Paper Template for Mini-Project

Author-1, *Student Member, IEEE,* Author-2, *Senior Member, IEEE,* and Author-3, *Fellow, IEEE*

***Abstract*—A1: Describe your domain of problem statement A2: Explain your problem statement and its challenges.**

**A3: Describe your approach to solve the problem. A4: What is your performance or results ?**

**A5: Conclude.**

***Index Terms*—keyword-1, keyword-2, keyword-3, ...**

1. INTRODUCTION

**M**INI-PROJECT PAPER LAYOUT

P1: Intro on your domain of the problem statement.

P2: Motivation for your problem statement. P3: State-of-the-art solutions.

P4: Drawbacks of the state-of-the-art. P5: Challenges of the problem space.

P6: Explain your approach to solve the problem here. P7: Point-wise contributions of your paper,

P8: Organization of the rest of the paper.

1. LITERATURE SURVEY

A bioinformatics method was developed by Ziqi He *et. al.,*[1] to find kidney stone diagnostic biomarkers[1]. Eight differentially expressed ferroptosis-related genes (DE-FRGs) linked to kidney stones were found by using the Ferroptosis Database and the Gene Expression Omnibus (GEO) database[2]. Four marker genes with appropriate diagnostic potential (FZD7, STK11, SUV39H1, and LCN2) were chosen for the suggested model using the LASSO and SVM-RFE algorithms[3][4]. With an area under the curve (AUC) of 0.893, the model demonstrated strong diagnostic performance. This work has the advantage of potentially identifying treatment targets and offering fresh perspectives on the pathophysiology of kidney stones. The study's drawback is that these biomarkers must first undergo additional validation before being applied in clinical settings.

A bioinformatics analysis methodology was developed by Sen-Yuan Hong *et. al.,*[2] to pinpoint key genes in kidney stone disease (KSD). In order to find important modules linked to KSD, the model use weighted gene co-expression network analysis (WGCNA) in conjunction with the GSE73680 dataset to filter differentially expressed genes (DEGs). After finding 30 hub genes, with SPP1 being the most prominent hub gene1, they produced noteworthy results. This work has the advantage of offering possible KSD treatment targets as well as insights into the function of macrophages in stone formation2. To validate the results, additional in vivo and in vitro research is necessary as the study does not have external validation.

Monali Gulhane *et. al.,*[3] proposed an improved deep neural network (DNN) architecture for the efficient detection of kidney stones[1] With the help of deep neural networks and conventional machine learning techniques, the model achieves 90% accuracy, 89% precision, 90% recall, and an F1-Score of 89.5%. This method's benefit is its capacity to spot complex patterns in datasets, guaranteeing adaptability in changing healthcare environments[2][3]. Large, non-skewed datasets are necessary for the model to perform well, though there may be issues with data privacy and ethical issues.

Fatemeh Mahmoodi *et. al.,*[4] proposed a machine learning-based system to predict symptomatic kidney stones using data from the Fasa Adults Cohort Study (FACS)[1]. Using five machine learning algorithms (SVM, RF, KNN, GBM, and XGB), they discovered that, with an AUC of 0.60[2][3], the XGB model worked the best. Their method has the benefit of identifying important predictors such as serum creatinine level, salt intake, hospitalization history, amount of sleep, and BUN level, which can direct early lifestyle changes[4][5]. Long-term follow-up is limited by the study's cross-sectional design, and the accuracy of predictions may be impacted by the absence of kidney stone imaging data.

Fransisco Lopez-Trio *et. al.,*[5], suggested a machine learning-based method for the in vivo recognition of kidney stones. Using endoscopic images of kidney stones, the system evaluates the effectiveness of three deep learning architectures and six shallow machine learning techniques[1]. With weighted accuracy, precision, recall, and F1-Score of 97%, 97%, 98%, and 98%, respectively, the InceptionV3 architecture produced the greatest results[2]. This system's great accuracy and ability to identify kidney stone kinds instantly during ureteroscopy are its advantages. However, variations in picture quality and acquisition conditions during endoscopic procedures may have an impact on the system's performance[3].

Robert Geraghty *et. al.,*[6] in his article "Role of Genetic Testing in Kidney Stone Disease:A Narrative Review" examines the substantial genetic component of kidney stone disease (KSD), citing evidence for polygenic risk as well as 46 recognized monogenic causes. For kids, young people under 25, and elderly patients with high-risk characteristics, he suggests genetic testing utilizing a gene panel. Depending on the parameters applied, genetic testing can have a diagnostic yield of 1–11% in adults and 12–21% in adolescents and young adults. Early genetic predisposition to KSD detection and focused care by a multidisciplinary team are two benefits of this method. The substantial expense of genetic testing and the paucity of data about the natural history of KSD in relation to monogenic causes, however, are significant drawbacks.

Monali Gulhane *et.al.,*[7] proposes several models for kidney stone detection, including Gradient Boosting Classifier, Light GBM, CatBoost, Support Vector Classifier (SVC), Random Boost, Logistic Regression, XGBoost, Deep Neural Network (DNN), and an Improved DNN. With an accuracy of 90% among them, the Improved DNN performed the best. These models have the main benefit of being able to improve kidney stone detection efficiency and accuracy, which can greatly help with early diagnosis and treatment. Nevertheless, a significant drawback is the processing power and intricacy needed to train and implement these models, which can restrict their usefulness in specific medical contexts.

Patrick Doyle *et.al.*,[8] Wu Gong,Ryan Hsi,Nicholas Kavoussi,proposes machine learning models (LASSO, Random Forest, XGBoost) to predict kidney stone to forecast the recurrence of kidney stones by utilizing 24-hour urine samples and electronic health records (EHR). With AUCs of 0.62 for 2-year and 0.63 for 5-year recurrence predictions, the LASSO model performed the best out of all of them. These models' main benefit is that they can combine several data sources to produce predictions that are more accurate, which could help with individualized patient care. The comparatively low performance measures, which show potential for increasing model accuracy and generalizability, are a significant drawback, though.

Manuel A. Anderegg *et.al.*,[9] , Eric G. Olinger, Matteo Bargagli,Rob Geraghty Rémy Bruggmann investigates the genetic factors influencing kidney stone formation using whole exome sequencing on 114 non-kidney stone formers (NKSFs) and 787 kidney stone formers (KSFs). To find genetic variations that predispose people to kidney stones, the suggested model/system analyzes 34 known nephrolithiasis genes. According to the study, 2.9% of KSFs had Mendelian kidney stone disease, and KSFs had genetic variations far more frequently than NKSFs did. This approach's main benefit is that it can find genetic variants that predispose patients to certain diseases, which can then be used to guide individualized therapy. The uncommon occurrence of Mendelian disease in unselected adult KSFs is a significant drawback, though, and it might restrict the wider application of genetic testing in this population.

Jivan jayawant Barale *et.al.,*[10] uses a dataset from Kaggle that contains features like urine gravity, pH, osmolality, conductivity, urea, and calcium levels to assess the predictive power of four different algorithms: decision tree, random forest, logistic regression, and k-nearest neighbor (KNN). Of them, the random forest method yielded the best accuracy (74.40%), closely followed by KNN (74.04%), and both decision tree and logistic regression (72.0%). The main benefit of employing these algorithms is their capacity to manage intricate information and offer quite high prediction accuracy, which can facilitate early detection and intervention. A significant drawback is that more work is required to improve their accuracy and generalizability, such as testing on various datasets and fine-tuning hyperparameters.

The genetic elements influencing the development of kidney stones are examined in the paper "Genetics of kidney stone disease—Polygenic meets monogenic" by Jan Halbritter *et.al.,*[11] from the University of Leipzig Medical Center12. The model that has been suggested emphasizes the interaction between polygenic and monogenic inheritance, with particular attention to genetic variations that impact renal function and calcium homeostasis. The study emphasizes the importance of identifying genetic predispositions for individualized treatment and preventative strategies. But it also highlights the drawbacks, namely the intricacy of genetic relationships and the underdiagnosis of kidney stone disorders caused by genetics, particularly in younger adults3. In order to improve clinical studies and patient outcomes, the research highlights the necessity of centralized patient registries.

The genetic elements influencing the development of kidney stones are examined in the paper "Genetics of kidney stone disease—Polygenic meets monogenic" by Jan Halbritter *et.al.*,[12] from the University of Leipzig Medical Center1. It talks about a scenario in which the CaSR–CLDN14–CLDN16/19 axis in calcium reabsorption is highlighted, and both polygenic and monogenic variables are involved. Better knowledge of genetic predispositions and possible drug targets for treatment are two benefits of this strategy. On the other hand, the drawbacks include the intricacy of genetic relationships and the requirement for centralized patient registries in order to enable thorough research.

The genetic elements of polygenic urolithiasis are examined in the article "Genetic factors of polygenic urolithiasis" by Filippova Tamara Vladimirovna *et.al.*,[13] and colleagues from Sechenov University and other institutions. They specifically focus on calcium metabolism. The authors provide a model that uses cutting-edge genetic and molecular technologies, such as high-throughput DNA sequencing and DNA microarray, to identify genetic risk factors1. This model makes it possible to identify genetic predispositions, which opens the door to customized care and preventative measures2. The advantages include early diagnosis and tailored treatment regimens, while the cons are the high cost and complexity of genetic testing, which requires specialized knowledge for effective interpretation.

The delicate relationship between vitamin D and kidney stones is examined in the article "The complex relationship between vitamin D and kidney stones: balance, risks, and prevention strategies" by Fan Zhang and Wenjian Li *et.al*.,[14]. The authors offer a thorough model for vitamin D supplementation and kidney stone prevention that takes into account lifestyle, genetic background, and environmental factors. The model's ability to customize tailored treatment plans, improve calcium-phosphorus metabolism, and lower the danger of kidney stones is what makes it so effective1. Personalized medicine and comprehensive preventive strategies are among the benefits; on the other hand, the intricacy of genetic and environmental connections and the requirement for lengthy, in-depth research to confirm the model's effectiveness are the drawbacks.

The intricate association between vitamin D and calcium supplementation and the risk of urolithiasis is examined in the paper "Vitamin D and Calcium Supplementation and Urolithiasis: A Controversial and Multifaceted Relationship" by Piergiorgio Messa *et.al.*,[15]. For individuals who require these supplements, the authors suggest a practical method for controlling the risk of urolithiasis1. They list the benefits of supplements—such as stronger bones and possible heart benefits—as well as the drawbacks, such as a higher chance of kidney stones because of increased excretion of calcium and oxalate in the urine. Their suggested model seeks to strike a compromise between the advantages and disadvantages of supplementing in individuals with a history of kidney stones, albeit it does not provide specific performance data.

Author-1 and Author-2 are with the Department of . (e-mail: author- [1@email.com,](mailto:1@email.com) author-2@email.com)

Author-3 is with . (e-mail:author-3@email.com)

* A table has to made (like Table [I.](#_bookmark0) In table, all 20 papers have to be listed with its parameters and compared.

1. PROBLEM STATEMENT AND BACKGROUND
2. *Problem Statement*
   * Describe your problem statement here with a scenario.
   * If possible build a mathematical model for your problem statement.
3. *Objectives*
   * List the objectives of your project here.
   * Every objective should have a title and a short description.
4. *Assumptions*
   * List the assumptions that you have made to implement the project.
5. *Background*
   * Describe the background/fundamentals of your project domain here. It can include basic definitions, equations, concepts, *etc*.
6. SYSTEM MODEL/ARCHITECTURE
   * Explain your proposed system model here.
   * You can have subsections for each module.
   * Draw and describe the system using UML notations.
   * Use tools like StarUML, Diagrams.net, PlantUML, Pa- pyrus, *etc*.
   * Make use of flowcharts or algorithm (sample algo. is given in Algorithm [1)](#_bookmark1) to describe the flow of your solution.
   * Make judicial use of the different software engineering design approaches.

TABLE I

EVALUATION OF REVIEWED RESEARCH PUBLICATIONS FOR TECHNIQUE.

**Author Year Approach 1 2 3 4 5**

1. parameter-1 2. parameter-2 3. parameter-3 4. parameter-4 5. parameter-5

**Algorithm 1** Algorithm for ...

**Input:** get data

**Output:** return results

*Initialisation* : 1: first statement *LOOP Process*

2: **for** *i* = *l* 2 to 0 **do**

*−*

3: statements..

4: **if** (*i* 0) **then**

5: statement..

6: **end if**

7: **end for**

8: **return** *P*

REFERENCES

[1] S. Pattar, S. K. Dwaraka, V. Darshill, R. Buyya, K. R. Venugopal, S. S. Iyengar, and L. M. Patnaik, “Progressive Search Algorithm for Service Discovery in an IoT Ecosystem,” *in Proceedings of the 2019 International Conference on Internet of Things (iThings) and IEEE Green Computing and Communications (GreenCom) and IEEE Cyber, Physical and Social Computing (CPSCom) and IEEE Smart Data (SmartData), Atlanta, USA*, pp. 1041–1048, 2019.

APPENDIX A

Appendix A goes here ...

APPENDIX B

Appendix B goes here ...

1. IMPLEMENTATIONS AND PERFORMANCE ANALYSIS
2. *Experimental Setup*
   * In detail explain your project implementation.
   * Describe the programming language, its libraries/packages you have used.
   * Give the specifications of the machine on which the experiments are performed.
   * Have you assumed somethings? Describe them.
   * Did you setup some parameters for experiments? Like network topology, ML hyperparameters, *etc.*, describe them here.
3. *Results*
   * List the experiments you have performed.
   * At least 5 experiments based on your objectives shall be done.
   * Each experiment will go into separate subsection.
   * For each experiment, draw graphs or tabulate results and analyze.
   * Make use of tikZ package in LATEXto draw graphs.
4. CONCLUSIONS

C1: What was your problem statement? C2: How did you solve it?

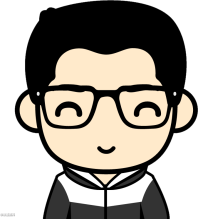
C3: What results you got?

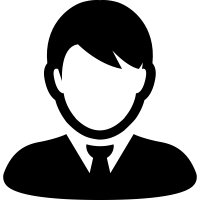
C4: How is your solution/approach better than the SOTA? C5: Future directions.

ACKNOWLEDGMENTS

List and thank the people who are not your co-authors but have helped you in successfully completing the project work.

**Author-1** received the Bachelor of Engineering de- gree in computer science from ... in ... and the Masters of Engineering degree from the ... in ... He is currently pursuing the Ph.D. degree in computer science with ... His current research interests include

... He is a student member of the IEEE.

**Author-2** is Professor of Computer Science and Software Engineering at the ... He is a Senior Member of IEEE.

**Author-3** ... He is a Fellow of IEEE.

