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VELS
INSTITUTE OF SCIENCE, TECHNOLOGY & ADVANCED STUDIES (VISTAS)
(Deemed to be University Estd. u/s 3 of the UGC Act, 1956)
PALLAVARAM, THALAMBUR, PERIYAPALAYAM-CHENNAI
ACCREDITED BY NAAC WITH 'A++' GRADE

BIORADARS
PROCEEDINGS AUGUST 2025

DEPARTMENT OF BIOINFORMATICS
SCHOOL OF LIFE SCIENCES
VELS INSTITUTE OF SCIENCE, TECHNOLOGY AND ADVANCED STUDIES (VISTAS)

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Sri Vidya Ganapathy (VISTAS Campus)

Dr. Ishari K. Ganesh -Founder-Chancellor, VISTAS

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Chancellor Message

Dr. Ishari K. Ganesh, M.Com. M.L., M.B.A., Ph.D.

Chancellor, VISTAS,

Founder- Chairman, VELS Group.

It gives me immense pleasure to know that the Department of Bioinformatics, VISTAS, has initiated the departmental club activity under the name **"BIORADARS"**. Involvement is a good way to develop relationships with other students and to create a sense of community for yourself and others. In this esteem, the club motivates the student to take part in both academics, extra-curricular well as develops the co-ordination capability.

Participation in student groups provides opportunities to get to know about their peer group and faculty members, to pursue a particular interest, to learn more about your major, to celebrate our culture.

I am confident that the magazine will provide a career-opening for students and research scholars of life science to know about issues relevant to the subject concerned. I hope that Bioradars will unravel the challenging issues in Bioinformatics.

I congratulate the faculty and students for taking timely initiative in releasing the magazine.

Dr. Ishari K. Ganesh.

Chancellor.

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About Bioradars

Bioradars Club was organized by the Department of Bioinformatics which is based & focused on the professional and personal development, and educational & cultural programming for students and the community. The club "BIORADARS" has been initiated to serve the purpose of enlightening the young minds about various prospects in extra and co-curricular activities.

The name of the club "BIORADARS" implies an acronym to detect or receive radiation from biological concepts. Bioinformatics an interdisciplinary and being versatile has been utilized in various fields to solve the problems as well as serve in the advancement of healthcare medicine. The club activities include several programs to ignite the young minds and a common platform to bring thought-provoking visionary solutions.

Editor's message

Bioradars intends to be a facilitating club for new kind of discussions about advance aspects of Biocomputing and Bioinformatics for student's community. I am proud of our team members and fortunate to be able to draw upon their individual and collective knowledge, talent, judgment and disciplinary backgrounds. On behalf of Bioinformatics Department, I must thank the university administration for supporting us for this effort. I must give special thanks to Dr. R. Dinakaran Michael, Dean, School of Life Sciences, who had the vision to embark on this work. His ability to draw together diverse talents and resources and his confidence that we could actually bring this manual to fruition is the mark of a true leader. Finally, I want to thank our students and faculty members, those we teach and with whom we partner. They make reciprocity a reality. They allow us into their lives and in so doing they teach and transform us and vice versa. I look forward to our journey together as we develop Bioradars magazine into its fullest potential.

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Founder-Chancellor

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RESEARCH ACTIVITIES

Patent filed / Published / Granted

S. No	Patent Title	Inventors /Faculty	Patent Application Filed No	Filed Date	Published Date	Status (Filed / Published / Granted	Department
1	Device for Psychologi Cal Profiling	Mrs.S.Shanmugavani , Dr. P.R. Kiresee Saghana	UK Patent-6350777	02-03-2024		16th April 2024.	Bioinform atics

Faculty Participation / Attended in Seminar / Conferences / Symposia / Workshop

Name of the Faculty	Type (National / International)	Title	Organized By Full Address	Date	Department	Year
Dr.R.Priya	National	Yoga for Physical and Mental Wellness	Vels Institute of Science, Technology and Advanced Studies,	21st Jun 2024	Bioinformatics	2024
Mrs.S.Shanmugav ani,	National	Yoga for Physical and Mental Wellness	Vels Institute of Science, Technology and Advanced Studies,	21st Jun 2024	Bioinformatics	2024
Dr.R.senthil	National	Yoga for Physical and Mental Wellness	Vels Institute of Science, Technology and Advanced Studies,	21st Jun 2024	Bioinformatics	2024

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Dr. P.R. Kiresee Saghana	National	Yoga for Physical and Mental Wellness	Vels Institute of Science, Technology and Advanced Studies,	21st Jun 2024	Bioinformatics	2024
Dr. R.Priya	International	International Conference on ICIT 2024	INTI UNIVERSITY MALAYSIA	26th & 27 Sep 2024	Bioinformatics	2024
Mrs.S.Shanmugavani,	International	International Conference on ICIT 2024	INTI UNIVERSITY MALAYSIA	26th & 27 Sep 2024	Bioinformatics	2024
Dr. P.R. Kiresee Saghana	International	International Conference on ICIT 2024	INTI UNIVERSITY MALAYSIA	26th & 27 Sep 2024	Bioinformatics	2024
Dr. P.R. Kiresee Saghana	International	"1st International conference on Microbes and Applied Biotechnology (ICMAB'24)"	St. Peter's Institute of Higher Education and Research	6th – 8th Nov	Microbiology, Biotechnology & Biochemistry,	2024
Dr. R.Priya	International	"1st International conference on Microbes and Applied Biotechnology (ICMAB'24)"	St. Peter's Institute of Higher Education and Research	6th – 8th Nov	Microbiology, Biotechnology & Biochemistry,	2024
Mrs.S.Shanmugavani,	International	"1st International conference on Microbes and Applied Biotechnology (ICMAB'24)"	St. Peter's Institute of Higher Education and Research	6th – 8th Nov	Microbiology, Biotechnology & Biochemistry,	2024
Dr. P.R. Kiresee Saghana	National	Five Day Faculty Development Programme"Integrating AI in Academic Research:	Scientific Research Reports	13th to 17th, 2024,	Scientific Research Reports	2024

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		Tools and Techniques"				
Dr. R.Priya	National	Five Day Faculty Development Programme"Integrating AI in Academic Research: Tools and Techniques"	Scientific Research Reports	13th to 17th, 2024,	Scientific Research Reports	2024
Mrs.S.Shanmugavani,	National	Five Day Faculty Development Programme"Integrating AI in Academic Research: Tools and Techniques"	Scientific Research Reports	13th to 17th, 2024,	Scientific Research Reports	2024
Dr. P.R. Kiresee Saghana	International	"1st International conference on Microbes and Applied Biotechnology (ICMAB'24)"	St. Peter's Institute of Higher Education and Research	6th – 8th Nov	Microbiology, Biotechnology & Biochemistry,	2024
Dr. R. Senthil	International	Seven days International FDB on " Various Aspects of Computational Modelling"	IQAC and PG & Research Department of Mathematics , Theivanai Ammal College for Women (Autonomous), Villupuram	03/01/25 to 09/01/25	School of Business and Technology	2025
Dr. R.Priya	International	Five days International FDB on " Innovative Research Advancements	Gojan School of Business and Technology , Chennai	27/01/25 to 29/01/25	School of Business and Technology	2025

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		in Medical Science				
Mrs. S. Shanmugavani	International	Five days International FDB on " Innovative Research Advancements in Medical Science	Gojan School of Business and Technology, Chennai	27/01/25 to 29/01/26	School of Business and Technology	2025
Mrs. S. Shanmugavani	International	Seven days International FDB on "Integrating AI in research writing	IVARIN PUBLICATION Chennai	6th to 12th Jan 2025	NA	2025
Dr. R. Senthil	International	Five days International FDB on " Innovative Research Advancements in Medical Science	Gojan School of Business and Technology, Chennai	27/01/25 to 29/01/27	School of Business and Technology	2025
Dr. P.R.Kiresee Saghana	International	Five days International FDB on " Innovative Research Advancements in Medical Science	Gojan School of Business and Technology, Chennai	27/01/25 to 29/01/28	School of Business and Technology	2025
Dr. R.Priya	International	Seven days International FDB on "Integrating AI in research writing	IVARIN PUBLICATION Chennai	6th to 12th Jan 2025	NA	2025
Dr. R. Senthil	National	Five days National Virtual FDB on " Exploring Hyper-Performance Quantum Computing System with	Department of Physics, School of Basic Science, VISTAS	19/02/25 to 23/02/25	Department of Physics, School of Basic Science, VISTAS	2025

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		Electrochemical- Nonlinear Optical Materials through DFT approach"				
Dr. R.Priya	National	Five days National Virtual FDB on " Exploring Hyper-Performance Quantum Computing System with Electrochemical- Nonlinear Optical Materials through DFT approach"	Department of Physics, School of Basic Science, VISTAS	19/02/25 to 23/02/25	Department of Physics, School of Basic Science, VISTAS	2025
Mrs. S. Shanmugavani	National	Five days National Virtual FDB on " Exploring Hyper-Performance Quantum Computing System with Electrochemical- Nonlinear Optical Materials through DFT approach"	Department of Physics, School of Basic Science, VISTAS	19/02/25 to 23/02/25	Department of Physics, School of Basic Science, VISTAS	2025
Dr. P.R.Kiresee Saghana	National	Five days National Virtual FDB on " Exploring Hyper-Performance Quantum Computing System with Electrochemical- Nonlinear Optical Materials through DFT approach"	Department of Physics, School of Basic Science, VISTAS	19/02/25 to 23/02/25	Department of Physics, School of Basic Science, VISTAS	2025

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Awards / Honours by the Faculty / Department

S.No.	Name of the Faculty	Name of the Award	Agency Name with Full Address	Level (State /National/ Internation Al	Date	Month & Year	Department
1	Dr. R.Priya	Research Contributor Award	VDGOOD Professional Association	International	19th Aug 2024	Aug-24	Bioinformatics
2	Mrs.S.Shanmugavani,	Research Contributor Award	VDGOOD Professional Association	International	19th Aug 2024	Aug-24	Bioinformatics
3	Dr.R.senthil	Research Excellence Award	VDGOOD Professional Association	International	19th Aug 2024	Aug-24	Bioinformatics
4	Dr. P.R. Kiresee Saghana	Research Contributor Award	VDGOOD Professional Association	International	19th Aug 2024	Aug-24	Bioinformatics
1	Dr. P.R. Kiresee Saghana	Excellence in Active Learning methods Award	SRR Publisher	National	15-10-2024	Oct-24	Bioinformatics
1	Dr. P.R. Kiresee Saghana	Certificate of Apperciation	Vels University	National	07-11-2024	Nov & 2024	Bioinformatics
2	Dr. R.Priya	Certificate of Apperciation	Vels University	National	07-11-2024	Nov & 2024	Bioinformatics
3	Mrs.S.Shanmugavani,	Certificate of Apperciation N	Vels University	National	07-11-2024	Nov & 2024	Bioinformatics
4	R. Senthil	Certificate of Apperciation N	Vels University	National	07-11-2024	Nov & 2024	Bioinformatics

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Paper presented by the Faculty Member in Conferences:

S. No.	Name of the Author	Title of the Paper	Organised by Full Address	Date	Department	Year
1	Dr. R.Priya	Insilico Analysis of polycystic kidney disease (PKD) using the polycystin -1 and 2 protein	International Conference on ICIT 2024 in INTI University Malaysia	26th & 27 Sep 2024	Bioinformatics	2024
2	Mrs.S.Shanmugavani,	A STUDY ON BIOCOMPATIBILITY AND BIODEGRADABILITY OF COLLAGEN USING CROSS-LINKED AGENT	International Conference on ICIT 2024 in INTI University Malaysia	26th & 27 Sep 2024	Bioinformatics	2024
3	Dr. P.R. Kiresee Saghana	IN SILICO ANALYSIS ON G PROTEIN-COUPLED RECEPTORS (GPCRS) – HORMONAL PROTEINS	International Conference on ICIT 2024 in INTI University Malaysia	26th & 27 Sep 2024	Bioinformatics	2024

Faculty member visit to Foreign Countries / Universities for academic purpose.

S.No	Name of the Faculty	Designation	Name of the Institution with Country Name	Purpose of Visit	Date of Visit	Year	Department
1	Dr. R.Priya	**Assistant Professor**	**INTI University, Malaysia**	**Conference**	26th & 27 Sep 2024	**2024**	**Bioinformatics**
2	Mrs.S.Shanmugavani,	**Assistant Professor**	**INTI University, Malaysia**	**Conference**	26th & 27 Sep 2024	**2024**	**Bioinformatics**
3	Dr. P.R. Kiresee Saghana	**Assistant Professor**	**INTI University, Malaysia**	**Conference**	26th & 27 Sep 2024	**2024**	**Bioinformatics**

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Book publication by faculty

S.No.	Name of the Faculty *	Name of the Book	ISBN No.	Name of the Publisher	Date	Month & Year	Department
1	Dr. P.R. Kiresee Saghana	Book chapter entitled :Unveiling Molecular Signatures: A Bioinformatics Exploration of Differential Gene Expression inVaricose Veins in "Recent Developments in Multidisciplinary Science and Technological Fields	978-81-980792-0-6	SRR Publisher	30-10-2024	**Oct-24**	**Bioinformatics**
2	Dr. R.Priya	Book chapter entitled :Unveiling Molecular Signatures: A Bioinformatics Exploration of Differential Gene Expression inVaricose Veins in "Recent Developments in Multidisciplinary Science and Technological Fields	978-81-980792-0-6	SRR Publisher	30-10-2024	**Oct-24**	**Bioinformatics**
3	Mrs.S.Shanmugavani,	Book chapter entitled :Unveiling Molecular Signatures: A Bioinformatics Exploration of Differential Gene Expression inVaricose Veins in "Recent Developments in Multidisciplinary Science and Technological Fields	978-81-980792-0-6	SRR Publisher	30-10-2024	**Oct-24**	**Bioinformatics**

4	Dr. P.R. Kiresee Saghana	Book chapter entitled : Computational modeling of unstructured protein in rabies employing swiss model	ISBN NO. 978-93-341-4952-4	Proceedings "1st International conference on Microbes and Applied Biotechnology (ICMAB'24)"	6th – 8th Nov	**Nov-24**	Microbiology, Biotechnology & Biochemistry,
5	Dr. R.Priya	Book chapter entitled :Pharmacophore modelling and molecular analysis of hexa gene	ISBN NO. 978-93-341-4952-4	Proceedings "1st International conference on Microbes and Applied Biotechnology (ICMAB'24)"	6th – 8th Nov	**Nov-24**	Microbiology, Biotechnology & Biochemistry,
6	Mrs.S.Shanmugavani,	Book chapter entitled :A review on computational techniques in Nanotoxicology	ISBN NO. 978-93-341-4952-4	Proceedings "1st International conference on Microbes and Applied Biotechnology (ICMAB'24)"	6th – 8th Nov	**Nov-24**	Microbiology, Biotechnology & Biochemistry,

ISBN: 978-81-991683-8-1

Details of Research projects submitted to the Funding Agencies by Department

S. No	Title of the R & D Project	Name of the Principal Investigator	Name of the Funding Agency	Duration of the project	Amount in Rs	Date of Submission	Department
1	Assessment of a membrane-active antimicrobial peptide from Arabidopsis thaliana for its therapeutic potential against airborne diseases	Dr. Radha Mahendran, Dr.Kiresee Saghana	ANRF (SREB)	3 Years	60 Lakhs	24-11-2024	Bioinformatics

Details of Seminar / Conference / Symposia / Workshop / FDP organized by Department

S.No	Title, Name of the Chief Guest / Resource Person with full Address	Seminar/Conferences /Symposia / Workshop) (State / National / International)	Department	Date	Month	Year
1	Mrs. S. Shanmugavani	FDP : Enhance the pharmacist skills- the AI Advantage	Bioinformatics	16th Dec to 21st Dec 2024	December	2024
2	Dr. R.Priya	FDP : Enhance the pharmacist skills- the AI Advantage	Bioinformatics	17th Dec to 21st Dec 2024	December	2024
3	Dr. P.R.Kiresee Saghana	FDP : Enhance the pharmacist skills- the AI Advantage	Bioinformatics	18th Dec to 21st Dec 2024	December	2024
4	Dr. R. Senthil	FDP: AI tools and Techniques for Research	Bioinformatics	9th to 13th Dec 2024	December	2024

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5	Dr. R. Senthil	FDP: Fundamentals of machine Learning	Bioinformatics	20th to 24th Dec 2024	December	2024
1	Mrs. S. Shanmugav Ani	FDP : Enhance the pharmacist skills- the AI Advantage	Bioinformatics	16th Dec to 21st Dec 2024	December	2024
2	Dr. R.Priya	FDP : Enhance the pharmacist skills- the AI Advantage	Bioinformatics	17th Dec to 21st Dec 2024	December	2024
3	Dr. P.R.Kirese e Saghana	FDP : Enhance the pharmacist skills- the AI Advantage	Bioinformatics	18th Dec to 21st Dec 2024	December	2024
4	Dr. R. Senthil	FDP: AI tools and Techniques for Research	Bioinformatics	9th to 13th Dec 2024	December	2024
5	Dr. R. Senthil	FDP: Fundamentals of machine Learning	Bioinformatics	20th to 24th Dec 2024	December	2024

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Research Papers Publication by faculty members

Sl.No	Author	Title	Journal	Year	Indexed (Scopus/ WOS / UGC)
1	Mahendran R, Mishra MR, Dey S, Srivastava D	Study of morphology and orchid mycorrhizal associations in Malaxis rheedei	App Biol Biotech	2024	Scopus
2	.R. Rajaganapathi, Radha Mahendran, D. Sivaganesan, Mr.R. Vadivel, M. Robinson Joel, V. Kannan	An IoT enabled computational model and application development for monitoring cardiovascular risks	e-Prime - Advances in Electrical Engineering, Electronics and Energy	2024	Scopus
3	V. S. Bhargavi, A. Dogra, A. Bhatt, P. Ghildiyal, S. R. Mahendran and R. Kaur	Accelerating Pharmaceutical Research and Development through AI-Driven Drug Discovery	Ninth International Conference on Science Technology Engineering and Mathematics (ICONSTEM)	2024	Scopus
4	Radha Mahendran, M. S. Khan, H. P. M P, A. J. Obaid, K. S. Mohsen and A. M. Shareef	IoT Based Health Monitoring System with AI-Powered Disease Prediction	Ninth International Conference on Science Technology Engineering and Mathematics (ICONSTEM)	2024	Scopus
5	R. Mahendran, A. Dogra, D. Mendhe, S. B. G. T. Babu, S. Dixit and S. P. Singh	Machine Learning-Assisted Protein Structure Prediction: An AI Approach for Biochemical Insights	Ninth International Conference on Science Technology Engineering and Mathematics (ICONSTEM)	2024	Scopus

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6	RadhaMahendran, A. Dogra, D. Mendhe, S. B. G. Tilak Babu, S. Dixit and S. P. Singh	Machine Learning for Drug Discovery: Predicting Drug-Protein Binding Affinities using Graph Convolutional Networks	5th International Conference on Recent Trends in Computer Science and Technology (ICRTCST	2024	Scopus

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Abstract

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A REVIEW ON "NEXT-GENERATION SEQUENCING (NGS)

Silviya Helan Mary,

B.Sc., Biocomputing, Department of Bioinformatics,

Vels Institute of Science, Technology and Advanced Studies, Pallavaram

Abstract:

The quick, high-throughput sequencing of DNA and RNA with unmatched accuracy and efficiency is made possible by Next-Generation Sequencing (NGS), a revolutionary development in genomics. Compared to more conventional techniques like Sanger sequencing, NGS technologies offer comprehensive genetic data at a substantially lower cost by enabling the simultaneous sequencing of millions to billions of DNA fragments. This has created new opportunities in clinical diagnostics, customized therapy, and genomic research. Important NGS platforms, such as Oxford Nanopore, Pacific Biosciences, Ion Torrent, and Illumina, use various sequencing technologies to serve a variety of applications. PacBio's single-molecule real-time (SMRT) sequencing, Oxford Nanopore's nanopore-based sequencing, Ion Torrent's semiconductor technology, and Illumina's sequencing-by-synthesis approach each provide special benefits like high accuracy, longer read lengths, and portability. These methods are widely used in many different fields, such as non-invasive prenatal testing (NIPT), infectious disease diagnostics, cancer genomics, and genomic research. In addition to improving diagnostic skills for infectious diseases and genetic disorders, NGS has been crucial in finding genetic alterations, comprehending disease mechanisms, and enabling targeted therapeutics in oncology. NGS has a number of obstacles in spite of its revolutionary influence. For efficient analysis and interpretation of the vast amount of data produced by NGS, advanced bioinformatics tools and computational resources are needed. Furthermore, error rates can still make it difficult to guarantee data fidelity, particularly with long-read technologies. Even while sequencing has become much less expensive over time, some areas or applications still find it too expensive. Furthermore, as NGS is increasingly incorporated into clinical practice, ethical issues pertaining to data privacy, genetic prejudice, and the handling of genomic information continue to be a critical topic of focus. With continuous developments aiming at enhancing sequencing accuracy, speed, and affordability, NGS has a bright future ahead of it. It is anticipated that when the technology develops further, it will be a standard component of clinical diagnostics and healthcare, providing individualized treatment options and deepening our

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knowledge of human disease and genomes. NGS integration into clinical workflows has the potential to transform medicine by increasing its precision, personalization, and predictiveness.

Keywords: *Next-Generation Sequencing, nanopore, diagnostics, Illumina, Pacific Biosciences.*

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A brief overview on advancements in sequence alignment algorithms

Roshan Roy Dayanicis,

B.Sc., Biocomputing, Department of Bioinformatics,

Vels Institute of Science, Technology and Advanced Studies, Pallavaram

Abstract:

Sequence alignment is a cornerstone technique in bioinformatics, used to compare biological sequences for functional, structural, and evolutionary insights. This article provides a concise review of key alignment algorithms—global, local, and heuristic methods—highlighting their applications, advantages, and limitations. With the growing complexity of genomic data, the article also explores recent advancements in machine learning and computational strategies aimed at improving alignment accuracy and efficiency.

Keywords: *Sequence Alignment, Bioinformatics, Algorithms, Genomics, Machine Learning.*

1. Introduction

Sequence alignment is essential in bioinformatics for comparing DNA, RNA, or protein sequences. The two main types are global alignment, which compares entire sequences, and local alignment, which focuses on regions of similarity. Alignment techniques have evolved significantly, driven by the increasing scale of genomic data and the need for computational efficiency.

2. Key Alignment Algorithms

2.1 Global Alignment

The Needleman-Wunsch algorithm (1970) performs global alignment by aligning two sequences from end to end using dynamic programming. It guarantees optimal results but is computationally intensive for large sequences.

Pros: Optimal for full sequence comparison.

Cons: Slow for long sequences.

2.2 Local Alignment

The Smith-Waterman algorithm (1981) allows for local alignment, finding high-scoring regions of similarity within sequences. It's more suitable for identifying conserved domains but also computationally demanding.

Pros: Identifies localized similarities effectively.

Cons: Computationally expensive.

2.3 Heuristic Methods

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BLAST and FASTA are heuristic algorithms designed to speed up the alignment process by using a seed-and-extend approach. They are much faster than dynamic programming but may sacrifice some accuracy.

Pros: Fast and scalable for large datasets.

Cons: Less accurate than exact methods.

3. Applications of Sequence Alignment

Genomics: Sequence alignment is crucial for genome assembly, variant detection, and gene annotation. Tools like Bowtie2 and BWA are commonly used for efficient alignment of DNA sequences to reference genomes.

Proteomics: In protein bioinformatics, tools like BLASTP are used to identify conserved protein domains, aiding in function prediction and structure analysis.

Phylogenetics: Sequence alignment underpins the construction of phylogenetic trees, helping to trace evolutionary relationships among species.

4. Challenges and Future Trends

4.1 Computational Efficiency

Handling large genomic datasets remains a major challenge. Advanced methods such as GPU acceleration and parallel computing are being integrated into alignment algorithms to improve speed and scalability.

4.2 Machine Learning Approaches

Machine learning, particularly deep learning, is being explored to enhance alignment accuracy. Models that predict optimal alignments based on sequence features are showing promise, potentially improving performance over traditional scoring systems.

4.3 Long-Read Sequencing

With the advent of long-read sequencing technologies (e.g., PacBio, Oxford Nanopore), new algorithms like Minimap2 are being developed to handle error-prone, long DNA reads efficiently.

5. Conclusion

Sequence alignment remains a crucial tool in bioinformatics for analyzing biological data. While traditional algorithms like Needleman-Wunsch and Smith-Waterman provide high accuracy, heuristic methods like BLAST offer faster solutions for large datasets. Emerging computational techniques, including machine learning, promise to further improve alignment accuracy and speed, especially as genomic data continues to grow in size and complexity.

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References:

Needleman, S. B., & Wunsch, C. D. (1970). A general method applicable to the search for similarities in the amino acid sequence of two proteins. Journal of Molecular Biology.

Smith, T. F., & Waterman, M. S. (1981). Identification of common molecular subsequences. Journal of Molecular Biology.

Altschul, S. F., et al. (1990). Basic local alignment search tool. Journal of Molecular Biology.

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Insilico Protein structure prediction for Thyroid using homology modelling

Surender.D,

B.Sc., Biocomputing, Department of Bioinformatics,

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Abstract:

Computational methods such as docking analyses and homology modelling are crucial for comprehending molecular interactions, especially in drug resistance research. The Ras and Rab interactor-like protein (RasL) linked to rheumatoid arthritis (RA), a chronic autoimmune illness marked by tissue damage and joint inflammation, was the main focus of this study. The pathophysiology of RA has been linked to RasL, a crucial mediator in the control of intracellular signalling pathways. We used homology modelling to estimate the 3D structure of RasL because experimental protein structures are limited. Using templates from closely related proteins with known structures, comparative modelling was carried out, producing a high-quality model that faithfully captures the functional domains of RasL. Natural plant extracts and compounds (NPECs), which originate from herbs or plants, have been used in the clinical treatment of rheumatoid arthritis (RA) for many years. Over the years, many scientists have carried out a series of studies on the treatment of RA by NPEC. RasL interactions with different inhibitors were evaluated using molecular docking in order to look into possible drug resistance mechanisms. Key residues in RasL that aid in drug binding were identified by docking simulations, indicating locations that could experience changes that result in resistance. These revelations on the structure-function relationship of RasL enhance our knowledge of drug resistance in RA and lay the groundwork for the logical development of innovative treatments targeted at reducing RasL-mediated resistance mechanisms in the management of RA. The binding pose energy is **-7.76205 kcal/mol**.

Keywords: *RASL, Natural plant, Homolgy modelling, Structure- function relationship*

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A Review about Bioinformatics

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HISTORY OF BIOINFORMATICS

BIOINFORMATICS

The phrase Bioinformatics was initially introduced in **1960** by Dutch biologists **Paulien Hogeweg** and **Ben Hesper**. Based on their research and findings, Bioinformatics was characterized as the examination of information processes within living systems.

Bioinformatics is a developing area of biological science that has arisen from the integration of biology and information technology. This interdisciplinary field encompasses various disciplines, including **Biology, Chemistry, Mathematics, Statistics, and Computer Science**, which have converged to create a unified area of study. This sector primarily focuses on the analysis of biological data and the creation of new software utilizing biological tools.

As stated by the NCBI - National Center for Biotechnology Information, which is part of the National Library of Medicine (NLM) and the National Institutes of Health (NIH), bioinformatics is defined as the computational technology-driven process of analyzing, collecting, classifying, manipulating, recovering, storing, and visualizing all types of biological information

WHY WE USE BIOINFORMATICS?

Bioinformatics has been developed to help scientists analyze and interpret biological data, which has led to advances in medicine, agriculture, and more.

Medical applications:

Drug discovery: Bioinformatics helps develop personalized medicines, drug delivery, and gene therapies.

Disease prevention: Bioinformatics helps identify pathogenic microorganisms and their virulence genes.

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Precision medicine: Bioinformatics helps determine the best course of treatment for a patient.

Agricultural application:

Crop improvement

- Bioinformatics helps identify agriculturally important traits and enhance crop productivity and resilience.
- Bioenergy feedstock
- Bioinformatics helps identify genetic traits that lead to increased biomass production and energy conversion efficiency.

Other applications:

Genome sequencing

- Bioinformatics helps clinicians make rare diagnoses and track infectious organisms.
- Understanding genetic diseases
- Bioinformatics helps scientists understand the variations in genetic codes and predict possible mutations.
- Bioinformatics uses a variety of tools, including databases, algorithms, online platforms, and software. Advancements in artificial intelligence (AI) and machine learning (ML) are helping to make bioinformatics faster and more accurate.

FIVE COMPONENTS OF BIOINFORMATICS

The bioinformatics covers many specialized and advanced areas of biology. Such areas are:

(1) Functional Genomics

(2) Structural Genomics

(3) Comparative Genomics

(4) DNA Microarrays and

(5) Medical Informatics.

Bioinformatics is the combination (or marriage) of biology and information technology.

HOW DOES BIOINFORMATICS WORK

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Bioinformatics operates through the application of computational tools and algorithms by bioinformaticians to address various challenges.

These professionals navigate extensive data sets through intricate processes to uncover insights that are valuable in clinical settings.

They employ software applications such as BLAST and Ensembl to facilitate their analyses.

RESEARCH INVOLVED IN BIOINFORMATICS

Bioinformatics research is predominantly concerned with the examination of extensive biological datasets, such as DNA and protein sequences, through computational techniques. This encompasses various tasks, including sequence alignment, gene identification, genome assembly, protein structure prediction, gene expression analysis, prediction of protein-protein interactions, and modeling of evolutionary relationships. The ultimate goal of these efforts is to gain insights into biological processes and mechanisms at the molecular level.

Significant domains of investigation within bioinformatics encompass the following:

Genomics:

- Sequencing and assembling genomes

- Identifying and annotating genes

- Conducting comparative genomics to analyze genomes across different species

- Performing genome-wide association studies (GWAS)

Transcriptomics:

- Analyzing RNA sequencing data

- Profiling gene expression

- Identifying regulatory elements

Proteomics:

-Protein sequence analysis

-Protein structure prediction

ISBN: 978-81-991683-8-1

-Protein-protein interaction prediction

Structural Bioinformatics:

-Protein structure modeling

-Molecular docking (predicting how small molecules bind to proteins)

Evolutionary Bioinformatics:

-Phylogenetic analysis (tracing evolutionary relationships)

-Sequence alignment algorithms

Systems Biology:

- Analysis of networks to identify interactions among genes and proteins

- Modeling of biological pathways

Medical Bioinformatics:

- Development of personalized medicine

- Discovery and design of pharmaceuticals

- Identification of genes associated with diseases

KEY ELEMENTS OF BIOINFORMATICS RESEARCH INCLUDE

1. **Development of data analysis algorithms:** Innovating computational techniques to process extensive biological datasets.

2**. Database design and management**: Establishing and overseeing databases that store biological information.

3. **Software development**: Designing intuitive tools for effective data visualization and analysis.

4**. Integration of high-throughput data**: Merging data from various sources to achieve a holistic understanding.

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CURRENT RESEARCH IN BIOINFORMATICS

- Geometrical and Physical Effects on the Instability of a Fluid-Conveying Pipe
- Physical and Geometrical Effects on the Vibratory Pattern of a Pipe Carrying Fluid Flow
- Numerical Study of Post-Buckling of Clamped-Pinned Pipe Carrying Fluid Under Different Parameters
- Optimization of Chelating Process of Polysaccharides of Lyophyllum decastes with Zinc and Its Antioxidant Activity
- Theoretical Investigation of Two Antiemetic Drugs at DFT Level.

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A Review on Thalassemia

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Abstract

Thalassemia syndromes are among the most serious and common genetic conditions. They are indigenous in a wide but specific geographical area. However, through migration they are spreading across regions not previously affected. Thalassemias are caused by mutations in the α (*HBA1/HBA2*) and β globin (*HBB*) genes and are usually inherited in an autosomal recessive manner. The corresponding proteins form the adult hemoglobin molecule (HbA) which is a heterotetramer of two α and two β globin chains. Thalassemia-causing mutations lead to an imbalanced globin chain production and consecutively to impaired erythropoiesis. The severity of the disease is largely determined by the degree of chain imbalance. In the worst case, survival is dependent on regular blood transfusions, which in turn cause transfusional iron overload and secondary multi-organ damage due to iron toxicity. A vigorous monitoring and treatment regime is required, even for the milder syndromes. Thalassemias are a major public health issue in many populations which many health authorities fail to address. Even though comprehensive care has resulted in long-term survival and good quality of life, poor access to essential components of management results in complications which increase the cost of treatment and lead to poor outcomes. These requirements are not recognized by measures such as the Global Burden of Disease project, which ranks thalassemia very low in terms of disability-adjusted life years (DALYs), and fails to consider that it ranks highly in the one to four-year-old age group, making it an important contributor to under-5 mortality. Thalassemia does not fulfil the criteria to be accepted as a target disease for neonatal screening. Nevertheless, depending on the screening methodology, severe cases of thalassemia will be detected in most neonatal screening programs for sickle cell disease. This is very valuable because: (1) it helps to prepare the affected families for having a sick child and (2) it is an important measure of secondary prevention.

Keywords: *Thalassemia, Burden of disease, Newborn screening, Hemoglobinopathies*

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Network Pharmacology in Cancer Treatment

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Abstract:

Anisomeles malabarica is a traditional medicinal plant known for its anti-inflammatory, anti-oxidant and anticancer properties. Network pharmacology offers a systematic approach to explore the multi-drug targets using bioactive compounds isolated from *Anisomeles malabarica* and study their interactions with key oncogenic regulators like AKT serine/threonine kinase 1, Tumor Necrosis Factor and signal transducer and activator of transcription 3, which are considered as crucial targets in tumor progression and metastasis. The protein-protein interaction (PPI) tool was used to identify the hub gene. Then the resultant network was exported to Cytoscape software visualize and study further. Pathway enrichment analysis was performed to determine the involvement of these targets in cancer-related signaling pathways, including Phosphoinositide 3-kinase-AKT serine/threonine kinase, Janus Kinase 3 -signal transducer and activator of transcription, nuclear factor kappa-light-chain-enhancer of activated B cells and epidermal growth factor receptor gene signaling. Molecular docking was conducted to evaluate the binding affinity of the compound obtained from the *Anisomeles malabarica* with the selected targets, including AKT1 Protein (PDB ID:7FCV), STAT3 Protein (PDB ID: 4Z1A), and TNF Protein (PDB ID:7YPC). Network analysis revealed that the selected targets play key roles in oncogenic signaling. Anisomelic acid is robust and capable ligand with strong binding affinities with the active sites of drug targets (-10.1 kcal/mol at AKT1), (-9.8kcal/mol at STAT3), (−10.8 kcal/mol at TNF). Those findings highlight the potential of multi-target therapy in cancer.

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Identification of an Allosteric Pocket: Dual site inhibition of *Mycobacterium tuberculosis* Thymidylate kinase by 4-hydroxy esterone

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Abstract

Thymidylate kinase of *Mycobacterium tuberculosis* (TMPKmt) is a crucial enzyme in the pyrimidine nucleotide biosynthesis pathway, playing a vital role in DNA replication and repair. Given its structural differences from the human homolog, TMPKmt serves as a promising pathogen-specific drug target for tuberculosis treatment. This study aims to identify an allosteric binding pocket in TMPKmt and screen potential inhibitors with dual activity at both the allosteric and active sites. The protein's structure (PDB ID: 1W2G) was analyzed using CASTp 3.0 to identify the active site, while PASSer was used to predict the allosteric site and confirmed by Molecular dynamic simulations for cryptic communication site. Virtual screening using MTiOpenScreen was performed against the FOOD-lib database, filtering compounds based on Lipinski's Rule of Five. Molecular docking using AutoDock Vina identified 4-hydroxyestrone (4HY) as a promising ligand with strong binding affinities at both sites (−11.5 kcal/mol at active binding site and -7.1 kcal/mol at allosteric site). The LD50 of 4HY is predicted as 5000mg/kg when compared to traditional first line anti-TB drugs Rifampicin and Isoniazid, 500mg/kg and 133mg/kg, respectively. Also, organ toxicity predicted is comparatively less. Molecular dynamics (MD) simulations using GROMACS confirmed the stability of the protein-ligand complex at allosteric site, with RMSD, RMSF, SASA, and binding free energy calculations supporting favorable interactions. The study highlights the potential of allosteric inhibitors in targeting TMPKmt, offering an alternative approach to combat tuberculosis and antibiotic resistance.

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Computational Identification of Anti-Burkholderia pseudomallei Agents: An Integrated QSAR and Molecular Docking Studies

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Abstract

The bacteria Burkholderia pseudomallei, which is mostly found in soil and water in Southeast Asia, northern Australia, and some regions of Africa, is the cause of melioidosis, an infectious disease that can be fatal. The pressing need for innovative treatment approaches is highlighted by B. pseudomallei's growing resistance to antibiotics and the scarcity of potent antimicrobial medicines. By focusing on important B. pseudomallei virulence variables, this in silico work seeks to find safe and efficient medications to treat melioidosis. The structure of the primary target protein, the type III secretion system (T3SS), was constructed using Modeller and analyzed using the Pymol. Building on evidence that plant-derived compounds are often regarded as safer alternatives to synthetic drugs, we selected 80 phytochemical compounds from various herbaceous plants like *Allium sativum* (garlic), *Curcuma longa* (turmeric),*Zingiber officinale* (ginger) based on a literature survey. The 2D and 3D structures of these compounds were analyzed using the PubChem database. Virtual screening and QSAR (Quantitative Structure-Activity Relationship) studies were performed, leading to the identification of promising phytochemical compounds. Various bioinformatics tools were used to conduct pharmacophore mapping studies, enhancing the prediction of protein-ligand interactions. Finally, molecular docking were carried out between the selected compounds and the target proteins, revealing the best binding energies and interactions with the active site. The results suggest that these phytochemical compounds could serve as potential leads for the development of novel melioidosis inhibitors. Further in vitro studies with the identified compounds could facilitate the discovery of new therapeutic options for melioidosis.

Keywords: Melioidosis, Burkholderia pseudomallei, T3SS, Modeller, Pharmacophore Mapping, QSAR, Molecular Docking.

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Computational Insights into Antimicrobial Resistance in Treponema pallidum: A Bioinformatics-Based Study

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Abstract :

The emergence of antimicrobial resistance (AMR) in Treponema pallidum, the causative agent of syphilis, poses a significant public health challenge, necessitating comprehensive genomic analyses. In this study, we employed a bioinformatics pipeline within the Galaxy platform to identify and characterize AMR determinants in T. pallidum. Whole-genome sequencing data were retrieved from NCBI SRA, followed by quality control using FastQC and Quast. Genome assembly was performed with SPAdes, and annotation was conducted using Prokka. BLAST analysis identified conserved regions and homologous sequences, while AMR gene screening using the Comprehensive Antibiotic Resistance Database (CARD) detected 91 antimicrobial resistance genes, including 90 loose matches and one perfect match. These genes encode diverse resistance mechanisms, suggesting potential multidrug resistance. Identified mechanisms include antibiotic target alteration (e.g., ermB) and efflux pumps (e.g., mtrA), which may confer resistance to antibiotics such as erythromycin, azithromycin, and penicillin. The presence of loose matches suggests potential resistance genes that require further investigation. This study highlights the utility of bioinformatics tools within the Galaxy platform for genomic analysis and AMR characterization.

Keywords: Antimicrobial Resistance, Galaxy, CARD, Treponema pallidum, Syphilis, Bioinformatics

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Phytochemical Profiling and Medicinal Potential of *Costus pictus*: A GC-MS and FTIR-Based Analysis

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ABSTRACT

Many medicinal plants play an essential role in medicine to prevent diseases due to the presence of several active chemicals. An effective strategy to combat non-communicable disease epidemics has been to introduce bioactive compounds from natural sources. *Costus pictus* is a versatile species which have exhibited beneficial properties against a variety of diseases. Multiple bioactive substances found in *C. pictus* have properties that are hypolipidemic, anti-hypertension, and anti-diabetic. GC-MS profiling revealed that the presence of (1alpha,2beta,5alpha)-2,6,6-trimethyl bicyclo [3.1.1] heptane, (*Z*)-9-Octadecenoic acid methyl ester, 1,2,4-Benzenetricarboxylic acid,-dodecyl dimethyl ester, 1-Hexanol, 2-ethyl-, 2,4-bis(1,1-dimethyl ethyl)-phenol, 2-Methoxy-4-vinylphenol, Benzeneethanamine, D-delta-tocopherol, Hexadecanoic acid, methyl ester, Methyl stearate, Phytol, and Phytol, acetate, β-Lapachone, 1,2,3-Propanetriol, 1-acetate, 2,6-Dihydroxynaphthalene, Benzene, (1- methyldodecyl)-, Curan-17-oic acid, 2,16-didehydro-20-hydroxy-, methyl ester, Phytol, (*R*)-(−)-(*Z*)-14-Methyl-8-hexadecen-1-ol, and Docosatrienoic acid and FTIR spectrum confirmed the presence of identified chemical compounds in *C. pictus.*

INTRODUCTION

Medicinal plants are the traditional source of chemical compounds in the field of biotechnology for the discovery of herbal medicine. Most of the pharmaceutical industries depend on these plants for the secondary metabolites for the development of health care products. The secondary metabolites are the phytochemical constituents present in the crude extracts of the plants [1]. In India, there is an increasing demand for natural products from plant sources due to their medicinal

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properties and safety issues. According to World Health Organization, about 80% of the population follow plant-based traditional medicines for primary healthcare [2]. Traditional systems of medicines are prepared from a single plant species or combinations of several plants species. The bioactive component of the plant may be derived from any parts of the plant like leaves, roots, bark, flowers, fruits, and seeds [3]. Plant-based medicines that are derived from crude leaf extracts contain different phytochemicals *Costus igneus*, popularly recognized as the insulin plant, belongs to the Spiral Flag family *Costaceae* and has been recently introduced in India after originating from South and Central America. Predominantly cultivated as an ornamental plant in southern India, its leaves are also utilized as a dietary supplement in diabetes mellitus treatment. Traditionally acclaimed for its diverse medicinal properties. In this study, comprehensive chromatographic and spectral analyses, particularly using Gas Chromatography-Mass Spectrometry (GC-MS), revealed the presence of various bioactive compounds in *Costus igneus extracts.* The presence of bioactive compounds justifies the use of plant leaves for treating various diseases with fewer side effects and recommended the plant of pharmaceutical importance. However, further studies are needed to undertake its bioactivity and toxicity profile. The importance of plants as future sources of natural antimicrobial agents holds great promise. Plants are inexpensive and proved to be effective medicines to cure myriad of diseases from mild microbial infections to complex diseases, including cancers and devastating infectious diseases, such as tuberculosis, caused by Mycobacterium tuberculosis with much less side effects when compared to the synthetic drugs (Abuzeid et al., 2014; Becklund et al., 2010; Koko et al., 2008).

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ARTICLE ON "INTEGRATING MULTI-OMICS DATA FOR PERSONALIZED MEDICINE

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ABSTRACT:

Life science is becoming more collaborative and sophisticated. Scientists use developing and diverse technologies to better comprehend organisms and illnesses at the molecular and system levels. To conduct relevant studies and extract actionable knowledge, researchers must examine heterogeneous data collected from various sources. Data capacity and availability have increased dramatically in recent years, thanks in large part to 'omics' technologies. Current breakthroughs in high-throughput and imaging technology are paving the way for next-generation healthcare that is personalized based on each patient's clinical and molecular characteristics. The Big Data generated by these technologies is of little use to society unless it can be processed, interpreted, and deployed in a relatively tailored and cost-effective manner. Our proposal is to provide some guidance on how to create your own local end-to-end personalized medicine service, from uploading raw data to intelligently integrating and exploring it to providing clinical medical reports with thorough analysis. Multiple abnormalities in the levels of DNA, RNA, and other molecules, including proteins, are the hallmarks of cancer, a complex disease that affects the entire body. The most frequently used data types in multi-omics models are:

- **Genomics** – To identify the nucleotide variants SNPs in the whole genome associated with clinical traits (GWAS – genome-wide association study)
- **Transcriptomics** – To quantify the expression levels of cellular transcripts (e.g. mRNA)

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- **Proteomics** - To characterize the protein expression levels of cells/samples
- **Metabolomics** – To characterize the abundance profile of metabolites and their relative ratios.

Integrating multi-omics data which mostly includes genomes, transcriptomics, proteomics, and metabolomics is causing a revolutionary change in the field of personalized medicine. Through the analysis of Genetic, molecular, and biochemical profiles, this synergy enables a thorough understanding of individual health. More accurate and customized therapeutic approaches are made possible by the creation and integration of multi-omics data, increasing treatment effectiveness and lowering side effects. Personalized medicine, also known as precision medicine, is a medical strategy that categorizes patients based on their expected response or disease risk, aiming to tailor treatment to each patient's unique characteristics, thereby transforming the medical field.

Keywords: *heterogeneous, personalized medicine, interpreted, proteomics, metabolomics, therapeutic, multi-omics data.*

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The Role of Bioinformatics in Parkinson's Disease: Genetic Analysis, Biomarker Discovery, and Precision Medicine

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Abstract

Parkinson's disease (PD) is a progressive neurodegenerative disorder primarily affecting motor function due to the loss of dopamine-producing neurons in the substantia nigra. It is characterized by tremors, rigidity, bradykinesia, and postural instability. The pathogenesis involves genetic and environmental factors, with mutations in genes such as SNCA, LRRK2, PARKIN, and PINK1 playing a crucial role. Bioinformatics has become essential in understanding PD by analyzing genomic data, protein interactions, and molecular pathways. Advanced computational tools like machine learning, network analysis, and next-generation sequencing (NGS) assist in early diagnosis, biomarker discovery, and drug development. Moreover, systems biology approaches help in identifying potential therapeutic targets for disease-modifying treatments. This paper explores the role of bioinformatics in PD research, focusing on genetic analysis, biomarker identification, and precision medicine approaches.

Keywords

Parkinson's disease, neurodegeneration, dopamine, bioinformatics, genomics, biomarkers, next-generation sequencing (NGS), machine learning, protein interactions, precision medicine.

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Gas Chromatography-Mass Spectrometry: A Powerful Tool for Molecular Analysis

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Abstract

Gas Chromatography-Mass Spectrometry (GC-MS) is a powerful analytical technique that integrates the separation capabilities of Gas Chromatography (GC) with the identification precision of Mass Spectrometry (MS). This technique is widely used for the qualitative and quantitative analysis of volatile and semi-volatile compounds in complex mixtures. In GC-MS, a sample is vaporized and carried by an inert gas through a chromatographic column, where compounds are separated based on their volatility and interaction with the stationary phase. The separated analytes then enter the mass spectrometer, where they undergo ionization, fragmentation, and mass-to-charge (m/z) analysis, producing unique mass spectra that facilitate compound identification.GC-MS is highly sensitive, selective, and precise, making it ideal for detecting trace compounds in environmental samples, biological matrices, food products, and forensic evidence. It provides comprehensive qualitative and quantitative data in a single run, making it invaluable for complex mixture analysis. The technique plays a critical role in various fields, including clinical diagnostics, toxicology, pharmaceuticals, metabolomics, and quality control. By coupling gas chromatography with mass spectrometry, GC-MS enables detailed molecular analysis and remains an indispensable tool in analytical chemistry and scientific research.

Keywords: Gas Chromatography, Mass Spectrometry, Analytical Chemistry, Volatile Compounds, Forensic Analysis, Metabolomics

ISBN: 978-81-991683-8-1

ADVANCING BIOINFORMATICS THROUGH MACHINE LEARNING: APPLICATIONS, CHALLENGES, AND FUTURE PERSPECTIVES

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Abstract

Bioinformatics, an interdisciplinary field integrating biology, computer science, and mathematics, has witnessed significant advancements with the incorporation of machine learning (ML) algorithms. ML techniques have revolutionized the analysis of large-scale biological data, enabling efficient pattern recognition, predictive modeling, and decision-making in various domains, including genomics, proteomics, and drug discovery. This paper explores the application of ML algorithms, such as deep learning, support vector machines, random forests, and neural networks, in bioinformatics research. These algorithms facilitate functional annotation of genes, protein structure prediction, disease classification, and biomarker identification, thereby accelerating precision medicine and personalized therapeutics. The integration of ML in bioinformatics not only enhances computational efficiency but also provides novel insights into complex biological processes. This study discusses recent advancements, challenges, and future perspectives in the application of ML for biological data analysis, emphasizing its role in transforming modern bioinformatics research.

Keywords:

Machine learning, Algorithms, deep learning, Bioinformatics and drug discovery.

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Computational Nanomedicine: Bioinformatics-Driven Design of Nanocarriers for Targeted Drug Delivery

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Abstract

The integration of bioinformatics and nanotechnology has revolutionized the field of precision medicine, particularly in targeted drug delivery. This interdisciplinary approach, known as computational nanomedicine, leverages bioinformatics tools to analyze genomic, proteomic, and molecular interaction data to identify optimal targets for nanocarrier-based drug delivery systems. Nanotechnology enables the development of advanced nanocarriers, such as liposomes, dendrimers, and polymeric nanoparticles, which can efficiently encapsulate therapeutic agents and deliver them to specific cells or tissues with minimal toxicity. Bioinformatics-driven simulations and molecular docking studies facilitate the rational design of these nanocarriers, optimizing their biocompatibility, stability, and efficiency in crossing biological barriers. In the context of cancer therapy, bioinformatics aids in understanding tumor microenvironments and identifying biomarkers for personalized treatment, while nanocarriers enhance drug solubility, bioavailability, and controlled release. This synergy between bioinformatics and nanotechnology holds immense potential in advancing nanomedicine, paving the way for next-generation targeted therapies with improved therapeutic outcomes and reduced side effects.

Keywords: *Nanomedicine, Nanotecchnology, Nanocarriers.*

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PREDICTING HEART DISEASE USING AI WITH PYTHON CODING

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Abstract:

Heart disease remains one of the leading causes of mortality worldwide, making early diagnosis and prediction crucial for effective treatment and prevention. This study explores the use of Artificial Intelligence (AI) and Machine Learning (ML) techniques to predict heart disease based on clinical data. Using Python, we develop a predictive model leveraging algorithms such as Logistic Regression, Decision Trees, Random Forest, and Neural Networks. The dataset is preprocessed through feature selection, normalization, and handling missing values to enhance model performance. The model is trained and evaluated using key performance metrics like accuracy, precision, recall, and F1-score. Additionally, we deploy the trained model using Flask or a cloud-based service for real-time prediction. This AI-driven approach aims to assist healthcare professionals in early detection and decision-making, potentially improving patient outcomes and reducing healthcare burdens.

Keywords: Heart Disease Prediction, Machine Learning, Artificial Intelligence, Neural Networks, Model Evaluation.

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Unravelling the Genomic Landscape of Candida Auris: Resistance Mechanisms, Virulence Factors, and Gene Expression Profiling

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Abstract:

The rising multidrug-resistant fungal infection Candida auris is a serious concern to public health around the world because of its high transmissibility, tenacious colonization, and resistance to antifungal medications. Its genomic structure, virulence factors, and methods of antibiotic resistance are all revealed by whole-genome assembly and annotation. Using a mix of long-read and short-read sequencing methods, we were able to achieve high-quality genome assembly of C. auris in this study, accurately and thoroughly representing its genome. Using structural and functional annotation, important genes linked to stress tolerance, biofilm development, and antifungal resistance were found. Additionally, under distinct environmental and drug-induced stress settings, differentially expressed genes (DEGs) were identified by comparative transcriptome analysis, identifying pathways essential for pathogenicity and survival. Important genetic factors linked to virulence, biofilm formation, and stress response were identified using functional annotation. Furthermore, we discovered and described antifungal resistance genes, such as mutations in transporter genes like CDR1 and MDR1 that lead to multidrug resistance, FKS1 (echinocandin resistance), and ERG11 (azole resistance).Our research advances our knowledge of the pathophysiology of C. auris and could help create new diagnostic and treatment approaches to fight infections brought on by this multidrug-resistant yeast.

Keywords: Candida auris, Multidrug Resistance, Genome Assembly, Antifungal Resistance, Transcriptome Analysis.

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Critiques

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An article on Morquio Syndrome

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Overview:

Morquio syndrome, also called mucopolysaccharidosis type IV (MPS IV), is a rare metabolic disorder in which the body is unable to break down certain sugar molecules known as glycosaminoglycans (GAGs), or mucopolysaccharides. In individuals with Morquio syndrome, keratan sulfate, a specific type of GAG, accumulates in the body. This condition, which is inherited in an autosomal recessive pattern, is classified as a lysosomal storage disorder. The buildup of GAGs affects multiple organ systems, leading to a wide range of symptoms. In the United States, the estimated incidence of Morquio syndrome ranges from 1 in 200,000 to 1 in 300,000 live births.

Signs and symptoms:

Patients with Morquio syndrome appear healthy at birth. While both Type A and Type B present similarly, Type B generally has milder symptoms. The condition typically becomes noticeable between the ages of 1 and 3. Morquio syndrome leads to progressive skeletal changes in the ribs and chest, which can result in neurological complications such as nerve compression. Other common symptoms include hearing loss and clouded corneas. However, intelligence is usually unaffected unless hydrocephalus develops and remains untreated.

Physical growth slows and often ceases around age 8. Skeletal abnormalities associated with Morquio syndrome include a bell-shaped chest, widely spaced teeth with thin enamel, spinal curvature or flattening, shortened long bones, and dysplasia of the hips, knees, ankles, and wrists. In some cases, the bones that stabilize the connection between the head and neck are malformed (odontoid hypoplasia), which may require spinal cervical fusion surgery to prevent life-threatening complications. These skeletal issues often cause gait abnormalities and frequent falls.

Cause:

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Morquio syndrome is an autosomal recessive disorder caused by defective genes that prevent the breakdown of keratan sulfate. When both parents carry a faulty gene, their child may inherit no functional copies, leading to toxic buildup in cells. Though babies appear healthy at birth, symptoms develop over time as damage accumulates.

Classification:

Morquio syndrome type	**Affected Gene**	**Missing enzyme**	**Chromosomal region**
Type A	GALNS	Galactosamine-6 sulfatase	16q24
Type b	GLB1	Beta-galactosidase	3p22

Treatment:

The treatment for Morquio syndrome includes prenatal identification and enzyme replacement therapy. On February 12, 2014, the U.S. Food and Drug Administration (FDA) approved elosulfase alfa (Vimizim) as a treatment for Morquio A (MPS IVA). However, there is currently no approved treatment for Morquio B (MPS IVB).

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An article on paraganglioma

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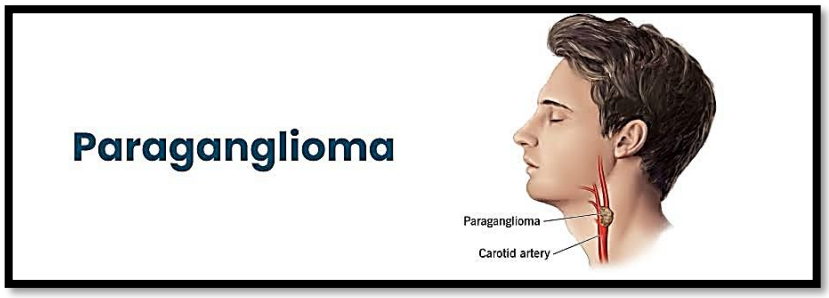
Paragangliomas are rare neuroendocrine tumors arising from paraganglia, collections of cells found throughout the body, and can be functional (secretory) or non-functional, manifesting as various symptoms depending on their location and hormone production



- **Origin:**

Paragangliomas originate from neural crest cells, which also form the paraganglia, a diffuse neuroendocrine system found from the skull base to the pelvic floor.

- **Function:**
    - **Functional Paragangliomas:** Some paragangliomas are functional, meaning they secrete catecholamines (hormones like adrenaline and noradrenaline), leading to symptoms like hypertension, sweating, and palpitations.
    - **Non-Functional Paragangliomas:** Others are non-functional and do not produce excessive hormones, and may be discovered incidentally during imaging studies.
- **Clinical Manifestations:**

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The symptoms depend on the tumor's location and whether it is functional:

- **Head and Neck:** Painless masses, hoarseness, hearing loss, tinnitus, and cranial nerve deficits.
- **Functional Paragangliomas:** Hypertensive episodes, headaches, sweating, and palpitations.

- **Diagnosis:**

Diagnosis involves a combination of imaging (CT, MRI, PET/CT scans), biochemical tests (measuring catecholamine levels), and potentially genetic testing.

- **Treatment:**

Treatment usually involves surgical removal, and in some cases, other approaches like radiation therapy or peptide receptor radionuclide therapy (PRRT) may be considered.

- **Prognosis:**

Paragangliomas can be benign or malignant, with malignancy being more common in extra-adrenal paragangliomas (PGLs) or those associated with hereditary syndromes.

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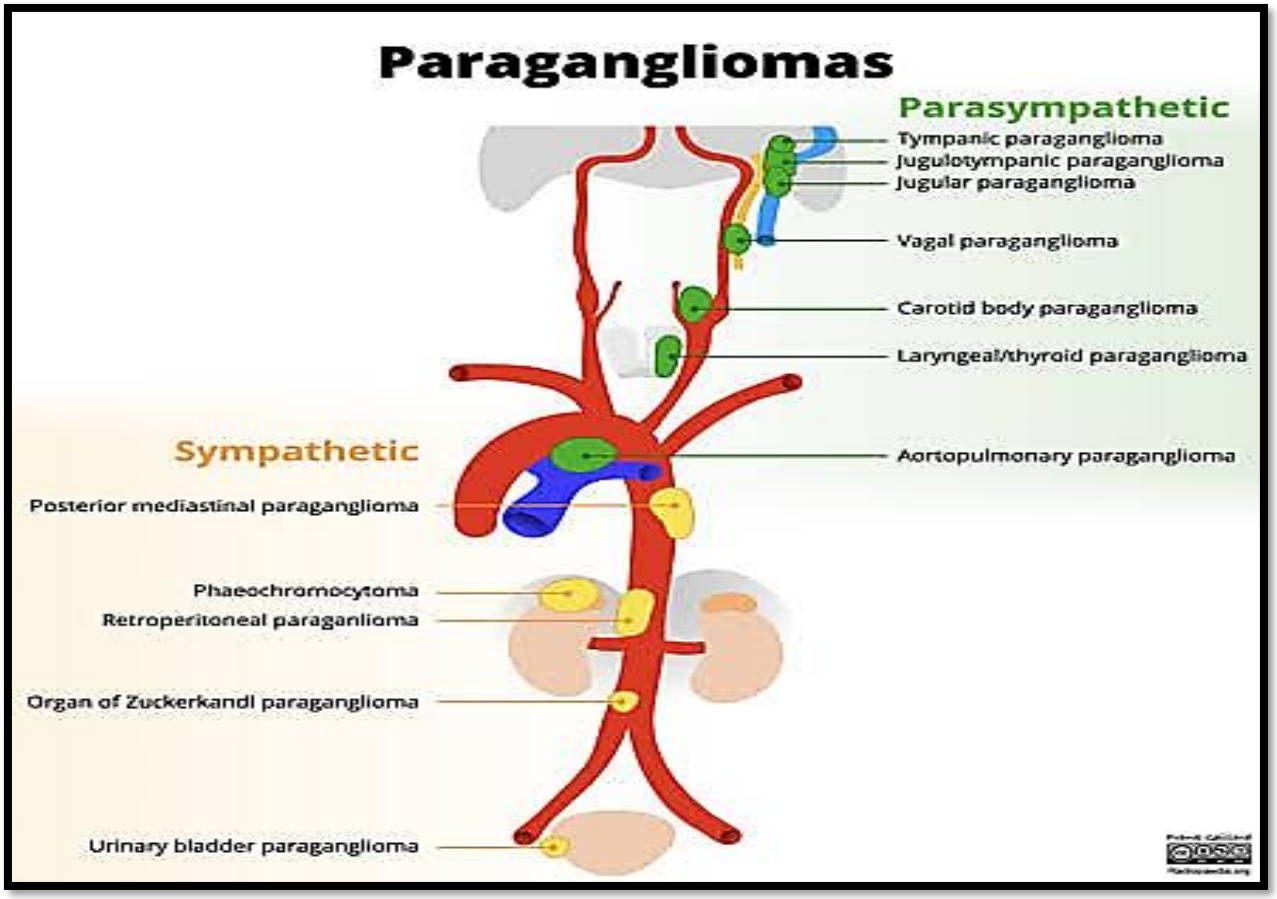

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An article on Fabry disease

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Fabry disease is the second most frequent lysosomal storage disorder. It is a X-linked genetic disease secondary to alpha-galactosidase A enzyme deficiency. This is a progressive and systemic disease that affects both males and females. Classical symptoms and organ involvements are acral pain crisis, cornea verticillata, hypertrophic cardiomyopathy, stroke and chronic kidney disease with proteinuria. Nevertheless, organ damages can be missing or pauci-symptomatic and other common symptoms are poorly recognised, such as gastrointestinal or ear involvement. In classical Fabry disease, symptoms first appear during childhood or teenage in males, but later in females. Patients may have non-classical or late-onset Fabry disease with delayed manifestations or with single-organ involvement. Recognition of Fabry disease is important because treatments are available, but it may be challenging. Diagnosis is easy in males, with dosage of alpha-galactosidase A enzyme activity into leukocytes, but more difficult in females who can express normal residual activity. Other plasmatic biomarkers, such as lyso-globotriaosylceramide (lyso-Gb3), are interesting in females, but need to be associated with GLA gene analysis. In this review, we aimed at summarize the main clinical manifestations of Fabry disease and propose a practical algorithm to know how to diagnose this complex disease.

Keywords: Alpha-galactosidase A; Angiokeratoma; Angiokératome; Diagnosis; Diagnostic; Enzyme replacement therapy; Enzymothérapie substitutive; Fabry disease; GLA; Lyso-Gb3; Maladie de Fabry; Migalastat; Traitement; Treatment.

Screening Test of Fabry Disease in Patients with Renal Replacement Therapy

Abstract

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Background: Fabry disease is a rare genetic lysosomal storage disease, inherited in an X-linked manner, characterized by lysosomal deposition of globotriaosylceramide due to deficient activity of the enzyme α-galactosidase A. Because the prevalence of this genetic disorder is unknown in the Emilia Romagna region, we conducted a screening study to assess the prevalence of Fabry disease in the city of Modena, Italy.

Material and methods: A screening study has been conducted in patients on renal replacement therapy at University Hospital of Modena. Screening tests have been performed using dried blood spot method. Alpha-galactosidase A activity and Lyso-Gb3 levels were evaluated in peripheral blood of all men. In women test based on genetic analysis; Lyso-Gb3 was measured only in patients with mutation of gene GLA.

Results: Screening tests have been performed on 388 subjects: 181 maintenance hemodialysis patients, 166 kidney transplant recipients and 41 peritoneal dialysis patients. About 40% of the patients did not had etiological diagnosis of renal disease. Lyso-Gb3 was more specific test than α- galactosidase A (100% vs. 82.5%) to diagnose Fabry disease. We found two different mutations: c.13 A >G p.(Asn5Asp), a variant likely benign and c.937 G >T p.(Asp313Tyr) a variant of uncertain significance. Both the patients carrying these genetic mutations had no symptoms or medical history compatible with Fabry disease.

Conclusion: Identification of variant of uncertain significance such as c.937G >Tp.(Asp313Tyr) showed the limits of genetic analysis to diagnose an inherit disease. Further studies are need to assess the diagnostic value of Lyso-Gb3 for screening for Fabry disease.

Keywords: Fabry Disease; D313Y; Lyso-Gb3; Screening; c.13 A>G p. Asn5Asp; c.937 G>T p.(Asp313Tyr); α-galactosidase A.

Fabry Disease and Inflammation: Potential Role of p65 iso5, an Isoform of the NF-κB Complex

Abstract

Fabry disease (FD) is an X-linked lysosomal storage disease, caused by mutations in the GLA gene on the X chromosome, resulting in a deficiency of the lysosomal enzyme α-GAL. This leads to the progressive accumulation of Gb3 in cells, causing multi-systemic effects. FD has been classified as a subgroup of autoinflammatory diseases. NF-κB is a family of ubiquitous and inducible

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transcription factors that play critical roles in inflammation, in which the p65/p50 heterodimer is the most abundant. The glucocorticoid receptor (GR) represents the physiological antagonists in the inflammation process. A novel spliced variant of p65, named p65 iso5, which can bind the dexamethasone, enhancing GR activity, has been found. This study investigates the potential role of p65 iso5 in the inflammation of subjects with FD. We evaluated in peripheral blood mononuclear cells (PBMCs), from over 100 FD patients, the p65 iso5 mRNA level, and the protein expression. The results showed significantly lower p65 iso5 mRNA and protein expression levels compared to controls. These findings, along with the ability of p65 iso5 to bind dexamethasone and the regulation of the glucocorticoid response in the opposite way of p65, strongly suggest the involvement of p65 iso5 in the inflammatory response in FD.

Keywords: Fabry disease; NF-κB; inflammation; p65; p65 iso5.

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An article on to perform the java program using selenium to retrieve primary, secondary, tertiary structures of proteins

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AIM:

To retrieve primary, secondarysequences & tertiary structure of proteins using java program automated using selenium. The sequences and structures retrieve using below mentioned tools.

The creation of an automated web application using Selenium WebDriver in a Java environment using the Eclipse IDE is demonstrated in this project.

Integrating bioinformatics tools such as ProtParam, GOR4, and SwissModel for the automated retrieval and analysis of protein sequence data from publically accessible databases is the project's main objective.

INTRODUCTION:

By creating an automated system with Java and Selenium WebDriver inside the Eclipse IDE, this project seeks to overcome these issues.

Selenium is a robust web automation framework that is commonly used for online application testing, but it may also be used to automate repetitive processes, such as bioinformatics analysis.

This system automates the retrieval and analysis of protein sequence data by combining bioinformatics tools like ProtParam, GOR4, and SwissModel, giving researchers a more streamlined and effective workflow.

TOOLS:

a. ProtParam: To retrieve physicochemical parameters of a protein sequence.
b. GOR4: To predict the secondary structure of a protein.
c. SwissModel: To retrieve the 3D tertiary structure of a protein.
d. Selenium WebDriver: To automate web interactions for retrieving data.
e. Java: The programming language for writing automation scripts.
f. Eclipse IDE: For developing and running the Java code.

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SYSTEM WORKFLOW:

Step 1: Launch Selenium WebDriver

- Initialize the WebDriver in the Java code, launching a browser (e.g., Chrome or Firefox) and navigating to the necessary tool websites (ProtParam, GOR4, SwissModel).

Step 2: Data Input

- Automate entering the protein sequence into the relevant form fields for each tool.
- Ensure that the input sequence is correctly formatted and that the tool accepts it. Use Selenium's WebElement locators to interact with form fields.

Step 3: Submit Form

- Submit the sequence data using Selenium's .submit() or .click() on the submit button. Handle any form submission delays with explicit waits to ensure the page is ready for the next action.

Step 4: Retrieve Results

- For each tool, wait for the results to load and use Selenium's WebDriver to extract the data (e.g., text or URLs). This can be done with .getText() for text data or .getAttribute("href") for links (like the link to the 3D model).
- For ProtParam, extract parameters like molecular weight, instability index, and other characteristics.
- For GOR4, extract the predicted secondary structure data (e.g., percentages of alpha-helices, beta-sheets).
- For SwissModel, download or extract information about the protein's tertiary structure.

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An article on Hypertension

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Introduction

Hypertension is also known as high blood pressure. It is defined as transitory (short-lived) or chronic elevation of the blood pressure in the arteries. This elevation may lead to cardiovascular damage. When left untreated, the damage to the circulatory system can cause heart attack, stroke, heart failure, heart disease and kidney failure. Types of hypertension The two types of hypertension are essential or secondary. High blood pressure with an unknown cause is essential hypertension and tends to develop over many years. High blood pressure with a known or direct cause is secondary hypertension. This type of hypertension tends to appear suddenly and can be caused by conditions such as obstructive sleep apnea, kidney disease, adrenal gland tumors, thyroid problems or medications such as use of birth control pills or illegal drugs like cocaine and amphetamines. Rates and risk factors Risk of hypertension increases with age. It is more common in men (50%), while women (44%) are more likely to develop hypertension after age 65. Hypertension is more common among non-Hispanic black adults (56%) compared with non-Hispanic white adults (48%), non-Hispanic Asian adults (46%) and Hispanic adults (39%). Conditions, such as stroke, heart attack and kidney failure, are also more common in the non-Hispanic black group as well. Treatment and prevention Hypertension is treated by changing lifestyle factors including eating, smoking and exercise habits. Pharmaceutical interventions include ACE inhibitors, ARB drugs, beta-blockers, diuretics, calcium channel blockers, alpha-blockers and peripheral vasodilators. The best way to prevent hypertension is to eat healthy and get exercise. Eating more fruits and vegetables and limiting saturated fats and eliminating trans fats are helpful ways to prevent hypertension. Reduction of stress, salt intake and alcohol intake are also helpful ways to prevent hypertension. Regularly checking blood pressure, staying on track with treatment (diet, exercise and medication) and managing other medical conditions can help patients manage their

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hypertension Epidemiology Elevated arterial pressure is one of the most important public health problems in developed countries. In the United States, for instance, nearly 30 percent of the adult population is hypertensive. High blood pressure is significantly more prevalent and serious among African Americans. Age, race, sex, smoking, alcohol intake, elevated serum cholesterol, salt intake, glucose intolerance, obesity, and stress all may contribute to the degree and prognosis of the disease. In both men and women, the risk of developing high blood pressure increases with age. Hypertension has been called the “silent killer” because it usually produces no symptoms. It is important, therefore, for anyone with risk factors to have their blood pressure checked regularly and to make appropriate lifestyle Complications The most common immediate cause of hypertension-related death is heart disease, but death from stroke or renal (kidney) failure is also frequent. Complications result directly from the increased pressure (cerebral hemorrhage, retinopathy, left ventricular hypertrophy, congestive heart failure, arterial aneurysm, and vascular rupture), from atherosclerosis (increased coronary, cerebral, and renal vascular resistance), and from decreased blood flow and ischemia (myocardial infarction, cerebral thrombosis and infarction, and renal nephrosclerosis). The risk of developing many of these complications is greatly elevated when hypertension is diagnosed in young adulthood.

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An Article on Malnutrition in Children

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What is malnutrition?

Your body needs a variety of nutrients, and in certain amounts, to maintain its tissues and its many functions. Malnutrition happens when the nutrients it gets don't meet these needs. You can be malnourished from an overall lack of nutrients, or you may have an abundance of some kinds of nutrients but lack other kinds. Even the lack of a single vitamin or mineral can have serious health consequences for your body. On the other hand, having an excess of nutrients can also cause problems.

The 4 types of malnutrition?

Malnutrition can mean undernutrition or overnutrition. It can also mean an imbalance of macronutrients (proteins, carbohydrates, fats) or micronutrients (vitamins and minerals).

Undernutrition:

Undernutrition is what most people think of when they think of malnutrition. Undernutrition is a deficiency of nutrients. You may be undernourished if you don't have an adequate diet, or if your body has trouble absorbing enough nutrients from your food. Undernutrition can cause visible wasting of fat and muscle, but it can also be invisible. You can be overweight and undernourished.

Macronutrient undernutrition:

Also called protein-energy undernutrition, this is a deficiency of macronutrients: proteins, carbohydrates and fats. Macronutrients are the main building blocks of your diet, the nutrients that your body relies on to produce energy to maintain itself. Without them — or even just one of them

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— your body soon begins to fall apart, breaking down tissues and shutting down nonessential functions to conserve its low energy.

Micronutrient undernutrition:

Micronutrients are vitamins and minerals. Your body needs these in smaller amounts, but it does need them, for all types of functions. Many people are mildly deficient in certain vitamins and minerals from a lack of variety in their diet. You might not notice a mild vitamin deficiency affecting you, but as micronutrient undernutrition becomes more severe, it can begin to have serious and lasting effects.

Overnutrition:

The World Health Organization has recently added overnutrition to its definition of malnutrition to recognize the detrimental health effects that can be caused by excessive consumption of nutrients. This includes the effects of overweight and obesity, which are strongly associated with a list of noncommunicable diseases (NCDs). It also includes the toxicity that can result from overdosing specific micronutrients.

Malnutrition among Children:

The estimated number of underweight, malnourished and severely malnourished children under 5 years of age is obtained under National Family Health Survey (NFHS) conducted by the Ministry of Health & Family Welfare. As per the recent report of NFHS-5 (2019-21), the nutrition indicators for children under 5 years have improved as compared with NFHS-4 (2015-16). Stunting has reduced from 38.4% to 35.5%, Wasting has reduced from 21.0% to 19.3% and Underweight prevalence has reduced from 35.8% to 32.1%. The detailed list of districts having highest and lowest prevalence of malnutrition among children in the country as per NFHS 5 is at Annexure I. State/UT wise details of malnutrition among children under 5 years as per NFHS 5 is at Annexure II. Government has accorded high priority to the issue of malnutrition and is implementing several schemes like Anganwadi Services, Scheme for Adolescent Girls and Pradhan Mantri Matru Vandana Yojana (PMMVY) under the Umbrella Integrated Child Development Services (ICDS) Scheme as direct targeted interventions to address the problem of malnutrition in the country. Children with Severe Acute Malnutrition are treated at the Nutrition Rehabilitation Centres established by the Ministry of Health and Family Welfare. Further, POSHAN Abhiyaan launched

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on 8th March 2018, aims to reduce malnutrition in the country by adopting a synergised and result oriented approach. Mission Poshan 2.0, an integrated nutrition support programme has been announced in budget 2021-2022 for all States/UTs. It seeks to strengthen nutritional content, delivery, outreach and outcomes with focus on developing practices that nurture health, wellness and immunity to disease and malnutrition. Steps have been taken to improve nutritional quality and testing in accredited labs, strengthen delivery and leverage technology under Poshan Tracker to improve governance. States/UTs have been advised to promote use of AYUSH systems for prevention of malnutrition and related diseases.

Causes of malnutrition in children:

The most common causes of hunger and malnutrition include poverty, wars and natural disasters. The latter are exacerbated by climate change, contributing to the loss of crops, livestock or income opportunities due to extreme weather events such as droughts or floods, and leaving them without food. The risk of malnutrition already starts in the womb. The mother's nutritional status has a significant influence on the development of the unborn child. Malnutrition during pregnancy usually results in children being born underweight and with a weakened immune system. The affected children are therefore more at risk of dying in infancy. The effects of early malnutrition are also noticeable later in life – these children are often delayed in their development and more susceptible to illness. How we treat children with acute malnutrition: The treatment of acutely malnourished or undernourished children follows a 10-point scheme developed by the World Health Organization (WHO). Treatment and prevention of low blood sugar with glucose: Glucose can be administered orally or intravenously. Treatment of hypothermia and monitoring of body temperature: Hypothermia (body temperature below 35 degrees Celsius) can easily be counteracted with blankets or heaters. Body temperature should be measured and recorded regularly. Treatment of dehydration: Special solutions for rehydration (ReSoMal) are best suited. Care must be taken not to overload the circulation. Close monitoring of pulse and respiratory rate is therefore recommended. Monitoring the electrolyte level: The aim is to bring it back into balance. This can be achieved primarily by administering liquid potassium and magnesium. Administration of a broad-spectrum antibiotic: As infections can occur without symptoms due to the weakened immune system, patients are given a broad-spectrum antibiotic as a precaution. In addition, children over the age of six months are vaccinated against measles if their condition is

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stable. Supplementation of vitamins and trace elements: Vitamin A, zinc, folic acid and iron are particularly important. Administration of supplementary food: The feeding of additional food should be started carefully at first so as not to overload the weakened body. Small, but several portions are given, which should contain around 100 kcal per kilogram of body weight in children. In addition, enough liquid (100-130 ml per kilogram of body weight) should be given. Monitoring the growth: The weight increase should be monitored at regular intervals and ideally be around 10 grams per kilogram of body weight within a day. Create a positive and encouraging environment: As malnutrition often causes a delay in mental development, it is important to provide a supportive and protective environment. Where possible, caregivers should be involved in the treatment. Monitoring and regular check-ups: This should involve the child's parents or caregivers, who will ensure that the follow-up appointments are kept.

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An Article on Application of Machine Learning in Bioinformatics

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Introduction:

Machine learning (ML) is rapidly changing the landscape in the field of bioinformatics with new tools to analyze and interpret complex biological information. Scientists can sift through vast amounts of information, spot patterns, make predictions, and fuel innovations in health and biotechnology using ML techniques.

Application:

Applications of ML in bioinformatics are extensive and potent. ML algorithms can be applied in genomics to predict genes, enhance sequence alignment, and detect mutations. This enhances genome annotation and our understanding about genetic diseases. Such breakthroughs like AlphaFold show ML's ability to predict protein structure and model protein-protein interactions, which inform drug design and disease research. ML extends to personalized medicine and drug discovery, enabling targeted therapy and screening in a virtual environment. In systems biology, ML unscrambles complex networks of metabolic pathways and regulation of genes and sheds light on diseases like cancer and metabolic disorders. Integration with diagnostics has led to breakthroughs in analysis of medical images, enabling early disease detection. Additionally, ML supports public health and epidemiology by making predictions about disease outbreaks, accelerating vaccine manufacturing, and forecasting antimicrobial resistance. Furthermore, ML plays a central part in microbiome analysis, making predictions about microbial species and gene function, and in evolutionary biology, reconstructing evolutionary relationships and identifying patterns in human migration.

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Conclusion:

Machine learning is redefining bioinformatics to enable faster, more precise, and more informative analysis. With advances in ML methods continuing, they will contribute to advances in biotechnology, personalized medicine, and health care, defining the future of these fields.

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An Article on EWING SARCOMA

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Introduction

Ewing sarcoma is a rare type of cancer that occurs in bones or the soft tissue around bones. This tumor is named after Dr.James Ewing in 1921, the pathologist who first described it.It most commonly affects children and young adults, typically between the ages of 10 age 30.Mostly Males are slightly More Likely to develop Ewing sarcoma than females.

Where does it occurs ?

It is Commonly found in long bones,pelvis, ribs, and spine,arm,feet, It can also occur in soft tissues.

What is the Cause of Ewing Sarcoma? The exact cause of Ewing Sarcoma is not Fully understood. However, researchers have discovered chromosomal changes in a cell's DNA that can lead to the formation of Ewing sarcoma. These changes are not inherited. Ewing sarcoma is associated with a genetic translocation between chromosomes 11 and 22, resulting in the EWSR1-Fusion gene. Protein known as EWS-FLI1

Symptoms Pain and swelling at the tumor site,A palpable lump or mass,Fever, fatigue, and weight loss (incases) and Reduced mobility if near a joint.

Diagnosis Imaging Tests:

X-rays, MRI, CT scans, and PET scans.Biopsy: Confirms the presence of cancerous cells.Molecular Testing: Detects the characteristic genetic translocation.

Treatment

Chemotherapy: To shrink the tumor before surgery or radiation. Surgery: Removes the tumor while preserving as much function as possible. Radiation Therapy: Often used if surgery is not feasible or as an adjunct to surgery. Gene Name ALK Protein Tyrosine-protein kinase receptor

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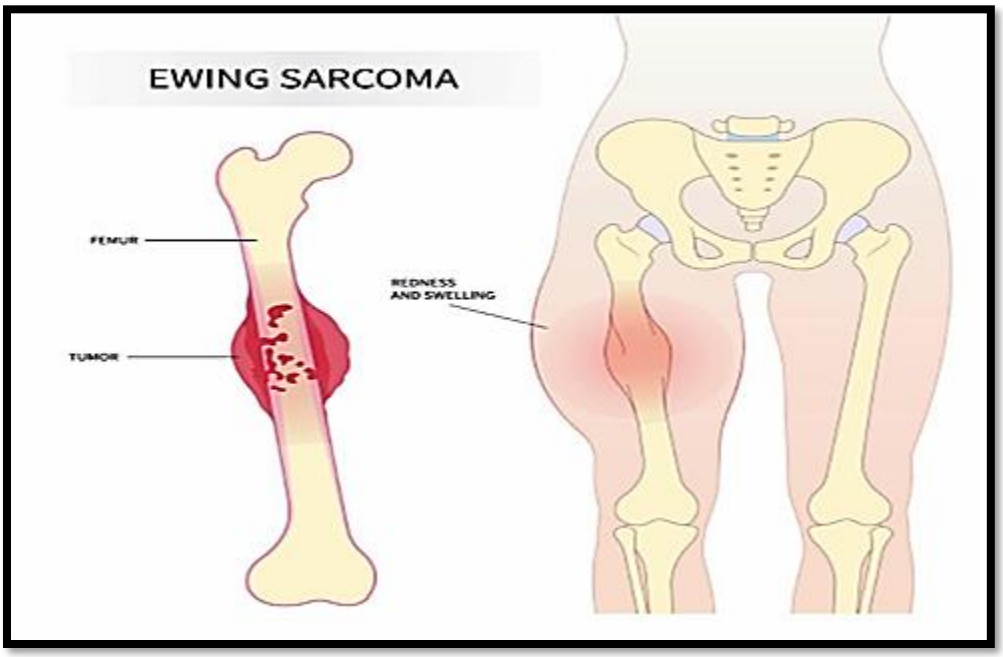
Protein Sequences from uniprot
MGAIGLLWLLPLLLSTAAVGSGMGTGQRAGSPAAGPPLQPREPLSRLQ
RKSLAVDFVVPSLFRVYARDLLLPPSSSELKAGRPEARGSLALDCAPLL
RLLGPAPGVSWTAGSPAPAEARTLSRVLKGGSVRKLRRAKQLVLELGE
EAILEGCVGPPGEAAVGLLQFNLSELFSWWIRQ

Reference article for Ewing's sarcoma. Balamuth NJ, Womer RB. Lancet Oncol. 2010 Feb;11(2):184-92. doi: 10.1016/S1470-2045(09)70286-4. PMID: 20152770 Review. Progress in the treatment of Ewing's sarcoma, the second most common bone tumour in children and adolescents, has improved survival from about 10% in the period before chemotherapy was introduced to about 75% today for patients with localised tumours.



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An Article on Next-Generation Sequencing

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Introduction

Imagine being able to read an entire book in minutes instead of days. That's what Next-Generation Sequencing (NGS) does for DNA. It allows scientists to decode genetic information faster, cheaper, and more accurately than ever before. This breakthrough is reshaping medicine, research, and even agriculture, bringing us closer to a world where diseases can be detected early, treatments are personalized, and crops are engineered to withstand harsh climates. Before NGS, researchers used Sanger sequencing, a slow and costly method that could only process small amounts of genetic data at a time. But with NGS, millions—or even billions—of DNA fragments can be sequenced simultaneously, making it possible to analyze entire genomes in just a few hours.

How Does Next-Generation Sequencing Work?

Think of NGS as a highly efficient assembly line for reading DNA. It takes raw genetic material, processes it, and outputs a complete sequence. Here's how:

1. Preparing the DNA Sample Before sequencing, DNA (or RNA) needs to be broken down into small fragments and labeled with special tags (adapters) so that sequencing machines can read them. Scientists often amplify these fragments using a method called PCR (Polymerase Chain Reaction) to ensure there's enough DNA for accurate sequencing.

2. Sequencing the DNA This is where the real magic happens! Different sequencing technologies use various methods to determine the order of DNA's building blocks—A, T, C, and G. Some of the most popular platforms include: Illumina (Sequencing by Synthesis): Uses fluorescent markers to detect each nucleotide as it's added. PacBio (Single-Molecule Real-Time Sequencing): Reads long DNA fragments in real time. Oxford Nanopore: Pulls DNA strands through tiny pores and measures electrical changes to determine the sequence. Each method has its strengths depending

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on the application. Some are better for detecting tiny mutations, while others can read long stretches of DNA, making them ideal for studying complex genetic structures.

3. Analyzing the Data Once the sequencing machine has done its job, scientists are left with huge amounts of raw data— sometimes terabytes per experiment. This is where bioinformatics comes in. Advanced computing tools help: Assemble the DNA sequence like a puzzle. Identify mutations, deletions, and variations. Compare the sequence to reference genomes. Make sense of the data for medical or scientific applications.

How Is NGS Changing the World?

NGS isn't just a cool technology—it's actively improving lives across multiple fields.

1. Personalizing Cancer Treatment

Cancer is caused by genetic mutations, and NGS helps pinpoint exactly which mutations are present in a patient's tumor. This means doctors can choose the most effective treatment based on a person's unique cancer profile rather than relying on one-size-fits-all chemotherapy. For example, in lung cancer, patients with an EGFR mutation respond well to targeted drugs that wouldn't work for others. This kind of precision medicine is revolutionizing cancer care.

2. Detecting Infectious Diseases NGS played a key role in tracking COVID-19, allowing scientists to quickly sequence the virus and monitor new variants. It's also used for diagnosing tuberculosis, HIV, and even antibiotic-resistant bacteria, helping doctors choose the right treatments faster.

3. Unlocking the Power of Personalized Medicine What if doctors could prescribe medications based on your DNA? NGS is making this possible by analyzing how different people process drugs. For instance, some people metabolize blood thinners quickly, while others process them slowly—NGS helps doctors determine the safest and most effective dose for each patient.

4. Non-Invasive Prenatal Testing (NIPT) Expecting parents can now get genetic insights about their baby without risky procedures like amniocentesis. A simple blood test can detect genetic conditions such as Down syndrome (Trisomy 21) as early as 10 weeks into pregnancy.

5. Transforming Agriculture and Environmental Science NGS isn't just for human health—it's helping feed the world and protect the environment. Scientists use it to: Improve crops by

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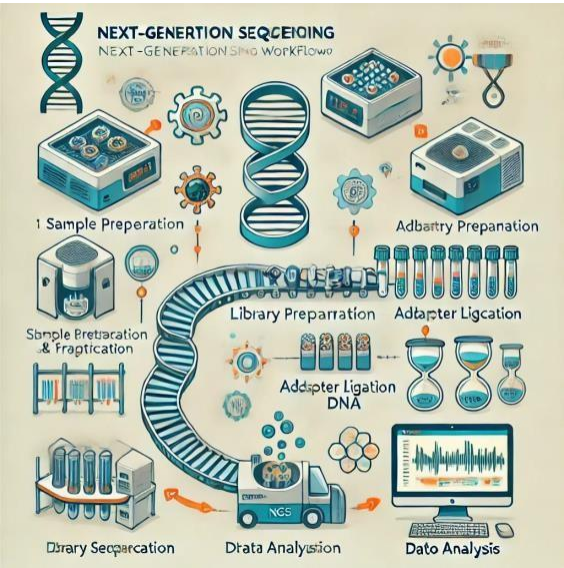
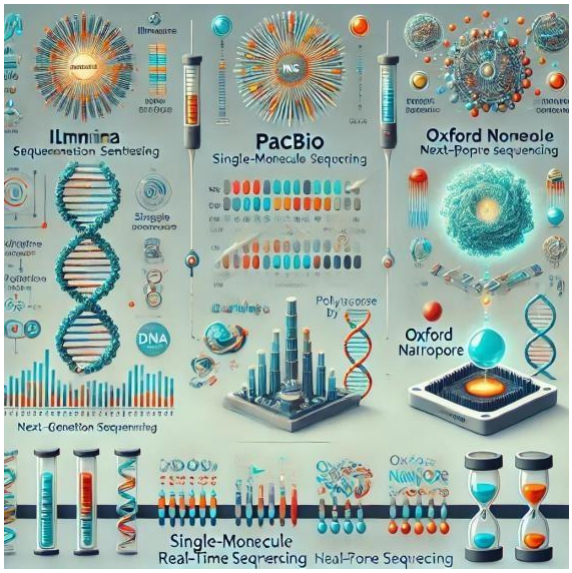
identifying genes for disease resistance and better yields. Track endangered species through environmental DNA (eDNA) left in water or soil. Study the microbiome of soil and oceans to understand climate change impacts. Challenges and The Future of NGS Despite its incredible potential, NGS has some hurdles to overcome: Cost: While sequencing is much cheaper than before, data analysis and storage remain expensive. Data Overload: A single human genome generates hundreds of gigabytes of data, requiring powerful computing resources. Accuracy: Some sequencing platforms have higher error rates, requiring cross-checking with different technologies. Ethical Concerns: As more people get their genomes sequenced, privacy and data security are major concerns.

Conclusion

NGS is more than just a scientific tool—it's reshaping medicine, research, and even the way we grow food. Whether it's fighting cancer, stopping pandemics, or making precision medicine a reality, this technology is changing lives every day. As sequencing becomes faster, cheaper, and more powerful, its impact will only grow. One day, having your genome sequenced might be as routine as a blood test, leading to a future where healthcare is truly personalized and diseases can be stopped before they even start.





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An Article on Prader-Willi syndrome

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A genetic disorder that causes obesity, intellectual disability and shortness in height. Prader-Willi syndrome is a genetic disorder usually caused by deletion of a part of chromosome 15 passed down by the father. The most common symptoms of Prader-Willi syndrome are behavioral problems, intellectual disability and short stature. Hormonal symptoms include delayed puberty and constant hunger leading to obesity. There is no cure for Prader-Willi syndrome but many patients will benefit from a supervised diet. Some symptoms can be treated with hormone therapy. Symptoms Requires a medical diagnosis The most common symptoms of Prader-Willi syndrome are behavioral problems, intellectual disability and short stature. Hormonal symptoms include delayed puberty and constant hunger leading to obesity. People may experience Developmental: delayed development, learning disability, delayed puberty, failure to thrive, short stature or speech delay in a child Behavioural: compulsive behaviour, self-harm or aggression Whole body: excessive hunger or reduced hormone production Muscular: flaccid muscles or abnormality walking Also common: infertility, obesity, baby feeding difficulties, excess sleepiness, lazy eye, scoliosis, sleep apnea or small feet Prader–Willi syndrome (PWS) is a rare genetic disorder caused by a loss of function of specific genes on chromosome 15. In newborns, symptoms include weak muscles, poor feeding, and slow development. Beginning in childhood, those affected become constantly hungry, which often leads to obesity and type 2 diabetes. Mild to moderate intellectual impairment and behavioral problems are also typical of the disorder. Often, affected individuals have a narrow forehead, small hands and feet, short height, and light skin and hair. Most are unable to have children.

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An article on bioinformatics in the age of AI opportunities, challenges, and future directions

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ABSTRACT

Bioinformatics is a rapidly evolving field that combines computer science, mathematics, and biology to analyze and interpret biological data. The advent of artificial intelligence (AI) has revolutionized bioinformatics, enabling researchers to analyze large amounts of data, identify patterns, and make predictions. This review aims to provide an overview of the current state of bioinformatics in the age of AI, its applications, challenges, and future directions.

INTRODUCTION

Bioinformatics is a crucial tool for analyzing and interpreting biological data, including genomic, transcriptomic, and proteomic data. The rapid advancement of high-throughput sequencing technologies has generated vast amounts of data, making it challenging to analyze and interpret. AI has emerged as a powerful tool to address this challenge.

BACKGROUND

AI has been increasingly applied in various fields of bioinformatics, including:

1. Genomic variant interpretation: AI can be used to analyze genomic variants and predict their functional impact on gene expression and disease susceptibility.

2. Gene expression analysis: AI can be used to analyze gene expression data and identify patterns and correlations associated with specific diseases or treatments.

3. Protein structure prediction: AI can be used to predict the three-dimensional structure of proteins, which is important for understanding their function and interactions.

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METHODS

A comprehensive literature review was conducted using PubMed, Google Scholar, and Web of Science databases. Keywords used included "AI in bioinformatics," "genomic variant interpretation," "gene expression analysis," and "protein structure prediction."

RESULTS

The review identified several applications of AI in bioinformatics, including:

1. Deep learning-based methods: Deep learning-based methods, such as convolutional neural networks (CNNs) and recurrent neural networks (RNNs), have been used for genomic variant interpretation, gene expression analysis, and protein structure prediction.

2. Machine learning-based methods: Machine learning-based methods, such as support vector machines (SVMs) and random forests, have been used for genomic variant interpretation, gene expression analysis, and protein structure prediction.

DISCUSSION

The integration of AI in bioinformatics has the potential to revolutionize the field, enabling researchers to analyze large amounts of data, identify patterns, and make predictions. However, there are several challenges that must be addressed, including:

1. Data quality and standardization: AI algorithms require high-quality, standardized data to produce accurate results.

2. Interpretability and transparency: AI algorithms must be interpretable and transparent to ensure that results are reliable and trustworthy.

3. Regulatory frameworks: Regulatory frameworks must be de to ensure that AI is used safely and effectively in bioinformatics.

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CONCLUSION

Bioinformatics is a rapidly evolving field that combines computer science, mathematics, and biology to analyze and interpret biological data. The advent of AI has revolutionized bioinformatics, enabling researchers to analyze large amounts of data, identify patterns, and make predictions. However, there are several challenges that must be addressed to ensure that AI is used safely and effectively in bioinformatics.

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An article on Smart Bioinformatics: The AI Revolution in Life Science

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ABSTRACT:

The fusion of artificial intelligence (AI) into bioinformatics has led to considerable expansion in the field, transforming biological research and healthcare. From the beginning of the 2000s, AI-based algorithms have improved data analysis across genomics, proteomics, drug discovery, and personalized medicine. Important milestones encompass the creation of AI-driven genome sequencing tools such as DeepVariant (2017) and AlphaFold (2020) for predicting protein structures. The precision, swiftness, and effectiveness of biological data interpretation have been enhanced by these developments. The article emphasizes the role of AI in speeding up drug discovery, forecasting protein interactions, and facilitating precision medicine. The outcomes show that AI has considerably diminished the time needed for genomic analysis, enhanced the success rate of identifying drug candidates, and aided in finding disease biomarkers. AI is anticipated to propel bioinformatics forward, resulting in significant progress in disease research and novel treatments over the next few years, despite challenges related to data quality, computational demands, and ethical issues.

KEYWORDS: Artificial intelligence (AI), Bioinformatics, Genomics, AI –Driven

INTRODUCTION:

Bioinformatics, the interdisciplinary science that integrates biology, computer science, and mathematics, has become essential in managing and analyzing vast biological datasets. The rapid advancements in genomic sequencing, proteomics, and drug discovery have led to an explosion of data that traditional computational methods struggle to process efficiently. Artificial intelligence (AI) has emerged as a transformative tool in bioinformatics, providing advanced analytical capabilities that enhance accuracy, speed, and scalability. This article explores how AI is revolutionizing bioinformatics, with applications in genome sequencing, protein structure prediction, drug discovery, and personalized medicine. This article explores the integration of AI

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in bioinformatics, its impact on genomic research, structural biology, and healthcare innovations, and the challenges and future prospects of AI-powered biological analysis. AI continues to push the boundaries of bioinformatics, promising groundbreaking advancements in disease understanding, treatment development, and precision medicine.

APPLICATIONS OF AI IN BIOINFORMATICS

1. GENE PREDECTION AND ANNOTATION
2. AI IN PROTEOMICS AND STRUCTURAL BIOLOGY
3. PERSONALIZED MEDICINE
4. GENOME-WIDE ASSOCIATION STUDIES (GWAS)

GENE PREDICTION AND ANNOTATION:

Gene prediction involves identifying coding and non-coding genes within a genome. AI enhances this process by learning patterns from large genomic datasets and predicting genes more accurately than traditional algorithms.

AI TOOLS FOR GENE PREDICITION:

1 . **Gene mark** (with AI): Uses deep learning for prokaryotic and eukaryotic Gene prediction

2. **Deep gene**: Identifying genes in large genomic datasets.

3. **GeneId**: A New AI tool enhances the discovery of genes involved in neurodevelopment conditions.

AI IN PROTEMICS AND STRUCTURAL BIOLOGY:

Proteomics is the large–scale study of proteins and their Structures, functions and interactions within a biological system.

Key AI Tools in Proteomics:

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AlphaFold (DeepMind, 2020): AI-driven protein structure prediction.

RoseTTAFold: AI-based modeling for protein folding.

Applications:

1. Protein structure prediction and folding.
2. Protein-protein and protein-ligand interactions.
3. AI in post-translational modifications analysis.

3. PERSONALIZED MEDICINE

Personalized medicine tailors treatments based on an individual's genetics, lifestyle, and environment. AI enhances this approach by analyzing vast datasets to predict disease risks, optimize drug responses, and personalize therapies.

Key AI Applications:

Genomic Analysis: AI tools like DeepVariant and IBM Watson for Genomics detect mutations and recommend treatments.

Drug Response Prediction: AI models such as DeepChem, predict how individuals react to medications.

Early Disease Detection: AI-powered diagnostics, like Google's LYNA, identify diseases at early stages.

Cancer Treatment: AI-driven platforms like Tempus AI design personalized cancer therapies.

4. GENOME-WIDE ASSOCIATION STUDIES (GWAS)

Genome-wide association Studies (GWAS) identify genetic variants linked to diseases by analyzing large genomic datasets. Traditional GWAS methods struggle with complexity, but AI improves accuracy, efficiency, and interpretation.

Key AI Tools in GWAS:

Deep WAS: Deep learning for detecting complex genetic associations.

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PLINK-AI: An AI-enhanced GWAS tool for large-scale genetic data analysis.

XGB-GWAS: Machine learning-based GWAS for improving variant prioritization

CONCLUSION:

AI has significantly enhanced bioinformatics by aiding scientists in the faster and more precise analysis of biological data. It is crucial for genome sequencing, predicting protein structures, discovering drugs, and studying diseases, which accelerates and enhances the precision of medical progress.

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An article on Sotos syndrome

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What Is sotos syndrome

Sotos syndrome is a rare genetic disorder that causes children to grow faster than normal, resulting in tall stature and macrocephaly. It's also known as cerebral gigantism. The excessive growth often begins in infancy and continues into the early teen years. Other characteristics include: Distinctive facial features** Down-slanting palpebral fissures, or downward-pointing outside corners of the eyes, are most noticeable in early childhood.

What causes Sotos syndrome?

A mutation in the NSD1 gene causes Sotos syndrome. The NSD1 gene gives your body instructions on how to grow and develop. When a mutation affects the NSD1 gene, your genes can't regulate your body's growth, causing children diagnosed with Sotos syndrome to be taller than their peers.

What is the diet for Sotos syndrome?

No special diet is required for Sotos syndrome although a well-balanced diet is important. Be aware, or ask parents, if the child has a medical alert bracelet.

Sotos syndrome treatable?

Mutations in specific genes cause Sotos syndrome. There is no specific treatment for Sotos syndrome, and doctors may refer people with the condition to specialists to treat specific symptoms.

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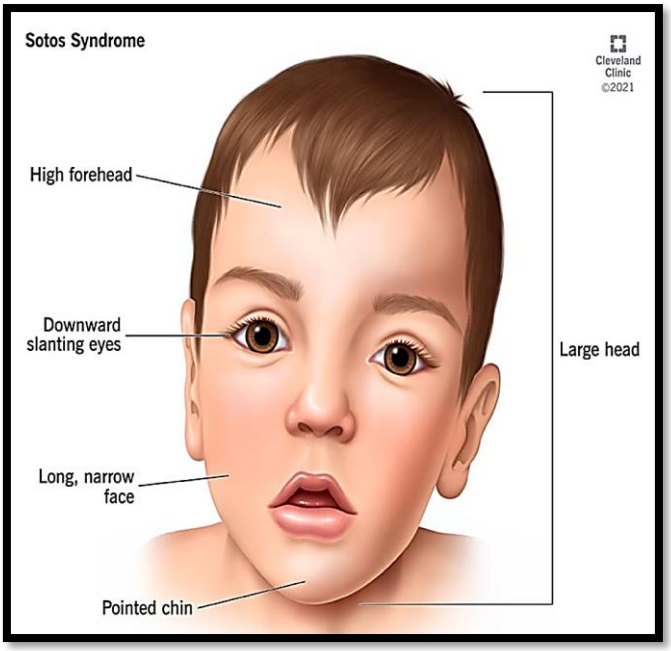
Diagram



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An article on The Digital Revolution in Biology

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Biology and technology have merged to create one of the most exciting fields of the 21st century—bioinformatics. This discipline, which combines biology, computer science, and mathematics, is transforming how we understand life at the molecular level. From decoding DNA to developing personalized medicine, bioinformatics is shaping the future of healthcare, agriculture, and biotechnology.

What Is Bioinformatics?

Bioinformatics is the science of analyzing biological data using computational tools. With the human genome containing over 3 billion DNA base pairs, traditional methods of studying genetic information would take centuries. Bioinformatics allows scientists to process massive amounts of data in seconds, revealing patterns and insights that were once impossible to detect.

How Does It Work?

At its core, bioinformatics involves:

Genome Sequencing – Deciphering the order of DNA bases in an organism.

Protein Structure Prediction – Understanding how proteins fold and function.

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Data Mining – Identifying disease-related genes and mutations.

Artificial Intelligence (AI) in Biology – Using machine learning to predict drug responses and develop new treatments.

Real-World Applications:

1. Personalized Medicine

Not all patients respond to drugs in the same way. Bioinformatics helps doctors design treatments based on an individual's genetic makeup. This is revolutionizing cancer therapy, where targeted drugs are tailored to a patient's specific genetic mutations.

2. Disease Detection and Prevention

By analyzing genetic markers, bioinformatics can predict the risk of diseases like diabetes, Alzheimer's, and even certain cancers. During the COVID-19 pandemic, scientists used bioinformatics to track virus mutations and develop vaccines in record time.

3. Agriculture and Food Security

Bioinformatics is helping scientists improve crop yields, develop pest-resistant plants, and create drought-tolerant crops. Genetic modification, powered by bioinformatics, ensures food security for a growing global population.

4. Drug Discovery and Development

Developing a new drug traditionally takes over 10 years and billions of dollars. Bioinformatics accelerates this process by identifying potential drug targets, simulating how drugs interact with proteins, and reducing the need for trial-and-error experiments.

5. Solving Evolutionary Mysteries

Scientists use bioinformatics to study ancient DNA and understand how species evolved. This helps in conservation efforts, tracking endangered species, and even identifying unknown viruses.

Future of Bioinformatics:

With advancements in AI, cloud computing, and quantum computing, bioinformatics will only become more powerful. In the future, we might see:

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*AI-powered doctors that analyze DNA in seconds.

*Custom-designed babies with selected genetic traits.

*Cures for genetic disorders before birth.

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கவிதைகள்

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நண்பர்கள்

கடலின் ஆழத்தை அளந்தவர்கள் உண்டு, ஆனால் நட்பின் ஆழத்தை அளந்தவர்கள் இல்ல…

நட்பே ..!!! என்னோடு நீ இருந்தாலும், இல்லை என்றாலும், மண்ணோடு மண்ணாகும் வரை… நெஞ்சோடு வைத்திருப்பேன் உன் நினைவுகளை … என் இதயம் ரோஜாவைவிட அழகானது… ஏன் தெரியுமா?? அதில் உன்னை போல் அழகான நண்பர்கள் இருப்பதால்!

உன்னுடைய மிக மோசமான எதிரியையோ, மிகச் சிறந்த நண்பனையோ,உன்னிடத்திலேயே நீ காணலாம்…!!!

நான் காதலுடன் பழகினேன், அவள் நட்புடன் பழகினாள், அவள் நட்பின் ஈர்ப்பில், நட்பாகியது என் காதலும்….

நான் காதலுடன் பழகினேன், அவள் நட்புடன் பழகினாள், அவள் நட்பின் ஈர்ப்பில், நட்பாகியது என் காதலும்…..

காதலை விட மிக கொடியது நம்முடன் உயிராய் பழகிய நல்ல நண்பனை இழப்பது.
கால பயணங்கள் தடுமாறலாம், நாம் கண்டகனவுகள் தவிடு பொடியாகலாம், நினைவுகளின் மாற்றங்கள் நம்மை நிலை குலைய செய்யலாம் ஆனால் நாம் அன்பாய் பழகிய அந்த நாட்கள் “நட்பு” என்ற சக்கரத்தில் இன்னும் உலாவி வந்த வண்ணமே உள்ளது.

என்னிடம் உள்ள சோகங்களை உன்னிடம் கொட்டி என் மனதின் பாரத்தை உன் தோள்களில் சுமந்து நம்பிக்கை எனும் விதையை நீ என்னில் தூவி வெற்றி எனும் விடையை எனக்கு அறிய செய்த நம் நட்பு என்ற மரம் இன்னும் செழித்து வளரனும் விருட்சமாய்.

என் நண்பன் என்னுடன் பேச கூட தேவை இல்லை அவன் கண்களின் செய்கையை வைத்தே கண்டு பிடித்திடுவேன் அவனின் மன நிலையை.

நட்பு என்ற ஒன்றின் ஏணிப்படி இருந்தால் போதும் மலையை கூட எழுதில் கடக்கலாம் நண்பனின் கரங்களை கைகோர்த்து கொண்டே.

நாம என்னதா கெத்தா செஞ்சாலும் நம்ம உயிர் நண்பனுக்கு நாம எப்போவுமே ஒரு டம்மி பீஸ் தான்.

வாழ்க்கையில் அனைத்து சிக்கல்களும் தீர்ந்த பாடில்லை தான். ஆனால்

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நண்பனிடம் பகிரும்போது அவன் தரும் ஆறுதல் தேடினாலும் கிடைக்காத ஒரு வரம்.

நல்ல குணம் பார்த்து காதல் கனியலாம். நல்ல மனம் பார்த்து அன்பு என்ற மழை பெருக்கெடுக்கலாம். ஆனால் டேய் மச்சான் என்ற ஒரு வார்த்தை போதும் இவை அனைத்தும் ஒன்று சேர.

அன்பு என்ற தூண்டினால் கோர்க்கப்பட்டு பாசம் என்ற வலையில் சிக்கி உனக்காக நானும் எனக்காக நீயும் உருகும் அதிசய நிகழ்வே " நட்பு ".

அழகில் மயங்கி உண்டாகும் காதல் உணர்வுகளை விட நிறம் குணம் கூட தெரியாமல் வரும் நண்பன் என்ற உணர்வு என்றுமே பெரிதே.

அன்று பெய்த அடைமழையால் அவளை பார்க்க சிறிது தாமதம் என் காதலி சொன்னாள் "என்னடா இவ்ளோ லேட்டா வேணாம் இனிமேல் என்ன பாக்குறது விட்று " அதே சமயம் தற்செயலாக வந்த நண்பனின் தொலைபேசி அழைப்பில் " மச்சி மழை ஓவர் ஹா பெய்யுது லேட்டா வந்தாலும் பரவயில்லை சேப்பா வா".

காற்று வீசுவதை உணர முடியும் ஆனால் பார்வையால் அதை பார்க்க முடியாது. நீரின் வேகத்தை அலச முடியும் ஆனால் கைகளால் அதை பிடித்து வைக்க முடியாது . வானின் அழகை ரசிக்க முடியும் ஆனால் அதனை நம்மால் தொட முடியாது . மின்னல் ஒளியை கண்ணால் காண முடியும் ஆனால் அதை நம்முன்கூட்டியே அறிய முடியாது. நட்பு என்ற ஒன்றில் மட்டுமே இவை அனைத்தும் மாறி மாறி நடக்கும். பிரிவு என்ற ஒன்று நட்பு என்ற அகராதியில் கிடையாது

வானத்தின் சொந்தம் விண்மீன்கள், மலரின் சொந்தம் வண்டுகள், காற்றின் சொந்தம் தென்றல், நட்பின் சொந்தங்கள் நல்ல நினைவுகள்.

கருத்தில்லா பாடலைக் கேட்கலாம்.. அன்பில்லா இதயமதை மாற்றலாம், உப்பில்லா உணவையும் உண்ணலாம்… நட்பில்லா வாழ்வு வாழலாமா… !

நான் சந்தோஷமாக இருக்கிறேன். ஏன் தெரியுமா? ஏனெனில் நான் அதிர்ஷ்டக்காரன். ஏன் தெரியுமா? ஏனெனில் கடவுள் என்னை நேசிக்கிறார். எப்படி தெரியுமா? அவர் எனக்கு சிறந்த நண்பனை அனுப்பியுள்ளார். அது யார் தெரியுமா? அது நீங்கள் தான்.

கல்யாணம் முடிந்த பிறகு , மாப்பிள்ளையம்-பொண்ணையும் விசாரிப்பவன் சொந்தக்காரன் , கல்யாணத்துக்கு வந்த பிகரை விசாரிப்பவன் பேச்சிலர் பசங்க தான் !!!! டேய் அந்த சிகப்பு கலர் சுடிதார்ல வந்த பிகரு யாருடா …

பனிப்போர் என்பது… ஒருவரிடம் தேன் ஒழுக ஒழுக நட்பு பாராட்டிக்கொண்டே ..சரியான சந்தர்ப்பங்களில் வார்த்தைகளால் குத்தி கிழித்து குழி பறிப்பது ..!!

ஆயிரம் உறவுகள் என் வசதியை நாடி வந்தாலும், என்னை விட்டு என்றும்

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விலகாத அறிய பொக்கிஷம் என் நண்பன் நீ.

வாழ்க்கை என்பது ஒரு காட்டாறு. அதில் இன்னொரு ஜென்மம் நிஜம் என்பது கிடையாது. அப்படி இருந்தாலும் உன்னை போல நட்பு கிடைக்குமா என்று தெரியாது. இருக்கும் வரை என் நண்பன் உன் முகம் எனக்கு மறக்காது.

அன்று சற்றும் எதிர்பாராமல் பழைய நண்பனை பார்த்த நொடியில் மனதில் ஓர் பரவசம் !!! “அடடா இவன் என் பழைய நண்பன் அல்லவா !!! ” என்று சட்டென்று பழைய நினைவுடன் நண்பனை அருகில் சென்று பெயரை சொல்லி அழைக்க பதிலுக்கு “ஜி” என்ற பெயரில் என்னை சொல்லி அழைத்தான் என் பெயரையும் மறந்து

தோழமை என்பது என்ன?
பாசம் என்பது என்ன?
தோழமை என்பது……..
உறவல்லா ஒரு நண்பனிடம் காட்டும்
உறவோ என பிரமிக்க வைக்கும்
ஆழ்ந்த பாசம்!
பாசம் என்பது……
உடன்பிறந்த சகோதரனிடம்…….
பெற்ற தாயிடம்…….
பெற்ற மகனிடம்…….ஏன்…….
நெருங்கிய எந்த உறவிடமுமே காட்டும்
ஆழ்ந்த தோழமை!
இதில் ஏன் ஒப்பீட்டு ஆராய்ச்சி?
இரண்டுக்கும் அடித்தளம்
புரிதல் வழி பிறந்த
இரு பக்க நம்பிக்கைதானே!
நம்பிக்கை வழி பாசம்தானே!
பழகும் நபரை எல்லாம் – நாம்
புரிந்து கொண்டோம் எனில்
புரிதல்கள் யாவும்
தோழமை ஆகிடுமே!

By

Ruba Shri

II B.Sc. Biocomputing

ISBN: 978-81-991683-8-1

பெண்மை

மண்டியிட்டு வாழ மனமில்லை மானுடனே
என்னை மாய்த்துக் கொள்ளவும் தயார்
மலடி என்பதிலிருந்து விடுபட
மாதவிடாய் தீட்டோ மாதத்திற்கு மூன்று நாள்தான்
ஆனால் மலடி என்னும் தீட்டோ வாழ்நாள் முழுவதும்
தீண்டாமைக்கும் உறவு முளைத்து விட்டது தீட்டு என்னும் நட்பினால்
மாட்டிக்கொண்டு முழிக்கிறேன்
மானங்கெட்ட சமுதாயத்தில்
இறப்பிலும் நிம்மதி இருக்கும் அவளுக்கு
உங்கள் கௌரவம் பெண்களின் கற்பை வந்தடைவதினால்

அபிநயா

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Moon

"The Moon's Gentle Watch"

The moon, a silver lantern high, In velvet skies it starts to fly.
A quiet sentinel, soft and bright, Casting whispers through the night.
It dances with the clouds so thin,
A glowing face, both shy and dim.
It watches over land and sea,
A timeless guard, forever free.
In silent grace, it reigns above, A symbol of eternal love.
A beacon for the dreams we chase, A light that time can't erase.
Beneath its glow, our hearts take flight, In the embrace of moonlit night

By

Sam seanan fernandus .P

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Luna's Birthday

The moon's bright sapphire dream cascade
Beneath the lantern's flickering glow
The lanern's warmth, the moon's cood thrill
A harmony of dark and bright.
Guiding hearts through silent night.
The lantern sways in quiet breeze,
In this calm, the world stand still,
Luna whispers soft and slow.
Whispering secrets with the gale.
Together they creat the night!

By

Shri Nivethaa S.M

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आशापूर्ण जीवन

मुझे उम्मीद है कि जीवन वह है जो एक व्यक्ति को बदल सकता है।

मुझे उम्मीद है कि दुनिया हमारे लायक के प्रति सच्ची होगी।

ब्रह्मांड जीवन को मौका देता है। जो उम्मीद रखता है।

एक मिलियन सपने मुझे जगाए रखते हैं।

जीवन केवल बहादुर के लिए है।

क्या आपको लगता है कि ब्रह्मांड आत्मा के लिए लड़ता है?

चली सबसे अच्छा की उम्मीद करें !

By

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Drawings

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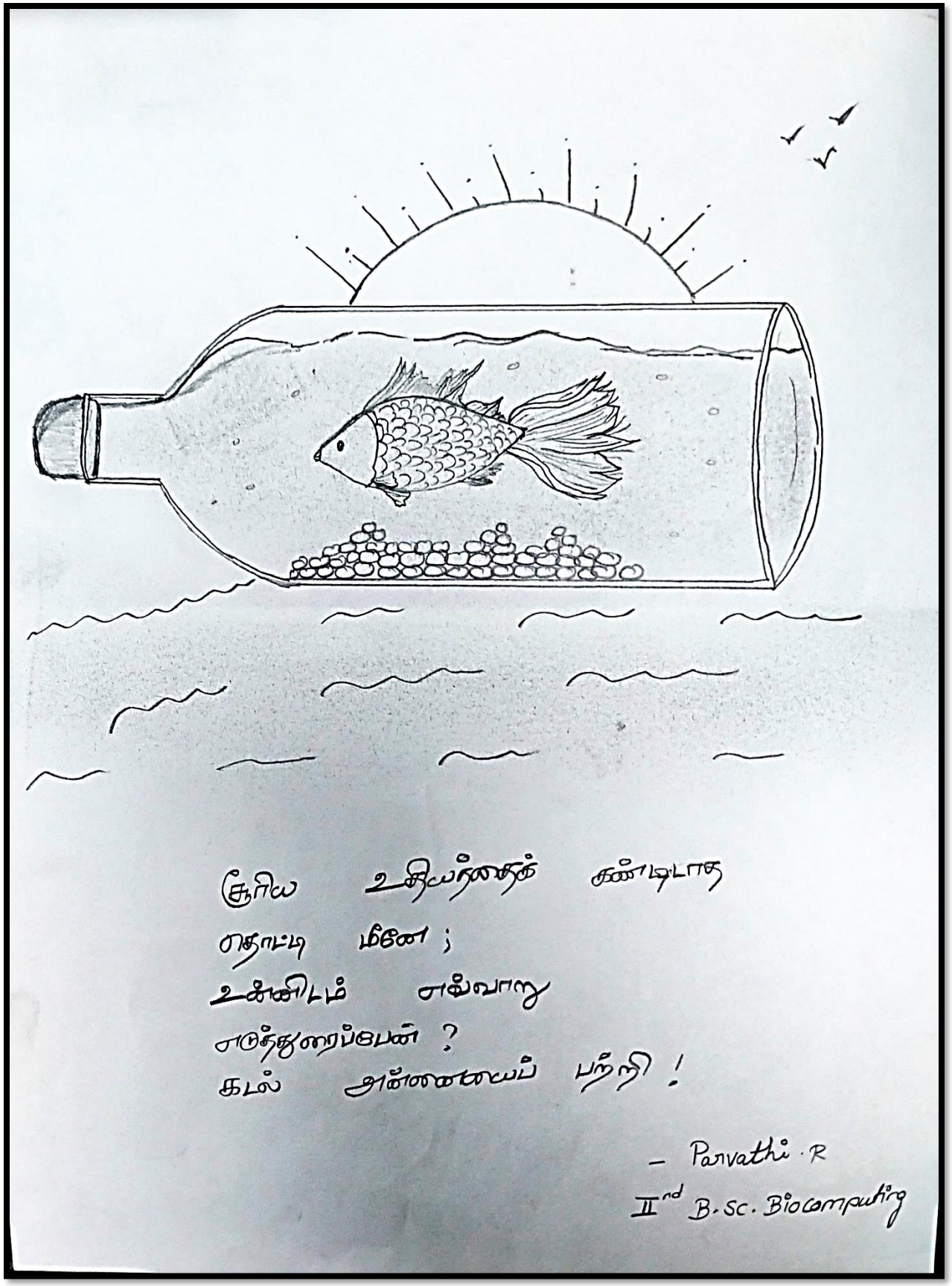

சூரிய உதயத்தைக் கண்டிடாத
சிறுமி மீனே ;
உன்னிடம் சில வார்த்தை
சற்றுரைப்பேன் ?
கடல் அன்னையைப் பற்றி !

– Parvathi . R
II nd B. Sc. Biomaterials

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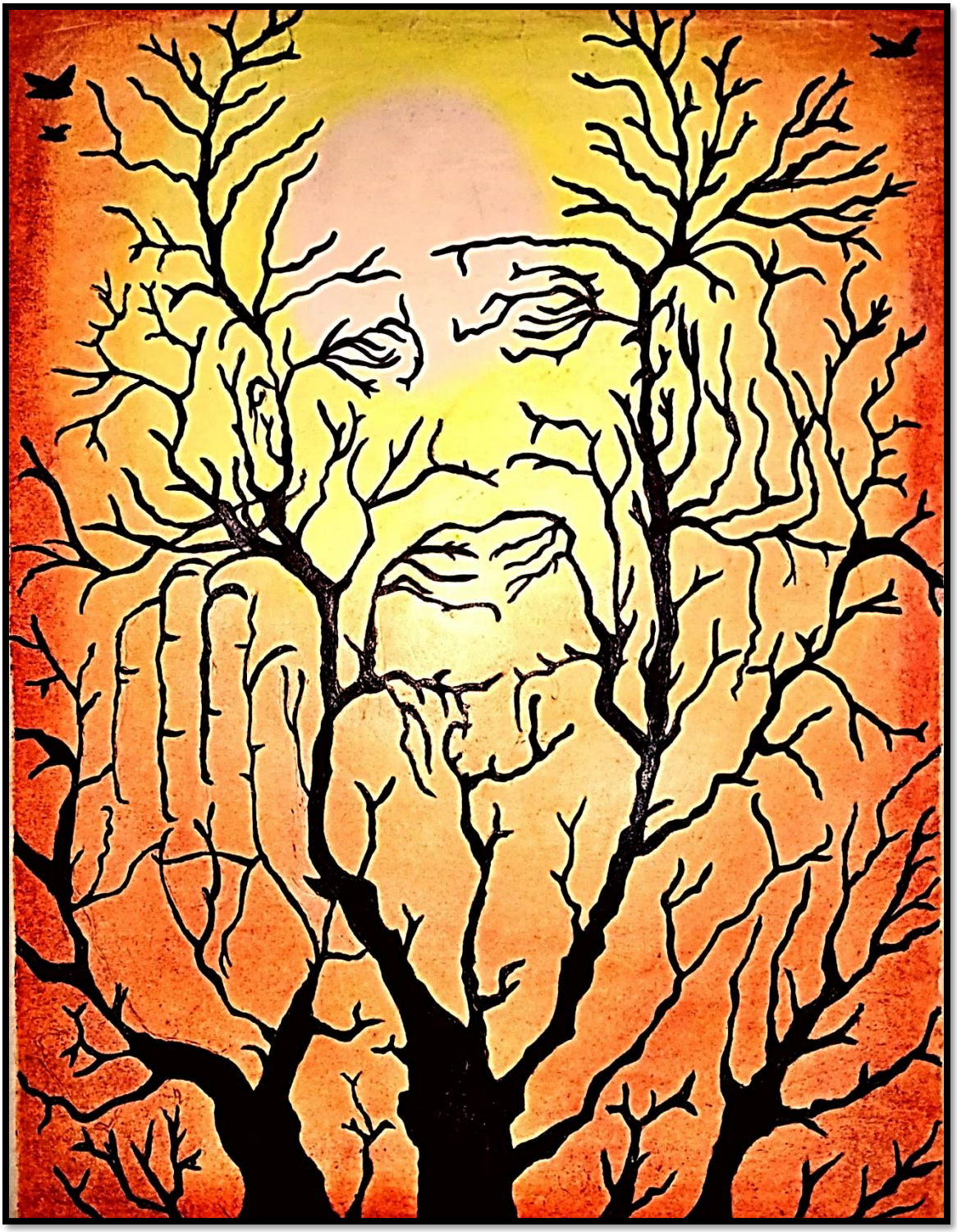

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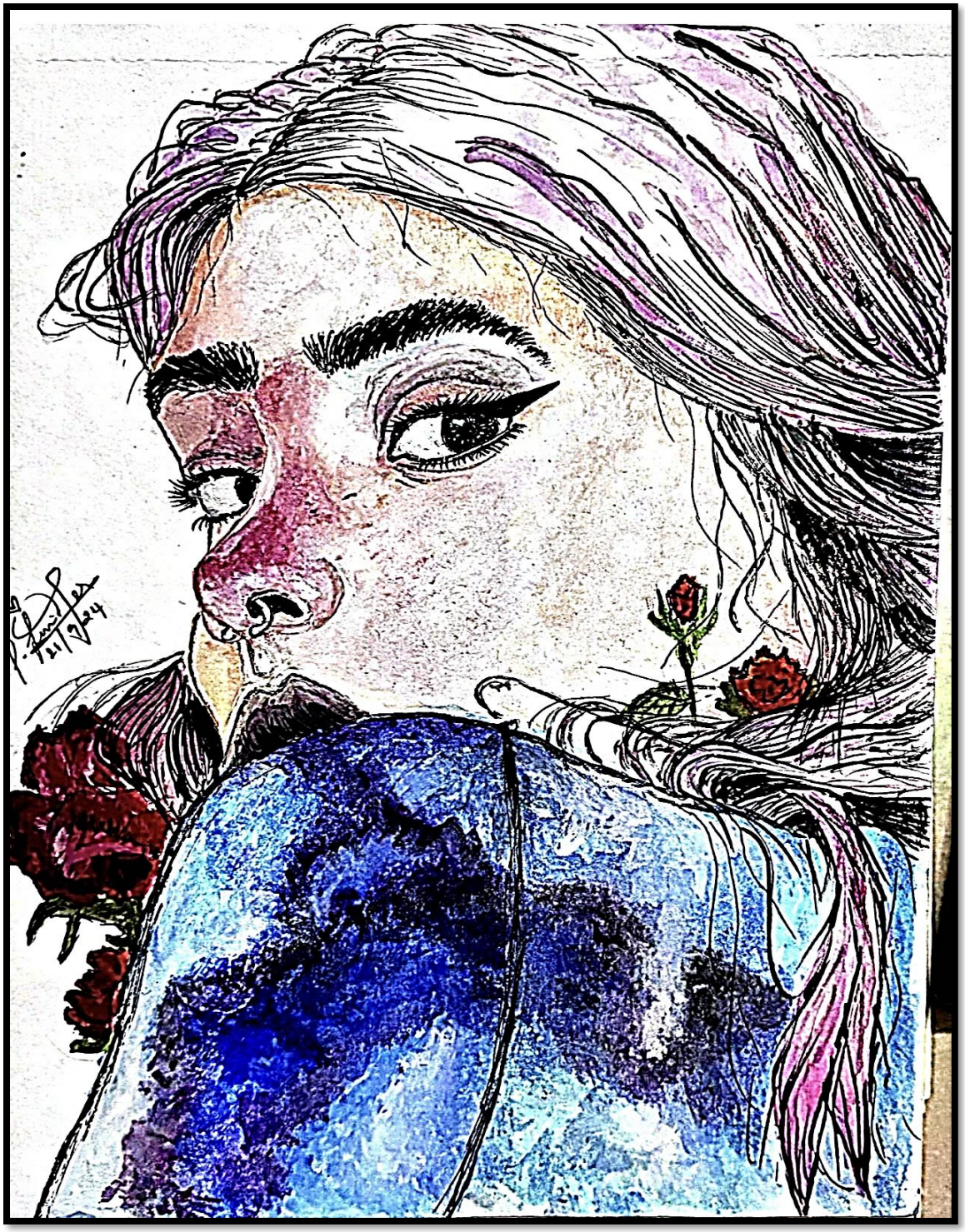

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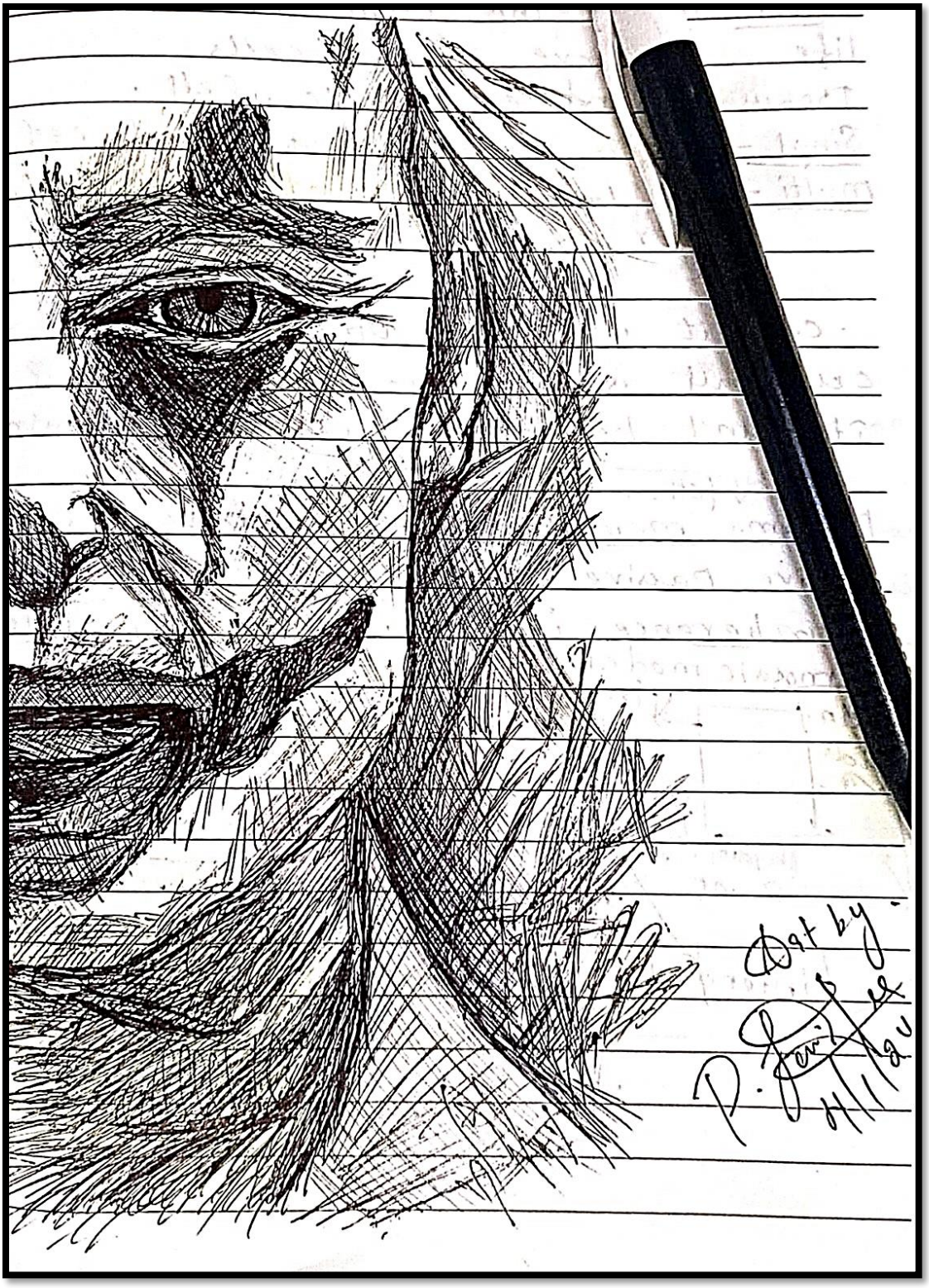

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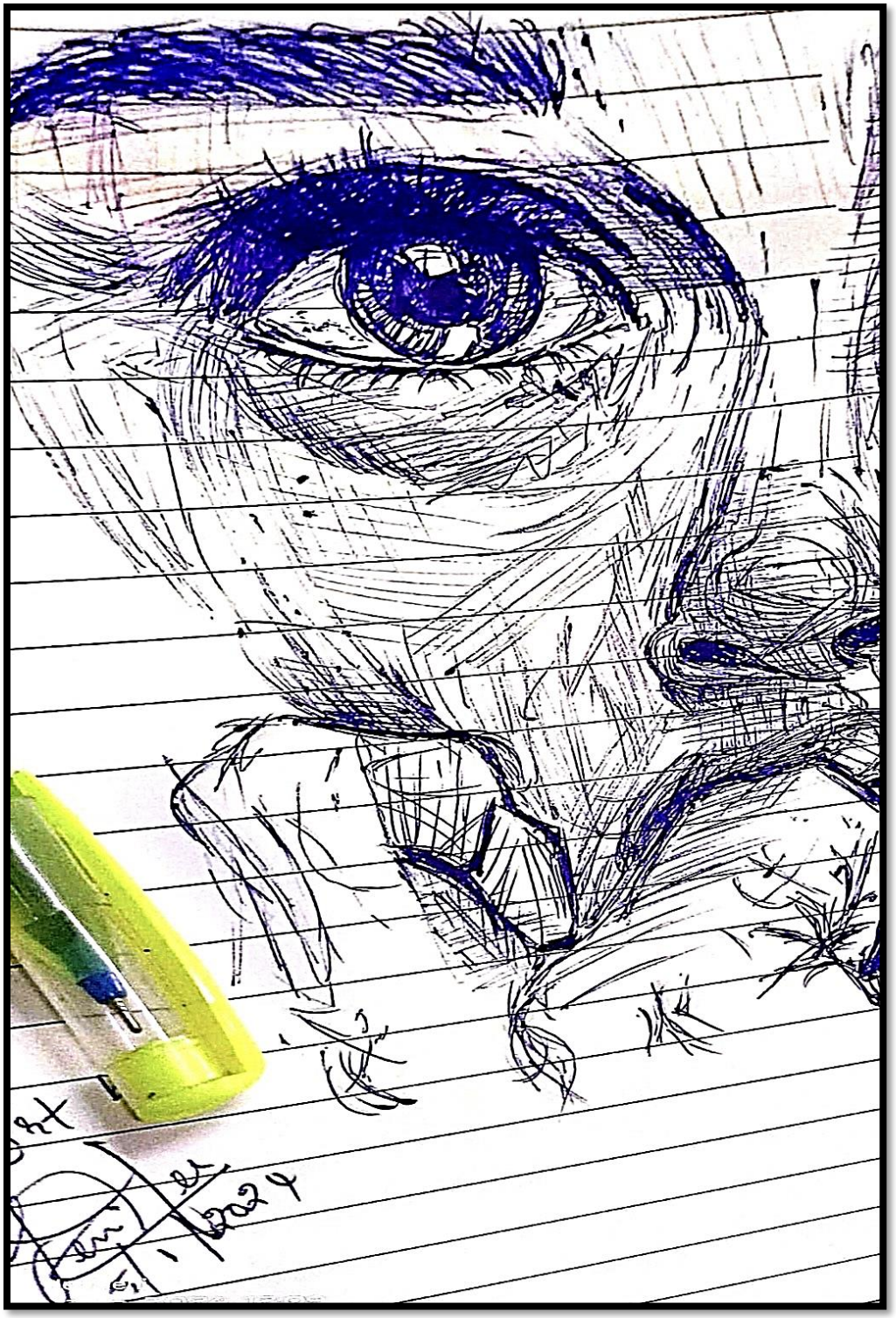

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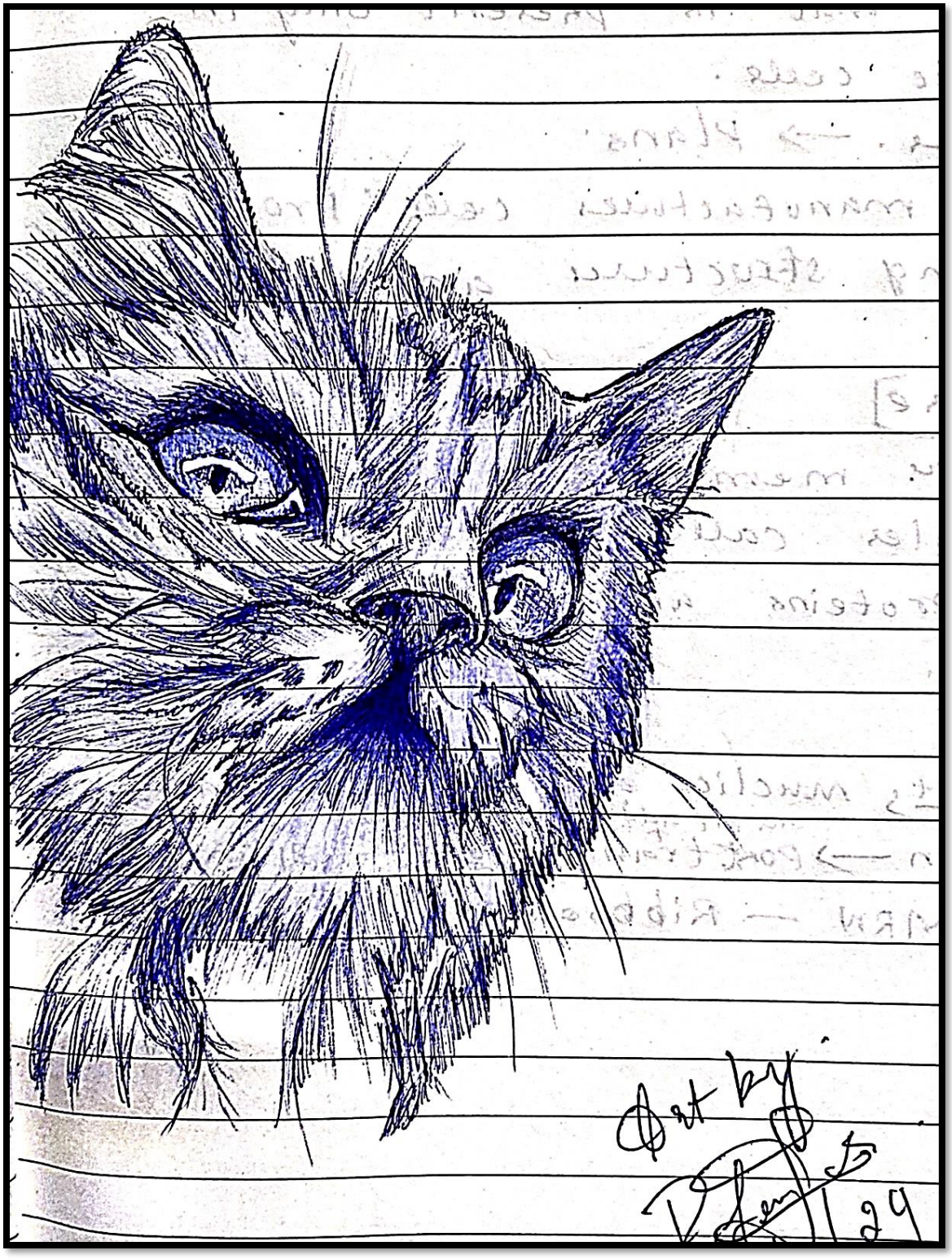

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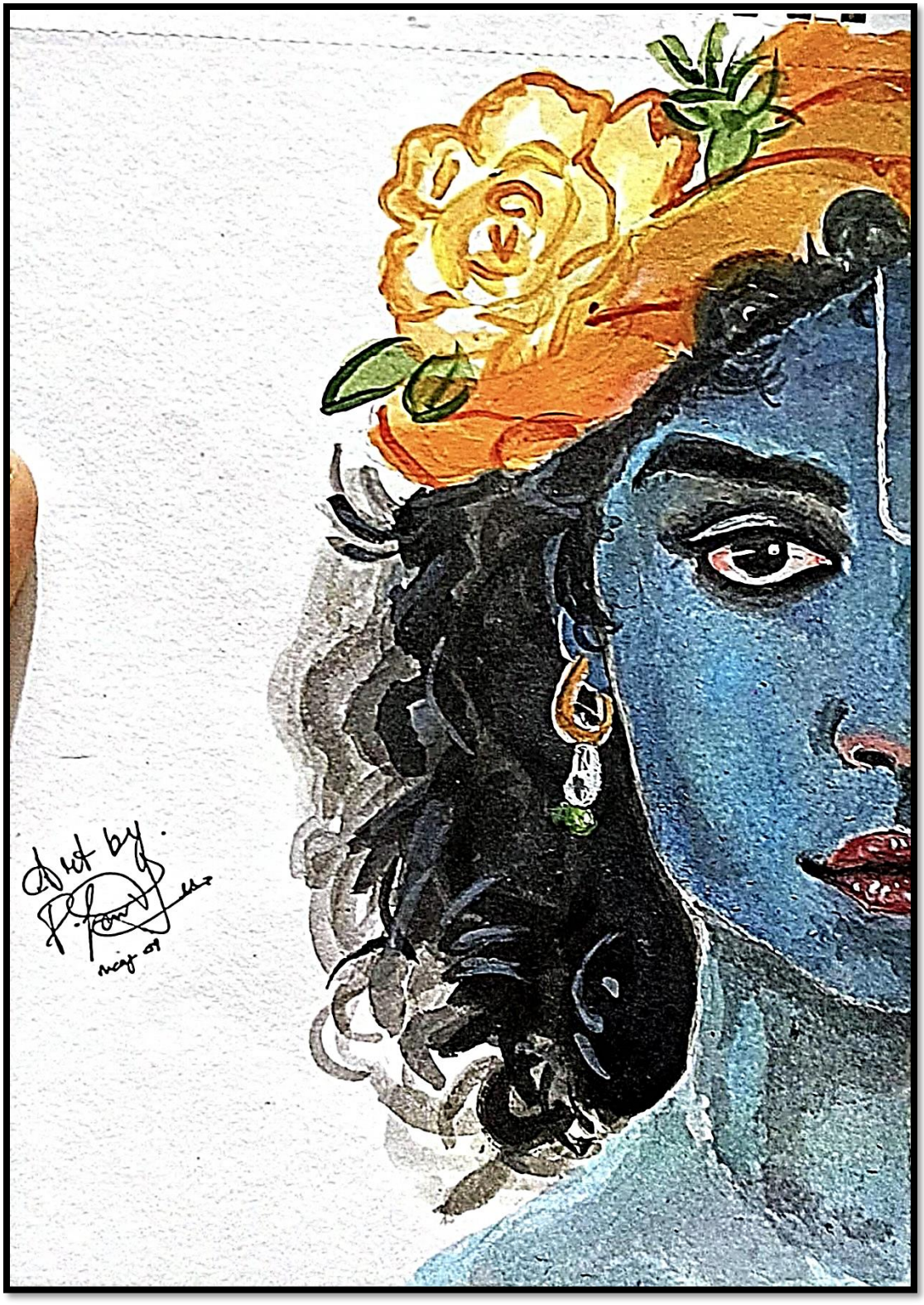

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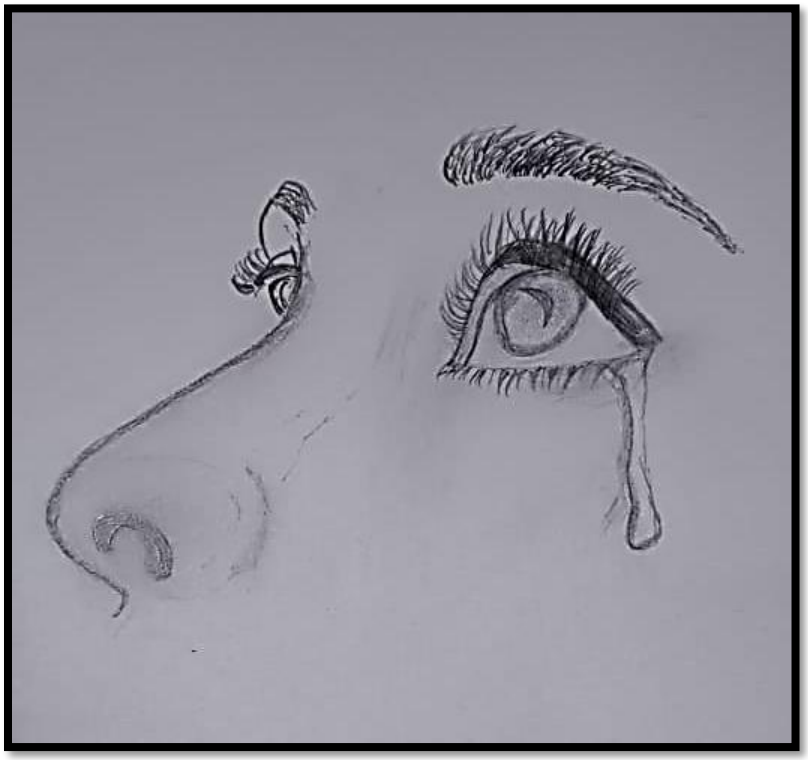

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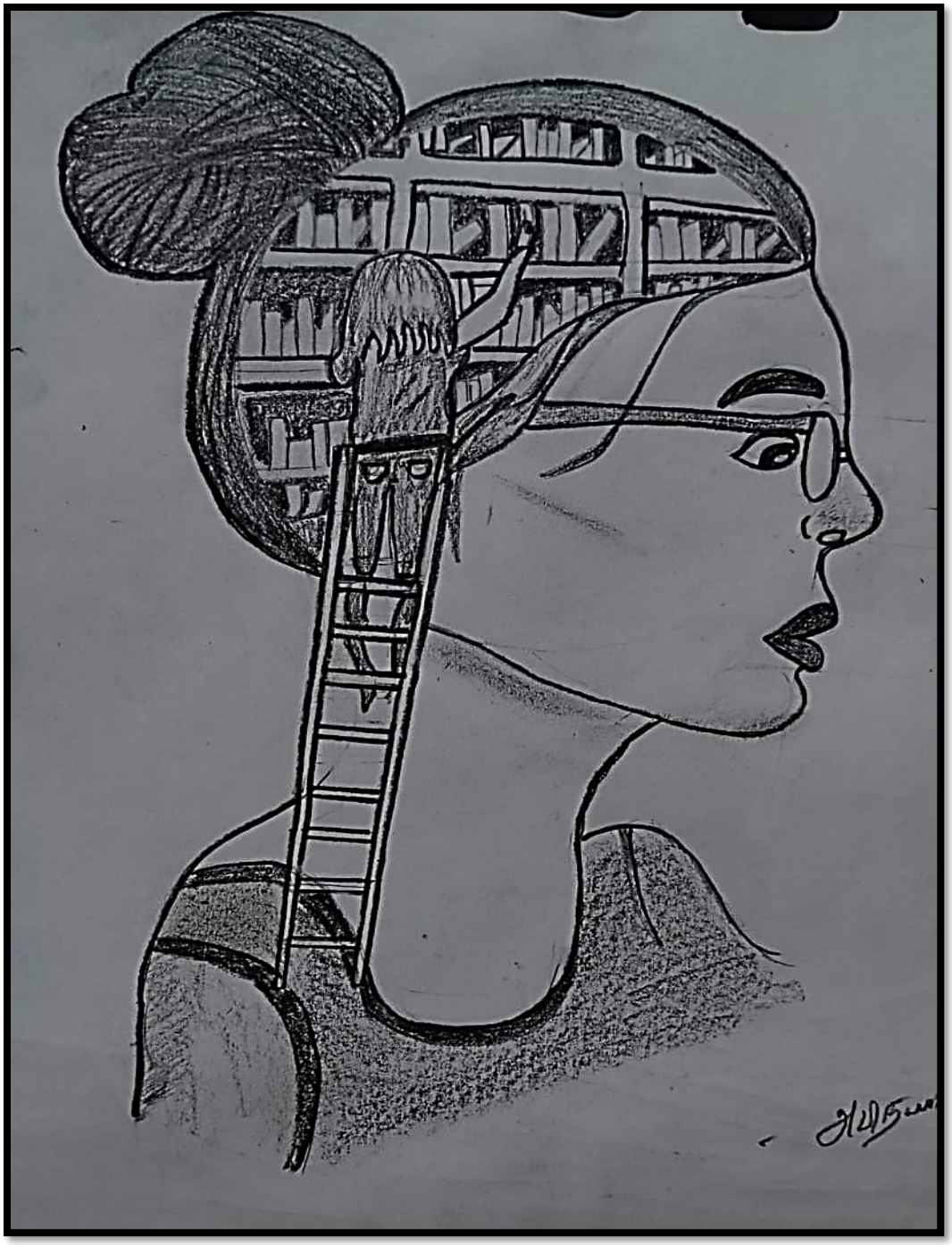

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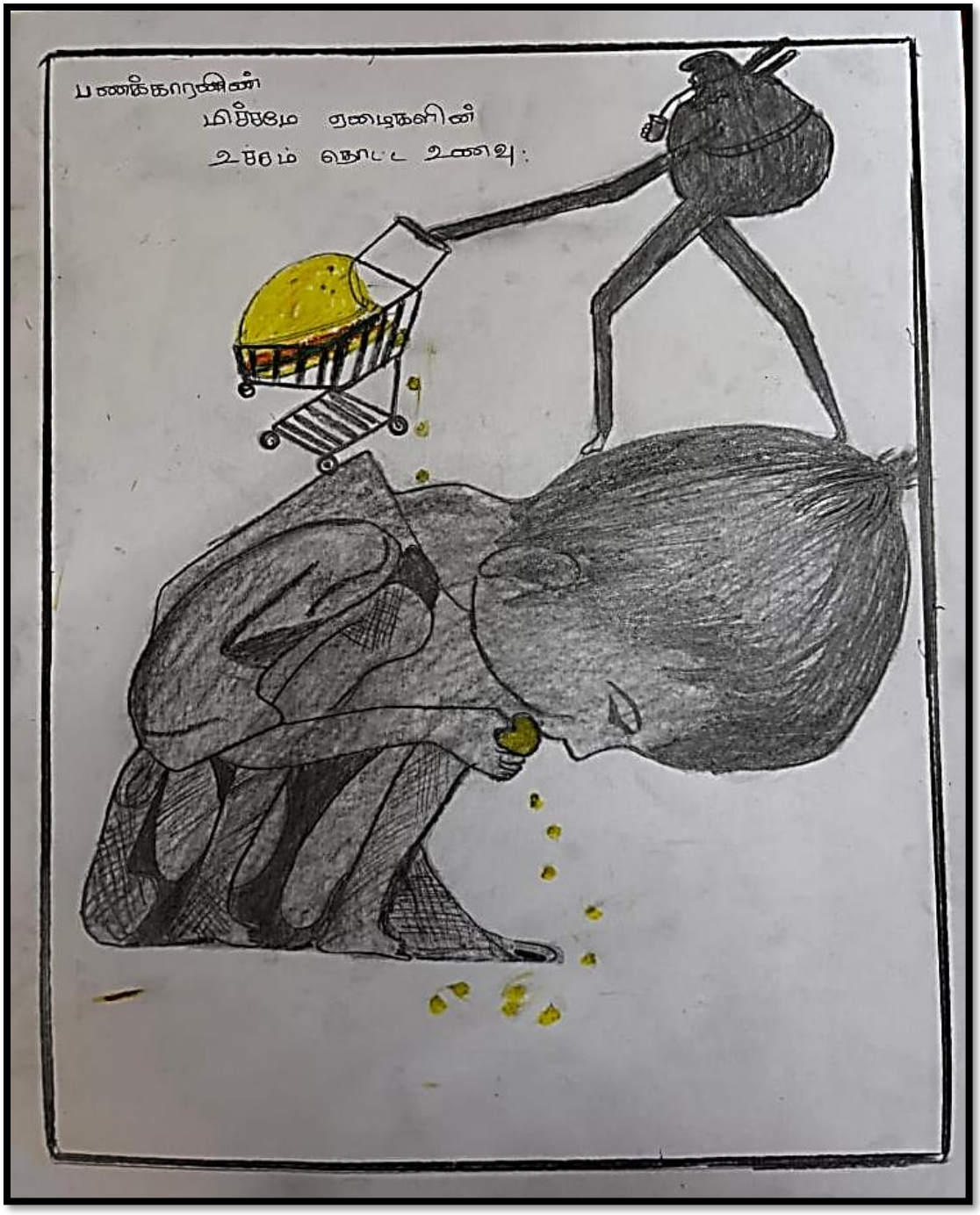

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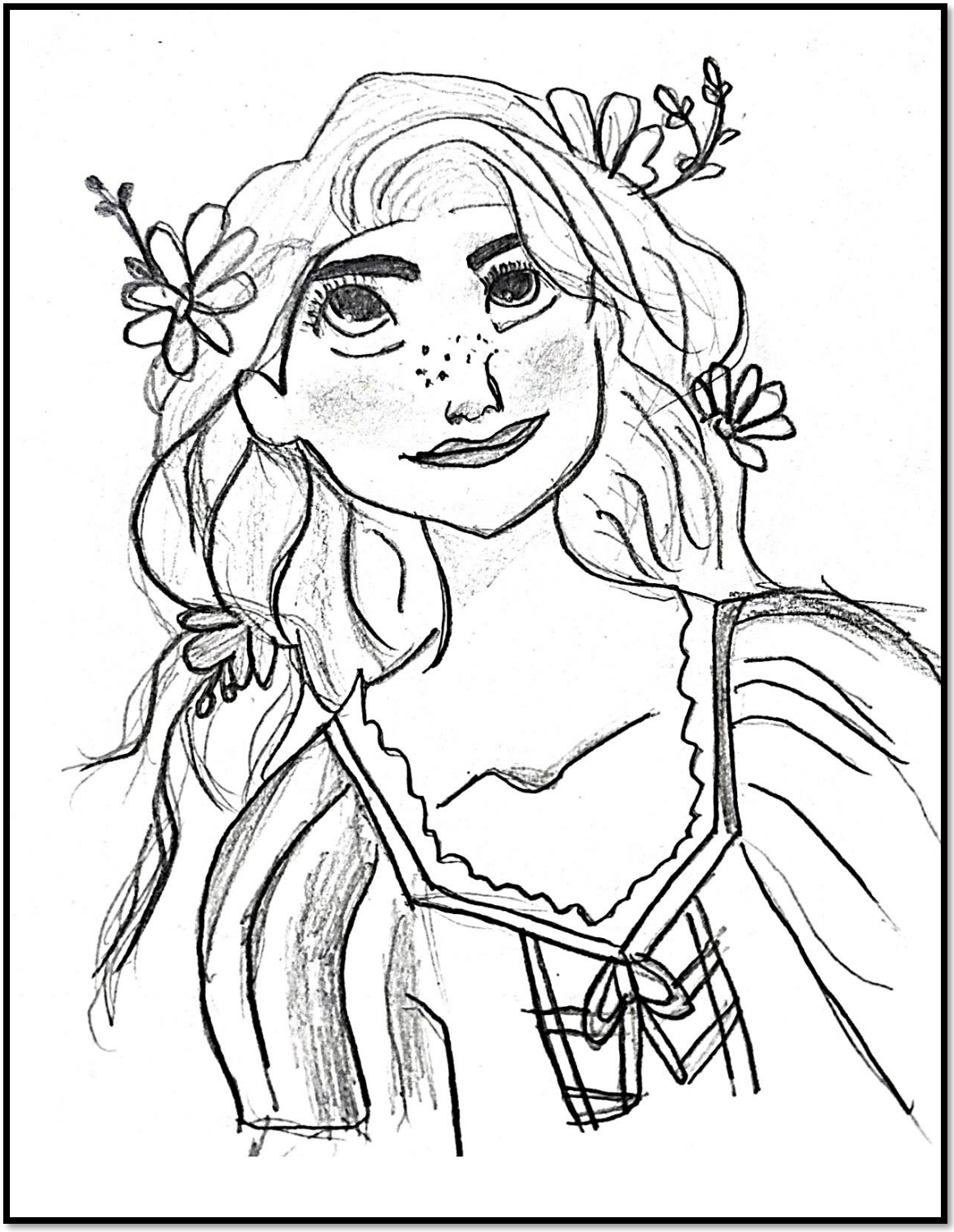

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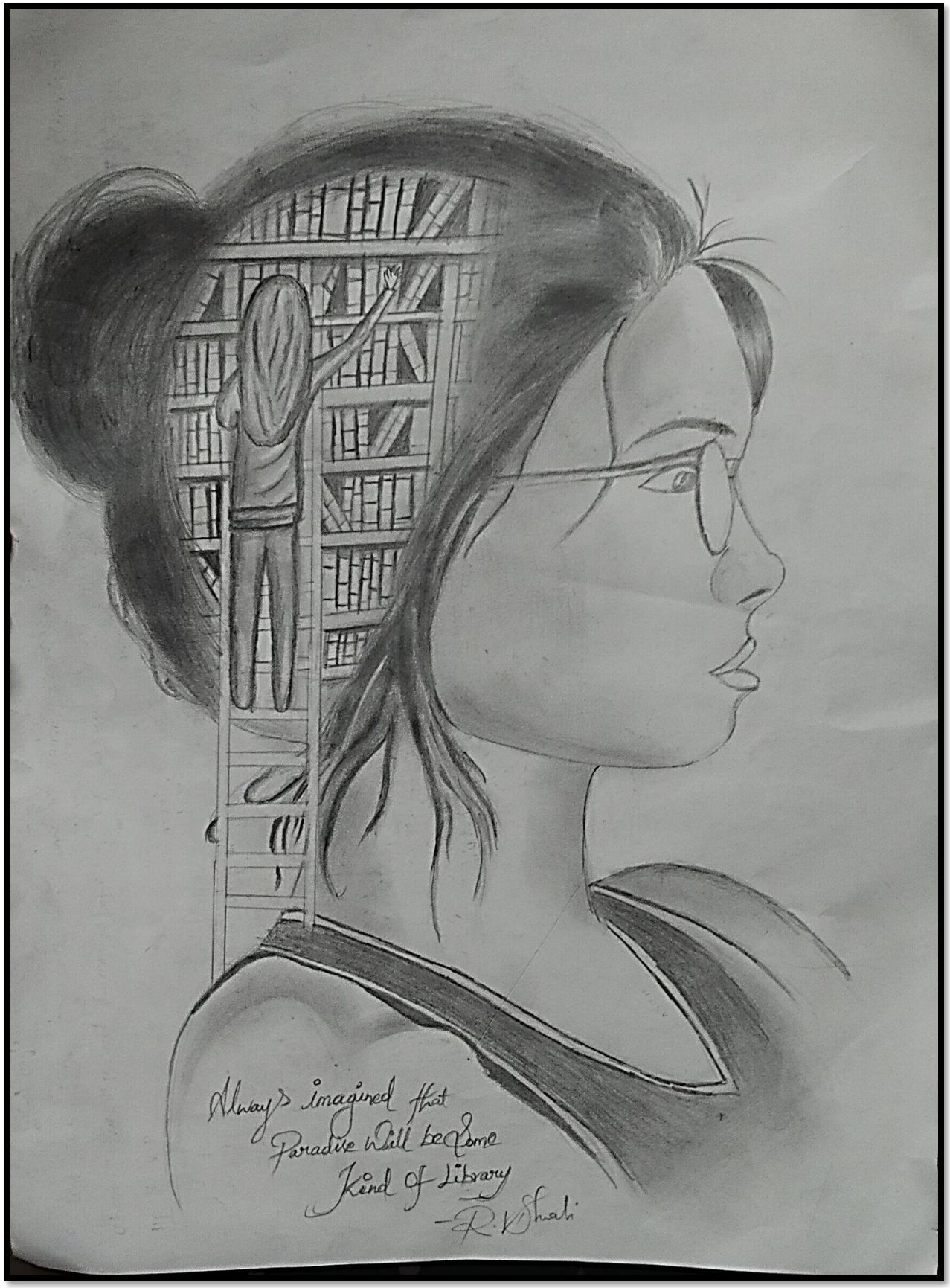

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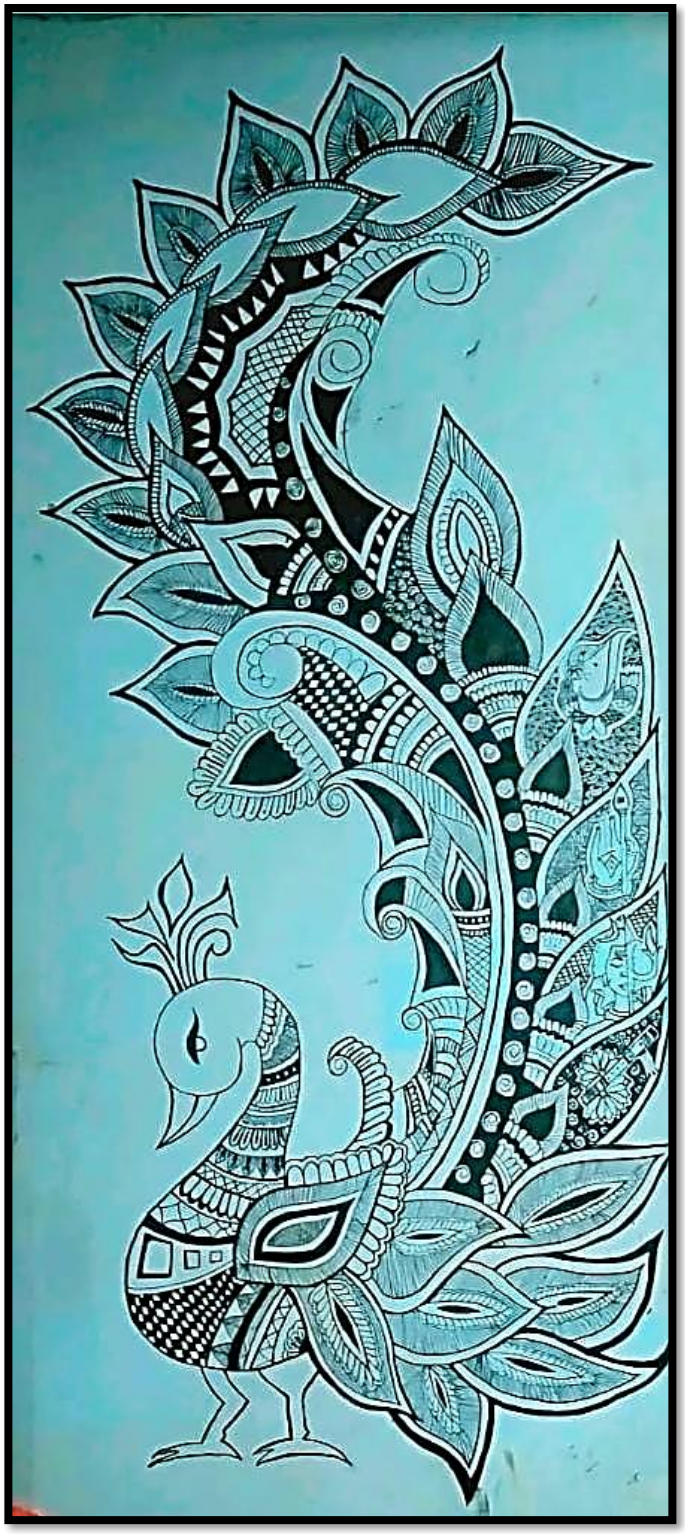

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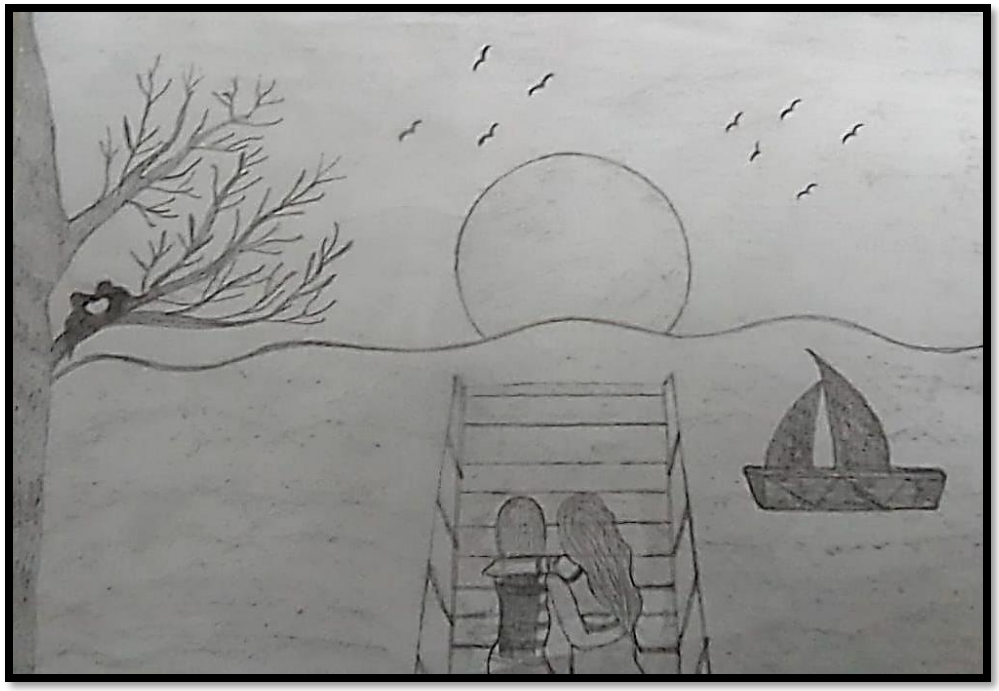

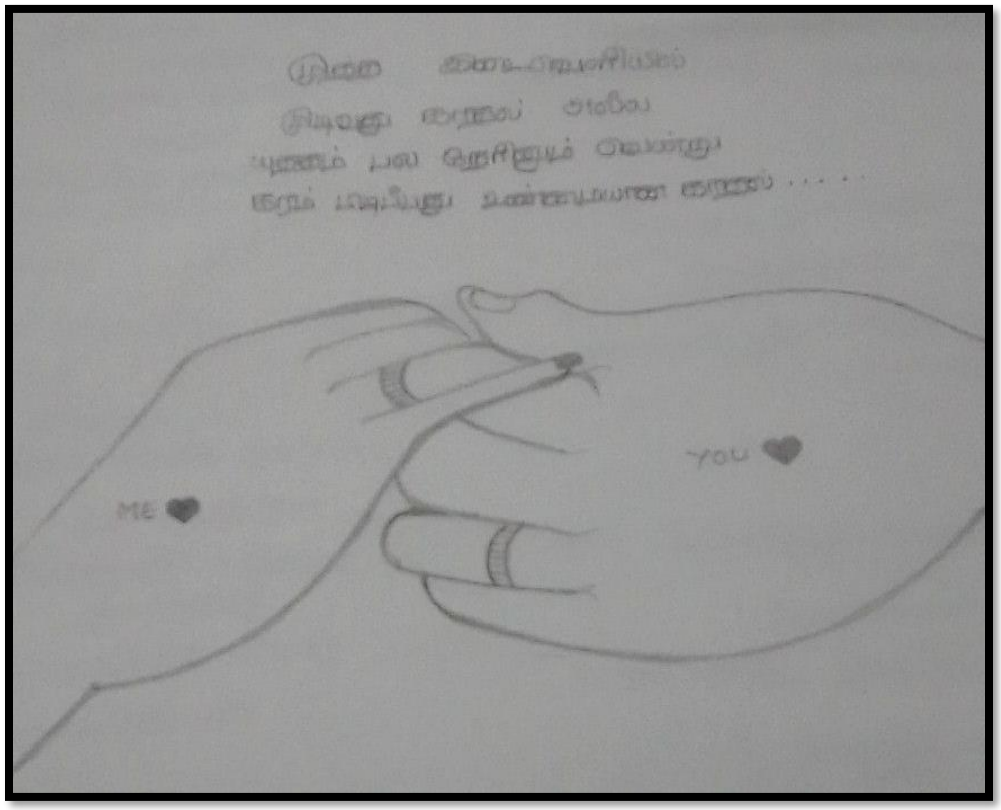

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