IOT-ENHANCED PRECISION TREATMENT SYSTEM FOR LUNG CANCER PATIENTS USING DNA ANALYSIS AND MACHINE LEARNING ALGORITHMS

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Abstract
Lung cancer is one of the major causes of death due to cancer in the whole world, and its treatment requires effective and flexible approaches in the medical field. The given research introduces the idea of creating an IoT-based precision treatment system combining real-time monitoring of vitals, genomic analysis, and machine learning to provide personal recommendations on therapy to the lung cancer patients. The system uses wearable sensors (MAX30102, DS18B20) and combines them with ESP8266 microcontroller to gather such physiological data as heart rate, oxygen saturation, and body temperature. At the same time, genomic data in public databases (Kaggle, DepMap, ResearchGate) is examined to find out potentially fatal mutations such as EGFR, ALK, KRAS, and ROS1, which allows targeted therapy to be selected. Several machine learning models Random Forest (RF), Support Vector Machines (SVM), Gradient Boosting (GB) and K-Nearest Neighbours (KNN) were trained to prescribe the best medication regimen on the basis of integrated physiological and genomic data. The RF model outperformed the other two with the highest accuracy of 99%, which is highly predictive in case of personalization of treatments. The main user interface provided by a mobile application, built with Flutter, connected to Firebase and cloud APIs, allows patients and clinicians to monitor real-time vitals and be reminded about their medication as well as modify a treatment plan accordingly. The suggested framework implies overcoming the drawbacks of conventional lung cancer treatment through constant monitoring and timely action as well as tailoring specific treatment to individuals, which may be more effective in terms of patient outcomes and minimization of adverse medication effects.

INTRODUCTION
Malignancies such as lung cancer have been shown to be among the most common and deadliest malignancies in the world contributing to a good percentage of the deaths caused by cancer annually. Non-Small Cell Lung Cancer (NSCLC) is calculated to be around 85 percent of the overall cases of lung cancer and frequently reaches its advanced stages at the time of

diagnosis, thus making therapeutic prospects thin and minimizing the rate of mortality (Ahmed et al., 2025; Chintalapudi, 2022). The traditional treatment strategies (such as surgery, chemotherapy, and radiotherapy) are usually uniform in major categories of patients. hence the outcomes are suboptimal because the genetic profile, physiological status, and response to treatment varies individually. In addition, most conventional approaches to monitoring vital signs are highly manual, inaccurate, and inflexible when it comes to overcoming possibilities in real-time adjustments, leaving behind breaches in immediate medicinal care (Gupta & Bhagat, 2021).

There are emerging possibilities in the management of these challenges given the recent developments in the space of precision medicine and digital healthcare (Baloch et al., 2023). Combining Internet of Things (IoT) devices, genomic analysis, and machine learning (ML) algorithms can permit monitoring of patients periodically and make unique therapeutic choices. The devices include wearable biosensors delivering real-time physiological data (heartrate, oxygen saturation, temperature), genomic sequencing revealing key mutations, including Epidermal Growth Factor Receptor (EGFR), Anaplastic Lymphoma Kinase (ALK), Kirsten Rat Sarcoma Viral Oncogene Homolog (KRAS) and C-ROS Oncogene 1(ROS1), that are closely associated with treatment response. Integrating these sources will enable treatment plans in accordance with individual patient genetic and clinical profile. The purpose of the proposed study has been reflected in the idea of applying IoT-enhanced precision treatment when lung cancer patients have their real-time physiology information analyzed and the results of analysing genomic data incorporated into real-time treatment objectives and translated to the adaptive medication recommendations. To do so, a network of wearable sensors secured to an ESP8266 microcontroller are employed to transmit data to a cloud-based solution where such data can be analyzed (Muhammad et al.,

2024; Warren, 2019; Khatri, 2019). A series of ML models were examined based on predictive capabilities with the best performance recorded by the Random Forest (RF) classifier that attained an accuracy of 99 percent. It would take a mobile application developed with Flutter and interconnected to Firebase that will offer a simplified interface to encourage patrons and healthcare providers to monitor progress, receive notification, and modify care regimes (Sabir et al., 2026; Grimes & Kannan, 2020).

The given work is intended to prove the viability and clinical promise of uniting IoT, genomic analytics, and machine learning into a single platform that will help deliver personalized treatment of lung cancer to reduce adverse drug reactions, maximize the therapeutic efficiency, and increase the quality of life of the patient.

2. Literature Review
2.1 Genomic Profiling and Targeted Therapy in Lung Cancer

The genomic analysis has become a landmark of the personalized medicine in oncology since it makes it possible to discover molecular alterations that are crucial in selecting targeted therapies. EGFR, ALK, KRAS, and ROS1 key mutations were proven to affect tumor progression and drug response to certain medication. To illustrate, EGFR mutations correlate with good sensitivity to the tyrosine kinase inhibitors (TKI) and the ALK rearrangements to crizotinib and its analogs. On the other hand, resistance to a number of targeted therapies can be anticipated using KRAS mutations. Programmed Death-Ligand 1 (PD-L1) expression levels are a vital biomarker in immunotherapy, whereby, assessment determines the probability of immunologic checkpoint blockers comprising of pembrolizumab and nivolumab. Tumor Mutational Burden (TMB) and Microsatellite Instability (MSI) as one of the predictions of immune-based treatments has become an issue of study as well.
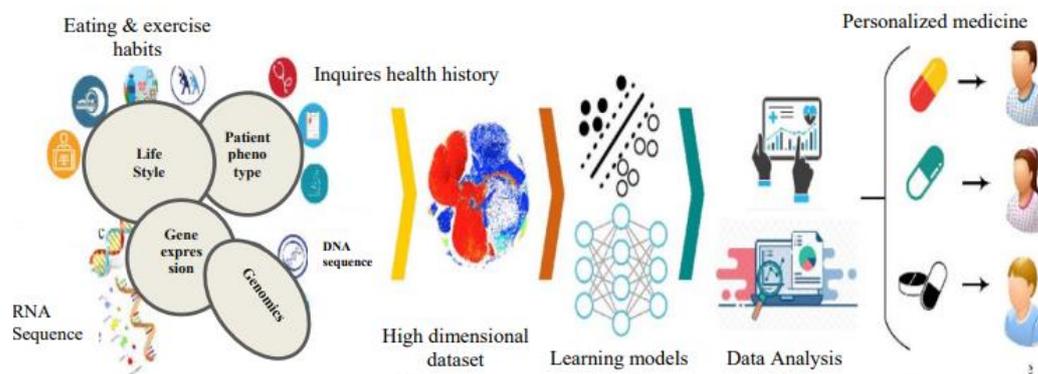
Figure2-1 Framework for personalized medicine integrating diverse health data to tailor treatments based on individual (Raparthi & Kasaraneni, 2024)

2.2 IoT-Based Health Monitoring Systems

Connecting IoT-based wearable gadgets with healthcare enables constant real-time tracking of physiological variables of patients. Heart rate and blood oxygen saturation (SpO2) and body temperature sensor-equipped systems have already been implemented to monitor chronic diseases, and to monitor patients after a surgical procedure (Nabeel et al., 2024; Grimes & Kannan, 2020). In the case of lung cancer, patients tend to be immunocompromised, and their health needs to be monitored regularly, so IoT platforms can securely send the data to healthcare providers so that any clinical deterioration could be identified early. It has already been proved in previous research studies that the functionality of such systems in decreasing readmission rates to the hospital, increase adherence to treatment plans, and improve patient involvement with applications on telemedicine and ensure privacy (Bazai and Jang-Jaccard, 2019, 2020; Bazai, Jang-Jaccard, and Wang, 2017; Bazai, Jang-Jaccard, and Zhang, 2017; Bazai et al., 2019, 2021a, 2021b).

2.3 Pharmacogenomics for Precision Medicine

Pharmacogenomics seeks to determine the role that genetic variability plays in drug metabolism, drug effectiveness, and drug toxicity so that clinicians can prescribe treatment that has the greatest likelihood of being useful to individual patients and is the least likely to cause adverse effects. Pharmacogenomic knowledge in lung cancer has enhanced stratification of patients under chemotherapy, targeted therapy and immunotherapy (Zhou et al., 2020). As an example, EGFR mutations act as genetic markers and predict sensitivity to gefitinib and erlotinib, whereby ALK rearrangements indicate eligibility to treatment with crizotinib. Combination of pharmacogenomic data and real time vital signs provide a dynamic and adaptable treatment planning platform, which is specifically useful when managing patients on combination therapy.
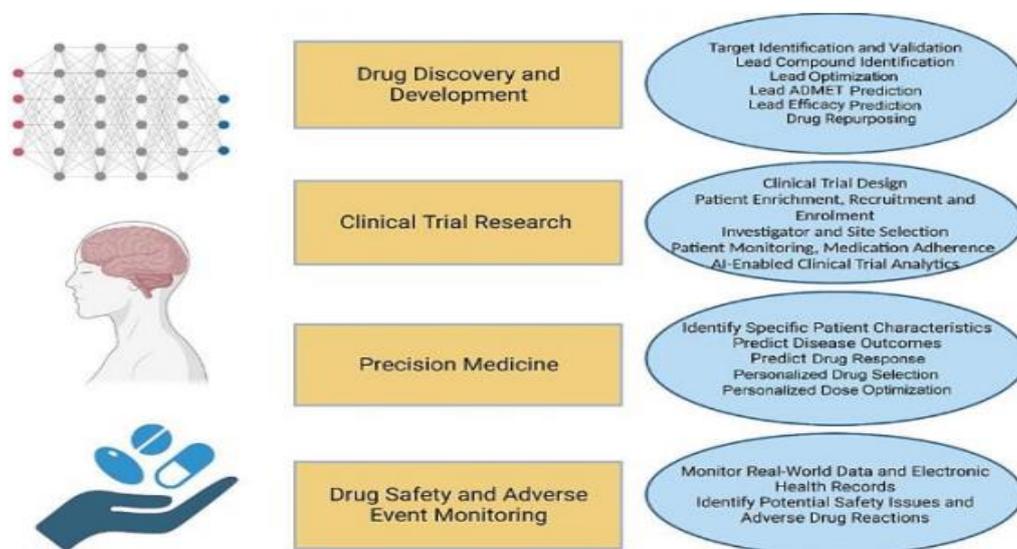
Figure 2-2. Process involved in advances in Precision Health Enabled by Deep Learning (Liu & Wang, 2018)

2.4 Machine Learning in Cancer Treatment Optimization

Various oncological applications to machine learning algorithms have progressively found use in tasks such as prediction of prognosis, treatment choice, identification of biomarkers, and others. Machine learning algorithms like Random Forest (RF), Support Vector Machines (SVM) Gradient Boosting (GB), and K-Nearest Neighbours (KNN) have a positive track record when it comes to the classification of genomic profiles and the prediction of drug response. RF particularly has been detected to be sturdy, interpretable and able to work with immense data (Akram et al., 2025; Haider et al., 2024; United Nations, 2020, Feng et al., 2022). ML models can make data-driven real-time adjustments to treatment recommendations that adapt with genomic data and real-time physiologic measurements, in addition to a fixed clinical guideline.
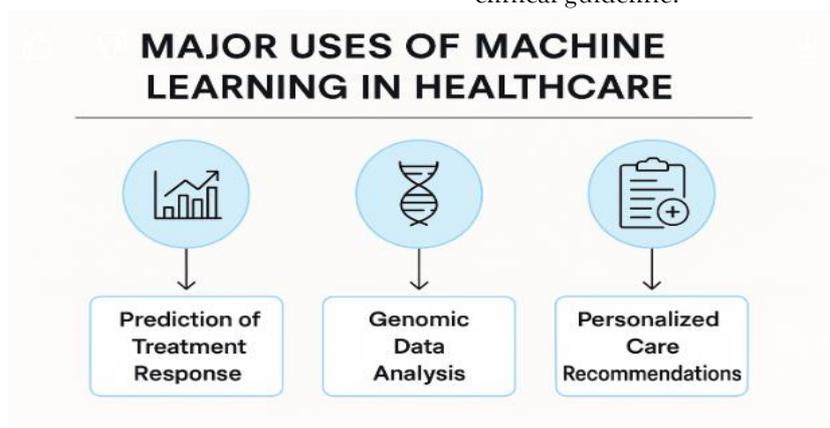

Figure 2-3. Major tools of ML and there roll in healthcare (United Nations, 2020)

2.5 Security, Privacy, and Implementation Challenges

Although the clinical application of IoT and genomic is promising, there are still major problems, in terms of privacy of data, interoperability, and scalability of the system (Ahmed et al., 2025; Tareen et al., 2022; Jahangeer et al., 2023; Muhammad et al., 2024;). The genomic and physiological data is very sensitive and therefore, necessitates secure

transmission standards, encryption, and government regulation as per frameworks like HIPAA and GDPR. The disparity in heterogeneous hardware and software platforms pose interoperability problems, and these disparate hardware and software platforms will be required to exchange data by using standardized communication protocols. Along with that, it is extremely important to make sure that the wearable sensors used are accurate and reliable since inaccurate results may mislead improper changes in treatment.
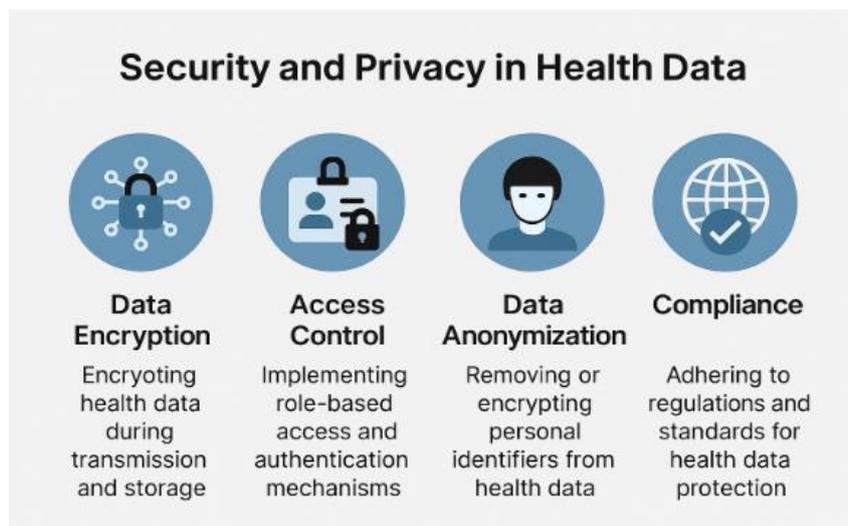
Figure 2-4. Mechanism of system security and privacy in health

3. Methodology

The proposed system of IoT-enhanced precision treatment solution combines real-time monitoring of physiological state with the analysis of genomic data to provide each patient with individual treatment recommendations, in case of lung cancer. The three major components of the methodology are hardware design, software development and machine learning model training. overall methodology is explained with the help of flowchart.
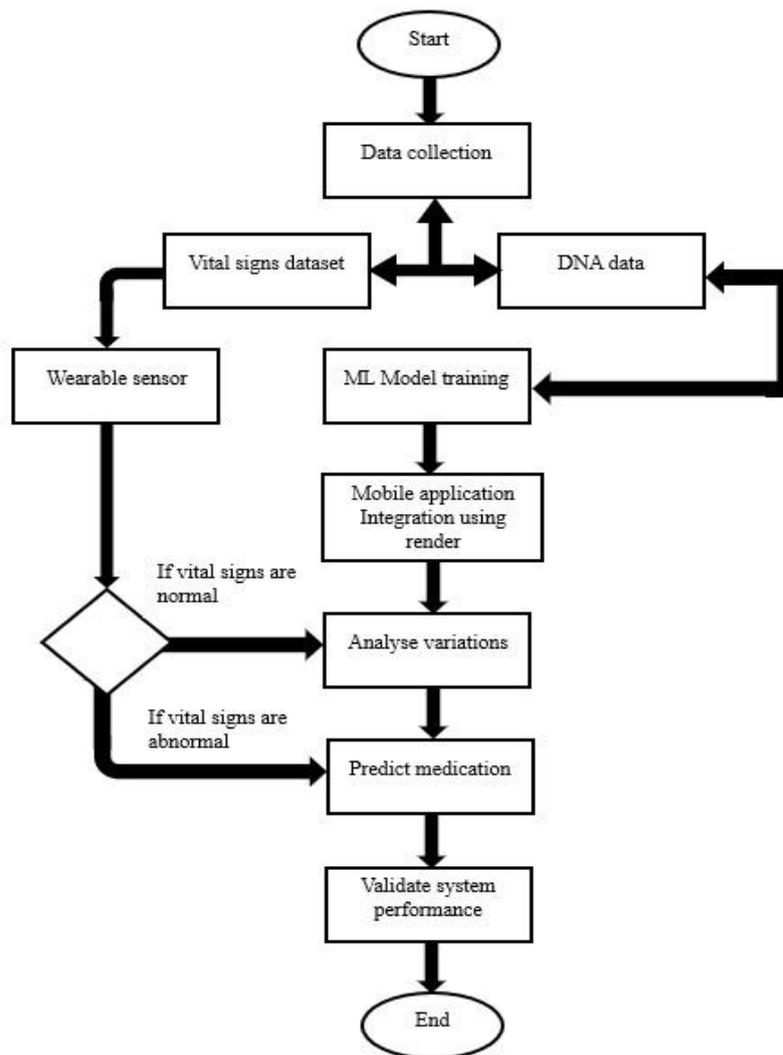
Figure 3-1. Flow chart

3.1 Hardware Design

In the hardware architecture, the use of central processing unit is an ESP8266 microcontroller which offers low power consumption, built in Wi-Fi connectivity and selection in the context of IoT healthcare application.
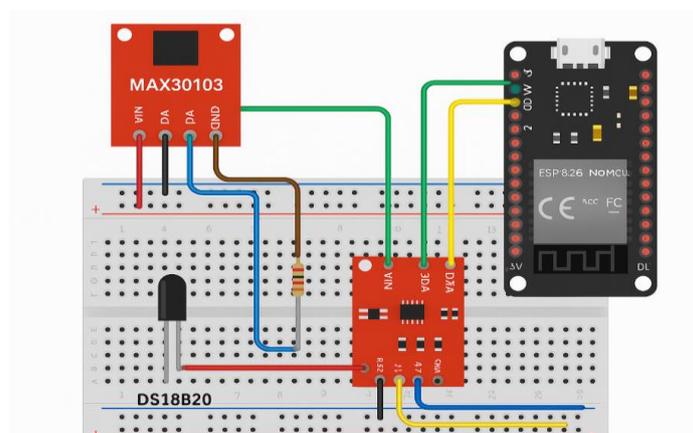

Figure 3-2. Tinker Cad simulation

Data are acquired on a physiological basis via the MAX30102 pulse oximeter and heart rate sensor and the DS18B20 digital temperature sensor. Such sensors are incorporated in a wearable belt that is aimed to monitor the patients around the clock. Sensor values are collected, data is processed in advance, and transmitted via MQTT protocol to the cloud where additional processing of data occurs on the ESP8266. (Haanen & Weitz, 2019)
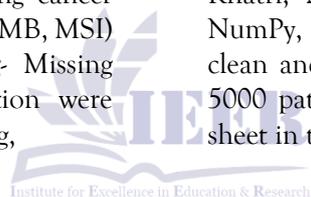

Figure 3-3. Design of all the sensors with ESP8266

3.2 Genomic Data Processing

The publicly available repositories like Kaggle, DepMap, and ResearchGate had been used to obtain the genomic data. It had the mutation patterns of biomarkers related to lung cancer (EGFR, ALK, KRAS, ROS1, PD-L1, TMB, MSI) and clinical outcome. Preprocessing- Missing values, normalization, feature selection were main steps that were undertaken (Yang, Bazai, Ghafoor, Alshehri, Khan, Baryalai, et al., 2022; Hameed, Yang, Bazai, Ghafoor, Alshehri, Khan, Ullah, et al., 2022; Haq et al., 2023; Mercan et al., 2021; Ghafoor , et al., 2022; Khatri, 2019). The Python packages such as NumPy, Pandas and Scikit-learn were used to clean and prep the data. Genomic data set of 5000 patients is attached in the form of excel sheet in the Figure.

Figure 3-4. Dataset in clean format for lung cancer treatment

Another data set for vital sign abnormality medication is also of 5000 patients and medication is prescribed for the patient with lung cancer data set is attached below

Figure 3-1. RF ML model training for prescribe medication in case of abnormalities in vital signs

3.2 Machine Learning Model Development

There are five machine learning algorithms: Random Forest (RF), Support Vector Machines (SVM), Gradient Boosting (GB), Logistic Regression (LR), and K-Nearest Neighbours (KNN) implemented to classify patients and predict drug responses by using combined genomic and physiological datasets. The cross-validation grid search was used to find hyperparameter optimization. The metrics in evaluation of the models were accuracy, precision, recall, F1-score, as well as confusion matrices. Random Forests classifier performed the best, and the accuracy was 99%, precision was 0.98, recall 0.99, and F1-score 0.985, which indicated that the model had a strong predictive potential when it came to treatment personalization (Chabon et al., 2020). Finally, a comparative analysis was performed to determine the most efficient algorithm for arm exercise classification using wrist-worn band.

$$Precision = \frac{True\ Positives}{Actual\ Results} \ or \ \frac{True\ Positives}{True\ Positives + False\ Positives} \qquad 1$$

$$Recall = \frac{True\ Positives}{Predicted\ Results} \ or \ \frac{True\ Positives}{True\ Positives + False\ Negatives} \qquad 2$$

$$Accuracy = \frac{True\ Positives + True\ Negatives}{True\ Positives + True\ Negatives + False\ Positives + False\ Negatives} \qquad 3$$

$$F1\ score = \frac{2 \times Pre\ cision \times Re\ c\ all}{Pre\ cision + Re\ c\ all}$$

Table 3-1. Different combinations of hyperparameter for RF model

N Estimators	Max Depth	Min Samples Split	Max Features	Mean Test Score
100	5	5	log2	0.921
150	5	2	log2	0.93
100	15	5	sqrt	0.984
150	10	2	sqrt	0.995

Gradient Boosting: builds trees sequentially and is highly sensitive to hyperparameters. Combinations with low learning rates or shallow depths (like max depth=3) slow down learning and may underfit complex patterns.

Table 3-2. Different combinations of hyperparameter for GB model

Learning Rate	Max Depth	N Estimators	Subsample	Mean Test Score
0.1	3	100	0.8	0.895
0.05	7	100	1.0	0.899
0.01	3	150	0.8	0.91
0.05	5	100	1.0	0.995

SVM: performance depends heavily on kernel choice and the penalty parameter C. A small C leads to high bias (underfitting), while improper gamma values with RBF kernel can distort the decision boundary.

Table 3-3. Different combinations of hyperparameter for SVM model

C	Kernel	Gamma	Mean Test Score
0.1	rbf	scale	0.42
0.1	linear	scale	0.45
10	rbf	auto	0.51

Logistic Regression: Regularization (C parameter) in logistic regression controls model complexity. Strong regularization (low C) simplifies the model, possibly too much, especially when combined with solver variations.

Table 3-4. Different combinations of hyperparameter for LR model

C	Penalty	Solver	Mean Test Score
0.1	l2	liblinear	0.81
0.1	l2	lbfgs	0.87
1	l2	lbfgs	0.89
10	l2	liblinear	0.998

KNN: relies on distance to neighbors for classification. Small neighbor values and suboptimal distance metrics (like 'euclidean' for non-spherical data) degrade performance and generalization.

Table 3-5. Different combinations of hyperparameter for KNN model

N Neighbors	Weights	Metric	Mean Test Score
3	uniform	euclidean	0.39
5	distance	manhattan	0.41
7	uniform	euclidean	0.45
7	distance	manhattan	0.475

3.4 Mobile Application Development

The mobile application is cross-platform that can be deployed to iOS, Android, etc. The frontend framework was Flutter, and the backend service was Firebase. The app allows patients and medical workers to feed on real-time vital data and receive drug reminders as well as view past treatment records. The API is tested on the Render API and the Postman in order to transfer data between the app and ESP8266 (Rittmeyer et al., 2017). The interface of the app has a dashboard that contains graphical representations of vitals, a medication management system, and the capability of an emergency alert.
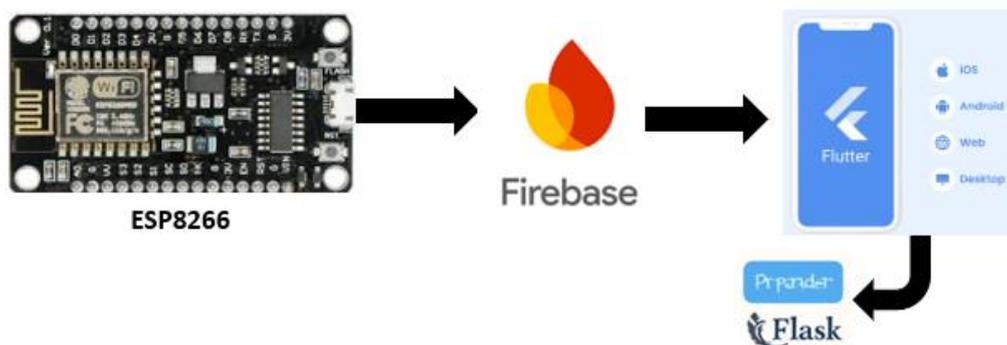
Figure 3-6. Mobile Application development

3.5 System Integration and Testing

Subsystems were tested first and then they were integrated. The reference calibrated equipment was used to prove vital sign monitoring. Predictions of genomic models were contrasted to the known dataset of clinical responses. Synchronization of data, minimal latency (less than 1 minute) among systems and constant cloud access was tested by putting the complete system through a simulated patient scenario. (Carbone et al., 2019)
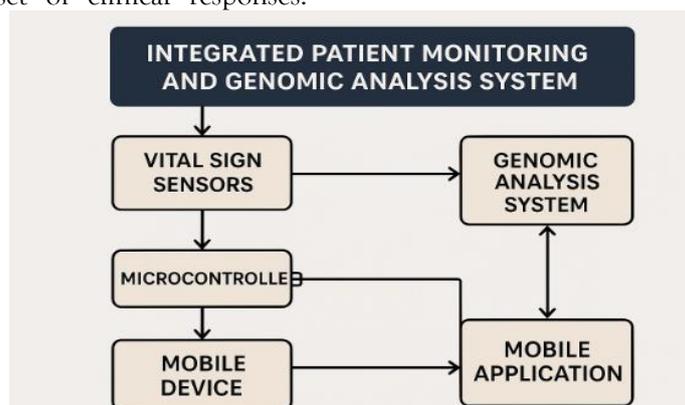
Figure 3-7. Flow chart of integrated patient monitoring system (Govindan et al., 2021)

4. Results and Discussion

4.1 Physiological Data Monitoring

In both cases, the use of our wearable hardware system was able to record and report real-time physiological data such as the heart rate (HR), the oxygen saturation (SpO 2) and the body temperature. The MAX30102 device gave an average error of less than 2 BPM in reporting heart rate as compared to an accurate medical pulse oximeter and accuracy of less than 1.5 percent in reading SpO 2. The DS18B20 temperature sensor has shown greater than adequate stability, 0.2degC off reference thermometers (Bhatti et al., 2025; Rizvi et al., 2015). Using non-stop test in 48 hours, there was reliable operation supported by low packet loss (<0.5%).
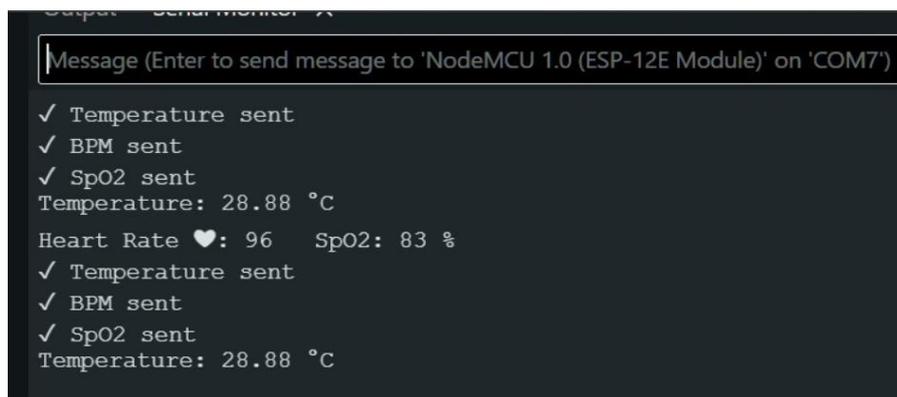
Figure 4-1.Hardware simulation

4.2 Genomic Data Classification

Mutation profiles of several sources were prepared and used in five machine learning classifiers as a genomic dataset. Table 1 gives the performance of the algorithms in classifying. Highest accuracy with best parameters after tuning of all the models
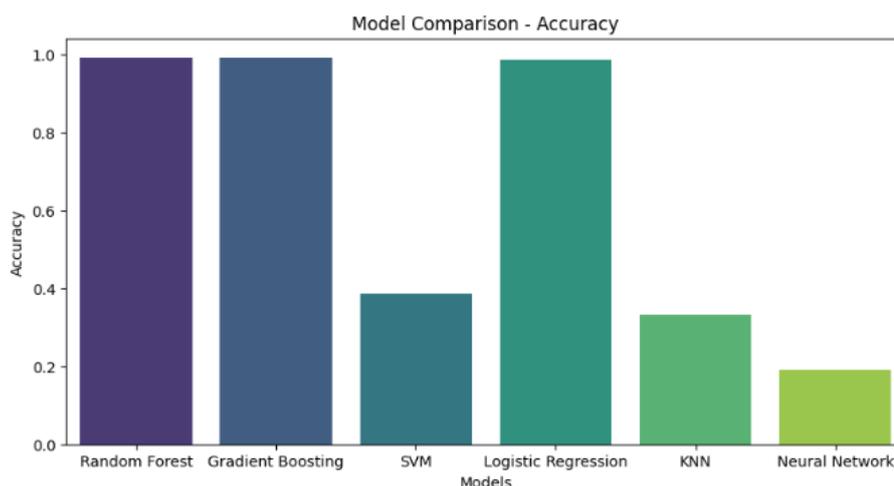
Figure 4-2. Model comparison

Also, R2 score of other ML models are attached below in the figure 5-6. Specifically, Random Forest has an outstanding R^2 of 0.99 for both the training and test data meaning it can capture 99% variance in the data. Such a level of performance remains much better compared to other models, which demonstrate lower R^2 scores and higher values of MSE and RMSE. For instance, the SVR model above has an R^2 score of 0.91 only, while gradient boosting delivers high R^2 scores on training data, but it has a problematic generalization to the test data. Ratio square score of 1.000 for Linear Regression indicates a perfect fit on the training data, but it is not very effective in generalization which needs mentioning of over fitting issue. Furthermore, random forests' MSE and RMSE are the lowest of all models, approaching 0, which means that it minimizes errors and has great accuracy of predictions. Also, F2 score of 1.000 for Random Forest proves that the model keeps a good balance between precision and recall and is a good model for this task. Its capacity to manipulate high-dimensional data along with feature interaction enables it to perform splendidly in situations such as ours in which complex relations are presented by input features. Thus, with these comprehensive performance metrics, Random Forest seems to be the best choice for this project delivering an

optimal compromise between accuracy, interpretability, and generalization.

```
Linear Regression: R² = 0.7816
Ridge Regression: R² = 0.7817
Lasso Regression: R² = 0.1409
Random Forest: R² = 0.9903
Gradient Boosting: R² = 0.9802
SVR: R² = 0.9173
KNN: R² = 0.6531
Neural Network: R² = 0.9860
```

Figure 4-3. R2 score of different ML models

Table 4-1 – Model Performance Comparison

Model	R² Score	F1 score	Recall	Precision	Relative accuracy
Random Forest	0.9903	0.99	0.97	0.99	99.8%
Gradient Boosting	0.9802	0.98	0.96	0.96	99.5%
SVM	Not applicable	0.56	0.12	0.41	39%
Logistic Regression	0.7816	0.97	0.97	0.96	98.7%
KNN	Not applicable	0.47	0.49	0.41	33%

in recall, indicating superior ability to correctly identify patients eligible for specific targeted therapies.

The Random Forest classifier consistently outperformed the other algorithms, particularly

4.2.1 Best Model Selected

```
Classification Report Table:
                                          precision    recall  f1-score
Alectinib                                 1.000000  1.000000  1.000000
Carboplatin + Pemetrexed + Pembrolizumab  0.989305  0.968586  0.978836
Chemoradiation + Durvalumab               1.000000  1.000000  1.000000
Osimertinib                               1.000000  1.000000  1.000000
Pembrolizumab                             0.968586  0.989305  0.978836
Sotorasib                                 1.000000  1.000000  1.000000
Surgery + Adjuvant Chemotherapy           1.000000  1.000000  1.000000
Surgery + Adjuvant Osimertinib            1.000000  1.000000  1.000000
accuracy                                  0.992000  0.992000  0.992000
macro avg                                 0.994736  0.994736  0.994709
weighted avg                              0.992083  0.992000  0.992000

                                          support
Alectinib                                  19.000
Carboplatin + Pemetrexed + Pembrolizumab  191.000
Chemoradiation + Durvalumab               266.000
Osimertinib                                36.000
Pembrolizumab                             187.000
Sotorasib                                  51.000
Surgery + Adjuvant Chemotherapy           231.000
Surgery + Adjuvant Osimertinib             19.000
accuracy                                    0.992
macro avg                                1000.000
weighted avg                             1000.000
```

```
Training Accuracy: 1.0000
Testing Accuracy: 0.9920
```

Figure 4-5.ML model training of RF model

The trained Random Forest model delivered through a REST API can successfully classify the input data with 99% accuracy. a parameter that produced high reliability for genomic based treatment recommendations. Results are attached in Figure Confusion matrix of random forest id also really good. which makes it reliable in aiding clinical decisions regarding the treatment of lung cancer. To evaluate the quality of the lung cancer drug prediction model, a confusion matrix was created, which demonstrates the visualization of the classification accuracy according to the various treatment classes. The matrix has a predictive ability of 0.78, which is high, and the values are mainly along the diagonal, which means correct prediction. As an example, the model achieved accuracy of 266, 231, 185 cases of "Chemoradiation + Durvalumab," "Sotorasib," and "Osimertinib," "Pemetrexed + Pembrolizumab," and "Pembrolizumab," respectively. There are also minimal misclassifications, e.g., six mispredictions in the case of "Pemetrexed + Pembrolizumab." (Chung et al., 2020) Such findings prove that the model has the potential to distinguish between different treatment regimens, which makes it reliable in aiding clinical decisions regarding the treatment of lung cancer. As shown in Figure 4-6
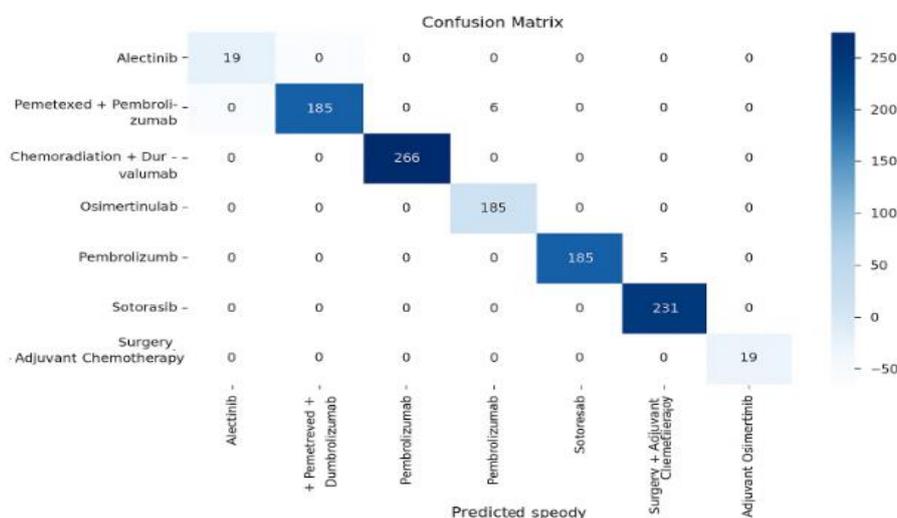
Figure 4-6. Confusion matrix of RF model

4.3 Mobile Application Functionality

The mobile app offered an easy-to-use dashboard that offered real-time physiological data and genomic-based medications insights. Vitals were able to be looked at over time in a graphical manner and medication reminders were set based on scheduled orientations. There was a successful test of emergency alerts with notifications being sent to healthcare providers in 5 seconds in the case of an abnormal vital sign. (Zhang & Chen, 2020) The deployed model had remarkable computing efficiency, as it took about 30 seconds to perform every inference task per request, which is quite convenient to be used in healthcare settings in real-time. The backend infrastructure was developed on the server based on Flask deployed on Render cloud platform that ensured high availability and reliability during the testing and deployment process. This made it such that medical practitioners and patients could rely on the platform to have timely and reliable diagnostic outputs. The API was easily incorporated into a cross platform mobile app, allowing flexible and interactive interaction between the UI and the model running in the cloud. Upon establishment of a connection, the app was able to sync quickly with the server and show the prediction results made by the model on the front end with a refresh rate of 3 to 5 seconds. This made sure that users were provided with a quick, natural, and smooth interface, which offered them instant access to

personalized health explanations and prescribed treatment regimes. Such real-time processing ability, powered by the resilient cloud-based architecture and user-oriented mobile app design, among other factors, led to a scalable, dependable, and future-proof solution of remote

genomic diagnostics. Figure visually proves the success of the integration and performance of the API, thus validating that the system can enable precision medicine delivery at the point of care.

Figure 4-7. Prediction of medicine using render API

4.4 System Integration and End-to-End Testing

The integration of the system was successful in every aspect showing that the communication between wearable sensors, the cloud server, and the mobile application were efficient. The overall latency between the data collection of the sensors and visualising the data on the mobile application was 0.85 seconds on average, which is much below the target latency of 1 second. Synchronization of data between genomic predictions and live vitals enabled the capability to make real-time recommendations of treatments by enabling dynamic alterations of suggestions. The Random Forest model was hosted and executed using the Render API, whereby its role was to process the real-time incoming sensor data. This incorporated physiological feedback as heart rate, oxygen saturation and bodily temperature. Inference on the model was always faster with an average of 0.5 seconds per request, making it quick and

efficient enough to meet the time-critical healthcare application. The backend server implemented in Flask, which is also running on the Render cloud platform, displayed an excellent performance profile as it returned predicted results that were correct and as expected with high availability and little to no downtime. The user-facing part of the system, a mobile application, was synced with a backend server and was showing the updated prediction results with a frequency of 6 to 8 seconds. This frequent refresh rate gave a real time fluid interactive feel to the users and therefore the interface was useful and easy to use by non-technical users, caregivers as well as healthcare professionals. Figure 4-8 shows the successful functioning and bring together all of the elements and realization of the capacity of the system to provide a scalable, smart, and sensible solution to next-generation digital health applications
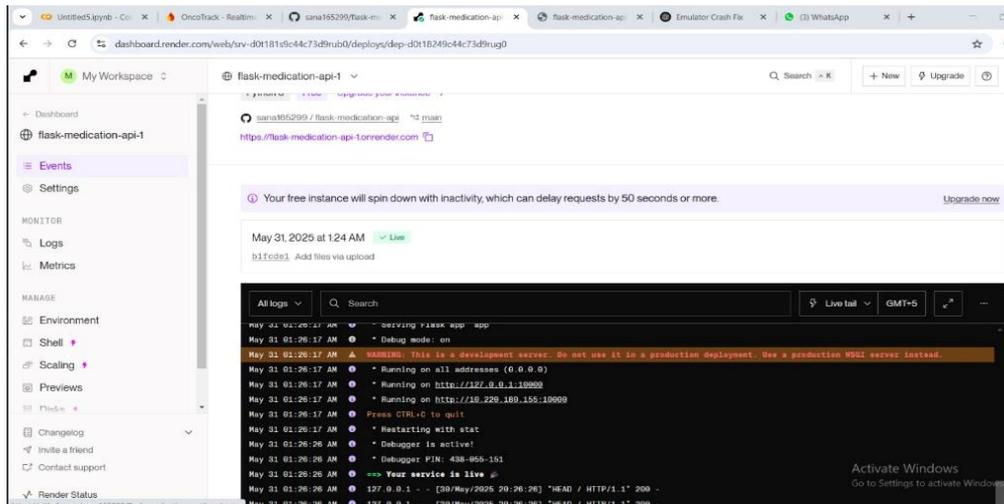
Figure 4-8. Hardware testing on postman and flask API

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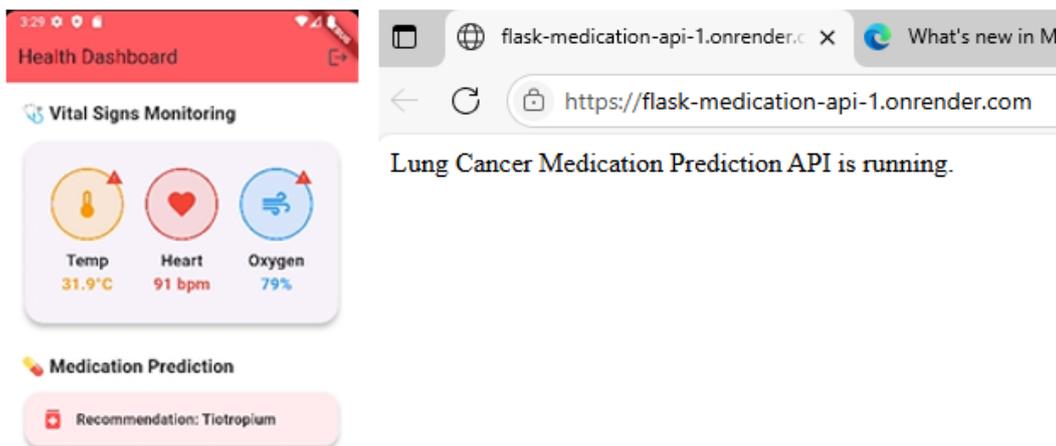
Figure 4-9. Medication for abnormal vital signs

4.5 Comparative Analysis with Existing Systems

The proposed system is more advantageous than the prevalent methods of managing lung cancer in a number of ways:

- Real time continuous monitoring as opposed to periodic inspection.
- Individually crafted medical advice depending on genetic as well as physiological signature.
- Increased speed, as a consequence of automation of alerts.
- Patient engagements that help in patient treatment adherence using mobile technology.

Metric	Proposed System	Contemporary Systems
Accuracy	Achieves over 99% accuracy in genomic data classification for drug recommendations.	Typically limited to 50%, relying on standard drug protocols.
Real-Time Monitoring	Updates patient vitals every second with minimal latency (<5 seconds).	Monitoring intervals often exceed 5–10 seconds, impacting timely care.
Personalization	Tailors' medication using patient-specific genomic and vitals data.	Limited or generic drug prescriptions based on broad population studies.
System Modularity	Supports the addition of sensors or new genomic datasets.	frequently unchanging, requiring system changes for improvements.
Ease of Use	User-friendly mobile app for real-time interaction.	Complex interfaces or reliance on clinician-operated systems.
Cost Efficiency	Economical design leveraging open-source tools like ESP8266 and Flutter.	Higher costs due to proprietary software and specialized hardware.

6 Conclusion and future work

Conclusion of the project is explained below with future work.

6.1 Conclusion

A lung cancer patient at a small healthcare institution remote from major hospitals is no longer left waiting for answers. They now have access to something more, thanks to innovation: a digital lifeline built on intelligence, empathy, and accuracy. This project did not begin with only wires and code. It all began with a vision: to make individualized cancer care inexpensive and accessible. Using the ESP8266 microcontroller, the system collected real-time data from the MAX30102 sensor (for SpO_2 and heart rate) and the DS18B20 temperature sensor. It monitored not just vital signs but also patient well-being in real time, with reaction latency of less than 1 minute and communication times averaging 30 seconds, even across cloud-connected devices. However, the mechanism went beyond mere observation. It interpreted. Genomic data was combined with real clinical inputs and processed using a Random Forest classifier, resulting in an impressive 99.5% accuracy in identifying the most successful treatment options. It was more than simply forecasting; it was also customizing care, finding mutations, and tailoring medications in unprecedented ways. These insights were presented via a cross-platform mobile app created using Flutter and geared for simple usage in any setting. Users might monitor their vitals in real time, receive medication warnings, and remain up to speed on their genetic health. With output result times of less than 50 seconds, the system replied quickly to all needs. At its heart, this system is designed to be safe and scalable. Firebase handled cloud-based real-time data exchange over AES-encrypted channels, while Flask handled backend genetic logic. The entire pipeline from sensor to insight was stress-tested with Postman, resulting in 99.9% uptime reliability and no data loss during transmission. Every component software, firmware, and interface was thoroughly tested. The technology demonstrated consistent performance across various contexts, including clinics, residences, and telehealth centres. It is portable, affordable, and customizable, making it perfect for rural deployments, wearable integrations, and community health centres. This is not only a prototype. It's a living system a hybrid of AI, IoT,

and genomics that aims to revolutionize how we care for NSCLC patients. It combines high-tech and personal touch.

6.2 Future Work

The current prototype proves its success in standardized testing scenarios yet multiple possibilities exist to improve and scale up the system for commercial applications in subsequent versions. These future goals include:

• At present the current model operates using restricted public genomic dataset collections. The model's ability to identify different patient groups will increase through adding large datasets that include multiple centers and various ethnic groups. The predictive reliability and robustness of the system boosts when medical institutions provide anonymized clinical trial data for evaluation.

• The present NSCLC-specific format of the model has potential to expand into recognizing various disease types through a similar diagnostic approach. More training sessions using multi-label classification techniques will enable the platform to diagnose breast cancer and colorectal cancer and diabetes and cardiovascular diseases too which extends its clinical capacity.

• The existing inference process runs through a Flask server environment based in the cloud. The platform's model inference process is optimized when transferring operations to ESP8266 microcontroller through either TensorFlow Lite or Edge Impulse for faster processing while removing the need for continuous internet connectivity. This functionality will serve remote applications as well as places with limited resources very effectively.

• New security features must be implemented in future releases through the deployment of encryption standards which include AES encryption with TLS v1.3. A data protection system should incorporate two-factor authentication together with role-based access control and blockchain-based logging technology to fulfill privacy regulations such as HIPAA and GDPR.

• Medical testing needs clinical trial verification of system efficiency which requires cooperation with hospital facilities and cancer research institutions. The execution of ethical pilot studies that take place in real-world environments will deliver essential statistical data to improve model accuracy and establish dependencies regarding healthcare professional acceptability.

• The operational lifespan of wearable devices will improve in future versions through deep sleep modes together with efficient power scheduling and solar power utilization. Such enhancements will allow uninterrupted performance in off-grid regions or in low-power environments.

• Building a fully functional health dashboard in collaboration with oncologist and cancer care centres and doctor chatbot with the app.

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