conditions

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Authors: [Chad Deal Cleveland Clinic](#)
- Genetic Approaches To Identifying Novel Osteoporosis Drug Targets [Robert Brommage](#) First published: 01 April 2015 <https://doi.org/10.1002/jcb.25179>
Citations: [24](#)

NEWSLETTER ARTICLE

Precision medicine through systems pharmacology: from theory to practice

INTRODUCTION

The Introduction With the ability to customize treatments for each patient according to their unique genetic, molecular, and clinical profiles, precision medicine has enormous promise. The integration of many data sources, like as omics, medication information, and clinical data, is essential to this strategy in order to understand disease causes and maximize treatment. But there are major obstacles to be overcome before precision medicine may be applied in clinical settings. In this review, the field of systems pharmacology—a multidisciplinary approach that combines network analysis, computational modelling, and experimental validation—is used to examine how precision medicine is developing. By utilizing pharmacokinetic, pharmacodynamic, and disease development models, systems pharmacology provides a viable remedy. It allows clinicians to predict both side effects and therapeutic outcomes at the same time by integrating many risk factors and validating them through experimental validation and computational simulations.

PHARMACOGENOMICS AND DRUG INDUCED ADVERSE EVENTS

People have used natural materials for their therapeutic benefits for ages. The eleventh-century Avicenna recorded hundreds of medicinal drugs in his "Canon of Medicine," while the Swiss alchemist Paracelsus stressed the significance of dosage in assessing if a material is poisonous. The thalidomide tragedy in the 20th century made the difference between desirable effects and adverse drug reactions (ADRs) clear, which prompted the creation of pharmacovigilance programs like the UK's Yellow Card system.

ADRs can be divided into two categories: type B, which is less predictable and frequently has immunological or genetic roots, and type A, which is predicted based on drug pharmacology and dosage. Type B reactions are not always recognized prior to a drug's licensure; however type A reactions might not be visible until after marketing surveillance. The study of pharmacogenetics—the way genetic variation affects drug response—has grown in significance. Using candidate gene studies and genome-wide association studies (GWAS) to find genetic variables linked to adverse drug reactions (ADRs) has resulted in the pharmacogenetic information that is now included on prescription labels.

To improve patient safety, regulatory organizations like the European Commission have made it mandatory for medicine labels to include pharmacogenetic information. Research has indicated variations in the quantity of pharmacogenetic data offered by various regulatory agencies and nations. To help with pharmacovigilance and the detection of ADRs, there is a rising trend toward adding more pharmacogenetic data on drug labels. Drug elimination pathways must be taken into consideration in order to comprehend the elements influencing genetic vulnerability to adverse drug reactions (ADRs). Drugs and their metabolites are either completely removed from the body or are removed from the body more quickly as metabolites. This biotransformation process is mostly carried out by the liver, though it also involves the kidneys, lungs, gastrointestinal system, muscles, and skin (Ionescu & Caira, 2005). When it comes to delivering foreign peptides to T cells, HLA gene products are essential. These genes, which are class I and class II types with significant polymorphism, are found on chromosome 6 of the major histocompatibility complex (MHC). Even though this polymorphism most likely developed to defend against infections, some HLA alleles have been linked to a higher risk of autoimmune conditions such as type 1 diabetes and multiple sclerosis. On a small scale, genetic testing has been used in clinical practice with the goal of preventing both type A and type B ADRs. In many countries, it is advised that individuals with type A reactions first have their TPMT status evaluated before receiving a prescription for thiopurine medication. Either genotyping or assessing the amounts of certain enzymes in red blood cells can be used to do this.

People.

INTEGRATING OMICS DATA FOR TAILORED TREATMENT STRATEGIES

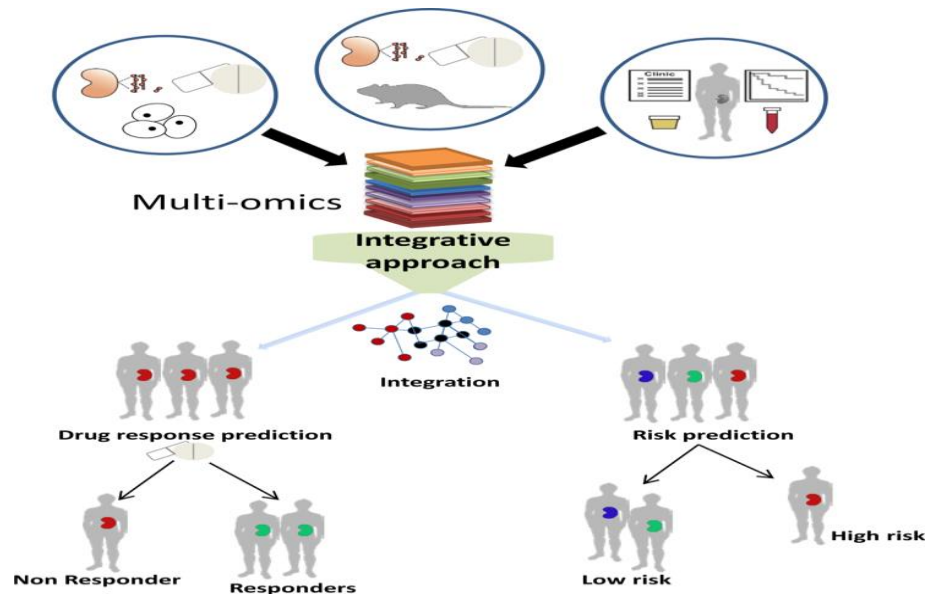
For precision medicine research, three main categories of data are essential: omics, drug-related, and clinical data. Both raw data obtained directly from patients and derived or summarized data, such as published research on the influence of genetics on medication reactions, are included in each class. The current therapeutic guidelines for the management of diabetic kidney disease (DKD) ignore the unique molecular variances across patients in Favor of a generic approach to medication. Different responses to therapies based on molecular subgroups within the disease have been shown in recent studies of DKD trials. This emphasizes the necessity of treating each patient individually based on their own molecular profile.

A customized treatment plan based on molecular traits is necessary to improve DKD patient care. Systems biology techniques can be utilized to comprehend the various reactions to treatments and find indicators that indicate the course of treatment. For example, a research by Lindhardt et al. examined how well a marker panel predicted individuals with type 2 diabetes and medication-resistant hypertension would respond to a particular drug. They discovered that a better response to therapy was connected with higher levels of a particular proteomic classifier.

By combining drug-specific molecular profiles, patient-specific molecular profiles representing kidney development, and bioinformatics techniques to match the two, systems biology can help predict patient response to approved DKD treatments.

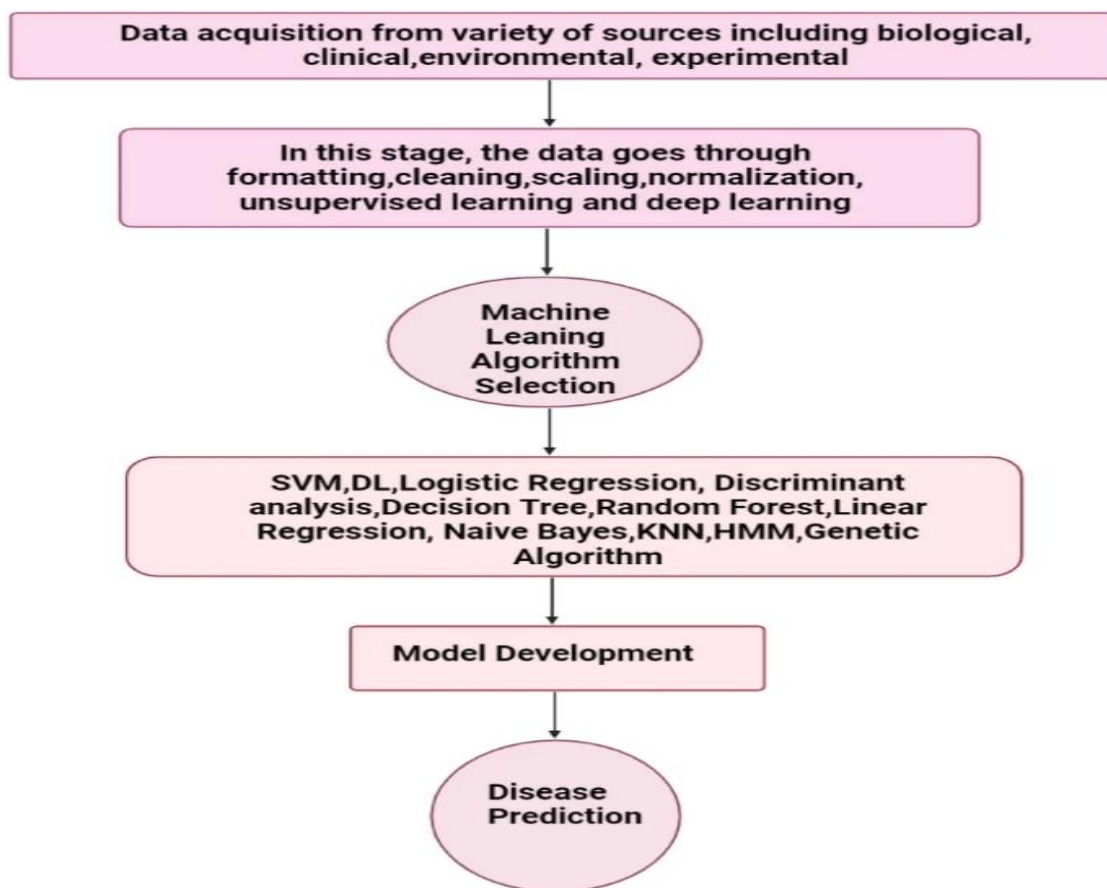
Drug processes can be better understood by employing multi-omics profiling in appropriate model systems to produce drug-specific molecular profiles. Identification of signals reflecting individual kidney progression is made possible by integrating this data with molecular profiles distinct to each patient. This method seeks to match each patient with the best medication, much like personalized medicine. Though DKD in humans may not be entirely replicated in animal and cell culture models, human biospecimen analysis from carefully planned treatment trials, along with insights from these models, might yield important information. By comparing the molecular profiles of patients who respond and

those who do not, clinicians can find potential markers linked to a patient's drug response, improving the accuracy of therapy prediction.



PERSONALIZED DRUG RESPONSE PREDICTION MODELS

By using computing advantages to guide both individual and population health, machine learning is transforming the healthcare industry. Observing patient conditions, analysing disease patterns, diagnosing and prescribing medications, providing patient centered care, reducing clinical errors, predictive scoring, supporting therapeutic decision-making, detecting sepsis, and identifying high-risk emergencies are just a few of the key roles it plays. It also helps in phenotypic identification, deciphering clinical statements from post-mortem reports and death certificates, identifying illnesses such as cancer and cardiovascular disease, identifying symptoms linked to various diseases, forecasting and mitigating risks, panelling, and resource allocation.



REGULATORY IMPLICATIONS AND FUTURE DIRECTIONS IN PRECISION PHARMACOLOGY

Significant developments have occurred in the fields of healthcare and pharmaceuticals, one of which is the growing importance of AI and ML in drug discovery, as demonstrated by Alphabet's DeepMind's success in protein structure prediction. Pharmaceutical manufacturing is being revolutionized by digital twins, as demonstrated by GSK's optimization of vaccine development. Regulatory experts must adjust to a more digitally-focused workplace in order to embrace Pharma 4.0, which merges digitalization and automation. This is especially true with the introduction of ISO's IDMP standards and real-time data interchange via cloud-based systems like Accumulus Synergy. Furthermore, regulatory agencies are adjusting to new technologies by means of initiatives such as the FDA's emerging technology program, which guarantees the smooth integration of

innovative technologies into the development of therapeutic products. Patient-centric methods are becoming more and more popular; programs like as EUPATI are increasing patient participation in research and development, affecting regulatory processes and determining reimbursement decisions, as demonstrated by the FDA's patient-focused drug development guidance series. Collaborative forums like IPRP and IMDRF are driving efforts toward global regulatory harmonization and convergence, but issues like governance and ethical concerns about the use of AI/ML still need to be addressed. To properly traverse this dynamic regulatory world, regulatory professionals need to arm themselves with digital literacy skills and a growth mindset that fosters ongoing learning and adaptation.

CONCLUSION

Precision medicine is replacing generic healthcare, and systems biology research is driving this change. Through molecular profile analysis, patients can be divided into many illness subgroups. While predictive biomarkers, with the aid of sophisticated bioinformatics tools, can match patients' genetic signatures with medication profiles to establish the most appropriate treatment approach, predictive biomarkers with greater accuracy can detect high-risk individuals in the early stages of the disease. By focusing on the "right patients," this strategy makes it possible for clinical trials and medication use in practice to be more effective. This results in smaller, more ethically conducted trials and more effective drug use in clinical settings.

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WORKSHOP ON EMBL-EBI SEQUENCE ANALYSIS TOOLS AND MAPPING BIOINFORMATICS WORKFLOWS.

DESCRIPTION

Date Attended:

Location: online platform

Introduction:

Attending the EMBL-EBI Sequence Analysis Tools and Mapping Bioinformatics Workflows workshop proved to be an invaluable experience, providing me with essential knowledge and practical skills in the field of bioinformatics. Over the course of two days, I had the opportunity to explore key bioinformatics tools and methodologies that are crucial for sequence analysis and workflow development.

Day 1: Sequence Analysis Tool

Day one of the workshop was packed with insights into fundamental sequence analysis tools such as BLAST, UniProt, InterPro, and InterProScan. Through hands-on sessions and guided demonstrations, I gained a deeper understanding of how these tools can be leveraged to unravel the mysteries hidden within biological sequences. The ability to conduct sequence similarity searches, annotate proteins, and identify functional domains has undoubtedly broadened my analytical toolkit and enhanced my capacity to interpret biological data effectively.

Day 2: Web Services and Workflows

The second day of the workshop focused on the practical aspects of building and executing bioinformatics workflows using web services and the Common Workflow Language (CWL). Learning about tools like Job Dispatcher (JD) and Course Web Service (CWS) provided me with valuable insights into automating analysis tasks and managing job submissions programmatically. Additionally, diving into CWL workflows exemplified the importance of reproducibility and scalability in bioinformatics analyses, equipping me with the skills necessary to design and execute robust workflows tailored to specific research objectives.

Conclusion:

My participation in the EMBL-EBI Sequence Analysis Tools and Mapping Bioinformatics Workflows workshop has been immensely beneficial, enabling me to acquire new skills and deepen my understanding of essential bioinformatics tools and methodologies. The knowledge and expertise gained during the workshop have already begun to positively impact my research endeavors, empowering me to tackle complex biological questions with confidence and

precision. I am incredibly grateful to the organizers and instructors for their dedication and expertise, which made this learning experience truly enriching and transformative.



EMBL-EB... 11/25/2023
to me ▾





Hi Abitha S,

Thank you for attending Exploring EMBL-EBI sequence analysis tools and managing bioinformatics workflows. We hope you enjoyed our event.

Please submit your questions or comments to: ajay@ebi.ac.uk.

We can confirm that you attended and completed the workshop.

All the resources, including the presentation slides, practical activities, and other useful links have been included in the handbook:
<https://docs.google.com/document/d/1sqxfWNjGe6JkevGfrq5GexLHugGHQe20HMPXI0IWVY/edit?usp=sharing>

Some of the questions which were answered via the Q&A box can be accessed here:
<https://docs.google.com/spreadsheets/d/1SkmEfAFsQAXuJIODp4NxbqbTRPdcsnG6agUfoP6lQA/edit?usp=sharing>

Your feedback is very important to us. It would be highly appreciated if you can provide feedback about the workshop, if you have not done so yet, - <https://docs.google.com/forms/d/e/1FAIpQLSc7PLjvck1YxnAPnv1t6iTtVYB7iu4dU3T5qNW5g-gJGwtGTw/viewform>

Happy learning!

Best wishes

Ajay, Nandana and Fabio

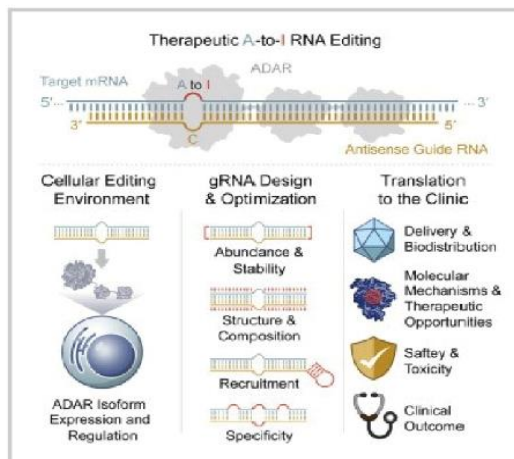
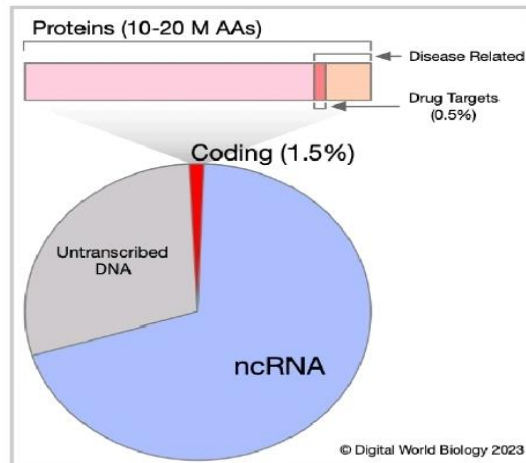
TRANSCRIPTOMICS

An Overview of ncRNA

The understanding of RNA's role has evolved beyond being a messenger between genes and proteins. Initially focused on housekeeping functions, such as tRNAs and rRNAs, this perception shifted with the discovery of microRNAs about 20 years ago. This revelation marked the beginning of exploring regulatory RNAs without significant protein-coding potential. Subsequently, various classes of non-coding regulatory RNAs, like endogenous small interfering RNAs (endo-siRNAs), PIWI-associated RNAs (piRNAs), and long non-coding RNAs, have been identified. Significant progress has been made in comprehending their expression, biogenesis, mechanisms, mode of action, and functions across diverse biological processes.

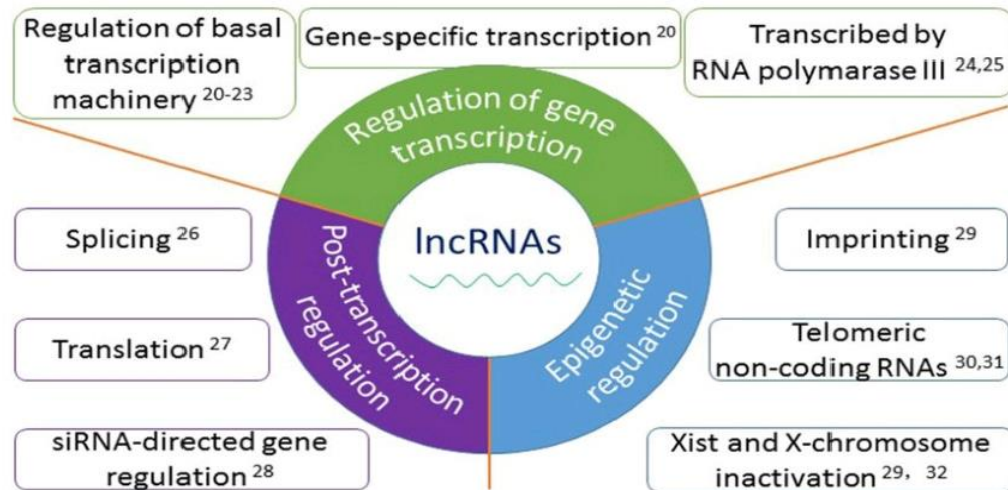
CircularRN (cirRNA)

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MicroRNA in disease regulation

Recent advances in microRNA (miRNA) research underscore their pivotal role in disease regulation across diverse physiological systems. Dysregulated miRNAs are implicated in cancer, neurological disorders, cardiovascular diseases, metabolic disorders, and infectious diseases. They serve as promising diagnostic biomarkers and therapeutic targets for various ailments, offering potential avenues for personalized medicine and novel treatment strategies. Understanding the intricate miRNA-mediated regulatory networks holds significant promise for advancing disease diagnostics, prognosis, and therapeutic interventions in clinical settings.



Therapeutic implication of ncRNA

Long non-coding RNAs (lncRNAs) play a crucial role in triple-negative breast cancer (TNBC) treatment responses, including chemotherapy, immunotherapy, and radiotherapy. Specific lncRNAs like H19 and LINK-A serve as biomarkers, influencing clinical outcomes. lncRNAs are involved in angiogenesis, cell proliferation, apoptosis, and drug resistance in TNBC, with examples like DRHC and HOTAIR inhibiting TNBC growth, and miR-377-3p delaying TNBC progression. Some lncRNAs, including HIF1A-AS2 and HOTAIR, are associated with overall survival and metastasis prevention.

Various lncRNAs act as stem cell markers, while others promote vasculogenic mimicry, facilitating tumor formation. MANCR inhibits DNA damage, AWPPH prevents tumorigenesis, and TUG1 enhances TNBC cell sensitivity to cisplatin. Preliminary studies highlight the significance of lncRNAs in tumor prevention, although further research is needed to explore treatment options.

RNA EDITING

Recent breakthroughs in RNA editing research highlight its significant role in disease regulation across various conditions. Dysregulated RNA editing is implicated in neurological disorders, cancer, cardiovascular diseases, genetic disorders, and infectious diseases. Aberrant RNA editing patterns affect key pathways involved in disease pathogenesis, offering potential targets for therapeutic interventions. Understanding RNA editing mechanisms provides insights into disease mechanisms and may lead to the development of innovative diagnostic tools and precision medicine strategies. Further exploration of RNA editing dynamics promises to improve our understanding of disease biology and enhance patient outcomes.

CONCLUSION

In conclusion, the burgeoning field of transcriptomics unveils the intricate landscape of RNA molecules, encompassing not only protein-coding transcripts but also a myriad of non-coding RNA species. From the dynamic regulation of gene expression by microRNAs to the post-transcriptional modifications mediated by RNA editing, and the emerging role of circular RNAs in gene regulation, our understanding of RNA biology has transcended traditional boundaries. The interplay between these diverse RNA species orchestrates intricate regulatory networks, influencing physiological processes and disease pathogenesis. As transcriptomic technologies continue to evolve, unraveling the complexities of RNA-mediated regulation holds immense promise for deciphering disease mechanisms and identifying novel therapeutic targets. With each discovery, we inch closer to unlocking the full potential of transcriptomics in revolutionizing diagnostics, personalized medicine, and therapeutic interventions.

MATLAB COURSE COMPLETION CERTIFICATES

I have completed 13 MATLAB Courses and attached the certificates below,

- Image Processing with MATLAB
- MATLAB Onramp
- MATLAB Programming Techniques
- MATLAB for Data Processing and Visualization
- Machine Learning with MATLAB
- Deep Learning with MATLAB
- Statistics Onramp
- MATLAB Fundamentals
- Reinforcement Learning Onramp
- Computer Vision Onramp
- Deep Learning Onramp
- Object-Oriented Programming Onramp
- Machine Learning Onramp

Image Processing with MATLAB

Unleash the power of MATLAB for image manipulation with our Onramp image editor. This hands-on course is designed to introduce you to the basics of image processing and show you how MATLAB can be used to perform a variety of image analysis tasks. Through interactive tutorials and real-world examples, you will learn techniques such as image enhancement, segmentation and feature extraction that enable you to efficiently process and interpret images.

MATLAB Programming Techniques

Take your MATLAB skills to the next level with MATLAB Programming Techniques Onramp. This advanced course is designed for experienced MATLAB users who want to

improve their programming skills. From optimization and debugging strategies to designing advanced data structures and algorithms, this Onramp covers a wide range of programming techniques to help you write powerful, robust, and maintainable MATLAB.

MATLAB for Data Processing and Visualization

It's a good idea to learn MATLAB for data processing and visualization, especially if you work with numerical data. Here are some things you might want to learn about processing and visualizing a data with MATLAB. These MATLAB capabilities enable you to handle a variety of data processing and visualization tasks, making it a powerful tool for data analysis and visualization.

Machine Learning with MATLAB

MATLAB is a versatile machine learning environment that contains rich built-in tools, functions, and documentation. Gaining knowledge of MATLAB machine learning will enable you to apply various machine learning techniques to real-world problems.

Image Processing Onramp

With an interactive, do-it-yourself approach, Image Processing Onramp offers short video courses and hands-on exercises to help you understand and use MATLAB image processing concepts. Complete the image processing onramp for a thorough understanding of image processing principles and methods. You will also gain hands-on experience using MATLAB to develop image processing algorithms.

Deep Learning with MATLAB

Explore the advancement of deep learning with MATLAB with Deep Learning Onramp. This interactive course provides a thorough introduction to deep learning concepts and shows how to use MATLAB to build, train, and deploy deep neural networks. Whether you're new to deep learning or want to deepen your knowledge, this Onramp gives you the skills to tackle complex problems.

Statistics Onramp

Dive into the world of statistical analysis and data interpretation with MATLAB Statistics Onramp. This interactive learning experience provides a comprehensive overview of statistical concepts, from basic descriptive statistics to advanced data modeling techniques. By learning the statistical capabilities of MATLAB, you can analyze data, generate meaningful insights, and make informed decisions in a variety of fields.

MATLAB Fundamentals

Learn the basics of MATLAB programming from the ground up with MATLAB Fundamentals Onramp. Designed for beginners, this interactive course provides a structured learning path covering basic MATLAB syntax, data types, control flow, and function writing. Whether you're new to programming or transitioning from another language, this Onramp provides a solid foundation for your MATLAB journey.

Reinforcement Learning Onramp

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

Computer Vision Onramp

Computer vision is where knowledge from the real world meets digital data. Data from multiple cameras and sensors can be combined to create a digital reconstruction. In this course, you will use object recognition to find, track, and count turtles in a video.

Deep Learning Onramp

Deep Learning Onramp is an interactive, self-paced course that uses MATLAB to teach you how to apply and understand deep learning concepts through short video tutorials and hands-on activities. After completing the Deep Learning Onramp, you will have a thorough understanding of deep learning theories and methods and hands-on experience building and improving deep learning models in MATLAB.

Object-Oriented Programming Onramp

Journey through object-oriented programming (OOP) principles with the MATLAB object-oriented programming onramp. This interactive course combines concise video tutorials with hands-on exercises to teach you the basics of OOP in MATLAB. By the end of this Onramp, you will have a good understanding of how to use OOP concepts to create modular and reusable code in MATLAB.

Machine Learning Onramp

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Course Completion Certificate

Abitha S

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

DIRECTOR, TRAINING SERVICES

1 March 2024



Course Completion Certificate

Abitha S

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MATLAB for Data Processing and Visualization

DIRECTOR, TRAINING SERVICES

7 March 2024



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