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Editorial

Advances in Science, Technology and Engineering Journal (ASTESJ) continues to provide a multidisciplinary platform for disseminating innovative research that addresses contemporary scientific, technological, and engineering challenges. The papers featured in this issue reflect the breadth of current research, ranging from advanced sensing systems, artificial intelligence, and cybersecurity to healthcare, sustainable materials, privacy-preserving data analytics, and bioinformatics. Collectively, these contributions demonstrate how emerging technologies and interdisciplinary approaches are driving practical solutions with significant scientific, industrial, and societal impact.

The issue opens with a study on the development of an electromagnetically actuated PCB-based resonating scanning micro-mirror for LiDAR applications. By introducing FR4 and polyimide substrates as cost-effective alternatives to conventional silicon MEMS devices, the research addresses limitations associated with fabrication cost and structural fragility while achieving enhanced optical scanning performance. The integration of optimized electromagnetic actuation with embedded sensing circuitry further demonstrates the potential of PCB-compatible micro-mirror technology for next-generation LiDAR and real-time control applications, highlighting an important advancement in precision sensing systems [1].

Artificial intelligence continues to transform medical diagnostics, as demonstrated by the proposed hybrid cascading framework for automated skin cancer detection. The integration of deep learning, machine learning, optimization techniques, and explainable artificial intelligence achieves remarkable diagnostic performance while improving computational efficiency and model transparency. The incorporation of Grad-CAM++ and LIME strengthens clinical interpretability by identifying lesion regions influencing predictions, illustrating the growing importance of trustworthy AI in healthcare decision-making [2].

The growing adoption of service-oriented communication in modern vehicles has created new cybersecurity challenges that require efficient and practical solutions. A novel detection and mitigation approach for SOME/IP server spoofing attacks provides an effective defense mechanism capable of identifying malicious activities during service discovery while minimizing processing and communication overhead. Comprehensive evaluation across multiple attack scenarios demonstrates the feasibility of implementing robust intrusion detection within resource-constrained in-vehicle networks, contributing to the advancement of secure automotive communication systems [3].

Advances in computer vision and physiological signal processing are further illustrated through a non-contact heart rate monitoring framework that combines remote photoplethysmography with pose estimation for exercise tracking. By integrating motion analysis with signal enhancement techniques, the proposed system significantly improves heart rate estimation under movement conditions while enabling real-time monitoring during physical activity. Such developments represent meaningful progress toward intelligent fitness systems capable of personalized exercise guidance and early detection of cardiovascular abnormalities [4].

Efficient neural network design remains a fundamental challenge as intelligent systems become increasingly embedded within robotics, smart cities, and Internet of Things environments. The proposed ElHa Net architecture presents a resource-efficient framework that combines self-feature extraction with an optimized classification mechanism to achieve competitive pattern recognition performance while minimizing computational requirements. The work contributes to

ongoing efforts aimed at developing lightweight artificial intelligence models suitable for modern autonomous and embedded applications [5].

Privacy-preserving healthcare analytics remains essential for unlocking the value of large-scale medical datasets without compromising sensitive patient information. The proposed Multi Attribute Stratified Sampling (MASS) framework introduces an automated optimization strategy that eliminates the need for manual configuration of privacy parameters while maintaining an effective balance between data protection and analytical utility. Validation across datasets of varying sizes demonstrates strong scalability, high recall retention, and practical feasibility, offering an important contribution to secure healthcare data sharing and privacy-aware analytics [6].

Sustainability is a recurring theme throughout contemporary engineering research, and this issue includes an investigation into the use of rice husk as a biomass additive for fired-clay cook-stove liners. The incorporation of agricultural waste significantly improves porosity, thermal insulation, and combustion efficiency while simultaneously promoting environmentally responsible waste utilization and greenhouse gas mitigation. The findings illustrate how locally available renewable materials can enhance energy efficiency and support the development of sustainable household technologies [7].

The final contribution introduces GC4miRNA, a bioinformatics pipeline designed to analyze GC content signatures in cancer-associated microRNAs. By examining sequence characteristics that influence miRNA-mRNA binding affinity and implementing the analysis through an accessible R Shiny application, the study provides researchers with a valuable computational tool for investigating gene regulation and disease mechanisms. The framework strengthens bioinformatics research by facilitating systematic exploration of sequence features associated with cancer-related microRNA dysregulation [8].

The diversity of contributions presented in this issue highlights the dynamic nature of scientific and engineering research and underscores the increasing convergence of artificial intelligence, advanced materials, biomedical technologies, cybersecurity, and sustainable engineering. Together, these studies offer novel methodologies, practical implementations, and valuable insights that advance both theoretical understanding and real-world applications. It is anticipated that the findings reported in this collection will inspire further interdisciplinary collaboration and stimulate future innovations that address emerging global challenges across science, technology, and engineering.

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Design and Electronic Interfacing of FR4 and Polyimide PCB-based Electromagnetic Resonating Micro-mirrors

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ABSTRACT

This paper presents the design and fabrication of an electromagnetically actuated PCB-based resonating scanning micro-mirror for LiDAR applications, with optimization targeted towards low-cost fabrication and a high scanning angle. Traditional silicon MEMS-based micro-mirrors, while offering high precision and compatibility with CMOS processing, are limited by fragility at low scanning frequencies and costly fabrication processes. To overcome these challenges, novel alternative polymer-based substrates, namely FR4 and polyimide (PI), were employed to implement PCB-compatible mirror prototypes. Electromagnetic actuation was chosen because it achieves a high scanning angle at low driving voltages and is therefore compatible with modern electronic drive circuitry. The resonant frequency and von Mises stresses were assessed via COMSOL finite element simulations. Various scanning mirror prototypes, each featuring an optical mirror aperture of 10 mm by 10 mm, were fabricated using two different materials: 0.3 mm-thick FR4 and polyimide substrates. Different electromagnetic coil structures, embedded on the mirror plate, were evaluated with the aim of optimizing the scanning performance. The magnetic field was generated using neodymium permanent magnets. The performance attained by each prototype is compared and discussed. The scanning mirrors were designed to have a low resonant frequency in the range of 250 Hz to 550 Hz. The maximum optical scanning angle achieved for the FR4 and polyimide substrates are 31.3° and 52.1°, respectively. The paper also delves into the design of a microcontroller-based electromagnetic actuation and sensing circuitry of the mirror. Custom electronic circuitry comprising a low-power STM32L432KC microcontroller, H-bridge motor drivers for mirror actuation, and INA241-based coil voltage and current sensing was designed for this purpose. The coil voltage and current sensing circuitry enable the eventual real-time sensor less angular position feedback of the micro-mirror.

1. Introduction

This paper presents an extended version of the preliminary work describing PCB-based micro-mirrors originally presented in the IEEE 31st International Conference on Electronics, Circuits, and Systems [1]. Scanning micro-mirrors are used in various applications, including miniature projection displays, LiDAR, micro-spectrometers, and biomedical imaging [2]. Previous work in this area includes an FR4-based micro-mirror featuring a 12 mm by 12 mm platform with a rectangular spring structure,

achieving an optical scanning angle of 11.2° at 361.8 Hz and requiring only 425 mV of driving voltage. This design also integrated an angle sensor for real-time feedback, demonstrating strong durability through long-term vibration and shock testing [3]. Another study, involving FR4-based scanning mirrors, evaluated three different configurations, with the most optimal one achieving a 140° scan angle at 417.4 Hz using serpentine springs, which were chosen for their lower spring constant [4]. Two other rectangular spring-based variants were also investigated: these achieved a scanning angle of 16.9° and 30° at an operating frequency of 1.787 kHz and 807 Hz, respectively, under similar conditions [4]. Another micro-mirror design was intended for a

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near infrared (NIR) spectrometer application and incorporated a 12 by 12 mm FR4-based diffraction grating with serpentine springs and reached a scanning angle of 13° at an operating frequency of 190 Hz [5].

In this work, polyimide (PI) is also considered and compared with FR4 as an alternative substrate material for its potential use in low-frequency resonating high scanning angle micro-mirrors due to its inherently low value of Young's modulus and mechanical robustness.

1.1. Substrate Material

While silicon (Si) MEMS-based micro-mirrors have been employed for high-frequency scanning, they tend to be fragile at low-frequency operation, in applications such as spectroscopy [6], [7] and LiDAR [8], [9]. Low-frequency Si mirror designs require springs with very low torsional stiffness. These are prone to fracture because of environmental impact forces, particularly in automotive applications [10]. Although there are alternative materials, such as silicon dioxide [11], silicon nitride [12] and metallic substrates, such as aluminum [13], [14], they are expensive and require extensive processing. The flexibility and toughness of polymer-based materials present an advantage over Si-based micro-mirrors in low scanning frequency applications [15], while also enabling a larger reflective aperture area to be achieved at low cost. Polymers have already been utilized for MEMS-based micro-mirror manufacturing, both as sacrificial and as structural materials: these include polydimethylsiloxane (PDMS) [16] and SU-8 photoresist [17], [18], which can be patterned using photolithography or soft lithography processes [19] and are thus compatible with standard MEMS manufacturing processes.

This paper presents a study on the use of FR4 and PI substrates for a cost-effective, large optical aperture and wide scanning angle micro-mirror design, together with its relative actuation and sensing electronic circuitry. The design is targeted at LiDAR applications. For low production volumes and niche applications, both PI and FR4-based solutions are significantly cheaper than Si-based designs, especially for large aperture designs exceeding 10 mm by 10 mm [3]. Furthermore, it should be noted that PI printed circuit boards (PCB) are relatively more expensive than the FR4 counterpart, but PI is also more flexible. Polyimide offers superior thermal stability since it can withstand temperatures of up to 200°C without any signs of degradation. On the other hand, FR-4 can sustain a lower temperature limit of around 120°C. Table 1 outlines the typical differences in material properties between FR4 [20], flexible PI [21] and single-crystal silicon [22].

Table 1: Comparison of typical material properties: FR4, flexible PI, and Silicon.

Property	Material		
	FR4	Flexible Polyimide	Silicon (single-crystal 100)

Material Type	Rigid laminate	Flexible laminate	Crystalline semiconductor
Glass Transition Temp (T _g)	130°C–180°C	200°C–250°C	N/A
Thermal Conductivity	0.3–0.4 W/m·K	0.12–0.22 W/m·K	~149 W/m·K
Decomposition Temp (T _d)	~300°C	>400°C	>1,414°C (melting point)
Moisture Absorption	0.10–0.20%	0.8–1.0%	0%
Ductility	Medium	High	Low
Cost	Lower	Medium	High
Mechanical Strength	High	Moderate	Very high (but brittle)
Ultimate Tensile Stress	~375 MPa	~230 MPa	~2 GPa

1.2. Actuation Method

The four main actuation principles used for micro-mirror actuation are electrostatic, electromagnetic, electrothermal, and piezoelectric. Electrostatic actuation is inherently low power but also requires high actuation voltages, which are typically not compatible with low-voltage electronic devices and require the use of dedicated high-voltage supplies and drivers in the range of about 10 to 100 V [23]. Electrothermal actuation can be used for low-frequency scanning applications [24], but this technique consumes significant power, is inherently non-linear, and prone to long-term degradation. Piezoelectric actuation can operate at lower voltages but requires the use of piezoelectric materials deposition, such as PZT or aluminum nitride [25], which are typically not available in standard PCB manufacturing processes. In this work, electromagnetic actuation is chosen due to its high electromechanical coupling and its capability to operate at relatively low voltages, without the requirement of special material depositions, making it compatible with standard PCB manufacturing processes and with standard low-voltage driving circuitry. Furthermore, electromagnetic actuation offers a more linear response than other actuation methods, making it ideal for slow linear scanning mirrors. The magnitude of the Lorentz force $F_{Lorentz}$ generated on a conductor of length L , inside a magnetic field B , and carrying a current i , is given by:

$$F_{Lorentz} = B \cdot i \cdot L \quad (1)$$

The corresponding mechanical torque T_{mag} generated by a coil having N turns is given by:

$$T_{mag} = 2 \sum_{j=1}^N B \cdot i \cdot l_j r_j \quad (2)$$

where r_j is the distance of the j^{th} coil (two coupled segments) from the centerline (refer to Figures 1 and 2). Unlike electrostatic and piezoelectric actuation, electromagnetic actuation generates considerable thermal I²R heat dissipation due to the finite resistance of the coil.

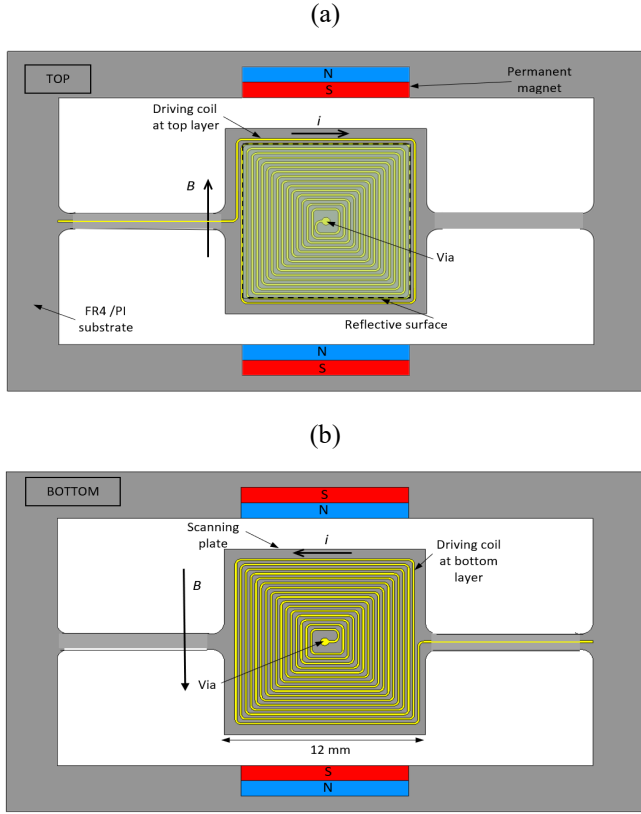


Figure 1: Coil design shown in the (a) top and (b) bottom layers of the PCB with a connection via placed at the center of the scanning plate.

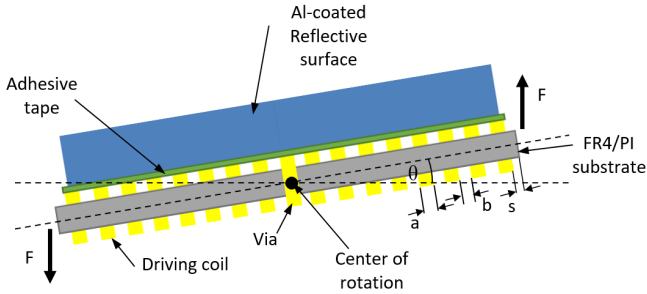


Figure 2: Scanning mirror shown with actuating forces.

In this paper, the use of PI substrate for scanning micro-mirrors is novel and is here compared to FR4-based substrates. Its low elastic modulus leads to enhanced scanning angles, which is advantageous for applications such as LiDAR. This choice of substrate is also attractive as a low-cost alternative to MEMS-based micro-mirror designs. Furthermore, novel electronic interface circuitry is presented for the eventual positional control of the micro-mirror without the requirement of additional sensors.

2. Micro-mirror Mechanical Design

2.1. Numerical Design

The PCB-based micro-mirrors consist of three main elements: the actuation coil, a pair of torsional springs, and the reflective aperture area. The mirrors are designed to operate at resonance in the out-of-plane torsional mode.

The resonant frequency f_r of the micro-mirror is given by [26]:

$$f_r = \frac{1}{2\pi} \sqrt{\frac{k_t}{I_m}} \quad (3)$$

where k_t is the torsional stiffness of the springs and I_m is the moment of inertia of the mirror plate around the rotational axis.

In this case, for straight springs, the torsional stiffness k_t is given by:

$$k_t = 2G \frac{J}{l_s} \quad (4)$$

where G is the material shear modulus and l_s is the spring length. The shape-factor term J for a spring having a rectangular cross-section, of width w_s and thickness t_s , ($w_s \geq t_s$), is given by [26]:

$$J = w_s t_s^3 \left[\frac{1}{3} - \left(0.21 \frac{t_s}{w_s} \left(1 - \frac{t_s^4}{12w_s^4} \right) \right) \right] \quad (5)$$

The shear modulus G can be inferred from the Young's modulus E and Poisson ratio ν , using [26]:

$$G = \frac{E}{2(1+\nu)} \quad (6)$$

The moment of inertia I_m of the rectangular mirror plate having width W_m , length L_m , thickness T_m , and density ρ_m is given by:

$$I_m = \frac{\rho_m L_m W_m T_m}{12} (W_m L_m)^2 \quad (7)$$

The various dimensions that determine the mirror's resonant frequency are depicted in Figure 3.

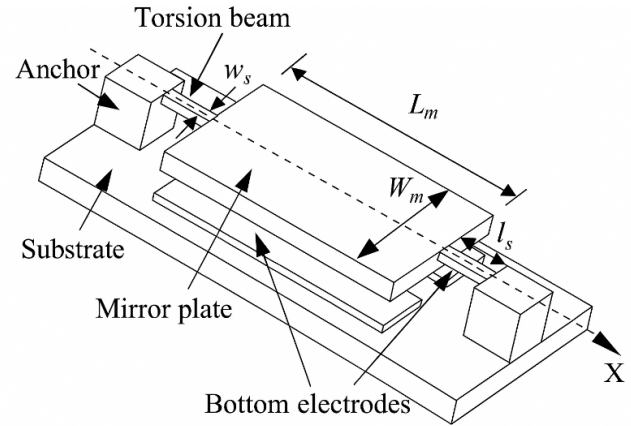


Figure 3: Principal dimensions of the scanning mirror [26].

Straight torsional beams with rectangular cross-sections are used to support the 10 mm by 10 mm mirror plate, where the spring width and length were selected to achieve the target resonant frequency.

The coil consists of two layers of copper turns in a rectangular spiral shape on both sides of the substrate. Different coil designs were considered with the aim of achieving the maximum magnetic coupling and the lowest actuation voltage. The external connections to the two coil layers are routed via the torsional

springs. The two coil layers are connected in series using a via placed at the center of the mirror plate area.

The coil designs (based on Figures 1 and 2) that have been investigated in this work are presented in Table 2. In each case, the copper thickness is fixed by the PCB process at 35 μm for both the FR4 and PI-based mirror substrates.

Table 2: Coil configurations examined in this study.

Coil trace width (a) (mm)	Total coil trace length (mm)	Number of turns/layer	DC Resistance (Ω)
0.503	278.5	5	0.265
0.152	591.7	15	1.878
0.102	712.5	20	2.261
0.102	899.7	25	4.725

The device dimensions for the FR4 and the polyimide PCB-based mirrors were calculated based on the material properties shown in Table 3.

Table 3: Material properties used for mechanical design.

Property	FR4	Polyimide	Polycarbonate (mirror)
Density (g/cm^3)	1.85	1.42	1.2
Young's Modulus (GPa)	22	3	2.4
Poisson ratio	0.11	0.34	0.38

The resulting PCB design for three different electromagnetic scanning micro-mirrors is shown in Figure 4. These designs have the same dimensions, but different coil designs.

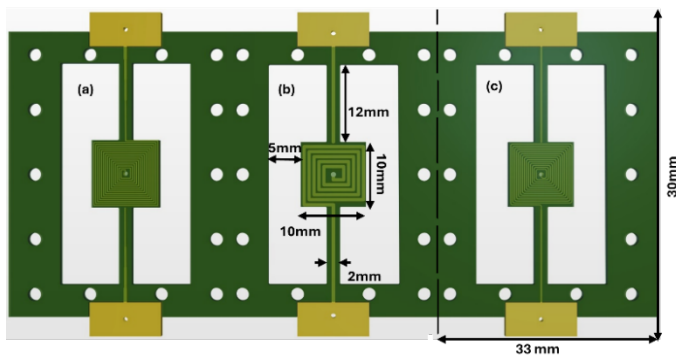


Figure 4: A sample of the PCB layouts of the designed micro-mirror having three different coil designs: (a) 20 turns/layer (b) 5 turns/layer and (c) 15 turns/layer.

Figure 5 shows the vertical cross-section of the designed micro-mirror. The PCB substrate and the coil were fabricated using the PCBway prototyping service. The reflective aluminum (Al) coated polycarbonate layer was extracted from a compact disc (CD) and attached to the PCB substrate using double-sided tape.

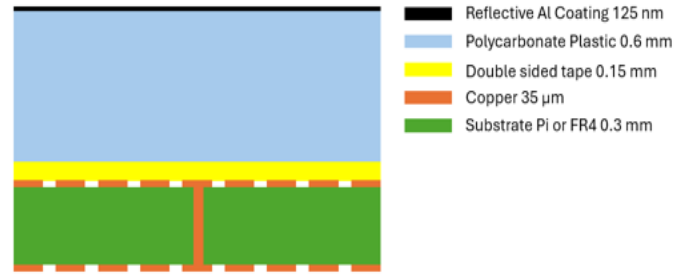


Figure 5: Vertical cross-section of the proposed resonant scanning micro-mirror showing the material stack with their respective thicknesses.

The mechanical design was verified by performing modal finite element analysis (FEA) using COMSOL Multiphysics to determine the torsional mode resonant frequency (refer to Figure 6). These simulations were also used to verify that adjacent modal frequencies were adequately separated, thus preventing spurious excitation of unwanted modes. Static structural FEA simulations were also carried out to determine the von Mises stress distribution and ensure that these are well below the maximum yield strength of the substrate material (refer to Figure 7). These simulations were carried out by applying an angular acceleration corresponding to an optical scanning angle amplitude of 40° at the first torsional modal frequency. Both simulations were carried out using swept hexahedral elements with 5 elements across the thickness of the device polymer layer and with fixed constraints (for the 6 degrees of freedom) applied to edge boundaries of the anchors attached to the torsional springs. The glass mirror was included in the simulations as this affects the moment of inertia. In each case, linear isotropic elastic material properties were considered: this is justified on the assumption that the maximum elastic strain developed at the maximum scanning angle is within the linear elastic limit of the polymer material. A mesh convergence study was performed to ensure that a negligible change in the maximum von Mises stress is obtained with further mesh refinement. The maximum von Mises stress values are 9.79 MPa and 79.95 MPa for the PI and FR4-based micro-mirrors, respectively. These von Mises stress values correspond to 4.2% and 21% of the respective material's ultimate tensile strength.

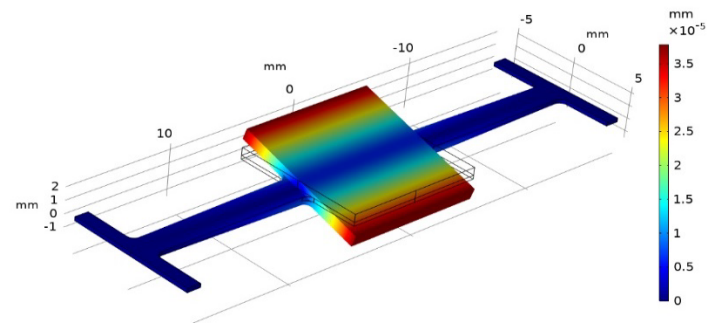


Figure 6: Contour plot showing the normalized mirror displacement in the torsional scanning mode at 285.15Hz obtained from an FEA modal analysis for the PI substrate. The corresponding resonant frequency value for the FR4 substrate is 792.9 Hz.

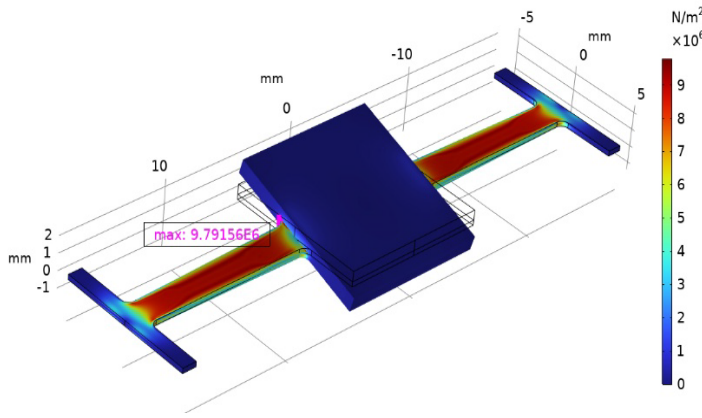


Figure 7: FEM simulation result showing the von Mises stress distribution at resonance and an optical scanning angle of 40° for the PI mirror. Maximum von Mises is 9.79 MPa for the PI mirror and 79.95 MPa for the FR4-based mirror.

2.2. Complete Micro-Mirror Assembly

The PCB-based micro-mirror was assembled, together with a pair of neodymium permanent magnets, in a 3D-printed polylactide (PLA) housing, as shown in Figure 8. The PCB substrate is clamped between two 3D-printed PLA blocks. The air gap between the magnets and the mirror plate was set to be 1 mm. This value was chosen as a compromise between mechanical tolerances and optimal electromagnetic coupling.

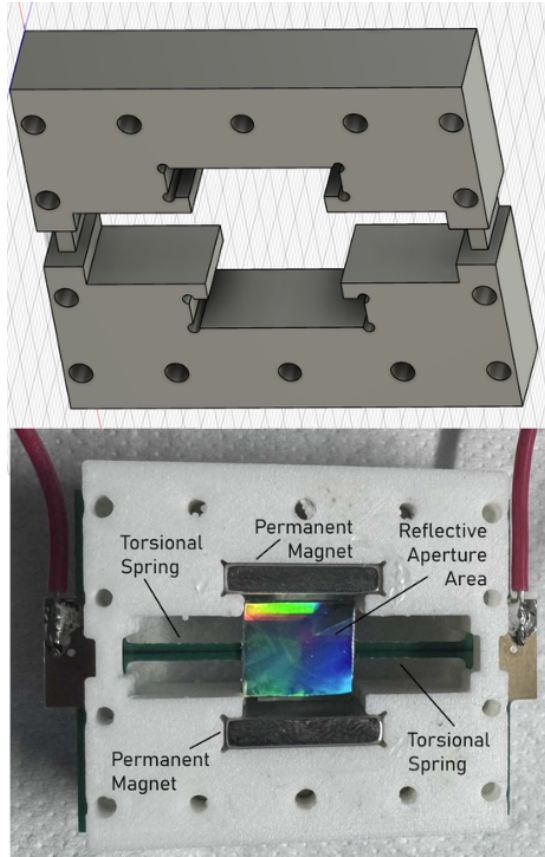


Figure 8: Photograph of half of the 3-D printed PLA frame (top), and the complete assembly (bottom), including the neodymium permanent magnets and the PCB-based micro-mirror with the aluminum-based reflective surface attached.

3. Micro-mirror Analytical, FEA, and Characterization Results

During characterization, the actual value of the mechanical resonant frequency of the mirror was obtained by manually applying an impulse mechanical torque and observing the resulting coil voltage on an oscilloscope, as shown in Figure 9.

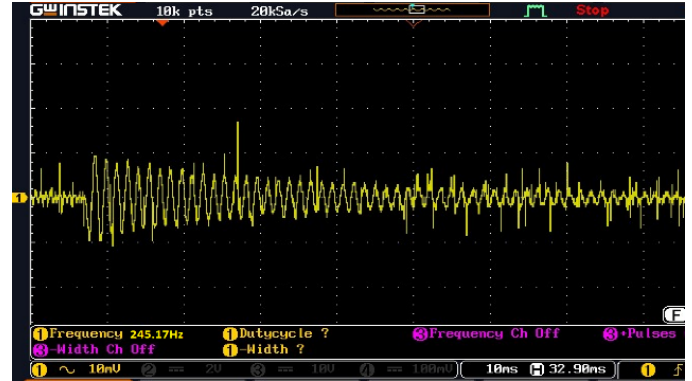


Figure 9: Transient response of the coil voltage for one of the free-running PI-based micro-mirrors, subjected to an initial mechanical torque impulse, confirming a resonant frequency of 245.17 Hz.

While eight micro-mirror prototypes were fabricated, a summary of the analytical, FEM, and experimental results for the two best-performing prototypes are presented in Table 4. Note that the values of the actual fabricated substrate thickness t (FR4 0.23 mm and PI 0.26 mm) are lower than the intended nominal value (0.3 mm), and therefore, simulations were also repeated for the actual thickness. Table 4 shows the maximum scanning angles achieved for each substrate and the resonant frequency f_r . The variation between the simulated and actual values of f_r is attributed to the manufacturing tolerances as well as material property variations. In this case, the measured resonant frequency was determined experimentally as the frequency which maximized the scanning angle. Table 4 also shows the simulated adjacent mode resonant frequency of the micro-mirror, which corresponds to the up-down translational mode.

Table 4: Mirror analytical, simulation, and measured results.

Parameter	Substrate Type	
	FR4	PI
Analytical ($t = 0.3$ mm) f_r (Hz)	692.3	321.7
Simulated ($t = 0.3$ mm) f_r (Hz)	792.9	285.2
Simulated f_r (corrected actual t) (Hz)	569.3	261.2
Simulated adjacent modal frequency (Hz)	440.3	180.1
Measured resonant frequency f_a (Hz)	550	250
Measured optical scanning angle (°)	31.3	52.1

Table 5 presents the measured optical scanning angle achieved for eight micro-mirror prototypes featuring coils of different number of turns per layer (n) implemented using either FR4 or PI substrate (sub). The optical scanning angle is four times the mechanical scanning angle [27]. Table 5 also provides the coil dimensions (trace width a and trace spacing b) together with the actuation frequency f_a as well as the coil current. In all cases, the

driving coil current was kept within the same range for ease of comparison. Coil designs 3 and 8, which have the highest number of turns, resulted in the highest optical scanning angle for the FR4 and PI substrates, respectively. This is expected due to the higher electromagnetic coupling, as can be inferred from (2).

Table 5: Characterization results for the fabricated mirrors having different substrates and actuating coil designs.

Coil	Sub	n	Trace width a, mm	Trace Spacing b, mm	Coil mA	f_a , Hz	θ (°)
1	FR4	5	0.503	0.203	265	650	5.5
2	FR4	15	0.152	0.152	250	550	11.4
3	FR4	20	0.102	0.102	226	550	31.3
4	PI	5	0.503	0.230	270	300	20.4
5	PI	15	0.152	0.152	235	250	27.6
6	PI	20	0.102	0.125	260	250	49.4
7	PI	25	0.102	0.102	260	250	52.1

4. Electronic Interface Design

4.1. Functional Description

The electronic interface for the scanning mirror is designed around the STM32L432KC microcontroller (MCU), as shown in the block diagram of Figure 10. The STM32L432KC can operate at an 80 MHz clock speed and has an in-built 12-bit ADC and complementary PWM channels. The PWM outputs are useful for generating the required signals to drive the actuation coil of the micro-mirror.

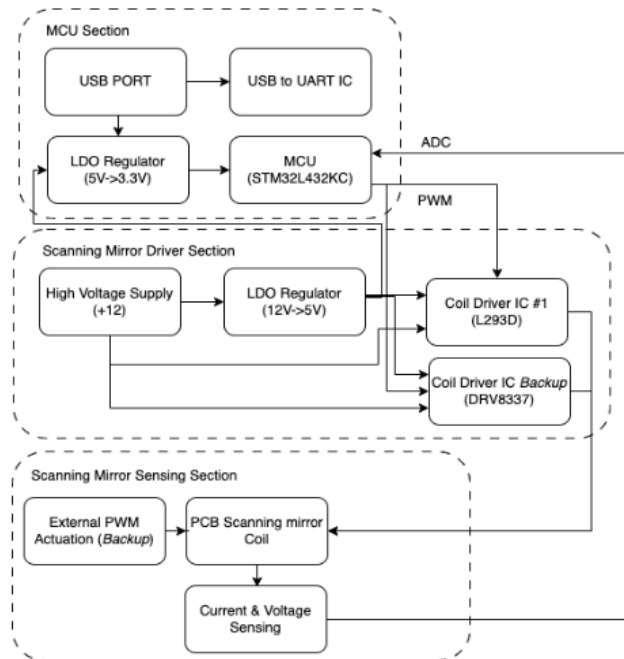


Figure 10: Functional block diagram of the electronic interface for the mirror control, built around the STM MCU, including USB interface, coil drivers, and coil voltage and current sensing.

An H-bridge driver configuration was chosen to maximize the coil driving voltage and minimize the power supply voltage

requirement. For this purpose, two different alternative driver integrated circuits were investigated, one based on the MOSFET DRV8837 and the other based on the bipolar L293. The interface also includes provision of USB communication for configuration purposes, as well as real-time measurement of the actuation coil current and voltage. Coil current sensing is achieved via the use of the INA241 sense amplifier, while voltage sensing is carried out using a potential divider. These analogue feedback signals are connected to two ADC channels of the MCU, with the aim of eventually determining the scanning mirror's angular position accurately without the use of additional optical sensors.

4.2. PCB Design

The prototype PCB development was split into three sub-systems to facilitate the testing and verification process: these consist of the MCU PCB, coil driver PCB, and the coil voltage and current sensing PCB. Each PCB section has a size of 30 mm by 30 mm and is stacked on one another.

4.2.1. Microcontroller PCB

The main function of the MCU PCB is to generate complementary PWM coil driving signals whose parameters, namely the frequency and duty cycle, are controlled via a personal computer using commands issued over the UART interface. This circuitry is built around the STM32L432KC microcontroller, as shown in Figure 11 (a). The MCU requires a 3.3 V supply, obtained via a low-dropout (LDO) regulator that lowers the 5 V USB supply voltage rail, as shown in Figure 11(b). The USB port allows a maximum sinking current of 500 mA, which is sufficient to power the MCU, LDO, and the FT232. However, the possibility of an external 5 V supply was included.

The FT232 is used as the USB-to-UART interface. The interfacing connections with the FT232 IC are shown in Figure 11(c). Two LEDs were connected to the data bus via pins 22 and 23 to provide visual feedback of the data transmission. Power supply stability was ensured via decoupling capacitors, which were placed physically close to the various ICs.

4.2.2. Coil Driver PCB

The coil actuation PCB makes use of either the L293D or the DRV8837 motor driver ICs. The L293D is a quadruple high-current half-H bridge driver that operates between 4.5 V and 36 V and can drive currents up to 600 mA in both directions. The control voltage range is 1.8 V to 7 V and is therefore compatible with the STM microcontroller. The DRV8837, on the other hand, is an H-bridge driver that uses N-channel power MOSFETs with an internal charge pump, providing an output current of up to 1.8 A and requiring a smaller PCB footprint.

4.2.3. Coil Sensing PCB

This PCB provides sensing of the mirror coil voltage and current feedback signals, which are fed back to the MCU via the ADC inputs. The INA241 amplifier is used for current measurement via a shunt resistor and was chosen due to its low input offset as well as high common mode rejection ratio (CMRR),

which is crucial for the accurate detection of the coil current waveform, which is superimposed on the high coil drive voltage swing. Voltage sensing is achieved via a resistive potential divider. This circuitry is shown in Figure 13.

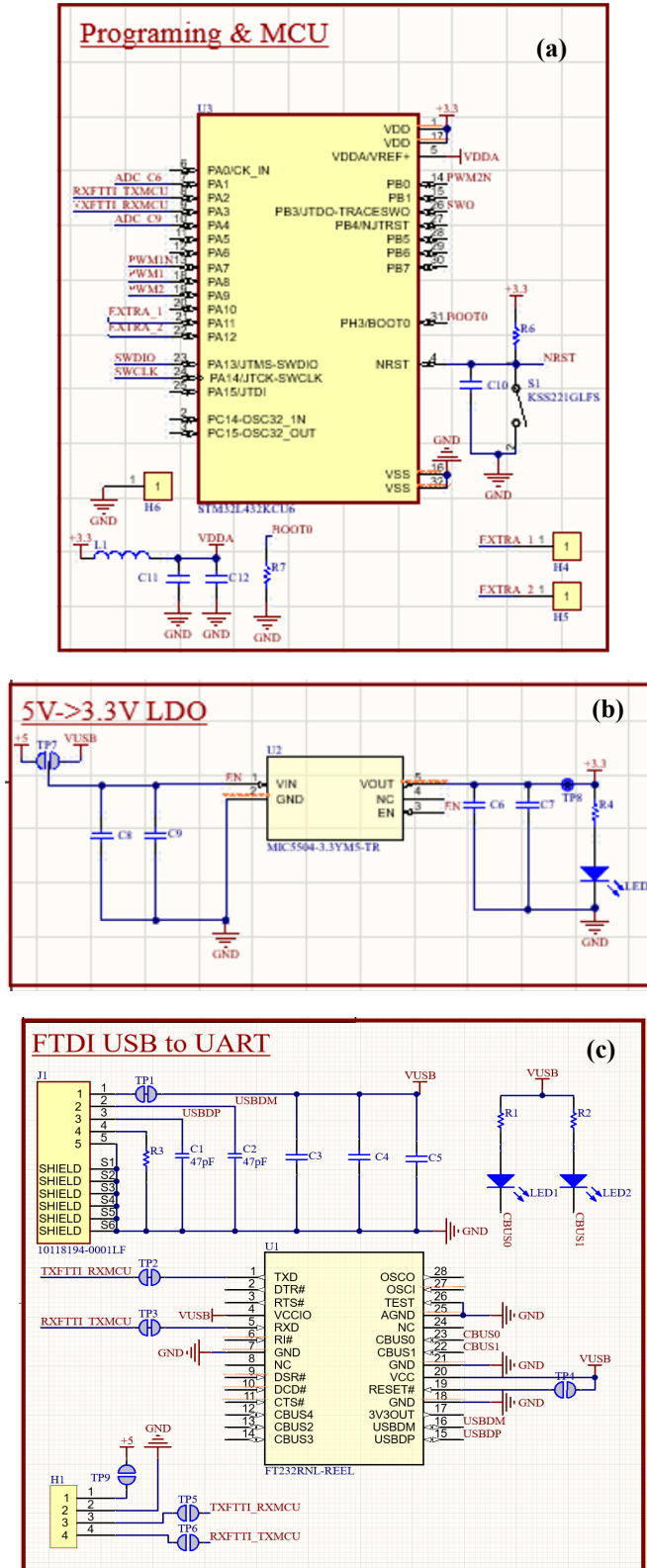


Figure 11: Schematic diagram of the main PCB, including (a) MCU section with programming port, (b) the power supply consisting of the 5 V to 3.3 V low drop-out regulator and (c) the FT232 USB-to-UART driver.

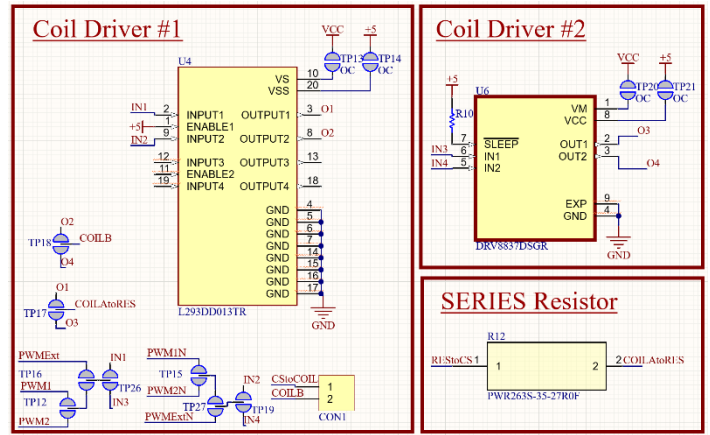


Figure 12: Schematic diagram of the L293D and DRV8337 bi-directional coil driver circuitry.

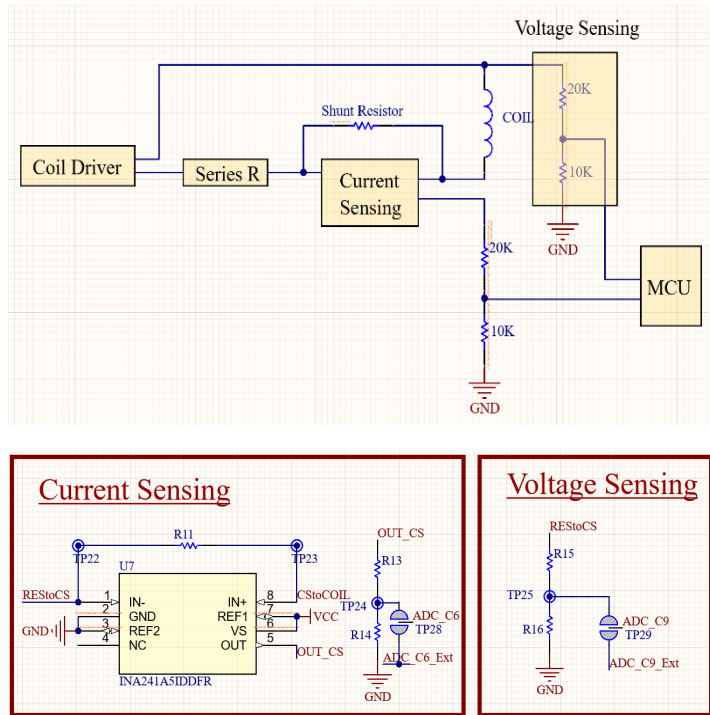


Figure 13: Coil voltage and current sensing feedback circuitry.

4.3. Firmware Design

The MCU firmware was designed to support various functions, including initialization of GPIO ports, PWM parameters for coil driving, direct memory access (DMA) and ADC, and UART. In addition, the MCU transmits the sensed coil current and voltage signals via the UART. The main firmware loop, which takes care of these processes, is shown in Figure 14. A UART-based protocol, shown in Figure 15, was developed, which enables setting up of the PWM frequency and duty cycle, as well as enabling and disabling of the PWM signals. A user interface was developed using C# to be able to control the PWM signal frequency and the duty cycle. The PWM frequency is configurable from 50 Hz to 10 kHz.

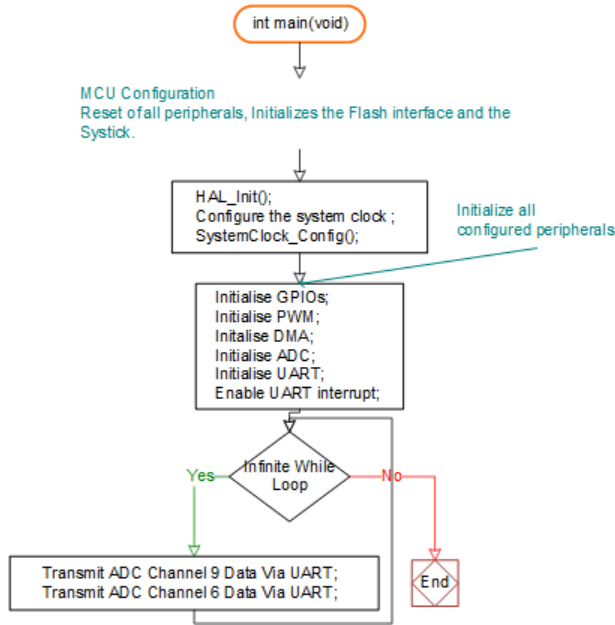


Figure 14: Main firmware loop catering for the initialization and feedback signal transmission to the personal computer via UART.

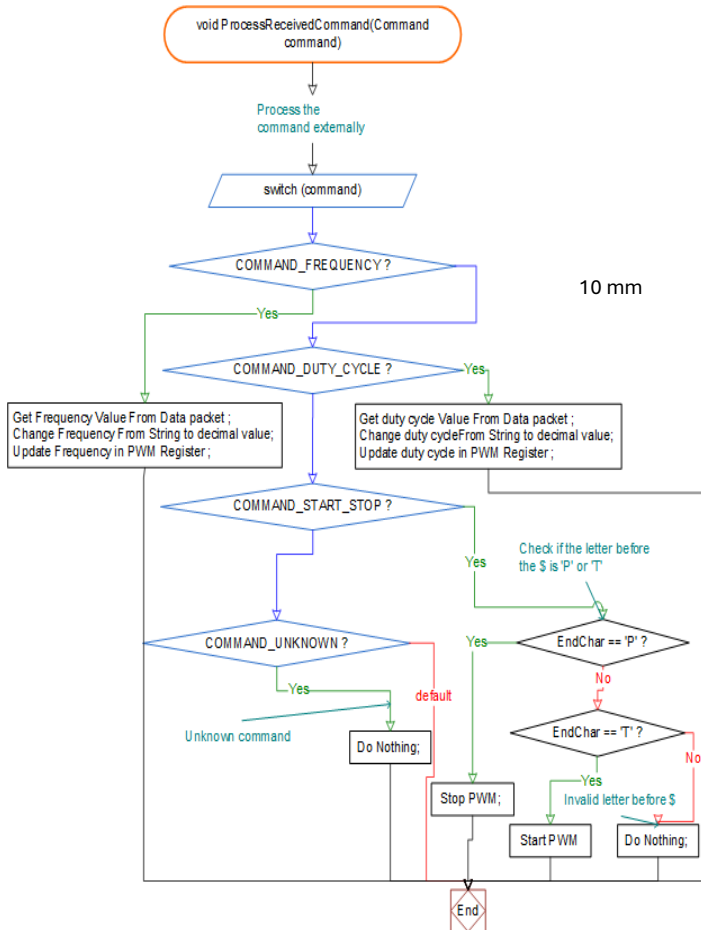


Figure 15: UART process logical flow block diagram.

5. Characterization of Scanning Angle variation with Duty Cycle

As explained in Section 4, the MCU design allows for PWM frequency and duty cycle control. Frequency control allows the mirror to be operated at resonance and caters for necessary tuning to compensate for process-related geometric variations as well as material property variations, which can also occur with temperature changes. It should be noted that FR4 and PI substrates are prone to mechanical property changes [3], which can occur due to aging related to mechanical stresses as well as exposure to elevated temperatures.

Duty cycle control allows for control of the scanning angle by effectively varying the electrical energy input to the actuation coil. The effect of duty cycle on scanning angle was investigated by varying the duty cycle from 10% to 50%. The corresponding scanning angle was geometrically calculated using the setup shown in Figure 16, consisting of a laser source and a projection screen. In this case, the PI-based micro mirror operating at a resonant frequency of 250 Hz is characterized.

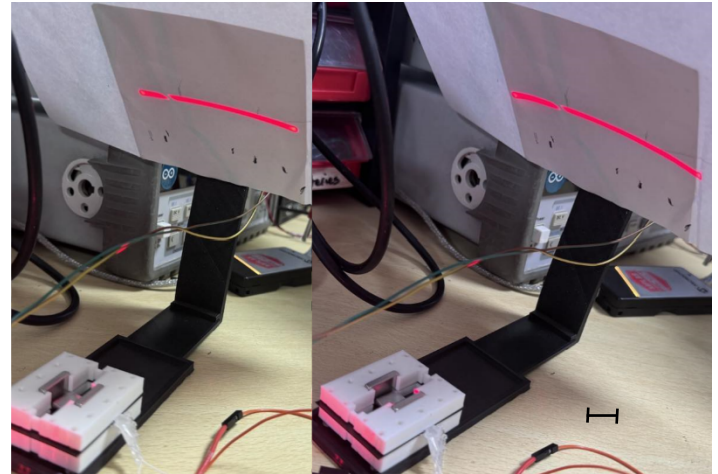


Figure 16: Optical Setup used to calculate the scanning angle at different applied voltage duty cycles. This figure shows the corresponding scanned trace, from the reflected laser source, at a duty cycle of 30% (left) and 40% (right) for the PI mirror.

Table 6 shows the corresponding scanning angles achieved at different values of duty cycle, as well as the corresponding recorded average coil voltage and current for the PI-based micro-mirror. A 22 mΩ shunt resistor is used in this case, followed by a voltage amplification of 200. The corresponding plot for the variation of the optical scanning angle with duty cycle is shown in Figure 17. As expected, the response exhibits a monotonically increasing scanning angle with duty cycle. However, non-linearity in the relationship can be observed, possibly arising from variations in coil resistance and material properties due to an elevated operating temperature at the higher duty cycle values, resulting from the coil I^2R losses, as well as other mechanical non-linearities.

Table 6: PI-based micro-mirror experimental results: scanning angle, coil voltage, and current at different values of applied voltage duty cycle, operated at a frequency of 250 Hz.

Duty Cycle (%)	Optical Scanning angle (°)	Average Coil Voltage (V)	Average Amplified Current-Sensing Shunt Voltage at the ADC input (V)	Average coil current (computed) (mA)
10	18.46	0.926	0.979	222
20	30.31	1.054	1.383	314
30	34.27	1.147	1.645	373
40	42.74	1.222	1.822	414
50	52.10	1.279	1.997	454

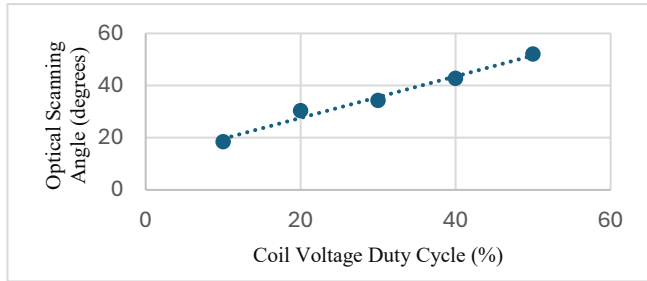


Figure 17: Measured optical scanning angle for different values of applied voltage duty cycle for the PI-based micro-mirror.

Table 7 presents a comparison of the key parameters with other electromagnetically actuated FR4-based micro-mirror designs. As expected, the novel PI-substrate lends itself to a higher optical scan angle when compared to the FR4-based mirrors, for the same driving current and spring geometry. This is expected due to its lower elastic modulus. Notable exceptions are FR4-based micro-mirrors employing serpentine springs, which have a lower effective spring constant for the same elastic modulus. This higher scanning angle is achieved at the expense of a slightly more complex fabrication process, which also complicates the electrical routing design to the actuation coil.

Table 7: Comparison with previous electromagnetically actuated micro-mirror designs with different spring designs (rectangular / serpentine).

	Substrate	Aperture (mm)	Res. Freq. (Hz)	Opt. Scan Angle (°)	Spring Type	Drive Current (mA)	Coil Resistance (Ω) / Number of turns
[3]	FR4	12 x 12	361.8	11.2	Rect.	115	3.7 / 11
[4]	FR4	5 x 5	1787	19.9	Rect.	250	N/A
[4]	FR4	5 x 5	417.4	140	Serp.	250	N/A
[4]	FR4	8 x 8	807	30	Rect.	250	N/A
[5]	FR4	12 x 12	190	52	Serp.	100	3.13 / 16
This work	FR4	10 x 10	250	31.3	Rect.	226	2.26 / 20
This work	PI	10 x 10	550	52.1	Rect.	260	4.73 / 25

6. Conclusion and Future Work

This work has demonstrated the feasibility of using FR4 and polyimide substrates to fabricate electromagnetic scanning mirrors through standard PCB processes. The resulting prototypes integrate planar copper coils, torsional springs, and reflective plates into compact devices that can be produced at a fraction of the cost of commercial MEMS mirrors, especially for low-volume applications. The integration of low-cost electronics, including a microcontroller, H-bridge drivers, and current/voltage sensing, may eventually be utilized for accurate positional control of the micro-mirror without the need for additional sensors.

The results clearly establish polyimide as the more suitable substrate for wide-angle scanning, with maximum optical deflections of up to 52.1°, achieved at a resonant frequency of around 250 Hz. This is the result of its lower value for the Young's modulus. While FR4 mirrors exhibited higher resonant frequencies and greater rigidity, their smaller deflections limit their applicability to systems requiring narrow scanning angles. In both cases, the prototypes confirmed the practicality of PCB-compatible designs for optical beam steering applications. Furthermore, it was noticed that PI-based micromirrors tended to achieve more repeatable results and were less susceptible to thermally induced stress. The repeatability of PI-based micromirrors is possibly explained by the fact that polyimide films tend to be more homogeneous than FR4 substrates. An interesting investigation would be a PI-based design employing serpentine spring structures, where a further enhancement of the optical scan angle for the same actuation current is expected.

Another consideration is system robustness. Unlike silicon MEMS mirrors, which are prone to brittle fractures, PCB-based mirrors are relatively robust under mechanical shock and vibration. The use of 3D-printed holders further contributes to mechanical stability, though long-term reliability testing remains necessary.

Despite these promising results, several limitations remain. The high-power consumption of the prototypes, of the order of 1.3 W, must be addressed to enable wider adoption in portable or battery-powered systems. Coil optimization, magnetic field enhancement, and resonant drive techniques represent promising directions to improve efficiency. Thermal effects also warrant closer study, particularly in polyimide mirrors, where repeated thermal cycling may induce material fatigue or delamination of copper traces. Therefore, reliability testing over extended periods is also necessary to evaluate the long-term durability of the substrates and coil under cyclic loading.

This work can contribute to further development within the area of low-cost scanning micro-mirrors. Dual-axis scanning mirrors, fabricated on polyimide, could be developed to provide full two-dimensional beam steering for advanced LiDAR systems. Closed-loop control schemes based on the existing voltage and current sensing still need to be developed and evaluated using position sensors or optical feedback to enhance accuracy and stability, particularly in environments prone to vibration.

Integration with existing LiDAR modules and field testing in automotive or robotic platforms will provide a more comprehensive assessment of system performance. Finally, further miniaturization and optimization of the drive electronics could reduce the footprint and improve overall efficiency.

In conclusion, PCB-compatible electromagnetic scanning mirrors based on PI or FR4 substrates represent a promising low-cost alternative to conventional silicon MEMS devices. They offer wide scanning angles, low resonant frequency operation, and scalable manufacturability, opening new opportunities for affordable LiDAR, biomedical imaging, and display technologies.

Conflict of Interest

The authors declare no conflict of interest.

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Computationally Efficient Explainable AI Framework for Skin Cancer Detection

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ABSTRACT

Skin cancer stands among some of the fastest growing and fatal malignancies of the world as a result early and accurate diagnosis of skin cancer is essential in order to enhance patient survival and treatment prognosis. Conventional methods of diagnosis including dermoscopy and histopathological examinations are expensive and time consuming also subject to inter-observer error. To address these shortcomings, this research suggests an optimized hybrid cascading framework that combines deep and machine learning strategies towards building an AI model for the detection of skin cancer. This study applied five different Convolutional Neural Network (CNN) as well as seven Machine Learning (ML) model and three optimization technique. Among them the suggested MobileNetV2 + LDA + LR model had the best accuracy of 99.33%, precision of 99.47%, recall of 97.33%, and F1-score of 98.31%. Moreover, it was found that the framework had better computational efficiency, with a time complexity of 35.1 ± 1.24 seconds and moderate memory usage. Later on, Explainable AI (XAI) including Grad-CAM++ and LIME techniques were employed to validate the interpretability of the model and revealed the clinically relevant areas of lesions that affected predictions, which increased the level of transparency and credibility.

1. Introduction

Cancer has become one of the major causes of death and disability worldwide [1], costing health systems, societies and economies an enormous burden. Recent estimates show nearly 20 million new cancer cases [2] and approximately 9.7 million cancer mortality cases worldwide in 2022 and that demographic projections indicate that the number of new cases would approach 35 million per year by 2050 if current trends continue [3]. Skin cancer is turning a devastating burden to the globe currently. Specifically, the most aggressive type of skin cancer melanoma

was estimated to result in 331,722 new cases and 58,667 deaths across the globe in the latest reports [4]; once the non-melanoma skin cancers are taken into consideration, the total number of skin cancer incidences is quite large, and it belongs to the most commonly diagnosed cancer groups [5]. As a matter of fact, it has a great setback in global economy as well. Recent studies on cancer costs worldwide indicate that the economic costs of cancer are immense and concentrated: China and the United States bear the most of the shares of world cancer costs, and it is estimated that over the next few decades, cancer will cost the world about

trillions of US dollars [5,6], in terms of productivity losses and medical expenses (one prominent statistics shows that the cancer will cost the world USD 25 trillion in the next 30 years when combined with productivity losses and medical costs) [6,7]. These statistics indicate that the urgent need to implement a cost-effective prevention, early detection and effective management strategies of cancer such as skin cancer [8].

Early and precise diagnosis of skin cancer has a significant positive impact on patients' survival rates [9]. However, the traditional clinical workflows clinical inspection, dermoscopy, biopsy and histopathology have been resource consuming and exposed to inter observer variability [10]. Also, the conventional diagnosis of skin cancer required a highly qualified and experienced oncologist without which the diagnosis is quite impossible [11]. Furthermore, accessibility to specialized dermatology services is also a limitation in remote and low resourceful areas as a result diagnosis become late which also may increase the costs of treatment and may mortality rate [12]. All of these real-world limitations have encouraged the creation of automated; image-based diagnostic to assist clinicians and increase screening accessibility.

Over the last few years, deep learning (DL) specifically Convolutional Neural Networks (CNNs) have demonstrated impressive performance on dermoscopic and histopathological images tasks regarding skin cancer detection [13]. Other recent studies have reported high classification rates and investigated the use of complementary technique including attention modules, metaheuristic optimization (e.g., Ant Colony Optimization, Particle Swarm Optimization), feature selection, and Explainable Artificial Intelligence (XAI) including Grad-CAM, LIME, SHAP and many more to enhance explainability and clinical trust [14]. In spite of these advancements, there are few gaps available which actually restrict the use of an automated system to the real-world settings including:

- (i) Robustness of validation: many studies lack k-fold (10-fold) cross-validation or other commensurately rigorous statistical validation of their models in independent cohorts.
- (ii) Computational cost and complexity: few studies quantify inference time, number of parameters, memory footprint, or time and space complexity to assess their model.
- (iii) Use of optimization strategies: only a fraction of studies use systematic metaheuristic or architecture-level optimization, and systematic comparison of optimization to alternative tun. Such methodological gaps decrease the trust of the reported performance and it is hard to determine the generalizability, scalability and affordability of health systems.

Based on these gaps, this study aims to design and evaluate an optimized, explainable, and computationally-sensitive hybrid cascaded deep learning framework in the detection and classification of skin cancer. The accuracy of the classification and generalization was also enhanced with higher feature selection and optimization techniques. The framework does not require large and unbalanced annotated datasets and more complex computing resources, as found in traditional methods; instead, it is specifically implemented to operate with relatively small and unbalanced datasets and with low resource requirements, therefore, simpler to fit into the standard clinical

workflow. This study would then want to make a contribution of a consistent, functionally and explainable computer aided diagnostic (CAD) model and this model not only could assist pathologists to make time sensitive and accurate diagnosis, but also address a very important gap in the environment of reliability and resource consumption [15]. Besides this, most currently implemented deep learning systems are Inconsistent black-box models, which do not provide much insight into the process of decision-making. They do not even have to be concerned with computational efficiency or scalability, which are the major concerns of a practical clinical use [16]. Indeed, as far as we know, few or, indeed, no research studies have broken down the problems of calculating their models in an explicit and analytical way (Complexity including time and space), a consideration that can debilitatingly hamper the role of transferring controlled research settings to the practice in a hospital. Overcoming these obstacles, our framework will not only be utilized to push the limits of the existing study, but also a step beyond that toward the creation of clinically practical, reliable, and sensible AI technique in the classification of skin cancer from the images. The major key contributions necessary to fill that research gaps addressed in this paper can be summarized as follows:

1. We suggest a hybrid automated system of Deep and Machine Learning in which DL is employed in terms of its effective learning-based feature extraction and ML is employed in terms of detecting skin cancer from the images.
2. The Pre-trained CNN models are applied with the purpose of extracting hierarchical features automatically and then feature selection of optimization techniques and dimensionality reduction methods are applied on the extracted features to ensure that the result is more robust and efficient.
3. The proposed model will be not only highly diagnostic but will also perform well on small datasets with minimal computing capabilities, hence it is applicable to real-time clinical practice.
4. In fact, we didn't just calculate the complexity of our proposed model but also all the remaining model's which perform comparatively higher.
5. In comparison with black-box DL models, our framework is more interpretable and reliable in the sense that it seeks to bridge the gap between AI-based predictions and clinical workflow decision-making by a pathologist.
6. Lastly we also applied XAI method including grad-cam++ and LIME in order to prove that proposed model's is more interpretable and scalable.

The headings represent the rest of our work: Section 2: Related work which illustrates the analysis of the literature of the current research based on the skin Cancer. Section 3: Methodology, the section outlines the system architecture, diagrams and requirements related to the system architecture. Section 4: Experimental Result presents the results in different tables, graphs and figures. Section 5: Conclusion and Future.

2. Literature Review

Several smart methods have been created in recent years to detect skin cancer based on images including: In [17], author

applied CNN algorithm to the HAM10000 dataset which had been collected from Kaggle and it has 10015 images as well as seven classes. In the image preprocessing phase this work applied the normalization and contrast enhancement techniques. The author also applied the Explainable AI techniques like GRAD-CAM and GRAD-CAM++ for making this work more reliable and understanding. This work acquired 82% classification accuracy and 0.47% loss accuracy. In [18], the study used ISIC2018 skin cancer dataset which has four classes like benign, malignant, nonmelanocytic, and melanocytic tumors and 3533 images. It used some image preprocessing techniques like image resizing, normalization and augmentation techniques. After that this research applied CNN, ResNet50, InceptionV3 and InceptionV3 & ResNet algorithms on this dataset and found the accuracy of 83.2%, 83.7%, 85.8% and 84% accordingly. In [19], the authors proposed a federated learning-based model and showed how the several hospitals exchange their private skin cancer data with a central server. The author applied DCNNs model on the three distinct dataset. They also split the dataset as a training, validation and testing dataset and for enhancing the image quality and the model's accuracy and this work also preprocessing the images like image augmentation and resizing techniques. In [20] the author applied DenseNet201 model on the Fitzpatrick 17k dataset which combines several skin condition images. This model is applied on the federated learning environment the author found 92% accuracy. The dataset was divided into 70% as training, 10% as validation and 20% as testing dataset. In [21] author applied multi class SVM model on the ISIC 2019 skin cancer dataset which has eight different classes and found the accuracy 96.25%. For preprocessing image, the author applied dull razor method for removing unwanted hair particle, gaussian filter for smoothing images and median filter for preserving edges. B. O. S. in [22] the author applied SVM and CNN model on the ISIC skin cancer dataset and found 85% accuracy. This dataset contains 23000 images and the author took 1000-1500 images for making training and testing dataset. In image preprocessing part this work removing hair, shade and glare from the images after that it did the segmentation technique. The overall summary of the literature review for this study can be summarized as follow in Table 1:

Table 1: Literature review

Ref.	Author	Method	Accuracy	Limitations
[17]	Mridha et al.	CNN	82.00%	Lower accuracy, No complexity analysis
[22]	B. O. S. Elgabbani et al.	SVM, CNN	85.00%	No Complexity, No cross validation, lower accuracy and no complexity analysis
[18]	Gouda et al.	Inception V3	85.80%	No complexity, Lower accuracy and no complexity analysis
[19]	Al-Rakhami et al.	DCNNs	90.00%	Overfitting, No cross validation and No complexity analysis
[20]	Karni et al.	DenseNet 201	92.00%	No complexity and no complexity analysis
[21]	Monika et al.	Multi class SVM	96.25%	No complexity, No cross validation and no complexity analysis

3. Methodology

The overall methodology of the proposed model is illustrated, in Figure 1, which is divided into five consecutive, but interdependent phases; these are the acquisition of datasets, preprocessing of the data, the architecture design of the system, model selection, and the interpretability of the proposed model with explainable artificial intelligence (XAI). The combination of these stages is to ensure that the model is more reliable, robust, and can minimize prediction errors. The data that was used in this study was collected from a secondary data source platform which contains dermatological image collections. The preprocessing stage was started with the use of advanced image enhancement methods to guarantee quality, uniform, and noise-free data. Contrast Limited Adaptive Histogram Equalization (CLAHE) was the most important of them in increasing contrast and at the same time decreasing noise in the image thus optimizing the raw dermoscopic and clinical skin photos to be further analyzed by the system [23]. Missing or inconsistent values were appropriately taken care of in order to maintain the integrity and methodological rigor of the dataset.

A set of pre-trained Convolutional Neural Network (CNN) model were applied on those preprocessed images in order to extract the features. These hierarchical based CNN models, which are characterized by their ability to extract hierarchical features, were used to break down the skin images into successively more discriminative and fine-grained feature representations, which could effectively classify the different skin cancer types. Dimensionality reduction and feature selection methods were then used to reduce redundancy, to keep only the most informative features and to reduce the computational overhead. After this step, the dataset was divided into testing (20%) and training (80%) sets thus making it easy to conduct rigorous experimentation.

Different classifiers were optimized using the training set, and this was done depending on the capability to capture complex, non-linear patterns that are considered to be linked with skin cancer, and the predictive ability of the models was confirmed with the testing set.

In order to enhance further interpretability and to bring transparency to the suggested diagnostic framework, the state-of-the-art methods of XAI, i.e., Local Interpretable Model-agnostic Explanations (LIME) and Gradient-weighted Class Activation Mapping++ (Grad-CAM++) were incorporated. LIME measures the impact of manipulations to the input information, which means that the results of the prediction are monitored in response to the alterations [24]. It then produces a linear surrogate model that reveals the most significant attributes that drive classification decisions. Instead, Grad-CAM++ generates high-resolution heatmaps, which visualize the discriminative regions of the skin lesion images, which affects the process of making a decision by the model [25]. Grad-CAM++ also provides better accuracy on tasks that have multiple target regions, compared to traditional Grad-CAM, because it computes more refined gradient-based distributions of weights over the feature maps [26]. The application of these XAI methods does not only lead to a better understanding of model behavior, but improves the clinical plausibility of the suggested skin cancer detection framework [27].

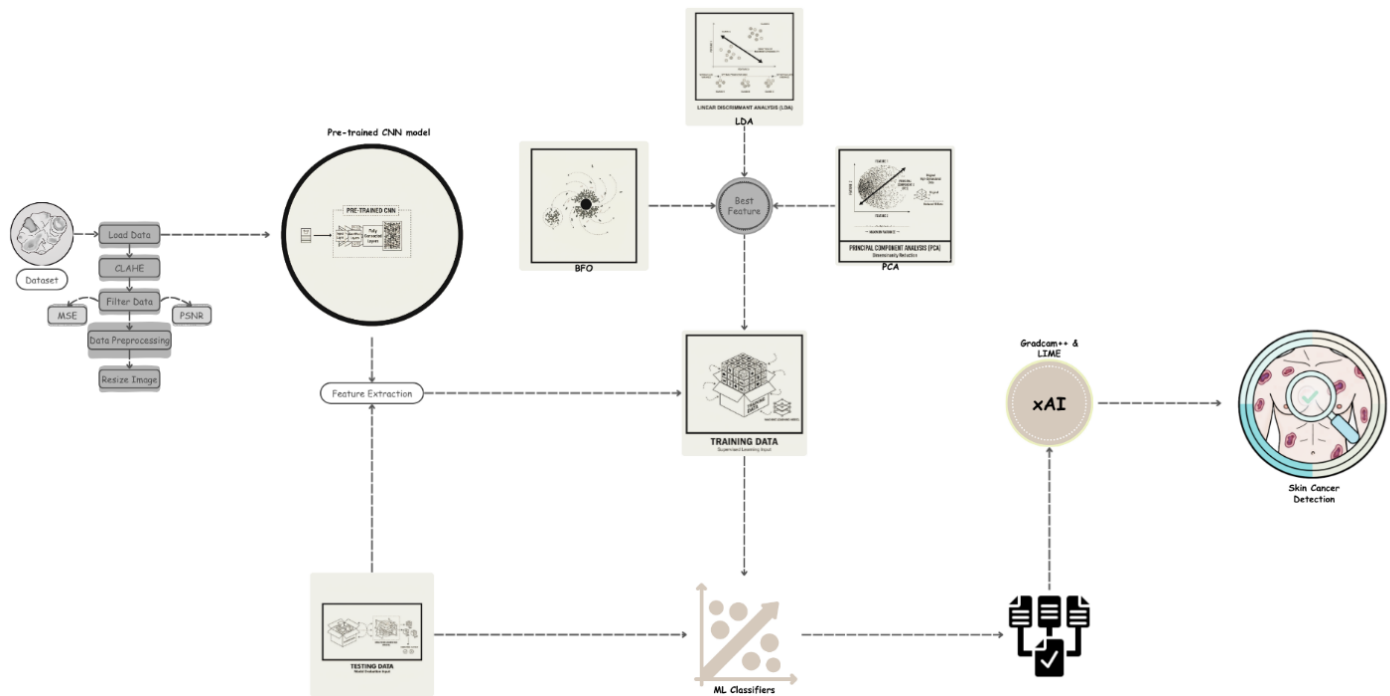


Figure 1: Workflow Diagram of this study

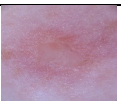
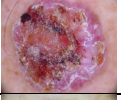
The framework provides a balance between predictive accuracy and explainability and, as a result, the practical interpretability requirements of dermatologists with advanced AI-driven analysis, further supporting trust and usability in the real-world healthcare environment.

3.1. Dataset

The dataset which were used in this study were collected from a secondary data resource platform called Kaggle [28]. A professional oncologist carefully examined and annotated the dataset and defined each image by the type and stage of lesion to guarantee reliability and clinical validity. A grading scale of 0 to 4 was used with a 0 indicating non-cancerous cases, 1 indicating Basal Cell Carcinoma, 2 indicating Malignant lesions, 3 indicating Melanoma, and 4 indicating Squamous Cell Carcinoma. The dataset is balanced between a variety of different classes, which includes 2,958 non-cancerous images, 2,093 Basal Cell Carcinoma images, 3,000 Malignant lesion images, 2,863 Melanoma images and 2,536 Squamous Cell Carcinoma images.

Table 2, provides a summary of the dataset distribution between these categories.

Table 2: Dataset Description of this study

Sample Image	Class Name	Class No.	No. of Sample image
	Non-Cancerous	0	2958
	Basal Cell Carcinoma	1	2093
	Malignant lesions	2	3000

	Melanoma	3	2863
	Squamous Cell Carcinoma	4	2536

3.2. Preprocessing

In order to enhance the quality of classifying skin cancer, a sequence of image processing methodologies was adopted in this research. Preprocessing is also an important part of medical image analysis because it improves the quality of data and minimizes background noise and presents models with more reliable inputs[29]. The preprocessing mechanisms used were tailor made to sharpen the skin images and facilitate extraction of their features to achieve precise classification. Some common challenges in skin images include noise, poor contrast, and unwanted artifacts that may interfere with the functionality of machine learning and deep learning models. A number of high-level preprocessing techniques were used to overcome these problems. Contrast Limited Adaptive Histogram Equalization (CLAHE) was one of the main methods, where the contrast of the images was enhanced by redistributing the intensity levels, hence emphasizing the slightest differences between cancerous and non-cancerous tissues and, by implication, are more pronounced in terms of analysis [30]. Besides contrast enhancement, noise reduction filters were also used to remove irrelevant details and enhance the meaningful tissue structures, eventually, simplifying the computation of the later models. Images that had been missed or corrupted were handled systematically to remain consistent with the data sets and image quality analysis and reconstruction methods were employed to make sure that only the data of high quality and reliability were retained. All these preprocessing measures reduced any artifacts that would affect the outcome of

the model and formed a solid base towards which machine learning and deep learning systems are cascaded to detect skin cancer, which in turn facilitated the construction of clinically viable diagnostic systems.

3.2.1. Image Filtering

Image filtering is a basic method of preprocessing of computer vision, which is essential in improving quality and trustworthiness of images in carrying out analysis tasks [31]. This is more crucial in the area of medical imaging where the smallest details can determine the difference between the diagnosis and the classification of the ailments. Image filtering also removes noises, highlights key features that makes images sharper, more contrasted and clearer, and may be more useful in machine learning and deep learning models [32]. The algorithm of filtering techniques which are used in this paper in order to enhance the quality of the of skin image consisted of the Gaussian filtering, median filtering and Contrast Limited Adaptive Histogram Equalization (CLAHE) etc., the random noise was removed through the use of the Gaussian filtering technique without damaging the significant edges and rendered the image smooth. Median filtering method was helpful in the fact that noise impulses were eliminated and edges in the tissue structures were preserved. Local contrast was improved through the application of CLAHE [33] to elevate the profile of minute changes in the regions of the tissue where change in intensities was minimal. By critically applying such filtering strategies, the dataset was reduced to focus on emphasis on the diagnostic patterns without distortions, which helped increase the model performance and classification rate. The initial step in converting raw skin image data to rich feature representations that can be exploited later in the medical imaging application by the image filtering. In this study there are about six types methods were used to reduce noise of the image data, including:

Average Filtering: Mean filtering is an image processing method that uses a sliding $n \times n$ sized window (or kernel) of an image to remove noise and smooth out the intensity changes [34]. This kernel is usually a square (e.g. 3×3 or 5×5) and as the kernel passes through the image, the pixel at the center is replaced by an average value of the other pixels in the neighborhood. This is one of the most effective methods to reduce high-frequency noise in the image and produce a smoother one, but at the cost of blurred edges and small details. Although average filtering may help increase the average similarity of the overall image, in medical imaging, where the edges hold more importance than the overall image then this filtering technique won't be that much fruitful. The mathematical equation of average filtering is given as follow:

$$f'(x, y) = \frac{1}{n \times n} \sum_{i=-k}^k \sum_{j=-k}^k f(x+i, y+j)$$

where $f(x, y)$ is the original pixel intensity, $f'(x, y)$ is the filtered pixel value, and $n \times n$ is the kernel size.

Median Filtering: Median filtering is another nonlinear image processing method that is extensively used in noise elimination especially in salt-and-pepper noise (also referred to as impulse noise) elimination [35]. In this method, an $n \times n$ sliding window is moved around the image and the median of the pixel values of the surrounding is used to substitute the central pixel. In contrast

to average filtering, which generally smooths edges, median filtering still maintains sharp edges and at the same time eliminates noise, which is particularly important in medical imaging, where structural boundaries are of primary importance. The mathematical equation of median filtering can be summarized as follows:

$$f'(x, y) = \text{median} \{f(x+i, y+j) \mid (i, j) \in W\}$$

where W represents the coordinates of the window of the kernel.

Bilateral filtering: It is an edge preserving nonlinear and noise reducing method that uses both spatial and intensity samples [36]. Unlike the Gaussian filtering which only smooth on the basis of the proximity of the pixels, Bilateral filtering takes into consideration the similarity between the pixel intensities, thus it preserve edges, but eliminate noise. The new value of each pixel is determined as a weighted average of the surrounding pixels with the weight being dependent on the distance between the pixels and the intensity difference. This filtering technique can be mathematically described as below.

$$f'(x, y) = \frac{1}{n \times n} \sum_{i=-k}^k \sum_{j=-k}^k f(x+i, y+j) \cdot G_s(i, j) \cdot G_r(f(x+i, y+j) - f(x, y))$$

where G_s refers spatial Gaussian kernel, G_r is the range Gaussian kernel, and $k(x, y)$ is the normalization factor.

Min filtering: It is also known as minimum entropy filtering as a morphological filtering method, is a process that replaces the pixel in the resulting image with the least brightness in its $n \times n$ pixel neighborhood [37]. This technique is especially useful in eliminating bright outlier noise (like salt noise) and is most frequently used in pre-processing of medical images to eliminate undesired brightnesses at the expense of darker detail. The mathematical equation of this filtering technique is shown below:

$$f'(x, y) = \min \{f(x+i, y+j) \mid (i, j) \in W\}$$

Max Filtering: Unlike min filtering, max filtering substitutes a pixel in the center of the neighborhood with the max intensity of the neighborhood [37]. This method is useful in getting rid of dark outlier noise (including pepper noise) without affecting bright structures in the image. In medical imaging, max filtering may prove to be convenient in improving bright objects, e.g. highlighted tissue in a medical image, stained objects in a histopathology microscope slide. The operation is defined as:

$$f'(x, y) = \max \{f(x+i, y+j) \mid (i, j) \in W\}$$

Gaussian Filtering: It is a linear smoothing technique used to reduce Gaussian noise and achieve image blurring while maintaining edge information more effectively than mean filtering [38]. It employs a kernel based on the Gaussian distribution, where neighboring pixels closer to the center contribute more weight than those farther away. Even areas are smoothed and edges are preserved by this weighted averaging. The Gaussian filter is mathematically defined as:

$$G(x, y) = \frac{1}{2\pi\sigma^2} e^{-\frac{x^2+y^2}{2\sigma^2}}$$

where $G(x, y)$: Gaussian kernel value at position, σ : standard deviation, which determines the spread of the Gaussian curve, and x, y : the position of the pixel in relation to the center of the kernel.

3.3. Architecture of the proposed system

Figure 1, shows the general structure of the proposed system, and the methodology is described stepwise in Algorithm 1. The pre-processing phase starts with the evaluation of image quality and removal of noise through the Contrast Limited Adaptive Histogram Equalization (CLAHE) algorithm which boosts the contrast values. Then, the images were further refined using six different filtering methods. The Image Quality Assessment Cell (I_{QAC}) assesses the sharpness and noise level of each image according to the approach suggested by [39]. The mean square error (MSE) analysis was applied to estimate the quality predictor coefficient based on which the quality index Q_i was calculated using a linear regression model. The higher the Q_i the lower the quality of the image. Therefore, images with $Q_{ih}=10$ or less had to be chosen as the subject of further processing. Upon I_{QAC} validation, the validated images were transformed into sRGB space in order to normalize colors and resize them to the input demands of the AI models. The above pre-processing steps especially the quality control step will help check that only good quality images are processed in the subsequent stages [40]. Among these six different filtering techniques we choose Bilateral filtering technique for further process in our proposed model.

Following the effective preprocessing, five CNN models ResNet50, DenseNet201, InceptionV3, MobileNetV2, and Xception were deployed, and MobileNetV2 was proven to be the most effective in terms of the feature extraction capability owing to their performance and applicability to the proposed framework. To reduce redundant features before the classification process, Bacterial Foraging Optimization (BFO), Principal Component Analysis (PCA), and Linear Discriminant Analysis (LDA) were used to feature optimize. These optimized features were then introduced to seven high-performing machine learning classifiers, K-Nearest Neighbors (KNN) classifier, Decision Tree (DT), Random Forest (RF), Support Vector Machine (SVM), Extreme Gradient Boosting (XGBoost), Gaussian Naïve Bayes (GNB) and Logistic Regression (LR) classifier to classify Non-cancerous, Basal Cell Carcinoma images, Malignant lesion images, Melanoma and Squamous Cell Carcinoma.

Explainable AI (XAI) methods were added to make the predictions more interpretable and transparent. In particular, Grad-CAM++ was used to visualize class-discriminative regions in the histopathological images, showing the most significant areas that drive CNN. Additionally, by examining local pixel perturbations that affect predictions, Local Interpretable Model-Agnostic Explanations (LIME) were utilized to provide feature-level interpretability. The combination of these methods is done in such a way that the proposed framework can not only provide high-quality classification results, but also provide clinically significant visualization explanations that will increase its suitability and acceptability in medical diagnostics.

3.4. Algorithm

Algorithm 1: Algorithm of the Proposed Model

Initialization:

$P \leftarrow \{P1, P2, P3, \dots, Pn\}$
 $B \leftarrow \{B1, B2, B3, \dots, Bn\}$
 $C \leftarrow \{C1, C2, C3, \dots, Cn\}$

while $I_{SRGB} \neq I_{NIL}$
do $I_{SRGB} = I_{QAC}(I_{RGB})$
 $I_R \leftarrow \text{Resize}(I_{SRGB} \text{ to } 224 \times 224)$
 $FM_i \leftarrow \text{Load feature extractor ResNet50 with parameters } P_i$
 $f_i \leftarrow FE_i$
 $BFO_i \leftarrow \text{Load BFO with parameters } B_i$
 $Sf_i = BFO_i(f_i)$
 $LDA_i \leftarrow \text{Load LDA with parameters } LDA_i$
 $Rf_i = LDA_i(Sf_i)$
 $PCA_i \leftarrow \text{Load PCA with defined components}$
 $Pf_i = PCA_i(Rf_i)$
 $CM_i \leftarrow \text{Load classifier Logistic Regression with parameters } C_i$
 $y = CM_i(Pf_i)$

if $y = 0$ then
 $\psi \leftarrow \text{Non-cancerous}$
else if $y = 1$ then
 $\psi \leftarrow \text{Basal Cell Carcinoma}$
else if $y = 2$ then
 $\psi \leftarrow \text{Malignant Lesion}$
else if $y = 3$ then
 $\psi \leftarrow \text{Melanoma}$
else
 $\psi \leftarrow \text{Squamous Cell Carcinoma}$
end if
end while
Output: ψ

Initialization: $\alpha, \beta, \gamma, Q_{ih}$
Load model with the $n + 1$ parameters α, β, γ
 $Q_i = \alpha + \beta \times \text{Sharpness} + \gamma \times \text{Noise}$
Sharpness and Noise are estimated

if $Q_i < Q_{ih}$ then
return NIL
end if

if $C_{linear} \leq 0.0031$ then
 $I_{SRGB} = 12.92 \times C_{linear}$
else
 $I_{SRGB} = 1.0552 \times C_{linear}^{1/2.4}$
end if
return I_{SRGB}

Function BFO(F_i)

Initialization: $a \leftarrow 2A - 1$, where $A = 1, 2, 3, 4, \dots$
 $P \leftarrow \text{Input Image}$
 $R_u \leftarrow \text{Respective Feature Vector}$
 $\text{Best-Filter} \leftarrow \text{apply-Filter}(P)$
 $Q_a \leftarrow \text{applyFilterToImage}(P, \text{BestFilter})$
 $A \leftarrow \text{image To Array}(PQ_a)$
for each A do
Use(P, Q_a) to get $R_a \mid R_a \{V_0, V_1, \dots, V_{14}\}$
end for
 $R_u \leftarrow R_a$
return R_u

Load PCA model with defined number of components
 $Pf_i \leftarrow \text{Apply PCA to } Rf_i$
return Pf_i

Load LDA model with parameters LDA_i
 $Rf_i \leftarrow \text{Apply LDA to } Sf_i$
return Rf_i

3.5. Performance Evaluation Matrix

To evaluate the model's performance four of the most dominating performance evaluation matrix were implemented those are:

Accuracy gives a general evaluation of how well the model is able to classify instances correctly in all classes, a broad perspective of how well the model is able to predict.

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN}$$

Precision is the fraction of cases of correct positive prediction among the cases which are predicted to be positive. It is the measure of how the model can reduce the false positives and mathematically determined as:

$$\text{Precision} = \frac{TP}{TP + FP}$$

Recall (or Sensitivity) is a standard to measure the fraction of the overall number of actual positive cases that is correctly predicted. It measures the efficiency of the model in detecting all the relevant samples and it is represented as:

$$\text{Recall} = \frac{TP}{TP + FN}$$

F1-Score This is the harmonic mean of Precision and Recall, which offers a balanced measure of evaluation; it is often useful when there is a class imbalance. It is calculated as:

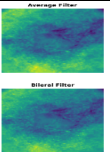
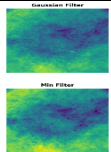
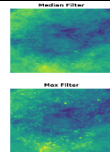
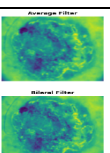
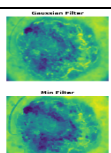
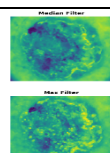
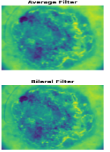
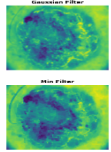
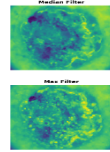
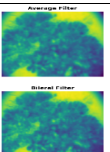
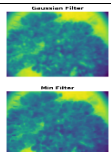
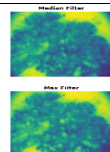
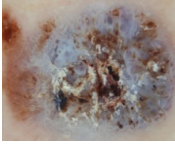
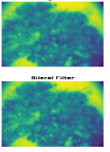
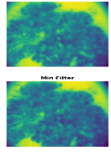
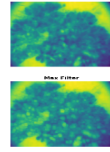
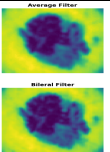
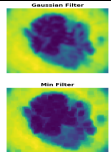
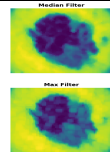
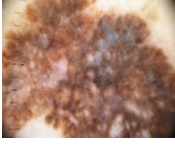
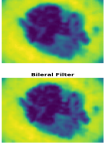
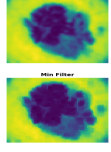
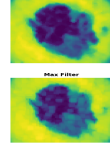
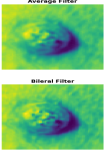
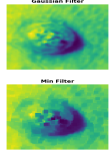
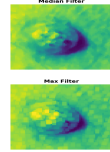
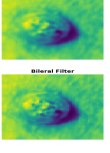
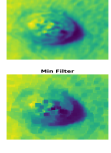
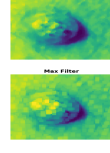
$$\text{F1-Score} = 2 * \frac{\text{Precision} + \text{Recall}}{\text{Precision} * \text{Recall}}$$

4. Result Analysis

4.1. Comparative Analysis of Filtering Methods in Different Image Classes.

A comparative analysis of diverse image filtering methods on five types of skin lesion images, which are Non-Cancerous, Basal Cell Carcinoma, Malignant Lesions, Melanoma, and Squamous Cell Carcinoma, is presented in the Table 3. The rows are presented with a sample picture of the respective class and continue to show a sequence of filtered results produced by six filters Average, Gaussian, Median, Bilateral, Min and Max with their quantitative measures of Mean Squared Error (MSE) and Peak Signal-to-Noise Ratio (PSNR). The findings reveal that the Bilateral Filter is the best one with the lowest MSE and maximum PSNR on all the classes, which is an indication of the quality of the filter in removing noise as well as maintaining important structural information. Indicatively, the Bilateral Filter yielded MSE and PSNR values of 5.58 and 40.66 respectively in Non-Cancerous picture, 35.84 and 32.58 in Basal Cell Carcinoma picture, 11.83 and 37.40 in Malignant Lesions picture, 7.18 and 39.56 in Melanoma picture and 20.00 and 35.11 in Squamous Cell Carcinoma picture. All in all, these results prove that the Bilateral Filter is indeed the best pre-processing method to improve the quality of the image before the classification.

Table 3: Filtering Method's MSE and PSNR Values for Different Image Classes

Sample Image	Filtered Images	Class	Filtering Technique	MSE	PSNR
	     	Non-Cancerous	Average Filter	119.15	27.36
			Gaussian Filter	6.05	40.30
			Median Filter	9.28	38.45
			Bilateral Filter	5.58	40.66
			Min Filter	34.59	32.74
			Max filter	39.24	32.19
	     	Basal Cell Carcinoma	Average Filter	115.40	27.50
			Gaussian Filter	37.33	32.40
			Median Filter	37.55	32.38
			Bilateral Filter	35.84	32.58
			Min Filter	72.86	29.50
			Max filter	73.40	29.47
	     	Malignant lesions	Average Filter	87.09	28.73
			Gaussian Filter	15.42	36.24
			Median Filter	13.34	36.87
			Bilateral Filter	11.83	37.40
			Min Filter	65.38	29.97
			Max filter	62.46	30.17
	     	Melanoma	Average Filter	108.56	27.77
			Gaussian Filter	9.12	38.52
			Median Filter	11.63	37.47
			Bilateral Filter	7.18	39.56
			Min Filter	77.80	29.22
			Max filter	79.05	29.15
	     	Squamous Cell Carcinoma	Average Filter	93.34	28.42
			Gaussian Filter	23.55	34.40
			Median Filter	25.94	33.98
			Bilateral Filter	20.00	35.11
			Min Filter	78.30	29.19
			Max filter	80.06	29.09

4.2. MACS, FLOPS, Feature, and parameter values for various CNN architectures

This Table 4, compares five deep learning models, DenseNet201, MobileNetV2, ResNet50, InceptionV3 and Xception, in terms of extracted features, number of parameters, Multiply- Accumulate Operations (MACS) and Floating-Point Operations per Second (FLOPS). The Number of Features column reflects the dimensionality of the data prior to and after optimization algorithms of Bacterial Foraging Optimization (BFO) and Principal Component Analysis (PCA).

MobileNetV2 is the lightweight and resource-efficient model since it has the lowest number of parameters of 3.505 million, 327.487 million MACS, and 654.973 million FLOPS, which is much lower than the rest of the models. ResNet50, InceptionV3, and XceptionV3, by contrast, are more complex with high computational complexity of all beyond 4 billion MACS and 8 billion FLOPS, but DenseNet201 is also moderately complex with 4.390G MACS and 8.781G FLOPS. Unlike dimensionality reduction, feature optimization generates reduced dimensions with high performance and low computation cost. In general, the findings highlight that MobileNetV2 is the most appropriate model to use in the development of an efficient feature extraction and real-time skin cancer image classification because of the small number of parameters and less computational intensity.

Table 4: The features, parameter, MACS and FLOPS of various model implemented in this study

Model	Number of Features			Parameter	MACS	FLOPS
	Without Opt	BFO	PCA			
DaseNet201	1024	498	600	20.014M	4.390G	8.781G
MobileNet V2	1024	724	600	3.505M	327.487M	654.973M
ResNet50	2048	1099	800	25.557M	4.134G	8.267G
InceptionV3	2048	887	800	23.835M	5.749G	11.498G
Xception	2048	1134	800	22.855M	4.146G	8.292G

4.3. The outcome of the Skin cancer analysis without optimization

The Table 5, represents the comparative performance of different pre-trained deep learning models with traditional machine learning classifiers on skin disease classification, without optimization, in terms of Accuracy, Precision, Recall, and F1-Score measures. MobileNetV2 showed the best overall performance in terms of accuracy, with the best results of 89.71, precision of 89.25, recall of 89.73, and F1-score of 89.80, and KNN classifier with a close result 84.56. This means that MobileNetV2 offers highly discriminative features that are appropriate to work with classification. Comparatively, DenseNet201 and InceptionV3 performed fairly well on all classifiers, whereas ResNet50 kept the accuracy rates steady but rather low. The Xception model had the least performance, especially in conjunction with the Gaussian Naïve Bayes (GNB) which had the lowest accuracy of 60.37. In general, MobileNetV2 with LR or KNN worked better than other combinations, which is why it is better suited to feature extraction and classification accuracy in the context of this unoptimized configuration.

4.4. Findings from Skin Cancer Analysis With BFO Optimization

The Table 6, shows the classification of various pre-trained models with the combination of conventional machine learning classifiers with the use of Bacterial Foraging Optimization (BFO). The findings indicate that the use of BFO optimization greatly enhanced the model accuracy in most settings compared to the un-optimized one. MobileNetV2, once again, outperformed all the others with overall performance of 92.45% accuracy, 92.54% precision, 92.56% recall, and 92.84% F1-score, which shows that BFO-tuned features have strong discriminative power. KNN under MobileNetV2 was also a competitive classifier with an accuracy of 85.55%. In the meantime, ResNet50 and DenseNet201 performed steadily, but relative moderate, and InceptionV3 demonstrated a weak increase, whereas Xception was quite low in comparison with the result of the non-optimized variant. Altogether, the combination of BFO optimization significantly improved the classification performance, in particular with MobileNetV2 + LR, which proved that BFO is an effective tool that reduces the quality of features and promotes the predictive potential of hybrid deep learning models.

4.5. Findings from Skin Cancer Analysis with PCA Optimization

In the Table 7, the comparison of performance between various pre-trained CNN models together with the standard machine learning classifiers after optimization with Principal Component Analysis (PCA) is presented and measured in terms of Accuracy, Precision, Recall, and F1-Score (percentage). The findings suggest that PCA has taken a significant role in enhancing consistency of classification and discrimination of features across models. The MobileNetV2 configuration displayed the most overall results, with the Logistic Regression (LR) classifier being the highest performing with an accuracy, precision, recall, and F1-score of 91.66, 91.64, 91.66, and 91.64, respectively, and the XGBoost (XGB) classifier coming in second with 87.33% accuracy. These results prove that MobileNetV2, optimized with PCA, removes very informative and concise features that boost the performance of the classifiers. In the meantime, ResNet50 turned out to be also competitive in its performance, with SVC reaching an accuracy of 77.52% and DenseNet201 and InceptionV3 showing moderate gains over the non-optimized counterparts. Conversely, Xception was once again the worst performing classifier. In general, the use of PCA optimization was successful in minimizing the data dimensionality and redundancy, enhancing computing efficiency and classification accuracy - most prominently with MobileNetV2 + LR combination.

4.6. Findings from Skin Cancer Analysis with LDA Optimization

The Table 9, shows the classification performance of various pre-trained CNN models coupled with standard classifiers following Linear Discriminant Analysis (LDA) optimization. Optimization using LDA resulted in a visible increase in the model performance in the majority of the combinations, with MobileNetV2 again performing better than other architectures. In particular the highest results were registered by the Logistic Regression (LR) classifier that demonstrated the accuracy of 99.33, precision of 99.47, recall of 97.33, and F1-score of 98.31, which depicts a highly discriminative and generalized

representation of features. The XGBoost (XGB) and KNN classifiers of MobileNetV2 performed also with high accuracies of 88.00% and 87.64, respectively, which confirms the strength of this pre-trained model when optimized using LDA. DenseNet201 and InceptionV3, in turn, showed moderate performance gains, and ResNet50 showed relatively constant results. The Xception model, though, was still presenting the poorest results, which is indicative of its low adaptability in this regard. On the whole, the findings show that LDA optimization is an effective predictor of maximizing the separability of the classes, and the MobileNetV2 + LR version had higher predictive accuracy and generalization than any other optimized and non-optimized options. (approximately 77.7%) with higher execution time and diverse memory utilization. ResNet50+SVC model was best but still with a moderate performance (89.07% accuracy) and had the highest peak memory (3139.07 MiB). In general, MobileNetV2 + LDA + LR was the best trade-off of all model configurations in terms of classification accuracy, computational time and memory efficiency.

Table 5: The Outcome of the Skin Cancer Analysis Without Optimization

Pre-trained model	Classifier	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
DenseNet201	SVC	70.06	70.73	70.71	70.76
	RF	76.20	76.17	76.10	76.12
	DT	72.07	72.00	72.76	71.77
	GNB	72.77	73.43	72.62	72.45
	XGB	77.25	77.27	77.14	77.17
	KNN	70.76	70.74	70.67	70.65
	LR	71.57	71.47	71.47	71.47
InceptionV3	SVC	77.03	77.77	77.13	77.75
	RF	74.75	74.77	75.06	74.71
	DT	65.06	65.55	65.07	65.23
	GNB	65.17	65.13	65.35	64.74
	XGB	77.74	77.77	77.03	77.71
	KNN	70.47	70.30	70.57	70.36
	LR	76.37	76.37	76.45	76.40
MobileNetV2	SVC	83.12	82.71	83.21	82.73
	RF	80.03	80.02	87.77	87.72
	DT	82.13	82.03	82.04	82.03
	GNB	81.17	81.75	84.27	81.27
	XGB	82.75	82.54	82.77	82.64
	KNN	84.56	84.54	84.45	84.47
	LR	89.71	89.25	89.73	89.80
ResNet50	SVC	89.07	89.42	89.77	89.17
	RF	75.77	76.60	75.50	75.77
	DT	77.70	70.10	70.07	70.07
	GNB	72.77	73.67	75.37	73.65
	XGB	77.43	77.71	77.33	77.51
	KNN	77.51	77.77	77.35	77.56
	LR	77.37	77.53	77.34	77.43
Xception	SVC	77.50	77.57	77.77	77.41
	RF	76.75	76.73	77.22	76.75
	DT	70.10	70.41	70.27	70.34
	GNB	60.37	70.57	71.17	67.51
	XGB	70.62	70.62	70.72	70.57
	KNN	77.75	77.71	77.73	77.72
	LR	70.70	70.71	70.74	70.76

Table 6: The Outcome of the Skin Cancer Analysis with BFO Optimization

Pre-trained model	Classifier	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
DenseNet201	SVC	75.71	75.77	75.75	75.76
	RF	72.51	72.43	72.42	72.42
	DT	75.13	74.74	74.76	74.73
	GNB	57.70	60.41	57.75	57.67
	XGB	74.40	74.34	74.27	74.30
	KNN	73.64	73.56	73.57	73.56
	LR	75.70	75.72	75.70	75.74
InceptionV3	SVC	76.03	76.01	76.07	76.03
	RF	77.47	77.46	77.54	77.47
	DT	65.71	66.13	65.71	65.77
	GNB	56.77	57.23	57.06	57.11
	XGB	74.57	74.53	74.61	74.56
	KNN	72.12	72.01	72.27	72.07
	LR	75.20	75.70	75.12	75.32
MobileNetV2	SVC	87.20	85.21	85.21	85.23
	RF	81.33	82.33	81.37	82.32
	DT	84.13	84.13	84.14	84.13
	GNB	84.12	84.12	84.14	84.17
	XGB	87.33	87.33	87.37	87.37
	KNN	85.55	84.46	84.76	84.52
	LR	91.66	91.64	91.66	91.64
ResNet50	SVC	77.52	77.61	77.64	77.62
	RF	70.41	73.26	77.47	70.27
	DT	74.10	74.46	74.25	74.32
	GNB	44.73	47.37	50.56	45.17
	XGB	75.36	75.73	75.27	75.47
	KNN	77.25	77.47	77.14	77.31
	LR	77.07	77.10	77.21	77.16
Xception	SVC	77.57	77.60	77.77	77.54
	RF	73.47	73.35	73.76	73.30
	DT	67.72	70.37	70.03	70.17
	GNB	47.31	53.77	46.71	46.13
	XGB	76.77	76.77	77.07	76.56
	KNN	77.50	77.47	77.73	77.57
	LR	74.67	74.74	74.77	74.77

4.7. Performance Evaluation of Pretrained CNN-Based Hybrid Model

It provides the comparison of the performance of different pretrained CNN-based hybrid models with their computational complexities. The results of the proposed MobileNetV2 + LDA + LR model outperformed other evaluated models with the highest accuracy of 99.33, precision of 99.47, recall of 97.33 and F1-score of 98.31, with a moderate time complexity of 35.1 ± 1.24 seconds and memory consumption of PM: 2548.77 MiB, INC: 1160.05 MiB. Comparatively, other architectures like ResNet50 + SVC and DenseNet201 + BFO + LR achieved lower accuracies of 89.07% and 77.75% respectively and had a high computational requirement. On the same note, InceptionV3 + LDA + XGB and Xception + BFO + XGB showed similar results with about 77 percent accuracy, only that they took more time and consumed more resources to execute. These results show that the hybrid model implemented using MobileNetV2 provides the best accuracy, efficiency, and cost of computation, and it can be used in real-time medical image classification in resource-restricted tasks.

Table 7: The Outcome of the Skin Cancer Analysis with PCA Optimization

Pre-trained model	Classifier	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
DenseNet201	SVC	77.31	77.43	77.33	77.27
	RF	76.12	76.12	76.02	76.03
	DT	70.70	70.57	70.53	70.53
	GNB	72.30	73.67	72.54	72.27
	XGB	77.47	77.46	77.45	77.45
	KNN	76.70	76.73	76.71	76.70
	LR	77.75	77.77	77.74	77.73
InceptionV3	SVC	75.45	75.30	75.57	75.33
	RF	75.20	75.27	75.26	75.26
	DT	65.71	66.37	65.72	65.77
	GNB	54.07	54.22	54.22	53.72
	XGB	77.45	77.37	77.52	77.41
	KNN	67.47	67.22	67.62	67.23
	LR	74.37	74.40	74.44	74.42
MobileNetV2	SVC	85.12	85.71	85.21	85.73
	RF	81.03	82.03	81.77	82.72
	DT	82.13	82.03	82.04	82.03
	GNB	81.12	81.72	84.64	81.67
	XGB	85.75	82.54	82.77	82.64
	KNN	85.55	84.46	84.76	84.52
	LR	92.45	92.54	92.56	92.84
ResNet50	SVC	76.72	76.72	76.77	76.77
	RF	75.54	75.71	75.37	75.62
	DT	77.53	77.54	77.72	77.72
	GNB	70.47	71.06	73.77	71.43
	XGB	77.71	77.16	77.77	77.76
	KNN	77.11	77.17	77.11	77.14
	LR	77.64	77.72	77.47	77.67
Xception	SVC	77.34	77.33	77.61	77.27
	RF	77.17	77.16	77.47	77.14
	DT	70.71	70.76	71.13	71.02
	GNB	60.37	70.72	71.37	67.37
	XGB	77.77	77.76	70.07	77.70
	KNN	76.70	76.65	76.76	76.67
	LR	70.21	70.23	70.36	70.27

Table 8: Comparison of pretrained CNN-based hybrid models and their computational complexities

Technique	A (%)	P (%)	R (%)	F1 (%)	Time Complexity	Space Complexity
Dasenet201 +BFO+LR	77.75	77.77	77.74	77.73	59.9 s ± 1.37 s	PM: 1840.90 MiB, INC: 989.61 MiB
Inception3 +LDA+ XGB	77.75	77.56	77.56	77.55	3.22 min ± 4.11 s	PM: 2337.03 MiB, INC: 1221.06 MiB
Xception +BFO+ XGB	77.77	77.76	70.07	77.70	8.33min ± 4.2ms	PM: 2165.42 MiB, INC: 997.95 MiB
ResNet50 + SVC	89.07	89.42	89.77	89.17	2.56 min ± 2.3s	PM: 3139.07 MiB, INC 1348.95 MiB
MobileNet V2 + LDA+LR	99.33	99.47	97.33	98.31	35.1 s ± 1.24 s	PM: 2548.77 MiB, INC: 1160.05 MiB

Table 9: The Outcome of the Skin Cancer Analysis with LDA Optimization

Pre-trained model	Classifier	Accuracy (%)	Precision (%)	Recall (%)	F1-Score (%)
DenseNet201	SVC	76.66	76.62	76.61	76.61
	RF	74.73	74.73	74.65	74.67
	DT	70.67	70.45	70.35	70.36
	GNB	72.65	72.77	72.50	72.35
	XGB	76.72	76.70	76.67	76.72
	KNN	74.45	74.37	74.27	74.27
	LR	76.77	76.77	76.76	76.71
InceptionV3	SVC	77.07	76.77	76.77	76.76
	RF	73.47	73.42	73.32	73.33
	DT	74.00	74.67	73.76	74.07
	GNB	64.77	64.63	64.54	64.33
	XGB	77.75	77.56	77.56	77.55
	KNN	74.50	74.04	74.12	74.06
	LR	75.77	76.07	75.77	75.70
MobileNetV2	SVC	87.20	87.21	87.21	87.23
	RF	82.33	82.33	82.37	82.32
	DT	85.13	85.13	85.14	85.13
	GNB	85.21	85.21	85.24	85.21
	XGB	88.00	87.01	87.01	87.02
	KNN	87.64	87.65	87.66	87.65
	LR	99.33	99.47	97.33	98.31
ResNet50	SVC	77.77	77.73	77.70	77.71
	RF	75.57	75.77	75.37	75.61
	DT	70.07	70.11	70.32	70.20
	GNB	70.45	71.77	74.25	71.47
	XGB	77.74	77.74	77.77	77.76
	KNN	77.34	77.65	77.11	77.37
	LR	77.57	77.54	77.67	77.60
Xception	SVC	76.74	76.75	77.10	76.73
	RF	77.55	77.51	77.71	77.57
	DT	70.04	70.47	70.25	70.35
	GNB	67.06	67.77	67.74	66.37
	XGB	70.32	70.30	70.53	70.36
	KNN	70.71	70.77	71.25	70.75
	LR	77.53	77.71	77.66	77.67

4.8. K(10) fold cross-validation result of the proposed model

Table 10, shows the outcomes of 10-fold cross-validation conducted on the MobileNetV2 + LDA + LR model to assess its consistency and generalization performance with various data partitions. The findings indicate that, the model has very stable and excellent results across all folds with Accuracy of between 99.31 and 99.36, Precision of between 99.42 and 99.47, Recall of between 97.26 and 97.35 and F1-Score of between 98.28 and 98.34. The average standard deviation values of $99.33 \pm 0.02\%$ (Accuracy), $99.45 \pm 0.02\%$ (Precision), $97.31 \pm 0.03\%$ (Recall) and $98.31 \pm 0.02\%$ (F1-Score) demonstrate the lack of differences in the average results of the folds and illustrate the strength and stability of the model. These results prove that the suggested MobileNetV2 + LDA + LR model has a high predictive stability, good generalization and stable classification results using different data splits.

Table 10: K(10) Fold Cross-Validation Performance of the MobileNetV2 + LDA + LR Model

Fold	Accuracy (%)	Precision (%)	Recall (%)	F1-Score(%)
1	99.34	99.45	97.28	98.31
2	99.35	99.46	97.31	98.33
3	99.32	99.43	97.29	98.30
4	99.31	99.42	97.26	98.28
5	99.36	99.47	97.33	98.32
6	99.33	99.45	97.34	98.31
7	99.34	99.46	97.32	98.30
8	99.32	99.44	97.30	98.29
9	99.35	99.47	97.35	98.34
10	99.33	99.45	97.31	98.32
Average $\pm$ SD	99.33 $\pm$ 0.02	99.45 $\pm$ 0.02	97.31 $\pm$ 0.03	98.31 $\pm$ 0.02

4.9. Learning curve of the proposed model

As depicted in Figure 2, the learning curve of proposed MobileNetV2+LDA+LR model shows the correlation between the size of both training and cross-validation sets and the model accuracy during both training and cross-validation processes. The training accuracy first grows quickly and levels to 0.90, which means that the model learns well on the training data available. On the other hand, the accuracy of the cross-validation begins with a lower value but exhibits a consistent increasing pattern with the size of the training set, which finally approaches the value of around 0.80. The decreasing difference between the training and validation curves indicates both less overfitting and better generalization with the increase of data. The gray area around the cross-validation curve is a measure of variance between folds, which is also small at larger training sizes, again giving evidence of model stability and stability in performance.

4.10. Receiver Operating Characteristic (ROC) curve of the proposed model

Figure 3, shows the Receiver Operating Characteristic (ROC) curve of the proposed model MobileNetV2+LDA+LR, which represents the trade-off between the True Positive Rate (TPR) and False Positive Rate (FPR) of all five classes. Class 0, class 1, and class 2 ROC curves attain an area under the curve (AUC) of 1.00, which means those curves are perfect classifiers with zero misclassifications. Class 3 and class 4 also have almost perfect performances with AUCs of 0.99 and 0.94 respectively. The general findings have shown a very discriminatory model that can be successfully used to differentiate the classes. The high position of all ROC curves at the top-left corner of the graph indicates the high sensitivity and specificity, which confirms the effectiveness and stability of the proposed method in multi-class classification processes.

4.11. Confusion Matrix of the Proposed model

The confusion matrix of the proposed MobileNetV2+LDA+LR model is shown in Figure 4, and this shows the classification performance of the model in five different types of skin lesion, Non-Cancerous, B.C.C (Basal Cell Carcinoma), Melanoma, S.C.C (Squamous Cell Carcinoma), and

Malignant. The matrix demonstrates that the model perceives most of the classes with almost perfect predictions with all the diagonal values being near 1 which means that there is a high agreement between actual and predicted labels. In particular, the model accurately classifies Non-Cancerous, B.C.C and Melanoma samples in a 100 percent accuracy. In the case of S.C.C, a misclassification rate of minimal 0.0044 is present and the Malignant cases are more accurate by 0.87 with a slight confusion of 0.13 having been misclassified as S.C.C. The general distribution of values of the diagonal indicates the very good discriminative capacity and a great accuracy of the model in differentiating similar lesion types, which shows that it is a very strong and reliable model in multiclass multimodal medical image classification.

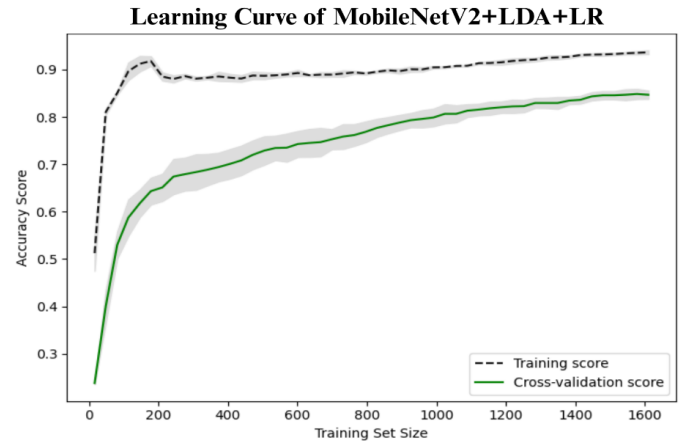


Figure 2: The proposed model's learning curve

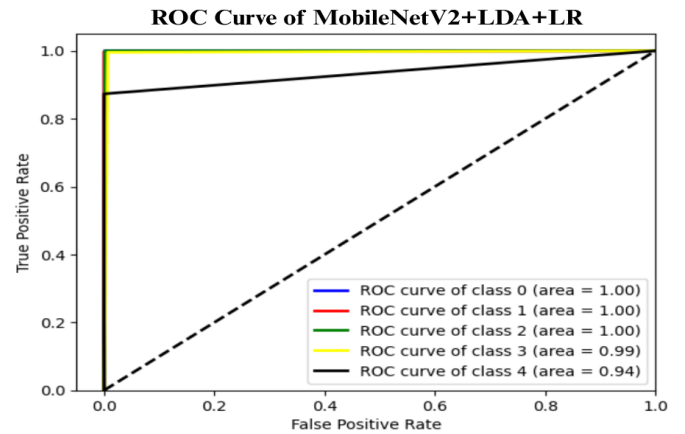


Figure 3: The proposed model's ROC curve

4.12. Outcome Explanation With XAI

Table 11 demonstrates the outcome interpretation of the proposed model using Explainable Artificial Intelligence (XAI) methods: Grad-CAM++ and LIME, with regard to four representative types of skin lesions, namely: Basal Cell Carcinoma, Malignant Lesions, Melanoma, and Squamous Cell Carcinoma. The Grad-CAM++ heatmaps are useful in that they are able to point out the discriminative areas in each lesion image with the red and yellow activation areas indicating the most important areas that the model ultimately relied on to make the final prediction. Equally, the LIME visualizations highlight which

super pixels are critical locally influencing the classification decision, and provide a more fine-grained view of the reasoning process of a model. These high correlations between the two visualization outcomes show that the model continuously targets the areas of the diagnostically significant lesions instead of the nonessential background sources. This level of interpretability does not only support the robustness and reliability of the model but also reinforces its possible application in real-world dermatological diagnostic systems by increasing clinical transparency and confidence of the decision.

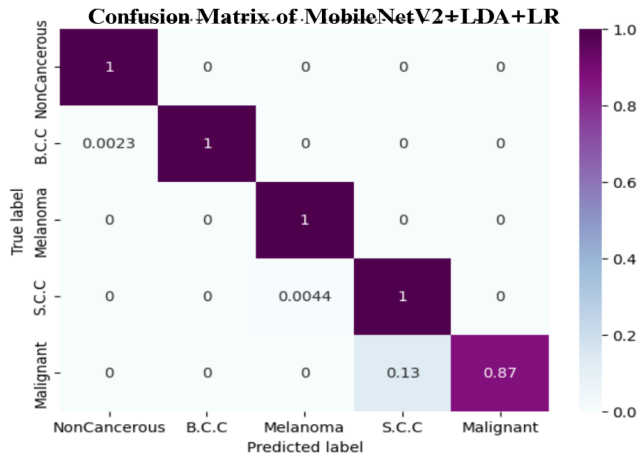


Figure 4: Confusion Matrix of the Proposed Model

Table 11: Explanation of the affected lung regions using XAI visualization

Sample Source	Actual Image	Grad-CAM++	LIME
Basal Cell Carcinoma			

Malignant lesions			
Melanoma			
Squamous Cell Carcinoma			

4.13. Discussion

A detailed comparison of the proposed MobileNetV2 + LDA + Logistic Regression model with a number of other available methods in skin cancer classification by their accuracy, optimization, explainable AI (XAI) integration, and computational complexity is provided in Table 12.

Current models, such as SVM, CNN, InceptionV3, DCNNs, and DenseNet201 reached the accuracy of between 85.00 and 96.25 with little or no optimization and XAI method. However, the suggested model has a better performance of 99.33 with the integration of various optimization models which include Bacterial Foraging Optimization (BMO), Principal Component Analysis (PCA), and Linear Discriminant Analysis (LDA). Moreover, the model uses XAI methods, namely LIME and Grad-CAM++, to improve interpretability and present visual explanations of the decision-making process. Although deep learning models are more complex, the presented approach is computationally efficient, with an execution time of $35.1s \pm 1.24s$, memory use of PM: 2548.77 MiB and INC: 1160.05 MiB, thus, providing a self-sustaining, reliable, and interpretable diagnostic framework in comparison to the current state-of-the-art approaches.

Table 12: Comparison between the Proposed Model and Existing Models

Ref.	Author	Method	A (%)	Opti.	XAI	Complexity	
						Time	Space
[22]	B. O. S. Elgabbani et. al.	SVM, CNN	85.00%	X	X	X	X
[18]	Gouda et al.	InceptionV3	85.80%	X	X	X	X
[19]	Al-Rakhami et al.	DCNNs	90.00%	✓	✓	X	X
[20]	Karni et al.	DenseNet201	92.00%	✓	✓	X	X
[21]	Monika et al.	SVM	96.25%	✓	✓	X	X
Proposed Method		MobileNetV2+ LDA+ Logistic Regression	99.33%	BFO, PCA, LDA	LIME, Grad-CAM++	$35.1s \pm 1.24s$	PM: 2548.77 MiB, INC: 1160.05 MiB

5. Conclusion & Future Work

The paper suggested a streamlined hybrid deep and machine learning architecture that can achieve reliable and explainable skin cancer detection, combining MobileNetV2, Linear Discriminant Analysis (LDA), and Logistic Regression (LR). The proposed model was shown to outperform in several assessment metrics and datasets, with the best results of 99.33% accuracy, 99.47% precision, 97.33% recall, and 98.31% F1-score and with a moderate computational cost. The framework demonstrated an incredible generalization, stability and robustness to all data partitions after extensive experimentation with 10-fold cross-validation. Its efficiency was further proven by the computational complexity analysis, which also exhibited moderate time and memory usage, which made it a viable diagnostic solution, which can be used in real-time scenarios in a clinical setting, particularly in resource-limited settings. Besides providing a high performance in classification, the integration of the Explainable Artificial Intelligence (XAI) models, including Grad-CAM++ and LIME, allowed the model to give a transparent and visual representation of how it makes its decisions. These visualizations verified the fact that the model always paid attention to the clinically relevant regions of lesions, which reinforced the credibility of the model and its clinical relevance. In contrast to traditional black-box CNN models, this aspect of interpretability ensures the disconnect between AI-based analysis and clinical decision-making, increasing the level of trust in physicians and the possibility of its integration into dermatological diagnostic processes. The main contributions of the study are its balanced design that incorporated accuracy, computational efficiency, and interpretability. The study was able to overcome constraints that were experienced in previous models especially in terms of model complexity, overfitting and scalability using lightweight architectures like MobileNetV2 and dimensionality reduction techniques like LDA and PCA. Additionally, metaheuristic optimization (BFO) integration presented a powerful approach to the enhancement of feature quality and the increase in classification performance. Nevertheless, even with such a good performance, this study recognizes some limitations. The model has been trained and tested with secondary datasets, as demonstrated, which, however diverse, might not be representative of the heterogeneity of real-world clinical images. Moreover, the paper was mostly oriented on image-based data; the inclusion of multi-modal data, including patient demographics or histopathological metadata, could be added to the work to enhance the quality of the diagnoses. Future research ought to then be based on applying this framework to multi-institutional datasets, applying federated learning techniques to improve data privacy and generalizability, and how real-time can be deployed on embedded or mobile medical devices to perform point-of-care screening. Altogether, the suggested MobileNetV2 + LDA + LR framework can be regarded as an important step in the development of skin cancer diagnostics as it provides a high level of accuracy, transparency, and computational efficiency. The model does not only expand the existing body of knowledge in computer-aided dermatological diagnostics but also opens a clinically viable route towards the use of artificial intelligence in the early detection of skin cancer, finally leading to more affordable, trustworthy, and interpretable AI-based healthcare systems.

Conflict of Interest

The authors declare no conflict of interest.

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Detection Method and Mitigation of Server-Spoofing Attacks on SOME/IP at the Service Discovery Phase

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ABSTRACT

Service-oriented architecture has attracted attention in automotive development. The Automotive Open System Architecture (AUTOSAR) specifies Scalable Service-Oriented Middleware over IP (SOME/IP) as a key middleware for service-oriented communication in-vehicles. However, SOME/IP-based networks are vulnerable to server spoofing during the service discovery phase, enabling attackers to cause man-in-the-middle attacks by impersonating legitimate services. This paper proposes a method for detecting attacks in which an attacker spoofs a server during service discovery using a packet switch in a network employing SOME/IP. In addition, a mitigation method is proposed to discard malicious messages. The proposed method addresses the limitations of conventional encryption-based approaches by reducing both processing and communication loads. It also improves anomaly detection rate and detection timing, which have been identified as shortcomings in intrusion detection systems proposed in previous studies. In this study, we evaluated the method using a dataset consisting of 36 attack patterns that combined attack types, attack initiation timing, and message categories. Real-world evaluations demonstrated that the proposed method detected all server spoofing attempts. Further analysis of processing time and memory resource usage confirmed its feasibility for in-vehicle system.

1. Introduction

Recently, there has been an increasing demand for software and hardware updates via over-the-air (OTA) and plug-and-play (PnP) after delivery for consumers to add new features and update existing ones. Advanced driver assistance systems are becoming popular, and automotive software is becoming increasingly large and complex. Service-oriented architecture has attracted attention as a solution to these issues. Automotive open system architecture (AUTOSAR), a global development partnership in the automotive industry, provides specifications for Scalable Service-Oriented Middleware over IP (SOME/IP) [1] and SOME/IP Service Discovery (SOME/IP-SD) [2], which are service-oriented communication middleware.

Communication in-vehicle systems has strict performance requirements for communication establishment and delays [3], [4]. To meet these performance requirements, SOME/IP suppresses the amount of bandwidth used across the entire network using multicast for certain communications. SOME/IP is designed to

communicate over the TCP/IP stack and does not have its own encryption and authentication mechanisms. In [5], the authors reported that analysis of the SOME/IP specification revealed the possibility of man-in-the-middle attacks, in which an attacker spoofs as a server providing a service or as a client using the service.

In [6], the use of IPSec and TLS/DTLS in SOME/IP was discussed; however, it was demonstrated that IPSec lack multicasting support, while TLS/DTLS incurred high communication overhead owing to its complex communication establishment process. In SOME/IP, both the server and the client perform event-triggered communications. The server periodically sends messages to registered clients using a unique publish/subscribe (Pub/Sub). Pub/Sub communication is used for communications where real-time performance, such as sensor information, is important. Pub/Sub employs multicast communication to reduce communication load because it sends the same information to multiple devices, which poses a challenge to the introduction of encryption and authentication. Therefore, it is important to develop an anomaly detection and mitigation method

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that minimizes communication load and delay while effectively addressing server spoofing attacks.

In [7], an Intrusion Detection System (IDS) that detects the spoofing attack using SOME/IP is proposed. The timing of anomaly detection in this method is during communication for service use; however, there is a possibility of misdetecting normal communication as an anomaly, and there is a concern that communication related to safety, such as vehicle operation, may be mistakenly obstructed. Therefore, it is difficult to perform actions, such as communication termination, when an anomaly is detected. Additionally, anomaly detection methods based on monitoring communication values struggle to detect man-in-the-middle attacks that only involve spoofed message reception. Therefore, an anomaly detection and mitigation method that can detect spoofing attacks, including man-in-the-middle attacks, during service discovery, that is, before service utilization begins, is necessary.

In this study, we propose a detection and mitigation method that detects and mitigates the possibility of spoofing as a server attack during service discovery in networks using SOME/IP. In the proposed method, anomaly detection is performed before the service starts. Therefore, even if normal communication is mistakenly detected as an anomaly, there are no safety concerns because the service has not started operating. The contributions of this study are as follows:

- We propose a method for detecting all spoofing attacks on SOME/IP using a simple algorithm requiring fewer than 100 operations per message, considering implementation in embedded devices.
- We classified attack patterns into 36 types based on the classification of the attackers' messages sent and attack timing, including man-in-the-middle attacks. Through a real-world evaluation, we demonstrated that the proposed method could detect spoofing attacks in all patterns. In particular, for the 24 attack patterns, normal communication and attacks were correctly classified, enabling continued service use.
- For the remaining 12 attack patterns, normal communications and attacks cannot be correctly classified. These cases occur only before service use begins. Thus, by blocking the target communications from the first use of the service, the system can be maintained in a safe state.

The remainder of this paper is organized as follows. Section 2 describes the requirements for in-vehicle networks and the characteristics of the SOME/IP and SOME/IP-SD protocols used in in-vehicle networks, introduces solutions for attacks on in-vehicle networks and their protection, and explains these issues. Section 3 describes the anomaly detection mechanism and mitigation mechanism in the proposed method. Section 4 presents the results of an evaluation using *vsomeip*[8], a prototype implementation of SOME/IP, to demonstrate the effectiveness of the proposed method. Section 5 discusses the evaluation results. Finally, Section 6 presents the conclusions.

2. Related Research

2.1. In-Vehicle Network Requirements

Reference [3] classified communications in-vehicle networks based on their strict real-time requirements as static, real-time, IP-

based, or web services. For various communications, such as sensor information, real-time performance is guaranteed by setting a communication cycle, and the maximum allowable communication delay is less than 10% of the communication cycle. In particular, for Static Real-Time Services used in Safety Electronics and Engine/Powertrain applications, communication is performed at a 1[ms] cycle; thus, the maximum allowable communication delay is 0.1[ms].

2.2. SOME/IP

SOME/IP is a service-oriented automotive middleware specification used to control communication messages [1]. SOME/IP is designed to communicate over TCP/IP or UDP/IP, and does not provide encryption or authentication mechanisms. It supports the following functions:

- **Serialization:**
Conversion of transmitted and received data into communication formats.
- **Remote Procedure Call (RPC) and message:**
Remote calls to functions and other messages.
- **Event Notifications:**
Notification from server to client.
- **Segmentation of UDP messages:**
Transfer SOME/IP messages that do not fit into a single UDP packet via UDP without fragmentation.

SOME/IP communicates using a TCP/IP protocol stack. It supports IPv4/IPv6 as the Internet layer and TCP and UDP as the transport layer. Table 1 lists the messages defined by SOME/IP. Each SOME/IP message contains a message ID composed of three components: a service ID, which specifies the type of service; a method ID, which specifies the type of method; and a session ID, which identifies communications between the same device pair. Attackers' ultimate goal is to tamper with these messages.

2.3. SOME/IP-SD

SOME/IP-SD is a middleware specification [2] that enables the discovery of available services on the system and the management of event message transmission on SOME/IP and supports the following functions.

- **Service Discovery:**
Dynamic service discovery, and access control.
- **Publish/Subscribe (Pub/Sub):**
Dynamic configuration of communication between Server and Client.

Table 2 shows a list of messages specified in SOME/IP-SD. SOME/IP-SD messages include a Service ID that indicates the type of service, and an Instance ID that identifies the server. In particular, in the case of SOME/IP-SD messages, the Message ID included in the lower-level protocol SOME/IP message is fixed at 0xFFFFF8100; thus, the target service is identified by the Service ID included in the SOME/IP-SD message. SOME/IP supports multiple servers providing services with the same Service ID, in which case, these servers will have different Instance IDs.

Table 1: SOME/IP Message Type List

Kind (Value)	Description
REQUEST(0x00)	Sent from Client (Unicast). Requests that require a response.
REQUEST_NORETURN (0x01)	Sent from Client (Unicast). Requests that do not require a response.
NOTIFICATION(0x02)	Sent from Server (Unicast or Multicast). One-way notification.
RESPONSE(0x80)	Sent from Server (Unicast). Response to REQUEST.
ERROR(0x81)	Sent from Server (Unicast). Error response.

The Service Discovery function uses the OFFER SERVICE, STOP OFFER SERVICE, and FIND SERVICE to share information about available services between the server and client. After starting, the server waited for a certain period before sending the OFFER SERVICE. The client detects that the target service is available by receiving the OFFER SERVICE and begins using the service. If the client cannot receive an OFFER SERVICE for a certain period after startup, it sends a FIND SERVICE to search for a server that provides the target service. When the server receives a FIND SERVICE, it sends an OFFER SERVICE to the client. When the server stops providing the service, it sends a STOP OFFER SERVICE to notify the client. Attackers may send these messages during an attack. The proposed method monitors these messages to detect attacks.

2.4. Attacks on Vehicle-Mounted Networks

Controller area networks (CAN), which are widely used in automotive networks, are vulnerable to spoofing attacks because they cannot identify source devices. Reports indicate that spoofing attacks can be conducted by injecting CAN messages into the CAN bus or OBD-II diagnostic port, causing unauthorized operation of automotive devices [9], [10]. In SOME/IP, although the source device can be identified, the absence of a standard authentication mechanism allows attackers to forge device information and conduct spoofing attacks. In such cases, legitimate communication from authorized devices continues alongside malicious activity, resulting in a combination of normal and spoofed messages. This study refers to such scenarios as “Normal and Anomaly (Attack).” The communication sequence of this attack pattern is shown in Figure 1. Furthermore, this attack has the lowest difficulty level.

It has been reported that a DoS attack called a bus-off attack [11] that disables the sending device is possible in a CAN. A spoofing attack [12] using a bus-off attack has been reported, and this attack has the characteristic that only spoofing attacks are performed because the communication of the legitimate device is disabled. The feasibility of a DoS attack with the same characteristics as a bus-off attack against SOME/IP has been examined in previous studies [13]. In this study, a comprehensive analysis of the state transition specifications of SOME/IP-SD concluded that while it is possible to disable legitimate device communications, an Offer Service must be sent at least once from the legitimate server. In this study, such an attack pattern is referred to as “Anomaly (Attack) Only.” The communication sequence of

Table 2: SOME/IP-SD Message Type List

Kind (Value)	Description
FIND SERVICE(0x00)	Send from Client (Multicast). Notification of service provider discovery.
(STOP) OFFER SERVICE (0x01)	Sent from Server (Unicast or Multicast). Notification of service provision status.
(STOP)SUBSCRIBE EVENTGROU (0x02)	Sent from Client (Unicast). Request to add/delete recipients of NOTIFICATION.
SUBSCRIBE EVENTGROUP ACK / NACK (0x03)	Sent from Server (Unicast). Success or failure of adding/deleting recipients of NOTIFICATION.

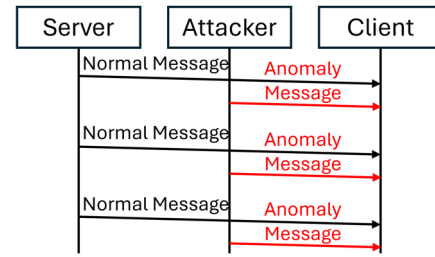


Figure 1: Communication Sequence of Normal and Anomaly (Attack)

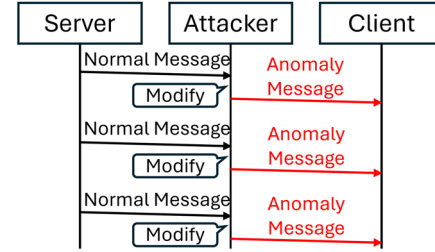


Figure 2: Communication Sequence of Man-in-the-middle attack

this attack pattern is shown in Figure 2. Furthermore, this attack has the highest difficulty level.

Because CAN always performs broadcast communication in a bus-type network topology, it is impossible to conduct a man-in-the-middle attack without physically changing the network connection. Man-in-the-middle attacks can be performed using the service discovery mechanism of SOME/IP [5]. Man-in-the-middle attacks against SOME/IP are conducted by attackers spoofing legitimate servers and sending an OFFER SERVICE, thereby inducing clients to use the services provided by the attackers. Furthermore, the difficulty level of this attack is medium.

2.5. Mitigation Measures Against Spoofing Attacks in Automotive Networks

For CAN, such as authentication and IDS, as countermeasures against spoofing attacks, have been proposed. AUTOSAR specifies a method for assigning MAC values to CAN communication messages between devices [14]. An IDS [15] that detects attacks based on the transmission cycle of information communicated in an in-vehicle network and the content of communications, such as sensor information, has been proposed. As a response to anomaly detection, [16] proposes a method that

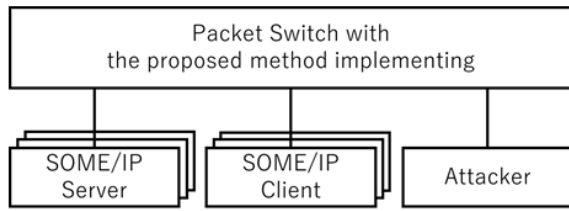


Figure 3: The proposed method assumes a network configuration where multiple servers, clients, and attackers are connected to different ports on a packet switch

discards CAN communication messages with invalid MAC values by monitoring all communications on the CAN bus.

In SOME/IP, encryption using IPSec and TLS/DTLS is being discussed; however, it has been demonstrated that high communication overhead is an issue owing to the lack of multicast support and the complex communication establishment process [6]. In [6], a mitigation method for SOME/IP using whitelists and authentication was proposed. However, there are concerns that flexibility may be reduced owing to whitelist management. An IDS [7] that monitors communication intervals, payload changes, and session counts as features has been proposed. However, because this method monitors communication related to service usage, there is a concern that false positives can affect safety-related communication, such as vehicle operation, making it difficult to take action, such as communication termination, when anomalies are detected.

3. Proposed Method

This paper proposes a detection and mitigation method to detect the possibility of spoofing as a server attack during service discovery in networks using SOME/IP.

3.1. Assumed Attacker

The network configuration targeted by the proposed method is shown in Figure 3, which is implemented using a packet switch and a server/client/attacker device connected in a one-to-many configuration. This study assumes that an attacker has the following characteristics:

- Connected to the same network as the attack server.
- Can send messages that do not follow the SOME/IP (-SD) specifications.
- No access to the internal information of devices other than the attacker.
- The physical connections of the network, including those of the attacker, cannot be changed.

Attacker communication can be classified into three types: Normal and Anomaly (attack), anomaly (attack) Only, and Man-in-the-Middle, as described in Section 2.4. Table 3 summarizes the characteristics of the communication patterns in these attacks from the perspective of communication between the server and attacker. In normal and anomalous cases, the attacker does not send a (STOP)OFFER SERVICE, a communication management service, but only sends messages for other actual data communications. Specifically, under Normal and Anomaly (attack) conditions, after the server starts providing services, the attacker spoofs as a server and sends a NOTIFICATION and RESPONSE. In a man-in-the-

Table 3: Feature of Spoofing Attacks

Attack Pattern	Server's communication	Attacker's communication
Normal and Anomaly (Attack)	Send all messages.	Send all messages except (STOP) OFFER SERVICE.
Anomaly (Attack) Only	Do not send.	Send all messages.
Man-In-The-Middle	Send all messages.	Send all messages.

middle attack, all messages, including (STOP)OFFER SERVICE, are sent. In Anomaly Only, the server's communication is blocked by the attacker, and as shown in previous research [13], the server only sends an OFFER SERVICE once at startup and does not subsequently send any messages.

Man-in-the-middle and anomaly only attacks share the common characteristic that the attacker and client communicate one-to-one and that both the server and attacker send OFFER SERVICE messages. The only difference between them is whether there is communication between the server and attacker. Because this study focuses on whether OFFER SERVICE messages are sent during service discovery, these two attack patterns have the same characteristics. Therefore, we treat them as man-in-the-middle attacks without distinguishing between them.

3.2. Concept of The Proposal Method

This paper proposes a mitigation method that satisfies the following requirements: The proposed method is intended to be implemented on the switch.

- Req.A) Prevent the Client from using services provided by the attacker in a spoofing attack with a pattern other than an anomaly (attack).
- Req.B) The service can continue even if an anomaly is detected after the client starts using it.
- Req.C) The increased communication latency for anomaly detection and mitigation method is within acceptable limits for communication in an in-vehicle network.
- Req.D) The amount of read-only memory (ROM) and random-access memory (RAM) required to implement the proposed method was within the capacity of the microcontroller used to implement the in-vehicle system.

By imposing restrictions on the design of the systems that comprise the network, we propose a method for detecting the presence of attackers during service discovery at the packet switch and for protecting communications from malicious activities by attackers. In the proposed method, the following restrictions were imposed on the system design:

- Cond.A) Have only one instance per Service ID (only one device to send an OFFER SERVICE per Service ID).
- Cond.B) The Client starts after the time elapses until the server sends the OFFER SERVICE for the first time (starts using the service).

The proposed method does not impose restrictions on the number of devices that can be connected to a packet switch. However, for

Table 4: Internal State of Proposed Method

Internal state	Server's communication	Client's communication
Not offered (Initial state)	Allow communication on all devices.	Allow communication on all devices.
Offered	Allow communication only for devices included in the list.	Allow communication on all devices.
Anomaly	Allow communication only for devices included in the list.	Allow communication only for devices included in the list.

the convenience of explanation and evaluation in this study, we assumed that a maximum of 32 devices can be connected to a single switch.

In the proposed method, the internal states Not-offered (0x00), Offered (0x01), and Anomaly (0x02) shown in Table 4, the list of servers and clients that communicated in the past (communication-permitted device list) are managed by the packet switch, and the transfer of messages is determined based on the internal states and communication-permitted device list. The procedure for updating the internal state and communication-permitted device list is called the “anomaly detection algorithm,” and the procedure for determining whether or not to forward messages according to the internal state and communication-permitted device list is called the “mitigation algorithm.” In the proposed method, an anomaly detection algorithm and a mitigation algorithm are executed to determine whether to forward the received message. The communication-permitted device list can be set as communication-not-permitted (0x00) or communication-permitted (0x01), with the initial value being communication-not-permitted (0x00). The internal state, communication-permitted device list for the server, and communication-permitted devices for the client were managed for each service ID.

In the anomaly detection algorithm, communication-permitted (0x01) is set for devices that communicate while Condition A is satisfied (i.e., Not-offered (0x00) or Offered (0x01) state), and the communication-permitted device list is not updated after detecting communication that does not satisfy Condition A (i.e., Anomaly (0x02) state). Communication is permitted between a server and client with a communication-permitted (0x01) set, regardless of the internal state, thereby achieving Requirement B. As clients cannot begin using the service when only attackers are providing it under Condition B, attackers and clients are never simultaneously granted communication. Thus, the proposed method satisfies Requirement A.

3.3. Anomaly Detection Algorithm

In the anomaly detection algorithm, as shown in the state transition diagram in Figure 4, when the switch receives an OFFER SERVICE for the first time, it transitions from the Not-offered (0x00) state to the Offered (0x01) state and sets the communication-permitted (0x01) for the sending device (port). When the switch receives an OFFER SERVICE from a device that does not have communication-permitted (0x01) set in the Offered (0x01) state, it transitions to the Anomaly (0x02) state. The communication-permitted device list for the servers is updated only when the switch transitions to the Offered (0x01) state. The

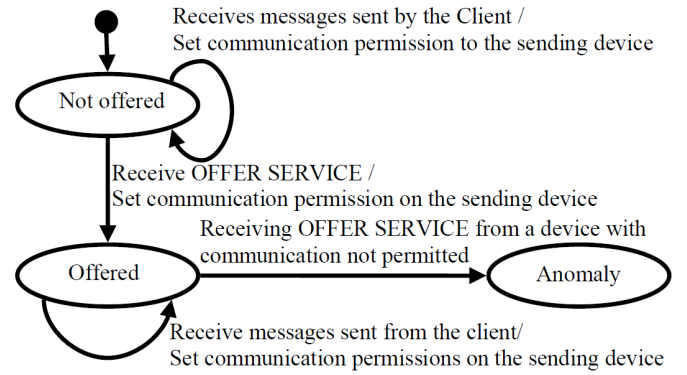


Figure 4: State machine in a proposal method where state transitions are triggered by communication from servers and clients

communication-permitted device list for clients is updated when the switch receives a message from a client in a state other than Anomaly (0x02).

The pseudocodes for the function that implements the anomaly detection algorithm is shown in algorithm 1. The process for determining whether the sender is a server or a client is shown in the pseudocode in algorithm 2 as a separate function. The pseudocode for the function that obtains the service ID targeted by the message from the SOME/IP and SOME/IP-SD headers is shown in algorithm 1. In these functions, the arguments *msg_id* and *msg_type* indicate the Message ID and Type contained in the SOME/IP message header, respectively; the arguments *sd_service_id* and *sd_type* indicate the Service ID and Type contained in the SOME/IP-SD message header, respectively; and the argument *src* indicates the port number to which the sending device is connected.

3.4. Mitigation Algorithm

The mitigation algorithm determines whether to forward a received message based on the internal state and the communication-permitted device list. Specifically, it identifies the internal status of the service ID included in the received message, and the values in the communication-permitted device list corresponding to the ports of the source and destination devices. If the internal status is not an Anomaly (0x02) or if communication-permitted (0x01) was set for both the source and destination devices in the communication-permitted device list, the message is judged to be transferable; otherwise, it is judged to be nontransferable. The pseudocode for the function that implements the mitigation algorithm is shown in algorithm 4. In this function, argument *dst* indicates the port number to which the destination device is connected. Other arguments were presented in Section 3.3.

4. Evaluation

In this section, we demonstrate that the proposed method can fulfill Requirement A-D described in Section 3.2. Requirement A-B, namely anomaly detection accuracy, will be evaluated on actual hardware. Requirement C-D, namely processing capacity and resource usage, will be evaluated on study.

4.1. Actual Machine Evaluation Environment

The evaluation uses a network configuration environment in which three devices—a legitimate server, legitimate client, and

Algorithm 1: Function to detect spoofing attacks

```

srv_lst, clt_lst: 32-bit integer array listing servers and clients
state: 8-bit integer array indicating the communication
permission status assigned to each port
service_id: 16-bit integer indicating the service ID
function ids(msg_id, msg_type, sd_service_id, sd_type, src)
    service_id = get_service_id(msg_id, sd_service_id);
    if sent_by_server(msg_id, msg_type, sd_type) then
        if state[service_id] == 0x00 then
            state[service_id] = 0x01
            srv_lst[service_id] = srv_lst[service_id] | (1 << src)
        else if state[service_id] == 0x01 then
            if ((srv_lst[server_id] >> src) & 0x01) == 0 then
                state[service_id] = 0x02
            end
        end
    else
        if state[service_id] != 0x02 then
            clt_lst[service_id] = clt_lst[service_id] | (1 << src)
        end
    end
end

```

Algorithm 2: Function to determine the sender

```

function sent_by_server (msg_id, msg_type, sd_type)
    if msg_id != 0xFFFFF8100 then
        return (msg_type & 0x82) != 0x00
    else
        return (sd_type & 0x01) != 0x00
    end

```

attacker are connected to an L2 switch that implements the proposed method. In this study, we implemented the proposed method assuming that only three ports were used for the L2 switch. These devices were personal computers running Ubuntu 22.04 and version 3.3.8, of vsomeip [8], a prototype SOME/IP protocol stack.

4.2. Anomaly Detection Rate

In this section, we evaluate the anomaly detection rate of the proposed method and demonstrate that it satisfies Requirement A and Requirement B shown in Section 3.2. The dataset used for evaluation is created by combining three factors: attack patterns, attack start timing, and SOME/IP(-SD) message types. The attack patterns are the two described in Section 3.1: normal and anomaly/man-in-the-middle patterns. Because the order of service provision by the server and service use by the client is determined by Condition B, shown in Section 3.2, only the timing of the attack by the attacker is varied.

The evaluation was performed using the following three patterns, in which communication started in the following order:

- A) Start attack → Start of service provision → Use of service
- B) Start of service provision → Start attack → Use of service
- C) Start of service provision → Use of service → Start attack

The attacker sends six types of messages that can be sent by servers other than those listed in Tables 1 and 2. In a man-in-the-middle attack, an attacker sends an OFFER SERVICE message

Algorithm 3: Function to get the service ID

```

service_id: 16-bit integer indicating the service ID
function get_service_id (msg_id, sd_service_id)
    if msg_id != 0xFFFFF8100 then
        service_id = (msg_id >> 16) & 0xFFFF
    else
        service_id = sd_service_id
    end
    return service_id
end

```

Algorithm 4:

Function to determine whether transfer is possible

```

srv_lst, clt_lst: 32-bit integer array listing servers and clients
state: 8-bit integer array indicating the communication
permission status assigned to each port
service_id: 16-bit integer indicating the service ID
function jdg_send (msg_id, sd_service_id)
    res: Boolean data indicating True (Permitted)/False (Not
Permitted)
    res = True
    if state[service_id] == 0x02 then
        if sent_by_server(msg_id, msg_type, sd_type) then
            res = (((srv_lst[service_id] >> src) & 0x01) != 0)
            and (((clt_lst[service_id] >> dst) & 0x01) != 0)
        else
            res = (((srv_lst[service_id] >> dst) & 0x01) != 0)
            and (((clt_lst[service_id] >> src) & 0x01) != 0)
        end
    end
    return res
end

```

before sending the attack message. The anomaly detection rate of the proposed method was evaluated using 36 sets of data combinations.

Table 5 presents the experimental results using this dataset. Under normal and anomalous conditions, the attacker does not send an OFFER SERVICE. Therefore, the proposed method continues to determine that the attacker is not allowed to communicate. In man-in-the-middle attacks, communication patterns A) and B) produce the same result, but pattern C) produces a different result. In A) and B), the server and attacker send an OFFER SERVICE before the client starts using the service and the proposed method detects an anomaly. If the client begins using the service when an anomaly is detected, the proposed method sets communication-permitted to deny the client, preventing the client from using the service. In C), the server sends the OFFER SERVICE first. Thus, the proposed method sets the communication-permitted for the server. Because the client begins using the service before an anomaly is detected, the proposed method sets the communication-permitted for the client. Subsequently, when the attack begins, the proposed method

Table 5: Result of Anomaly Detection Rate

Attack Pattern	True	False Negative	False Positive
Normal and Anomaly	18 cases	0 case	0 case
Man-In-The-Middle	6 cases	0 case	12 cases

detects the anomaly and sets the communication permission to deny the attacker.

Based on the evaluation results in Table 5, there were no false-negative cases; therefore, the proposed method satisfied Requirement A. The only false-positive cases were communication patterns A) and B) in the man-in-the-middle attacks. These cases occur only before service use begins; thus, the proposed method satisfies Requirement B.

4.3. Processing Time and Resource Usage

In this section, we demonstrate that the proposed method satisfies Requirement C and Requirement D, as shown in Section 3.2, by evaluating the processing time and ROM/RAM usage based on the pseudocode of the proposed method shown in Section 3 and the performance of the processor used in the in-vehicle system. To demonstrate that the proposed method is feasible as an in-vehicle system, we established evaluation criteria based on the specifications of STMicro Stellar P series microcontrollers [17], which are being developed with the implementation of devices that connect multiple networks, such as Gateways and Zone Controllers, in an in-vehicle network and perform packet transfer. The Stellar P series microcontroller supports a 32-bit CPU operating at up to 1.6 GHz (Cortex-R52+ [18]), 2.3 to 8.2 MB of RAM, and 15.5 MB of ROM. While the CPU operating clock and memory size vary by product, this study employs a CPU operating clock of 1.6 GHz, RAM size of 2.3 MB, and ROM size of 15.5 MB as the baseline to demonstrate the feasibility of implementing the proposed method on microcontrollers used in automotive systems.

Table 6 lists the number of instructions contained in the pseudocode for the method described in Section 3. However, function arguments and return values are assumed to be stored in general-purpose registers; therefore, they are excluded from the number of memory accesses. Assuming that bit operations, arithmetic operations, comparison operations, branch instructions, and memory accesses can all be executed in one clock cycle, the number of instructions in the proposed method is 76. Therefore, the processing is completed in 76 clock cycles, or 0.00005[ms] at 1.6 GHz. As explained in Section 2.1, the acceptable communication delay in an in-vehicle network is 0.1[ms]. Therefore, the increase in processing time owing to the proposed method is within the acceptable range, and the proposed method meets Requirement C.

As shown in the pseudocode of the proposed method in Section 3, dedicated memory areas are required as global variables for the communication-permitted device list and the internal state of the server/client. The communication-permitted device list is a 32-bit variable, and the internal state is an array of 65,536 8-bit variables (the maximum number of service IDs supported by SOME/IP). Therefore, the required RAM size for the proposed method was 576 Kbytes per packet switch. However, the stack memory was required regardless of whether the proposed method was implemented; therefore, it was excluded from the evaluation. The global variables used in the proposed method had no initial values (initial value = 0); thus, the ROM area was not used. Therefore, considering only instruction size, if 76 instructions (32-bit) are stored in the ROM, the required ROM size for the proposed method is 304 bytes per packet switch. The usage of RAM and ROM was 24.5% and 0.002%, respectively, which fits within the

Table 6: Number of Instructions for Proposed Method

Function name	Bitwise/ quadrature/ comparison operations	bifurcation process	memory access
Ids	10 times	4 times	22 times
sent by server	5 times	1 time	4 times
get service id	3 times	1 time	4 times
jdg_send	8 times	2 times	12 times

Table 7: The Position of Proposed Method

Method	Anomaly detection rate	Availability	Processing load
IPSec/TLS/DTLS [6]	Excellent	Excellent	Poor
IDS for SOME/IP [7]	Good	Good	Excellent
Proposed method	Excellent	Good	Excellent

capacity of the microcontroller considered in this study. Therefore, the proposed method satisfies Requirement D.

5. Consideration

In this section, we discuss the following three points based on the evaluation results:

- Comparison between the proposed method and previous studies.
- False positives during man-in-the-middle attacks.
- Application to large-scale networks with multiple switches.

Table 7 presents the results of the comparison between the proposed method and those of previous studies. The anomaly detection rate indicates the detection rate of spoofing attacks, which determines whether normal communication can be continued when a spoofing attack, including false positives, occurs, and the processing load indicates the CPU load and network load for anomaly detection. The existing IDS [7] cannot detect all spoofing attacks; however, the proposed method can detect all spoofing attacks. These methods show differences in detection rates for Anomaly Only attacks and Man-in-the-middle attacks where payloads and communication timing are normal. Similar to the IDS, the proposed method generates false positives, and there are cases where normal communication and spoofing attacks cannot be correctly distinguished, thereby preventing the use of the target service. This is a disadvantage compared with methods that employ IPSec or TLS/DTLS. By contrast, the proposed method was implemented using a simple algorithm with fewer than 100 operations, thereby resolving communication delay issues that are problematic in IPSec or TLS/DTLS. The proposed method is considered superior to existing methods in terms of availability. Subsequently, the impact of availability constraints was examined.

As shown in Section 4.2, false positives occur in man-in-the-middle attacks; if an attacker launches an attack before the client starts using the service, the client would not use the service, resulting in reduced availability. However, if the client detects an anomaly after starting to use the service, it can continue using the service. In automobiles, passenger safety is the top priority; therefore, availability during operation (i.e., while using the service) should be guaranteed. If the possibility of reduced availability is detected before operation (i.e., before starting to use the service), passengers should be notified of the anomaly to ensure safety and prevent operation. In the proposed method,

safety is prioritized over availability by preventing clients from accessing services if a potential spoofing attack is detected before service initiation.

Next, we discuss the application of the proposed method to networks that contain multiple switches, similar to actual in-vehicle systems. In SOME/IP-SD, the OFFER SERVICE is multicast to all devices using SOME/IP. Client devices utilize the target service after receiving the OFFER SERVICE. Consequently, attackers must also send the OFFER SERVICE to client devices. Regardless of the network configuration, packet switches connected to client devices receive both the legitimate and malicious OFFER SERVICE messages. By deploying the proposed method on all packet switches within the network, spoofing attacks can be detected in the same manner as in a single-switch configuration. However, since all packet switches must maintain the same internal state and communication-permitted device list, resource utilization becomes inefficient, raising concerns that the implementation cost may exceed that of a system monitored by a device [7]. If necessary, This method removes condition A and allows multiple instances per service ID. The designer must configure the number of instances allowed, and an anomaly will only be flagged if that number is exceeded.

6. Conclusion

In this study, we propose a mitigation method that detects server spoofing attacks during service discovery in SOME/IP networks packet switching in a network using and discards malicious messages. For the attack evaluation, 36 attack patterns, including man-in-the-middle attacks, were classified, constructed, and verified using actual devices. The proposed method can detect spoofing attacks in all patterns, and in 24 patterns, it can distinguish between normal communication and attacks, allowing for continuous service accessibility. Although it cannot distinguish among the remaining 12 patterns, security can be maintained by blocking the initial communication. The proposed method can detect attacks during the service discovery stage, thereby enabling safe communication blocking. In addition, it successfully mitigates man-in-the-middle attacks while remaining significantly lighter than encryption-based approaches.

Future work will explore integration with cryptographic mechanisms and complementary intrusion detection methods, as well as investigate applicability to other service-oriented protocols such as DDS. This research demonstrates that packet switches can respond to vulnerabilities to man-in-the-middle attacks by supporting dynamic service discovery with SOME/IP, contributing to the introduction of service-oriented architectures in automobiles.

Conflict of Interest

The authors declare no conflict of interest.

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Beyond Fitness: Revolutionary Exercise Tracker Combining Pose Recognition with Heart Rate Monitoring using Remote Photoplethysmography (rPPG)

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ABSTRACT

Heart rate (HR) is a critical indicator in fitness monitoring, athletic performance evaluation, and injury prevention. However, traditional motion-sensitive wearable devices are highly susceptible to movement artifacts, which degrade measurement accuracy during physical activity. Remote photoplethysmography (rPPG) offers a non-contact alternative for HR measurement, though it too remains sensitive to motion. This study proposes a novel framework that integrates MediaPipe's BlazePose for bicep-curl motion tracking with rPPG-based real-time HR monitoring. The system leverages pose-estimation data to accurately track arm movements and applies advanced signal-processing techniques to suppress motion-induced noise in the rPPG signal, thereby enhancing HR estimation accuracy. The extracted signal is pre-processed using filtered, normalized, and transformed from the time domain to the frequency domain, enabling reliable HR extraction during continuous exercise. The green color channel is selected for BPM estimation, as it exhibits a strong correlation with cardiac pulse signals. Experimental results demonstrate that motion-corrected rPPG can effectively support real-time, non-contact HR monitoring during exercise. This approach shows strong potential as a platform for personalized fitness coaching and AI-based workout optimization. Future work will focus on extending the system to support multi-exercise tracking and continuous performance monitoring. The proposed framework enhances user safety by enabling early detection of abnormal heart rate patterns during exercise, such as tachycardia or irregular fluctuations caused by overexertion. By correlating physiological signals with biomechanical movement data, the system can adapt workout intensity in real time, ensuring exercises remain within safe cardiovascular limits. This closed-loop feedback mechanism supports individualized training plans tailored to the user's fitness level and physiological response.

1. Introduction

The heart rate (HR) is an important physiological metric that reflects cardiovascular health, exercise intensity, and stress levels. It is used for fitness monitoring, medical diagnostics, and performance tracking [1]. Conventional HR measurement techniques, such as electrocardiography (ECG) [2] and photoplethysmography (PPG) [1] sensors, involve direct skin contact, which leads to discomfort and motion artifacts during dynamic activity. Wearable devices, although ubiquitously

employed, have problems with accuracy in dynamic movement, limiting their real-time exercise tracking reliability.

To overcome these limitations, remote photoplethysmography (rPPG) has emerged as a non-contact alternative for HR measurement, extracting heart rate from subtle skin color variations in video footage [3], [4]. rPPG eliminates the need for physical sensors, making it suitable for continuous monitoring in fitness applications. Remote photoplethysmography employs camera hardware that detects

minor changes in color due to the flow of blood, thus providing it with significant physiological quantities that include heart rate. This occurs during either the systolic phase, where higher oxygenated blood causes red coloration of the area involved, or the diastolic phase, whereby the red color is reduced in the area. This is essential for the functionality of rPPG. However, whereas temperature, light wavelength, and breathing all affect the normal PPG readings, they have little effect on rPPG readings, along with skin tone differences that introduce significant noise in rPPG-based HR estimation, reducing its accuracy [5]. Although green light is sensitive to volume variations of blood because it travels a shorter distance inside the skin than red or infrared light, it is relatively insensitive to motion in either PPG or rPPG, making it effective for real-time heart rate monitoring [9], [7].

Simultaneously, pose estimation methods, including DeepPose [8], Convolutional Pose Machines [9], OpenPose [10], and BlazePose [11], [12], have improved real-time exercise monitoring by precisely identifying body movement and joint locations. Of these, MediaPipe BlazePose is designed for mobile and embedded platforms and is thus particularly suited for real-time fitness monitoring [13]. Nevertheless, although pose estimation offers precise movement analysis, it does not include physiological information, such as HR monitoring.

This research introduces a new method that combines BlazePose pose estimation with rPPG real-time HR monitoring. Arm movement in exercises such as bicep curls is monitored using BlazePose from MediaPipe, and signal filtering algorithms are employed to mitigate rPPG noise to further enhance HR estimation accuracy. The Fast Fourier Transform (FFT) converts the discrete-time signal to the frequency domain, and finally, the magnitude of the signal is determined, which usually corresponds to the heart rate.

A contactless heart rate measurement system using remote photoplethysmography (rPPG) and body pose estimation was presented in this study. The system can process real-time video streams to determine a person's heart rate from skin color changes while simultaneously following the person's body movement. Instead of traditional wearable sensors, this novel approach allows HR monitoring that is comfortable and easy to use because it is non-invasive.

Using MediaPipe BlazePose for pose tracking and rPPG for signal extraction, the system can produce an accurate real-time HR estimation. Therefore, the subject carried out exercises, such as bicep curls, at an optimal camera distance of 1 meter under fixed light conditions. The results show the reps for the bicep curl along with heart rate in the form of BPM (beats per minute). The average heart rate was determined every minute, which represented the BPM. In addition, the system shows an alert message when the BPM surpasses the safe range of the BPM. OpenCV and Python were used in this implementation, which included computer vision-based tracking, delivering better HR estimation.

The remainder of this article is organized as follows. In related work, we describe the previous work, which has two parts: A. pose estimation algorithms and B. research on PPG and rPPG. The Proposed Method presents the methodology employed, including decoding BlazePose, along with the techniques applied

for rPPG. Experimental Results describe the experimental setup implementation details and needs for performance evaluation. Finally, the Conclusion and Future Scope conclude the paper with a discussion of Future Work.

2. Related Work

2.1. Pose Estimation Algorithms

Recent state-of-the-art pose estimation has provided progress in both single-pose and multi-pose estimation. While single-pose estimation is also an effective way of tracking an individual's movements, multi-pose estimation, on the other hand, is a non-negotiable point for real-world situations where many people are involved, for example, sports, fitness exercises, or crowd monitoring. The task is to successfully capture all key points that are visible and reduce occlusions. The challenge lies in maintaining precision despite rapid movements, occlusions, and variations in lighting or viewpoint.

In [14], The authors have used the blaze-pose to identify the behaviour of the driver and raise an alarm, if he is found drunk or sleepy to avoid accidents.

In [8], the author proposed DeepPose, which is a deep-learning-based approach for human pose estimation. Deep Pose is a deep neural network (DNN)-based regression algorithm for human pose estimation that encodes body joints as pose vectors and normalizes them relative to a bounding box for consistency. The Convolutional Neural Networks CNN specifically AlexNet, predict the joint coordinates directly from the image, process the rectified linear units (ReLU), and locally normalize the responses (LRN) for feature extraction. A sequence of regressors enhances each other by iteratively correcting inference errors. When it comes down to speed, DeepPose is not the case for improving the process speed, neglecting real-time fitness tracking and motion analysis software.

In [9], the author developed Convolutional Pose Machines, a multi-stage CNN that aims to iteratively refine human pose estimation by exploiting contextual information and spatial relationships. The entire process begins with feature extraction; here, convolutional layers examine the input image to derive pose-related features of vital importance. The computed heat maps provide probabilities for each of the body's key points. During training, intermediate supervision is reinforced as predicted heatmaps are compared with ground truths, which allows the model to learn stepwise. Through such iterative refinement, the CPM model improves predictions through the application of probabilistic heat maps, thus resulting in more accurate localization of the joints. The final pose estimation comes from the precise localization of key points with the aid of finer heatmaps. In [9], the use of multiple stages and intermediate supervision allows CPMs to better capture occlusions and enhance the accuracy of pose estimation. However, the added complexity of multi-stage processing also makes real-time applications challenging. Nevertheless, CPMs gave a major push in the progress towards deep learning-based human pose estimation that ushered many lines of follow-up research to further improve body tracking systems.

In [10], the author introduced OpenPose, a real-time multi-person posture estimation framework to track and identify important human body points in a single image. By initially recognizing individual body parts and connecting them to create a complete pose, OpenPose employs a bottom-up methodology. To detect body parts, a convolutional neural network (CNN) with a two-stage architecture is used. The first stage predicts confidence maps, whereas the second stage estimates the Part Affinity Fields (PAFs) to create connections between parts. The framework uses a VGG-19 network to extract features and then a custom network to iteratively refine predictions.

In [11], the author presented BlazePose, an efficient and lightweight pose estimation model optimized for real-time use on mobile devices. It builds on MobileNetV1 and uses depth-wise separable convolutions to reduce computational overhead [13]. BlazePose is better suited for tracking a single individual and offers more detailed movement analysis. In total, 33 important points were supported. The two-stage pipeline begins with a person's detection and joint location approximations. Subsequently, pose estimation was improved using regression-based approaches. BlazePose is particularly helpful for real-time applications, such as fitness tracking and posture correction, but it has a disadvantage in that it cannot track multiple persons at once.

The intersection over union (IOU), which increases bounding box accuracy, and non-maximum suppression (NMS), which filters redundant key-point detections, further boost BlazePose's efficiency. It is a better framework for real-time pose estimation because it does not undergo iterative refinement, which delays the extraction of correct joint points. In addition, BlazePose uses a depth-wise Separable CNN, which increases the efficiency and reduces the computation cost, which is further explained in the proposed method. BlazePose is a powerful substitute for AI-driven fitness apps because it runs 25–75 times faster on mobile CPUs than its counterparts. The lack of multi-person tracking is a significant drawback. The proposed method captures the joints of a single individual in real-time, and BlazePose is considered a better choice.

2.2. Heart Rate Estimation using PPG and rPPG

Photoplethysmography (PPG), a popular optical method for tracking heart rate, detects changes in light absorption or reflection via the skin to determine blood volume changes. A photodetector measures the reflected or transmitted light according to the blood volume in the lighted region, and PPG sensors typically use red, green, or infrared light to record arterial blood volume variations [5]. PPG is less dependable in dynamic situations such as exercise because it is greatly impacted by motion aberrations, ambient light interference, and skin tone fluctuations, even if it is very accurate in static situations such as the supine position with an error margin of approximately 5% [15].

Remote photoplethysmography (rPPG) is a contactless alternative to traditional PPG for measuring physiological signals such as blood volume changes and heart rate. Unlike conventional PPG, which requires direct skin contact with optical sensors, rPPG analyzes subtle color changes in the facial skin caused by blood flow using video-based techniques [8]. This technology has gained significant interest in telemedicine, fitness tracking, and

healthcare owing to its non-invasive nature. However, real-world challenges such as variations in skin tone, lighting conditions, and motion artifacts still hinder its accuracy. This section explores the key advancements in rPPG research, focusing on methods to enhance real-time performance, address environmental challenges, and improve signal quality.

In [16], the author proposed a procedure for extracting the blood volume pulse (BVP) waveform using signal processing, face detection, and source signal reconstruction based on the camera-recorded video signals. ROI selection followed by the selection of the green channel was made in the RGB signal, then spatially averaging the channel, processing the average signal through an eleven-point moving-average filter that smoothed it out, and then removing the trend and standardizing it. Independent Component Analysis (ICA) was used to find the most vital component by decomposing all the signals into independent components and selecting the component with the maximum peak in the power spectrum. The BVP waveform was deconvolved using five frequency extraction techniques: Discrete Time Fourier Transform (DTFT), Discrete Short-Time Fourier Transform (STFT), Discrete Wavelet Transform (DWT), Peak Counting, and Mean Value of Inter-beat Interval (IBI). The findings of experiments on 15 participants in both resting and post-exercise states, verified by a wearable pulse sensor, demonstrated that IBI performed better than all other methods in HR accuracy.

In [17], the author proposed a continuous HR measurement method that employs a video of the face, focusing on the cheek region as a stable ROI. RGB signals are sent to the chrominance space to be filtered and analyzed using the FFT. A temporal HR distribution model was introduced to increase stability, while the median fusion of sub-ROIs was employed to enhance accuracy.

In [18], the ascertained heart rates were evaluated by evaluating various types of skin over time. They relied on face detection with Haar cascades for forehead tracking of the entire video. Each frame representing the average pixel intensity within the ROI was processed using FFT to obtain heart rate frequencies (0.5–3 Hz) with an error of 3%, practically remaining constant in the case of various skin tones. Accuracy was confirmed through testing and comparing the Ambiotex and Fitbit Alta HR wearable devices.

In [19], the researchers proposed a real-time heart rate measurement framework that integrates Viola-Jones face detection, tracking, and skin detection to robustly extract the region of interest (ROI) from video frames. Linear Discriminant Analysis reduces dimensionality to enhance the quality of the green-channel plethysmographic signals. Heart rate frequencies (0.7–4 Hz) were isolated using a Hamming window-based band-pass filter, followed by spectral analysis to extract the peak heart rate.

In [20], the author demonstrated that heart rate can be estimated from facial videos by detecting the face as a Region of Interest ROI using the HSV color space. The extracted face was then decomposed into RGB channels with an average pixel intensity. Signal processing was implemented to enhance the signal quality using baseline removal and band-pass filtering. Cross-correlation is applied between two signals to measure their similarity and identify shared periodic components, thereby

reducing the uncorrelated noise. Independent Component Analysis was employed for signal separation, and the dominant frequency corresponded to the heart rate identified using the Fast Fourier Transform.

In [21], the author proposed an algorithm that turned out to be a deliberately improved way to measure heart rate on fitness videos using precise motion compensation that used optical flow and Viola-Jones for face detection. Illumination changes and heart rate isolation were performed by using a bandpass filter. The proposed method demonstrated Root Mean Squared Error RMSE (1.1 bpm) and a relative error (0.58%). However, video-based heart rate monitoring methods typically perform poorly during strenuous exercises of high-motion-induced motion, where rapid movements and partial or total body occlusions cause artifacts that are difficult to remove. Adaptive filtering or motion-aware segmentation can be realized in the future to eliminate these obstacles.

In the proposed work, a combination of a Butterworth bandpass filter and Fast Fourier Transform is employed to enhance the signal quality and extract meaningful features. The Bandpass filter discards unwanted noise, allowing only the accepted frequencies (0.7 Hz – 3.0 Hz). The filtered signal is converted into the frequency domain from the time domain by Fast Fourier transform, allowing for easier feature extraction and identification of dominant frequency components. For ICA, PCA, and LDA, which focus predominantly on signal separation or dimensionality reduction rather than on frequency analysis, FFT analyzes frequency patterns with a high resolution for near-signal patterns that are challenging to evaluate. The Butterworth Bandpass filter and FFT enhance the efficiency and accuracy of the model, thereby rendering it robust for signal processing and pattern recognition.

3. Proposed Method

3.1. BlazePose from Mediapipe

Media Pipe is a powerful and versatile framework for building ML solutions. Through the prebuilt component "BlazePose," Media Pipe offers a complete solution for estimating human poses. The BlazePose was designed for efficient and accurate pose estimation in real-time applications. The BlazePose model is the most basic and supports 33 key points. Media Pipe Pose Estimation uses a two-stage pipeline to estimate the 3D pose of a person in an image or a video frame. In the first stage, a Robust Pose Detection model is used to detect the presence of a person in the frame and estimate the approximate rough location of the person's body joints. In the second stage, a Pose Estimation model is used to refine the location of a person's body joints and estimate the 3D pose of the person [11], [12]. The BlazePose training dataset consists of 60K images with a single or few people in common poses and 25K images with a single person performing fitness exercises.

The BlazePose from MediaPipe offers a pre-trained pose estimation model. A real-time compact pose estimation algorithm was created by Google. It operates effectively across platforms, including web applications and mobile devices. For joint detection and regression, BlazePose employs a variant of the Single-Shot Multi-Box Detector (SSD) and Part Affinity Fields

(PAFs) to record the connections between body joints. The BlazePose can estimate the 2D connections and locations of numerous body joints in real-time.

BlazePose in MediaPipe uses a CNN architecture based on the MobileNetV1 architecture [13]. For effective inference on mobile and embedded devices, MobileNetV1 is a compact CNN architecture. To reduce computational complexity while maintaining a reasonable accuracy level, it uses depth-wise separable and pointwise convolutions. The BlazePose key-point topology is illustrated in Figure 1. The Figure 1 shows 33 anatomical points used by BlazePose for pose estimation, Note. Adapted from [12].

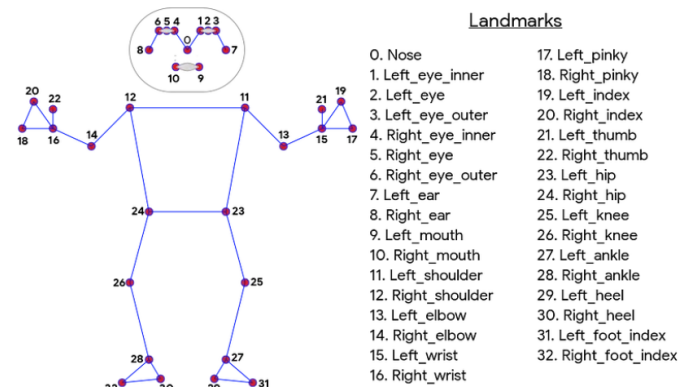


Figure 1: BlazePose Key-Points Topology

3.1.1. Model Architecture and Pipeline Design

As shown in Figure 2, BlazePose uses a detector-tracker architecture for inference, which exhibits excellent real-time performance for tasks such as hand landmark prediction and dense face landmark prediction. A pose tracker network follows a lightweight body-pose detector in the pipeline. The tracker predicts the key-point coordinates, the person's presence in the current frame, and the refined region of interest for the current frame. A flow chart in figure 2, illustrates the two-stage pipeline of BlazePose, with key-point detection followed by refinement of the key-point position.

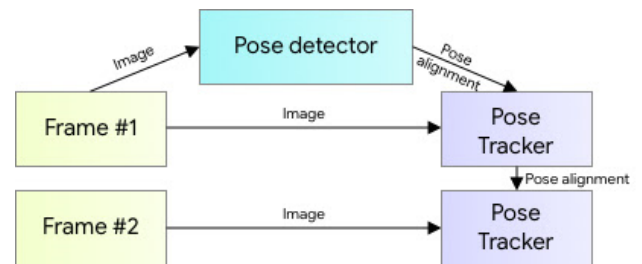


Figure 2: Human pose estimation pipeline overview [9]

BlazePose Detector: The BlazePose Detector locates the body joints and calculates the initial pose. It uses the Single-Shot Multi-Box Detector (SSD) framework, a well-liked object-detection system. In real-time object detection, SSDs are renowned for their effectiveness and efficiency. The BlazePose Detector extract features by processing an input image through several convolutional layers. Regression and detection are performed using these features. The network estimates the

bounding boxes enclosing each body joint while forecasting the confidence scores for the presence of each joint. The BlazePose Detector runs an input image through multiple convolutional layers to extract information. These features were then used for both detection and regression. The network predicts confidence scores for the existence of each bodily joint and calculates the bounding boxes surrounding each joint.

The Single Shot Multi-Box Detector (SSD) framework uses a Convolutional Neural Network (CNN) to estimate the pose in an image. The CNN creates feature maps with default boxes for body joints. Each box is classified and regression-trained, with the CNN forecasting confidence scores and regression offsets. A non-maximum suppression algorithm eliminates overlapping detections and results in a clear set of pose estimations, as illustrated in Figure 4.

3.2. Non-maximum Suppression

Input: Lists of proposal boxes B , matching confidence scores S , and overlap threshold N are inputs. The anchor and proposal boxes were identical. From Figure 3, the Intersection Over Union (IOU) is a method used to measure the overlap between the two proposals.

Output: A filtered list of D 's proposals.

- Choose the proposal with the highest confidence score, move it out of B , and include it in List D of the final proposals. D is initially empty.
- At this point, we compare this proposal to all others and determine its Intersection over Union (IOU). Consider the proposal out of B if the IOU exceeds the threshold N .
- Select the proposal again from B with the highest degree of confidence, remove it from B , and add it to D .
- Compute the IOU of this proposal with all of the proposals in B once more, and then cross out the boxes whose IOU is greater than the threshold.
- This process was repeated until no additional proposals remained.

An illustration shows in figure 3, how the Intersection over Union (IOU), which is used to determine object detection accuracy, is computed by dividing the area that two bounding boxes overlap by the total area that both boxes cover.

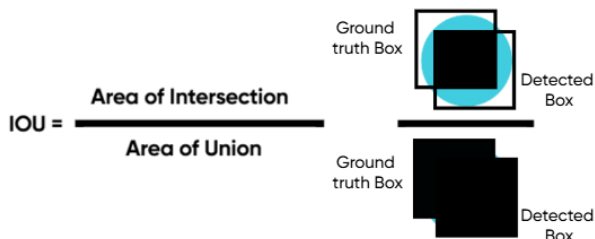


Figure 3: Intersection Over Union.

The figure 4, demonstrates how non-maximum suppression filters overlapping bounding boxes and considers only the most confident predictions.

Without Non Max Suppression With Non Max Suppression



Figure 4: Non-Max Suppression.

The BlazePose Refiner enhances the initial pose estimates from the BlazePose Detector using Part Affinity Fields (PAFs) to calculate the relationships between body joints. These 2D vector fields store information regarding the direction and strength of the connections between the joints. BlazePose can infer the relative positions and orientations of joints and build the entire pose estimation by estimating these connections. With the initial joint detection, the BlazePose Refiner predicts the PAFs for joint connections, resulting in more precise and thorough pose estimations.

The CNN architecture in BlazePose uses heatmap and offset losses to manage lightweight embedding, which represents the presence and location of body joints in the heat maps. Heatmap loss helps supervise lightweight embedding, whereas offset loss refines joint positions by predicting the offset values. During inference, the output layers associated with the heatmap and offset were removed, resulting in only the regression encoder network being used. This network takes lightweight embedding as input and performs regression to predict precise joint positions based on the embedded information. Figure 5 illustrates the BlazePose CNN architecture, highlighting heatmaps and offsets for joint localization.

3.3. BlazePose CNN Architecture.

Block diagram of the BlazePose model architecture in figure 5, showing layers for feature extraction, regression, and pose refinement.

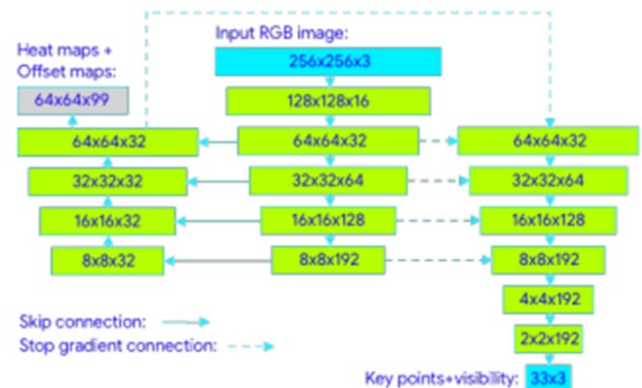


Figure 5: BlazePose CNN Architecture [12]

3.3.1. How Depth-wise Separable Convolution is better than Conventional Convolution Neural Networks?

Figure 6 represents the conventional convolutional neural network, where a filter or kernel convolves the input data to produce a feature map. A convolutional neural network uses an RGB image with dimensions of $6 \times 6 \times 3$ for the height, width, and channels, respectively. There must be an equal number of channels in the filter and the image. The result is a 4×4 image. Note that the final image is now $4 \times 4 \times 1$ instead of $4 \times 4 \times 3$.

Output Dimension: $(n-f+2p) / s + 1$, where p and s are the padding and stride, respectively.

Input Dimension: n

Kernel Dimension: f

The kernel size was $3 \times 3 \times 3$, representing the height, width, and number of channels. The kernel cube of size $3 \times 3 \times 3$ slides the RGB image, and in each move, it covers the nine cells of each RGB image. After the entire traversal, the extracted feature has a size of 4×4 . Figure 6 is illustrating a 2D convolution applied to a $6 \times 6 \times 3$ RGB image with a $3 \times 3 \times 3$ kernel to generate a 4×4 output feature map.

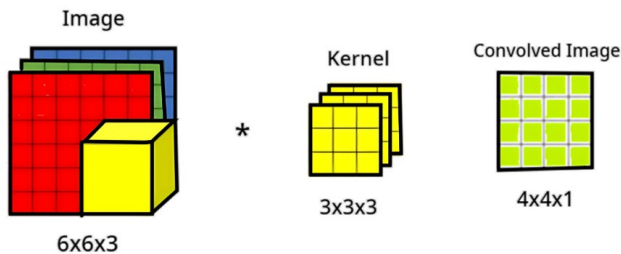


Figure 6: Conventional Convolution on an RGB Image.

3.3.2. Depth-wise Separable Convolution Neural Network

The architecture of a Depth-wise Separable Convolutional Neural Network consists of d Depth-wise and Point-wise Convolutional layers [13].

3.3.3. Pointwise Convolution

The pointwise convolution, 1×1 convolution, is the second stage. Figure 7 shows that the feature maps generated from the depth-wise convolution are subjected to a 1×1 filter. The bottleneck layer, that is, pointwise convolution, increases the number of channels while maintaining the same spatial dimensions. Pointwise convolution, which employs a 1×1 filter, enables linear combinations of channels, allowing the model to learn intricate correlations between features.

3.3.4. Depth-wise Convolution

The depth-wise convolution is the initial phase in depth-wise separable convolution. In Figure 7, depth-wise convolution applies a separate 3×3 filter to each independent input channel, unlike typical convolutions that employ a single 3×3 (generally $n \times n$) filter across all input channels. This implies that each input channel is analysed independently to capture the spatial information contained within that channel. Depth-wise separable

convolution, which splits conventional convolution into two phases to reduce computing complexity, is illustrated. First, depth-wise convolution applies different $k \times k \times 1$ filters to each input channel (red, green, and blue) to maintain spatial properties. Then, point-wise convolution merges them across channels using $1 \times 1 \times C$ filters, where C is the number of output channels in the final feature map.

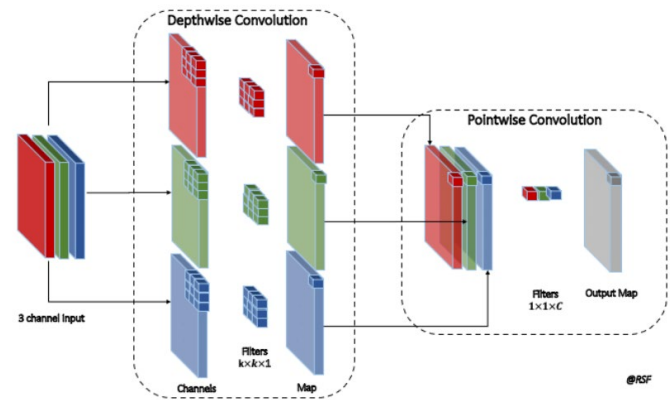


Figure 7: Depth-Wise and Point-Wise Convolutions [22].

3.4. Conventional CNN vs Depth-wise Separable CNN

Figure 6 shows an input RGB image with three input channels of $6 \times 6 \times 3$ and a kernel size (f) of $3 \times 3 \times 3$ in a conventional convolutional neural network that generates a feature map of 4×4 .

Input Image size(n): (6,6)

Kernel size(f): (3,3)

Number of Channels: 3

Output Image size: $(n-f+2p)/s + 1$, where the padding = 0 and stride = 1

Output Image size: $(6-3+2 \times 0)/1 + 1 = 3+1 = 4$

For one tensor, there are $(3 \times 3 \times 3) \times 16$, i.e., 27×16 , i.e., 432 tensor operations. For 256 such feature maps, there are $27 \times 16 \times 256$, i.e., 110592 operations that take place.

For the same dimensions of the input image of $6 \times 6 \times 3$, in a depth-wise separable Convolutional Neural Network, a depth-wise convolution is performed on each $6 \times 6 \times 1$ with a filter size (k) of $3 \times 3 \times 1$ each. Because the number of input channels is three, an output image of $4 \times 4 \times 3$ is obtained.

The number of tensor operations in a depth-wise separable convolutional neural network for one tensor is $(3 \times 3 \times 3) \times 16$, i.e., 432.

The output of the Depth-wise separable Convolutional Neural Network was $4 \times 4 \times 3$. For 256 such feature maps, the number of operations required is $(4 \times 4 \times 3) \times 256$, i.e., 12288. In total, the number of operations for 256 tensors is $432 + 12288$, i.e., 12,720, which is far less than 110592. The output after the pointwise convolution is $4 \times 4 \times 1$ by applying a filter of $1 \times 1 \times 3$ to the output of the depth-wise convolution $4 \times 4 \times 3$.

Table 1: CNN vs Depth-wise Separable CNN

Aspects	Conventional CNN	Depth-wise Separable CNN
Input Image Size (n)	(6,6)	(6,6)
Kernel Size (f)	(3,3)	(3,3)
Number of Channels	3	3
Padding	0	0
Stride	1	1
Output Image Size (per channel)	(4, 4)	(4, 4)
Number of Tensors	256	256
Operations on Tensor	(3x3x3) x 16 = 432	(3x3x3) x 16 = 432
Total Operations on 256 Tensors	110,592	12,720
Layers Included	Convolutional, Pooling, Fully Connected	Depth-wise Convolution, Point-wise Convolution
Operation Philosophy	Single filter applied across all channels	Different filters for each channel (Depth-wise), Linear combinations (Point-wise)
Efficiency Benefit	Standard performance, higher computation	Reduced computation, maintains performance with lower computation
Parameter Efficiency	Higher parameter counts per channel	Lower parameter counts per channel
Computational Efficiency	Lower efficiency due to redundant computation	Higher computational efficiency by applying depth-wise and point-wise separately
Execution Speed	Slower due to higher computations	Faster due to reduced computations
Feature Extraction	Channels combined for feature extraction	Channels are independently extracted and combined later (Depth-wise)

The Depth-wise Separable Convolution Neural Network performs Depth-wise and Pointwise Convolutions separately, reducing computational complexity and improving efficiency. The differences between a conventional convolutional neural network and a depth-wise separable convolutional neural network, based on various aspects, are demonstrated in Table 1. The parameters in Table 1 are based on the example described in Figures 6 and 7.

3.5. Remote Photoplethysmography (rPPG)

Remote photoplethysmography uses camera hardware to measure subtle color changes caused by blood flow, providing important physiological data such as heart rate. This occurs either during the diastolic phase, when the red color shrinks in the affected area, or during the systolic phase, when increased

oxygenated blood causes the area to become red. An image of the RGB channel was captured. In the proposed methodology, the green channel is used to capture the heart rate frequency, as it corresponds highly to the heart rate signals [16], [8].

3.6. Face Detection and ROI Selection

The two computer vision technologies used in this study are (1) face identification and (2) pose estimation with MediaPipe's BlazePose. The purpose of the experiment was to measure the heart rate (measured in beats per minute) while engaging in a simple bicep curl exercise. OpenCV uses Haar cascades, first presented in [23], to implement face detection. With varying weights, the identified faces were separated into three regions of interest (ROIs). The first ROI was assigned the highest weight of 0.5, which spans from the forehead to the eyes. A weight of 0.3 is given to the second ROI, which covers the nose and cheeks, and 0.2 is given to the second ROI and to the third ROI, which extends from the upper lip to the chin. Because it is more likely to move than the forehead, which remains mostly stationary, the lower portion of the face is given less weight. During the bicep curl exercise, arm movements were tracked using the MediaPipe's BlazePose estimate. The elbow flexion angle was calculated using important landmarks of the wrist, elbow, and shoulder. The up and down phases of the movement are determined by the system based on the angle. When the change from the down phase to the up phase was observed, a repetition was recorded.

3.7. Heart Rate Estimation

The methodology consists of three key stages: (1) Signal Preprocessing, (2) Frequency Analysis, and (3) Heart Rate Computation.

3.8. Signal Preprocessing

A Butterworth bandpass filter was used for signal preprocessing to allow frequencies within a specific range while attenuating frequencies outside of this range [24]. The Butterworth filter is preferred because it has a maximum flat frequency response in the passband, resulting in minimal signal distortion. It is based on the Nyquist theorem (1), which asserts that a continuous signal may be reliably reconstructed if sampled at a rate at least twice that of the highest frequency component of the signal.

$$f_N = \frac{f_s}{2} \quad (1)$$

where f_N is the Nyquist frequency and f_s is the sampling rate in hertz.

According to the Nyquist rule (2), the sampling rate must be at least twice the maximum frequency component f_{max} of the signal, given by (2)

$$f_s \geq 2f_{max} \quad (2)$$

This approach ensures that all of the frequency components of the signal are captured without losing information. For example, if a signal oscillates at a maximum frequency of 10 Hz, the minimum required sampling rate is calculated as in (3)

$$f_s \geq 2 \times 10 = 20\text{Hz} \quad (3)$$

Thus, at least 20 samples per second must be captured to accurately reconstruct a 10-Hz signal. This technique ensures effective filtering and signal integrity while limiting sampling artifacts and distortions.

After calculating the sampling rate, the frequencies were normalized by dividing by the low-cut f_L and high-cut f_H frequencies based on the Nyquist frequency. This ensures that the filter performs correctly in the normalized frequency domain. The normalized frequencies were calculated using (5).

$$f'_L = \frac{f_L}{f_N} (4), f'_H = \frac{f_H}{f_N} (5)$$

f'_L and f'_H are the normalized low-cut and high-cut frequencies, respectively.

Butterworth remove unwanted frequencies and preserve the desired frequencies. The order in the Butterworth filter specifies the steepness of the transition between the bandpass and stopbands. The Butterworth filter eliminates undesirable frequencies while retaining permitted frequencies. The filter order controls the steepness of the transition between the passband and the stopband. In the proposed model, the frequency range considered is between 0.7 Hz to 3.0 Hz, which highly corresponds to the heart rate frequency in Hz [25]. The Butterworth filter transfer function $H(s)$ is represented as in (6), where s represents the complex frequency and n denotes the order of the filter, which indicates how strong the filter is or determines the frequency to allow. ω_c represents the cut-off frequency.

$$H(s) = \frac{1}{\sqrt{1 + \left(\frac{s}{\omega_c}\right)^{2n}}} (6)$$

For instance, if the cutoff frequency is 1.0 Hz, consider two scenarios: 1. A signal frequency below the cutoff of 0.5 Hz, 2. A signal frequency above the cutoff of 5.0 Hz.

For the frequency $f = 0.5$ Hz, with order $n = 2$ gives the $H(s) \cong 0.970$. This implies that 97% of the signal passes through, and the filter attenuates the signal by 3%. For the cutoff frequency $f = 1.0$ Hz, with order $n = 2$ computes the $H(s) \cong 0.707$. This indicates that 70% of the signal strength remains, and the filter attenuates the signal by 30%. Here, the $f = 5.0$ Hz, with order $n = 2$ calculates the $H(s) \cong 0.040$, which says only 4% of the signal passes through.

Digital filters are essential for selectively permitting or suppressing particular frequency components of signals during signal processing. The function of a filter is determined by its coefficients, which define the stop-band (attenuated frequencies) and band-pass (permitted frequencies). Usually, a difference equation of the following type is used to apply a digital filter, where $y[n]$ calculated using (7), is the output signal at the timestep n and $x[n]$ is the input signal at the time n . b and a represent the set of coefficients that determine the influence of the input signal $x[n]$ on the output signal $y[n]$ and the impact of previous output values $y[n-1]$ on the current output $y[n]$ respectively.

$$y[n] = b_0x[n] + b_1x[n-1] + b_2x[n-2] + \dots - a_1y[n-1] - a_2y[n-2] - \dots (7)$$

The filter was applied twice, and phase shifts were introduced in the forward direction. The phase shifts introduced in the forward pass were eliminated when the filter was used again in the reverse direction. This technique, called zero-phase filtering, successfully eliminates noise while maintaining the timing of the important signal properties.

3.9. Frequency Analysis: Frequency Resolution and Sampling

The Fast Fourier Transform (FFT) is utilized for the frequency analysis to convert the time domain to the frequency domain [26]. The resolution of the FFT is defined as the ratio of the sampling rate f_s to the number of samples N .

$$\Delta f = \frac{f_s}{N} (8)$$

For instance, if $f_s = 100$ Hz and $N = 1000$ samples, the resolution is generated as in (8) is $\Delta f = \frac{100}{1000} = 0.1$ Hz. Closely spaced frequency components, such as 1 Hz and 1.1 Hz, can be easily distinguished with greater resolution (e.g., 0.1 Hz). In comparison, with $f_s = 100$ Hz and $N = 200$ samples, the resolution was $\Delta f = \frac{100}{200} = 0.5$ Hz. FFT with a lower resolution cannot clearly distinguish two peaks of frequency that are close (e.g., 0.1 Hz). The heart-rate signal must be captured at a high-resolution frequency.

3.10. Discrete Fourier Transform (DFT)

The Fast Fourier Transform (FFT) computes the Discrete Fourier Transform (DFT), which transforms a discrete-time signal $x[n]$ into its frequency domain $X[k]$ representation as calculated (9). The DFT identifies the frequency components in a filtered heart rate signal and measures the amplitude (or strength) of each frequency component in the signal. The identification of significant frequencies is essential for an analysis of heart rate variability. The Discrete Fourier Transform equation is as follows

$$X[k] = \sum_{n=0}^{N-1} x[n] e^{-j\frac{2\pi}{N}kn}, \quad \text{for } k = 0, 1, \dots, N-1 (9)$$

Any periodic signal, including the heartbeat, can be broken down into the Fourier Series, which is a sum of sine and cosine functions. The amplitudes of the cosine components (horizontal oscillations) and the sine components (vertical oscillations) are represented by the real and imaginary parts of the complex number $X[k]$. This transformation measures the amplitude of each frequency component by computing the magnitude of $X[k]$.

The sampling period, which is calculated as the inverse of the frame rate, is the time that passes between successive frames. For example, if the frame rate was 10 fps, the sample period would be $T_s = \frac{1}{10} = 0.1$ seconds. This implies that 10 samples were acquired per second. The largest frequency that can be accurately measured, or the Nyquist frequency, is equal to half the sampling rate according to the Nyquist theorem. Thus, at a sampling rate of 10 Hz, the Nyquist frequency is $f_{\text{Nyquist}} = \frac{10}{2} = 5$ Hz; which is the highest frequency identified in the signal.

3.11. Heart Rate Computation

The FFT outputs a symmetric spectrum with negative and positive frequencies as defined by Hertz. However, only the

magnitudes corresponding to the positive frequencies were considered in the computation. The frequency with the maximum amplitude, or the peak frequency, was then determined to be the principal frequency of the signal. In the proposed model, the BPM ranges from 42 to 180 BPM when the frequency is considered in the range of 0.7 Hz to 3.0 Hz. The heart rate (beats per minute) was calculated by multiplying the recorded peak frequency (in Hz) because 60 seconds make up one minute. For instance, the heart rate was 60 beats per minute (BPM) when the peak frequency was 1 Hz. The $f_{(peak)}$ denotes the significant frequency obtained from the FFT, and the HR is computed as follows: $HR = f_{peak} \times 60$ (10).

4. Experimental Results

In this study, four candidates with varying skin tones, such as light, medium, and brown, participated in experiments with ages ranging from 20 to 25 were considered. The candidates were not wearing any makeup or face accessories that covered their faces, such as scarves, spectacles, or caps. The experiment was performed twice, and each participant was tested five times. The experiment was first performed in a room with a 20-watt tube light. The second experiment was performed with the same candidates in the same room under a 40-watt tube light. The distance between the candidates and the camera was 1 meter. During each session, participants performed bicep curls for one minute, and the system recorded their heart rate in beats per minute (BPM). BlazePose was used to continually track the candidate's motions and show the number of repetitions on the screen, ensuring that participants maintained a consistent level of intense activity throughout the test. After each session, a Dr. Trust Signature Series oximeter provided reference BPM readings for each trial, which takes approximately 5 to 10 seconds to show the oximeter readings. This dual-measurement method directly compared the BPM estimates from our rPPG model and oximeter readings.

The BPM values calculated using the rPPG approach were compared and contrasted with the oximeter reference readings to test the effectiveness of our methodology. Metrics such as the Mean Absolute Error (MAE), Root Mean Squared Error (RMSE), and Mean Absolute Percentage Error (MAPE) were used to calculate the error rate. MAPE (10) is particularly convenient because it states the error as a percentage of the true value, allowing intuitive interpretation and easier comparison between subjects or conditions with differently sized BPMs. MAPE was calculated as follows:

$$MAPE = \frac{100}{5} \sum_{j=1}^5 \left| \frac{BPM_{model}(j) - BPM_{oximeter}(j)}{BPM_{oximeter}(j)} \right| \quad (10)$$

For each candidate, the experiment was conducted five times, where j represents the count, BPM_{model} is the system's BPM value, and $BPM_{oximeter}$ denotes the oximeter reading for the BPM value for j_{th} trial.

Table 2 represents the features such as age, gender, and skin tone of each candidate. MAPE I and MAPE II in Table 2 represent the mean absolute percentage error for the respective candidate in the room with ambient light intensities of 20 watts and 40 watts, respectively. The above table figures show that the percentage error is high for low ambient light intensity, and the percentage

error is low for high ambient light intensity, irrespective of skin tone and gender.

Table 2: Experimental Results

Candidate	Features			Results	
	Age	Gender	Skin Tone	MAPE I	MAPE II
Person 1	25	Female	Medium	15%	10%
Person 2	21	Male	Light	14%	7%
Person 3	22	Female	Light	16%	7%
Person 4	20	Female	Brown	13%	8%

5. Conclusion

The results show that the non-contact method is promising for real-time cardiovascular monitoring, despite the difficulties caused by high-motion activities and slight differences in the testing distance. A mechanism that alerts users when the BPM exceeds a predetermined intensity range was also included. By providing real-time alerts, this feature not only makes the system more helpful but can also be used for personal health monitoring, allowing users to be promptly notified if their heart rate exceeds permissible limits. However, these findings also target at the possible areas for development, such as improving motion compensation methods and fine-tuning the rPPG signal-processing pipeline to lower the error margin. The aim of the proposed system is to continuously monitor an individual's heart rate and generate timely alerts in the event of abnormal or risky fluctuations that could severely impact health. In addition, the system supports and optimizes fitness activities through AI-based workout recommendation and optimization techniques. In today's fitness-driven culture, activities such as Zumba, gym workouts, Aerobics, Dance fitness, Cardio workouts, CrossFit, Circuit training, and yoga to name a few exercise routines; that are often performed without expert supervision or medical guidance. This proposal addresses the associated health risks by enabling intelligent monitoring and personalized fitness optimization.

6. Future Scope

Future research will focus on enhancing motion compensation and ROI tracking to improve rPPG accuracy in numerous applications, along with a shift to include gyroscope data to enhance body-orientation tracking and movement identification. The use of exercise volumes that are more AI-driven can potentially lead to better versions of exercise becoming a reality, such as providing constant posture correction and real-time heart rate monitoring. Physiotherapy and telemedicine health monitoring are two medical application scenarios that can be explored to aid patients' recovery and avoid heart stress. In addition, non-invasive heart rate monitoring and posture detection methods can be attained by combining exercise apps, fitness centers, and AI-powered coaching to support the modernization of health and activity tracking.

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Author Contributions

Dr. Fahmina Tarannum conceived the study idea, supervised the research process, and provided guidance throughout the work. Sadaf Kauser conducted the literature review, developed the methodology, implemented the system, performed data analysis, and wrote the manuscript draft. Dr. Maniza Hijab has helped to execute the idea, Dr. Gouri Patel did the literature review and Dr. Fouzia reviewed and suggested the changes. All the Authors reviewed and approved the final version of the manuscript and agree to be accountable for all aspects of the work.

Competing Interests

The authors declare no competing interests.

Data Availability Statement

No datasets were generated or analyzed during this study. However, the source code used in this research is available from the corresponding author upon reasonable request.

Informed Consent Statement

Before the experiment, all participants gave their verbal informed consent. Every participant was fully informed about the study's purpose, methodology, and voluntary nature, even though no formal consent form was used.

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Efficient Pattern Recognition Resource Utilization Neural Network

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ABSTRACT

Neural Networks derives intelligent systems and modern autonomous applications. With the complexity introduced in today's systems, designing architectures remains open research problem in all fields. Despite many efforts to generalize, the resources required by neural architectures remain challenge. Robots design, Smart cities, IoTs ...etc. become the leading industry and driving the fourth industrial revolutions. All these challenges dictate the search for efficient utilization of resources. This paper demonstrates details of the architecture *ElHa Net*. The architecture finds the minimum resources required for pattern recognition domains. Composed of two stages, Extraction stage followed by classification stage. The extraction stage is a self-extraction, performed by convolutions like processes. The classification stage receives the extracted patterns and associates them through weighting to defined classes. The architecture is found to compete with many reported in literature.

1. Introduction

The industry and the fourth industrial revolution witness automation in all systems. With the realization of Artificial Intelligence, deep learning plays an important role in generalization of Neural Networks. Deep learning results in huge architectures and resources to perform computing tasks. Thus it becomes essential to introduce the issue of complexity in finding solutions towards efficient resources to address this problem.

In search for enhanced architectures in machine learning, convolution neural networks and deep learning play significant roles. Deep learning proves its efficiency in learning patterns using huge volume of inputs to train machines for self-efficient extraction utilizing convolution in the extraction of features. Recent architecture *ElHa Net* originally presented at ISAS symposium addresses deep learning pattern recognition neural networks architecture [1].

The research on Hand written digits recognition is a benchmark for neural network in pattern recognition. Many models were developed and tested on the MNIST data set. Originally, models based on feature extraction of LeCun in 1989 [2]. Then emergence

of convolution nets become the state of the art. To Develop and train complex convolution architectures requires huge volume of data composed of thousands of neurons. LeCun ideas based on the concepts of local receptive fields, shared weights, and spatial/temporal sub sampling. Zip codes digits used LeNet as the first convolution neural network [2]. Then appear AlexNet in 2012 in computer vision, beside others. The Network architecture is similar to LeNet of LeCun, utilizing deeper, bigger, and featured Convolution Layers stacked on top of each other followed by a Pool layer [3] - [5]. Many developments took place across the years [6], [7]. In 2013 Matthew Zeiler and Rob Fergus developed ZF Net (short for Zeiler& Fergus Net). It was an improvement over AlexNet architecture hyper parameters, it expands the middle convolution layers and modify the stride and filter size on the first layer [8]. Google Net 2014, from [9] developed an Inception Module that reduced the number of parameters in the network. The authors use Average Pooling instead of Fully Connected layers at the top of the ConvNet, which reduces parameters that do not contribute to the classification process [9]. In 2014 also appeared VGG Net. Karen Simonyan and Andrew Zisserman that became known as the VGG Net. Identifies good performance as a result of

the depth in the network [9]. 2016 witness the appearance of ResNet. Residual Network developed by [10]. The architecture uses heavy batch normalization, the fully connected layers at the end of the network disappeared. ResNet are currently the state-of-the-art Convolution Neural Network models [10]. Despite the success of these models, remain the challenge of huge architecture and the connectionist model among the cascaded layers of the networks. These result in demands for computing resources that beyond individual systems.

In this paper, we developed *ElHa Net* Neural Network utilizing the efficiency of deep learning and the convolution neural network of self-extraction. The architecture used the hand written digit characters of the MNIST data set. The MNIST data set is used as the bench mark across the literature. The approach is found to perform favorably with minimal computation and time resources. By computation resources we refer to the neurons architecture and the connections required, while time resource refers to the processor's time [11], [12].

The organization of the paper includes an Introduction. In section 2 we demonstrate the model in a top-down approach. We give the functions, then the structure of the components, followed by the overall architecture. The data flow demonstrated in section 3. Results discussions and conclusions of the implementation using MNIST data set is demonstrated in section 4.

2. *ElHa Net* Neural Network

2.1. *ElHa Net* Model

ElHa Net model is a hybrid architecture utilizing the advantages of the k-Means approach and the Convolution Neural Networks. The network is a self-extraction Neural Network. Composed of two stages, a feature extraction Network and a classification Network, Figure 1.

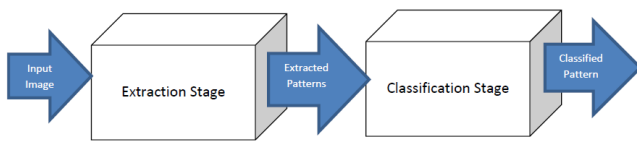


Figure 1: *ElHa Net* Block Diagram

Figure1 demonstrates the block diagram for the two stages of *ElHaNet* Neural Network composed of two stages, An input stage is the feature extraction network. Output of this stage is the input patterns to the classification stage. The classification network will perform on the extracted features and produced output. Training the network is a backpropagation algorithm.

2.2. *ElHa Net* Functions and Structure

We follow a Top-Down approach to define *ElHa Net*, first we start with the functions, then define the structure for the building blocks defined in Figure 1.

ElHa Net Functions:

- Extraction; features extraction measured based on Euclidean distance. The feature extraction is a self-process.

- Dimensionality reduction and preserve spatial invariance with pooling.
- Classification; classify the patterns detected as belong to particular classes, as probability of image.
- Pattern recognition; recognize patterns of different objects based to their present in the input. Through none linearity and training

ElHa Net Structure:

The main building blocks of Figure 1 structured in extraction stage, and a classification stage. The extraction stage is capable of self-extraction. Neurons in the first layer accepts inputs from an input image. The weights of the neural network store kernels that produce feature maps. The feature maps are distance-base operation using Euclidean distance as the square root of the quantity in the summation of equation (1)

$$D = \sum_{i=1}^n (x_i - y_i)^2 \quad (1)$$

In the above equation x, y are two points in Euclidean n -space x_i, y_i Euclidean vectors, starting from the origin of the space (initial point).

n is the n -space

The extraction operation produces feature maps based on the minimal distance obtained for a particular kernel. Receptive fields in the image are then represented by the kernel that produces this minimal distance.

To reduce dimensionality, the minimum distance kernel is searched, the kernel representing an area is averaged and forms the input to the feature map produced from the pooling operation. The feature maps are passed through a ReLU function (2) to finalize the extraction stage.

$$f(x) = \begin{cases} 0 & x < 0 \\ 1 & x \geq 0 \end{cases} \quad (2)$$

The classification stage is a fully connected network. Composed of a flattened pattern layer, formed from the extraction stage, one hidden layer, and an output layer. Neurons are fired as a result of sigmoid activation, equation (3)

$$f(x) = \frac{1}{1+e^{-x}} \quad (3)$$

3. *ElHa Net* Architecture

ElHa Net Architecture Figure 2 shows the two stages of the network. The extraction pipeline network accepts $n \times n$ input image. The classification stage accepts flattened patterns detected by the extraction network.

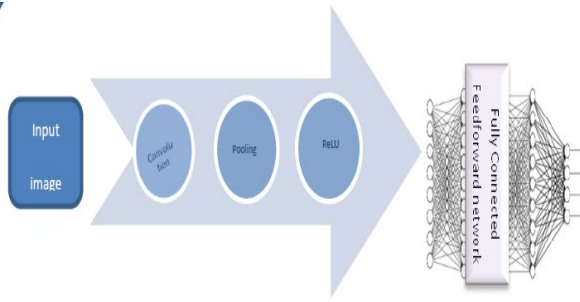


Figure 2: ElHa Net Architecture

3.1. ElHa Net Operations

The extraction stage of the network specifies the number of kernels -code words-, two-dimensional array of real values. Each has a square dimension of $kSize \times kSize$. Typical kernel dimensions are 2X2, 3X3, or 5X5, Figure 3. Initialized at the beginning of the training and adjusted gradually.

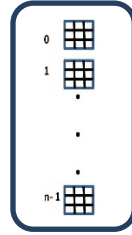
Figure 3: A set of $n \times 3 \times 3$ kernels.

Figure 3 gives typical $n \times 3 \times 3$ kernels that is designed specific. The size of such kernels is based on the application domain. Feature maps are computed for an input image according to the distance of a frame from the kernel, Figure 3. By frame we mean portion of the image that will be convolved with the kernel.

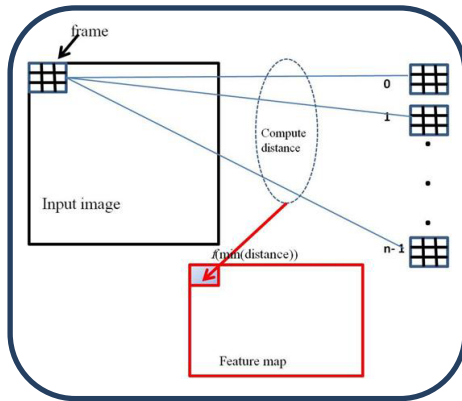


Figure 4: A Feature Map Entry Computation

Figure 4 gives the computation of one entry in the feature map. An input image is scanned from left to right, top to bottom partitioning it into frames. Each is of size, $kSize \times kSize$. A frame will be represented by the nearest kernel. This will be the entry in the feature map, equation (4).

$$Fmap_{ij} = F(\min(\text{distance}(\text{frame}_{ij}, \text{kernel}_0 \dots \text{no. of kernels}))) \quad (4)$$

The feature map is then pooled for dimensionality reduction. This step also achieves spatial invariance. The pooling is done by

averaging the kernels present in the feature map. Passes through a ReLU, then flattened to produce a one-dimensional array for the classification network.

3.2. ElHa Net Learning

The training algorithm is a backpropagation algorithm. Errors are backpropagated to update the kernels. Kernels are randomly initialized, and are updated according to the backpropagation in the extraction network, as well as weights in the fully connected network for enhanced recognition rate. The training continues to reach a preset target or the maximum number of the training epochs reached. Kernels are $kSize \times kSize$ stored as weights. Feature maps are produced based on the distance measure. The minimum distance kernel is the input to the feature map. Pooling is the dimensionality reduction process that produces an averaged kernels to represent the code word for the detected features. The rectified linear unit Figure 5, works on the code words to normalize the detected features. The output of the feature extraction is then flattened to compose the input to the classification stage.

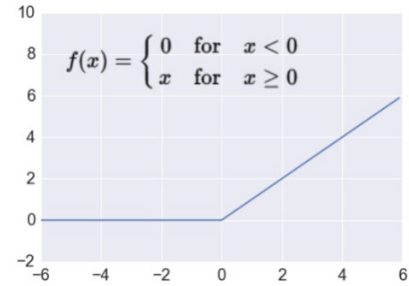


Figure 5: Rectified Linear Unit

The classification stage is a two-layer dense network. Neurons in the hidden layer uses sigmoid activation to fire. Figure 6. This process classify the detected patterns as one of the output classes.

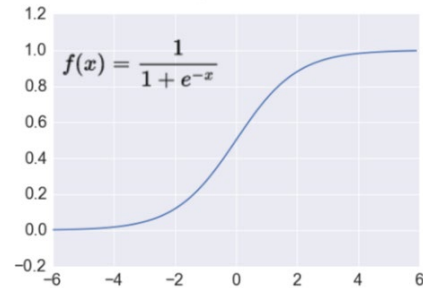


Figure 6: Sigmoid activation

Output of the network, Algorithm 1 specifies the process of pattern detection present in the input image.

Algorithm 1: Network Output Computation

Compute_feature_map (input image x) returns feature map $fmap$

Kerns $\equiv$ array of kernels, each of dimension $kSize \times kSize$
for $i := 0 \dots N - 1$

for $j := 0 \dots M - 1$

set $frame := x[i..i+kSize][j..j+kSize]$

```

set fmap[i][j] := min(distance(frame, kernels))
netOutput(inputs: image x, weights matrices W1,
W2)
returns netStruct, classIndex
fmap:=Compute_feature_map(x)
y := Flatten(fmap) //y: input to the fully connected
layer
y :=relu(y)
netStruct.y:=y
//Full connected layers
o1 := matrixMultiply(y, W1)
netStruct.ot1 := o1
o1 := sigmoid(o1)
netStruct.o1 := o1
o2 :=matrixMultiply(o1, W2)
netStruct.ot2 := o2
o2 := sigmoid(o2)
netStruct.o2 := o2
classIndex:=argMax(o2)
end
end

```

Algorithm 1 gives the algorithm for computing the output. The feature extraction stage produces features for the classification stage. The dense network as mentioned is two fully connected layers that accept the flattened output of the extraction stage. Neurons activation uses sigmoid activation both in the hidden layer and the output. One of the output neurons will fire based on activation.

To produce the output, the network is trained to recognize the pattern present in the input image, Algorithm 2, *ElHa* Net learning algorithm uses backpropagation to recognize the input pattern. A set of training images is used for the training process.

Algorithm 2: Network Training

```

Initialize weights to small random values
Initialize kernels
Initialize training parameters
set N :=feature map number of rows
set M :=feature map number of columns
repeat
for each training sample tsmpt do
// compute network output
netStruct, class :=netOutput(tsmpt, W1, W2)
out1, out2, ot1, ot2, y :=netStruct.( out1, out2, ot1, ot2, y)
for k := 0 . . . length(out2)
diff := target - out2k
 $\delta 2k := \alpha \times \text{diff} \times \text{sigmoid}(\text{out1}k)$ 
for j := 0 . . . W2 rows
 $W2_{jk} := W2_{jk} + \delta 2k$ 
sum :=  $\sum_{j=0}^{W2 \text{ rows}} \delta k \times W2_{jk}$ 
sd = 0.0
for j := 0 . . . W1 cols
for k := 0 . . . W1 rows
 $\delta t_j := \text{sum} \times \text{sigmoid}(\text{o1}t_j)$ 

```

```

 $\delta 1_{kj} := \delta t_j \times \text{inp}_k$ 
 $W1_{kj} := W1_{kj} + \delta 1_{kj}$ 
sd:=sd +  $\delta t_{kj} \times W1_{kj} \times \text{reluD}(\text{inp}_k)$ 
// update kernels
for p:= 0 . . . noofKernels - 1
kernMp:=mean(all frames belong to kernelp)
for i, j := 0 . . . kSize
kernpij:= 2×sd×(kernMpij - kernpij)
until either number of epoch = maxepoch or error < eps

```

Algorithm 2 used to train the network. The kernels are updated according to the propagation of the error. The successive iterations continue to meet a criterion, or a stated number of epochs expired.

3.3. MNIST Implementation

The MNIST is a world bench mark data set used globally to test novel architectures. The data set is used in order to recognize hand written digits. The data set composed of 60000 Hand written digit images each is 28X28. Data is divided into training and testing sets.

ElHa Net accepts MNIST images and apply kernels to filter the images. This process produces the feature maps. The feature maps consist of kernels that matches certain patterns in the presented image. Pooling produces a reduced feature plane by averaging each kernel present in the feature map. ReLU applied to the pooled plane. Output of the ReLU is then flattened to compose the input to the classification stage. This is the two layer fully connected network that classify the extracted features as one of the ten decimal digits.

4. Results, Discussions and Recommendations

The architecture *ElHa* Net applied MNIST data set. Results are demonstrated together with recommendations that can foster further research..

4.1. Results and Discussions

ElHa Net uses 2X2 kernels in the extraction stage of the network for the MNIST application, Figure 7. This size was approached after extensive experimentation with first 5x5 kernels, then a 3x3 kernels due to poor recognition rates. The size then reduced to 2x2 kernels.

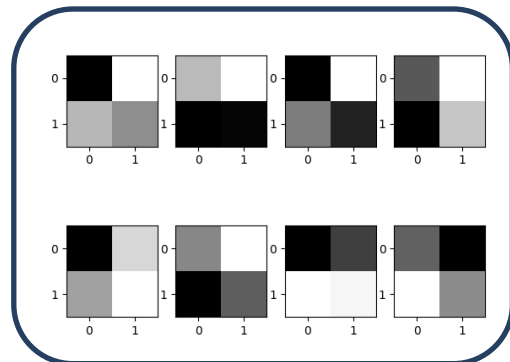


Figure 7: 2X2 Kernels in the extraction stage of the MNIST Application

Figure 7 visualizes 8 kernels used in the *ElHaNet*. Figure 8 visualizes sample feature maps produced in extraction stage.

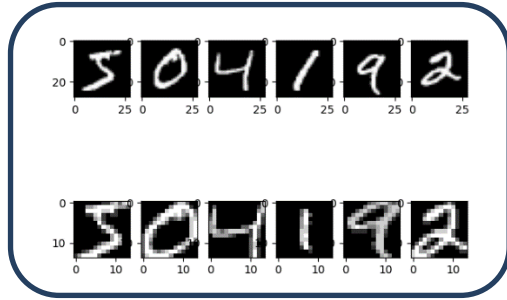


Figure 8: Sample Feature maps of the extraction stage , first row original digits, second row output.

As seen in the figure 8, the feature map reduces the 28X28 input image into half the size, which is 14X14, thus reduced dimensionality by 50%. This achieved through extraction and pooling explained earlier. These extracted patterns are then flattened to form the input to the classification stage. The classification network initializes the weights randomly. The backpropagation, propagates the errors across the network back and forth to meet a threshold of $1e^{-4}$, Figure 9.

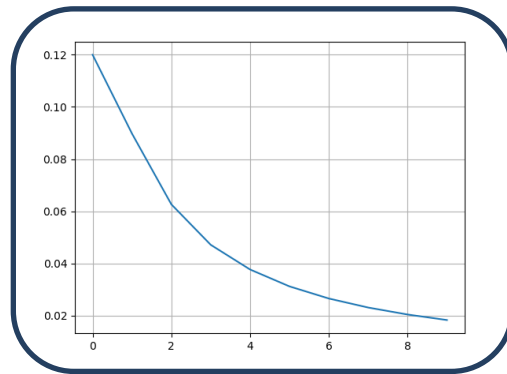


Figure 9: Visualizing the Training Error

Figure 9 shows the error during the training of the network. Due to random initialization, the curve shows an improvement as the time progress, and the network learns the pattern of interest.

Figure 10 visualizes the digits in the test set. The figure shows 969 for digits 0, 1127 for digits 1, 1015 for digit 2, 989 for digits 3, 961 for digit 4, 858 for digit 5, 933 for digit 6, 1005 for digit 7, 955 for digit 8, and 974 for digit 9.

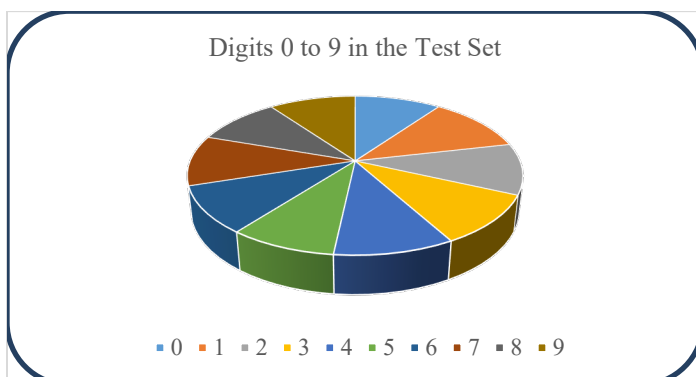


Figure 10: Digits 0 through 9 in the Test Set

Figure 11 shows the training and testing accuracy for the handwritten digit's application. *ElHa Net* achieved 99.96 accuracy during the training, and 99.53 in the testing.

```
Training accuracy = 99.96159690103688
Testing accuracy = 99.52994073165748
[5918. 6742. 5947. 6117. 5836. 5409. 5913. 6245. 5836. 5928.] 59891.0
[ 969. 1127. 1015. 989. 961. 858. 933. 1005. 955. 974.] 9786.0
[ 2. 0. 0. 5. 2. 2. 1. 3. 4. 4.] 23.0
[ 1. 0. 4. 7. 2. 1. 0. 0. 5. 8. 9.] 46.0
[ 0 1 2 3 4 5 6 7 8 9]
```

Figure 11: Training and Testing Accuracy

The recognition for individual digits is shown in Figure 12. The network capability to recognize the ten digits varies considerably. Figure 13 detailed the frequency of the miss classified digits.

```
c = [ 99.89680083 100. 99.60591133 99.29221436 99.79188345
      98.83449883 100. 99.50248756 99.16230366 99.07597536]
[0.10319917 0. 0.39408867 0.70778564 0.20811655
 1.16550117 0. 0.49751244 0.83769634 0.92402464]

PS = 0.9952449892041173
RS = 0.9951620753892669
FIS = 0.9951991801112723
0.9952035305697337
```

Figure 12: Recognition of Individual Digits 0 Through 9

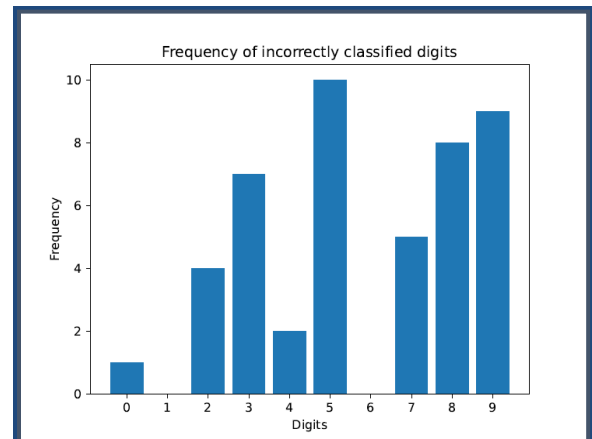


Figure 13: Incorrectly Classified Individual Digits 0 Through 9

As seen in the above figure, some digits are well recognized, produced 100% recognition rate, as in digits 1 and 6. Other digits vary. The most challenging digit to be recognized is digit 5, with 98.83% recognition rate.

```
[[ 968 0 0 0 0 0 1 0 0 0]
 [ 0 1127 0 0 0 0 0 0 0 0]
 [ 0 0 1011 2 0 0 0 0 2 0]
 [ 1 0 0 982 0 2 0 1 2 1]
 [ 0 0 0 0 959 0 0 1 0 1]
 [ 2 0 0 6 0 848 1 0 1 0]
 [ 0 0 0 0 0 0 933 0 0 0]
 [ 0 0 3 1 1 0 0 1000 0 0]
 [ 1 0 2 2 0 2 0 1 947 0]
 [ 0 0 0 2 5 0 0 0 2 965]]
```

Figure 14: Confusion Matrix

Figure 14, confusion matrix, shows the performance of the network on individual digits. For digit 0, 968 out of 969 images are

successfully recognized. While one image missed and classified as 6. For digit 1, represented by 1127, all are successfully recognized. Digit 2, from 1015, 2 were classified as 3, and 2 as 8. For digit 3, 989 images were used, 982 are correctly recognized, 1 classified as 0, 2 as 5, 1 as 7, 2 as 8, and 1 as 9. For the digit 4, we have 961 images, 959 were well recognized, while 1 classified as 7 and another as 9. Digit 5 represented by 858 images, 848 were recognized, 2 classified as 0, 6 classified as 3, 1 as 6 and 1 as 8. Digit 6 images are 933 all recognized. Digit 7 images are 1005, 1000 were correctly recognized, 3 missed as 2, 1 as 3, 1 as 4. For digit 8, the total images are 955, 1 classified as 0, 2 as 2, 2 as 3, 2 as 5 and 1 7. For digit 9 from 974, 965 were recognized, 2 classified as 3, 5 as 4, and 2 as 8.

```
Precision = [99.89680083 100. 99.60591133 99.29221436
99.79188345 98.83449883 100. 99.50248756
99.16230366 99.07597536] -1.4210854715202004e-14

Recall = [ 99.58847737 100. 99.50787402 98.69346734
99.3782383 99.53051643 99.78609626 99.70089731
99.26624738 99.79317477]

F-measure= [99.74240082 100. 99.55686854 98.99193548
99.58463136 99.18128655 99.89293362
99.60159363 99.2142483 99.43328181] 99.51991801112723
```

Figure 15: Precision and F Matrix

The Precision matrix, Figure 15 again shows the precision for individual digits, which is a measure of how well the network recognizes a certain pattern. Recall is a measure of how well the network remembers a pattern of interest; it gives the percentage of actual positive predictions correctly classified. The F-measure lay the foundation for comparison and useful to bench the performance of the algorithm with other produced on similar applications. It is a weighted average of the precision and recall. Figure 16 visualizes the accuracy of individual digits 0 through 9.

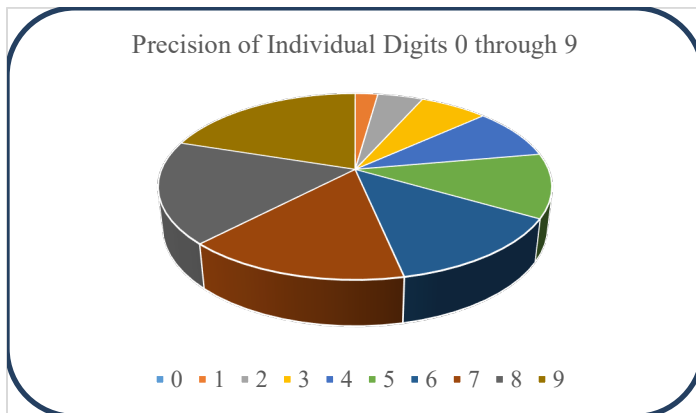


Figure 16: Precision of Individual Digits 0 Through 9

Table 1 reports performance of different architectures referenced in the literature, the first row reports the performance of *ElHa* Net architecture. The recognition rate based on the MNIST data is found to compare favorably with other architectures reported in the literature.

Table 1: Recognition of different Architectures on the MNIST Data Set

Architecture	Recognition Rate	Reference
<i>ElHa</i> Net	99.5	Current work
CNN	98.32	[2]
ResNet	99.16	[10]
CNN (Keras & Zeano)	98.7	[13]
DNN	98.08	[14]
LeNet-4-CNN	98.9	[15]
SVM	98.6	[16]
Robert Edge	99.01	[17]
Adaptive MLP	98.3	[18]
ANN	97.32	[19]
CNN	99.15	[20]
CNN	98	[21]
CNN and Multi-Level Fusion	≥ 98	[22]
DenseNet	99.37	[23]

ElHa Net developed on CPU Intel core i7 (8750H) @2.2 GH GPU NVIDIA Geforce GTX1050 with 16GB RAM, 128GM and 1 TB HDD, USB SSD (Ubuntu) 500 GB. Windows 11&Ubuntu C++ Compiler: gcc, g++. These specifications contribute to the processing time spent on training and testing. Table 2 compare the performance of *ElHa* Net with reported architectures on the same data set [24]-[29].

Table 2: *ElHa* Net Architectural Training and Size Comparison

Model	Training Time (s)	Model Size (MB)
<i>ElHa</i> Net	600	10.8
GoogleLeNet	512	49.7
MobileNet V2	498	13.6
ResNet-50	510	97.8
ResNeXt-50	549	95.8
Wide ResNet-50	540	132

The time required for training can be attributed to the computational power of the machine. Table 2 reported the least model size for *ElHa* Net.

4.2. Recommendations

The architecture developed in this paper aims to provide an efficient off line recognition that can be implemented in many applications. Excellent recognition rate on the MNIST application demonstrated the efficiency of this approach. Utilizing code word approach enable reducing architecture [30], [31]. The architecture can be implemented on other scenarios for testing efficiency and robustness.

Conflict of Interest

The authors declare no conflict of interest.

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Multi Attribute Stratified Sampling: An Automated Framework for Privacy-Preserving Healthcare Data Publishing with Multiple Sensitive Attributes

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ABSTRACT

The accumulation and analysis of large-scale patient data have led to breakthrough discoveries in potential flags for diseases based on pattern recognition, highlight medication efficacy, and local population health trends that would be impossible with traditional paper-based records. However, these benefits come with unique challenges posed by the application of data sharing for research and analysis, and mandatory requirements that require careful balance between privacy protection and usefulness of data especially when the data contains several sensitive information. We propose a framework, Multi Attribute Stratified Sampling (MASS), to achieve automatic parameter optimization by separating the sanitization process from manual privacy parameter configuration. Most traditional privacy-preserving techniques require experts to specify privacy parameters such as k, l, and t values for k-anonymity, l-diversity, and t-closeness respectively based on intuition or trial and error resulting in sub-optimal privacy-utility-trade-offs. In contrast our framework employs a self-tuning paradigm which uses GetAnonymized, CandidateBuilder, and Optimizer modules. CandidateBuilder produces multiple anonymized versions of the original preprocessed data by iteratively calling GetAnonymized on a range of anonymization levels creating a solution space. The Optimizer then scans through the solution space using an objective function to determine the optimal anonymized version. The objective function utilizes privacy and information losses along with the classification recall to discover the privacy parameters that yield the best balance between privacy protection and data utility, eliminating the burden of manually fine tuning the privacy parameters and ensuring reproducible outcomes across various healthcare datasets and analytical contexts. Experimental validation on four datasets (1k, 10k, 100k and 10M) demonstrates that MASS achieves strong privacy protection across datasets with a privacy loss < 0.25 while maintaining $>95\%$ recall retention on datasets exceeding 10k records. Given that the computational complexity to generate anonymized dataset is NP-hard, MASS presents a polynomial-time heuristic solution which validates practical implementation and scalability for real-world deployment.

1. Introduction

In the current digital era, healthcare organizations across the world have welcomed Electronic Health Records (EHRs) as a fundamental building block to support modern healthcare practices and clinical trails. EHR systems have transformed healthcare access and delivery by providing healthcare professionals with instant access to patient information, minimizing errors, and enabling data-driven decision making. Apart from clinical care, the non-volatile health data repositories stored in EHR data warehouses

hold extraordinary potential in healthcare policy development, public health surveillance, medical research, and government initiatives.

The transition to EHR has altered how data is collected, stored, and shared. Healthcare data publishing serves various objectives that extend beyond archival preservation. While research and analysis remain the primary focus, the application and landscape of data publishing have grown through government regulatory mandates, ethical obligations, and funding requirements that compel organizations to make data publicly accessible.

The American Food and Drug Administration Amendments Act of 2007 (FDAAA 801) [1] established mandatory registration and result reporting for clinical trials by the sponsors. Noncompliance carries civil penalties reaching 10,000 USD per day. The European Union (EU) Clinical trials Regulation 536/2014 [2] implemented transparency requirements by mandating that trial protocols, results, and clinical study reports be publicly available through EU Clinical trial Register. Effective January 25, 2023, all National Institutes of Health funded research are required to share data management and sharing policies regardless of funding level. These mandates create knotty commitments that must be balanced against privacy protection by the Health Insurance Probability and Accountability Act (HIPAA) in the USA and the General Data Protection Regulation (GDPR) in the EU. This very tension between mandate disclosure requirement and privacy obligations drives the privacy engineers to innovate techniques in the field of Privacy Preserving Data Publishing (PPDP). Figure 1 illustrates the pathway of data publication from Data Owners to Data Users.

Organizations and agencies (Data Holders/Custodians) that collect patients' data (Data Owners—whose personal health information must be protected) with the patients' consent are responsible for security, compliance (HIPAA, GDPR) and access control. Data publishers (a team of privacy engineers) who may be within the same organization as Data Holders or a separate entity, transform and anonymize data using privacy preserving approaches before publishing that data. Data Publishers face the privacy-utility trade-off challenge that differentiates healthcare data from social media or commercial data.

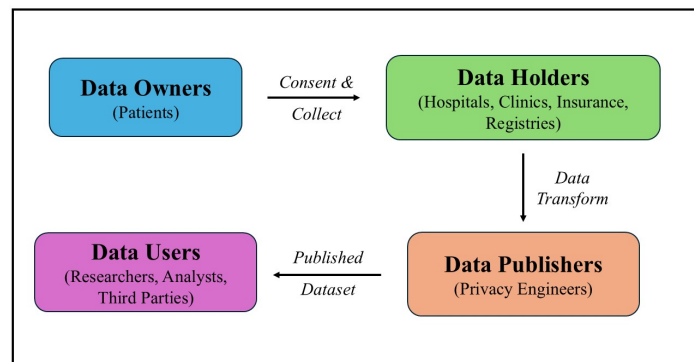


Figure 1: Data Publishing Flow

Healthcare data can be categorized into:

- **Administrative Attributes (AA):** serves as the backbone of healthcare operations that capture logistic and financial aspects of patient information. These attributes hold Personal Identifiable Information (PII) (PatientID, Patient Name, emailID, and SSN), Sensitive Information (SI) (charges, payments, and reimbursements), Quasi Identifiers (QI) (length of stay and scheduling data), and Operational Information (OI) (Department/Unit, Institution ID, and VisitID).
- **Demographic Attributes (DA):** describes the characteristics of the patient population (age/DOB, gender, race, ethnicity,

etc.) and usually contains QI (information that does not identify the patient but a combination of them might).

- **Clinical Attributes (CA):** constitutes the core medical content of healthcare data that holds diagnoses, laboratory results, medications, vital signs, and allergies to list a few. These usually hold SI that must be protected.
- **Socio-Economic Attributes (SEA):** provides context about patients' social and economic circumstances that may impact health outcomes. They include, but are not limited to education level, employment status, income level, marital status, neighborhood characteristics, and behavioral and lifestyle data. They hold both SI and QI.

PPDP provides techniques and approaches to safeguard SI while restoring high data usage. The k -anonymity privacy model [3, 4] set up the elementary foundations for PPDP by requiring each record to be like $k - 1$ other records in terms of QIs. While groundbreaking, researchers identified significant limitations since k -anonymity does not take SIs into consideration. Extensions like l -diversity [5] (requiring minimum distinct sensitive values in each equivalence class) and t -closeness [6] (preserves SI distribution in each equivalence class that is close to the SI distribution in pre-anonymized data) were proposed to k -anonymity that specifically considers SIs.

This work makes the following key contributions to the field of privacy preserving healthcare data publishing:

- We propose a novel framework that presents an end-to-end solution that generates publishable healthcare data containing multiple SI attributes.
- Our methodology automatically discovers the optimal privacy configurations through systematic solution exploration coupled with data-driven optimization there by eliminating the requirement to specify the privacy parameters.
- We address the NP-hard problem of forming optimal equivalence classes with minimum information loss through a similarity based heuristic that operates in polynomial time.

The rest of the paper is organized as follows, Section 2 provides a brief literature review on the existing work in publishing medical data. Section 3 gives the framework of our approach, and Section 4 lays out the experiments and discusses the findings. The paper concludes in Section 5.

2. Related Work

The challenge of releasing healthcare data while safeguarding patient privacy has directed large-scale exploration on various dimensions. The challenge enhances when handling data that contains several private medical information. This section reviews existing approaches focused on healthcare context to identify potential research gaps.

In [7], a method was proposed to prevent over-generalization in medical data using k -anonymity and h -ceiling. The method preserves data utility by inserting counterfeit records to the EHR

that contains demographics and diagnosis. While the approach substantially prevents unreasonable information loss that occurs with k -anonymity based full-domain generalization, it does not extend to l -diversity or t -closeness. The insertion of counterfeit records may introduce artificial patterns that impact the results of medical data analysis especially when handling a rare disease or condition.

An investigation in [8] addressed a problem in PPDP where traditional anonymization techniques used in published datasets frequently underrepresent minority groups. Existing methods, such as k -anonymity and l -diversity, can mask or delete minority patterns when data is widely generalized, potentially compromising the quality of decisions made based on this data, and subsequently affecting the benefits derived from it. Their method automatically identifies “equity-vulnerable” QI attributes and prevents them from being erased, while still maintaining considerable privacy. Preserving this information is crucial for ensuring fair representation in healthcare data and serves as a solution to the privacy-equity trade-off (PET) often observed in data publishing scenarios.

A new privacy-preserving technique that partitions data both horizontally and vertically known as slicing was proposed in [9]. This new approach overcomes problems found in popular anonymization techniques (generalization and bucketization), as it can handle high-dimensional data while preserving attribute correlations and l -diversity through random permutation of values across columns within each bucket. By leveraging the strengths of both techniques simultaneously, slicing is demonstrated to be particularly suitable for complex healthcare data, where a clear separation between QI and SI is normally required.

An enhanced k -anonymity algorithm, KAPP, that integrates t -closeness and an improved African vultures optimization algorithm (AVOA) was introduced in [10] to counter challenges found in common k -anonymity methods. Traditional methods can lead to clustering inconsistencies and are still vulnerable to skewness and similarity attacks. Additionally, other models, like l -diversity, have specific weaknesses when it comes to protecting SIs. KAPP enhances clustering accuracy by featuring a multi-dimensional SI clustering algorithm, while ensuring that equivalence classes remain distinct.

A comparative evaluation of three anonymization algorithms was reported in [11] highlighting the Multi-Objective Optimization-Based Anonymization Model (MO-OBAM) as the most effective for maintaining data utility while protecting against homogeneity and linkage attacks. When compared to the basic k -anonymity model, MO-OBAM significantly decreases vulnerability in groups at a higher risk of linkage attacks. By pointing out the need for more advanced anonymization methods that protect vulnerable populations without compromising model performance, this analysis supports the increased use of advanced anonymization models, such as MO-OBAM, to balance the privacy-utility trade-off in published data.

In [12], the authors discuss a flaw with k -anonymity and similar metrics like t -closeness or l -diversity, being that they are static and only account for a limited time span. This means that dynamic trajectory data fails to be fully obscured as time moves forward. To solve this problem, they propose a method which involves partitioning the data by time, then scanning their trajectories for efficient

clustering and privacy protection under (k, δ) security constraints. They have tested their method on various real-world trajectory data examples, and have concluded that it successfully preserves privacy and the data's utility and integrity.

A new way of understanding k -anonymity within the context of moving objects' data was identified in [13]. The authors state that because a moving object has an inherent uncertainty due to sampling and positioning systems, a new version of k -anonymity using co-localization can be utilized for privacy preservation. The trajectory of a moving object is not a line in three-dimensional space, but a cylindrical volume containing its potentiality; this means any object within that same cylinder is indistinguishable from all others. Due to this quality, they define (k, δ) -anonymity, where δ represents the possible location imprecision, then develop a method tailored to space translation called Never Walk Alone (NWA). This method achieves (k, δ) -anonymity by first minimally distorting the spatial data, then utilizing a greedy clustering algorithm based on clustering and ad hoc pre-processing and outlier removal. Rethinking privacy algorithms based on the field knowledge and context of the data itself leads to valuable innovations in data privacy.

An anonymization algorithm which includes dimensionality reduction by applying feature selection, then uses feature and attribute suppression to satisfy k -anonymity was proposed in [14]. This k -anonymous pattern-based multidimensional suppression algorithm (kPB-MS) was tested by comparing the performance of five anonymized datasets against the originals using four distinct classifiers. In the majority of test cases, the accuracy of the classifiers was not diminished by using the anonymized datasets, proving the algorithm's viability for maintaining the usability of the data. The primary shortcomings of the research are the reliance of the algorithm on the manual definition of k values and the potential to miss interacting features with low main effects due to its use of a forward selection method.

A k -Anonymity based on Center Point Clustering (KACPC) was introduced in [15] to improve data utility while guaranteeing k -anonymity in EHR. The algorithm defines new similarity metrics between healthcare records and clustering technique decrease information loss as compared to traditional generalization methods. Although the algorithm achieves higher data utility than the Samarati's [4] baseline while maintaining polynomial time complexity it requires a predefined k value and does not apply to EHR with more than one sensitive attribute.

A framework was developed in [16] to achieve (k, l) -diversity in healthcare records with multiple sensitive attributes. It first vertically slices the data into QI buckets and SI buckets, later applies hierarchical classification to retain effective data utility since it does not treat all attributes uniformly. Even though their framework allows various levels of privacy for different attributes providing flexibility in safeguarding several sensitive attributes, the vertical slicing breaks the correlation between QI and SI that are critical for medical research analysis especially in epidemiological studies.

3. Multi Attribute Stratified Sampling (MASS)

In this section, we present a comprehensive end-to-end framework for MASS where we transform a raw healthcare data into

privacy protected version of the original data. This anonymized data is suitable for publication and sharing with high analytical usefulness. Our methodology starts by preprocessing the raw data which involves cleaning the data and mapping the healthcare attributes to privacy classes. We then pass this preprocessed data through three modules: the first module is the core anonymization engine (*GetAnonymized*) that generate a sanitized version, using a stratification-based approach that partitions records by SI combinations before forming equivalence classes, for an anonymity level and stores the privacy and information losses. This anonymized version achieves implicit l -diversity and t -closeness without explicitly specifying the l and t parameters. The second module (*CandidateBuilder*) generates a solution space of anonymized data variants for a range of anonymity levels. In this module we test for the data utility (i.e., the ability of the anonymized healthcare data to perform on predictive analytics) of all the variants by capturing the classification recall metric. The final module (*Optimizer*) uses an objective function to scan through the solution space and select the best anonymized version to publish and share. For each of the modules we perform time-space analysis. This approach eliminates the need for manual parameter tuning and provides a practical solution in a polynomial time, for a NP-hard problem.

3.1. Data Preprocessing and Feature Engineering

Data preprocessing is a crucial step to ensure data integrity for privacy modeling and successive analytical utility. We begin by cleaning the raw data to address the common quality issues such as:

- Missing values (Null/NaN, empty strings, placeholders): for example, unrecorded/omitted vital signs, lab results, or diagnosis codes in EHRs.
- Duplicate records: for example, multiple records for the same patient caused by system migrations between healthcare providers, slight variation in patient information, or re-enrollments.
- Data inconsistencies (capitalization, spelling errors, mixed data formats, units of measurement, invalid/incorrect data, encoding/formatting, structural errors).
- Outliers.

Once the quality issues are resolved we proceed to mapping healthcare attributes to privacy classes. We define a function $\varphi : H \rightarrow P$ that associates healthcare-related attributes with standard privacy categories. Let $H = \{AA, DA, CA, SEA\}$ represent the healthcare attributes and $P = \{PII, QI, SI, OI\}$ represent the privacy attributes where AA, DA, CA, and SEA are mapped to PII, QI, SI, and OI respectively. We then drop the PII attributes since they directly identify the patient.

3.2. Data Representation

We denote the preprocessed healthcare data, $\mathcal{H}^C$, as a set that relates each patient record to a tuple h_i ,

$$\mathcal{H}^C = \{h_1, h_2, h_3, \dots, h_n\} \quad (1)$$

$$h_i = \{a_{i,1}, a_{i,2}, a_{i,3}, \dots, a_{i,m}\} \quad (2)$$

where n is the total number of records, m is the total number of attributes after preprocessing, $a_{i,j}$ is the value of j^{th} attribute in the i^{th} record. The m attributes represent the three privacy classes.

Table 1: Attribute Categorization

Privacy Classes	Attributes	Cardinality
QI	$\{a_1, a_2, \dots, a_q\}$	q
SI	$\{a_{q+1}, a_{q+2}, \dots, a_s\}$	$s - q$
OI	$\{a_{s+1}, a_{s+2}, \dots, a_m\}$	$m - s$

3.3. GetAnonymized

The *GetAnonymized* module serves as the core sanitization engine to transform the preprocessed healthcare dataset into a privacy-preserved version that balances the necessities of patient privacy and data utility preservation. The algorithm deploys an applied k -anonymity principle that indirectly achieves l -diversity and t -closeness within the context of data anonymization. This module accepts the $\mathcal{H}^C$, QI and SI column names, and anonymity level (privacy parameter k) to generate an anonymized version of the preprocessed dataset, $\mathcal{H}^C$. During the sanitization process, *GetAnonymized* computes and records two key metrics:

- Privacy Loss (PL): quantifies the level of privacy protection achieved on the SI through the t -closeness principle using Earth Mover's Distance [17], also known as Wasserstein distance. It measures the distributional divergence between SI values in the original and anonymized datasets by estimating the amount of work done in successfully converting one distribution into another. This gives us the privacy parameter t .
- Information Loss (IL): measures how much the data has been altered from its original form through generalizing the QIs within each equivalence class using General Loss Metric [18].

GetAnonymized module is a three-step process, where we first cluster $\mathcal{H}^C$ into non overlapping subsets such that each subset contains patient records that share the same combination of SI values. This approach ensures that the subsequent QI generalization operation do not internationally create equivalence classes that homogenize SIs, which would ironically increase privacy risks by making SIs more inferrable. For example, consider a scenario where all records in an equivalence class share the same diagnosis, an attacker knowing that a patient belonging to this equivalence class will immediately infer their medical condition with certainty, even if their QI characteristics remain hidden.

The second step involves the anonymization mechanism that operates independently on each subset produced in the first step. For each subset, we use a similarity-based clustering approach to identify records whose QI values are in comparable range there by naturally minimizing the information loss required to achieve the desired anonymity, i.e., for each group satisfying the minimum size constraint ($|group| \geq k$), we select $|group|/e$ records, where e is the size of equivalence class calculated as n/k . This selective sampling strategy is vital for optimizing privacy preservation through t -closeness since every equivalence class gets equal portion

of records from each subset which retains the semantic closeness of SI values and similar QI values thereby reducing the privacy loss and information loss respectively. The final step implements metric computation to quantify the privacy protection achieved through t -closeness principle and the information utility sacrificed during the generalization of QI. These metrics act as key components in decision making process for the third module, *Optimizer*.

3.3.1. Implicit l -diversity, t -closeness and Low Information loss Achievement

The *GetAnonymized* module offers reliable privacy guarantees beyond k -anonymity through its architectural design implementation to satisfies l -diversity and approximates t -closeness without requiring explicit privacy parameter specifications. During the module's first two steps where we cluster the patient's records by unique SI combinations into non-overlapping subsets and form equivalence classes by selecting equal portions of records inherently prevents homogeneity attacks, i.e., the records within each SI-homogeneous subset share identical sensitive values, and the final equivalence classes combine records from multiple different subsets, the resulting anonymized dataset naturally exhibits SI diversity. An equivalence class in this anonymized version contains records originating from different SI subsets which guarantees that SI are not homogeneous within the equivalence class. This design approach achieves high SI diversity as an emergent property rather than through explicit constraint enforcement there by avoiding the additional information loss and computational overhead required by traditional l -diversity implementations, i.e., after forming each equivalence class the implementations must verify the diversity constraint for each iteration. As stated earlier, during equivalence class creation selecting records whose QI values are close results in low cardinal generalization which reduces the information loss

Also, the module addresses t -closeness objectives without requiring specification of the t parameter. It is a critical advantage given that determining appropriate t values lacks principled methodology. Unlike, l -diversity that requires minimum l distinct SI values within each equivalence class, the t value is subjective i.e., distinguishing whether $t = 0.15$ versus $t = 0.18$ is adequate. To address this distribute SI combinations equally among equivalence classes during clustering by ensuring each SI-homogeneous subset contributes proportionally to equivalence classes. Now the module minimizes distributional distance between individual equivalence classes. This equal distribution strategy reduces the overall distance between the original SI distribution and the distributions within each equivalence class, effectively approximating t -closeness by making all equivalence class distributions similar to each other.

Key Advantages:

- Eliminates the need to determine appropriate l or t values
- Privacy properties emerge from SI-based clustering design rather than explicit checking
- Achieves diversity through subset combination rather than forced mixing
- Equal SI distribution minimizes distances between subset distributions and the original distribution
- No runtime diversity or closeness constraint checking required

3.3.2. Algorithm

Algorithm 1: GetAnonymized: Core Sanitization Engine

Input: $\mathcal{H}^C$ (preprocessed dataset), QI columns, SI columns, k (anonymity level)
Result: $\mathcal{H}^{C^*}$ (anonymized dataset), PL (Privacy Loss), IL (Information Loss)

// Step 1: Cluster by Sensitive Information
 $Subsets \leftarrow \emptyset$;
foreach unique combination of SI values **do**
 $subset \leftarrow$ all records in $\mathcal{H}^C$ with this SI combination;
 $Subsets \leftarrow Subsets \cup \{subset\}$;
end
// Step 2: Form Equivalence Classes
 $\mathcal{H}^{C^*} \leftarrow \emptyset$;
foreach $subset \in Subsets$ **do**
 Group records in $subset$ by similar QI values;
 foreach group of size $\geq k$ **do**
 Select $|group|/e$ records with similar QI values;
 Generalize QI values for selected records;
 Add generalized records to $\mathcal{H}^{C^*}$;
 end
end
// Step 3: Compute Metrics
 $PL \leftarrow$ ComputePrivacyLoss($\mathcal{H}^C, \mathcal{H}^{C^*}$) using Earth Mover's Distance;
 $IL \leftarrow$ ComputeInformationLoss($\mathcal{H}^C, \mathcal{H}^{C^*}$) using General Loss Metric;
return $\mathcal{H}^{C^*}, PL, IL$;

3.3.3. Time Complexity Analysis

Creating subsets based on unique SI combinations requires scanning all n records and grouping them by s sensitive attributes. This operation takes $O(n \cdot s)$ time. For each subset, grouping records by similar QI values and generalizing them involves: sorting or comparing QI values: $O(n \log n)$ in the worst case, and electing and generalizing n/k records per group: $O(n \cdot q)$ where q is the number of QI attributes. Computing the Privacy Loss (Earth Mover's Distance) takes $O(n^2 \cdot m)$ in worst case, and Information Loss (General Loss Metric) takes $O(n \cdot m)$

Overall Time Complexity: $O(n^2 \cdot m + n \log n)$, dominated by the Earth Mover's Distance computation.

3.3.4. Space Complexity Analysis

- **Input Storage:** Original dataset $\mathcal{H}^C$ requires $O(n \cdot m)$ space.
- **Subsets Storage:** In worst case, each record could have unique SI values, requiring $O(n \cdot m)$ space for all subsets.
- **Output Storage:** Anonymized dataset $\mathcal{H}^{C^*}$ requires $O(n \cdot m)$ space.
- **Metrics:** Privacy Loss and Information Loss values require $O(1)$ space.

Overall Space Complexity: $O(n \cdot m)$

3.4. CandidateBuilder

The *CandidateBuilder* module systematically generates a comprehensive solution space Ω to explore the tradeoff present in PPDP. Our strategy is to let go of complexity constraints to avoid sub-optimal parameter selection that could result in week data analytics or lack of better privacy protection. To this end, we build a lattice of anonymized versions of the preprocessed data by iteratively invoking the *GetAnonymized* module for a range of anonymity levels (extracted from the dataset itself and not a user defined range) rather than producing a single anonymized data variant. Each point in this solution space represents a unique privacy-utility-trade-off point. This enables our framework to identify best configuration that satisfy an objective function in the later stage.

This module initially computes the maximum cardinality l_v across all SI columns in the original dataset, defined as

$$l_v = \max(l_1, l_2, l_3, \dots, l_s) \quad (3)$$

where, l_x is the total number of unique instances of sensitive values in the x^{th} SI column, where $(q + 1 \leq x \leq s)$. This maximum cardinality serves as a vital benchmark to define the upper bound of the anonymity parameter exploration range. We set $4l_v$ as the upper bound. The rationale for using this as the upper bound reflects two important considerations on the practical limits of anonymization:

- This upper bound guarantees that the module explores k values well beyond the diversity of SI attributes, testing configurations where the groupings are considerably larger than the number of distinct SI values. This is essential because k -anonymity alone do not guarantee diverse SI.
- As k approaches and exceeds $4l_v$, the equivalence classes become large that generalization typically destroys the QI information leading to high information loss.

The fundamental computational loop of *CandidateBuilder* cycles through k values from 2 to $4l_v$, generating $4l_v - 1$ unique anonymized dataset by calling the *GetAnonymized* module as shown in Figure 2. The choice of $k = 2$ as the lower bound indicates the minimum meaningful k -anonymity guarantee, $k = 1$ would provide no anonymization as each record would belongs to its own equivalence class and returns the original data as anonymized data.

The organized iteration produces a solution space Ω containing $4l_v - 1$ candidate solutions, each representing a heterogeneous point in the utility-privacy tradeoff ecosystem. For each candidate solution ω_i , the module computes a comprehensive collection of metrics to capture the anonymization quality. The privacy loss and information loss metrics are inherited directly from the *GetAnonymized* module. However, recognizing that the terminal merit of anonymized healthcare data is situated in its capacity to support valid inferential and analytical tasks, we introduce an additional practical utility metric through classification recall (R) computation, which quantifies the proportion of relevant information retained after sanitization. (The choice of recall as a metric rather than classification accuracy or precision demonstrates the domain-specific priorities). Recall is a significant measure in healthcare data analysis and research as it measures model's sensitivity in detecting positive cases. The goal is to reduce the False Negatives

(FN) in the actual prediction. FN represents the number instances where a patient is having a disease and the model predicted not having disease. The module trains a classifier on each anonymized variant $\mathcal{H}^C$ and computes its recall performance.

$$\Omega = \{\omega_1, \omega_2, \dots, \omega_{4l_v-1}\} \quad (4)$$

where $|\Omega| = 4l_v - 1$. Each candidate solution $\omega_i \in \Omega$ is a tuple

$$\omega_i = (\mathcal{H}^C, PL, IL, R)_i \quad (5)$$

containing the anonymized dataset along with its respective privacy loss, information loss, and recall. These tuples together populate the solution space which serves as input to subsequent optimization module that select the most appropriate candidate.

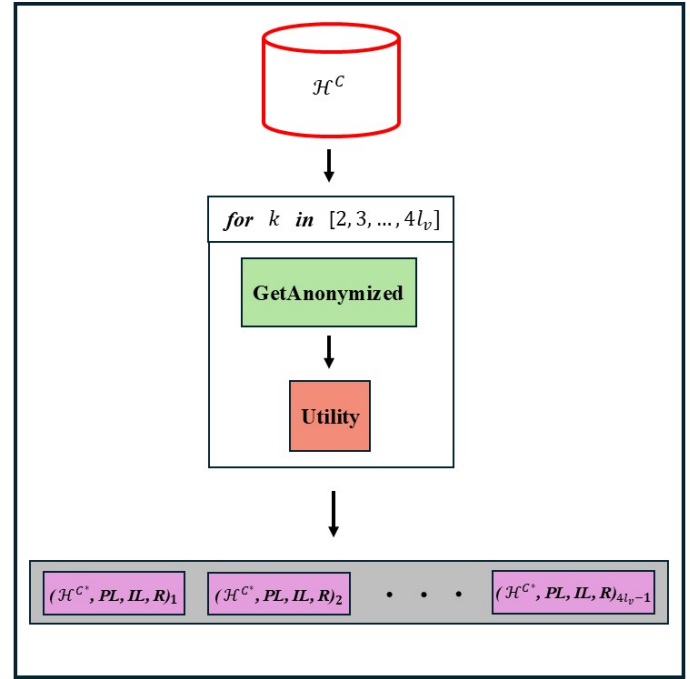


Figure 2: CandidateBuilder flow diagram

3.4.1. Recall Computation Methodology

Before invoking the *GetAnonymized* to create a solution space and soon after the preprocessing we set up a benchmark to ensure that the classification recall measurements accurately capture the practical analytical value of the anonymized datasets by training multiple classification algorithms on the $\mathcal{H}^C$ to identify and eliminate algorithms exhibiting overfitting, i.e., we set a threshold of 15% as the accuracy gap between the training and testing data. The algorithms demonstrating stable performance across the classification accuracy form the evaluation ensemble. We use this ensemble algorithms during the *CandidateBuilder*'s iteration process, to get the classification recall across each anonymized version. The recorded recall R for the each candidate solution ω_i is the average recall across all classifiers in the ensemble

$$R_i = \frac{1}{m} \sum_{j=1}^m \text{Recall}_{ij} \quad (6)$$

where m is the number of classifier algorithms in the valid ensemble and Recall_{ij} is the recall value of the j -th algorithm on the i -th anonymized dataset calculated as:

$$\text{Recall} = \frac{\text{TruePositive}}{\text{TruePositive} + \text{FalseNegatives}} \quad (7)$$

By averaging the recall rather than depending on a the behavior of the single model, we reduce the bias that the classification algorithms introduce.

3.4.2. Solution Space Properties

The solution space Ω possesses several key structural properties that underpin its interpretation and practical use:

- The candidates are tacitly organized in increasing order of the privacy parameter k that corresponding to decreasing information loss and increasing privacy protection. The ordering naturally facilitates efficient visualization of the privacy-information tradeoff as seen in Figure 4(A).
- The solution space captures non-linear relationships between k and the metrics that enables to identify *sweet spots* where privacy and utility are optimally balanced as seen in Figure 4(B).
- Although the losses captures valuable theoretical insight into the anonymization process, they do not directly answer the pragmatic question: “Can this anonymized dataset still support clinical predictions we care about?” By contrast, recall explicitly addresses this question directly. Incorporating and tracking recall as an additional utility measure bridges this gap between the measure of privacy loss and information loss and their practical implications.

3.4.3. Algorithm

Algorithm 2: CandidateBuilder: Solution Space Generator

Input: $\mathcal{H}^C$ (preprocessed dataset), QI columns, SI columns
Result: Ω (solution space of sanitized dataset variants)
 // Compute maximum cardinality
 $l_v \leftarrow \max(l_1, l_2, l_3, \dots, l_s);$
 // where l_x is the number of unique instances in x^{th} SI column
 $\Omega \leftarrow \emptyset;$
 // Generate candidate solutions
for $k \leftarrow 2$ **to** $4l_v$ **do**
 $(\mathcal{H}^C, PL, IL) \leftarrow \text{GetAnonymized}(\mathcal{H}^C, \text{QI}, \text{SI}, k);$
 // Compute data utility through recall
 Train classifier on $\mathcal{H}^C$;
 $R \leftarrow \text{ComputeRecall}(\text{classifier});$
 // Store candidate solution
 $\omega_{k-1} \leftarrow (\mathcal{H}^C, PL, IL, R);$
 $\Omega \leftarrow \Omega \cup \{\omega_{k-1}\};$
end
return $\Omega;$

3.4.4. Time Complexity Analysis

Finding the maximum cardinality l_v among s SI columns requires scanning each SI column which takes $O(n \cdot s)$ time. Generating each solution candidate involves calling GetAnonymized algorithm iteratively from $k = 2$ to $k = 4l_v$, creating $(4l_v - 1)$ iterations. Each GetAnonymized iteration takes $O(n^2 \cdot m + n \log n)$. Training ensemble classifiers and computing the aggregate recall takes $O(n \cdot m \cdot d)$ where d is the ensemble classifier complexity.

Overall Time Complexity: $O(l_v \cdot (n^2 \cdot m + n \cdot m \cdot d))$

3.4.5. Space Complexity Analysis

- **Input Storage:** Original dataset $\mathcal{H}^C$ requires $O(n \cdot m)$ space.
- **Solution Space Ω :** Stores $(4l_v - 1)$ candidate solutions, where each ω_i contains:
 - Anonymized dataset $\mathcal{H}^C$: $O(n \cdot m)$
 - Metrics (PL, IL, R): $O(1)$

Total for Ω : $O(l_v \cdot n \cdot m)$

- **Classifier Storage:** Temporary space for training classifier: $O(n \cdot m)$

Overall Space Complexity: $O(l_v \cdot n \cdot m)$. This is the dominant space requirement as it stores all candidate anonymized datasets.

3.5. Optimizer

The *Optimizer* module implements the decision-making logic to select the optimal sanitized dataset from the solution space Ω generated by *CandidateBuilder*. This module employs a composite objective function $\mathfrak{J}(\omega)$ that consolidates the multidimensional metrics into a single scalar optimization criterion to systematically evaluate every candidate and returns the best balance across all three metrics. The optimization problem is formally defined as:

$$\omega^* = \arg \min_{\omega \in \Omega} \mathfrak{J}(\omega) \quad (8)$$

where ω^* represents the solution that minimizes the objective function,

$$\mathfrak{J}(\omega_i) = \frac{PL_i + IL_i}{R_i} \quad (9)$$

The rationale behind the objective function is to achieve maximum analytical utility while incurring minimum privacy and information costs. The numerator $PL_i + IL_i$ represents the total cost of anonymization, where lower PL indicates stronger privacy protection and lower IL indicates better data quality preservation. The function treats both losses as equally important costs to minimize. The denominator R_i represents the analytical utility in the anonymized dataset through classification recall. Higher recall means the model is better at identifying actual positives. Placing recall in the denominator ensures that the configuration in Ω maintain high utility. The ratio structure creates an inherent tradeoff mechanism. Configurations with low total cost and high recall achieve low objective function values and are preferred.

The *Optimizer* uses an exhaustive search strategy that evaluates every candidate solution in Ω against the objective function to identify the global minimum. This exhaustive linear search is computationally feasible because it requires simple arithmetic operations on pre-computed metrics.

3.5.1. Algorithm

Algorithm 3: Optimizer: Optimal Solution Selector

Input: $\Omega = \{\omega_1, \omega_2, \dots, \omega_{4l_v-1}\}$ (solution space)
Result: ω^* (optimal sanitized dataset with metrics)
 $\mathfrak{I}_{min} \leftarrow \infty$;
 $\omega^* \leftarrow \text{null}$;
 // Evaluate each candidate solution
foreach $\omega_i \in \Omega$ **do**
 Extract $(\mathcal{H}^C_i, PL_i, IL_i, R_i)$ from ω_i ;
 // Compute objective function
 $\mathfrak{I}(\omega_i) \leftarrow \frac{PL_i + IL_i}{R_i}$;
 // Update optimal solution if better
 if $\mathfrak{I}(\omega_i) < \mathfrak{I}_{min}$ **then**
 $\mathfrak{I}_{min} \leftarrow \mathfrak{I}(\omega_i)$;
 $\omega^* \leftarrow \omega_i$;
end
end
 // Extract optimal components
 $(\mathcal{H}^{C^*}_{optimal}, PL^*, IL^*, R^*) \leftarrow \omega^*$;
return $\mathcal{H}^{C^*}_{optimal}, PL^*, IL^*, R^*$;

3.5.2. Time Complexity Analysis

The optimizer module evaluates $(4l_v - 1)$ candidates in the solution space and for each candidate it computes the objective function in a constant time of $O(1)$.

Overall Time Complexity: $O(l_v)$

3.5.3. Space Complexity Analysis

- **Input Storage:** Solution space Ω requires $O(l_v \cdot n \cdot m)$ space.
- **Working Variables:** Minimum objective value $\mathfrak{I}_{min}$ and optimal solution ω^* require $O(n \cdot m)$ space.

Overall Space Complexity: $O(l_v \cdot n \cdot m)$

Unlike traditional approaches where practitioners or data engineers must pre-define privacy constraints (k or t) through trail and error, MASS's integrated system of *GetAnonymized*, *CandidateBuilder*, and *Optimizer* operates as a self-tuning framework that automatically identifies the anonymized dataset with optimal privacy-utility balance.

3.6. Solving the NP-Hard Problem

Give a dataset with n records, QI, privacy parameter k , and an information loss metric, finding the anonymized version that minimizes the information loss while upholding k -anonymity requires exploring an exponentially large solution space which fundamentally is a NP-Hard [19, 20]. When explicit constraints for l -diversity and t -closeness are introduced, the computational complexity dramatically increases [5, 6]. The algorithms must verify these additional constraints by checking at each partition step which further expands the exponential search space. Enforcing explicit l and t constraints results in a nested optimization loops, where the algorithms first partition for k constraint, check diversity constraints, then measure SI distributional distance, and backtracking when the constraints are not satisfied [21, 22]. When handling datasets

with several SI columns, finding the combination of SI values that satisfy both l and t constraints across all attributes concurrently compounds the difficulty, making optimal solutions computationally infeasible even for moderately sized datasets.

The MASS framework addresses this intractability through a decomposition-based polynomial-time heuristic that achieves near-optimal information loss, without claiming to compute the global optimum. The time complexity of $O(l_v \cdot (n^2 \cdot m + n \cdot m \cdot d))$ implicitly satisfies l -diversity and t -closeness without additional computational overhead. The partitioning of $\mathcal{H}^C$ into SI-homogeneous subsets transforms the global optimization problem into several independent smaller problems. Then we employ a similarity based greedy clustering within each subset which reduces generalization distance and thus the information loss. Critically our framework achieves l -diversity and t -closeness as emergent properties of the decomposition design and not through explicit constraint checking. The SI-based subset creation ensures that equivalence classes naturally contain records from multiple different subsets that ensures diversity in SI columns (implicit l -diversity). The identical allocation strategy dispenses SI combinations proportionally across all equivalence classes which leads to minimizing distributional distances (implicit t -closeness). These privacy properties are achieved without any additional computational cost beyond the base k -anonymity algorithm, i.e.,

- no diversity verification loops,
- no SI distribution distance verification loops,
- no constraint-violation backtracking.

MASS's polynomial-time complexity enables practical anonymization of large datasets where optimal algorithms are infeasible, i.e., $O(l_v \cdot (n^2 \cdot m + n \cdot m \cdot d))$ time complexity remains unchanged regardless of whether we consider only k -anonymity or the combination of k -anonymity, l -diversity, and t -closeness which is a significant notable advantage over methods that must explicitly enforce these three constraints, positioning the framework as a scalable heuristic rather than an exact solver. The time and space complexities are summarized in Table 2.

Table 2: Time and Space complexities

Algorithm	Time Complexity	Space Complexity
GetAnonymized	$O(n^2 \cdot m + n \log n)$	$O(n \cdot m)$
CandidateBuilder	$O(l_v \cdot (n^2 \cdot m + n \cdot m \cdot d))$	$O(l_v \cdot n \cdot m)$
Optimizer	$O(l_v)$	$O(l_v \cdot n \cdot m)$
Overall	$O(l_v \cdot (n^2 \cdot m + n \cdot m \cdot d))$	$O(l_v \cdot n \cdot m)$

4. Experimental Evaluation and Results

We conduct wide-range experiments on synthetic healthcare datasets of varying sizes to validate and study the effectiveness and scalability of the MASS framework. The experimental design systematically examines MASS's performance across settings ranging from small-scale pilot studies to large-scale institutional data repositories. Since publicly available healthcare datasets are typically pre-anonymized, which would confound our analysis of the anonymization process, we use synthetically generated datasets that allow us to control the original data characteristics and systematically evaluate the impact of our anonymization framework.

4.1. Setup

We generate four synthetic healthcare datasets with realistic attribute distributions and correlation patterns representative of electronic health records. The datasets contain identical schema with multiple QIs (age, gender, zip code, occupation, race), multiple SIs (diagnosis, treatment, symptoms, total bill, high risk), and OI (visit date, blood pressure systolic, blood pressure diastolic, heart rate, bmi, temperature) but vary in size:

- **Small-scale (1K records):** Representative of specialized clinical studies or rare disease registries
- **Medium-scale (10K records):** Typical of single-institution research datasets
- **Large-scale (100K records):** Representative of multi-institutional collaborative studies
- **Very large-scale (10M records):** Approaching national-level healthcare databases

This scale progression enables evaluation of MASS across realistic deployment scenarios while assessing computational scalability as dataset size increases by four orders of magnitude. Each feature is generated from empirically validated distributions to ensure clinical realism.

All experiments were run on Dell XPS series laptop (2.60 GHz 13th gen i9 processor with 32 GB RAM and 8 GB graphics card) using Python 3.13 to implement the framework.

4.2. Evaluation Objectives

Our experiments investigate three key research questions as we apply MASS to varying data sizes:

- We examine how different classification algorithms behave on anonymized data compared to original data. While recall drives our optimization function, we also track classification accuracy to understand the broader impact of anonymization on predictive modeling. This reveals whether accuracy and recall degrade similarly or exhibit different sensitivity patterns as anonymization strength increases. We expect the anonymized datasets to perform slightly better due to the fact that we introduce additional data points while generalizing the QIs.
- We analyze the multidimensional tradeoff between privacy loss, information loss, and utility as k increases which is expected in PPDP. This analysis helps us to understand if the privacy gains justify utility costs at various k levels and examine how information loss correlates with actual utility degradation.
- We validate the computational scalability of our approach by measuring how execution time scales with dataset size and k value to confirm that our polynomial-time heuristic achieves practical runtime performance. We expect the time per- k execution to show a slight decrease as k increases for smaller dataset because fewer equivalence classes need to be formed and should execute in seconds. As the data size increases the execution should increase.

For each dataset, we follow a systematic protocol beginning with classifier validation, proceeding through comprehensive anonymization testing, and concluding with boundary validation.

4.3. Classifier Ensemble Validation

We begin by identifying a valid ensemble of classifiers that demonstrate dependable generalization on $\mathcal{H}^C$ to ensure robust and meaningful utility evaluation. We train seven widely used classification models—Logistic Regression, Decision Trees, Random Forests, Support Vector Machines (SVM), k-Nearest Neighbors, Gradient Boosting (XGBoost), and Naive Bayes—on $\mathcal{H}^C$. Each model is assessed on held-out test data where both training and test accuracy are recorded. The generalization behavior of each model is quantified via an accuracy gap measured as the absolute difference between their training and test accuracy. Those models that exhibit an accuracy gap of 15% are deemed to overfit the data and are excluded from subsequent evaluation. This screening ensures that our utility measurements are driven by true predictive capability rather than artifacts of model memorization. The validation results are summarized in Table 3, showing training and test metrics for each algorithm along with overfitting status. The accuracy gap is visualized in Figure 3 with the 15% threshold marked in black dashed line.

Decision Trees and Random Forests display pronounced overfitting across all four dataset sizes, achieving perfect training accuracy (1.000) while test accuracy remains around 55-66%. In both cases, they consistently show accuracy gaps exceeding 34% which are well above the established 15% threshold. Consequently, these classifiers are removed from the validated ensemble. Gradient Boosting similarly overfits on the small-scale dataset, exhibiting an accuracy gap of 18.08%. However, its performance stabilizes on larger datasets, indicating that limited training data exacerbates its tendency to memorize patterns.

We note that the decision tree-based models can often be stabilized through parameter tuning like pruning or depth constraints. However, we intentionally avoid classifier-specific optimization in this study since the objective in this study is to evaluate how anonymization generalizes under a uniform and minimal-configuration setting. Applying classifier-specific optimization would introduce additional degrees of freedom.

In contrast, the remaining four classifiers, i.e., Logistic Regression, SVM, K-Nearest Neighbors, and Naive Bayes, exhibit consistent generalization across all dataset sizes with accuracy gaps below 15%. Logistic Regression demonstrates remarkable consistency with gaps of under 1% across all scales. SVM and Naive Bayes maintain gaps under 7% and 3% respectively. K-Nearest Neighbors exhibits slightly higher gap but still acceptable around 13%. On the medium, large, and very large datasets, Gradient Boosting also joins the validated ensemble with gaps under 5%. Interestingly, test accuracy remains relatively stable across dataset sizes for most classifiers, typically ranging from 60-66% suggesting the synthetic data's inherent complexity rather than sample size determines predictive capacity. The validated ensemble of 4-5 classifiers (depending on dataset) provides a robust foundation for evaluating anonymization impact, with ensemble-averaged baseline test accuracy around 63-65% across all scales.

Table 3: Baseline classification performance on original (non-anonymized) data

Dataset	Classifier	Training Accuracy	Test Accuracy	Accuracy Gap (%)	Overfit?
Small-scale	Logistic Regression	0.670	0.665	0.42	No
	Decision Tree	1.000	0.606	39.33	Yes
	Random Forest	1.000	0.660	34.00	Yes
	SVM	0.791	0.663	12.83	No
	K-Nearest Neighbors	0.736	0.606	13.00	No
	Gradient Boosting	0.830	0.650	18.08	Yes
	Naive Bayes	0.633	0.660	2.67	No
Medium-scale	Logistic Regression	0.660	0.659	0.05	No
	Decision Tree	1.000	0.553	44.65	Yes
	Random Forest	1.000	0.643	35.70	Yes
	SVM	0.721	0.653	6.80	No
	K-Nearest Neighbors	0.728	0.603	12.52	No
	Gradient Boosting	0.695	0.653	4.24	No
	Naive Bayes	0.639	0.621	1.80	No
Large-scale	Logistic Regression	0.658	0.649	0.83	No
	Decision Tree	1.000	0.555	44.42	Yes
	Random Forest	1.000	0.638	36.20	Yes
	SVM	0.699	0.646	5.32	No
	K-Nearest Neighbors	0.735	0.596	13.94	No
	Gradient Boosting	0.672	0.650	2.16	No
	Naive Bayes	0.645	0.630	1.50	No
Very large-scale	Logistic Regression	0.6510	0.645	0.56	No
	Decision Tree	1.000	0.559	44.01	Yes
	Random Forest	1.000	0.635	36.42	Yes
	SVM	0.682	0.644	3.80	No
	K-Nearest Neighbors	0.731	0.593	13.78	No
	Gradient Boosting	0.657	0.645	1.25	No
	Naive Bayes	0.640	0.628	1.24	No

By excluding the Decision Trees and Random Forests from the majority of datasets, our utility assessment focuses on algorithms with demonstrated generalization capability. This is appropriate since we aim to measure how anonymization affects genuine predictive patterns rather than memorization. To format the results into tables and visualize the patterns efficiently, we exclude Gradient Boosting too. The validated ensemble spans diverse learning paradigms from linear (Logistic Regression), to distance-based (SVM, K-Nearest Neighbors), and probabilistic (Naive Bayes) which enables comprehensive and balanced assessment of utility across diverse modeling approaches.

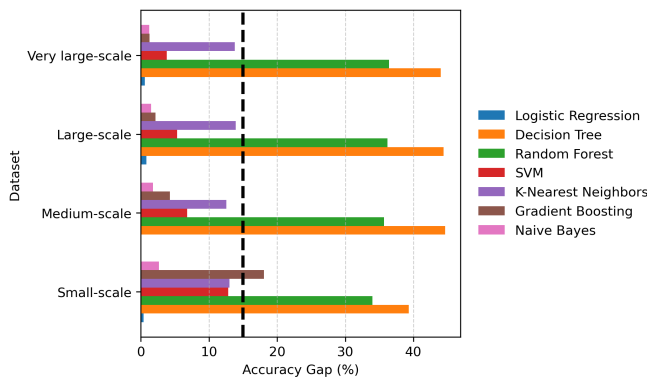


Figure 3: Classification accuracy gap across dataset

4.4. Solution Space Generation and Evaluation

After establishing the validated ensemble, we find each dataset's SI structure to determine the range of k . Table 4 presents the maximum cardinality for each dataset, which we use to determine the upper bound of $4l_v - 1$. While we execute the anonymization process for every value of k within the exploration range, presenting all the results is space extensive and obscure the

key trends (for example: the Medium scale data has 43 set of results, instead we prune it to 15). Therefore, we also show the representative k values for which the results are recorded in the subsequent utility measurement. These values are chosen after completing all the experiments and identifying the optimum anonymized version for each dataset. This presentation strategy ensures that we are not unintentionally biased by selectively displaying only convenient values. We provide transparency about the solution quality by including dense sampling around the data-driven optimal k .

We present the five core anonymization metrics (privacy loss, information loss, computational time, ensemble-averaged recall, and the objective function) in Table 5 across the representative anonymity levels for all four datasets. These aggregate metrics are visualized in Figure 4(A) revealing the fundamental privacy-information tradeoffs present in PPDP (i.e., how they evolve inversely as anonymization strength increases). Figure 4(B) tracks the execution time in seconds across the datasets and Figure 5 displays the objective function $\mathfrak{J}(\omega)$ showing where optimal configurations emerge.

MASS upholds the classic privacy-information loss trade off, i.e., as k increases, privacy loss consistently decreases which indicates stronger privacy protection and information loss monotonically increases which indicating the effect of anonymization through generalization. The tradeoff pattern is consistent across all four datasets, for small-scale data, privacy loss drops from 0.367 at $k = 2$ to 0.078 at $k = 27$ which accounts to a 79% reduction, while information loss rises from 0.076 to 0.462 a 508% increase. On medium-scale, large-scale, and very large-scale datasets privacy loss declining from 0.402 to 0.051 (87% reduction), 0.412 to 0.045 (89% reduction), and 0.506 to 0.011 (98% reduction), and information loss increases from 0.074 to 0.436 (489% increase), 0.072 to 0.515 (615% increase), and 0.073 to 0.512 (601% increase) respectively.

Table 4: Dataset Characteristics and k -Parameter Exploration

Dataset	I_v	$4I_v - 1$	Representative k
Small-scale	7	27	2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 27
Medium-scale	11	43	2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 43
Large-scale	16	63	2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 45, 55, 63
Very large-scale	19	75	2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 45, 55, 65, 75

Despite the persistent growth of information loss with k , Table 5 shows that ensemble-averaged recall remains remarkably stable, fluctuating within narrow ranges: 0.631-0.749 for small-scale, 0.750-0.778 for medium-scale, 0.780-0.791 for large-scale, and 0.781-0.792 for very large-scale.

This stability is achieved due to the addition on a data point while generalizing the QI columns and allows the objective function to identify meaningful optima where the combined burden of privacy and information loss is minimized relative to preserved utility. Figure 5 visualizes these U-shaped objective function curves, with minima occurring at $k = 4$ (small), $k = 9$ (medium), $k = 8$ (large), and $k = 9$ (very large). These optimal points correspond to configurations in Table 5 where objective values reach their minima: 0.533, 0.559, 0.479, and 0.547 respectively. These optimal configurations achieve privacy loss values below 0.25 while maintaining recall above 0.70.

The computation time on small and medium scale datasets decrease with increase in k due to fewer equivalence classes. Small-scale shows clear descent from 0.507s to 0.231s and medium-scale drops from 5.66s to 2.44s. Large scale dataset shows modest decrease from 493.5s to 421.1s. The very large scale shows relatively stable times fluctuating around 3000s to 3500s across k values rather than a strictly monotonic trend. This behavior is seen due to the interaction between MASS's stratification-based processing and system-level effects. At this scale, the algorithmic variations are further amplified by Python runtime overhead, memory access patterns, and cache misses. These variations dominate execution time once the dataset no longer fits entirely in fast memory reflecting data-dependent partitioning and hardware-level effects rather than instability in the MASS algorithm itself.

Table 6 provides detailed per-classifier performance data showing accuracy, recall, accuracy retention percentage, and recall retention percentage at each representative k value. The detailed breakdown enables us to understand the effect of anonymization effectively. The retention patterns are visualized in Figure 6(A) for accuracy and Figure 6(B) for recall across all four datasets. These retention patterns are re-framed as percentage gains or losses from the baseline in Figure 7 highlighting where anonymization provides unexpected benefits (values above 0%) versus expected degradation (values below 0%).

The retention percentages are computed as:

$$\text{Recall Retention (\%)} = \frac{\text{Recall}_{\text{anonymized}}}{\text{Recall}_{\text{original}}} \times 100 \quad (10)$$

$$\text{Accuracy Retention (\%)} = \frac{\text{Accuracy}_{\text{anonymized}}}{\text{Accuracy}_{\text{original}}} \times 100 \quad (11)$$

Table 5: Metrics across dataset

Dataset	k	Info Loss	Privacy Loss	Time (s)	Recall (avg)	$\mathfrak{Z}(\omega)$
Small-scale	2	0.076	0.367	0.507	0.730	0.607
	3	0.098	0.323	0.454	0.749	0.562
	4	0.131	0.243	0.401	0.702	0.533
	5	0.160	0.211	0.381	0.663	0.560
	6	0.215	0.198	0.353	0.731	0.565
	7	0.279	0.201	0.338	0.729	0.658
	8	0.302	0.178	0.313	0.711	0.675
	9	0.328	0.161	0.309	0.694	0.705
	10	0.358	0.151	0.303	0.676	0.753
	15	0.385	0.121	0.284	0.652	0.776
	20	0.418	0.104	0.274	0.721	0.724
	25	0.443	0.091	0.260	0.642	0.832
	27	0.462	0.078	0.231	0.631	0.856
Medium-scale	2	0.074	0.402	5.66	0.778	0.612
	3	0.101	0.391	5.02	0.773	0.637
	4	0.113	0.361	4.62	0.750	0.632
	5	0.119	0.314	4.16	0.772	0.561
	6	0.147	0.311	3.92	0.775	0.591
	7	0.174	0.280	3.67	0.757	0.600
	8	0.193	0.261	3.67	0.768	0.591
	9	0.227	0.202	3.55	0.768	0.559
	10	0.236	0.194	3.52	0.767	0.561
	15	0.316	0.145	3.31	0.770	0.599
	20	0.360	0.109	3.22	0.763	0.615
	25	0.368	0.094	3.11	0.764	0.605
	30	0.390	0.081	3.01	0.765	0.616
	35	0.423	0.068	2.84	0.766	0.641
	43	0.436	0.051	2.44	0.766	0.636
Large-scale	2	0.072	0.412	493.5	0.787	0.615
	3	0.107	0.381	486.8	0.786	0.621
	4	0.133	0.311	431.6	0.784	0.566
	5	0.154	0.284	477.6	0.782	0.560
	6	0.176	0.256	446.7	0.784	0.551
	7	0.187	0.201	471.2	0.784	0.495
	8	0.195	0.179	435.7	0.780	0.479
	9	0.237	0.201	415.7	0.786	0.558
	10	0.253	0.210	461.0	0.791	0.585
	15	0.344	0.175	450.8	0.786	0.661
	20	0.374	0.124	448.9	0.783	0.636
	25	0.398	0.101	447.9	0.781	0.639
	30	0.421	0.087	441.7	0.781	0.651
	35	0.448	0.061	437.1	0.781	0.652
	45	0.459	0.055	434.8	0.789	0.652
Very Large-scale	55	0.485	0.047	431.3	0.785	0.678
	63	0.515	0.045	421.1	0.782	0.716
	2	0.073	0.506	2819.97	0.788	0.735
	3	0.107	0.478	2919.72	0.786	0.744
	4	0.132	0.423	3653.78	0.784	0.708
	5	0.153	0.388	3385.69	0.789	0.686
	6	0.170	0.341	3340.55	0.791	0.646
	7	0.188	0.301	3880.88	0.791	0.618
	8	0.207	0.268	3562.65	0.791	0.601
	9	0.219	0.213	3459.25	0.790	0.547
	10	0.238	0.201	3360.35	0.789	0.557
	15	0.341	0.181	3580.39	0.789	0.662
	20	0.358	0.162	3202.45	0.792	0.657
	25	0.388	0.143	3182.46	0.781	0.680
	30	0.403	0.115	3415.12	0.790	0.656
	35	0.445	0.091	3645.22	0.791	0.678
	45	0.463	0.062	3125.54	0.790	0.665
	55	0.486	0.041	2987.71	0.789	0.668
	65	0.507	0.024	3076.84	0.787	0.675
	75	0.512	0.011	3176.52	0.792	0.660

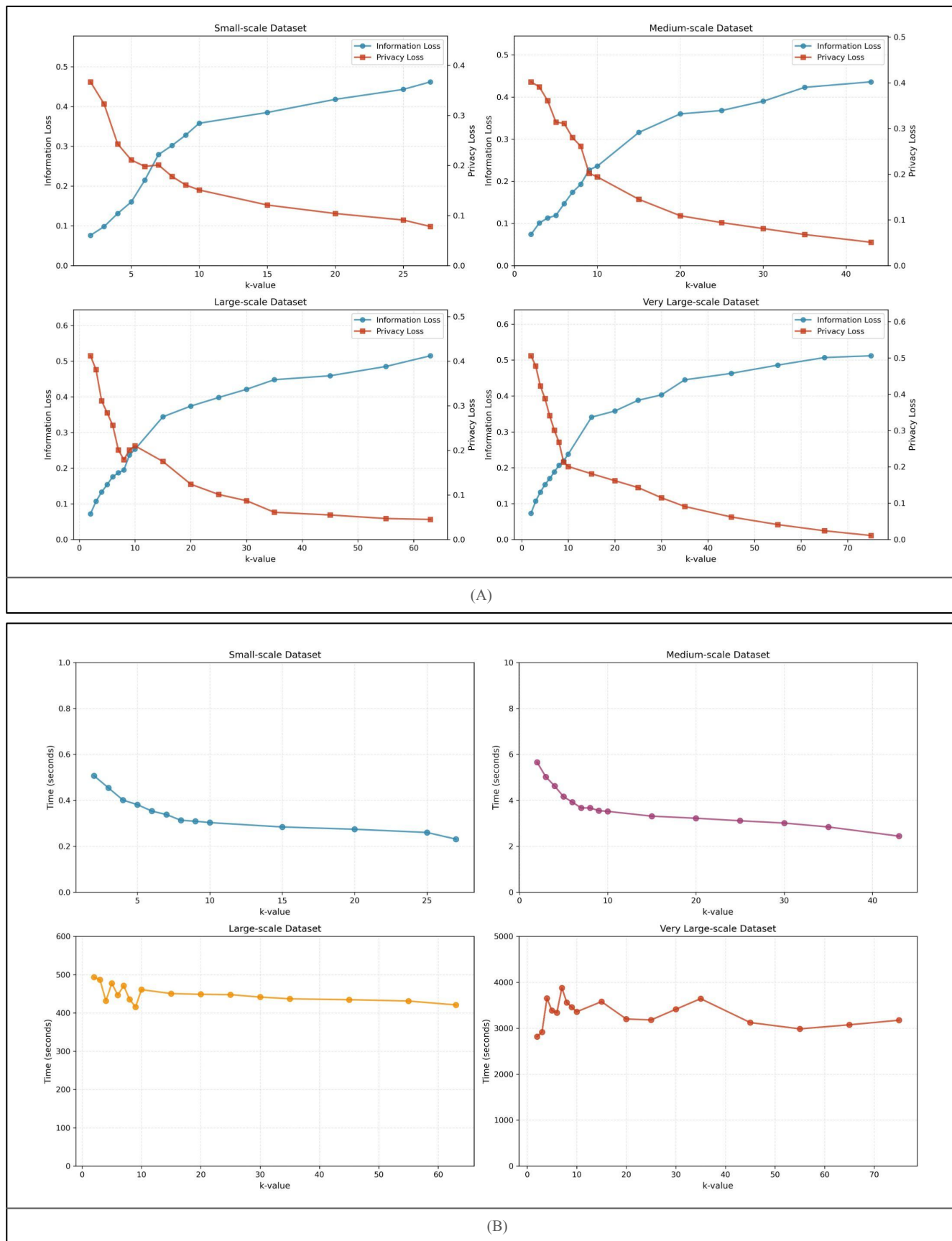


Figure 4: Anonymization metrics: privacy loss and information loss trade-off (A), computational time (B)

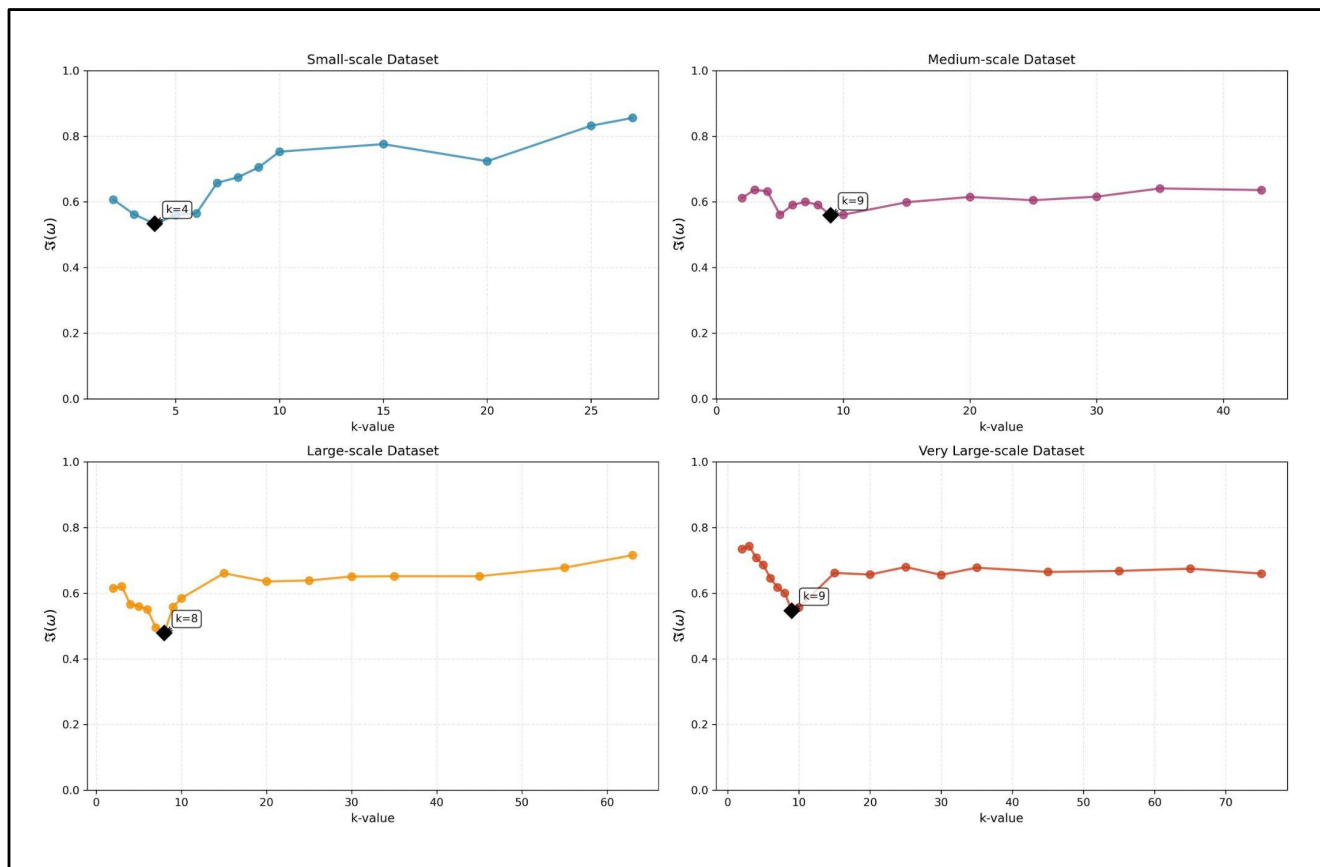


Figure 5: Objective function indicating optimal k across datasets

Table 6: Accuracy and Recall Across k Values for All Dataset Scales

Dataset	k	Logistic Regression				SVM				k-NN				Naive Bayes			
		Acc	Rec	Acc _{Ret}	Rec _{Ret}	Acc	Rec	Acc _{Ret}	Rec _{Ret}	Acc	Rec	Acc _{Ret}	Rec _{Ret}	Acc	Rec	Acc _{Ret}	Rec _{Ret}
Small-scale	2	0.621	0.733	93.27	93.85	0.597	0.709	89.71	90.78	0.573	0.703	94.45	97.44	0.652	0.773	98.79	97.72
	3	0.639	0.768	95.94	98.34	0.597	0.732	89.71	93.73	0.556	0.708	91.64	98.13	0.642	0.786	97.27	99.37
	4	0.612	0.703	91.92	90.01	0.601	0.679	90.31	86.94	0.520	0.703	85.71	97.44	0.605	0.721	91.67	91.15
	5	0.605	0.725	90.86	92.83	0.605	0.681	90.91	87.20	0.504	0.575	83.09	79.70	0.583	0.669	88.33	84.58
	6	0.651	0.776	97.78	99.36	0.632	0.724	94.97	92.70	0.550	0.667	90.67	92.45	0.658	0.756	99.70	95.57
	7	0.645	0.766	96.88	98.08	0.630	0.753	94.67	96.41	0.521	0.675	85.88	93.56	0.611	0.721	92.58	91.15
	8	0.631	0.776	94.77	99.36	0.627	0.776	94.21	99.36	0.484	0.585	79.78	81.08	0.591	0.707	89.55	89.38
	9	0.631	0.769	94.70	98.40	0.619	0.744	92.94	95.20	0.515	0.589	84.82	81.57	0.574	0.674	86.97	85.21
	10	0.630	0.761	94.62	97.44	0.610	0.711	91.66	91.04	0.545	0.592	89.85	82.05	0.557	0.641	84.39	81.04
	15	0.633	0.711	95.04	91.04	0.575	0.656	86.40	83.99	0.511	0.617	84.22	85.52	0.575	0.625	87.12	79.01
	20	0.571	0.761	85.75	97.44	0.561	0.735	84.30	94.11	0.561	0.752	92.47	104.23	0.535	0.637	81.06	80.53
	25	0.593	0.756	89.06	96.80	0.647	0.709	97.22	90.78	0.480	0.523	79.13	72.49	0.573	0.581	86.82	73.45
	27	0.598	0.752	89.80	96.30	0.655	0.701	98.50	89.80	0.468	0.505	77.20	70.00	0.566	0.565	85.70	71.40
Medium-scale	2	0.658	0.806	99.85	99.26	0.636	0.762	97.40	97.57	0.575	0.720	95.36	100.14	0.665	0.822	107.09	101.59
	3	0.665	0.822	100.91	101.23	0.641	0.763	98.16	97.70	0.557	0.693	92.37	96.38	0.661	0.813	106.44	100.48
	4	0.654	0.804	99.24	99.01	0.624	0.739	95.56	94.62	0.537	0.673	89.05	93.60	0.638	0.783	102.74	96.78
	5	0.643	0.812	97.57	100.00	0.612	0.765	93.72	97.95	0.550	0.699	91.21	97.22	0.646	0.810	104.03	100.11
	6	0.647	0.816	98.18	100.49	0.618	0.759	94.64	97.18	0.563	0.715	93.37	99.44	0.641	0.810	103.22	100.11
	7	0.641	0.795	97.27	97.91	0.611	0.743	93.57	95.13	0.545	0.687	90.38	95.55	0.645	0.802	103.87	99.13
	8	0.642	0.814	97.42	100.25	0.622	0.764	95.25	97.82	0.544	0.692	90.21	96.24	0.644	0.802	103.71	99.13
	9	0.646	0.821	98.02	101.05	0.621	0.757	95.02	96.86	0.551	0.694	91.38	96.52	0.641	0.798	103.14	98.64
	10	0.650	0.827	98.63	101.85	0.619	0.749	94.79	95.90	0.558	0.696	92.54	96.80	0.637	0.794	102.58	98.15
	15	0.647	0.831	98.18	102.34	0.617	0.766	94.49	98.08	0.541	0.680	89.72	94.58	0.632	0.803	101.77	99.25
	20	0.636	0.813	96.51	100.12	0.615	0.763	94.18	97.70	0.540	0.677	89.55	94.16	0.625	0.798	100.64	98.63
	25	0.639	0.828	96.97	101.97	0.623	0.765	95.41	97.95	0.533	0.678	88.39	94.30	0.632	0.785	101.77	97.02
	30	0.641	0.835	97.45	102.90	0.629	0.767	96.50	98.40	0.528	0.679	87.60	94.60	0.636	0.777	102.40	96.00
	35	0.643	0.842	97.95	103.80	0.635	0.769	97.60	98.80	0.523	0.680	86.80	95.00	0.640	0.769	103.10	95.00
	43	0.647	0.853	98.70	105.30	0.645	0.773	99.20	99.50	0.515	0.682	85.50	95.30	0.648	0.755	104.40	93.40
Large-scale	2	0.664	0.815	102.31	96.79	0.660	0.794	101.54	96.71	0.594	0.720	99.66	100.14	0.665	0.817	105.56	99.76
	3	0.657	0.812	101.23	96.44	0.654	0.800	100.62	97.44	0.584	0.710	97.99	98.75	0.660	0.820	104.76	100.12
	4	0.652	0.813	100.46	96.56	0.648	0.800	99.69	97.44	0.576	0.703	96.64	97.78	0.654	0.821	103.81	100.24
	5	0.649	0.811	100.00	96.32	0.644	0.799	99.08	97.32	0.575	0.704	96.48	97.91	0.651	0.814	103.33	99.39
	6	0.647	0.814	99.69	96.56	0.644	0.807	99.08	98.29	0.570	0.698	95.64	97.08	0.650	0.817	103.17	99.76
	7	0.647	0.814	99.69	96.56	0.643	0.803	98.92	97.81	0.575	0.702	96.48	97.63	0.649	0.816	103.02	99.63
	8	0.644	0.814	99.23	96.56	0.639	0.800	98.31	97.44	0.564	0.691	94.63	96.11	0.644	0.815	102.22	99.51
	9	0.646	0.820	99.54	97.27	0.643	0.806	98.93	98.11	0.568	0.697	95.38	96.95	0.646	0.820	102.54	100.12
	10	0.648	0.825	99.85	97.98	0.647	0.811	99.54	98.78	0.573	0.703	96.14	97.78	0.648	0.825	102.86	100.73
	15	0.643	0.817	99.08	97.03	0.637	0.805	98.00	98.05	0.568	0.703	95.30	97.78	0.642	0.819	101.90	100.00
	20	0.641	0.814	98.77	96.56	0.636	0.802	97.85	97.69	0.565	0.698	94.80	97.08	0.642	0.816	101.90	99.63
	25	0.641	0.819	98.77	97.27	0.634	0.800	97.54	97.44	0.565	0.691	94.80	96.11	0.640	0.814	101.59	99.39
	30	0.640	0.818	98.62	97.21	0.632	0.797	97.16	97.07	0.564	0.696	94.63	96.80	0.639	0.812	101.43	99.20
	35	0.639	0.818	98.46	97.15	0.629	0.794	96.77	96.71	0.563	0.701	94.46	97.50	0.638	0.811	101.27	99.02
	45	0.644	0.825	99.23	97.98	0.639	0.810	98.31	98.66	0.563	0.698	94.46	97.08	0.645	0.823	102.38	100.49
Very large-scale	55	0.643	0.822	99.15	97.59	0.637	0.807	98.05	98.25	0.561	0.692	94.09	96.31	0.643	0.820	102.11	100.15
	63	0.643	0.819	99.08	97.27	0.636	0.804	97.85	97.93	0.559	0.688	93.79	95.69	0.642	0.818	101.90	99.88
	2	0.665	0.814	103.10	97.84	0.665	0.805	101.22	98.29	0.597	0.717	100.67	99.72	0.668	0.816	106.37	99.51
	3	0.656	0.814	101.71	97.84	0.656	0.801	99.85	97.80	0.588	0.708	99.16	98.47	0.660	0.822	105.10	100.24
	4	0.654	0.811	101.40	97.48	0.652	0.801	99.24	97.80	0.584	0.705	98.48	98.05	0.656	0.817	104.46	99.63
	5	0.650	0.819	100.78	98.44	0.649	0.808	98.78	98.66	0.581	0.704	97.98	97.91	0.653	0.823	103.98	100.37
	6	0.651	0.822	100.93	98.80	0.650	0.811	98.93	99.02	0.582	0.706	98.15	98.19	0.652	0.825	103.82	100.61
	7	0.650	0.826	100.78	99.28	0.649	0.808	98.78	98.66	0.583	0.707	98.31	98.33	0.652	0.824	103.82	100.49
	8	0.648	0.821	100.47	98.68	0.645	0.812	98.17	99.15	0.580	0.708	97.81	98.47	0.649	0.823	103.34	100.37
	9	0.648	0.821	100.39	98.62	0.645	0.811	98.17	99.02	0.580	0.706	97.73	98.19	0.649	0.823	103.34	100.37
	10	0.647	0.820	100.31	98.56	0.645	0.810	98.17	98.90	0.579	0.704	97.64	97.91	0.649	0.823	103.34	100.37
	15	0.646	0.822	100.16	98.80	0.644	0.810	98.02	98.90	0.575	0.703	96.96	97.77	0.646	0.822	102.87	100.24
	20	0.647	0.827	100.31	99.40	0.646	0.815	98.33	99.51	0.573	0.702	96.63	97.64	0.647	0.825	103.03	100.61
	25	0.644	0.820	99.84	98.56	0.643	0.811	97.87	99.02	0.574	0.699	96.80	97.22	0.647	0.825	103.03	100.61
	30	0.643	0.823	99.69	98.86	0.642	0.812	97.72	99.15	0.573	0.700	96.63	97.36	0.646	0.824	102.87	100.49
	35	0.642	0.825	99.53	99.16	0.641	0.813	97.56	99.27	0.572	0.701	96.46	97.50	0.645	0.824	102.71	100.49
	45	0.642	0.822	99.53	98.80	0.640	0.813	97.41	99.27	0.571	0.702	96.29	97.64	0.645	0.824	102.71	100.49
	55	0.642	0.819	99.46	98.44	0.640	0.811	97.34	98.97	0.571	0.703	96.29	97.77	0.644	0.822	102.47	100.24
	65	0.641	0.816	99.38	98.08	0.639	0.808	97.26	98.66	0.571	0.703	96.29	97.77	0.642	0.820	102.23	100.00
	75	0.639	0.826	99.07	99.28	0.637	0.814	96.96	99.39	0.572	0.707	96.46	98.33	0.640	0.820	101.91	100.00



Figure 6: Classification performance study: (A) % accuracy retention, (B) % recall retention

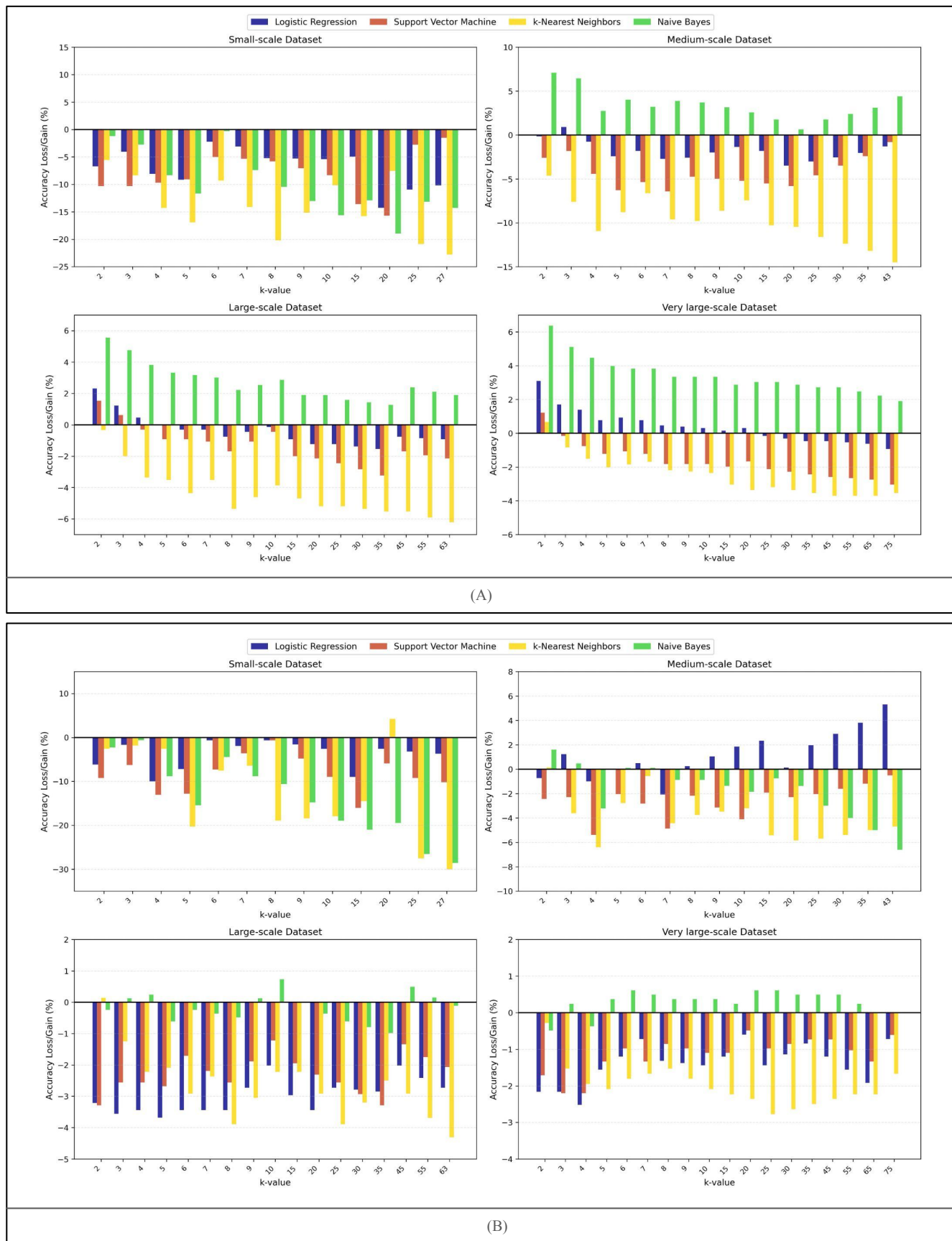


Figure 7: Classification performance study: (A) Accuracy gain/loss, (B) Recall gain/loss from the baseline

5. Conclusion and Future Work

This study addresses fundamental challenges in PPDP for healthcare datasets containing multiple sensitive attributes. We have presented MASS, a comprehensive framework that eliminates the need for manual privacy parameter specification, provides polynomial-time solution to the NP-hard problem of optimal anonymization, and implicitly achieves l -diversity and t -closeness guarantees through architectural design rather than explicit constraint enforcement.

Our experimental validation across four dataset scales demonstrates that MASS successfully navigates the privacy-utility-information loss tradeoff space. The framework achieves strong privacy protection (privacy loss < 0.25 at optimal configurations) while maintaining excellent utility preservation, with recall retention exceeding 95% on datasets with 10,000 or more records. The remarkable retention stability observed in larger datasets where accuracy and recall retention remain within 93-106% and 95-101% ranges respectively throughout the entire k parameter space validates that the stratification approach enables aggressive anonymization without catastrophic utility degradation. The occasional performance gains exceeding baseline, where anonymized data outperforms original data, reveal an unexpected benefit: generalization can act as beneficial regularization that improves classifier performance rather than degrading it.

MASS represents a significant advancement in making privacy-preserving healthcare data publishing both theoretically sound and practically deployable. By addressing the dual challenges of multiple sensitive attributes and automated parameter selection, while maintaining computational tractability through our polynomial-time heuristic, we enable organizations to publish valuable health data that advances medical research, supports clinical decision-making, and informs public health policy all while rigorously protecting patient privacy. The framework's open architecture supports future extensions including integration of differential privacy mechanisms, incorporation of alternative anonymization techniques beyond generalization, and adaptation to other domains beyond healthcare where multiple sensitive attributes require protection. Future work will focus on three directions: parallelization to achieve further scalability improvements for very large datasets, integration of multiple anonymization techniques (microaggregation, anatomization, permutation, noise addition) with adaptive selection mechanisms, and extension to dynamic data publishing scenarios where datasets evolve over time. The comprehensive framework presented here provides a solid foundation for these enhancements while already delivering production-ready capabilities for static healthcare data publication. Privacy-preserving healthcare data publishing for multiple sensitive attributes is no longer a theoretical challenge requiring expert intervention and MASS makes it a practical, automated reality where the framework is be applicable to:

- Multi-institutional research databases require standardized de-identification across diverse healthcare systems and data warehouses to track multiple health conditions over time.
- Public health surveillance needs to publish patterns and trends while protecting individual patient privacy.

- Clinical trial requirement where patient characteristics and findings must be released to the public.
- Health information exchanges facilitate data sharing among healthcare providers.

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Investigating the Influence Biomass Additive on the Thermal Performance of a Fired-Clay for Producing the Inner Liner of a Biomass Cook-stove

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ABSTRACT

This study investigated the influence of a biomass additive on the thermal performance of the inner liner of fired-clay cook-stoves. Fired-clay cook-stoves are essential cooking devices, particularly in areas with limited access to modern energy resources. The study aimed to enhance the thermal efficiency of the cook-stoves by incorporating rice husk into the inner liner material. The shrinkage, porosity, bulk density, thermal conductivity and heat retention performance of the produced fired-clay were evaluated. Different proportions of rice husk mixed with clay were examined to determine the desired combinations. It was found that the sample with 30% rice husk has apparent porosity of 71.41% and bulk density of 0.995343g/cm³ and that of the sample with no rice husk, was 41.38% and 1.526922g/cm³ respectively. The results indicated improvement in thermal insulation performance with the rice husk additive, and thus improved combustion efficiency of the cook-stove. This study offered a valuable insight in using rice husk as a sustainable biomass additive to enhance insulation performance of a fired-clay for producing cook-stoves, thereby contributing in producing a more efficient and environmentally friendly cooking device. The use of rice husk as a biomass additive offers additional environmental benefits, as such re-purposing the use of agricultural waste and emission mitigation of greenhouse gases.

1. Introduction

Millions of people around the world, especially in the developing countries, still depend on open-fire and three-stone stoves that depend on biomass fuels for heating and cooking [1]. However, the development of cook-stoves has changed over the past few decades with modifications from the three-stone fire to better efficient cook-stoves with good aesthetic and quality insulation materials. The cook-stoves with a much better thermal efficiency are expensive due to high quality materials and insulators used by the manufacturers, though they tend to have improved performance efficiency [2]. The need for more efficient cook-stoves is on the rise and much effort to modify the previous ones aimed at improving the thermal performance and reducing emission. Since most insulation materials used for producing the

inner liner of a cook-stove are clay-based materials, deciding the best performing clay mixtures in respect to its thermal resistance is essential to improve insulation performance of cook-stoves. Heat is always lost from the body of cook-stoves by conduction and radiation, thus it is necessary to make use of proper insulation to help reduce heat loss.

Cook stoves are designed to increase fuel efficiency and reduce smoke alongside the pollution emissions due to poor fuel combustion efficiency. Improving the insulating part of the inner liner cook-stove reduces the amount of fuel used and improves the quality of heat transferred to the cooking pot [3]. Improved cook-stoves design focused on the approach to increase combustion and insulating efficiencies through a series of design structures. Heat transfer quality in a stove indicates the extent of thermal energy

absorbed by the cooking pot compared to the amount of thermal energy released during the combustion processes and the level of insulation of the inner liner. The combustion efficiency and thermal performance of cook-stoves are key factors in ensuring their energy conservation and minimizing their environmental impact [4]. The inner liner of a cook stove plays a vital role in improving the combustion efficiency and thermal performance of energy efficient cook-stoves, making it essential to investigate how to improve the insulation performance of the inner liner of cook-stoves. Adding combustible organic pore-forming additives in the clay body can improve the insulation performance by creating porosity in the clay body when they are burnt off during firing [5]. The pore-formers can also help to reduce the heat absorbed by the liner and modify other properties like water absorption, thermal performance and density. The possibility of using straw and reed residue generated during bleached pulp production was determined during clay brick formation. It was seen that besides the composition of the additive, it also depends on the clay body's porosity and internal structure and also the thermal conductivity is determined by the clay body [6].

In [7], the authors carried out some laboratory tests on samples made of brick clay with up to 30% volume of sawdust and/or paper-making sludge as pore-forming agents. During firing, it was observed that the sawdust and the sludge helped to reinforce the structure of the body and prevented cracking. A very porous structure was then obtained after firing at a temperature of up to 920°C [2]. Also, determination of the water absorption, porosity, bulk density and compressive strength of the fired samples were achieved. Incorporating biomass particles into the clay mixture could be envisaged in creating voids during the firing process, and thus modifying clay properties was seen to improve the structure and properties of clay. Making ceramic materials lighter by creating air cavities was found to be the most effective way of increasing thermal technical properties. In [8], the authors found that cook-stoves enhanced with biomass additives saved 35–50% on fuel compared to other conventional stoves, lowering household expenses. Each family might save up to 300 kg of fuel each year as a result of this and cook in a much healthier environment. In [9], the authors evaluated the improved biomass cookstove by considering the water boiling test, and the results indicate that the thermal efficiency for boiling 5 L of water was 25%. In [10], the researchers state that coffee husk pellets, which is a byproduct gotten from the waste coffee husk production considered as a very potential solid fuel. They further evaluated stoves with hole system design by considering the Water Boiling Test (WBT) and emission test. The results showed that 16.47 % and 298 ppm were the maximum thermal efficiency and CO emissions respectively.

From the above studies, there is a paucity of published information on the thermal and insulation performance of cook-stoves based on the material used in producing the combustion chamber inner liner and biomass additives in the clay material. This work focused on addressing the insulation performance of the inner liner of a biomass cook-stove. The heat lost from the inner liner of a cook-stove during fuel combustion can reduce the overall efficiency of the stove. Biomass additives can have various influences on the production and performance of the combustion chamber in a cook-stove. Thus, the influence of biomass additives (such as rice husk in this case) in improving the insulation performance of fired clay for production of the inner liner of a

cook-stove are investigated in this study to reduce heat losses and improve the insulation performance of the cook-stove. Different mixtures of clay materials (ball clay, kaolin) and a biomass additive (such as rice husk) are used in this study to obtain the mixture compositions that could be used to produce the inner liner with improved insulation performance of the cook-stove.

2. Materials and Methods

The materials used in this study are the metal boxes used to mold the mixed clay, kaolin and rice husk into a rectangular shape, the LPG cylinder used for firing the samples in the kiln, the kiln used for firing the formed samples. The infrared thermometer device was used to measure temperature at a distance, without touching the object.

2.1. Clay and Rice Husk Preparation

The ball clay and kaolin used for this study were gotten from the National Stove Eligibility Laboratory (NSEL) in the National Center for Energy Research Development (NCERD), University of Nigeria, Nsukka (UNN) and the rice husk from a rice mill in Enugu state, Nigeria. The ball clay was first crushed into fine powder and dirt removed. The rice husk was sieved to obtain a uniform particle sizes and dirt removed. All the samples were mixed in varying ratios summing up to 300g for each sample.

2.2. Samples Preparation

The ball clay, kaolin, and rice husk were mixed to form the samples (S). Tables 1 to 4 are the percentage by weight composition mixture of the clay (C), kaolin (K), and the biomass additive (rice husk, R). For each of the mixtures, water was added to create plasticity and molded using rectangular metal molds with dimensions of 11cm length, 8cm breadth and 3cm thickness. The weights of the samples after moulding, after sun drying and after firing in the kiln, and % weight loss after firing samples are presented in Tables 1 to 4.

Table 1: Samples mixed with 0% Rice husk (R)

Sample (S)	S1	S2	S3	S4
Mixture of Rice husk (R), Clay (C) and Kaolin (K)	40%C, 60%K, 0%R	30%C, 70%K, 0%R	20%C, 80%K, 0%R	10%C, 90%K, 0%R
Weight after moulding (g)	372.7	391.9	382.4	389.5
Weight after sun drying (g)	281.5	288.3	283.9	287.9
Weight after firing (g)	245.3	250.4	244	248.5
Weight loss (%)	34.18	36.11	36.19	36.20

Table 2: Samples mixed with %10 Rice husk (R)

Sample (S)	S5	S6	S7	S8
Mixture of Rice husk (R), Clay (C) and Kaolin (K)	35%C, 65%K, 10%R	25%C, 65%K, 10%R	15%C, 75%K, 10%R	5%C, 85%K, 10%R
Weight after moulding (g)	386.2	397.4	393.1	389.8
Weight after sun drying (g)	285.2	295.5	288.6	286.1
Weight after firing (g) in the kiln	231.5	238.7	232.1	228.6
Weight loss (%)	40.06	39.93	40.96	41.35

Table 3: Samples mixed with 20% Rice husk (R)

Sample (S)	S9	S10	S11	S12
Mixture of Rice husk (R), Clay (C) and Kaolin (K)	30% C, 50% K, 20% R	20% C, 60% K, 20% R	10% C, 70% K, 20% R	0% C, 80% K, 20% R
Weight after moulding (g)	399.9	397.4	396.1	394.1
Weight after sun drying (g)	291.7	288.0	288.2	287.5
Weight after firing (g) in the kiln	220.5	215.0	214.9	212.7
Weight loss (%)	44.86	45.90	45.75	46.03

Table 4: Samples mixed with 30% Rice husk (R)

Sample (S)	S13	S14	S15	S16
Mixture of Rice husk (R), Clay (C) and Kaolin (K)	25% C, 45% K, 30% R	15% C, 55% K, 30% R	5% C, 65% K, 30% R	0% C, 70% K, 30% R
Weight after moulding (g)	409.8	401.9	402.7	404.7
Weight after sun drying (g)	287.2	294.2	297.0	291.3
Weight after firing (g) in the kiln	195.2	200.2	203.1	198.8
Weight loss (%)	52.37	50.19	49.56	50.88

The produced samples were sun dried for two weeks, after which they were fired using a LPG fired kiln shown in Figure 1. The mini kiln insulated with ceramic fiber was developed at the NCERD, UNN. The firing process in the kiln was done in three stages.



Figure 1: Preheating stage in the kiln



Figure 2: The gas inlet part of the kiln and the kiln not yet completely closed

Stage 1 is the preheating, which involved raising the temperature of the kiln to less than 100°C, while leaving the door of the kiln opened as shown in Figure 1, for 2 hours to gradually drive off the moisture still trapped in the samples, which would cause busting during firing of the samples.

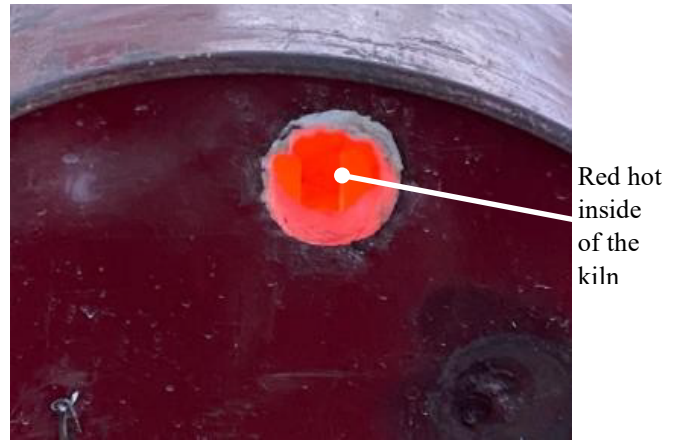


Figure 3: Firing stage of the samples in the kiln



Figure 4: Samples after 6 hrs firing in the kiln and allowed to cool over the next day

At stage 2, the door of the kiln was further lowered, but not completely closed as shown in Figure 2 and the temperature rose to above 100°C for 1 hour to ensure that any remaining moisture in the samples had completely evaporated. After preheating, (i.e. at stage 3), the door of the kiln was completely closed. As shown by the red hot colour inside of the kiln in Figure 3, the temperature inside the kiln gradually increased to about 1000°C to 1300°C, which is the firing temperature range for 6 hours. At this temperature, the pore forming agents (ie. rice husk) had burnt completely and pores are formed. After the 6 hours firing, the gas supply was turned off and the samples were allowed to cool inside the kiln until room temperature was achieved on the next day. This was to prevent thermal shock, which could occur where a material experiences abrupt change in temperature and developed stresses and strains in their internal structure, that could cause cracking. Figure 4 shows the fired samples that were removed from the kiln on the next day and kept in an open air environment.

2.3. Fired Sample Shrinkage

Even though the samples appeared very dry after the sun drying, but they still contain some water, the chemically bonded water and the residual moisture. During the firing stage, this water was burnt out, thereby make the samples to shrink. Also, during the firing, the rice husk in the samples also burnt out, making the samples to shrink further. The shrinkage of the fired samples was determined by measuring their dimensions before and after firing them in the kiln. The percentage shrinkage is calculated based on Equation (1).

$$\text{Fired shrinkage (\%)} = \frac{D_o - D_f}{D_o} \times 100 \quad (1)$$

D_o = dimension after sun drying, D_f = dimension after firing. The dimensions include length, breadth and thickness.

2.4. Porosity and Bulk density

After firing, the rice husk had burnt out completely and created pores in the internal structure of the samples. The porosity and bulk density tests were carried out by immersing each of the samples in a bowl with one liter of water as shown in Figure 5 and leaving it for 15 minutes to absorb water into the pores.

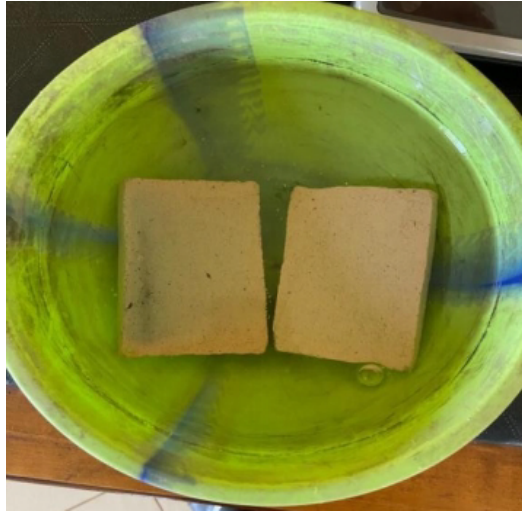


Figure 5: Samples submerged in water



Figure 6: Wet samples being weighed

After 15 minutes, the sample was taken out of the water and weighed as shown in Figure 6 to get the saturated weight. The porosity measures the volume of pore spaces formed within the material, and an increase in porosity means there are more empty spaces within the sample. The bulk density on the other hand measures the weight of the solid per unit volume, including both solids and pores. The porosity and bulk density of the samples are determined based on Equations (2) and (3) respectively.

$$\text{Apparent porosity, } P(\%) = \frac{w - D}{w - S} \times 100 \quad (2)$$

where w = saturated weight, D = dried weight, S = suspended weight.

$$\text{Bulk density, } D = \frac{W}{V} \quad (3)$$

where W = dry weight, V = Volume of sample = $L \times B \times H$

2.5. Thermal Conductivity Test

For the purpose of determining the thermal conductivity of the samples, the following procedures were carried out. As shown in Figure 7, each sample was wrapped with ceramic fiber on the four sides to prevent the heat losses from those sides to the surrounding, and instead the heat be directed vertically upwards to the outer surface of the sample. The unwrapped surface of each sample was in turn placed on a hot plate with a steady heat supply at 450°C , to allow heat transfer through the surface in direct contact with the hot plate to the outer surface exposed to the ambient air. After every 5 minutes, the temperature of the outer surface exposed to the ambient air was measured using an infrared thermometer until a steady state was reached. The temperatures were recorded in order to determine the thermal conductivity of the respective samples.

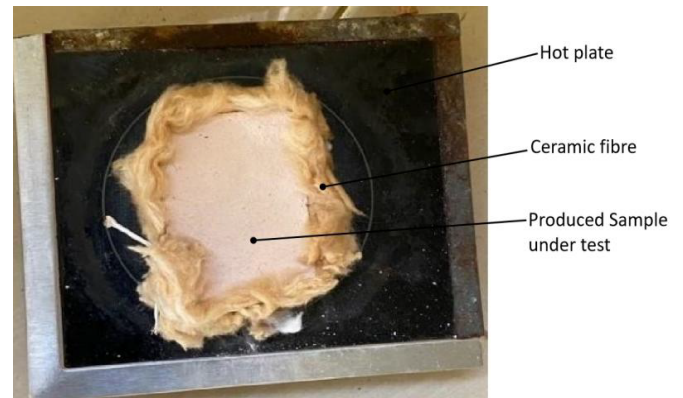


Figure 7: Thermal conductivity test set-up

The thermal conductivity [11] of the samples was determined based on Equation 4.

$$\text{Thermal conductivity, } k = \frac{Q \times \Delta x}{A \times \Delta T} \quad (4)$$

where Q = quantity of heat transferred,

Δx = distance between two isothermal planes,

A = surface area of each sample,

ΔT = temperature difference

Equation 4 gives the first order approximation in determining thermal conductivity of the samples, which is very essential considering the complex differential equations prior to numerical modelling. The sample material properties were assumed constant and independent of temperature.

3. Results and Discussion

The design and structure of the inner liner of cook stoves are to minimize heat loss to the surrounding and to improve the thermal efficiency. The samples made of clay, kaolin, with rice husk as a biomass additive were fired in a kiln to determine the mixture

composition that could minimize heat loss and improve the thermal efficiency of cook-stoves. In this section, the shrinkage, porosity, bulk density and thermal conductivity tests results of the sample are analyzed.

3.1. Shrinkage and Breadth

Clay shrinks when dried and fired because of the organic materials that burnt out at high temperature forming pores, leading to loss in dimensions and weight. The amount of shrinkage depends on the type of clay in use. In depth understanding of how clay shrinks is an important factor when taking the final size of the product into consideration. The influence of biomass additive on the shrinkage and weight loss after firing the considered sample mixtures of clay, kaolin and rice husk in Tables 1 to 4 are presented in Figures 8 to 12.

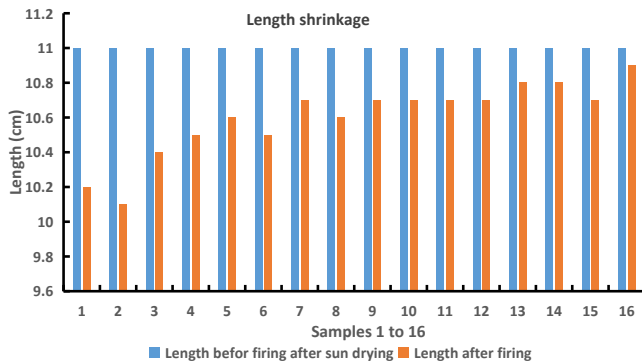


Figure 8: Length shrinkage of the samples

Figure 8 shows the influence of the rice husk additive on the length shrinkage of the fired samples. As expected, it can be seen the length of the samples shrunk after firing in the kiln depending on the quantity of the additive added in the mixture.

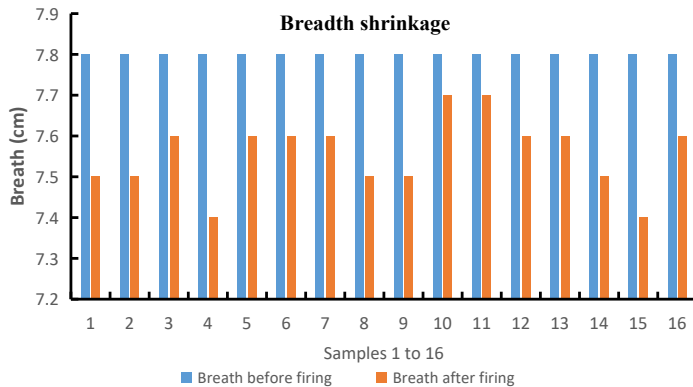


Figure 9: Breadth shrinkage of the samples

Figure 9 shows the influence of the rice husk additive on the breadth shrinkage of the samples. It can be observed that the breadth of the samples decreased after firing due to the different percentages of the added additive that burnt out at high temperature of the kiln.

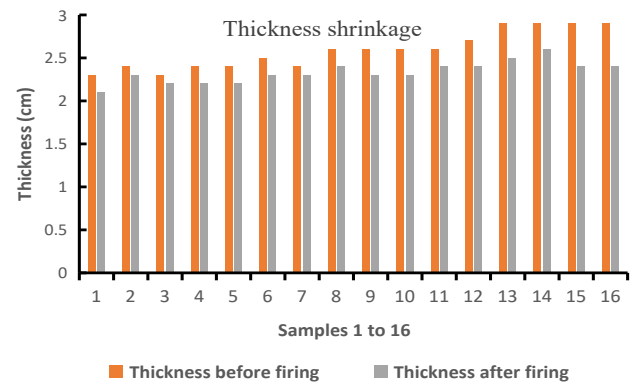


Figure 10: Thickness shrinkage of the samples

Figure 10 shows the influence of the additive on the thickness shrinkage of the fired samples. It can be seen that the thickness also shrunk after firing the samples in the kiln.

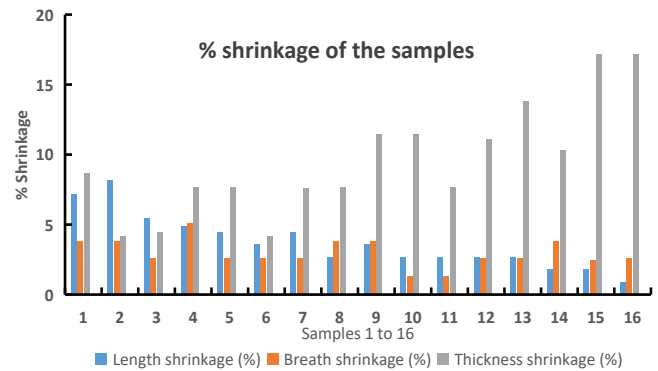


Figure 11: % Shrinkage of the samples

Figure 11 compared the shrinkage effect on the length, breath and thickness of the samples. It can be observed that the shrinkage affected the thickness more than the case of the length and breath of the samples.

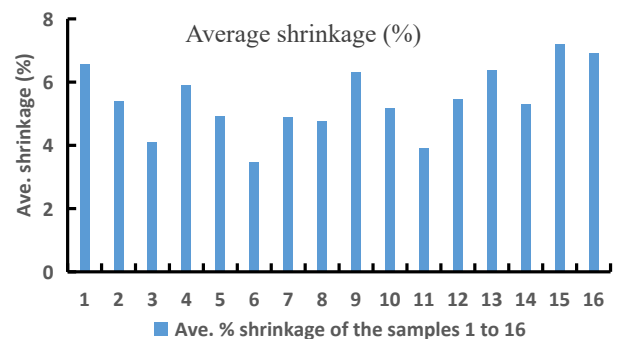


Figure 12: Average shrinkage of the samples

Figure 12 shows that the shrinkage are different for different proportion of the additive added in the samples.

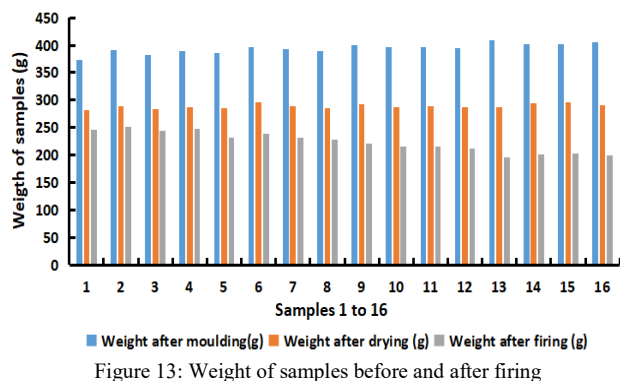


Figure 13: Weight of samples before and after firing

Figure 13 shows that weights of the samples are different and decreased after firing due to the different percentages of the rice husk additive that burnt out at high temperature of the kiln.

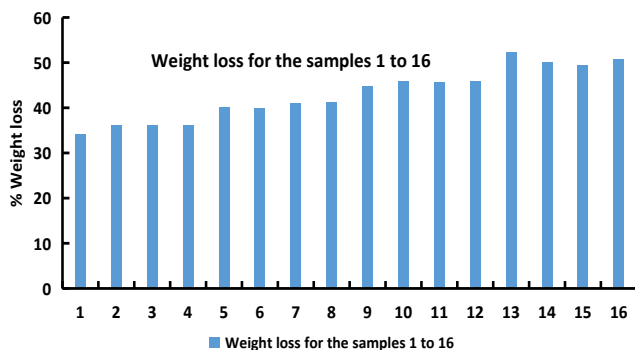


Figure 14: Weight loss of the samples

Figure 14 shows that samples with 30% rice husk lost more weight compared to those with 20%, 10% and 0% rice husk additive. The samples with 30% rice husk lost about half of its weight, while those without rice husk lost only about 35%. This result is in agreement with that of Arthur [12]. It confirms that, the higher the shrinkage, the denser and less porous the material. They observed relatively higher values of firing shrinkage with decreasing amount of additives may be attributed to conversion of additives into ashes.

3.2. Porosity and Bulk Density of the Samples

Porosity is an important factor in determining the heat conduction through the clay samples. Samples with high porosity often have a low thermal conductivity and hence better insulation. Also, such samples possess a low bulk density, which reduces the overall weight.

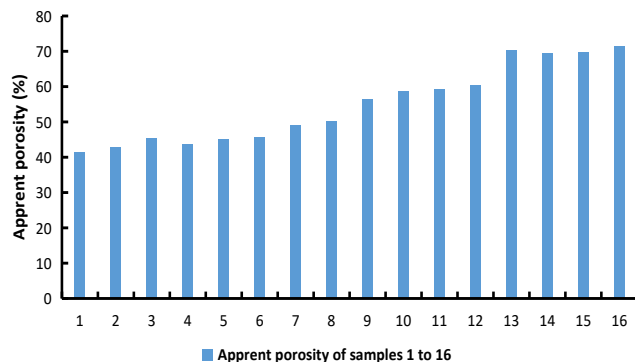


Figure 15: Apparent porosity the samples

Figure 15 show the influence of the rice husk additive on the porosity of the samples considered in this study. It indicates that the porosity increased with an increase in the percentage of rice husk in the samples (S_1 to S_{16}).

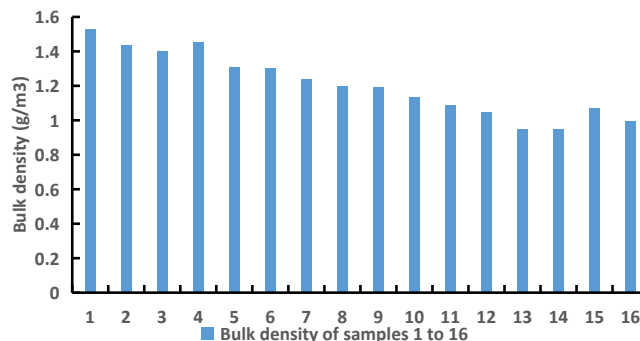


Figure 16: Bulk density of the samples

Figure 16 shows the influence of the rice husk additive on the bulk density of the samples. It can be observed that the bulk density of the samples decreased with the increase in the percentage of rice husk in the samples (S_{1-4} = 0% rice husk, S_{5-8} = 10% rice husk, S_{9-12} = 20% rice husk, to S_{13-16} = 30% rice husk,).

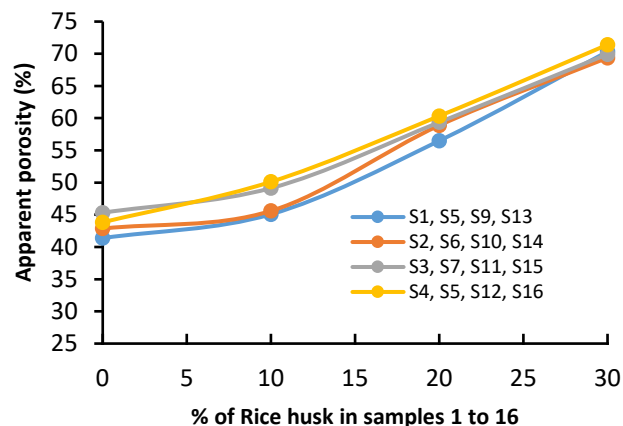


Figure 17: Influence of % rice husk on the % apparent porosity of the sample

Figure 17 shows an increase in the porosity of the samples as the percentage of the rice husk increased. This indicates that the bulk density is indirectly proportional to the percentage of rice husk additive in the sample.

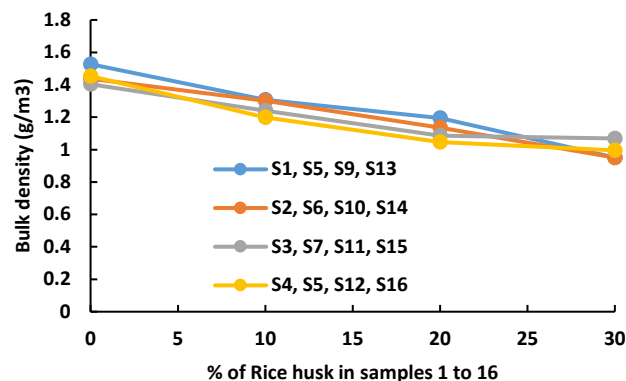


Figure 18: Influence of % rice husk on the bulk density of the samples

Figure 18 shows a decrease in the bulk density of the samples as the percentage of the rice husk increased. From Figure 17, S_{16} which has 30% rice husk has a higher porosity value (71.41%) than S_5 (45.08%) which has 10% rice husk. This result is in line with the tests carried out by [13] and [14] on the effect of rice husk and rice husk ash on properties of clay bricks, which indicated that the porosity increased from 21% to 64% and bulk density decreased from 1.78g/cm^3 to 0.73g/cm^3 as the percentage of rice husk in the sample increased from 0% to 30%. Also in [15] and [16], the authors worked porosity tests and found that the apparent porosity of the clay was 15.38% while those with the additives were 23.91, 34.09, 44.89, and 42.85 for 5%, 10%, 15% and 20% respectively.

3.3. Thermal Conductivity of the Samples

Thermal conductivity tests are important for insulation applications where thermal gradients dictate the use of a material for refractory applications. Thermal conductivity depends not only on the properties of clay but also on the geometry and quantity of the additives. Figure 19 shows the influence of percentage (%) by weight of rice husk additive on the thermal conductivity of the samples (S_1 to S_{16}), based on the procedure presented in Figure 7. For all the tested samples, the value of thermal conductivity is lower with the higher percentage of the rice husk additive, which is in line with work of Arthur [12].

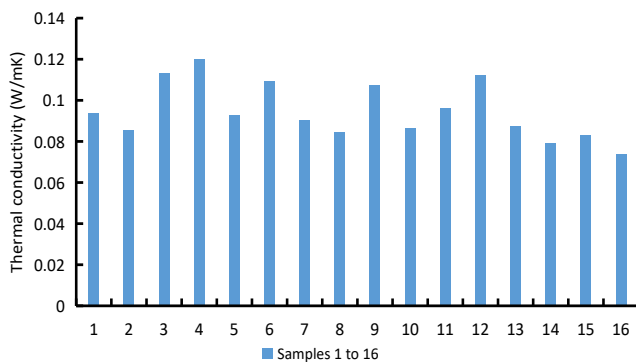


Figure 19: Influence of % rice husk on the thermal conductivity of the samples

This can be due to the increase in pores arising from the burning off the additive that created pores in the internal structure of the samples. This reduces the heat flow rate in a porous medium causing a decrease in thermal conductivity of the samples. As such, the percentage increase in the rice husk additive improves the sample's thermal insulating properties as more pores were created in the micro-structure of the samples. This indicates that the mixture of clay and kaolin with rice husk is more insulating than the unreinforced clay, since the rice husk is primarily responsible for creating the thermally insulating pores.

Figures 20 to 23 show the temperature variations at interval of 5 minutes where the considered samples with 0%, 10%, 20% and 30% of rice husk additives were subjected to a steady heating for 25 minutes during the thermal conductivity tests experiment presented in Figure 7.

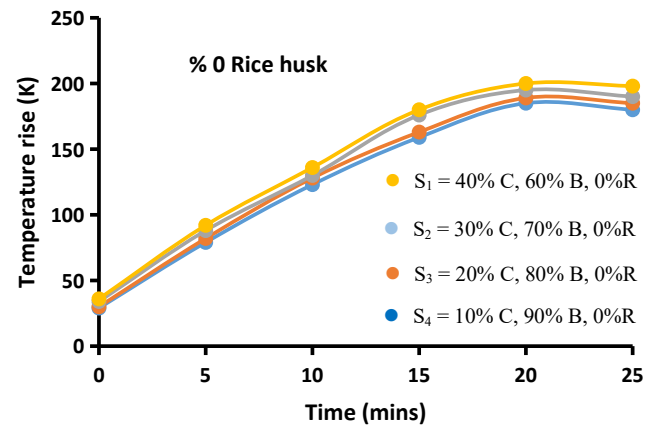


Figure 20: Temperature rise for samples with 0% rice husk

Figure 20 shows the temperature rise for the samples case with 0%, of rice husk additive subjected to a steady heating for 25 minutes.

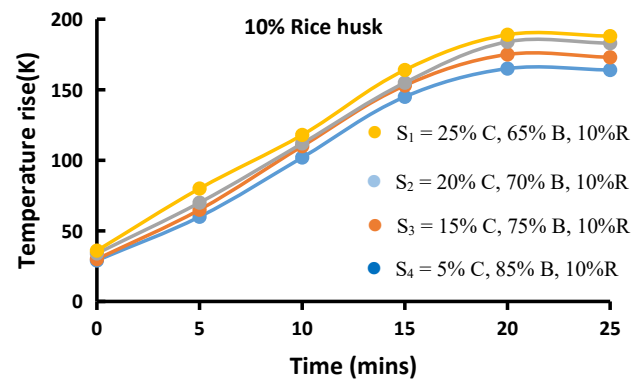


Figure 21: Temperature rise for samples with 10% rice husk

Figure 21 shows the temperature rise for the sample case with 10%, of rice husk additive subjected to a steady heating for 25 minutes.

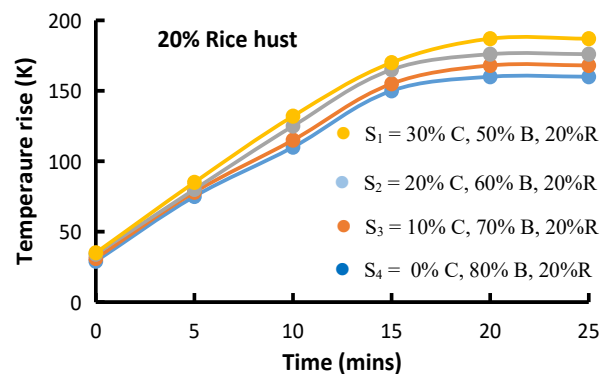


Figure 22: Temperature rise for samples with 20% rice husk.

Figure 22 shows the temperature rise for the sample case with 20%, of rice husk additive subjected to a steady heating for 25 minutes.

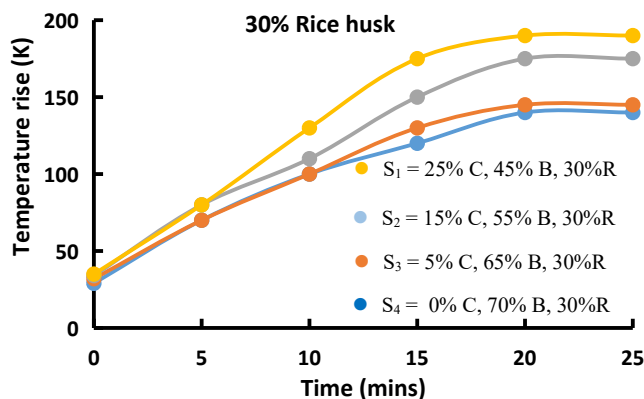


Figure 23: Temperature rise for samples with 30% rice husk

Figure 23 shows the temperature rise for the sample case with 30%, of rice husk additive subjected to a steady heating for 25 minutes. It can be observed from Figures 20 to 23 that the temperature of the samples with 0%, 10%, 20% and 30% rice husk additives increased steadily till they reached steady state at approximately 25 minutes. It can also be observed that the temperature of the samples decreased with an increase in the percentage (%) of rice husk additive in the samples. Figures 20 to 23 also showed different thermal performance capability of the samples with the rice husk additives in reducing the heat loss by conduction across the wall thickness of the samples, if such rice husk additive is used in producing the inner liner of a biomass cook-stove. The difference in thermal performance of the samples could be due to the increase in porosity created by the increase in the rice husk additive, as well as the micro-structural changes that occurred when the samples were fired at high temperature. Obviously, the thermal conductivity value decreases with an increase in the percentage of the rice husk additive resulting from the increase in pores created in the micro-structure, which reduces the heat flow rate in the porous medium, thereby causing a decrease in thermal conductivity of the samples.

4. Conclusion

The inner liner of a biomass cook-stove is a vital part of the combustion chamber of a cook-stove. This study has investigated the influence of rice husk additive on the fired clay and kaolin mixture to determine the suitable proportion for producing the inner liner of a cook-stove that improves its insulation performance and thermal efficiency, and still maintain low bulk density. It was found that the apparent porosity of the samples increased with an increase in the rice husk additive and the bulk density decreased. This indicates that the rice husk is very effective in creating pores in the produced samples making them more porous and reducing the bulk density, hence reducing the overall weight. It was also found that the thermal conductivity of the samples decreased with an increase in the rice husk additive due to the increase in pores, which reduces the heat flow rate in a porous medium, and thus causing a decrease in thermal conductivity of the samples. This study shows the prospect of using rice husk additive to enhance the insulation performance of the inner liner of cook-stoves, thereby contributing in producing a more efficient and environmentally friendly cooking device.

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Data availability: The datasets generated during and/or analysed during the current study are available from the corresponding author on reasonable request.

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GC4miRNA - a Pipeline for Examining Impact of GC Content in miRNA Seed Sequences on Expression in Tumor Samples

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ABSTRACT

MicroRNAs (miRNAs) are small RNA molecules that play a crucial role in regulating gene expression by binding to and degrading targeted mRNAs. miRNAs targeting a specific mRNA have a region known as the “seed sequence”, which typically has a high affinity for its complementary sequence in the targeted mRNA. Single Nucleotide Polymorphisms (SNPs) are mutations that refer to the substitution of a single nucleotide. Alterations in the nucleotides of seed sequences can have a significant impact on the targeting strength between miRNAs and mRNAs, potentially resulting in dysregulation of genes, and causing various diseases, including cancers. It is crucial to assess the impact of SNPs will have on nucleotides in specific seed sequences by gauging a common factor (e.g. GC content) reflecting the binding affinity.

GC content is an essential aspect in miRNA binding, since high GC content miRNAs are frequently more stable, and may have a stronger affinity for their targets. To reveal the GC content signature for cancer-associated miRNAs, we developed a bioinformatics pipeline called GC4miRNA, which can calculate GC percentage enrichment in a sequence and perform statistical analysis to compare the GC content between the seed sequence and whole sequence for targeting miRNAs using customized BASH and R scripts. The pipeline was implemented as an R Shiny application that carries out several tasks/modules, such as measuring similarities between miRNAs whose dysregulation is linked to cancer and identifying common patterns within miRNAs with greater GC content.

1. Introduction

The Cancer Genome Atlas (TCGA) is a project initiated by the National Cancer Institute to characterize cancer-causing biomarkers(<https://www.cancer.gov/tcga>) through the storage of omics data. There are 33 cancer subtypes that have been studied in the project. Much of this data has already been examined in different aspects; however, there are still many areas that have yet to be fully explored, particularly in the realm of miRNA.

MicroRNAs (miRNAs) are small molecules that regulate gene expression by targeting the 3'UTR region of genes. The specific targeting relationships between miRNAs and mRNAs can become incredibly complex because miRNAs can target multiple mRNA, or multiple miRNAs might be needed to target one mRNA [1]. The seed sequence of each miRNA is a region that facilitates the binding between miRNA and mRNA. This binding affinity is usually affected by the GC content of the seed sequence [2].

Single Nucleotide Polymorphisms (SNPs) are mutations that alter a single nucleotide. In cancers, miRNA could undergo mutations in their target sequences, or mutations could also affect the 3' UTR of genes. Perfect base pairing between most of the seed sequence and its target is often needed for functional miRNA binding [3]. SNPs in seed sequences could disrupt the binding affinity between miRNAs and mRNAs. Over the years, many efforts have been made to elucidate the variations caused by SNPs across individuals, such as the 1000 Genome Project [4].

Motifs are short nucleotide sequences which usually have biological significance, such as acting as binding locations. Existing tools, such as MEME [5], are commonly used to identify motifs, which can then be analyzed for specific functions. So far, many bioinformatics tools have been developed to identify motif sites in the context of miRNA binding mechanisms using different computational approaches.

There is an urgent need to develop bioinformatics tools and methods to reveal the GC content signature for cancer-associated miRNAs. In this project, we developed a RShiny application that utilizes a pipeline of bioinformatics resources to calculate GC content, characterize differential expression patterns of miRNAs, perform statistical analysis for identified patterns, and determine important motifs within miRNA sequences.

2. Experimental Methods

To create this pipeline, we aimed to use the following steps to analyze the GC content signatures of the test dataset. The workflow of pipeline is shown in figure 1.

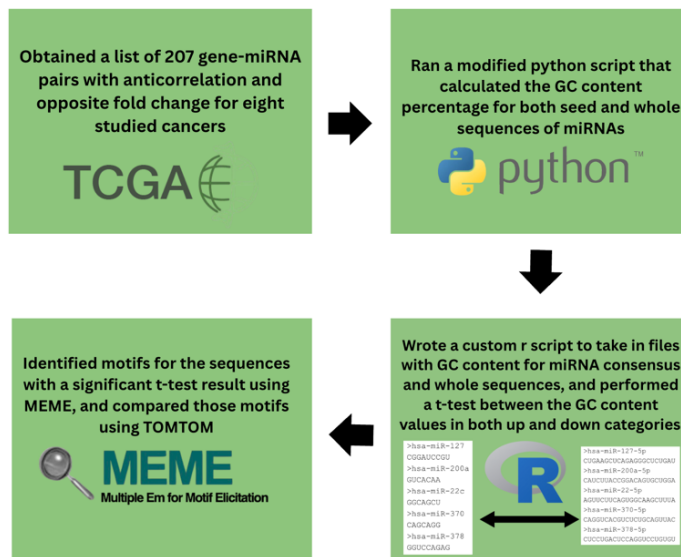


Figure 1: Workflow of the pipeline to analyze GC content in seed sequences

1.1. Locate Seed Sequences of Cancer-Associated miRNAs

We downloaded a dataset from a previously published study [6] that found 238 miRNA-gene pairs whose dysregulation was associated with eight TCGA cancers. These pairs were initially discovered using the miRNA target prediction tools targetScan [7], targetProfiler [8], and miRanda [9], so these same tools were

used with default parameters to find seed sequences for each miRNA-Gene pair. To find seed sequences with targetProfiler, we looked at the hairpin sequence that was generated, and recorded the nucleotides that were in a row, and thus more likely to be the seed sequence. Algorithm results could differ slightly in nucleotide sequence and length, so we kept only the sequences where at least two algorithms predicted the same result, or only one algorithm predicted a result. We generated logos (example shown in Figure 2) with WebLogo [10] for the consensus sequences with positive and negative correlation coefficients in tumor samples.

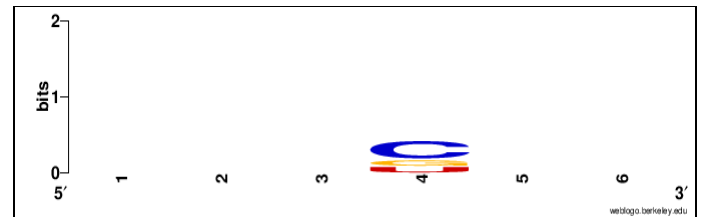


Figure 2: Logo generated for Consensus Sequences with a negative correlation coefficient for Head and Neck Squamous Cell Carcinoma (HNSC)

1.2. Retrieve miRNA 5p and 3p Sequences

We downloaded a file from miRbase [11] to find the complete sequences of miRNAs within our dataset. In order to efficiently search through this file for the relevant information, we compiled a list of every unique miRNA within our data and found the nucleotide sequence of the 5p and 3p strands of mature miRNA, before processing it. In some cases, it was unspecified whether the only given sequence was the 5p or 3p strand, so it was categorized as “Unclassified”. (Supplementary Table 1)

1.3. Calculate Normalized GC content

In order to calculate GC content for our Consensus, 5p, and 3p Sequences, we employed VectorBuilder’s “GC content Calculator” [12], which found GC content as well as the number of G’s and C’s in each sequence. To speed up the process, we also used a BASH script available in Github [13] that could calculate GC content for all sequences within a FASTA file. Due to the varying lengths of the seed sequences (6-8 nucleotides), we developed a formula (eq. 1) to calculate normalized GC content for each miRNA. When calculating normalized GC content for 5p and 3p sequences, we disregarded unclassified sequences from the total count of miRNAs.

$$norm(GC) = \frac{\#GC \times 100}{\#NC \times \frac{\#Total\ GC}{\#miRNA}} \quad (1)$$

Formula for normalizing GC content of miRNA sequences. (Note: #NC is the nucleotide count in that specific miRNA, #Total GC is the total number of G’s and C’s for that specific kind of miRNA sequence in the cancer, and #miRNA is the number of miRNAs that are associated with the cancer)

1.4. Identify Differentially Expressed miRNAs

Next, we utilized the dbDEMC database [14] of experimental data to find whether the miRNAs we were examining were being upregulated or downregulated within the cancers their

dysregulation was associated with. We downloaded a file containing all the experimental and expression information from dbDEMC, before applying Unix commands to retrieve the necessary information. We only kept experiments that analyzed TCGA data, since our original pairs were selected by studying TCGA datasets. Finally, we reported the differential expression of miRNAs, as well as the experimental ID of the experiment where the information was drawn from.

1.5. Calculate Statistical Significance of GC content in Consensus Sequences

We created an R script to run a Student's t-test on the GC content between consensus and 5p sequences within groups with different differential expressions for each cancer. We considered any result with a p-value below 0.05 to be significant.

1.6. Identify Significant Motifs for Differentially Expressed miRNAs

After finding out which 5p sequences had a significant difference in GC content from their consensus sequences, we ran MEME with default parameters to find the top three motifs of all miRNA 5p sequences with a certain differential expression. We considered any motif with an E-value below 0.05 to be significant.

2. Results

2.1. Identified Sequences of Mature miRNAs

We found mature sequences for all our miRNAs, but roughly 14 sequences had an unclassified rating, and were not included in any of our mature-miRNA analysis. Although LUSC has the highest proportion of unclassified miRNA sequences, there were only four pairs within our study associated with LUSC. The miRNAs associated with KICH had no unclassified sequences.

2.2. Calculated and Normalized GC content of miRNA Sequences

We reported that the average normalized GC content for all mature miRNAs was similar between most cancers. The average GC content for 5p and 3p miRNA sequences were very similar (~5%). However, the average normalized GC content for upregulated seed sequences was higher (by 4% or more) than downregulated seed sequences for BLCA and THCA. In LIHC and LUSC, downregulated miRNAs had average normalized GC contents that were higher (by 3% or more) than upregulated miRNAs. There was a less than 1% difference in average GC content between the two groups for HNSC, KICH, and THCA.

Table 1: Average normalized GC contents of miRNAs for consensus, 5p, and 3p sequences in investigated cancers, with the parentheses containing the averages for upregulated and downregulated miRNAs only

Cancer	Average normalized GC content for consensus sequences	Average normalized GC content for 5p sequences	Average normalized GC content for 3p sequences
BLCA	14.45% (19.64%,12.94%)	4.89% (5.67%, 5.15%)	4.95% (6.04%, 4.62%)

HNSC	14.13% (13.75%,14.65%)	4.51% (4.42%, 4.65%)	4.54% (4.14%, 4.72%)
KICH	13.89% (13.18%,13.23%)	4.55% (4.51%, 4.64%)	4.55% (4.67%, 4.70%)
KIRP	13.98% (15.04%,11.42%)	4.50% (4.60%, 4.39%)	4.52% (4.69%, 3.98%)
LIHC	13.98% (13.51%,16.59%)	4.48% (4.24%, 5.08%)	4.52% (4.35%, 5.27%)
LUSC	14.29% (13.45%,16.81%)	4.55% (4.41%, 4.81%)	4.61% (4.23%, 5.37%)
THCA	13.78% (13.99%,14.41%)	4.51% (4.39%, 5.52%)	4.57% (4.48%, 5.78%)
UCEC	14.49% (17.36%,13.30%)	4.51% (4.21%, 4.93%)	4.52% (4.56%, 4.44%)

2.3. Differential Expression and Gene Analysis results

We identified differential expression patterns based on TCGA data for most of our miRNAs, and found that for most cancers excluding THCA, there were more cases where miRNA was upregulated or downregulated. To elucidate the functions of the genes which these miRNAs were targeting, we used gProfiler [15] and ClueGo [16] to find commonly enriched terms in each cancer (Supplementary Table 2). In KIRP, three genes were annotated by ClueGo which are involved within the process of aldehyde metabolism. In LIHC, two genes: *PRKCZ* and *ADCY4*, were reported to be involved in eight different pathways, such as G-Protein, Relaxin, Chemokine, and Rap1 signaling. SiRNA knockdowns of *PRKCZ* have been known to decrease cancer cell migration and invasion [17] and shown in figure 3.

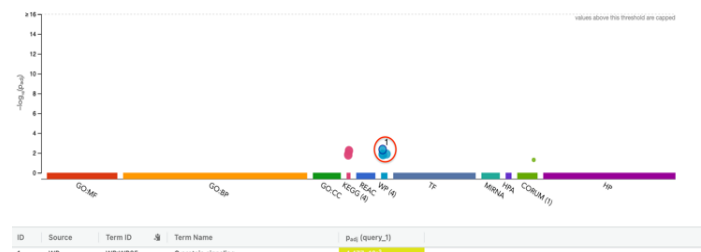


Figure 3. gProfiler gene annotation result for LIHC, circled cluster contains *PRKCZ* and *ADCY4*.

2.4. Statistical Analysis results

Our Student's t-test confirmed the significance of the GC content within all our miRNAs except for LUSC, which had only 4 miRNA sequences. Overall, the p-values were below 0.01 for all cancers (Table 2), and the GC content difference between consensus and whole sequences for upregulated miRNAs seemed to be more significant than downregulated ones in most cancers, possibly indicating that upregulated miRNAs were more enriched with GC content within their seed sequences, though this needs further testing on a much larger scale. For KIRP, a very significant p-value could be due to its bigger sample size (more than 40 miRNA-gene pairs).

Table 2: T-test statistics (p-value for seed sequence of miRNA when compared to the whole sequence)

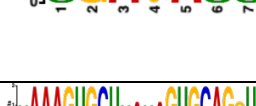
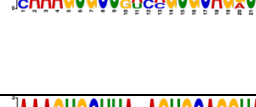
Cancer	Up	Down
BLCA	p-value = 0.008733	p-value = 0.005622
HNSC	p-value = 3.059e-06	p-value = 5.553e-06
KICH	p-value = 5.52e-08	p-value = 0.0002546
KIRP	p-value < 2.2e-16	p-value = 0.0001013
LIHC	p-value = 9.975e-07	p-value = 0.001259
LUSC	p-value = 0.2229	"not enough 'x' observations"
THCA	p-value = 4.863e-12	p-value = 0.02901
UCEC	p-value = 0.00305	p-value = 0.009271

(Note: bolded p-values are significant)

2.5. Motif Analysis results

After generating logos for the miRNAs with a significant GC content with MEME and inspecting their E-values, we discovered five significant (E-value<0.05) motifs for upregulated miRNAs in HNSC, KICH, KIRP, LIHC, and UCEC (Table 3). We also found one significant logo for BLCA in downregulated miRNAs (data not shown). There are more GC content-based motifs in upregulated miRNA sequences compared to downregulated miRNA sequences, which could be explained by our previous observation that there is more enriched GC content in upregulated miRNA sequences.

Table 3: Significant motifs present in upregulated miRNA sequences for selected cancers

Cancer	miRNA IDs	E-value	Logo
HNSC	<i>hsa-mir-183</i> <i>hsa-mir-182</i> <i>hsa-mir-1296</i>	3.6e-002	
KICH	<i>hsa-mir-182</i> <i>hsa-mir-1266</i> <i>hsa-mir-629</i> <i>hsa-mir-183</i> <i>hsa-mir-222</i> <i>hsa-mir-589</i>	9.5e-003	
KIRP	<i>hsa-mir-17</i> <i>hsa-mir-20a</i> <i>hsa-mir-106b</i> <i>hsa-mir-93</i>	4.1e-011	
LIHC	<i>hsa-mir-17</i> <i>hsa-mir-20a</i>	2.7e-002	
UCEC	<i>hsa-mir-106b</i> <i>hsa-mir-17</i> <i>hsa-mir-183</i> <i>hsa-mir-301a</i>	3.3e-002	

2.6. GC4miRNA RShiny App

We combined all our developed modules into one application, and we uploaded a variety of resources along with

individual programs and instructions into a GitHub page (<https://github.com/braydonlu/GC4miRNA>), so that it could be downloaded and run locally.

Module 1 was the customized GC content calculator, which was made by converting the source code from “Abby’s Amazing GC Calculator” publicly available in GitHub into a RShiny script. A screenshot of Module 1 is shown in figure 4.

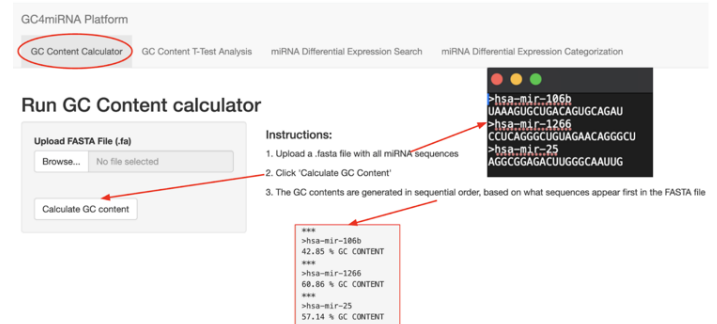


Figure 4. Layout of Module 1 as well as how instructions on how to use

Module 2 can take GC content information to test the statistical significance between miRNA seed sequences and whole sequences for each category using a Student's t-test. A screenshot for Module 2 is shown in figure 5.

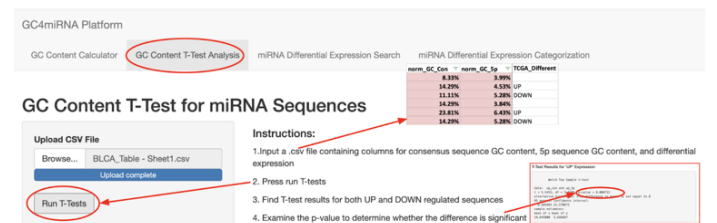


Figure 5. Layout of Module 2 as well as how instructions on how to use

Module 3, which we developed, can search through dbDEMC to find expression data, by using an input list of miRNAs to search through a dbDEMC dataset. A screenshot for Module 3 is shown in figure 6.

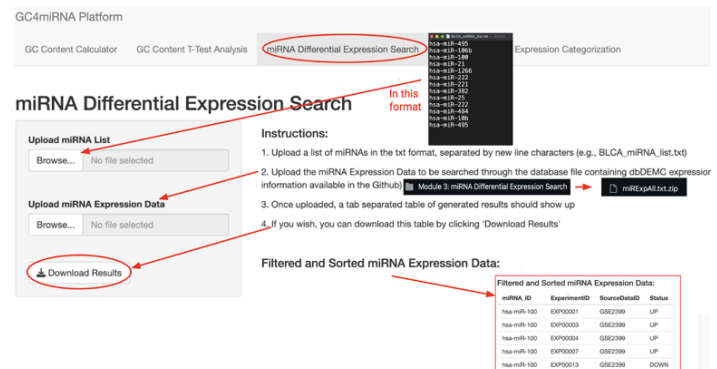


Figure 6. Layout of Module 3 as well as how instructions on how to use

Module 4 can generate FASTA files used for running motif detection software. Specifically, it works by reformatting a list containing miRNA IDs and sequences into FASTA files. The screenshot for Module 4 is shown in figure 7.

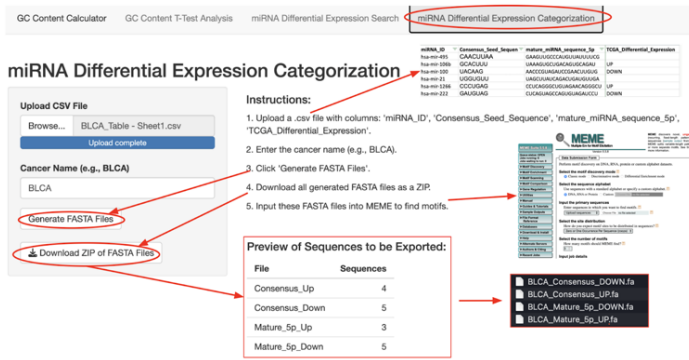


Figure 7. Layout of Module 4 as well as how instructions on how to use

3. Discussion

In this study, we developed a RShiny application with several modules to evaluate GC content within seed sequences of cancer-associated miRNAs, and to identify significant motifs within these miRNA sequences. We also utilized a novel method of normalizing GC content for miRNA seed sequences, so that sequence length would not bias our results. This allows us to analyze the relationship between miRNA expression in tumor cells and the GC content in seed sequences, helping to explain changes in binding affinity that can lead to gene dysregulation in cancer.

We used the GC content statistical analysis module to identify if any miRNA seed sequences would have significantly more GC content within its seed sequence than the whole sequence. After normalizing our calculated GC content, we found that every input list of miRNAs associated with studied cancer types, except those associated with LUSC, had seed sequences with a significant (p -value < 0.05) GC content compared to the rest of the sequence. This is interesting, because for miRNA seed sequences to have strong binding affinities, they could have high GC content. According to a previous study [18], high GC content within miRNA seed sequences has been associated with higher percentages of seed-pairing targets, and our results suggest that miRNAs with GC-rich seed sequences are highly important in regulating multiple gene pathways.

After categorizing most of our miRNAs with the miRNA differential expression search module, we also found that most upregulated miRNAs tended to have more significant p -values than downregulated miRNAs based on the results from Student's t -test. This could imply that changes in seed sequences with high GC content are likely to cause that miRNA to lose some of its functionality and thus lead to its upregulation to achieve the normal level of gene regulation.

Additionally, many of these upregulated miRNAs had significant (E -value < 0.05) motifs within its 5p miRNA sequence, which could indicate these motifs are important to the functionality of miRNA binding. Alteration of GC content, as well as conserved motifs, might imply a role in how that miRNA is expressed within tumor samples [19].

We have demonstrated that our pipeline is able to conduct analysis on GC content relating to its effect on regulation of miRNAs in tumor cells. Through working with an example dataset of 207 miRNA-gene pairs, we were able to identify some interesting results for several TCGA cancer types we studied. KICH had extremely low p -values ($< 3e^{-4}$) for its Student's t -test, and when we used MEME to find motifs, KICH had a significant motif, with an E -value of $9.5e^{-3}$. We further examined the 7-nucleotide long motif we found by checking TOMTOM [20], and we found matches to motifs within genes coding for zinc finger formation in mouse analogs. Some members in the zinc finger protein family have been found to be important biomarkers in kidney cancer [21,22].

The gene ontology results for KICH also had consistently low p -values for each enriched term. In our gene functional analysis, we determined that two genes, *FTCD* and *MTHF1D*, were enriched with terms such as "Histidine Metabolic Processes" and "Disorders of folate metabolism and transport". These processes are crucial in many different types of cells, but can also prolong the longevity of tumors; upregulation of *MTHF1D* in cancer cells has been associated with worse prognosis for oral squamous cell cancer patients [23]. We looked at the miRNAs associated with these two genes and discovered both were targeted by *has-miR-625*. A previous study on renal carcinomas specifically examined the impact of *hsa-miR-625-3p*, and found that it promoted cell migration and invasion, and reduced apoptosis [24]. However, this study did not mention the impact of *FTCD* and *MTHF1D* in its gene ontology results. Additionally, *has-miR-625* was not found in the list of miRNAs containing the significant motif for LIHC, indicating that it might have a different conserved sequence.

Through our pipeline, we were able to analyze GC content rich seed sequence motifs that may play important roles in gene regulation involving oncogene or tumor suppressor pathways. For future research, we hope to uncover the roles of specific mutations in disrupting binding patterns, and how the dysregulation of genes could cause certain cancers. We could apply machine learning methods to predict the specific effects of miRNA mutations on its binding affinity by analyzing how these binding patterns impact both primary sequence recognition and secondary sequence conformation. This machine learning algorithm could be trained on trained on experimentally validated miRNA-mRNA interaction datasets, and its results could be cross-referenced with publicly available transcriptomics profiles from cancer patient cohorts. This way, we could potentially identify specific mutations within seed sequences that are most associated with dysregulated oncogenic pathways.

We worked with a very limited dataset in this study, so we believe that our findings could be strengthened through incorporating more samples. This may be achieved through studying the International Cancer Genome Consortium Accelerating Research through Genomic Ontology (ICGC ARGO) database (<http://platform.icgc-argo.org>) [25].

Conflict of Interest

The authors declare no conflict of interest.

Acknowledgment

The results published here are in whole or part based upon data generated by the TCGA Research Network: <http://cancergenome.nih.gov/>

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