[11]Mr. U. Udayakumar,

[2]Dr. J. Jebamalar Tamilselvi

A Machine Learning Approach to Improving the Accuracy of Similarity Evaluation of DNA Genetic Codes using Proposed Longest Common Subsequence Algorithm

Journal of Electrical Systems

ABSTRACT

DNA sequence analysis in biological and computational applications, such as studying evolution discovering genes and diagnosing genetic diseases. It is crucial to identify similarities between codes in these fields. Traditional methods like the subsequence (LCS) algorithm have been widely used to compare DNA sequences. However, this research paper introduces an approach that utilizes machine learning techniques to address the challenges of evaluating DNA sequence similarity. The proposed algorithm combines the effectiveness of sequence alignment with the power of data driven models. By leveraging a trained machine learning model, it predicts alignment scores reducing burden while maintaining high accuracy. Using NCBI GenBank nucleotide sequence dataset and Proposed LCS Algorithm implement and deployed with Support Vector Machines. The Algorithm is randomly tested with 10000 samples NCBI GenBank nucleotide sequence dataset and among the different samples. The result of the SVM Classification Algorithm and it computes the sequence similarity between HUMAN to ANIMAL DNA Sequence among them Human and Chimpanzee shows the best result with the prediction of 98%.

Keywords: DNA Genetic Codes, Proposed Longest Common Subsequence Algorithm, Similarity Evaluation, Diagonal Edges, DNA Sequencing, Machine Learning

INTRODUCTION

The analysis of DNA sequences is a fundamental task in biological research and has far-reaching implications in various domains, such as evolutionary studies, gene discovery, and genetic disease diagnosis. DNA processing, the performing of calculations utilizing natural particles, as opposed to conventional silicon chips. The possibility that singular particles (or even molecules) could be utilized for calculation dates to 1959, when American physicist Richard Feynman introduced his thoughts on nanotechnology. Nonetheless, DNA processing was not genuinely acknowledged until 1994, when American PC researcher Leonard Adleman demonstrated the way that particles could be utilized to tackle a computational issue. A calculation might be considered the execution of a calculation, which itself might be characterized as a bit by bit rundown of obvious guidelines that takes a few information, processes it, and produces an outcome. In DNA registering, data is addressed utilizing the four-character hereditary letters in order (A [ADENINE], G [GUANINE], C [CYTOSINE], and T [THYMINE]), as opposed to the parallel letter set (1 and 0) utilized by customary PCs. A calculation's feedback is thusly addressed (in the least difficult case) by DNA particles with explicit groupings, the directions are done by research facility procedure on the particles, (for example, arranging them as per length or hacking strands containing a specific aftereffect), and the outcome is characterized as some property of the last arrangement of atoms (like the presence or nonappearance of a particular succession).

[1] Ph.D(Research Scholar) & Assistant Professor, Department of Computer Science, College of Science and Humanities, SRM Institute of Science and Technology, Ramapuram Campus, Chennai

[2]Associate Professor, Department of Computer Science & Applications (B.Sc CS), College of Science and Humanities, SRM Institute of Science and Technology, Ramapuram Campus, Chennai

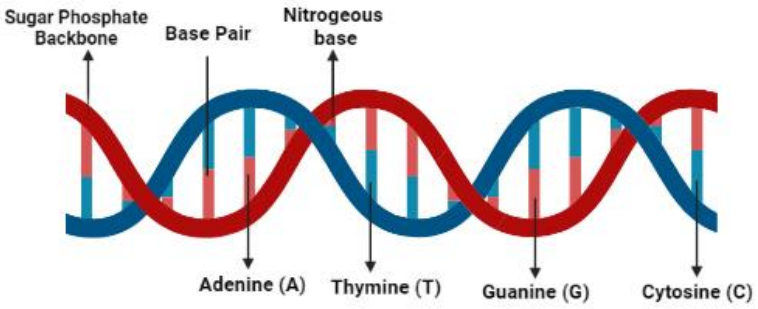

Figure 1.1. double helix structure of DNA

However, in most difficult problems the quantity of potential arrangements develops exponentially with the size of the issue (for instance, the quantity of arrangements could two-fold for each town added). This implies that even somewhat little issues would require unmanageable volumes of DNA (on the request for huge baths) to address every single imaginable response. Adleman's trial was critical on the grounds that it performed limited scope calculations with organic atoms. More significantly, in any case, it opened the chance of straightforwardly customized biochemical responses. One of the key challenges in this field is to determine the degree of similarity between genetic codes, which aids in understanding evolutionary relationships, identifying functional regions, and uncovering genetic variations associated with diseases. Traditional sequence alignment methods, such as the longest common subsequence (LCS) algorithm, have been widely employed for comparing DNA sequences and detecting similarities. The LCS algorithm aims to find the longest subsequence that is common to two given sequences. It has been a popular choice for DNA sequence comparison due to its simplicity and effectiveness. To overcome these challenges, recent advancements in machine learning have shown promise in various bioinformatics applications. Machine learning models can capture complex patterns and dependencies in DNA sequences, enabling efficient and accurate analysis. In this context, integrating machine learning techniques with the LCS algorithm can enhance its performance by reducing computational requirements and improving alignment accuracy. The design of DNA comprises of two long entwined stands that structure the well-known twofold helix structure as displayed in Figure 1.1. Each strand is worked from a little arrangement of constituent particles called nucleotides. A nucleotide comprises of three sections. The initial two sections are utilized to shape the lace like spine of the DNA strand, and are indistinguishable in all nucleotides.

LITERATURE SURVEY

Emre Delibas and Ahmet Arslan [1] performed a Dim level surface were made by the qualities doled out to the nucleotides in the DNA groupings. Closeness estimations were made between these surfaces utilizing histogram-put together surface examinations based with respect to first-arrange measurements. The surface highlights for 3 distinct DNA informational collections of various lengths, and determined the likeness grids. Christian Blum, Marko Djukanovic, Alberto Santini ,Hua Jiang, Chu-Min Li, Felip Manyà, Günter R. Raid [2] mentioned examples of the old style longest common subsequence issue and of a portion of its variations into occurrences of the greatest club issue. In addition, procedure to decrease the size of the subsequent charts. At last, a thorough exploratory assessment utilizing late definite and heuristic most extreme inner circle solvers is introduced. Weiyang Chena, Bo Liao,Weiwei Li [3] proposed a technique to calculate the image features of a DNA sequences. Utilizing similitude distance framework can be figured and connections from the measured highlights, we found that the DNA grouping of people has the most noteworthy entropy and least energy. From human to chimpanzee, orangutan, gorilla, and different species, the entropy diminishes and energy increments. Toan Thang Taa, Yi-Kung Shieha, Chin Lung Lu [4] developed a unique programming calculation that can accurately register a LCAIS between any two successions with rehashed components in O(nm) space, where n and m are the lengths of two info groupings and l is the length of the result LCAIS. Jiaoyun Yang, Yun Xu, Yi Shang [5] developed a productive equal calculation for tackling LCS issues on GPUs. By changing the information reliance in the score table utilized by unique programming, the calculation

empowers more serious level of parallelism and accomplishes a decent speedup on GPUs. Costas S. Iliopoulos, M. Sohel Rahman [6] find an answer for Inflexible Fixed Hole LCS to $O(n^3)$. Outstandingly, in each of the above cases, we accept that the two given strings are of equivalent length for example n. However, our outcomes can be effectively reached out to deal with two strings of various length. B.Lavanya, A.Murugan [7] developed and implemented MLCS in a profoundly equal manner, and can be reached out to numerous different information mining applications moreover. In future, tackling all the more constant issues in sub-atomic biology is conceivable. Qingguo Wang, Dmitry Korkin, and Yi Shang [8] proposed an calculation is fundamentally quicker than the best existing successive strategies, arriving at up to 2-3 significant degrees quicker speed on enormous size issues. At last, we present a productive equal execution of the calculation. Assessing the equal calculation on a benchmark set of both irregular and natural successions uncovers a close direct speedup concerning the consecutive calculation. Junpeng Bao, Ruiyu Yuan, Zhe Bao [9] analyzed DNA groupings similitude metric is one of the central issues of bunching. The arrangement free strategy is an extremely well-known method for computing DNA succession closeness. It ordinarily changes over a grouping into a component space in light of words' likelihood dissemination as opposed to straightforwardly matches strings. Machbah Uddin, Mohammad Khairul Islam, Md. Rakib Hassan, Farah Jahan, Joong Hwan Baek [10] developed a proficient framework for tracking down the places of k−mer in the count network. We apply our framework in six different datasets. We accomplish the high level for two benchmark datasets from AFproject, 100 percent exactness for two datasets (16 S Ribosomal, 18 Eutherian), and accomplish an achievement for time intricacy and memory utilization in contrast with the current review datasets (HEV, HIV-1). Hence, the near aftereffects of the benchmark datasets and existing examinations exhibit that our strategy is profoundly successful, proficient, and exact.

PROPOSED METHODOLOGY

The proposed machine learning approach offers several advantages over traditional approaches to improving the accuracy of the LCS algorithm. First, the proposed approach is more efficient, as it does not require the construction of a table of all possible subsequences. Second, the proposed approach is more accurate, as it considers the statistical properties of DNA sequences. Third, the proposed approach is more flexible, as it can be easily adapted to different DNA sequences. Machine learning can be used to classify DNA sequences into different categories, such as genes, proteins, or regulatory elements. This can be used to identify new genes, discover new mutations, and understand the function of DNA sequences. One common approach to DNA sequence classification is to use a support vector machine (SVM).

SVMs are a type of machine learning algorithm that can be used to classify data points into two or more categories. In the case of DNA sequence classification, the data points are the DNA sequences, and the categories are the different types of DNA sequences. Another approach to DNA sequence classification is to use a deep neural network (DNN). DNNs are a type of machine learning algorithm that can learn complex patterns in data. This makes them well-suited for classifying DNA sequences, which can be very complex. DNA sequence alignment is the process of comparing two DNA sequences to identify similarities and differences. This can be used to identify mutations, track evolutionary relationships, and reconstruct ancient genomes. One common approach to DNA sequence alignment is to use the Needleman-Wunsch algorithm. The Needleman-Wunsch algorithm is a dynamic programming algorithm that can align two DNA sequences efficiently. Another approach to DNA sequence alignment is to use a DNN. DNNs can learn to align DNA sequences by being trained on a dataset of aligned DNA sequences.

Machine learning techniques, such as Support Vector Machines (SVM), have been applied to analyze DNA sequences and extract valuable insights. In this approach, SVM is used as a classification algorithm to classify DNA sequences into different categories based on their patterns and features.

DNA Sequencing and Data Preparation:

DNA sequencing produces raw data in the form of nucleotide sequences. These sequences can be quite lengthy, so they are typically transformed into fixed-length vectors by encoding the nucleotides (A, C, G, T) into numerical representations or converting them to k-mer representations (substrings of length k). This process converts each DNA sequence into a numerical format suitable for feeding into machine learning algorithms.

Feature Extraction:

In Feature Extraction, data will be extracted from the DNA sequences. These features could include k-mer frequencies, nucleotide compositions, or any other relevant statistical or sequence-based features that capture the unique characteristics of the DNA sequences.

Data Labeling:

Data Labeling involves associating each DNA sequence with a specific class or category. For instance, the sequences could be labeled as disease-related or healthy, functional or non-functional, etc., depending on the specific application.

Model Training:

The SVM model is then trained on the labeled training data to learn the patterns and relationships between the extracted features and the corresponding class labels. SVM aims to find an optimal hyperplane that best separates the different classes in the feature space.

Model Evaluation:

After training the SVM model, it is evaluated on the testing set to assess its performance in classifying unseen DNA sequences accurately. Common evaluation metrics include accuracy, precision, recall, F1 score, etc.

Hyperparameter Tuning:

SVM has various hyperparameters, such as the kernel type, regularization parameter (C), and gamma, which can significantly impact the model's performance. Hyperparameter tuning is essential to find the best combination of parameters that yield the highest classification accuracy.

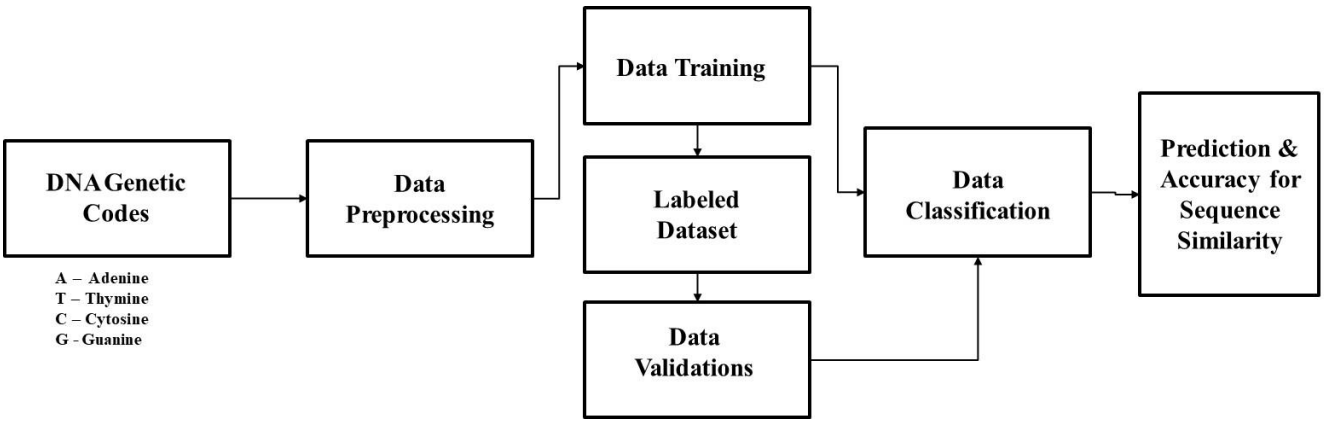

Figure 1.2. Systematic Representation of Machine Learning SVM Classification for Similarity Evaluation of DNA Genetic Codes

In Figure 1.1 states that Machine learning, specifically Support Vector Machine (SVM) classification, can be effectively utilized for similarity evaluation of DNA genetic codes. DNA similarity evaluation is a crucial task in bioinformatics and genomics, as it helps in understanding evolutionary relationships, identifying conserved regions, and detecting functional elements in DNA sequences. SVM classification offers a powerful approach to compare and classify DNA sequences based on their genetic similarities.

EXPERIMENTAL RESULT

Name of the DNA 1	DNA 1	Name of the DNA 2	DNA 2	Proposed LCS Solution	Matching sequence value	% of similarity
HUMAN	GTCACGATTTGGG GGATGCTTCTGGC TC_A-	CHIMPANZEE	GTCAGATTTGGGGGA TGCTTCTGGCTC------	GTCACGATTTGGGGGAT GCTTCTGGCTC------A-	36	100
HUMAN	GTCACGATTTGGG GGATGCTTCTGGC TC------A-	GORILLA	GTCACGATTTGGGGG ATGCTTCTGGCTC------A-	GTCAGATTTGGGGGATG CTTCTGGCTC------	36	100
HUMAN	GTCACGATTTGGG GGATGCTTCTGGC TC------A-	ORANGUTAN	GTCACGATTTGGGAG ATGCTTCTGGCTC-----G-	GTCACGATTTGGGGGAT GCTTCTGGCTC------A-	33	91.67
HUMAN	GTCACGATTTGGG GGATGCTTCTGGC TC------A-	BABOON	GTCAGAATTTGGGGG ATGCTTCTGGCTC-----T-	GTCACGATTTGGGGATG CTTCTGGCTC------	33	88.89
HUMAN	GTCACGATTTGGG GGATGCTTCTGGC TC------A-	MACAQUE	GTCAGAATTTGGGGG ATGCTTCTGGCTC-----T-	GTCAGATTTGGGGGATG CTTCTGGCTC------	33	88.89
HUMAN	GTCACGATTTGGG GGATGCTTCTGGC TC------A-	VERVET	GTCAGAATTTGGGGG ATGCTTCTGGCTC-—-T-	GTCAGATTTGGGGGATG CTTCTGGCTC—-—	33	88.89
HUMAN	GTCACGATTTGGG GGATGCTTCTGGC TC------A-	MOUSE-LEMUR	ATCACAG-TTGGGGGATGCCACT GGCCT—-C-	GTCAGATTTGGGGGATG CTTCTGGCTC------	28	75
HUMAN	GTCACGATTTGGG GGATGCTTCTGGC TC------A-	LEMUR	ATCACAA-TTGGGGG-TGCCACGGTCCT—– C-	TCACGTTGGGGGATGCC TGGCT-----	26	69.44
HUMAN	GTCACGATTTGGG GGATGCTTCTGGC TC------A-	RABBIT	ATCACAATTTGGGGA ACACCACTGGCAT----- C-	TCACATTGGGGGTGCCG GCT------	26	69.44

HUMAN	GTCACGATTTGGG GGATGCTTCT GGC TC------A-	RAT	GTCACAATTTGG AGG ATGTTACTGGCA T----- C-	TCACATTTGGGGAC CTG GCT-----	30	77.78
HUMAN	GTCACGATTTGGG GGATGCTTCT GGC TC A-	MOUSE	GTCACATTTGGG GAT GTTCTGGCT- ----	GTCACAGTTTGGAG GAT GTTACTGACAT– –C-	29	72.22
HUMAN	GTCACGATTTGGG GGATGCTTCT GGC TC A-	HEDGEHOG	GTCAGTTTGATTTT G GCT------	GTCATAGTTT— GATTATATGGGCTT— C-	24	58.33
HUMAN	GTCACGATTTGGG GGATGCTTCT GGC TC A-	DOG	GTCACATTTGGGGG A TCTCTGGCT-----	GTCACAATTTGGGGGA T ACTACTGGCAT—C-	30	80.56
HUMAN	GTCACGATTTGGG GGATGCTTCT GGC TC A-	CAT	GTCACGTTTGGGG GA CTCTGGCT-----	GTCACAGTTTAGGGGG T ACTACTGGCAT—C-	29	72.22
HUMAN	GTCACGATTTGGG GGATGCTTCT GGC TC A-	HORSE	GTCACATTTGGG TGC CTGGCT——	GTCACAATTTAGGA AGTG CCACTGGCCT—-C-	27	71.12
HUMAN	GTCACGATTTGGG GGATGCTTCT GGC TC------A-	COW	GCCTCTCTTT-------- --- CTGCCCTGCAGG C---- --	GTCACAGTTTGGAG GAT GTTACTGACAT– –C-	17	33.33
HUMAN	GTCACGATTTGGG GGATGCTTCT GGC TC_A-	ARMADILLO	---------- TGCTACTAATAT— T-	GTCATAGTTT— GATTATATGGGCTT— C-	19	36.11

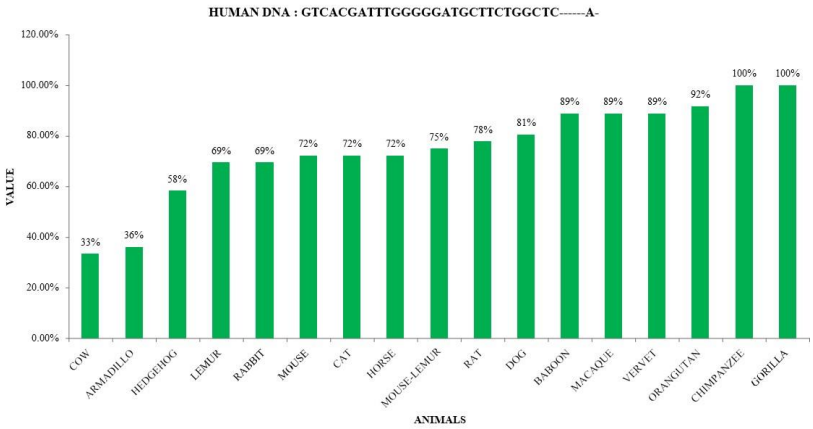

Figure 1.3. Graphical Representation of DNA Sequence Similarity

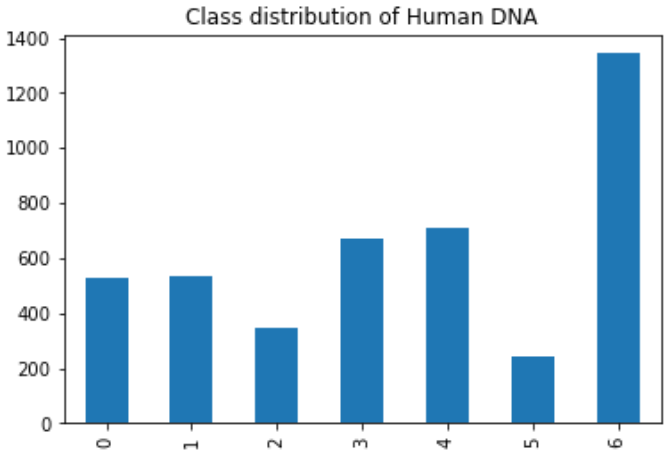

Figure 1.4. Class distribution of Human DNA

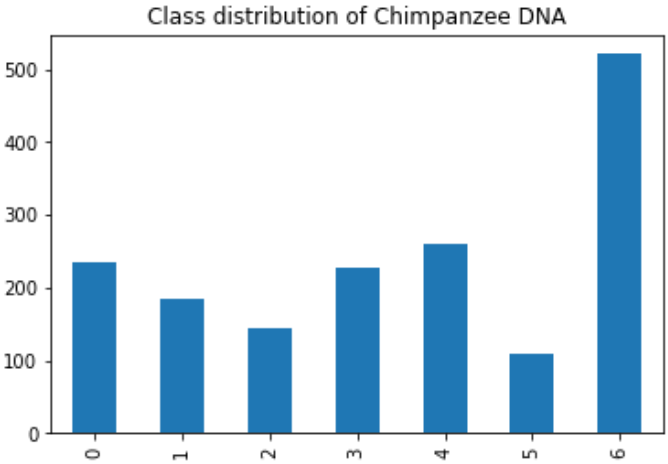

Figure 1.5. Class distribution of Chimpanzee DNA

Evaulation on chimpanzee genes

print("Confusion matrix for predictions on Chimpanzee test DNA sequence\n")

print(pd.crosstab(pd.Series(y_chim,name='Actual'), pd.Series(y_pred_chimp, name='Predicted')))

```
accuracy, precision, recall, f1 = get_metrics(y_chim, y_pred_chimp)

print("accuracy = %.3f \nprecision = %.3f \nrecall = %.3f \nf1 = %.3f" % (accuracy, precision, recall, f1))
```

Predicted	0	1	2	3	4	5	6
Actual							
0	232	0	0	0	0	0	2
1	0	184	0	0	0	0	1
2	0	0	144	0	0	0	0
3	0	0	0	227	0	0	1
4	2	0	0	0	254	0	5
5	0	0	0	0	0	109	0
6	0	0	0	0	0	0	521

```
accuracy = 0.993
precision = 0.994
```

Figure 1.3. Confusion Matrix for Predictions on Human DNA to Chimpanzee DNA Sequence

CONCLUSION

The Proposed longest common subsequence algorithm is used to find closeness between two strings utilizing longest normal aftereffect (LCS). It computes the longest normal aftereffect (LCS) by staying away from superfluous correlations with works on its exhibition. It assists with finding the DNA hereditary code arrangement closeness between two strings. It ascertains the matching rate between two strings by utilizing longest normal aftereffect and alter distance approach by staying away from superfluous correlations that decrease its time intricacy. The running time is superior to the powerful program-based calculations happen to its time control boundary. The DNA succession likeness calculation is tried on 100 examples with two info DNA hereditary code grouping strings and arbitrarily chose in Pentium processor machines and it shows great outcomes. The model appears to deliver great outcomes on human information. It likewise does on Chimpanzee which is on the grounds that the Chimpanzee and people share a similar hereditary order. The exhibition of the canine isn't exactly as great which is on the grounds that the canine is more wandering from people than the chimpanzee.

REFERENCES

1. Neil C.Jones and PavelA.Pevzner, “An Introduction to Bioinformatics Algorithms” (2004)
2. Jiaoyun Yang, Yun Xu and Yi Shang, “An Efficient Parallel Algorithm for Longest Common Subsequence Problem on GPUs”, World Congress Engineering, 2010.
3. Maier. D, “The Complexity of some problems on subsequences and super sequences”, ACM, (25), 1978, 332-336.
4. Wu. T. D and Brutlag.D.L, “Identification of protein motifs using conserved amino acid properties and partitioning techniques”. Proceedings of the 3rd International conference on Intelligent Systems for Molecular Biology, 1995, 402-410.
5. Isabelle da Piedade, Man-Hung Eric Tang, and Oliver Elemento, “DISPARE: discriminative pattern refinement for position weight matrices”. BMC Bioinformatics, 10(388): 2009, 1471-2105.
6. B.Lavanya and A.Murugan, “Discovery of Longest Increasing Subsequences and its Variants Using DNA Operations”, International Journal of Engineering and Technology (IJET),5(2), 2013, 1169-1177.
7. B.Lavanya and A.Murugan, “Mining Longest Common Subsequence and other related patterns using DNA operations”, International Journal of Computer Application, (18), 2012, 38-44.
8. B.Lavanya and A.Murugan, “Discovering sequence motifs of different patterns parallel using DNA operations”, International Journal of Computer Applications, 2011.
9. A.Murugan and B.Lavanya, “A DNA Algorithmic approach to solve GCS Problem”. Journal of Computational Intelligence and Bioinformatics. 3(2), 2010, 239-247.

10. Nikhil Bansal, Moshe Lewenstein, Bin Ma, and Kaishong Zhang, “On the longest common rigid subsequence problem”. Algorithmica, 2010, 270-280.
11. Hirosawa et al, “Comprehensive study on iterative algorithms of multiple sequence alignment”. Computational Applications in Biosciences, 1995, 13-18.
12. Neuwald.A.F and Green.P, “Detecting patterns in protein sequences”. Journal of Molecular Biology, 1994, 698-712.
13. Mahdi Esmaieli and Mansour Tarafdar, “Sequential Pattern Mining from multidimensional sequence data in parallel”, International journal of Computer theory and engineering, 2010, 730-733.
14. Smith. T. F. and Waterman. M. S, “Identification of common molecular subsequences”. Journal of Molecular Biology, 1981 147:195- 197.
15. Benson. G. and Waterman .M.S. “A method for fast database search for all k-nucleotide repeats”. 2nd International conference on Intelligent Systems for Molecular Biology, 1994, 83-98.
16. Neville-Manning. C. G., Sethi. K .S., Wu. D.,andBrutlag. A. D, “Enumerating and ranking discrete motifs”. Proceedings of Intelligent Systems for Molecular Biology, 1997, 202-209.
17. Stormo. G, “DNA binding sites: representation and discovery”. Bioinformatics, 2000, 16:16-23
18. Kyle Jensen. L., Mark Styczynski. P., IsidoreRigoutsos, and Gregory Stephanopoulos. V, “A generic motif discovery algorithm for sequential data”. Bioinformatics, 22(1) 2006, 21-28.
19. Wang. L. and Jiang. T, “On the complexity of multiple sequence alignment”. Journal of Computational Biology, 1994, 337-348.
20. Nan Li and Tompa. M, “Analysis of computational tools for motif discovery”. Algorithms of molecular biology, 2006, 1-8.
21. Lo. D and Khoo. S. D. Liu, “Efficient mining of iterative patterns for software specification discovery”. International Conference.on Knowledge Discovery and Data Mining, 2007, 460-469.
22. Annila. H. M., Toivonen. H., and Verkamo. A.I, “Discovery of frequent episodes in event sequences”. Data Mining and Knowledge Discovery, 1(3), 1997, 259-289.
23. Martinez. M, “An efficient method to find repeats in molecular sequences”. Nucleic Acid Research, 1983, 4629-4634.
24. Suyama. M., Nishioka. T., and Junichi. O, “Searching for common sequence patterns among distantly related proteins”. Protein Engineering, 1995,1075-1080.
25. Smith. H. O., Annau. T. M., and Chandrasegaran.S, “Finding sequence motifs in groups of functionally related proteins”. Proceedings of National Academy (USA), 1990, 826-830.
26. Bin Ma, "A polynomial time approximation scheme for the closest substring problem". LCNS Springer, 2000, 99-107.
27. https://www.dyclassroom.com/dynamic-programming/longest-common-subsequence
28. Sahoo, A. K., Gulavani, S., Manwal, M., Medidha, R., Bhaskar, T., & Manohara, M. (2023). Faulty diagnostics model in e-commerce using AI. Measurement: Sensors, 25, 100634.
29. Sahoo, A. K., Dash, S., & Rath, S. S. (2020). The application of garrett scoring techniques for assessment of the farmer problems in obtaining and repayment of agricultural credit. International Journal Of Scientific & Technology Research, 9(03), 5192-5199.
30.
31. SAHOO, A. K. (2018). Structure of agricultural credit system in India. REQUEST FOR FEEDBACK & DISCLAIMER 41.
32. Sahoo, A. K., Gakhreja, S., Rakesh, C., Gupta, M., Bhavsar, H., & Kumar, T. C. A. (2024). Green Manufacturing Innovations Fuelling the Transition to a Sustainable Industry 5.0. In Powering Industry 5.0 and Sustainable Development Through Innovation (pp. 237-250). IGI Global.
33. SAHOO, A. K., DASH, S., & RATH, S. S. (2020). Agricultural financing for agricultural development in India: a perceptional study on Sambalpur district. Revista Espacios, 41(08).
34. Sahoo, A. K., & Scholar, M. P. A Study of Bancassurance undertaken by Private Sector Banks in India. Int. Journal of Engineering Research and Application www. ijera. com ISSN, 2248-9622.

35.
36. Sahoo, A. K., Alekhya, V., Raj, V. H., Kumar, A., & Shelke, C. (2024). An In-Depth Analysis of Industry 5.0 in Next-Gen Manufacturing and Differentiations From Industry 4.0. In Powering Industry 5.0 and Sustainable Development Through Innovation (pp. 154-169). IGI Global.
37. Ealla KKR, Veeraraghavan VP, Ravula NR, Durga CS, Ramani P, Sahu V, Poola PK, Patil S, Panta P. Silk Hydrogel for Tissue Engineering: A Review. J Contemp Dent Pract. 2022 Apr 1;23(4):467-477. 10.5005/jp-journals-10024-3322
38. Adel, S. M., Vaid, N. R., El-Harouni, N., Kassem, H., & Zaher, A. R. (2022). TIP, TORQUE & ROTATIONS: How accurately do digital superimposition software packages quantify tooth movement?. Progress in Orthodontics, 23(1), 8.
39. Bhalerao, A., Marimuthu, M., Wahab, A., & Ayoub, A. (2023). Dynamic navigation for zygomatic implant placement: A randomized clinical study comparing the flapless versus the conventional approach. Journal of Dentistry, 130, 104436.
40. Iqbal, A., Karobari, M. I., Alam, M. K., Khattak, O., Alshammari, S. M., Adil, A. H., ... & Issrani, R. (2022). Evaluation of root canal morphology in permanent maxillary and mandibular anterior teeth in Saudi subpopulation using two classification systems: a CBCT study. BMC Oral Health, 22(1), 171.
41. Pandiyan, I., Sri, S. D., Indiran, M. A., Rathinavelu, P. K., Prabakar, J., & Rajeshkumar, S. (2022). Antioxidant, anti-inflammatory activity of Thymus vulgaris-mediated selenium nanoparticles: An: in vitro: study. Journal of Conservative Dentistry and Endodontics, 25(3), 241-245.
42. Kravitz, N. D., Dalloul, B., Zaid, Y. A., Shah, C., & Vaid, N. R. (2023). What percentage of patients switch from Invisalign to braces? A retrospective study evaluating the conversion rate, number of refinement scans, and length of treatment. American Journal of Orthodontics and Dentofacial Orthopedics, 163(4), 526-530.
43. Singh, S., & Sharma, S. (2017). Performance analysis of spectrum sensing techniques over TWDP fading channels for CR based IoTs. AEU-International Journal of Electronics and Communications, 80, 210-217.
44. Kaur, A., Sharma, S., & Mishra, A. (2017). Sensing period adaptation for multiobjective optimisation in cognitive radio using Jaya algorithm. Electronics Letters, 53(19), 1335-1336
45. Bansal, A., Sharma, S., & Khanna, R. (2019). Compact meandered RFID tag antenna with high read range for UHF band applications. International Journal of RF and Microwave Computer-Aided Engineering, 29(11), e21695.
46. Bansal, A., Sharma, S., & Khanna, R. (2020). Platform tolerant dual-band UHF-RFID tag antenna with enhanced read range using artificial magnetic conductor structures. International Journal of RF and Microwave Computer-Aided Engineering, 30(2), e22065.
47. Sah, B. K., Singla, G., & Sharma, S. (2020). Design and development of enhanced bandwidth multi-frequency slotted antenna for 4G-LTE/WiMAX/WLAN and S/C/X-band applications. International Journal of RF and Microwave Computer-Aided Engineering, 30(7), e22214.
48. Bansal, A., Sharma, S., & Khanna, R. (2020). Linearly tapered meander line broadband monopole tag antenna with T-match for Ultra High Frequency Radio Frequency Identification applications. International Journal of RF and Microwave Computer-Aided Engineering, 30(11), e22423.
49. Masood, M., Ishrat, M. M., & Reddy, A. S. (2007). Computational combustion and emission analysis of hydrogen–diesel blends with experimental verification. International Journal of Hydrogen Energy, 32(13), 2539-2547.
50. Masood, M., & Ishrat, M. M. (2008). Computer simulation of hydrogen–diesel dual fuel exhaust gas emissions with experimental verification. Fuel, 87(7), 1372-1378.
51. Reddy, K. V. P., Mirzana, I. M., & Reddy, A. K. (2018). Application of Additive Manufacturing technology to an Aerospace component for better trade-off's. Materials Today: Proceedings, 5(2), 3895-3902.
52. Ramamurty, G. (2013). Applied Finite Element Analysis. IK International Pvt Ltd.
53. Shaik, A. S., & Mirzana, I. M. (2016). Stress concentration of rectangular plate with a hole made with composite material using finite element analysis. IOSR J Mech Civil Eng, 13(4), 2278-1684.

54. Mirzana, I. M., Rao, G. K. M., ur Raheman, S., & Ahmed, M. Z. (2016). Fabrication and micro-structural study of functionally graded material disc of SS316/IN625. Materials Today: Proceedings, 3(10), 4236-4241.
55. Lakshmi Kumari, N. B. V., Jagadeesh, A., Mirzana, I. M., Subbiah, R., Dixit, S., Joshi, A., ... & Medikondu, N. R. (2024). Thermal analysis of convective-radiative porous fin heat sinks made from functionally graded materials using the Galerkin method. Cogent Engineering, 11(1), 2393238.