# Quantum Lattice Learning and Explainable Artificial Intelligence for Maternal and Child Healthcare

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A thesis submitted to the Department of Computer Science and Engineering
in partial fulfillment of the requirements for the degree of
Master of Science in Computer Science and Engineering

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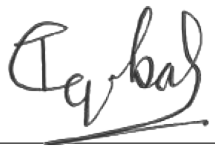

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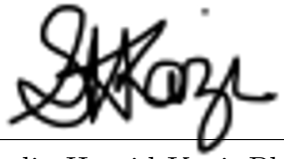

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# Ethics Statement

This thesis was carried out in complete compliance with research ethics, norms and codes of practices set by BRAC University. I have ensured that all the sources have been cited.
As the Author of this thesis, I take full responsibility for any ethics code violations.

# Abstract

The current approach to maternal and child healthcare is extremely patient-centred, it requires costly, risky surveillance and testing before diagnosis besides treatment accompanied with uncertainty despite the essential combination of healthcare expertise, skills and experience in medical care and public health for medical practitioners to support maternal and child health.
With the recent maternity and prenatal engagement besides the availability of health data and information, we interpretably revolutionize advances in maternal medicine by turning massive amounts of data into proactive, predictive, preventive, personalized and participatory optimal treatment plans through predictive and preventive medicine for maternal and child well being.
This work focuses on interpretable predictive and Machine Learning (ML) modelling of Artificial Intelligence (AI) algorithms to be used in predictive analytics of health data for maternal precision medicine and explainable preventive insights for physicians and patients' medical decision making. We also introduced the concept of Quantum Lattice Learning for building Explainable Machine Learning models in Quantum Space.
Due to the uncertainty caused by abstracted black-box AI and ML models (algorithms) used to support the maternal-child medical decisions, there is ambiguity of safety and trust of all the existing and proposed AI models. That hinders reliability and trust in adoption of the developed models by physicians and patients. We, therefore, implemented Explainable Artificial Intelligence (XAI) and feature interpretability analysis to allow clinicians like obstetricians, perinatologists, gynecologists and midwives to understandably trust, comprehensively assess connections and transparently analyze and use the important derived features for strategic maternal and child predictive, preventive and precision medicine.
The adoption of the proposed XAI approaches (models) on health data usage could potentially strengthen health systems, public health, primary and surgical care for mothers and children globally. They can significantly improve accountability, reliability and adoption of safe and trusted artificial intelligence applications for improved maternal-fetal medicine besides global health. Moreover, our transparent models provide useful insights for healthcare management and policy-making to improve the health and well-being of patients and physicians.

**Keywords:** Explainable Artificial Intelligence (XAI); Quantum Lattice Learning (QLL); Machine Learning (ML); Maternal and Child Health (MCH); Predictive, Preventive and Precision Medicine (PPPM); Patient Monitoring and Management;

# List of Publications

1. **Ggaliwango Marvin**, Md. Golam Rabiul Alam (2021). "A Machine Learning Approach for Predicting Therapeutic Adherence to Osteoporosis Treatment" IEEE CSDE 2021 (Asia-Pacific Conference on Computer Science and Data Engineering 2021).- - - *[**Won the IEEE CSDE 2021 Developing Country Researcher Award]***

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5. **Ggaliwango Marvin**, Md. Golam Rabiul Alam. (ICISET) 2022. "Explainable Augmented Intelligence and Deep Transfer Learning for Pediatric Pulmonary Health Evaluation. (2022 International Conference on Innovations in Science, Engineering and Technology)

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By signing below I confirm that Ggaliwango Marvin was the principle investigator of the research projects and significantly contributed to the Conception, Research Design, Data collection, Analysis, Article Drafting, Critical Revision and Final Presentation of the research project outcomes for the research papers and poster presentation entitled the following:

1. A Machine Learning Approach for Predicting Therapeutic Adherence to Osteoporosis Treatment.
2. Cardiotocogram Biomedical Signal Classification and Interpretation for Fetal Health Evaluation.
3. Explainable Feature Learning for Neonatal Intensive Care Unit (NICU) Admissions.
4. Explainable Artificial Intelligence for Hematologic Pediatric Patient Survival Prediction upon Stem Cell Transplantation.
5. Explainable Augmented Intelligence and Deep Transfer Learning for Pediatric Pulmonary Health Evaluation.
6. An Explainable Lattice based Fertility Treatment Outcome Prediction Model for TeleFertility.
7. Explainable Artificial Intelligence for Maternal and Child Predictive and Preventive Medicine

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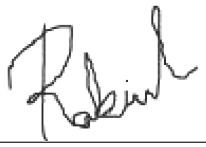

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*"We cannot improve what we cannot measure"*
*I therefore dedicate this thesis to everyone who taught me how to measure the right metrics.*

**"In the name of Allah, Most Gracious, Most Merciful"**

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# Nomenclature

The next list describes several symbols & abbreviation that will be later used within the body of the document

$ADASYN$ Adaptive Synthetic

$AI$ Artificial Intelligence

$BMI$ Body Mass Index

$BTMs$ Bone Turnover Markers

$CART$ Classification and Regression Tree

$CD19$ Cluster of Differentiation 19

$cGFS$ chronic GVHD-free surviva

$COVID-19$ Coronavrus Disease 2019

$CTscan$ Computed tomography scan

$CTG$ Cardiotocogram signal

$DBA$ Diamond-Blackfan Anemia

$DL$ Deep Learning

$E-Health$ Electronic Healthcare

$ECG$ Electrocardiogram

$EFB$ Exclusive Feature Bundling

$ELI5$ Explain Like I'm 5

$GOSS$ Gradient-based One Side Sampling

$HLA$ Human Leukocyte Antigen

$HSCT$ Hematopoietic Stem Cell Transplantation

$ICE$ Individual Conditional Expectation

$IVF$ In vitro fertilization

$LcMHC$ The Life Cycle Approach to Maternal and Child Health

$LIME$ Local Interpretable Model-Agnostic Explanations

$LRP$ Layer-wise Relevance Propagation

$MCH$ Maternal and Child Health

$ML$ Machine Learning

$NICU$ Neonatal Intensive Care Unit

$OCT$ Optical Coherence Tomography

$PD$ Partial Dependence

$PPPM$ Predictive, Preventive and Personalized Medicine

$PPPM$ Predictive, Preventive and Precision Medicine

$QLL$ Quantum Lattice Learning

$S-matrix$ Scattering matrix

$SDG$ Sustainable Development Goal

$SHAP$ SHapley Additive exPlanations

$SMOTE$ Synthetic Minority Oversampling Technique

$SMOTESVM$ Synthetic Minority Over-sampling Technique Support Vector Machine

$SVM$ Support Vector Machine

$TB$ Tuberculosis

$XAI$ Explainable Artificial Intelligence

# Chapter 1

# Introduction

## 1.1 Background

Osteoporosis is one of the huge socioeconomic burdens revealed by demographic patterns with a liability to meeting the financial and social needs yet it is increasing with the growing number of elders [4][8] who are greatly constraining the Health care systems. Moreover 1 in 3 women over the age of 50 years and 1 in 5 men will experience osteoporotic fractures in their lifetime according to the International Osteoporosis Foundation statistics [34][95][16]. Unfortunately Adherence to neridronate therapy in pregnant women due to pregnancy osteoporosis during postpartum or last trimester due to vertebra fractures is also obscured [22].This calls for an urgent need to strategically and sustainably control the health care costs and survival of the elderly and vulnerable pregnant women.
While services offered at maternal antenatal care units have been greatly interrupted by the covid-19 crisis, the authority measures for preventing the spread of the disease have continuously stressed the healthcare systems in limited resource settings besides the in-access to affordable maternity services [68]. The scarcity of experienced skilled health workers to attend to the mothers in and out of the maternal health centers has even made this situation worse hence leading to an increase in maternal and neonatal mortality and morbidity rates globally [109][84][74]. Despite the fact that pregnant women need social, emotional and psychological support, there is extreme scarcity of these services to mothers in low resource settings. Moreover some of the pregnant mothers are faced with gender-based violence besides extreme poverty and lack of necessary tools and technologies to support them during maternity. This necessitates a need for an urgent, affordable approach to monitor and support maternal and fetal health. Prior studies have reflected an an overwhelming increased number of stillbirths amongst communities in constrained settings most especially minority groups and developing countries [119][74]. This justifies the need for cost effective, proactive maternal and fetal monitoring and surveillance to reduce maternal morbidity and mortality across communities. With reliable monitoring systems of fetal and labor activities, physicians can efficiently manage maternal and fetal health with guided informed medical decisions and choices.
Maternal and Fetal complications are the leading contributors to Neonatal mortality and morbidity which is one of the biggest global burdens hindering achievement of Sustainable Development Goal Three (SDG-3) [7]. To make matters worse, neona-

tal healthcare medical costs attributed to the need for NICU services are reportedly one of the fastest growing expenses in healthcare. This Maternal and Child Health (MCH) problem is causing a lot of toxic emotional stress to pregnant mothers hence fueling an infinite loop of fetal and neonatal health risks. Moreover, most of the preventive initiatives taken to reduce these risks are very expensive and obstructed by outcome uncertainties most especially in resource constrained settings[99][15]. The limited access to neonatal emergency services globally hardens the prenatal quality management and this generally reduces the quality of healthcare provided to mothers. The abrupt maternal-fetal emergencies also limit quality of maternity facility or service management in health centers. Unfortunately, there are lots of interdisciplinary contributing factors (features) to neonatal emergencies that render existing solutions obsolete for NICU service management [107][58]. With healthcare Big Data, we can preventively predict NICU admissions to improve health facility management and reduce neonatal mortality and morbidity using machine learning and artificial intelligence. We can reduce toxic stress among pregnant mothers and NICU service providers by explainably identifying the interdisciplinary contributing factors (features) to neonatal emergencies [21]. This AI approach to Neonatal Electronic Healthcare (E-Health) can affordably improve access to quality maternal and neonatal care services most especially in constrained resource settings [40].

It is important to note that the innovative technology emerging trends coupled with accumulated patient and healthcare records have greatly disrupted the approaches to medicine. Leveraging these readily available but underutilized technological tools could greatly boost the health and well-being of mothers and children. With the power provided by healthcare records and biomedical informatics, we can innovatively optimize data utilization for predictive, preventive and personalized medicine to not only reduce healthcare costs but also increase access and reliability of quality healthcare solutions across the globe [97]. Hematologic and blood disorders in children are one of the most complex inherited or acquired bone marrow failure syndromes that contribute to child mortality and morbidity globally. Despite the expertise provided by physicians in response to these complications, the survival rates of the diagnosed pediatric patients are still very low besides the high costs and in-access to these Hematologic healthcare services most especially in low resource settings [98].

Despite the innovative technological trends in healthcare, Biomedical research about preventive and predictive medicine for COVID-19 in pediatric patients and other pulmonary diseases like Tuberculosis (TB), Pneumonia, and Bronchitis among others is still extremely limited. Open chest X-ray datasets to pediatric biomedical image processing are also extremely scarce. This domain of pediatric biomedical image processing is literally unexplored yet child mortality and morbidity arising from pulmonary diseases and infections is rapidly increasing since the discovery of COVID-19. It has been confirmed that COVID-19 can emerge, before, during or after any kind of pediatric pulmonary infection or disease and this is extremely lethal due to the similarities between the COVID-19 symptoms to other pulmonary disorders [108]. Biomedical instrumentation health services in infants and children are quite expensive and inaccessible in low resource settings yet these pulmonary diseases pose a significant burden on child health. The pediatric evaluation of pulmonary health since the discovery of COVID-19 introduced new diagnostic and therapeutic challenges for the physicians besides the uncertainties in medical diag-

nosis and limited access to quality healthcare in low resource settings. Annotated (labeled) pediatric chest X-ray Image data for the medical image processing is very scarce and a little expensive to access which reduces the effectiveness of pediatric medical image processing and transfer learning.
In addition to the universal maternal mortality, there is a global disruption in peoples ability to reproduce. Globally, women under 35 are exhibiting a decline in birth rates for nearly all age groups yet there is an increase in birth rates for those in the 30s and early 40s [115] in developed societies. The lack of both quantity and quality eggs for women in their late 30s and early 40s would make it difficult for them to conceive besides other risk factors that lower rates of successful conception. Fortunately, availability and rise of fertility health interventions has made it possible for women who are choosing to become mothers at a later age thus making fertility solutions a norm for many families today. This has become a global increasing trend for the future for women in both developed and developing countries.The growing market for fertility services is inspiring academia and industry to innovate better products and services for fertility customers for example egg freezing services. Unfortunately, the minority, less privileged and under-served groups faced with a more unconventional path to pregnancy still have limited choices. This is because the products, services and markets for reproductive medicine are still concentrated among the privileged and developed communities.

## 1.2 Motivation

Clinicians offer various pharmacologic and therapeutic treatments for several healthcare problems including but not limited to infertility and osteoporosis although the offered adherence to treatments is not satisfactory [44][106]. The perceptions and experiences of patients during treatment greatly affects their adherence to osteoporosis therapy [10] yet they are extremely unpredictable hence a need for interdisciplinary collaboration to improve long term treatment approaches [66][59]. This is what motivated us to use Machine Learning Models to predict the adherence of patients in order to develop improved strategies patient adherence to medications individually most especially for the elderly and vulnerable pregnant women.

Despite the strategic electronic prenatal safety monitoring tools deployed for maternal and neonatal health for example the Electronic Fetal Monitoring (EFM} strips, uncertainty and ambiguity of cardiotocogram signal results still hinders correct inter- and intra-observer signal interpretation. This births interpretation discrepancies among physicians and patient caretakers thus stirring poor communication and opinion variation for precise medical decisions [90]. Electrocardiography as a field of biomedical research has greatly contributed towards developing maternal-fetal technologies and a gold standard database for Fetal heart rate (FHR) signal processing to support Electronic Fetal monitoring and evaluation but this requires a highly sophisticated skillset to operate the expensive inaccessible equipment most especially for economically disadvantaged and highly populated regions to implement the clinical procedures for sophisticated medical practices and applications [80] hence a need for a more feasible approach.

In worst case scenarios, an Explainable Feature Learning approach to Predictive

Neonatal medicine could enable maternal and neonatal medical practitioners to precisely identify and proactively monitor high risk expectant mothers and neonates. With a multidisciplinary maternal and child health dataset, physicians can obtain interdisciplinary insights on additional information necessary for handling neonatal emergencies and risky pregnancies [55][86].
Interpretable Prediction of NICU admission with machine learning can guide on efficient utilization and management of the NICU facilities. It can also guide on optimal predictive and preventive maternal and neonatal health interventions with reduced room for errors and uncertainty [30]. With the disruptive AI innovation and technology trends today besides open healthcare big data, the need for data utilization has grown towards developing novel and strategic data-driven solutions to healthcare problems [105][89].
Therefore an explainable feature learning approach for predicting NICU admissions is a step towards a better, equitable and global contribution to health data utilization for a better future. Since we are solving an interdisciplinary problem, we need to obtain data that gathers multiple perspectives across domains for capturing interdisciplinary contributions (features) to Neonatal emergencies for Maternal and Child Health. With this kind of data, we can tackle this interdisciplinary problem with big data techniques and Artificial Intelligence. Explainable feature learning is very important in this case for optimal selection based on feature importance. Since we have a pool of interdisciplinary contributors in the dataset, robust machine algorithms can proficiently learn to predict NICU admissions.

Neonatal Hematology is another scope of hematology and blood disorders that includes but is not limited to bone marrow transplantation, acute myeloid leukemia, Non-Hodgkin's lymphoma, blood count disorders, anemias, hemobiology, leukemias, blood clotting disorders, multiple myeloma, lymphocytic disorders, immune system disorders, stem cell disorders, transfusion medicine, hematology, thrombocytopenia, thalassemias, Hodgkin's lymphoma, red cell biology, immunobiology among others [71][7]. Unfortunately the application of Machine learning and Artificial Intelligence methods for medical interventions in all these scopes is still limited for pediatric medicine despite the massive volumes of data available for use. With interdisciplinary collaborative research, predictive, preventive and personalised medicine, we can innovatively establish reliable pediatric comprehensive bone marrow failure treatment plans for diagnostic, therapeutic and support services for children with acquired and inherited bone marrow disorders [87].

We can now agree on the importance and contribution of healthcare data for Pediatric health yet for all the digital health initiatives taken in data mining of medical image data for pediatrics, the reliability of diagnostics developed still remains untrustable and unsafe since it is not easily understandable to physicians and pediatric patient caretakers. Image Processing, Machine Learning (ML) and Deep Learning (DL) are the pillars of augmented intelligence which is a technique of computer vision tailored to improve accuracy of digital image processing with less resources like computational power or image data access [96]. Augmented intelligence for health care can greatly help developing countries and nations with limited tools and technologies in mining medical image data. With the few existing open Chest X-ray Image datasets, we can leverage augmented intelligence, transfer learning, artifi-

cial intelligence and biomedical image processing to improve pediatric diagnostics of pulmonary diseases besides improving pediatric pulmonary treatment plans for the physicians and patients. Pattern recognition and classification of pulmonary diseases in X-ray Images using a deep convolutional Neural Network would help us identify lethal patterns in pediatric patients and to evaluate the pediatric pulmonary health of patients for early treatment and health attention.

In addition to costliness, the ambiguity of uncomfortable reproductive medical procedures for infertility treatment and evaluation, the fertility customers require advanced, proactive, predictive, preventive and personalized treatment plans that are feasible enough to synchronize with advancing healthcare data driven solutions to comfortably administer reproductive medicine. Moreover the field of reproductive medicine is so sensitive for its combination of philosophy, cognitive psychology and human medicine for successful fertility diagnosis. This necessitates an accessible technological approach to fertility medical diagnosis, treatment and evaluation. The technological solution must also be interpretable and explainable for fertility physicians and customers (fertility patients) to transparently adopt.

Generally, we identified and focused our work on mainly four stages of maternal and child health and we were mainly motivated by the way they were interrelated in forming up a huge convoluted problem of Maternal and Child Mortality and Morbidity.

## 1.3 Research Scopes (Gaps addressed)

In this subsection, we summarise and clarify on the specific research gaps in the existing works that we are are addressing in this thesis.

Firstly, numerous osteoporosis treatment plans have been developed by physicians but there has not been any work done to predict therapeutic adherence of patients to osteoporosis treatment in order to develop strategies to improve adherence to medications individually.

Secondly, several CTGs signal exploration and deployment avenues have been done but no focus has been put on classical representation of feature based extracted results of ML classifiers in a less ambiguous interpretable manner for fetal health evaluation.

Also, no work has been done to explainably explore maternal significant multidisciplinary features for NICU admission prediction using ML and AI techniques. There is also no work identified to focus on exploring feature Learning and interaction in predictive maternal and neonatal healthcare.

We also realised that there is very limited work done to predictively evaluate influential determinants of prolonged survival of pediatric risks upon stem cell transplantation procedures. Moreover all the exiting statistical methods used are not interpretably sufficient.

Based on the exiting literature, all works on pediatric biomedical image processing do not cover the computer vision techniques that are comparatively comprehensible for pediatricians to assess connections between pulmonary health diseases. We did not find any works that interpretably articulate important features for precise predictive and preventive pediatric medicine using any computer vision techniques.

Lastly, despite the various fertility treatment plans developed by fertility physicians, we found no work done to predict the success of any of the treatment plans prescribed for the fertility patients. There is no work done with any statistical techniques to handle uncertainty of feature interaction for machine learning models in reproductive health.

Generally, the application of Machine Learning and Artificial Intelligence techniques in the field of maternal and child health is still an under researched thematic area yet its potential in stopping preventable deaths is very enormous.

## 1.4 Conceptualization of the Research Gaps

Since available works support the application of integrated life course approaches to examine reproductive health, it was very applicable in the field of maternal and child health because it examines the whole human life course in consideration of continuity of reproduction with a focus on correlation between indicators of reproductive health [12] [6][65].

We therefore developed a research design that used a life course approach to study Maternal and Child health by exploring features across life, human generations that influence pregnancy outcomes, gynaecological disorders, fertility and age. We also recognised significant influences on maternal and child health like chronic disease risks. We then synthesized a summarized cycle of Maternal and Child health events based on reproductive life sequential events.

The cycle synthesised is based on the observations made in the research patterns after rigorous maternal and child health literature review. It is called "**The Life Cycle Approach to Maternal and Child Health (LcMCH)**."

The research scope summary is illustrated in The Life Cycle Approach to Maternal and Child Health (LcMCH) where we picked at least one problem at each stage of the cycle to demonstrate the purpose of our works in this thesis through the research Objectives derived.

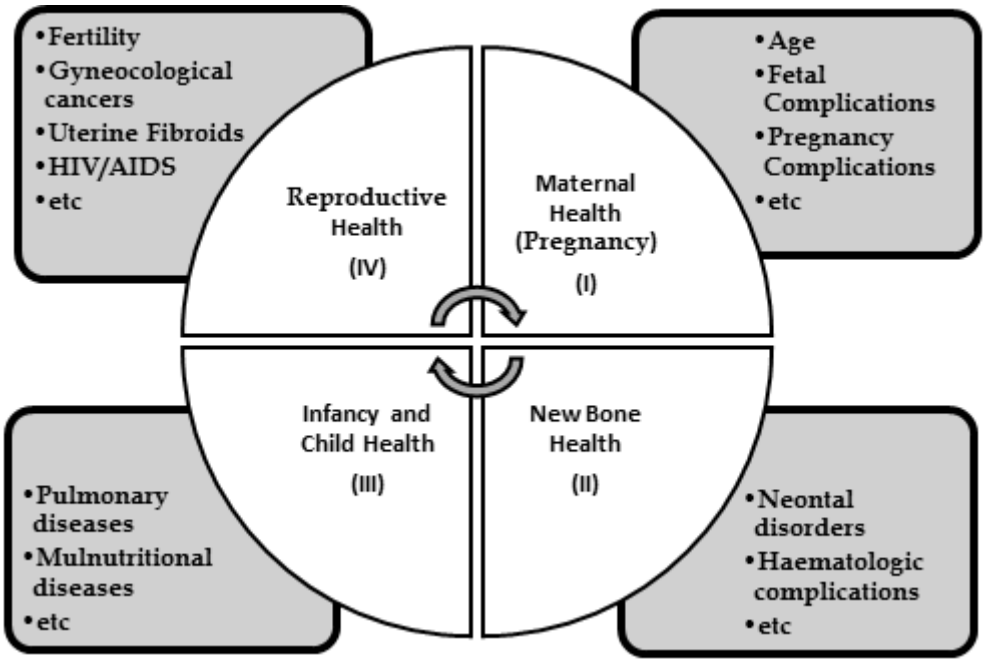


Figure 1.1: The Life Cycle Approach to Maternal and Child Health

## 1.5 Research Objectives

(a) To prove the concept of predictive, preventive and precision medicine using Machine Learning (ML) and Artificial Intelligence (AI) techniques for Maternal and Child Health (MCH) using real datasets.

(b) To improve ML and AI interpretability for MCH physicians and care takers by using explainable AI techniques in more transparent and insightful means for predictive, preventive and precise MCH medical decision making.

(c) To derive and comprehensively illustrate the most important features (factors) that require extra attention for specific MCH predictive, preventive and precise medical decision making.

(d) To create a new Explainable Predictive Machine Learning Model that is capable of transparently illustrating feature interaction of the most influential features leading to a precise medical decision for MCH.

The above core research objectives of this thesis were investigated through a series of scientific international conference papers centered on the core subjects namely; Maternal and Child Health (MCH), Machine Learning (MCH) and Artificial Intelligence (AI) at the different Stages of The Life Cycle Approach to Maternal and Child Health (LcMCH) as illustrated in Table 1.1

| Paper Short Form | Research Contributions | Objectives Investigated | Stage of LcMCH |
|---|---|---|---|
| ML-4-Osteoporosis-Treatment | A Machine Learning Approach for Predicting Therapeutic Adherence to Osteoporosis Treatment | a | (I) |
| XAI-4-Fetal-Health-Evaluation | Cardiotocogram Biomedical Signal Classification and Interpretation for Fetal Health Evaluation | a, b, c | (I) |
| XAI-4-NICU-Admissions | Explainable Feature Learning for Neonatal Intensive Care Unit (NICU) Admissions | a, b, c | (II) |
| XAI-4-StemCell-Transplantation | Explainable Artificial Intelligence for Hematologic Pediatric Patient Survival Prediction upon Stem Cell Transplantation | a, b, c | (II) |
| XAI-4-Pulmonary-Health-Evaluation | Explainable Augmented Intelligence and Deep Transfer Learning for Pediatric Pulmonary Health Evaluation | a, b, c | (III) |
| QLL-XAI-4-Fertility-Treatment | An Explainable Lattice based Fertility Treatment Outcome Prediction Model for TeleFertility | a, b, c, d | (IV) |

Table 1.1: Scientific Research papers for each research objectives at each of The Life Cycle Approach to Maternal and Child Health (LcMCH) Stage

## 1.6 Research contributions

### 1.6.1 A Machine Learning Approach for Predicting Therapeutic Adherence to Osteoporosis Treatment (ML-4-Osteoporosis-Treatment) | LcMCH: I | Objective: a.

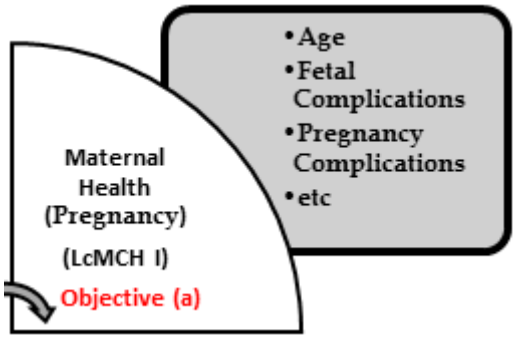


Figure 1.2: Stage I of The Life Cycle Approach to Maternal and Child Health

We developed Machine Learning models for predicting therapeutic adherence of patients to osteoporosis treatment and tested them on a real dataset for Drug Persistence [12] with 69 features and about 3414 samples. We optimized and tested the accuracy of different ML models and classified the accuracy metrics of the results depending on the training, testing or overall dataset where the ExtraTree Model showed the finest accuracy of 100%, 85.0% and 94.5% with respect to the datasets. The outcomes of the tests prove that the implementation of Machine Learning Predictive Models that use the ExtraTree Classification algorithms with SMOTESVM enable health professionals to compatibly decide on the individualized therapeutic treatments and approaches for osteoporosis treatment and pharmacologic management of their patients. The summary of the contributions is stated below.

1. We proposed and developed Machine learning Models for predicting therapeutic adherence to osteoporosis treatment for physicians and researchers to develop suitable adherence-improving interventions.

2. We optimized the Models with various sampling techniques for the imbalanced data on osteoporosis.

3. We evaluated the performance and accuracy of the models with both synthesized and real datasets for Drug Persistence classification.

4. Finally, we recommended the most accurate Machine Learning Models for adoption and deployment for researchers, physicians and investors in the therapeutic adherence domain.

### 1.6.2 Cardiotocogram Biomedical Signal Classification and Interpretation for Fetal Health Evaluation (XAI-4-Fetal-Health-Evaluation) | LcMCH: I | Objectives: a, b, c.

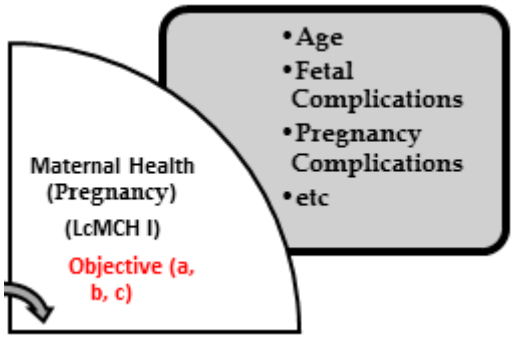


Figure 1.3: Stage I of The Life Cycle Approach to Maternal and Child Health

We took advantage of the generated open cardiotocography biomedical signal dataset [26] to build Machine learning models that classified and interpreted fetal heart rate and uterine contraction signals with reduced EFM maternal-fetal signal ambiguity for efficient maternal-fetal assessment by the maternal caretakers/specialists and

with easy interpretation of FHR tracings for improved fetal health evaluation. We are focused on testing and optimization of ML models for affordable advances in electronic fetal evaluation and testing perinatology to improve maternal-fetal wellbeing of pregnant women.
The summary of the contributions is stated below.

1. We proposed ML biomedical signal classifiers to reduce maternal-fetal signal ambiguity for efficient fetal evaluation.

2. The Models illustrated maternal-fetal classical results for EFM interpretation of FHR tracings in a more interpretable presentation for maternal-fetal assessment.

3. Moreover, we performed feature extraction and comprehensively test the various classification models and recommend the best classifier for fetal health evaluation.

4. Finally, we evaluated the performance and accuracy of biomedical signal classifiers with both synthesized and real datasets obtained for purposes of 10 class or 3-class diagnostic fetal experiments with clear model explainability.

### 1.6.3 Explainable Feature Learning for Neonatal Intensive Care Unit (NICU) Admissions (XAI-4-NICU-Admissions) | LcMCH: II | Objectives: a, b, c.

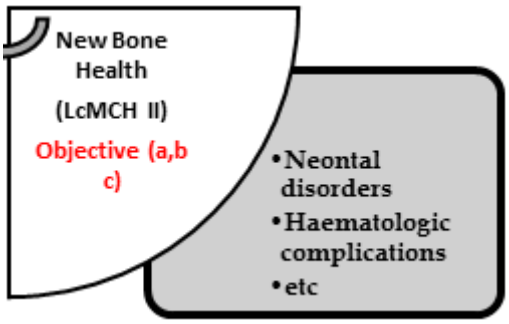


Figure 1.4: Stage II of The Life Cycle Approach to Maternal and Child Health

We proposed Interpretable Machine Learning Models for predicting NICU admission using maternal health profiles that capture interdisciplinary maternal and child health features. We used interpretable approaches to explain the features contributing to the predicted results for physicians and patients to understand how the machine learning algorithms came up with the predicted results. The demonstrated predictive models can be integrated in mobile medical applications for Maternal-Fetal Telemedicine to increase access to quality healthcare for mothers through E-health.
The summary of the contributions is stated below.
a) We proposed and build reliable interpretable machine learning algorithms for predictive and preventive Neonatal Medicine.

b) We demonstrated 'black box' machine learning explainability techniques for interpreting and understanding Machine Learning predictions for Maternal and Child Health.
c) We illustrated feature importance identification and learning for effective medical predictions using large interdisciplinary datasets comprising of very many health features for precision medicine.

### 1.6.4 Explainable Artificial Intelligence for Hematologic Pediatric Patient Survival Prediction upon Stem Cell Transplantation (XAI-4-StemCell-Transplantation) | LcMCH: II | Objectives: a, b, c.

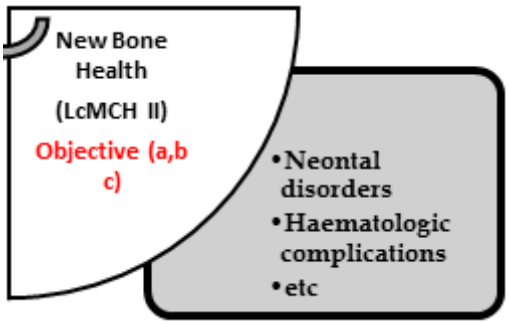


Figure 1.5: Stage II of The Life Cycle Approach to Maternal and Child Health

Since the application of interpretable machine learning to survival analysis and prediction transparently overcomes the constraints of reactive and statistical approaches to medicine, we can significantly improve the quality of healthcare and survival of the vulnerable pediatric populations with the application of machine learning and artificial intelligence for predictive, preventive and personalized pediatric medicine. Below is the summary of our contributions.

1. We proposed an interdisciplinary innovative approach for Predictive, Preventive and Personalized transplantation and cellular therapeutic medicine for hematologic pediatric patients and demonstrated how it can improve their survival.

2. We modelled and built Explainable Pediatric Survival Predictors for safer precision stem cell transplantation.

3. We interpretably simulated the stem cell transplantation outcomes and illustrated the most important factors influencing the success or failure of the transplantation procedure.

4. We tested and evaluated the accuracy of the machine learning models and recommended the most optimal models for predictive and preventive pediatric treatment.

5. Finally, we collaboratively shared insights about the applications of Artificial Intelligence and machine learning for personalized pediatric medicine and informed decision making for pediatric physicians and patient caretakers.

### 1.6.5 Explainable Augmented Intelligence and Deep Transfer Learning for Pediatric Pulmonary Health Evaluation (XAI-4-Pulmonary-Health-Evaluation) | LcMCH: III | Objectives: a, b, c.

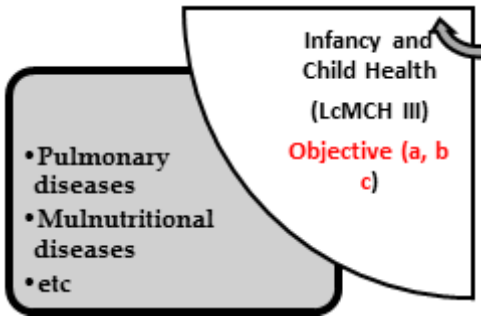


Figure 1.6: Stage III of The Life Cycle Approach to Maternal and Child Health

Since Scientific Innovation and interdisciplinary collaborative research have proven a positive contribution towards interdisciplinary medicine, we leverage innovative tools it provides for prediction and transparently overcome the constraints of reactive and statistical approaches to medicine. We interdisciplinarly improve the quality of healthcare and in vulnerable pediatric populations with the application of interpretable machine learning and explainable augmented intelligence for predictive, preventive and personalized pediatric pulmonary medicine.
Below is the summary of our contributions.

1. We presented an interpretable approach to medical image processing for lethal pediatric pattern recognition in order to proactively, predictively, preventively, personalize and participate in optimal pediatric pulmonary treatment plans.

2. We demonstrated a combination of computer vision tools and techniques for reliable pediatric pulmonary diagnosis regardless of the scarcity of pediatric chest X-ray Image datasets for a safe and trustable approach to pediatric pulmonary health evaluation.

3. Finally, we demonstrated and recommended safe and reliable approaches to efficient biomedical image processing with limited medical image data and computational resources.

### 1.6.6 An Explainable Lattice based Fertility Treatment Outcome Prediction Model for TeleFertility (QLL-XAI-4-Fertility-Treatment) | LcMCH: IV | Objectives: a, b, c, d.

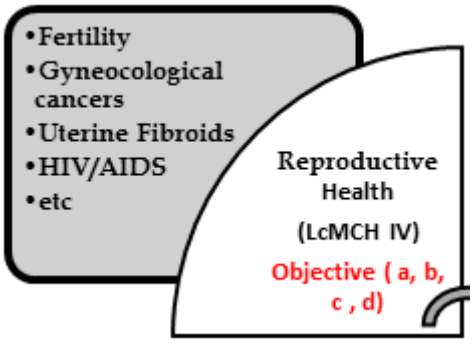


Figure 1.7: Stage IV of The Life Cycle Approach to Maternal and Child Health

We proposed, modelled and simulated interpretations of fertility intervention predictions to enable fertility patients and physicians to understand the health contributors to the predicted possibilities of any selected fertility treatment plan in lattice space. There are lots of therapeutic and diagnostic possible interventions for infertility but the ambiguity and uncertainty about the most appropriate treatment plan hinders precise selection. Fertility Physicians propose many possible treatment plans that are costly, risky and possibly unhealthy to patients in the long run since most of them involve body intake of various medicines with hope to discover that which works best for them. Swallowing too much medicine is unhealthy and medical adherence is hard. That is why we proposed the use of machine learning for predictive medicine and lattice models to explain the predictions to the physicians and patients in lattice space. With the simulated explanations, physicians and patients can make an informed choice with the help of the fertility health feature interactions displayed. This approach to fertility medical precision is very cost effective, less ambiguous and preferable to patients.
Below is the summary of our contributions.

1. We introduced the concept of Quantum Lattice Learning using the Feynman's technique for Medical Machine Learning model Interpretability and Explainability in lattice space.

2. We proposed and modelled interpretable predictors for precise fertility intervention evaluation using Lattice based Models.

3. We explainably simulated the predicted fertility intervention outcomes in lattice space for informed decision making on fertility treatment plans.

4. We tested and evaluated the accuracy of the lattice models and recommended optimal models for TeleFertility (remote assessment of fertility interventions).

5. Finally, we shared insights about Artificial Intelligence Innovation for telemedicine ( E-Health) evaluation of fertility to make this technology globally accessible to everyone.

## 1.7 Thesis organization

The thesis organization is based on research scope Conceptualization and Objectives of the research. The research Objectives are investigated by a series of six research papers coded as with Research Paper Short Formats in Table 1.1. At every stage of **The Life Cycle Approach to Maternal and Child Health** (LcMCH), a specific objective is achieved by investigating as chosen problem with consideration of Observations and Lessons Learned (Chapter 5) of each research paper at every stage of Maternal and child health life cycle. The tabular visualization of the thesis organization can be studied in Table 1.2.

<table>
<tr><td>Chapter 1: Introduction</td><td colspan="5">Background<br>Motivation<br>Research Scope<br>Research Scope Conceptualization<br>Research Objectives<br>Research Contributions<br>Thesis Organization</td></tr>
<tr><td>Chapter 2: Existing Works</td><td colspan="5">Machine Learning Modelling<br>Biomedical Signal Classification<br>Neonatal Intensive Care Unit Admissions<br>Pediatric Transplantation and Stem cell therapy<br>Pediatric Pulmonary Health<br>Predictive, Preventive and Personalized Medicine<br>Explainable Artificial Intelligence</td></tr>
<tr><td rowspan="2">Chapter 3: Methodology<br><br>Chapter 4: Results and Discussion</td><td colspan="2">LcMCH Stage I</td><td colspan="2">LcMCH Stage II</td><td>LcMCH Stage III</td><td>LcMCH Stage IV</td></tr>
<tr><td>ML-4-Osteoporosis-Treatment<br><br>Objective:<br>a</td><td>XAI-4-Fetal-Health-Evaluation<br><br>Objectives:<br>a, b, c</td><td>XAI-4-NICU-Admissions<br><br>Objectives:<br>a, b, c</td><td>XAI-4-StemCell-Transplantation<br><br>Objectives:<br>a, b, c</td><td>XAI-4-Pulmonary-Health-Evaluation<br><br>Objectives:<br>a, b, c</td><td>QLI-XAI-4-Fertility-Treatment<br><br>Objectives:<br>a, b, c, d</td></tr>
<tr><td>Chapter 5: Conclusion</td><td colspan="5">Major Observations and Lessons Learned<br>Conclusion derived from the Observations<br>Future Works derived from the Observations</td></tr>
</table>

Table 1.2: Tabular visualization of the thesis organization

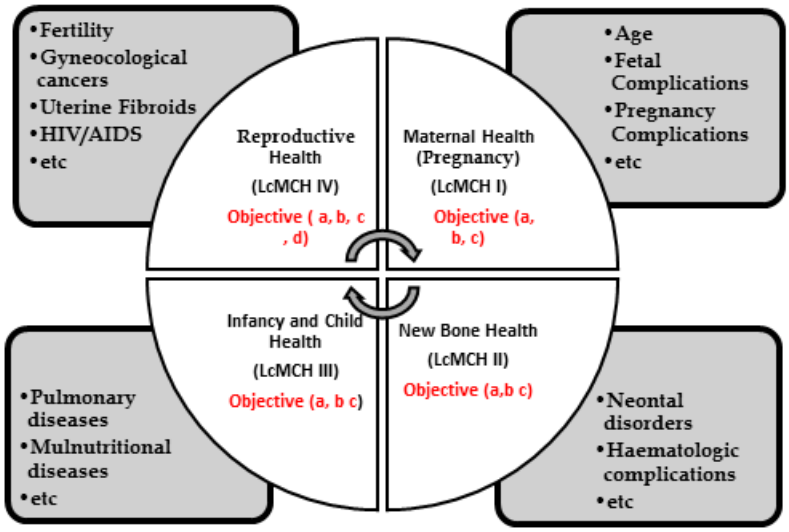


Figure 1.8: Thesis Methodology Organisation based on The Life Cycle Approach to Maternal and Child Health

# Chapter 2

# Existing Works

## 2.1 Machine Learning Modeling.

Machine Learning (ML) Modeling and algorithm choice selection is often dictated by the purpose and the problem to be solved. ML Algorithms are categorized as supervised learning, semi-supervised learning, unsupervised learning, and reinforcement learning. Predominantly, supervised learning is further divided into the classification and regression, unsupervised learning is divided into clustering and dimension reduction among others [93]. For ML model optimization in supervised learning, the goal is to find an optimal mapping function to minimize the loss function of the training samples. In our work, we had to optimize the ML Models by selecting optimal parameter values for sampling in the shortest time possible. Since we had to classify imbalanced data, we deployed optimal sampling techniques with SVM (Support Vector Machine) to optimize the Models accordingly [72]. We focused on tuning Machine Learning Models for accurate prediction of therapeutic adherence to osteoporosis treatment in a more generalizable manner among other MCH precision medical outcomes.

### 2.1.1 Handling the imbalanced data in Machine Learning.

Due to the highly imbalanced registered medical data in fields like therapeutic medicine, we apply Synthetic Minority Oversampling Technique (SMOTE) and Adaptive Synthetic (ADASYN) Sampling Approach to independently handle Imbalance because majority of the machine learning algorithms never consider the distribution of the data sample by default. Imbalanced data often skews results towards the majority sample class distribution if the model is built using an Imbalanced data which is extremely misleading both in practice and theory if the imbalance is ignored [93].

## 2.2 Biomedical Signal Processing

### 2.2.1 Cardiotocography

Cardiotocography has been deployed in many maternal fetal technological applications for example fetal heart rate monitoring using doppler ultrasound technology,

morphological analysis of fetal electrocardiograms for noninvasive fetal monitoring, prediction of vaginal or caesarian deliveries, qualitative assessment of fetal state by -Hyperballs simplification of fuzzy rules, Phonocardiography advanced signal processing for passive fetal monitoring, digitization and analysis of cardiotocography records, detection of change in fetal heart rate, feature selection for fetal health status classification, convergent cross mapping of cardiotocography signals with Gaussian processes to discover causalities [61] and fetal health classification based on machine learning [91].

### 2.2.2 Classification of biomedical signals.

Classification of biomedical signals is a step of biomedical signal processing to obtain information out of signals for medical diagnosis. This classification has been implemented in a number of applications for example; Ensemble learning classification to determine signal quality of radar-recorded heart sound signals, detection and classification aortic stenosis using seismo-cardiogram and gyrocardiogram signals, classifying electrocardiogram signals to detect atrial fibrillation from intensive care unit patients, arrhythmia recognition and classification using ECG signals [78], classification of heart sound signals to detect abnormal cardiac valves, physiological heart sound audio classification for heat status monitoring, automatic classification and evaluation of ECG signal quality by channel for subsequent processing, Classification and detection of Atrial fibrillation from premature atrial contraction and premature ventricular contraction using novel density poincare´ plots [82], classification of Biofeedback signals for intelligent biofeedback augmented content comprehension, classification of capnographic signals to diagnose chronic obstructive pulmonary disease and congestive heart failure and classification of cardiotocograms to analyze dimensionality techniques on big data [70][120]. With relevance to CTG signals, the noise due to measurement, inadequate training samples, non-discriminative features and inherent ambiguity of classification greatly affect the classification results.

## 2.3 Neonatal Intensive Care Unit (NICU) Admissions

NICU Admissions have attracted a lot of attention recently that most scientists have actively participated in solving this problem. Technological approaches to length of stay in NICU analysis [85], automatic extraction of impulsive cries of preterm newborns [83], Forecasting NICU admissions in near-term and term infants with low illness acuity [92] all geared towards understanding the future actions of artificial intelligence in management of newborns [47] and pregnancy disease strategic management by prediction and identification of maternal risk factors for neonatal intensive care admissions [92].

## 2.4 Pediatric Transplantation and Cellular Therapy

Bone marrow transplantation also referred to as stem cell transplantation is a medical treatment that replaces human bone marrow with healthier bone marrow cells usually for treatment of blood disorders. The high morbidity and mortality caused by transplant-related uncertainties is worrying despite the necessity of prolonging life and treatment of blood disorders with hematopoietic cell transplantation in hematologic malignant patients. The risk of cardiac toxicity in old chronic patients and pediatric patients is still life threatening to these vulnerable populations yet there is not yet a safe trustable proactive solution to handle health risk [37]. This calls for an urgent need for a collaborative interdisciplinary innovative scientific solution to save lives of these vulnerable populations across the globe.

There are a lot of patient survival interventions put in place to increase the overall survival rates of blood disordered patients upon stem cell transplantation. Hematopoietic Stem Cell Transplantation (HSCT) is one of the best approaches that have resulted in an excellent probability of overall survival and chronic GVHD-free survival (cGFS) in patients with Diamond-Blackfan anemia (DBA) [37]. Haploidentical hematopoietic stem cell transplantation graft manipulation prevented graft-versus-host disease, improved survival in pediatric leukemia [111]. Allogeneic hematopoietic stem cell transplantation (HSCT) from an Human Leukocyte Antigen (HLA)-haploidentical relative (haplo-HSCT) was proven to be a suitable option for pediatrics with acute leukemia [24]. T-cell receptor (TcR)/Cluster of Differentiation 19 (CD19) -depleted HLA-haploidentical HSCT is an effective strategy for children with several non-malignant disorders. HLA-haploidentical HSCT after T-cell/B-cell depletion (haplo-HSCT) also exhibited efficiency in effectiveness in children [11]. Also aggressive interventions with critical care is encouraged for pediatric hematopoietic stem cell transplant patients having respiratory failure [35]. One comparative analysis to confirm increasing the CD34+ cells / kg dosage prolongs general survival time of patients without synchronous occasions of unpleasant events affecting patients' quality of life besides learning rule sets performed for survival data synthesis [35].

All the reactive medical approaches proposed are extremely patient centered. To the best of our knowledge, there is no work performed to predictively and preventively improve pediatric patient survival before stem cell bone marrow transplantation using ML and AI techiques.

## 2.5 Pediatric Pulmonary Health

Automatic classification of fetal heart rate based on convolutional neural network has been done before as a solution exhibiting mixed approaches of transfer learning for faster feature extraction and learning improved diagnostic approaches of healthcare [52]. Some scholars followed the sound of children's hearts using a deep-learning-based computer-aided pediatric diagnosis system in order to improve the health infants and children [77]. There are some approaches discussed on unveiling

COVID-19 from Chest X-ray with deep learning. The authors shared knowledge about the hurdles race with small data which is the exact problem in X-ray pediatric datasets [73][64].

The complexity of diagnosis of pulmonary diseases among covid-19 patients is reflected in a case study for diagnostics and management of tuberculosis and covid-19 in a patient with pneumothorax where the scholars described a first case where tuberculosis and COVID-19 were diagnosed concomitantly in a Russian patient with pneumothorax [101]. A data augmented approach to transfer learning for covid-19 detection clarifies the possibilities of how we can still be able to do more with less availability of data for medical image processing and deeply explain how transfer learning can been used for pulmonary disease detection using X-ray, ultrasound, and CT scans [88]. Scholars also discussed about classification of pulmonary diseases from x-ray images using a convolutional neural Network. The niche was not pediatric pneumonia but instead tomographic identification and evaluation of pulmonary involvement due to sars-cov-2 infection using artificial intelligence and image segmentation techniques [102].

Inception-v4, inception-resnet and the impact of residual connections on learning have greatly exhibited advances in image recognition performance [26], this makes them so applicable in pediatric medical imaging since we have even more issues to handle with less data access and much needs for computational resources. A novel augmented deep transfer learning for classification of COVID19 and other thoracic diseases from X-ray was developed, where augmented ensemble transfer learning techniques showed substantial performance gain over the conventional transfer learning [81]. Alternatively, covid-19 detection using chest x-ray images with a regnet structured deep learning model was also presented by other scholars in identifying medical diagnoses and treatable diseases by image-based deep learning [39] although the pediatric niche was not addressed even in the critic evaluation of methods for covid-19 automatic detection from x-ray images discussed by authors in [63].

The works on the occurrence of COVID-19 in pediatric patients and other pulmonary diseases like Tuberculosis (TB), Pneumonia, bronchitis among others is extremely limited. This domain of biomedical image processing is literally ignored hence the existence of open datasets to address cross cutting issues is very scarce. It has been proven that COVID-19 can transpire before, at the time of, or after the diagnosis of TB, Pneumonia or any other pulmonary infection and more reliable evidence is often required to regulate or control the spread of any of these pulmonary diseases whether they are reactive or not [69]. The sole purpose of our work is to reduce the worst case scenario of each of the detected pediatric pulmonary abnormalities on pediatric patients. Data on the association between TB, Pneumonia, COVID-19 and other pulmonary diseases are not conclusive enough, nevertheless most scholars believe that a pediatric carrier of more than one of these infections is likely to worsen the condition of any of them most especially TB. We believe that an explainable augmented intelligence approach with deep transfer learning for pediatric pulmonary health evaluation would greatly reduce the worst case scenario in pediatrics patients.

## 2.6 Predictive, Preventive and Personalized Medicine (PPPM).

Reactive patient centered medicine is extremely risky and life threatening. Fortunately, biomedical informatics and computational Intelligence have the potential to innovatively disrupt these reactive approaches to medicine by allowing for interdisciplinary collaboration of biology and engineering research for proactive improved medical interventions. Using health data records, big data and analytic techniques, it is possible to predictively approach medical diagnostics by forecasting possible msedical outcomes before making any medical decision. This is referred to as predictive medicine. Additionally, preventive approaches to medicine can be leveraged to avoid worst case scenarios among patients by using medical data forecasts. Data-driven innovative approaches can allow for pediatric personalized medicine such that the various important feature interactions are virtually performed by machines through machine learning upon modeling the necessary patient metrics in order to generate the most appropriate medical intervention insights that can guide physician decisions [17][100].
With the available predictive power and improved computational intelligence, we can feasibly deploy machine learning and artificial intelligence for predictive, preventive and personalized medicine to identify the most important metrics affecting the success or failure of blood medicine in vulnerable populations.

### 2.6.1 Hematologic Predictive, Preventive and Personalized Medicine.

Besides the delayed interventional medical approaches of reactive medicine, the insufficient economy of healthcare systems and in-access to appropriate specialized training programs for specific subjects like pediatric medicine makes it so hard to build sufficient expertise and capacities to handle Hematological emergencies in children. Moreover the problematic ethical aspects of several pediatric treatments as well as inadequate communication among professional medical groups and healthcare policy makers complicate medical outsourcing interventions to save lives of the vulnerable pediatric population

### 2.6.2 Predictive Models for Medical Adherence.

Machine learning Algorithms have been deployed in prediction of various aspects of Medical Adherence which include predicting patients' non-adherence risks [76], fibromyalgia therapies adherence for mitigation of inaccuracy of social health forum data [49], predicting medication non-adherence in Crohn's disease maintenance therapy [75], examining medication adherence thresholds and risks of hospitalization [20], use of medical claims data in medication adherence prediction, identifying post-menopausal women at high risk of osteoporosis [14], predicting short-term fracture risks [57], among others. Most of the research is focusing on predicting results of non-adherence and other dynamics associated with non-adherence, no work has been done about prediction of adherence to osteoporosis therapeutic treatment. That is the research gap we are addressing for better adherence-improvement interventions for patients.

### 2.6.3 Maternal and Neonatal Predictive Medicine.

With the availability of massive historical and incoming health data, Artificial Intelligence has become the future of reproductive healthcare. It has the power to detect patterns and formulate neat simulations from large amounts of highly folded, complex distributed data using machine learning. This often helps in development of intelligent reproductive diagnostic and treatment plans [60][104]. Artificial Intelligence has been used for In vitro fertilization (IVF) outcome prediction, sperm analysis and selection, embryo and occyte selection and it has been proven to improve accuracy with increase in patient data provision thus an increase in accuracy of predictive and precision medicine besides treatment plans [56].

## 2.7 Explainable Artificial Intelligence (XAI).

The complexity and convolution of ethical components of critical decision-making in neonatology and other aspects of pediatrics often require proper understanding and explanation to not only the physician but also the patient managers [2] and that is what necessitates interpretable technologies. Explainable Artificial Intelligence (XAI) is what gives humans ability to not only explain but also validate the outcome or Machine Learning (ML) models. It illuminates learning 'black box' to allow humans interpret and reliably understand how the model works. Locally Interpretable Model-agnostic Explanations (LIME) explainable Feature Learning uses surrogate models. It bases on predictor variable relationships with the output predictions to learn and explain the 'black box' models within local regions [108][54]. "Explain Like I'm 5." (ELI5) feature learning in random forest algorithm with multidisciplinary datasets is achieved through the Inspection of Machine learning pipeline processes. ELI5 python package is used to compute feature importance by permutation for specific compatible 'black box' estimators with in the pipelines [48]. SHapley Additive exPlanations (SHAP) Feature Learning encompasses LIME techniques with additive feature attribution methods within a general framework for learning and visually simulating feature interactions and importance [116][31][32].
XAI insightfully suggests features that drive ML decisions and highlights redundant features that have little influence on the predictive results. With these insights, physicians can make precise critical decisions and programmers can build better and more accurate ML models [23]. XAI is what can interpretably prove that the ML model does not contain biases and can be safe for acceptance and distribution in production and critical medical environment with sincere trust and confidence to humans [94] while providing practical and applicable perceptions on what to do to improve the medical outcomes [110].

### 2.7.1 Feature Relevance Interpretation in Explainable AI (XAI).

A lot of explainability techniques have been developed and tested for transparent interpretation of machine learning models. "Blackbox" or opaque Artificial Intelligence algorithms require post-hoc explanations to transparently understand and interpret their procedures of how they come up with medical predictions, this is the only way users can be able to trust these algorithms in making medical decisions

[103]. Some of the explainability methods of these algorithms include but are not limited to;
Feature relevance interpretations to quantify the model input variables in order to explain the model for example the Layer-wise Relevance Propagation (LRP), Local interpretations with concentrated specific model areas of interest to explain the model, Visual interpretations which simplify model explainability by generating multiple visualizations of the model. Text explanations use symbols for example natural language text in order to generate explainable representations. Exemplification explanations extract instances from training datasets that represent operations of the model as a live demonstration [53].
Other Model-agonistic explainability methods used in demystifying "blackbox" machine learning models depend on intrinsic model architectures to relate the input to outputs. They perform the explanations by simplification, feature relevance explanations or visual explanations. Interpretation by Simplification may include Local Interpretable Model-Agnostic Explanations (LIME) which bases on the target prediction surrounding area to locally approximate a model during explanation. Some are based on coalitional Game theory (Shapley values) to derive explanations while others use visual explanations for model-agonistic interpretations for example Partial Dependence (PD) and Individual Conditional Expectation (ICE) plots to explain the models [46][118][114].

### 2.7.2 Safe and Trustable AI.

Explainable Artificial Intelligence is what gives lay humans like physicians and patients the ability to comprehend and validate the outcome of Machine Learning models. It illuminates the abstracted 'black box' to allow humans understand how the model works. An example is when humans understand the health features that guide the health predictive decisions and those that least contribute to the final prediction. Using these insights, humans can build simpler and more accurate models and physicians can choose better fertility treatment plans. XAI is what can interpretably proves that the Machine Learning model does not contain biases and that it is safe for adoption and deployment in medical (production) environment with trust and confidence to humans while providing actionable insights on what to do to improve the outcome [53].

# Chapter 3

# Methodology

## 3.1 ML-4-Osteoporosis-Treatment | LcMCH: I

### 3.1.1 Summary

Osteoporosis is a great disability burden with an expected cost increase of almost 50% by 2025. Due to its long term treatment, 50–70% of the patients withdraw from their osteoporosis medications within the first year of initiation. This necessitates an urgent need for improved osteoporosis and pharmacologic management tools most especially for pregnant women, postmenopausal women and the elderly to ensure therapeutic adherence of the patients during treatment. In this paper, we developed and tested accuracy of Machine Learning Models for predicting therapeutic adherence of patients to enable health professionals to compatibly decide on the therapeutic treatments and approaches for osteoporosis treatment and pharmacologic management of their patients. We were the first to develop and test Machine Learning Models for Predicting Therapeutic Adherence treatments. The ML Model accuracy results are summarized as classical metrics where the ExtraTree Model exhibited the highest accuracy of 100%, 84.1%, 94.2% on the training, testing and overall dataset respectively using Synthetic Minority Over-sampling Technique Support Vector Machine (SMOTE-SVM).

In this research work, we achieved our first objective (a) of proving the concept of predictive, preventive and precision medicine using Machine Learning (ML) and Artificial Intelligence (AI) techniques for Maternal and Child Health (MCH) using real datasets.

### 3.1.2 Methodology

#### Approach

Predicting patient therapeutic adherence to osteoporosis treatment. Although Bone Turnover Markers (BTMs)/ Biomarkers are currently used for prediction and management of osteoporosis [9], Machine learning is more appealing to support strategic

clinical decisions based on predictive patient management tools and applications. Our proposed ML Models were typically limited to objective prediction of patient adherence to therapeutic treatment based on features that affect drug persistence among patients.
We proposed ML Models to classify features that affect patient adherence based on predictive analytics performed on drug persistence data. The proposed predictive models are built on application of machine learning classification algorithms to categorize patients based on features that influence drug persistence.

### Dataset Description and Features

Despite the fact that [62] doubts the accuracy of machine learning-based prediction of medication adherence, most of the factors pointed out to hinder accuracy of our developed ML Models are taken care of by the dataset we used. The dataset [119] used had 69 features and about 3414 samples which is sufficient information to develop ML Models for the prediction problem in this domain. Lastly, the biggest problem of imbalanced registered medical data on osteoporosis [28] is handled by deploying appropriate sampling techniques.

**Data Exploration** We examined the data types in the dataset and the significance of NULL data together with the frequency of each category visually separated by labels as shown in Figure 3.1.
According to the histograms plotted, we observed not significant or special correlation between the variables with the target function. Also, the categorical variables could not determine the correlation factor between the variables and the target functions.

**Data Cleaning** We removed numerical columns and apportioned each categorical variable a value number to be mapped to since correlation cannot be calculated for categorical variables. Then we examined the results, considering the correlation between "pseudo categorical variables" and the "target" independent function.
Figure 3.2 illustrates the correlations among all variables where Grey fields signify no correlation, while the comparative intensity of the red and blue colors signify a rise in correlation, red indicates a positive correlation and blue indicates a negative correlation.
We further restricted some of the variables with low correlation results by setting and choosing the correlation above 0.01 or below -0.01 as illustrated in Figure 3.3.
Since the correlation between the variables in the training and test data in Figure 3.4 is nearly the same, good predictive results could be expected if a good train result is obtained.

**Sampling and Training.** For data balance since Persistency Flag 0 had the majority samples after checking, it would affect the accuracy of the Models.
We deployed optimal sampling techniques to obtain sufficient synthetic data for training the Models for optimal results, they included: SMOTE to aid creation of more synthetic data for the minority class 1, Borderline-SMOTE which is a new Over-Sampling Method for Imbalanced Data Sets Learning, SMOTE-SVM to aid identification of misclassified examples on the decision boundary and ADASYN to

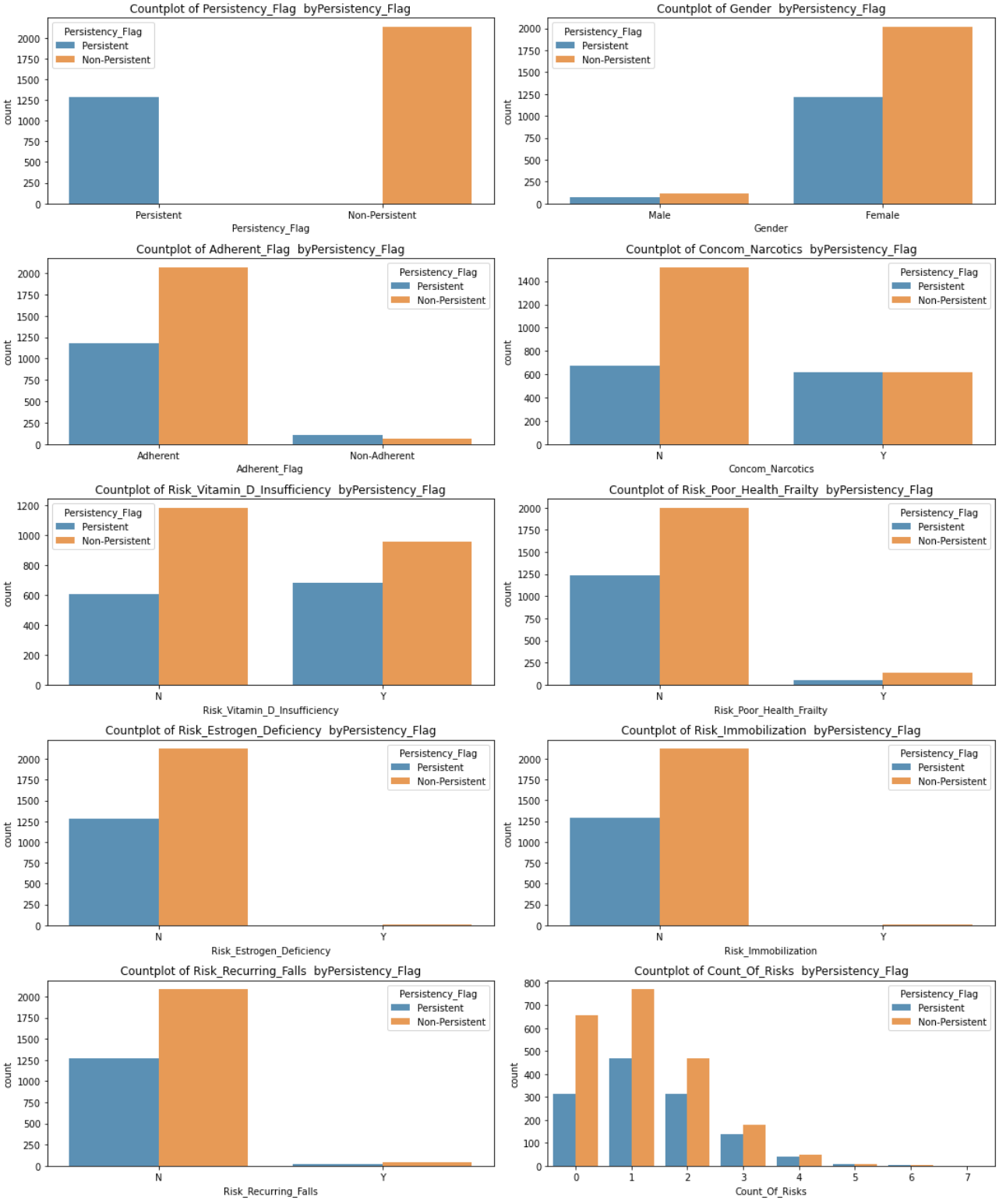


Figure 3.1: Sample count plot Histograms

generate more synthetic instances in regions of the feature space where the density of minority was low and fewer or none where the density was high [93].

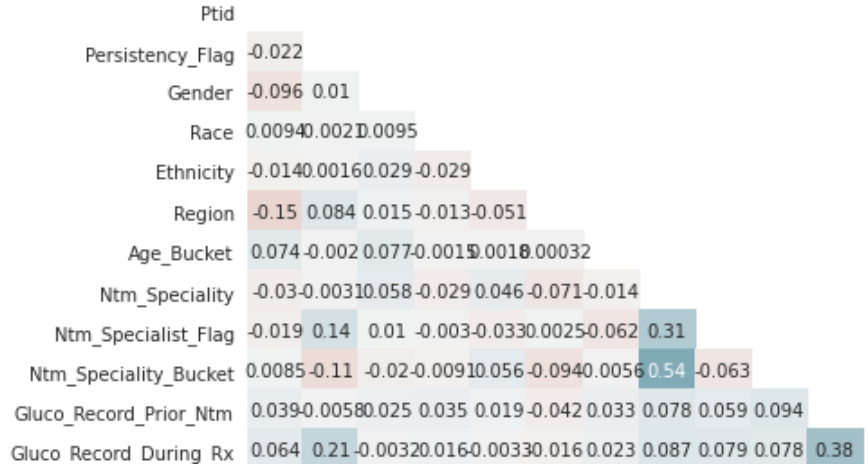


Figure 3.2: Correlation Heat map of features in train dataset (Partial)

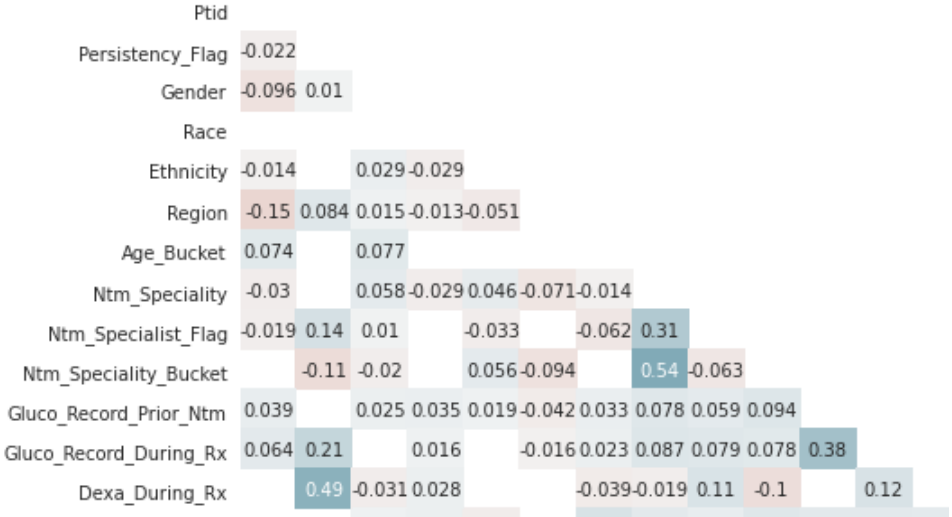


Figure 3.3: Correlation Heat map of features after restricting variables with low correlation results (Partial)

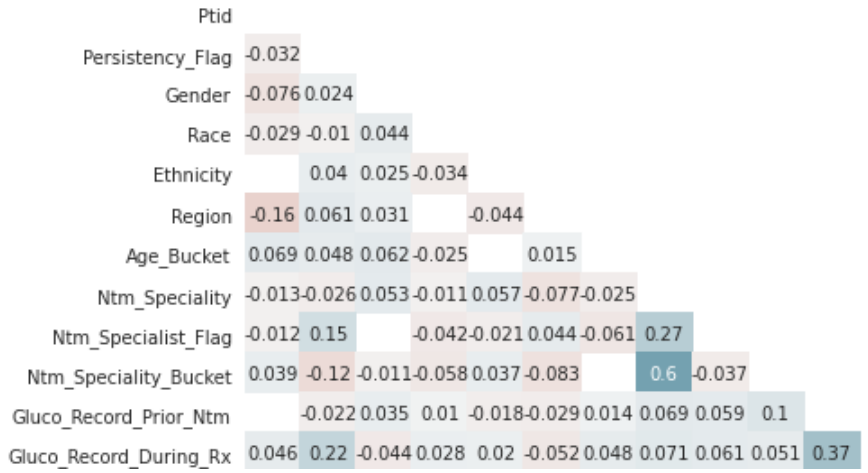


Figure 3.4: Correlation Heat map of features in test dataset (Partial)

## 3.2 XAI-4-Fetal-Health-Evaluation | LcMCH: I

### 3.2.1 Summary

Maternal and Neonatal health has been greatly constrained by the in-access to essential maternal health care services due to the preventive measures implemented against the spread of covid-19 hence making maternal and fetal monitoring so hard for physicians. Besides maternal toxic stress caused by fear of catching covid-19, affordable mobility of pregnant mothers to skilled health practitioners in limited resource settings is another contributor to maternal and neonatal mortality and morbidity. In this work, we leveraged existing health data to build interpretable Machine Learning (ML) models that allow physicians to offer precision maternal and fetal medicine based on biomedical signal classification results of fetal cardiotocograms (CTGs). We obtained 99%, 100% and 97% accuracy, precision and recall respectively for the LightGBM classification model without any GPU Learning resources. Then we explainably evaluated all built models with ELI5 and comprehensive feature extraction.

In this research work, we achieved the objectives a,b and c thus, we proved the concept of predictive, preventive and precision medicine using Machine Learning (ML) and Artificial Intelligence (AI) techniques for Maternal and Child Health (MCH) using a real dataset, improved ML and AI interpretability for MCH physicians and care takers by using explainable AI techniques in more transparent and insightful means for predictive, preventive and precise MCH medical decision making, then derived and comprehensively illustrate the most important features (factors) that require extra attention for specific MCH predictive, preventive and precise medical decision making.

### 3.2.2 Methodology

#### Approach

Explainable Biomedical Signal Classification.
Machine learning is appealing to enhance maternal fetal medicine through electronic fetal monitoring and evaluation applications or frameworks in telemedicine in constrained resource settings. Our proposed ML Models are typically limited to objective classification and unambiguous interpretation of cardiotocogram biomedical signal features that affect evaluation of fetal health. With feature extraction, the ML Models classify signals to evaluate fetal health in a probabilistic approach for informed maternal-fetal health decisions by physicians or caretakers. We compressively evaluate the ML models for optimal accuracy and represent EFM interpretations as classical results for minimal ambiguity.

#### Dataset Description and Preparation

We obtained 2126 instances of real, multivariate cardiotocography biomedical signal dataset [120] containing measurements of fetal heart rate and uterine contraction features classified by expert obstetricians based on fetal state and the morphology

patterns with 23 attributes. We first explored the signal density of each feature in our dataset in order to understand and establish the boundaries and limits for the fetal health state categories ie {Normal (1), Suspect (2) and Pathological (3) as illustrated in Figure 3.5. } We then checked for the missing values and assessed the distribution of the target fetal health classes.

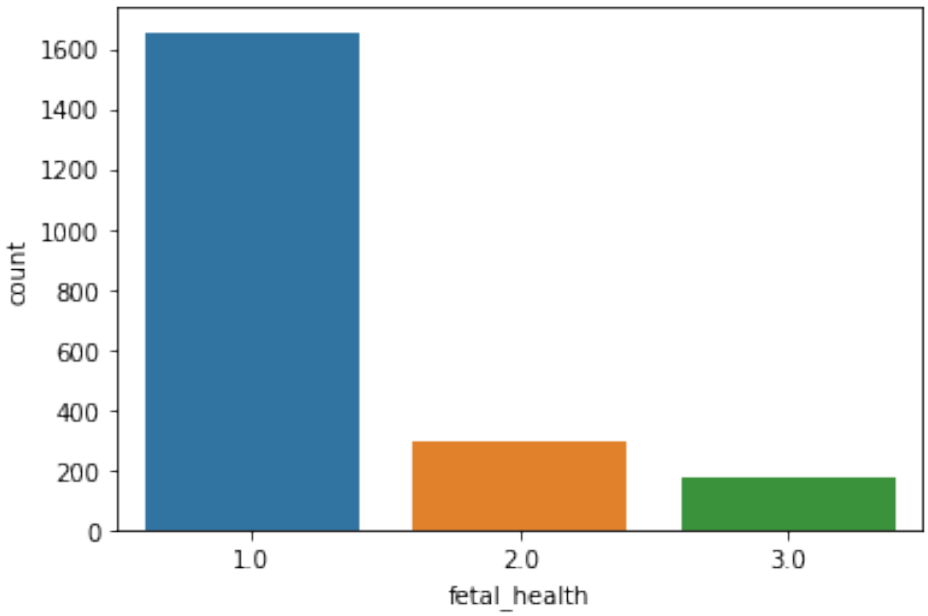


Figure 3.5: Cardicotogram Target Variables

On Exploring the dataset, we realized extreme data imbalance in amongst the target variables and handled it by resampling. In order to choose an appropriate resampling technique, we needed to explore the outliers as shown in Figure 3.6 and set the upper and lower thresholds to filter the signals.
We then calculated the signal correlation and examined the results, considering the correlation between "pseudo categorical variables" and the "target" objective function. The heat map in Figure 3.7 illustrates the correlations among all variables as blue-green fields represent no correlation, while the relative intensity of the aeroblue and blue colors represent an increase in correlation. In particular, blue reveals a positive or direct correlation (the variation of one characteristic directly affects the other) and aeroblue reveals a negative or indirect correlation (the variation of a characteristic inversely affects that of the other).

### Sampling, Feature Extraction and Training

Due to the signal class imbalance, we resampled the data before training the ML Models to prevent highly skewed signal class distributions and ensure high classification performance by up sampling the minority classes. Therefore, we first separated signal target classes, sampled with replacement to match the majority signal class then we randomly reproduced results which we combined with the majority class after up sampling. We extracted the features with 23 dimensions and separated target variables then scaled the extracted features for standardization before training and evaluating the ML Models.

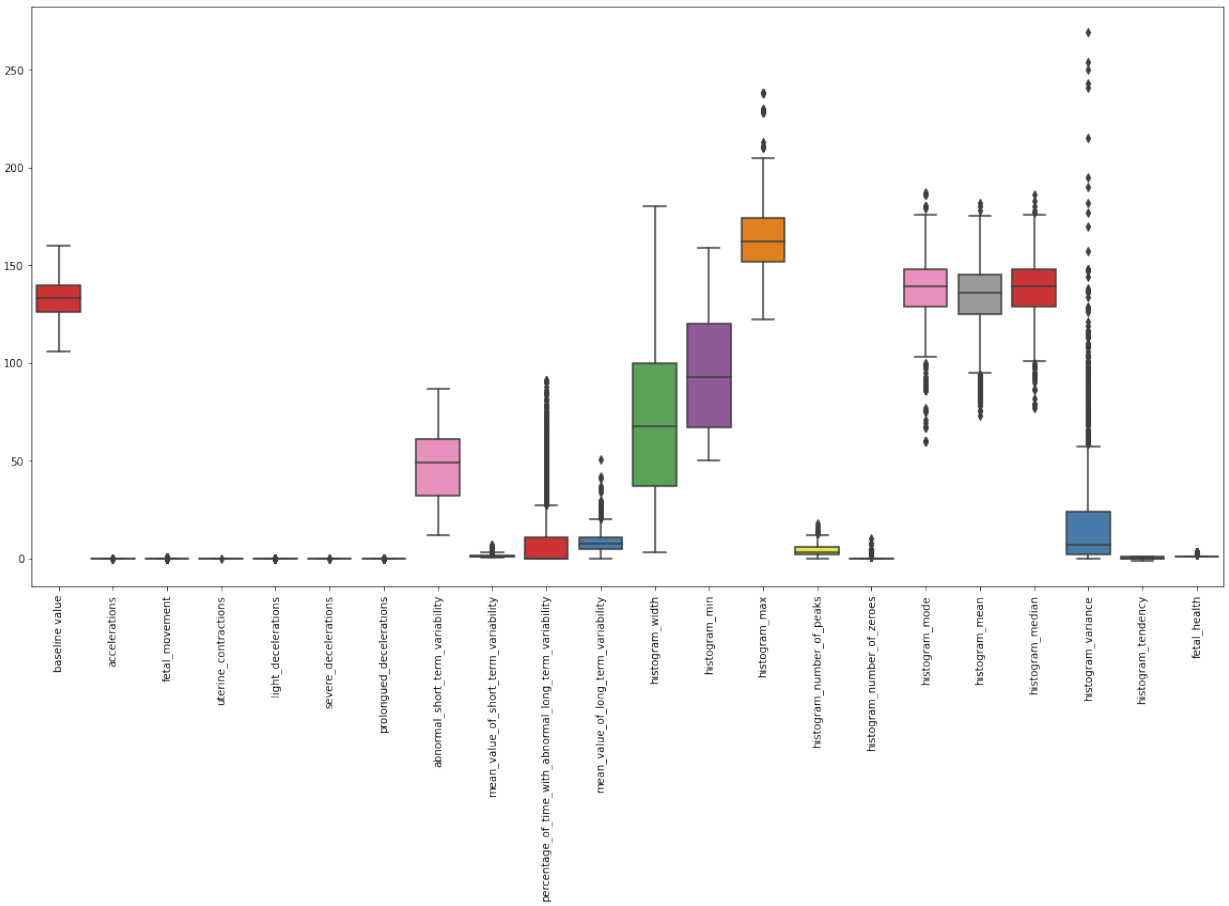


Figure 3.6: Exploring signal outliers

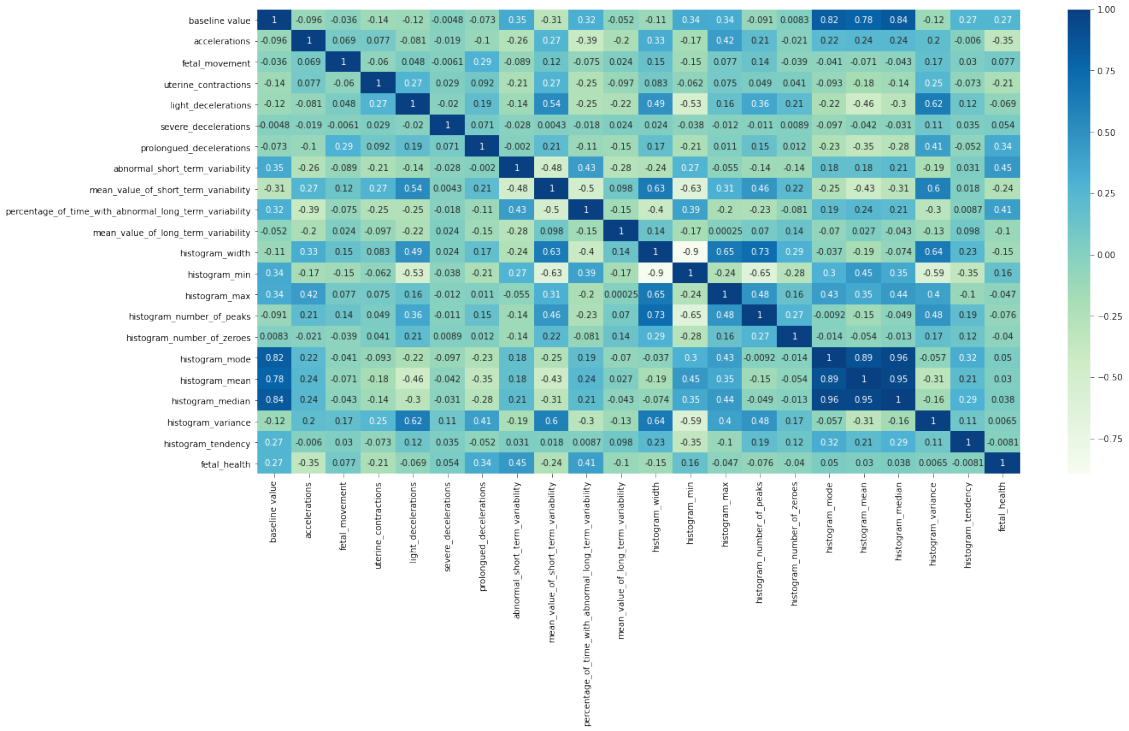


Figure 3.7: Correlation matrix Heat map of all features in the dataset

**Model Selection and Description.**

**Gradient Boost Classifier:** This iterative functional gradient ensemble method builds an additive model by combining both Gradient Descent to minimize loss function of the predecessor and Boosting where several weak learners are sequentially merged into a strong learner in a forward stage-wise manner. The 3 components of gradient boosting are; **Loss function** (to estimate the accuracy of the model at making predictions), **weak learners** (decision trees to classify data) and **additive model** (to sequentially and iteratively add weak learners). For the functional gradient descent, if we look for approximations $\hat{f}(x)$ as functions on an iterative basis, the function of approximations is initialized as a sum of approximations $\hat{f}_0(x)$ such that:

$$\hat{f}(x) = \sum_{i=0}^{M} \hat{f}_i(x) \tag{3.1}$$

Since $\hat{f}(x)$ is a description of functions that pretend to pass into functional space, we restrict the search to certain functions of the $\hat{f}(x) = h(x,k)$. It is important to note that;
The sum of the models is more complex compared to any family model but choose the optimal, we consider $\mathbb{E}$ for the coefficient of every step. Consider the expression below;

$$\hat{f}(x) = \sum_{i=0}^{t-1} \hat{f}_i(x), \tag{3.2}$$

$$(p_t,\ \theta_t) = arg_{p,\theta}\text{min}\mathbb{E}_{x,y} \quad \left[L\left(y, \hat{f}(x) + \rho.h(x,\theta)\right)\right], \tag{3.3}$$

$$\hat{f}_t(x) = \rho.h(x,\theta_t) \tag{3.4}$$

Since having a trained model h(x,) for any loss function L(y,f(x,)) is so hard in practice, we use expression of the loss function gradient to measure its value on our data and use least quadratic squares to correct residual predictions after training the models with predictions similar to the obtained gradient.
The square difference between pseudo-residuals r and our estimates for regression, and classification tasks are then minimized as shown below;

$$\hat{f}(x) = \sum_{i=0}^{t-1} \hat{f}_i(x), \tag{3.5}$$

$$r_{it} = -\left[\frac{\partial L(y_i, f(x_i))}{\partial f(x_i)}\right]_{f(x)=\hat{f}(x)}, \ for\ i = 1, \ldots, n, \tag{3.6}$$

$$\theta_t = arg_\theta min \sum_{i=1}^{n} \left(r_{it} - h(x_i,\theta)\right)^2, \tag{3.7}$$

$$\rho_t = arg_\rho min \sum_{i=1}^{n} L(y_i, \hat{f}(x_i) + \rho.h(x_i,\theta_t)) \tag{3.8}$$

**Light Gradient Boost Model**
This architectural framework sequentially trains numerous trees to boost the gradient weights learning with a reduced error by giving more weight to the misclassified

points in the subsequent iterations with a reduction in memory usage [93]. It uses Gradient-based One Side Sampling (GOSS) and Exclusive Feature Bundling (EFB) techniques to overcome constraints in Gradient Boosting Decision Tree frameworks. All LightGBM solutions are built on the following function to gain estimated variance $V_j{}^*(d)$ over the subset $A \cup B$.

$$V_j^*(d) = \frac{1}{n}\left(\frac{\left(\sum_{x_i \in A_l} g_i + \frac{1-a}{b}\sum_{x_i \in B_l} g_i\right)^2}{n_l^j(d)} + \frac{\left(\sum_{x_i \in A_r} g_i + \frac{1-a}{b}\sum_{x_i \in B_r} g_i\right)^2}{n_r^j(d)}\right) \tag{3.9}$$

Where $A_l = \{x_i \in A : x_{ij} \leq d\}$,$A_r = \{x_i \in A : x_{ij} > d\}$, $B_l = \{x_i \in B : x_{ij} \leq d\}$,$B_r = \{x_i \in B : x_{ij} > d\}$,$d$ is the point for computing the split in the dataset to find the optimal variance performance.

**Categorical Boosting (CAT)**

his gradient boosting framework developed by the Yandex team was designed to handle categorical variables by obtaining the best gradient through an ensemble of decision trees. It makes use of categorical features for integrative learning during training instead of preprocessing stage. Encoding techniques are used during runtime to convert categorical values to numerical values to reduce over-fitting by using random permutations of training data. Since CAT uses target statistics (TS) for efficiency improvement, yet it replaces the original category $Xk^i$ of $k^{th}$ training variables with a single feature equivalent to some target statistic $\hat{x}_k^i TS$, we must obtain $\hat{x}_k^i \approx \mathbb{E}\ y|x^i = x_k^i$ .Such that the random permutation for choosing the tree structure first calculates the average of leaf values.

If a permutation is $\theta = [\sigma_1, \ldots, \sigma_n]_n^T$, it is replaced with

$$x_{\sigma_{p,k}} = \frac{\sum_{j=1}^{p-1}\left[x_{\sigma_{j,k}} = x_{\sigma_{p,k}}\right].Y_{\sigma_j} f.P}{\sum_{j=1}^{p-1}\left[x_{\sigma_{j,k}} = x_{\sigma_{p,k}}\right].Y_{\sigma_j} f.P} \tag{3.10}$$

After altering the equation, we obtain the estimated $\mathbb{E}\ y|x^i = x_k^i$ by using the average value of $y$ over the dataset for training with the same category $x_k^i$.

**Decision Tree Classifier**

This is a supervised technique for building a tree using Classification and Regression Tree (CART) algorithm where internal nodes represent the features of the signal dataset, decision nodes with multiple branches represent the decision rules and leaf nodes represent the outcome. It is an illustration of all the likely solutions to a decision based on specified conditions. The algorithm continuously calculates the measure of purity of the sub split for each feature after every split that helps us build a suitable decision tree by choosing the best feature to split accordingly. This is called entropy and it is given by;

$$H(s) = -P(+)\,log_2 P(+) - P(-)log_2 P(-) \tag{3.11}$$

$$\frac{P(+)}{P(-)} = \frac{\%\ of + ve\ class}{\%\ of - ve\ class} \tag{3.12}$$

Alternatively, Gini impurity of features after splitting can be used to split the tree appropriately, it can be computed by formula below;

$$GI = 1 - \sum_{i=1}^{n} P^2 \tag{3.13}$$

$$GI = 1 - \left[P(+)^2 + P(-)^2\right] \tag{3.14}$$

**Voting Classifier**
This is an ensemble combination of different multiple models to overcome bias of a single model towards particular factors in order to attain a generalized and confident fit of all models. The two implementations of Voting are Soft Voting where we sum and average the predicted probability vectors of the combined models and Hard Voting where we classify model output then obtain the final output value by calculating the mode value of combined individual model output. E. ML Model Interpretability and Explainability. Black-box Machine Learning (ML) predictions and decisions require explanation for trust and reliability in the field of medicine.

**Explainability of the CTG Signal Classification Models.** In this paper, we used ELI5 Python package XAI Libraries to explain the ML models using weights associated with each feature to depict the feature's importance in of each ML model for reduced ambiguity and better interpretability of CTG Signals [113]. Since ELI5 shuffles the removed variable attribute values and randomizes the chosen variable to analyze the model's performance decrease, we used it to compute and interpret the global explainability of the selected models in analysis of the variable global influence in the fetal health evaluation [48].

## 3.3 XAI-4-NICU-Admissions | LcMCH: II

### 3.3.1 Summary

Neonatal Intensive Care Units (NICU) service costs are rapidly growing due to the higher resource utilization intensity. This in turn increases the healthcare costs for NICU patients besides the inaccessibility and unpreparedness of both NICU service providers and patient caretakers hence an increase in neonatal mortality and morbidity. There are a lot of contributors to NICU admissions but the existing methods consider very limited features to precisely predict NICU admissions. In this paper, we present a robust Explainable Artificial Intelligence approach that allows machines to interpretably learn from a pool of possible contributing features in order to predict an NICU admission. Our machine learning approach interpretably illustrates the thought process of admission prediction to the physician and patient. This provides transparent and trustable insights for the precise, proactive, personalized and participatory NICU medical diagnostics and treatment plans for the patient. We statistically and visually present Random Forest and Logistic Regression prediction explanations using SHAP, LIME and ELI5 techniques. This predictive technological approach can preventively increase success of maternal and neonatal monitoring and treatment plans. It can also enhance proactive management of NICU facilities (resources) by the responsible facility administrators most especially in resource constrained settings.

In this research work, we achieved the objectives a,b and c thus, we proved the concept of predictive, preventive and precision medicine using Machine Learning (ML) and Artificial Intelligence (AI) techniques for Maternal and Child Health (MCH)

using a real dataset, improved ML and AI interpretability for MCH physicians and care takers by using explainable AI techniques in more transparent and insightful means for predictive, preventive and precise MCH medical decision making, then derived and comprehensively illustrate the most important features (factors) that require extra attention for specific MCH predictive, preventive and precise medical decision making.

### 3.3.2 Methodology

#### Approach

Explainable ML for predicting NICU Admission.

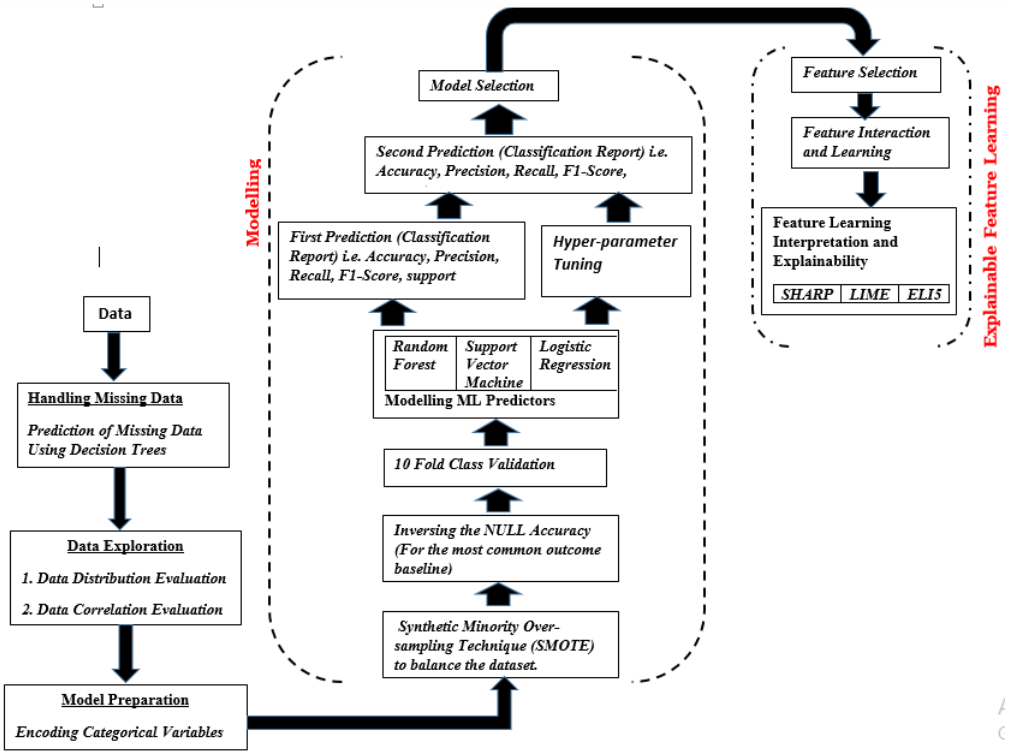


Figure 3.8: High Level diagram for the proposed NICU XAI approach

We are proposing an Explainable Machine Learning (ML) approach to NICU Admission prediction. It will help patients cut costs for preventable NICU services and help the Neonatologists improve the precision in maternal and neonatal medicine. This approach will improve neonatal treatment plans with interpretable Machine Learning (ML) predictions for NICU service interventions. In this paper, ambiguity and technophobia to Neonatal AI preventive medicine is achieved by explaining driven NICU predictions with feature importance as outlined in the Illustration of Figure 3.8.

#### XAI Approach Description

The three Explainability Techniques used in this approach are;

**SHapley Additive exPlanations (SHAP):**
In 2017, Lundberg and Lee published a game theoretical approach that explains outputs of ML models by connecting optimal credit portions with local descriptions using the Shapley values of game theory and their related extensions which created the SHAP AI framework. This average marginal contribution of a feature value over all possible coalitions defines the Shapley values which are unified measures of a feature importance derived by;

$$\varphi_i(v) = \sum_{SN\{I\}} \frac{|S|!(|N| - |S| - 1)!}{|N|!}(v(S \cup \{i\}) - v(S) \tag{3.15}$$

where marginal contribution of the feature $[v(S \cup i) - v(S)]$ is computed out of all the subsets S to get the Shapley value for a feature $i$, such that model estimates of all subsets with and without the feature are calculated and added to get the Shapley value for that feature to make the Additive exPlanations [116].

**Local Interpretable Model-Agnostic Explanations (LIME):**
This algorithm illuminates black box predictions of any classifier (f) in a correct way, by estimating it locally with an interpretable model $g$ $Gg \in G$. where $G$ is a class of interpretable models such as a linear classifier or a decision tree. The measure of complexity Omega $(g)\Omega(g)$ of the model is also a significant factor of how easily the explanations are generated. In addition, the error of $g$ is calculated by approximating f using a loss or distance function, denoted as $L(f, g)$. Finally the explanation $(g)(g)$ is calculated from the optimization of;

$$(g)\Omega = \text{ ar}g\text{minL(f,}g\text{)} + \Omega(g) \tag{3.16}$$

LIME is used to train a linear model to approximate the local decision boundary for that instance in the dataset. It is used by non-experts to pick classifiers that generalize better in the real world and improve trustworthiness of classifiers by doing feature engineering with guidance on when and why to trust a model. With respect to a single prediction, this model-agnostic method generates an explanation by training a local interpretable classifier where its training data is generated by taking a specific input, permuting it, and labeling the permutations using the model [118][31].

**Explain it Like I'm 5 (ELI5)**
It is a python package with in-built support for several ML frameworks inspect ML classifiers and explain their predictions. It allows for visualization and debugging of various machine learning algorithms such as sklearn regressors and classifiers, XGBoost, CatBoost, Keras etc. using a unified API by providing weights of the features from most common Python Libraries. Since it has local (how and why a specific prediction is made) and global (how an overall model works) properties, ELI5 explains the ML models interpretably and computes the contribution selected features to execute feature importance for final prediction [114][46].

**Dataset Description and Features.**

From IEEE Data port, we obtained a multidisciplinary Mother's Significant Feature (MSF) Dataset for multidisciplinary collaborative scientific research towards woman

and child health improvement for use. With 450 records and 130 maternal and child health feature attributes, features are traced about the mother, father and health outcomes. The 5 categories of the features are; physical, social, lifestyle, stress level, and health outcomes. All child health, maternal health and pregnancy outcomes of all possible abnormalities are covered in the dataset based on thorough literature review and brainstorming phases with doctors (gynecologists and pediatricians) [86].

### Data Preparation and Processing

We performed general data visualization to recognize and learn any features that are indicative of NICU admission. We used decision trees to predict the missing values for (miscarriage history and weight before delivery) in our dataset before replacement. Then we explored the data by first inspecting the numeric variable distribution as illustrated in Figure 3.9.

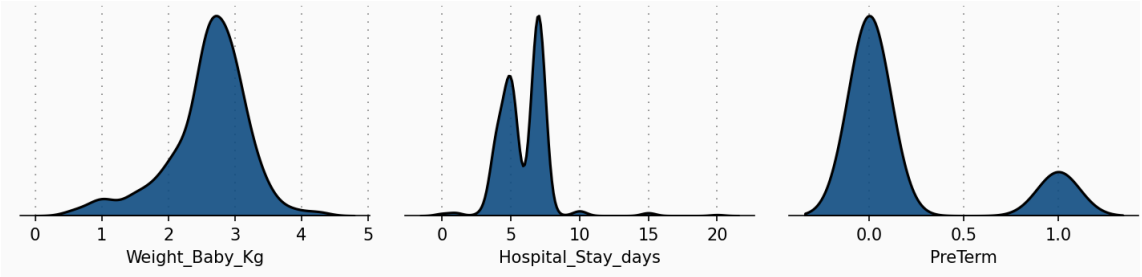


Figure 3.9: Display of some variable distribution curves of features

We implemented Synthetic Minority Over- sampling Technique (SMOTE) to balance the dataset.

### Handing Imbalanced Data

Synthetic Minority Over-sampling Technique (SMOTE)
In 2002, Chawla proposed SMOTE as an algorithm to add synthetic minority class observations based on the k-nearest neighbors' algorithm for the minority class observations to add minority class observations data to smoothen the imbalance between the classes. It interpolates between the original minority class samples and its neighboring samples by:

$$X_{new} = X_{origin} + rand\,(0,1) \times (X_i - X_{origin})\,,\ i = 1, 2, \ldots N \tag{3.17}$$

where $X_{new}$ represents the minority class samples which are newly synthesized; $X_{origin}$ between 0 and 1; $X_i$ denotes a sample that is selected from original sample randomly and used to create new samples; rand(0, 1) denotes a random number which is between 0 and 1; $X_i$ denotes a sample that is randomly chosen of the minority class sample $X_{origin}$ from the $k$ neighboring samples. Although SMOTE results in over generalization, it generates synthetic instance with the same number. Therefore the minority class after applying SMOTE can look very different from the original data and may not return the fundamental distribution of the minority class. In order to beat the null accuracy of NICU admission, we took the inverse of the baseline to predict the most common outcome of our ML models.

**Model Selection and Description.**

We build Logistic Regression, SVM and Random Forest ML models with a 10 fold cross validation then selected the best predictor based on F1 scores as the primary metric due to the dataset imbalance.

**Logistic regression**

This preferred simple classification model for multiple explanatory variables is given by;

$$p^{(Y_i|X_i,\ldots,X_p)} = \frac{e^{\beta_0+\beta_1 X_1+\cdots+\beta_p X_p}}{1+e^{\beta_0+\beta_1 X_1+\cdots+\beta_p X_p}} \tag{3.18}$$

where $X = (X1, \ldots, Xp)$ are $p$ explanatory variables for predicting the response variable Y, it can also be expressed as;

$$\log\left(\frac{p\left(Y_i \mid X_i, \ldots, X_p\right)}{1-p(Y_i \mid X_i, \ldots, X_p)}\right) = \beta_0 + \beta_1 X_1 + \cdots + \beta_p X_p. \tag{3.19}$$

where the logit function of $p$ to exhibits linearity in explanatory variables for estimated multiple logistic regression models to classically predict the probability of a given observation as positive or negative for correct classification of new observations in untrained labels. Here, the tested error rate is reduced by assigning each observation to its most likely class trained on the values of the explanatory variables hence a test observation with explanatory vectors $x_1, \ldots x_p$ should be assigned to the class $j$ for which

$$p\left(Y = j \mid X_1 = x_1, \ldots, X_p = x_p\right) \tag{3.20}$$

is largest. This corresponds to assigning a test observation to class 1 if

$$p\left(Y = 1 \mid X_1 = x_1, \ldots, X_p = x_p\right) > 0.5 \tag{3.21}$$

and to class -1 otherwise in binary setting [11].

**Support Vector Machines (SVM)**

This group of similar classifiers generalizes the maximal margin classifier using a separating hyper-plane to classify observations. Consider a hyper-plane to be a subspace of $\mathrm{p}-1$ dimensions in p-dimension space defined by;

$$\beta_0 + \sum_{i=1}^{p} \beta_i x_i = 0 \tag{3.22}$$

For feature space of dimension 2, the hyper-plane is a straight line such an observation $x = (x_1, \ldots, x_p)$ given by;

$$\beta_0 + \sum_{i=1}^{p} \beta_i x_i > 0, \tag{3.23}$$

OR

$$\beta_0 + \sum_{i=1}^{p} \beta_i x_i < 0 \tag{3.24}$$

The Hyper-plane can only be used as a classifier if observations are classified without errors. For divided data, there numerous possible hyper-planes of which maximal margin classifier selects one that lies extreme of the training observations (support

vectors). SVM is a linear classifier extending support vector classifier with accommodation of non-linear class boundaries represented as;

$$f(x) = \beta_0 + \sum_{i=1}^{n} \alpha_i \langle x, x_i \rangle , \tag{3.25}$$

Where $\alpha_i, (\mathrm{i} = 1, ..., \mathrm{n})$ are parameters, one per observation. The inner product computation of new point x and each of the training points estimates the parameter which are nonzero for the support vectors only. On replacing every inner product with a generalization $K(x_i, x_{i'})$ where $K$ is a function that measures the similarity of two observations (kernel), expression becomes;

$$f(x) = \beta_0 + \sum_{i \in S}^{n} \alpha_i K(x, x_i) . \tag{3.26}$$

Where S represents a set of all observations that are support vectors. The radial basis kernel is generally given by;

$$K(x_i, x_i) = \exp(-\gamma + \sum_{j=1}^{p} (x_{ij} - x_{i'j})^2) \tag{3.27}$$

where  is a cross validation positive constant determinant.

**Random forest**
It is a decision tree based classifier for predicting qualitative responses by dividing the predictor space into different and non-overlapping regions for the same prediction to be made for every observation in that region (majority group) during classification which can be regarded as Bayes classifier. Predictor space is partitioned iteratively based on the highest reduction of some measure of classification error by recursive binary splitting often using the Gini index;

$$G = \sum_{k=1}^{K} \hat{p}_{mk}(1 - \hat{p}_{mk}) \tag{3.28}$$

where $\hat{p}_{mk}$ is the quantity of training observations that belong to the $k^{th}$ class in the $m^{th}$region. Overfitting data during learning is addressed by bootstrap driven bagging where the model is trained on the individual bootstrapped training sets in order to get $B$ classification functions by;

$$f^{*1}(x), \ldots, f^{*B}(x) \tag{3.29}$$

In order to average the predictions of all the models for the final result as;

$$\hat{f}_{bag}(x) = \frac{1}{B} \sum_{b=1}^{B} \hat{f}^{*b}(x) \tag{3.30}$$

,observation prediction is done by recording the class prediction by each of the B trees and summing the predictions with the most frequent class among the B predictions as a majority vote. As extension of bagged trees, random forest aims at

model variance reduction by choosing a random sample of the m predictors as split candidates from the full set of $p$ predictors at each split which is given by; $m \approx \sqrt{p}$. Thus reducing the total variance of averaged models with a slight increase in bias when deco-relating the trees.
On comparing performance of the 3 models on positive seen data (1) and negative seen data (0), the report below was obtained as illustrated in table 3.1

| **Metric** | **Precision** | **Recall** | **F1-Score** | **support** |
|---|---|---|---|---|
| **Negative(o)** | 0.84 | 0.83 | 0.84 | 238 |
| **Positive (1)** | 0.49 | 0.51 | 0.50 | 77 |
| **Accuracy** | | | 0.75 | 315 |
| **Macro Average** | 0.67 | 0.67 | 0.67 | 315 |
| **Weighted Average** | 0.75 | 0.75 | 0.75 | 315 |
| **Accuracy Score: 0.75** | | | | |

Table 3.1: Random Forest (RF) Classification Report

RF exhibited good accuracy but poor recall so we optimized it with a grid-search, bootstrapped with a maximum of 5 features and 100 estimators to find its optimal parameters and obtained the results in table 3.2.

| **Metric** | **Precision** | **Recall** | **F1-Score** | **support** |
|---|---|---|---|---|
| **Negative(o)** | 0.84 | 0.87 | 0.85 | 238 |
| **Positive (1)** | 0.55 | 0.51 | 0.53 | 77 |
| **Accuracy** | | | 0.75 | 315 |
| **Macro Average** | 0.70 | 0.66 | 0.69 | 315 |
| **Weighted Average** | 0.77 | 0.78 | 0.77 | 315 |
| **Accuracy Score: 0.77** | | | | |
| **F1 Score: 0.52** | | | | |

Table 3.2: Tuned Random Forest (RF) Classification Report

Since Logistic Regression (LR) had the highest F1 Score, we tuned its parameters for better results in table 3.3.

We also tuned the SVM to obtain the results in Figure 3.4 to make a fair comparison. Despite the low accuracy, Logistic Regression had the best recall amongst all ML models.

The comparison illustrated in Figure 3.10 showed that a tuned RF gave a higher accuracy score, it was likely that the model would best predict the likelihood of NICU admission rather than the less likelihoodness of admission.
We visually compared the performance of the selected ML models to assess their performance on each prediction. RF performs the best for overall accuracy in Figure 3.11

| Metric | Precision | Recall | F1-Score | support |
|---|---|---|---|---|
| **Negative(o)** | 0.85 | 0.72 | 0.85 | 238 |
| **Positive (1)** | 0.41 | 0.60 | 0.49 | 77 |
| **Accuracy** | | | 0.69 | 315 |
| **Macro Average** | 0.63 | 0.66 | 0.63 | 315 |
| **Weighted Average** | 0.74 | 0.769 | 0.71 | 315 |
| **Accuracy Score: 0.69** | | | | |
| **F1 Score: 0.48** | | | | |

Table 3.3: Parameter Tuned Logistic Regression (LR) Classification Report

| Metric | Precision | Recall | F1-Score | support |
|---|---|---|---|---|
| **Negative(o)** | 0.82 | 0.76 | 0.79 | 238 |
| **Positive (1)** | 0.39 | 0.47 | 0.42 | 77 |
| **Accuracy** | | | 0.69 | 315 |
| **Macro Average** | 0.60 | 0.61 | 0.61 | 315 |
| **Weighted Average** | 0.71 | 0.69 | 0.70 | 315 |
| **Accuracy Score: 0.68** | | | | |
| **F1 Score: 0.42** | | | | |

Table 3.4: Parameter Tuned Support Vector Machine (SVM) Classification Report

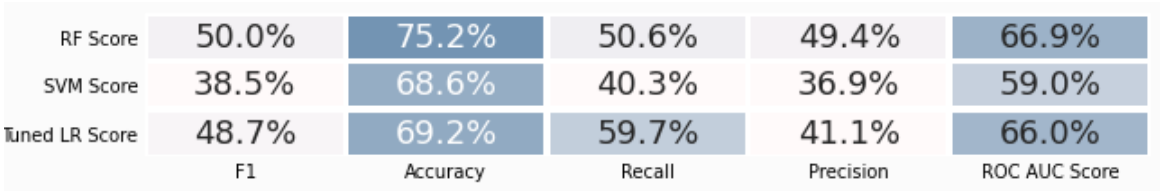


Figure 3.10: Summary of the Machine Learning Model Performance Comparisons

In this domain of maternal and neonatal healthcare, the healthcare medical practitioners' choice of predictive model depended on the purpose of prediction. When we opted to use the model for medical advice or preventive maternal-fetal medicine (treatment), the model with the highest recall was preferably Logistic Regression (LR) with detail illustrated in Figure 3.15.
This LR option is not final for all maternal and neonatal medical decisions because the recall variance of the models and accuracy of the models are great factors to consider for model selection in this medical domain.

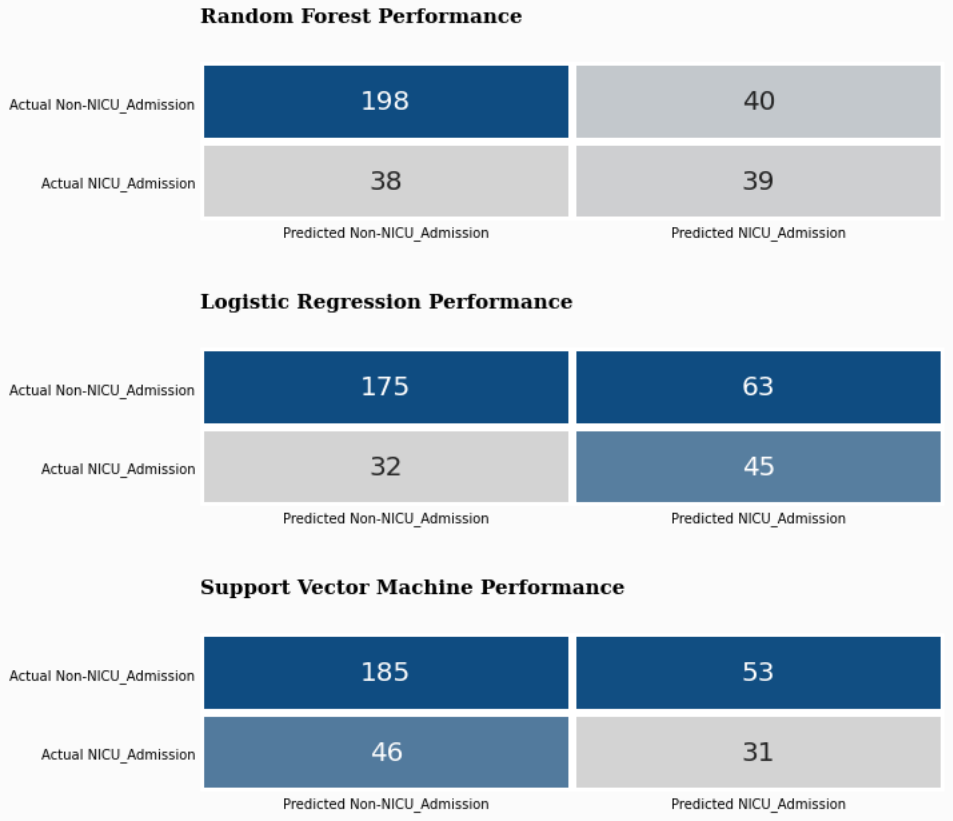


Figure 3.11: Individual Performance of each Model on Each Prediction

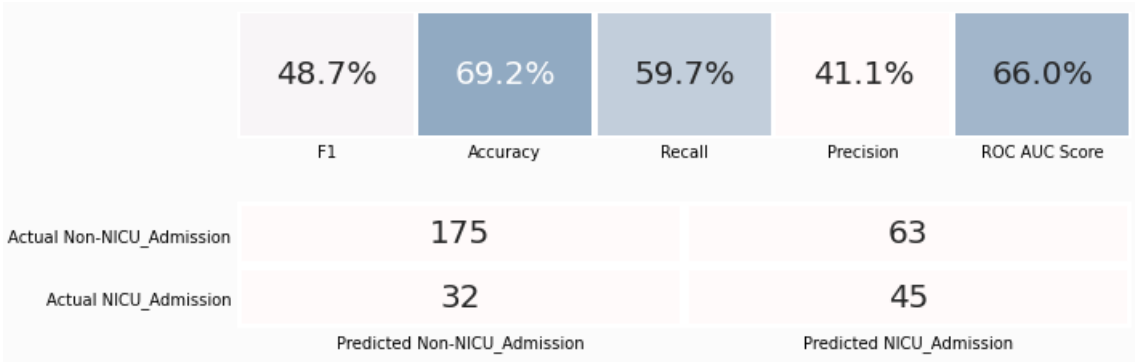


Figure 3.12: Logistic Regression Overview

## 3.4 XAI-4-StemCell-Transplantation | LcMCH: II

### 3.4.1 Summary

Pediatric bone marrow failure syndromes are therapeutically and diagnostically strenuous, costly and yet extremely risky to pediatric patients despite their necessity for pediatric survival. To make matters worse, the current approach to the treatment of hematology and blood disorders in pediatric patients is extremely patient-centred and uncertainly lethal. In this work, we innovatively leveraged machine learning and artificial intelligence techniques to predictively and explainably identify important factors influencing the success or failure of cell transplantation

in pediatric patients using SHapley Additive exPlanations (SHAP). We also demonstrated a reliable approach to predict the survival of the pediatric patient based on the important feature interactions before the cell transplantation is performed. For this role, Catboost, LigtGBM and XBoost algorithms obtained 82%, 92% and 94% accuracy respectively. As much as we validate Kawłak's hypothesis that increasing the CD34+ cells/kg dosage prolongs general survival time of patients without synchronous occasion of unpleasant events affecting patients' quality of life (Kawłak et al., 2010), we discovered that pediatric risk group and recipients' age are likely to be more influential determinants of prolonged survival as compared to CD34+ cell reception. Our predictive and preventive approaches to pediatric medical transplantation beat the existing delayed interventional approaches of reactive pediatric medicine. They can greatly reduce child mortality and improve the survival of children with personalized medicine hence transparently improving maternal and child healthcare.

In this research work, we achieved the objectives a,b and c thus, we proved the concept of predictive, preventive and precision medicine using Machine Learning (ML) and Artificial Intelligence (AI) techniques for Maternal and Child Health (MCH) using a real dataset, improved ML and AI interpretability for MCH physicians and care takers by using explainable AI techniques in more transparent and insightful means for predictive, preventive and precise MCH medical decision making, then derived and comprehensively illustrate the most important features (factors) that require extra attention for specific MCH predictive, preventive and precise medical decision making.

### 3.4.2 Methodology

#### Approach

Explainable Predictive Artificial Intelligence for Hematologic Pediatric Patient Survival upon Stem Cell Transplantation using Model-agonistic Interpretation methods. Our explainability approach flexibly depends on intrinsic model architectures to exclusively relate the input to outputs by feature relevance techniques. The proposed explainability approach is based on coalitional Game theory (Shapley values) where Shapley Additive exPlanations (SHAP) focus on the instance to be interpreted in order to build liner models, then use feature importance as the explanation coefficients for the used machine learning algorithms.
SHapley Additive exPlanations (SHAP): In 2017, Lundberg and Lee published a game-theoretical approach that explains outputs of ML models by connecting optimal credit portions and related extensions which created the SHAP AI framework. This average marginal contribution of a feature value over all possible coalitions defines the Shapley values which are unified measures of feature importance derived by;

$$\varphi_i(v) = \sum_{SN\{I\}} \frac{|S|!(|N| - |S| - 1)!}{|N|!}(v(S \cup \{i\}) - v(S) \tag{3.31}$$

Where the marginal contribution of the feature $[v(S \cup i) - v(S)]$ is computed out of all the subsets S to get the Shapley value for a feature $i$, such that model estimates

of all subsets with and without the feature are calculated and added to get the Shapley value for that feature to make the Additive exPlanations.

**Dataset Description.**

We obtained a pediatric hematologic dataset with 187 examples of pediatric patients characterized by 37 attributes describing hematologic diseases and malignant disorders among pediatric patients who were subjected to unmanipulated allogeneic unrelated donor hematopoietic stem cell transplantation [16].

**Artificial Intelligence Model Selection and Description**

**LightGBM**

It is an algorithm that uses Gradient-based One Side Sampling (GOSS) and Exclusive Feature Bundling (EFB) methods to overcome limitations in Gradient Boosting Decision Tree frameworks [15].
For the given training dataset

$$X = \{(a_i, b_i)\}_{1=1}^{m}. \tag{3.32}$$

LightGBM aims to search for an approximation $\hat{f}(x)$ to the function $f^*(x)$ for minimizing expected values of specific loss functions;

$$L(y,\ f(x)) : \hat{f}(x)\, argminEL(y,\ f(x)) \tag{3.33}$$

LightGBM then combines many T regression trees for predicting the eventual model defined as;

$$f_T\ (X) = \sum_{t=1}^{T} f_t\ (X) \tag{3.34}$$

The model then trains in the additive form at step t as illustrated below;

$$P_t \cong \sum_{j=1}^{M} L(y_i,\ F_{t-1}\ (a_i) +\ f_t\ (a_i)) \tag{3.35}$$

Equation 3.35 is simplified when the constant term is removed

$$P_t = \sum_{j=1}^{M} (g_i f_t(a_i) +\ \frac{1}{2}\ h_i f_t^2(x_i)) \tag{3.36}$$

Equation 3.36 is further converted to 3.37 if the sample set of leaf j is represented by$I_j$:

$$P_t = \sum_{j=1}^{J} ((\sum_{i \in I_j} g_i)c_j + \frac{1}{2} \left( \sum_{i \in I_j} hi +\ \lambda \right) c_j^2) \tag{3.37}$$

In terms of the tree structure q(x), the optimum leaf weights of the leaf nodes $c_j^*$ and extreme values of $P_t$ are figured out by Equation 3.38 and Equation 3.39:

$$c_j^* = -\frac{\sum_{i \varepsilon I_j} g_i}{\sum_{i \varepsilon I_j} hi +\ \lambda} \tag{3.38}$$

$$P_T^* = -\frac{1}{2}\sum_{j=1}^{J}\frac{\left(\sum_{i\in I_j} g_i\right)^2}{\sum_{i\in I_j} hi + \ \lambda} \tag{3.39}$$

where is the weight function measuring the quality of tree structure $q(x)$. The objective function is eventually obtained by integrating the split:

$$Q = \frac{1}{2}\left(\frac{\left(\sum_{i\in I_l} g_i\right)^2}{\sum_{i\in I_l} hi + \ \lambda} + \frac{\left(\sum_{i\in I_r} g_i\right)^2}{\sum_{i\in I_r} hi + \ \lambda} + \ \frac{\left(\sum_{i\in I} g_i\right)^2}{\sum_{i\in I} hi + \ \lambda}\right) \tag{3.40}$$

where $I_l$ and $I_r$ are samples of the left and right branch respectively.

**Extreme Gradient Boosting (XGboost):** It is a an algorithm that implements optimized distributed gradient boosting decision trees in an open-source gradient boosting framework using ensemble learning techniques [93]. This model inputs a training set as $\{(x_i, y_i)\}_{i=1}^{N}$,a differentiable loss function $L(y,\ F(x))$, a number of weak learners M and a learning rate $\alpha$. Then we run the inputs through an algorithm where we initialize a constant value to pass through M when m=1. After which we fit the weak learner ( base learner, e.g. tree) using a selected training set to compute an optimization who's output can be used to update the model such we obtain an output defined as;

$$\hat{f}\,(x) = \hat{f}_M\,(x) = \sum_{m=0}^{M}\hat{f}_m\,(x) \tag{3.41}$$

**Categorical Boosting (CatBoost):** It is an algorithm developed by YANDEX as gradient boosting framework [93]. It uses target statistics ( $TS$) to improve efficiency in classification tasks by replacing the original category of features $Xk^i$of $k^{th}$ training variables with a single feature equivalent to some target statistic $\hat{x}_k^i TS$. We must obtain $\hat{x}_k^i \approx \mathbb{E}\ y|x^i = x_k^i$ Such that the random permutation for choosing the tree structure first calculates the average of leaf values. If a permutation is $\theta = [\sigma_1, \ldots, \sigma_n]_n^T$ , it is replaced with;

$$x_{\sigma_{p,k}} = \frac{\sum_{j=1}^{p-1}\left[x_{\sigma_{j,k}} = x_{\sigma_{p,k}}\right].Y_{\sigma_j} f.P}{\sum_{j=1}^{p-1}\left[x_{\sigma_{j,k}} = x_{\sigma_{p,k}}\right].Y_{\sigma_j} f.P} \tag{3.42}$$

After altering the equation, we obtain the estimated $\mathbb{E}\ y|x^i = x_k^i$ by using the average value of y over the dataset for training with the same category $x_k^i$.

## 3.5 XAI-4-Pulmonary-Health-Evaluation | LcMCH: III

### 3.5.1 Summary

Biomedical Instrumentation is one of the fastest health emerging innovative technologies with proven contribution towards the interdisciplinary medicine, it helps physicians to diagnose complex medical problems and provide treatment to patients precisely and safely. With this technological trend, explainable artificial intelligence, biomedical image processing and augmented intelligence can provide a tool that can help pediatricians and other experts in the fields of pulmonology and otolaryngology as well as experts from epidemiology and pediatric practice to interpretably and reliably offer clinical and diagnostic services to infants, children, and adolescents with acute and chronic respiratory disorders. In this work, we presented a reliable interpretable deep transfer learning approach for pediatric pulmonary health evaluation regardless of the scarcity and limited annotated pediatric chest X-ray Image dataset sizes that affect the reliability of digital image processing for pediatric pulmonary disease diagnosis. This approach leverages a combination of computer vision tools and techniques to reduce child morbidity and mortality through predictive and preventive medicine for reduced surveillance risks and affordability in low resource settings. With open datasets, the deep neural networks classified the generated augmented images into 4 classes namely; Normal, Covid-19, Tuberculosis and Pneumonia at an accuracy of 97%, 97%, 70%, and 73% respectively with recall of 100% for Pneumonia and overall accuracy of 79% at only 10 epochs for both regular and transferred learning.

In this research work, we achieved the objectives a,b and c thus, we proved the concept of predictive, preventive and precision medicine using Machine Learning (ML) and Artificial Intelligence (AI) techniques for Maternal and Child Health (MCH) using a real dataset, improved ML and AI interpretability for MCH physicians and care takers by using explainable AI techniques in more transparent and insightful means for predictive, preventive and precise MCH medical decision making, then derived and comprehensively illustrate the most important features (factors) that require extra attention for specific MCH predictive, preventive and precise medical decision making.

### 3.5.2 Methodology

#### Approach

Explainable Augmented Intelligence and Deep Transfer Learning for Pediatric Pulmonary Health Evaluation. With collaborative interventions of Computer Science in Biology, we took advantage of scientific innovations like Image augmentation, Interpretable Artificial Intelligence, Deep and Transfer Learning to propose a transparent, accurate pulmonary disease detection and classification approach that leverages a

combination of deep and transfer learning of chest X-ray images to detect and differentiate the most deadly pediatric pulmonary diseases for precise and personalized diagnosis, treatment and management. Since specific signs and symptoms common to COVID-19, Pneumonia and TB facilitate a rapid access to imaging services, we proposed use of Explainable AI as a reliable tool for biomedical image processing of the newly augmented extracted chest X-ray images dataset.

**Dataset Description.**

We obtained three different well annotated chest image datasets. One was a small COVID-19 chest X-ray (CXR) dataset collected from Northern Italy by a major emergency hospitals during peak of the COVID pandemic, this dataset is hosted at github [112]. We obtained another small pediatric Pneumonia dataset of Labeled Optical Coherence Tomography (OCT) and Chest X-Ray Images from with directories CNV, DME, DRUSEN, and NORMAL from Mendeley [38], we the obtained one last small chest X-ray Tuberculosis image dataset form kaggle including (training, testing and validation) images [117]. In total we managed get up to a total of 7135 x-ray images for the work. We then created a Google cloud repository to host the obtained datasets with in their organized folders and subfolders. Then we build a data pipelines towards the Google cloud directory for efficient assess by Keras during data processing.A sample of the images obtained in the datasets is illustrated in Figure 3.13.

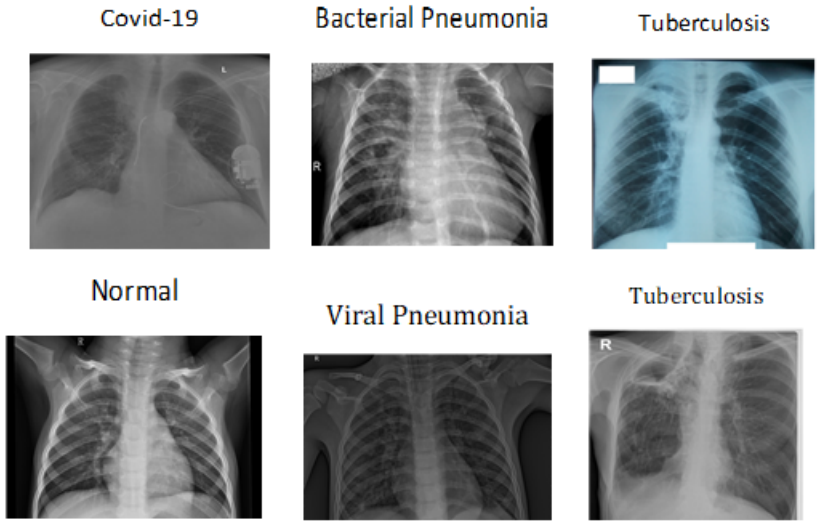


Figure 3.13: Sample Chest X-ray Images of used datasets before Augmentation

**Image Data Augmentation for Augmented Intelligence**
Since conventional image processing uses statistical or machine learning classifiers as a computer vision methodology to segment images and recognized objects/ patterns, they often require large well labeled datasets to effectively predict or classify objects. This is a very huge problem in the medical setting most especially pediatric pulmonology.

Due to the scarcity of pediatric chest X-ray image datasets and limited access to annotated chest X-ray images for biomedical image processing, we proposed and deployed image data augmentation in order to generate a relatively large, balanced

and sufficient dataset for effective machine learning and computer vision. For this particular experiment, we set up and executed a Keras image generator through the dataset cloud directory hosting the dataset with a configured validation split of 0.2, rotation range of 5, width shift of 0.05, height shift of 0.05, zoom range of 0.05 and a compulsory horizontal flip with some samples shown in Figure 3.14.

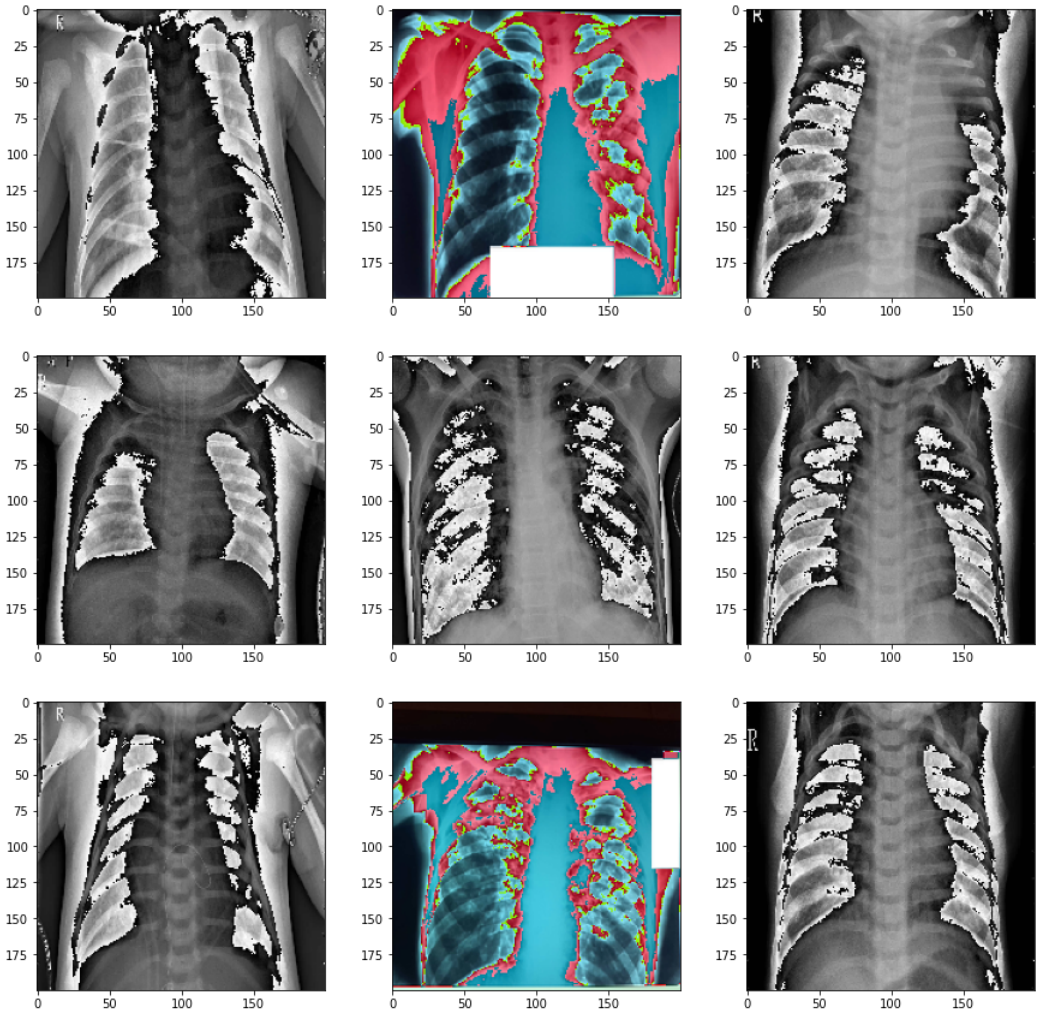

Figure 3.14: Generated Augmented Pediatric Chest-X-ray Images

**Deep Learning with Convolutional Neural Network**

We proposed and built a deep convolutional neural network (CNN) to accurately learn, detect and classify the pediatric pulmonary diseases within the newly generated augmented pediatric chest X-ray images at only 10 epochs as demonstrated in Table 3.6. The deep network will also act as the base for transfer learning in order to reduce computation costs of pulmonary disease detection among pediatric patients. The CNN often generates image abstracts for representative classification as a way of improving biomedical image classification although it requires computationally intensive equipment and demands vast amounts of training samples for accurate pattern recognition and image processing. This is what necessitates transfer learning for pediatric pulmonary health evaluation. We set up a two Dimension (2D) sequential CNN with a total of 3,409,688 parameters which were all trainable

as illustrated by the CNN architecture in Table 3.5

| **Model: "sequential"** | | |
|---|---|---|
| **Layer (type)** | **Output Shape** | **Param** |
| **conv2d (Conv2D)** | (None, 198, 198, 16) | 448 |
| $\mathbf{max}_{p}ooling2d(MaxPooling2D)$ | (None, 99, 99, 16) | 0 |
| $\mathbf{conv2d}_{1}(Conv2D)$ | (None, 97, 97, 32) | 4640 |
| $\mathbf{max}_{p}ooling2d_{1}(MaxPooling2$ | (None, 48, 48, 32) | 0 |
| **dropout (Dropout)** | (None, 48, 48, 32) | 0 |
| $\mathbf{conv2d}_{2}(Conv2D)$ | (None, 46, 46, 64) | 18496 |
| $\mathbf{max}_{p}ooling2d_{2}(MaxPooling2$ | (None, 23, 23, 64) | 0 |
| **flatten (Flatten)** | (None, 33856) | 0 |
| **dense (Dense)** | (None, 100) | 3385700 |
| $\mathbf{dropout}_{1}(Dropout)$ | (None, 100) | 0 |
| $\mathbf{dense}_{1}(Dense)$ | (None, 4) | 404 |
| **Total params: 3,409,688** | | |
| **Trainable params: 3,409,688** | | |
| **Non-trainable params: 0** | | |

Table 3.5: Convolutional Neural Network Architecture

| | |
|---|---|
| **Validation loss:** | 0.0011364993406459 69 |
| **Validation accuracy:** | 1.0 |
| **Test loss:** | 2.207593202590942 4 |
| **Test accuracy:** | 0.787289261817932 1 |

Table 3.6: Convolutional Neural Network Training Metrics with 10 epochs

The base model saved for transfer learning exhibited a test loss of 2.20 and test accuracy of 0.78 yet it was able to attain a total percentage of 97%, 97%, 73%, and 70% for the pattern recognition and detection of covid-19, normality, pneumonia and tuberculosis respectively. It even exhibited a total recall of 100% for pneumonia yet 36% for the normal state of patients as illustrated in Figure 3.15 and Table 3.7

**Transfer Learning**

We proposed and used a pretrained CNN model to accelerate deep learning of the augmented pediatric X-ray chest dataset for accurate pediatric pulmonary disease detection. Besides low computational requirements for accurate pulmonary health evaluation of pediatrics, transfer learning is faster by using backward propagation and a feed-forward neural network. It fine-tunes lower layer weights during pattern detection and retains upper layer weights for unique feature recognition for necessary image classification. The first adopted base model for transfer learning exhibited

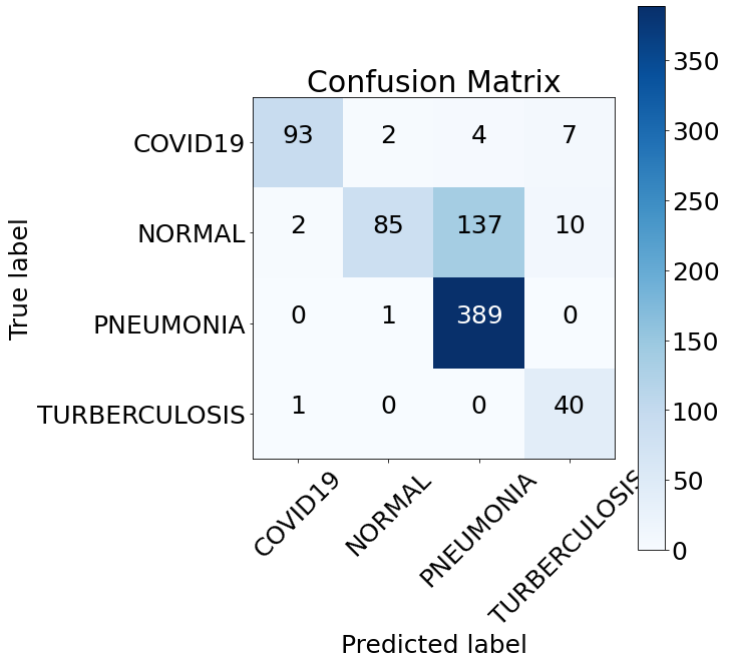


Figure 3.15: Confusion matrix of detected pulmonary diseases before transfer learning

| Classification Report | | | | |
|---|---|---|---|---|
| | **precision** | **recall** | **f1-score** | **support** |
| **COVID19** | 0.97 | 0.88 | 0.92 | 106 |
| **NORMAL** | 0.97 | 0.36 | 0.53 | 234 |
| **PNEUMONIA** | 0.73 | 1.00 | 0.85 | 390 |
| **TURBERCULOSIS** | 0.70 | 0.98 | 0.82 | 41 |
| **accuracy** | | | 0.79 | 771 |
| **macro avg** | 0.84 | 0.80 | 0.78 | 771 |
| **weighted avg** | 0.83 | 0.79 | 0.76 | 771 |

Table 3.7: Pediatric pulmonary classification report before Transfer Learning

a total validation loss of 0.001 and a validation of accuracy of 1.0 at 10 epochs as shown in Table 3.6 while the later exhibited a loss validation loss of 0.002 with the same validation accuracy as the base model as shown in Table 3.8 after transfer learning.

| | |
|---|---|
| **Validation loss:** | 0.00272019207477569 6 |
| **Validation accuracy:** | 1.0 |
| **Test loss:** | 1.474593520164489 7 |
| **Test accuracy:** | 0.785992205142974 9 |

Table 3.8: Training Metrics of the transferred learning model with 10 epochs

## 3.6 QLL-XAI-4-Fertility-Treatment | LcMCH: IV

### 3.6.1 Summary

The global trends of women in the reproductive age have significantly altered due to their personal and career development engagements besides adoption of contraceptive methods. Since women are extending birth to their late ages where natural conception is quite hard besides other factors, it has globally boosted the fertility service market which is a projected 41.4 billion industry by 2026. Despite the growing market for fertility services, infertility evaluation is still uncomfortable, expensive, inaccessible and ambiguous for both the customers and the fertility service providers. In this work, we deploy Machine Learning and Explainable Artificial Intelligence to predict the outcomes of fertility treatment using interpretable Machine Learning Lattice Models for predictive, preventive and precision reproductive medicine. We also introduced the concept of Quantum Lattice Learning in Artificial Intelligence for Machine Learning Interpretability.

In this research work, we achieved the objectives a,b, c and d thus, we proved the concept of predictive, preventive and precision medicine using Machine Learning (ML) and Artificial Intelligence (AI) techniques for Maternal and Child Health (MCH) using a real dataset, improved ML and AI interpretability for MCH physicians and care takers by using explainable AI techniques in more transparent and insightful means for predictive, preventive and precise MCH medical decision making, then derived and comprehensively illustrated the most important features (factors) that require extra attention for specific MCH predictive, preventive and precise medical decision making and we created a new Explainable Predictive Machine Learning Model that is capable of transparently illustrating feature interaction of the most influential features leading to a precise medical decision for MCH.

### 3.6.2 Methodology

#### Approach

We are proposed an Explainable Artificial Intelligence (XAI) approach to reproductive medicine that births a fragmented market of Fertility care solutions to serve

reproductive endocrinologists and fertility patients with immediacy. This approach is a combination of interpretable Machine Learning (ML) predictors for fertility health interventions using Lattice Models (LM). In this paper, this transparency is achieved by simulating the process of lattice model prediction of fertility intervention outcomes in lattice space. This simulation is what interpretably explains the 'blackbox' machine learning prediction process to aid understandability of the predictive models.

**Dataset Description**

We obtained a Mother's Significant Feature (MSF) Dataset [86] intended for scientists aiming at women and child health improvement. With 450 records and 130 attributes entailing mother's features, father's features and health outcomes, the features are divided into 5 categories namely physical, social, lifestyle, stress level, and health outcome. All probable complications related to child health, mother's health and gestation results are covered in the dataset, which were realized after comprehensive literature review and brainstorming sessions with doctors (gynecologists and pediatricians) [86].

**Data Preparation and Processing**

We first explored the dataset for data balance and missing values. We performed mean substitution (imputation) to handle missing values. It worked by substituting missing values of the defined variables with the mean of non-missing cases of defined variable. We plotted all features against the targeted variable to assess their numeric variation and relationship as shown in Figure 3.16.

Figure 3.16 shows a strong relationship between mothers' age and conception success. The higher the age, the lower the conception success after fertility medical intervention. It also shows numerous other features contributing to the success of reproductive medicine for example the father's age, Body Mass Index (BMI) of the mother among others.

Secondly, we split our data into train and test sets. Due to the heavy imbalance in the output variable, we stratified the split with 'Fertility_Treatment' to fix the proportion of Fertility Treatment events. We applied sample weighting to our algorithm by assigning a weight to each observation according to the prevalence of 'Fertility_Treatment'. In practical terms, this means that 'Fertility_Treated' individuals weighed about 20 times more than non-'Fertility_Treated' individuals since 'Fertility_Treated' individuals constituted around 5% of the total population. We then applied stochastic gradient descent to our models and correctly specified a 'Fertility_Treated' individual in order to reward the model 20 times as much as a non-'Fertility_Treated' individual [13].

### 3.6.3 Lattice Learning

We have utilized Quantum Lattice Learning which is a supervised approach to Machine Learning that builds mathematical models between inputs and outputs of the

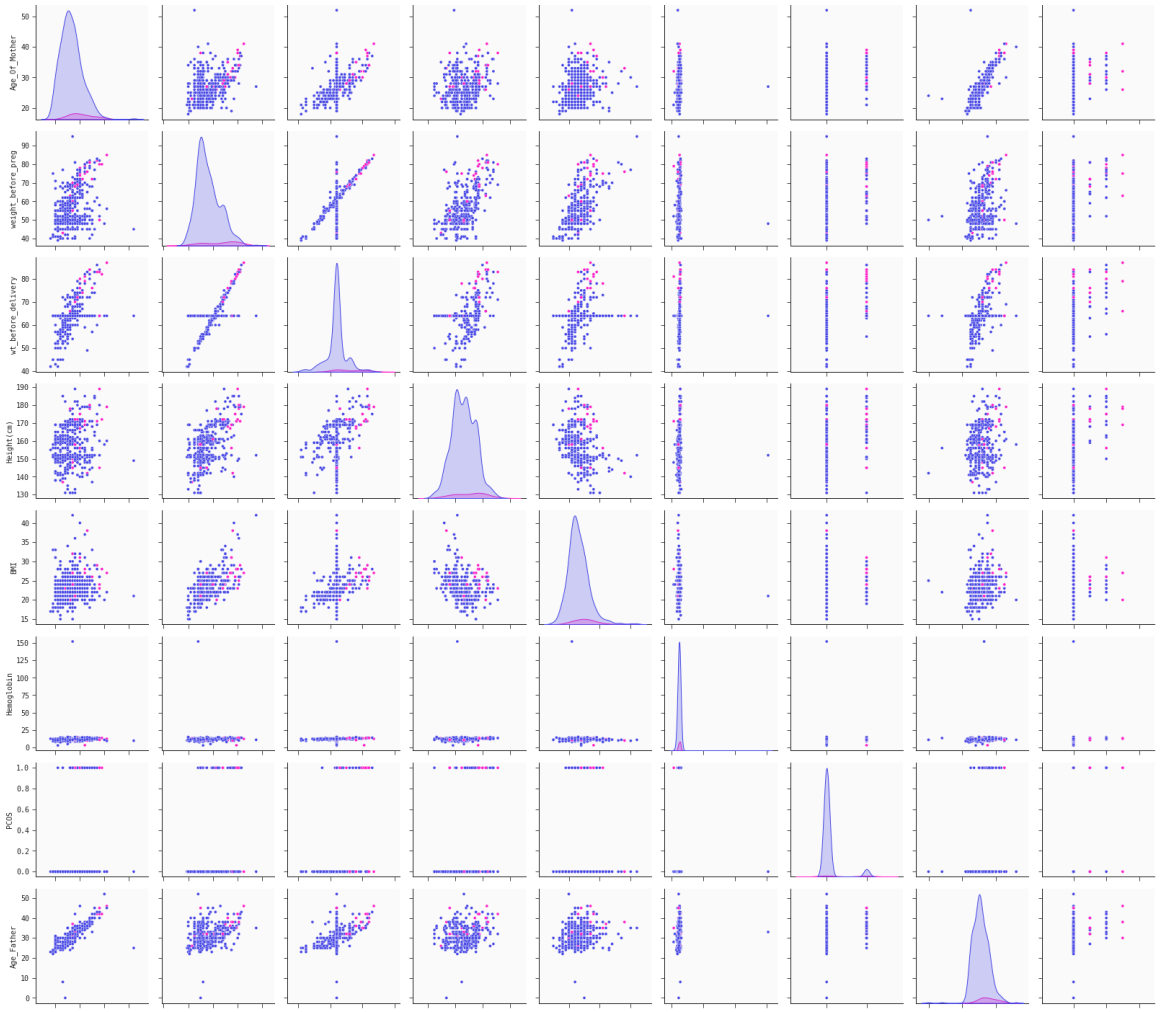


Figure 3.16: Partial Seaborn pair plot of the dataset features

datasets based on the Feynman's Path Integral.

With lattice learning, Quantum Lattice learns the structure of the problem and the probability fields of spatial paths within the lattice space and updates them such that the best mathematical model to explain the input data becomes more likely. The search is a list of probable functions A = f (B) sorted by match efficiency (explanation simplicity} given a set of observations B [3].

The premise of Feynman's technique is that; to explain something well, it must be explained simply. The way the simplicity of the explanation is attained by continuous repetitive learning of what works best with discard of what least works as demonstrated in Figure 3.17.

**In the Quantum Lattice Space :**

1. We sample thousands of models at a time,

2. Fit them using a form of back propagation, and assess them on a selected criteria (e.g. variety of loss function and information criteria).

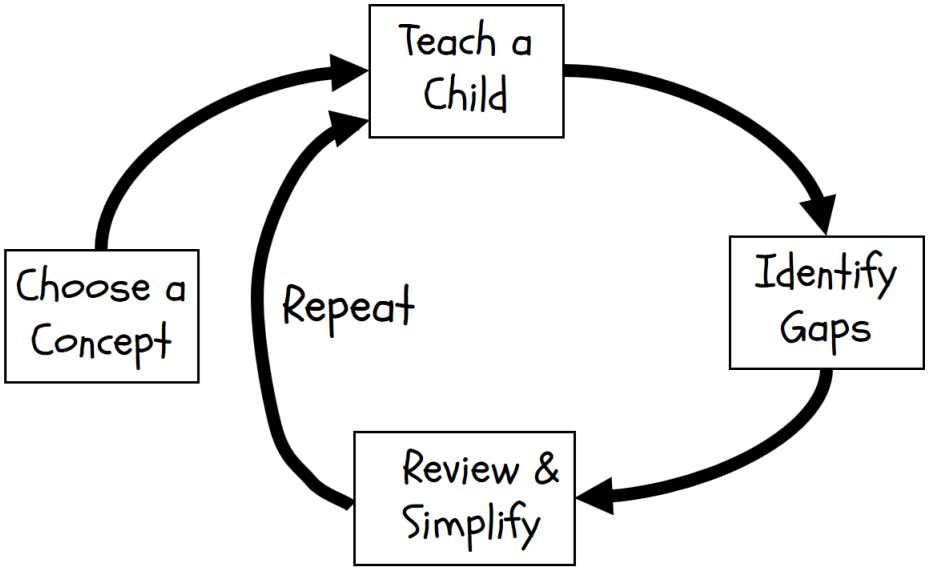


Figure 3.17: Feynman's Learning Technique

3. Abandon the worst models based on a couple of options such as dropout and decay,

4. Lattice Learning happens as we update Quantum Lattices with structures of the best mathematical models ( usually the top 10 structures that are divergent enough to ensure decent optimal learning.

5. We start over from 1, and add a couple of new samples to our list of mathematical models to evaluate. The newly added sample models then compete with the ones which were kept from the previous loop.

Each model is tested from the Quantum Lattice space, then its probability distribution is considered and modified over time. Initially, this distribution is uniform but through this process, the Quantum Lattice converges to multiple shapes the distributions towards better solutions.

Lattice Models take advantage of samples of each built model based on probability distribution turned over time to unite shapes and distributions towards an optimal solution. It takes advantage of lattice and quantum properties to simulate discrete paths from numerous inputs through lattice space paths before emerging to outputs.

Lattice Models utilize random sampling which is form of selection of computational functions (interactions). This Random sampling continuously transforms the inputs along the path integral formation until a solid path is formed such that convergence happens to the path most likely to explain the problem. Lattice model random sampling via path integral formation is illustrated by the model in Figure 3.18 with probability distributions on top of each interaction towards the predicted decision. The probability based Function (interactions) are directed by repetitive reinforcement of the best solutions discovered as numerous models are fitted. During repeated reinforcement, quantum islands with independent evolution form in the Quantum Lattice space hence narrowing the search space, and giving way to many separate evolutionary spaces.

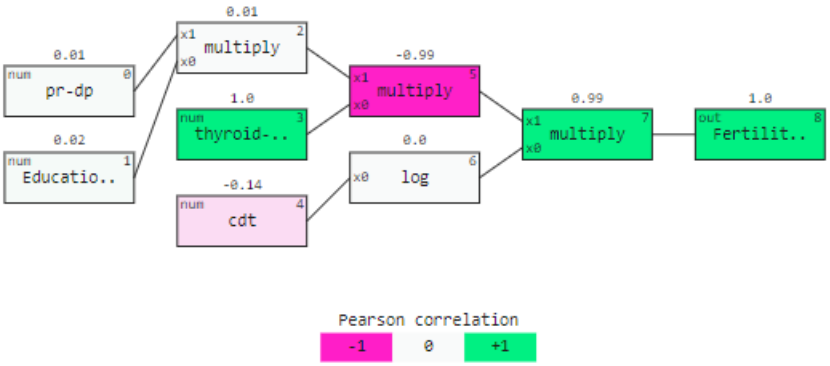


Figure 3.18: Lattice Model illustrating the function interactions with 4 inputs to form an explainable solid convergence path towards prediction the outcome of the fertility intervation

**Model Interpretability and Explainability.**

Lattice Learning allows to keep track of disintegrated representations (rules) of a signal by its probability distribution. Each rule is a coarsened signal executed to gain some human-interpretable perception of what could govern the nature of the original signal.
The multiple disentangled rules arranged in a hierarchy are used to summarize the signal based on the formalized lattice structure. Lattice learning focuses on explainability and generalizability from "small data" and it aims for rules similar to those humans extract from experience instead of an illustration improved for specific tasks like classification.
If a signal exists, the Quantum Lattice will always find it. Therefore, we can trust the model prediction if our problem is best explained with a complex non-linear mathematical equation, or a simple linear model.

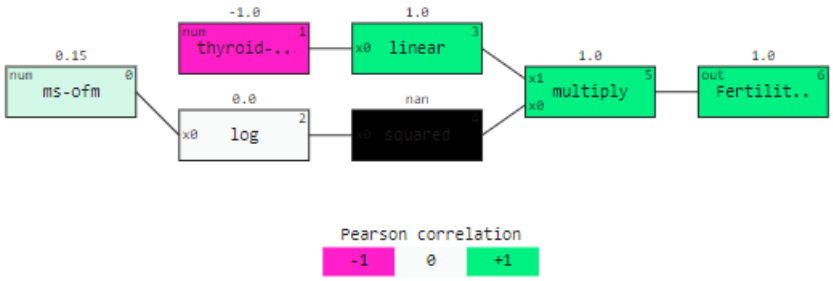


Figure 3.19: An explainable simple Linear Lattice Model of 2 inputs with a double scalar error along the predictive convergence path.

For all illustrations, Pearson correlation demonstrated in Figure 3.20 is color-coded for:

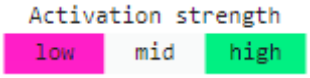


Figure 3.20: Feature Correlation Scale.

### 3.6.4 Quantum Lattice Learning Preliminaries

#### Lattice and Quantum SPACE

The feasibility of conditional probability approaches in spatial processes makes them preferable to joint probability approaches. This is because conditional probability approaches are intuitively applicable to Statistical Analysis of Lattice Space compared to joint probability approaches.
With the application of Hamersley-Clifford theorem, consistency problems are almost entirely removed which makes it easy to use as a tool for constructing conditional probability models in multiple situations [18].
This makes lattice models yield great results with the conditional probability techniques to a very simple parameter estimation procedure (the coding technique) for the binary and Gaussian variants to a straightforward goodness-of-fit tests such that Gaussian variants [18], maximum likelihood appears equally available for both simultaneous and conditional probability models of similar complexity [36].
The strength of genetic programming approaches to symbolic regression [42] coupled with the predictive power of dynamic particles taking multiple paths as evidenced by Feynman's in quantum mechanics through the Richard Feynman's path integral formation reveal implication of crossing symmetry or distribution probabilities to allow for building predictive models in the lattice space [1][79].

#### Quantum Lattice Learning (QLL)

QLL is a supervised ML approach that is inspired by the Feynman's Technique derived from Feynman's Path Integral. In this approach, the algorithm iteratively searches through an infinite list of potential mathematical models generated to solve the problem until it selects the most optimal model.
The quantum properties of this learning technique stir simulation of decision pathways through data exploration to give better understanding of the data relationships thus connecting scientific inquiry to data science. Quantum Lattice Learning is fully based on theories of Feynman's path integral to Quantum Mechanics.

#### The path Integral Formation.

In 1933, Dirac observed that action performed a central role in classical mechanics but that it assumed to have no critical role in Quantum Mechanics even if he wondered about possible explanations before he proposed the propagator (Green's function) to approve the essence of proportionality.
The matrix elements of the scattering matrix (S-matrix) in momentum space in Quantum Mechanics must be proportional to the phase factor given by $e^{iS/h}$; where S is the classical action evaluated along the classical path.
Feynman developed Dirac's idea and completed deriving the path integral formula of Quantum Mechanics in 1948. Since the propagator can be written as a sum over all possible paths between the initial and final points, each path contributes with a weight and the probability, the formed amplitude given by;

$$P\left(A \to B\right) = \left|\Re\left(A \to B\right)\right|^2 = \sum_{paths} \omega\left(A \to B\right) e^{\frac{iS_C}{h}} \tag{3.43}$$

While Dirac only studied the classical path, Feynman showed that all paths contribute.
From the Path Integral; Quantum Lattice models form (generate) infinite possible spatial paths of A to B as mathematical expressions which are interpreted as mathematical equations by their interactions amongst themselves in lattice space. The model searches this space for the parameter and expressions that best explain the output prediction in terms of the input [29][67].

# Chapter 4

# Results and Recommendations

## 4.1 ML-4-Osteoporosis-Treatment | LcMCH: I

### 4.1.1 Predictive Modeling and Classification.

#### Gaussian Naive Bayes Model

Based on Bayes' theorem, it performs classification by assuming independence between predictors where presence of a particular feature in a class does not depend on the presence of any other feature as illustrated in Figure 4.1. This model is useful for very large datasets and it is relatively easier to build. It is fast, simple, and suitable for very high-dimensional datasets. It can be optimized if used with SMOTE-SVM

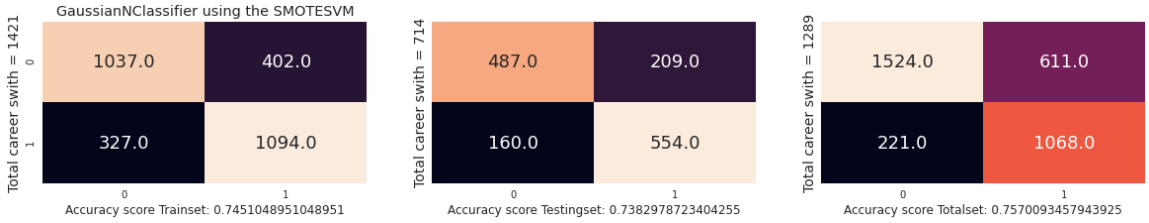


Figure 4.1: Gaussian using SMOTE-SVM

#### Logistic regression Model

As part of the linear classifiers, this Model is necessary for binary classification as shown in Figure 4.2. It is faster with easy result interpretation and effective at handling multiclass problems. This Model also gives optimal results if deployed with SMOTE-SVM.

#### Extreme Gradient Boosted Model

This Model deploys both linear and tree learning algorithms which give it great predictive power of almost 10x faster than already existing gradient boosting techniques. It is suitable for handling structured data as it tolerates several objective

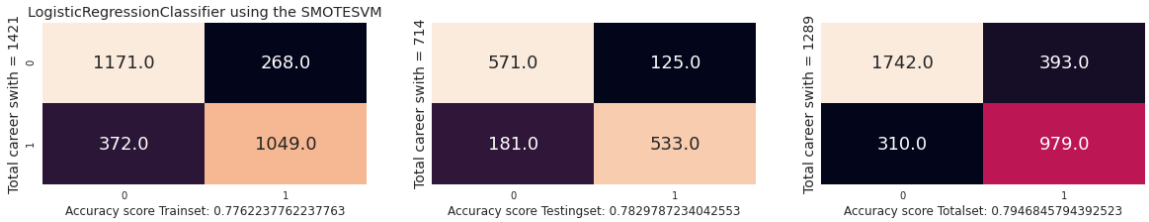


Figure 4.2: Logistic Regression using SMOTE-SVM

functions as well as regression, classification and ranking. It is gives the best results when deployed with SMOTE-SVM in this domain as shown in Figure 4.3.

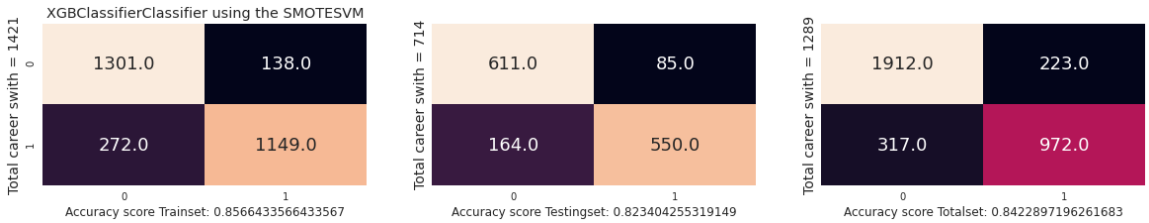


Figure 4.3: XGB using SMOTESVM

### Gradient Boosted Model

It deploys ensemble boosting for both classification and regression tasks when handling plenty of data for high prediction. This model combines prediction of several base estimators to expand robustness over a single estimator. For prediction accuracy on the validation set, we can assess the model by checking its accuracy on confusion matrix creation and then specify the finest learning rate based on results. It gives optimal results if deployed with SMOTE-SVM as demonstrated in Figure 4.4.

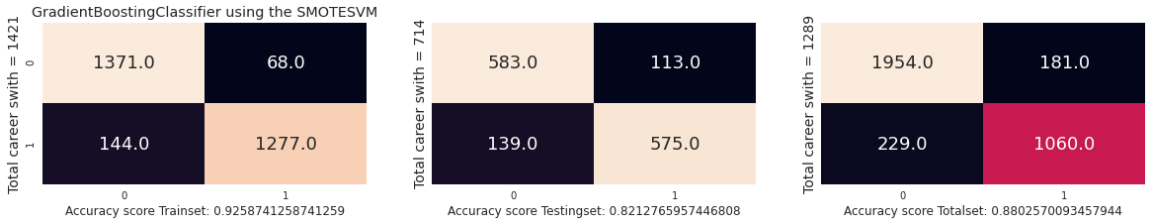


Figure 4.4: Gradient Boosting using SMOTE-SVM

### Decision Tree Model

This supervised ML model is generally used for classification problems with both categorical and continuous dependent variables as shown in Figure 4.5. It has faster training time compared to neural network models. It is a distribution-free or non-parametric model, independent of probability dissemination assumptions and can resolve high dimensional data with better accuracy. It yields optimal results if deployed with SMOTE.

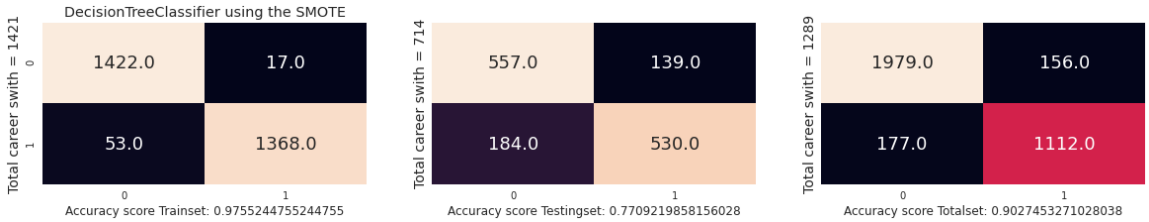


Figure 4.5: Decision Tree using SMOTE

### K-nearest Neighbors (KNN) Classification Model

This model is computationally expensive despite its comprehensibility and adaptability. It is often deployed for classification than regression, modest, and one of the best machine learning models. It requires variable normalization to prevent bias from high range variables and results if 0 and 1 are the ranges used for the same scale data. This model need dimensionality reduction for better performance, therefore it is unfitting for the large dimensional data. Its performance can also be improved by controlling missing data. It yields optimal results if deployed with ADASYN as shown in Figure 4.6.

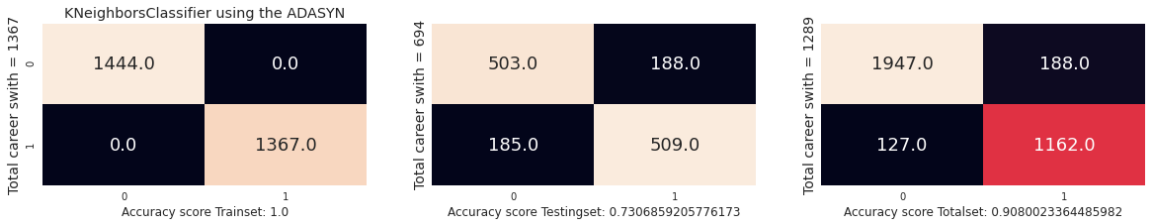


Figure 4.6: KNN using ADASYN

### Light Gradient Boosted Machine Model

This gradient boosting Model framework deploys tree based learning algorithms with a quicker training speed and higher efficiency. It utilizes lower memory, parallelism, GPU learning with better accuracy at handling large-scale data as demonstrated in Figure 4.7. Since it is a leaf-wise algorithm decreases extra loss compared to the level-wise algorithm, its accuracy is higher compared to other boosted models if deployed with SMOTE.

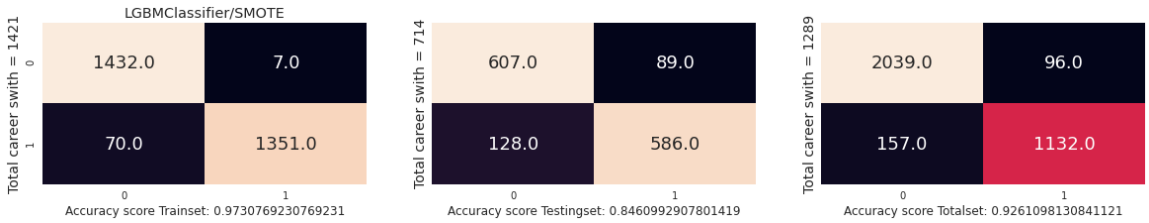


Figure 4.7: LGBM using SMOTE-SVM

### Random Forest Model

This Model ensembles learning by merging dissimilar types of algorithms or similar algorithms multiple times to form a more powerful prediction model usable for both regression and classification tasks as shown in Figure 4.8. It is very stable, effective with a mixture of categorical and numerical features, efficient with missing or poorly scaled data. It is computationally expensive due to the massive combination of decision trees and expensive to train compared to other models.

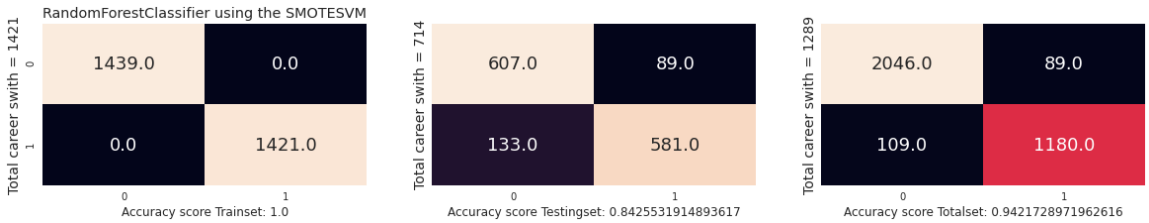


Figure 4.8: Random Forest using BSMOTE

### Extra Trees Classification Model

This ensemble machine learning model works by generating numerous unpruned decision trees from the training dataset to enhance prediction. It is handy at prediction of the decision trees in the case of regression or using majority voting in the case of classification as shown in Figure 4.9.

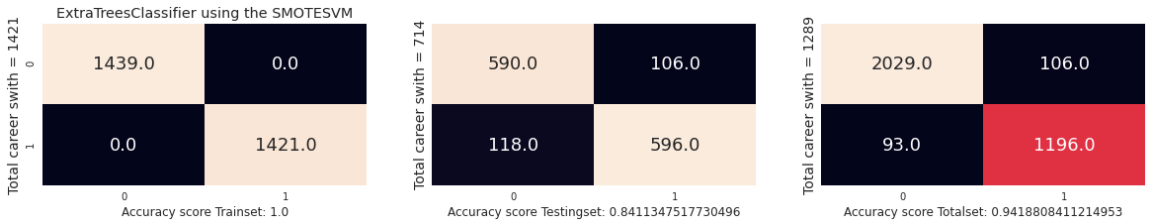


Figure 4.9: Extra trees using SMOTE-SVM

## 4.1.2 Summary of the Machine Learning Classical Results

The summary of the performance of all the used ML algorithms in this work to achieve Objective "a" are illustrated in Table 4.1.

### Receiver Operating Characteristic curve of the best Model.

We then plotted the ROC curve in Figure 4.10 of the best Machine Learning Classifier that predicted therapeutic adherence in comparison to to other algorithms.

| Model & Optimal Sampling Technique | Training dataset | Testing Dataset | Overall | ROC curve (AUC) |
|---|---|---|---|---|
| Random Forest Model with SMOTE-SVM | 100 | 85.0 | 94.4 | 0.941 |
| KNN Classification Model with ADASYN | 100 | 73.05 | 90.7 | 0.905 |
| Logistic Regression Model with SMOTE-SVM | 78.0 | 79.5 | 79.7 | 0.788 |
| Gaussian Naïve Bayes Model with SMOTE-SVM | 75.7 | 75.9 | 76.7 | 0.778 |
| Decision Tree Model with SMOTE | 97.5 | 76.7 | 90.1 | 0.894 |
| Extra Trees Classifier with SMOTE-SVM | 100 | 85.0 | 94.5 | 0.943 |
| Gradient Boosted Model with SMOTE-SVM | 92.2 | 83.0 | 87.7 | 0.868 |
| Extreme Gradient Boosted Model with SMOTE-SVM | 85.3 | 84.0 | 84.0 | 0.825 |
| Light Gradient Boosted Machine Model with SMOTE-SVM | 97.4 | 86.5 | 92.8 | 0.919 |

Table 4.1: Therapeutic Adherence Table of Results

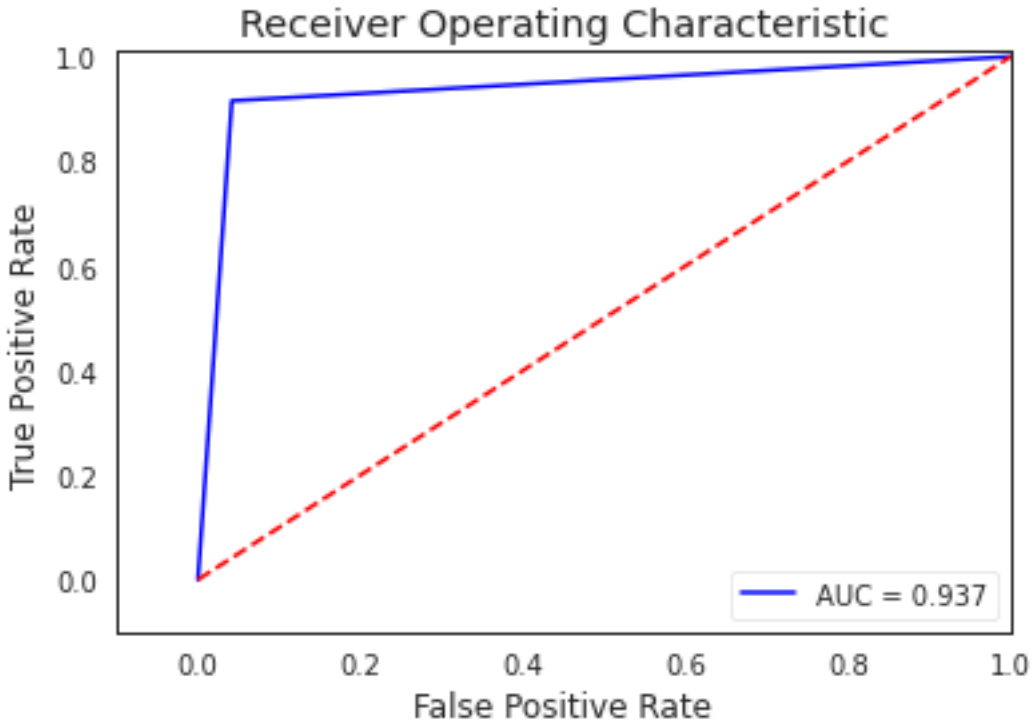


Figure 4.10: Extra Tree Classification Model ROC curve

**Feature Permutation Importance**

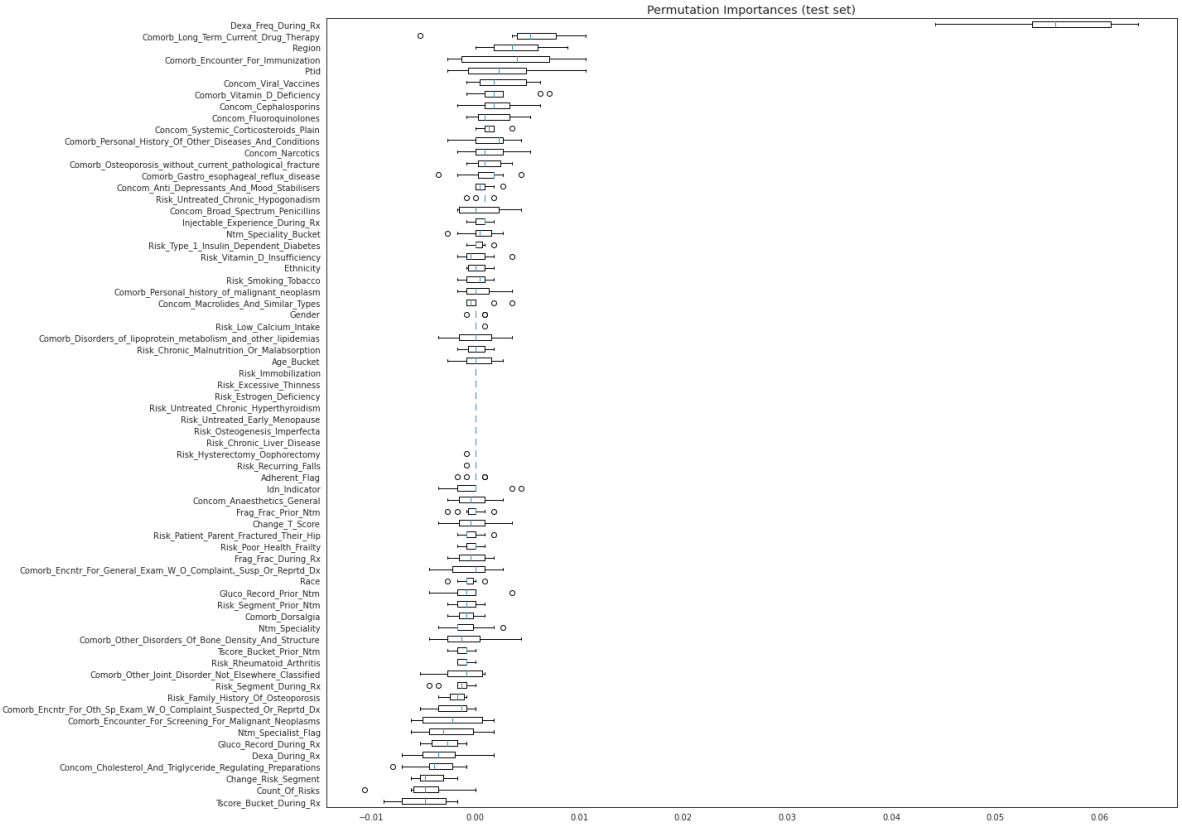


Figure 4.11: Feature Permutation Importance in the test set

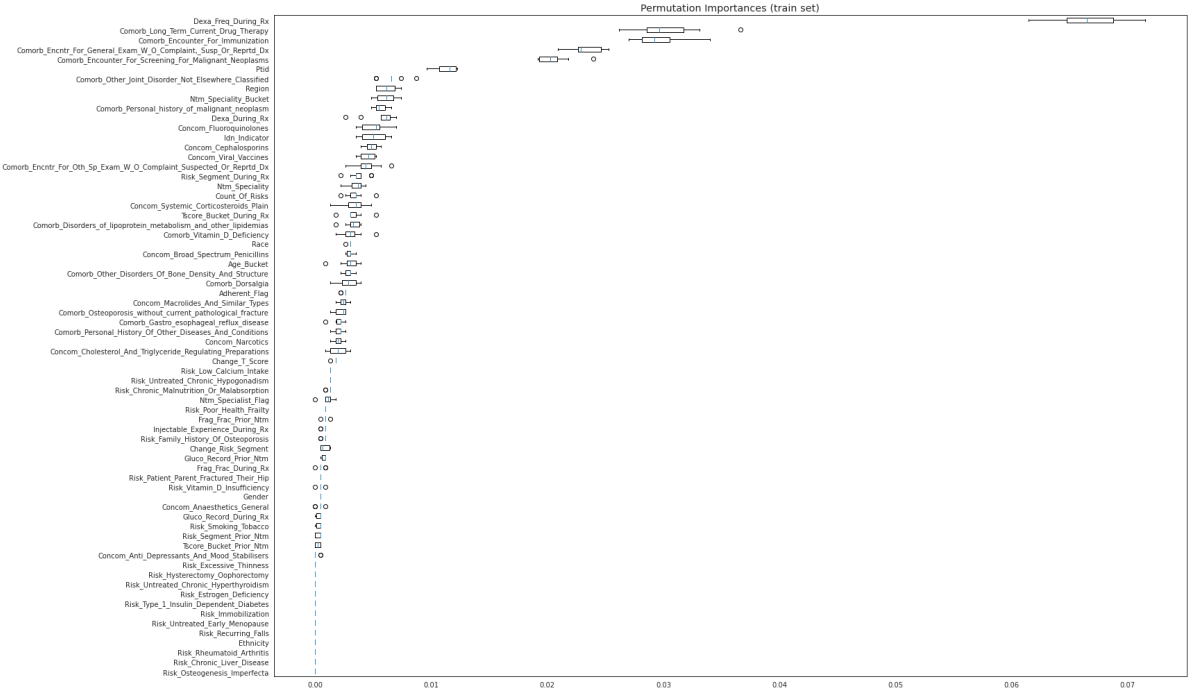


Figure 4.12: Feature Permutation Importance in the train set

## 4.2 XAI-4-Fetal-Health-Evaluation | LcMCH: I

Since we had randomly split our CTG dataset of 2126 instances in a ratio of Training: Testing, we obtained 3:1, thus 1594.5 Training and 531.5 Testing sample instances in the respective sets. We evaluated each algorithm based on various performance expressions on the 3 signal classes as illustrated in Table 4.2.

### 4.2.1 Biomedical Signal Class Interpretation and Evaluation

#### Gradient Boosting Classifier

Often used as a supervised signal detection tool, this signal classifier is effective for feature extraction based on classification generalization of boosting to arbitrary differentiable loss functions and effective for both classification and regression instances.

| y=1.0 (probability 0.002, score -3.700) top features | | | y=2.0 (probability 0.004, score -2.758) top features | | | y=3.0 (probability 0.994, score 2.693) top features | | |
|---|---|---|---|---|---|---|---|---|
| Contribution? | Feature | Value | Contribution? | Feature | Value | Contribution? | Feature | Value |
| 0.057 | prolongued_decelerations | -0.49 | 0.095 | percentage_of_time_with_abnormal_long_term_variability | 2.147 | 1.687 | uterine_contractions | -1.145 |
| 0.007 | histogram_mean | 0.142 | 0.082 | mean_value_of_short_term_variability | -1.118 | 1.279 | abnormal_short_term_variability | 1.353 |
| 0.001 | histogram_variance | -0.694 | 0.025 | histogram_mean | 0.142 | 0.443 | accelerations | -0.501 |
| -0.022 | histogram_number_of_peaks | -0.587 | 0.021 | uterine_contractions | -1.145 | 0.437 | mean_value_of_long_term_variability | -0.491 |
| -0.023 | mean_value_of_long_term_variability | -0.491 | 0.016 | histogram_min | 1.019 | 0.133 | fetal_movement | -0.217 |
| -0.027 | fetal_movement | -0.217 | 0.006 | mean_value_of_long_term_variability | -0.491 | 0.063 | light_decelerations | -0.577 |
| -0.029 | histogram_min | 1.019 | 0.001 | light_decelerations | -0.577 | 0.052 | histogram_max | -1.035 |
| -0.045 | light_decelerations | -0.577 | -0.01 | histogram_median | -0.018 | 0.043 | histogram_median | -0.018 |
| -0.046 | histogram_median | -0.018 | -0.013 | baseline value | -0.179 | 0.011 | histogram_number_of_peaks | -0.587 |
| -0.048 | histogram_number_of_zeroes | -0.376 | -0.043 | histogram_max | -1.035 | 0 | histogram_tendency | -0.481 |
| -0.049 | percentage_of_time_with_abnormal_long_term_variability | 2.147 | -0.057 | histogram_width | -1.277 | -0.002 | histogram_mode | -0.093 |
| -0.057 | histogram_mode | -0.093 | -0.113 | fetal_movement | -0.217 | -0.016 | histogram_variance | -0.694 |
| -0.141 | histogram_max | -1.035 | -0.191 | histogram_number_of_zeroes | -0.376 | -0.038 | histogram_mean | 0.142 |
| -0.152 | histogram_width | -1.277 | -0.291 | histogram_mode | -0.093 | -0.044 | baseline value | -0.179 |
| -0.177 | accelerations | -0.501 | -0.387 | histogram_number_of_peaks | -0.587 | -0.1 | prolongued_decelerations | -0.49 |
| -0.222 | mean_value_of_short_term_variability | -1.118 | -0.804 | abnormal_short_term_variability | 1.353 | -0.146 | percentage_of_time_with_abnormal_long_term_variability | 2.147 |
| -0.424 | baseline value | -0.179 | -1.093 | <BIAS> | 1 | -1.11 | <BIAS> | 1 |
| -0.476 | abnormal_short_term_variability | 1.353 | | | | | | |
| -0.733 | uterine_contractions | -1.145 | | | | | | |
| -1.093 | <BIAS> | 1 | | | | | | |

Figure 4.13: GBC Model Explainability

#### CatBoost Classifier

Yandex introduced Categorical Boosting in 2018 for efficient classification of categorical data of various data types with short learning time [7]. It calculates the leaf values during tree structure selection using ordered boosting and processes extracted categorical signal features during training.

#### LGBM Classifier

By using decision tree learning algorithms, this gradient boosting framework handles high dimensional CTG extracted signal features in large amounts with a distributed and faster training efficiency [7]. It uses a leaf-wise algorithm to grow trees vertically and exclusive feature bundling algorithm to handle sparsity in the signal dataset.

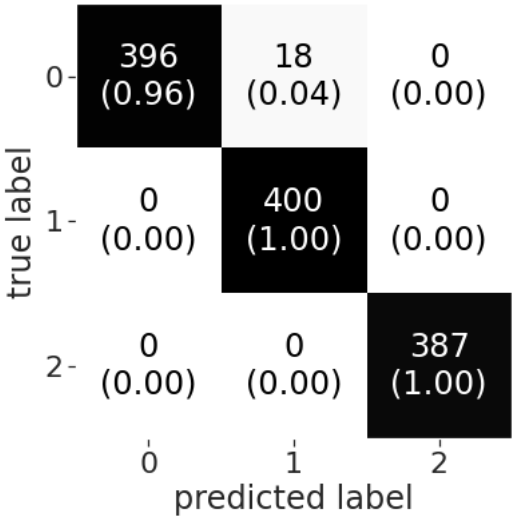


Figure 4.14: Fetal Health classical results using CAT

This ensemble classifier combines mutually exclusive extracted signal features in a lower lossless way to reduce the number of features while reserving the most informative ones.

| y=1.0 (probability 0.000, score -5.999) top features | | | y=2.0 (probability 0.000, score -5.264) top features | | | y=3.0 (probability 0.999, score 2.539) top features | | |
|---|---|---|---|---|---|---|---|---|
| Contribution? | Feature | Value | Contribution? | Feature | Value | Contribution? | Feature | Value |
| 0.219 | histogram_mean | 0.142 | 1.863 | percentage_of_time_with_abnormal_long_term_variability | 2.147 | 6.841 | abnormal_short_term_variability | 1.353 |
| 0.125 | prolongued_decelerations | -0.49 | 0.211 | accelerations | -0.501 | 0.285 | fetal_movement | -0.217 |
| 0.032 | histogram_min | 1.019 | 0.113 | light_decelerations | -0.577 | 0.236 | baseline value | -0.179 |
| 0.024 | histogram_mode | -0.093 | 0.073 | mean_value_of_long_term_variability | -0.491 | 0.235 | uterine_contractions | -1.145 |
| 0.003 | histogram_number_of_peaks | -0.587 | 0.073 | histogram_mean | 0.142 | 0.101 | accelerations | -0.501 |
| 0 | histogram_variance | -0.694 | 0.067 | mean_value_of_short_term_variability | -1.118 | 0.061 | histogram_width | -1.277 |
| -0.003 | baseline value | -0.179 | 0.055 | baseline value | -0.179 | 0.005 | light_decelerations | -0.577 |
| -0.012 | histogram_max | -1.035 | 0.054 | uterine_contractions | -1.145 | 0.001 | mean_value_of_short_term_variability | -1.118 |
| -0.013 | histogram_tendency | -0.481 | 0.033 | histogram_median | -0.018 | -0.064 | prolongued_decelerations | -0.49 |
| -0.018 | histogram_width | -1.277 | 0.017 | histogram_min | 1.019 | -0.125 | histogram_tendency | -0.481 |
| -0.037 | light_decelerations | -0.577 | 0.015 | histogram_number_of_peaks | -0.587 | -0.255 | histogram_median | -0.018 |
| -0.04 | mean_value_of_long_term_variability | -0.491 | 0.013 | histogram_variance | -0.694 | -0.671 | histogram_mean | 0.142 |
| -0.17 | percentage_of_time_with_abnormal_long_term_variability | 2.147 | -0.004 | fetal_movement | -0.217 | -1.373 | percentage_of_time_with_abnormal_long_term_variability | 2.147 |
| -0.221 | fetal_movement | -0.217 | -0.006 | histogram_width | -1.277 | -2.739 | <BIAS> | 1 |
| -0.521 | uterine_contractions | -1.145 | -0.021 | histogram_max | -1.035 | | | |
| -0.684 | mean_value_of_short_term_variability | -1.118 | -0.097 | histogram_mode | -0.093 | | | |
| -1.058 | abnormal_short_term_variability | 1.353 | -2.512 | <BIAS> | 1 | | | |
| -1.502 | accelerations | -0.501 | -5.213 | abnormal_short_term_variability | 1.353 | | | |
| -2.122 | <BIAS> | 1 | | | | | | |

Figure 4.15: LGBM Model Explainability

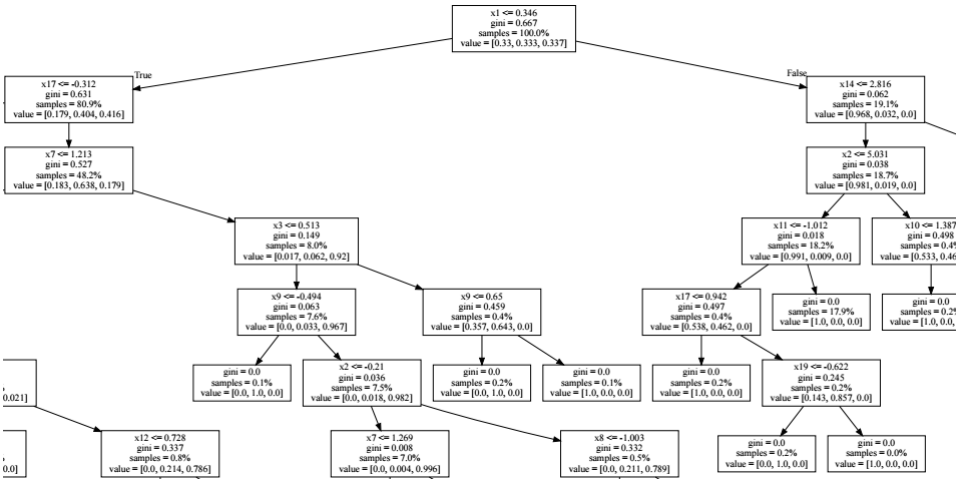


Figure 4.16: Fetal Health classical results using CAT (Partial)

**Voting Ensemble Classifier (VEC)**

It is an ensemble classifier of numerous models that aggregates the results of all models into a voting classifier to predict the output class depending on the highest majority of voting. By soft voting, the 3 ensemble models output a prediction based on their average probability for an optimal voting classifier which was made of CAT, LGBM, and DT.

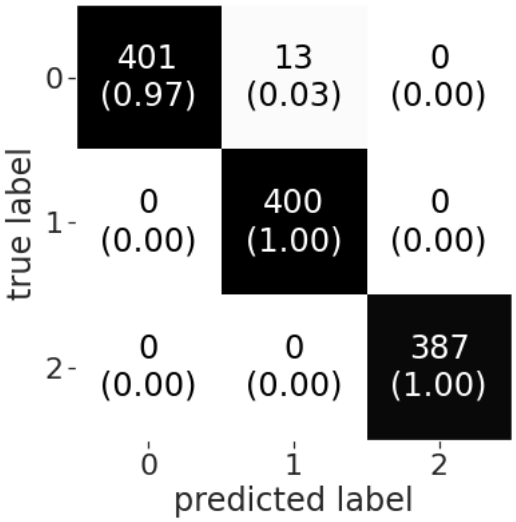


Figure 4.17: Fetal Health classical results using VEC

### 4.2.2 Summary of the Biomedical Signal Classification Results

Feature Importance provided insights into the signal dataset, and influenced the predictive modeling of the classifier since it gave us a basis for dimensionality reduction and feature extraction to help us improve the efficiency and effectiveness of our signal classifiers.

**Feature Importance**

We obtained feature importance for all classifiers.

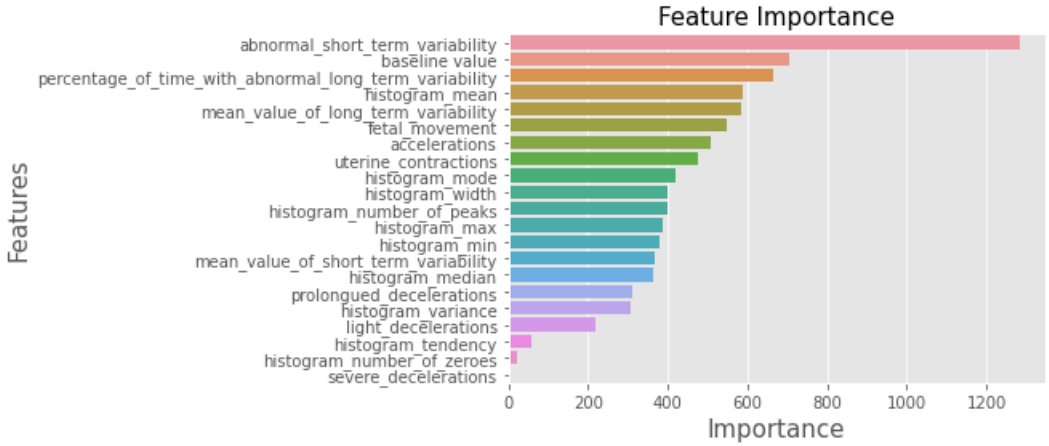


Figure 4.18: CTGs Signal Feature Importance

**Table of Results.**
Since we had randomly split our CTG dataset of 2126 instances in a ratio of Training: Testing, we obtained 3:1, Thus 1594.5 Training and 531.5 Testing sample instances in the respective sets. We evaluated each algorithm based on various performance expressions on the 3 signal classes as illustrated in Table 4.2.

| **Metric** | **Fetal Signal Classes** | **Gradient Boosting Classifier** | **CategoricaBoosting Classifier** | **Light Gradient Boosting Model** | **Decision Tree** | **Voting Ensemble Classifier** |
|---|---|---|---|---|---|---|
| **Accuracy** | | 0.981 | 0.990 | 0.990 | 0.984 | 0.989 |
| **AUC** | | 0.986 | 0.99 | 0.993 | 0.988 | 0.992 |
| **Macro Average** | | 0.98 | 0.99 | 0.99 | 0.98 | 0.99 |
| **Weighted Average** | | 0.98 | 0.99 | 0.99 | 0.98 | 0.99 |
| **Precision** | **Normal** | 1 | 1 | 1 | 1 | 1 |
| | **Suspect** | 0.95 | 0.96 | 0.97 | 0.95 | 0.97 |
| | **Pathological** | 1 | 1 | 1 | 1 | 1 |
| **Recall** | **Normal** | 0.95 | 0.96 | 0.97 | 0.95 | 0.97 |
| | **Suspect** | 1 | 1 | 1 | 1 | 1 |
| | **Pathological** | 0.97 | 1 | 1 | 1 | 1 |
| **F1-Score** | **Normal** | 0.97 | 0.98 | 0.99 | 0.98 | 0.98 |
| | **Suspect** | 0.97 | 0.99 | 0.99 | 0.98 | 0.98 |
| | **Pathological** | 1 | 0.99 | 1 | 1 | 1 |

Table 4.2: CTG classification Table of Results

## 4.3 XAI-4-NICU-Admissions | LcMCH: II

**Random Forest (RF) Feature Selection** Since accuracy is not the appropriate metric for assessing suitability of Machine Learning models for NICU predictions, Random Forest was dropped but a detailed study of accuracy can greatly contribute to understanding and bench-marking features for optimizing the selected ML model i.e. Logistic Regression.

### 4.3.1 Feature Importance

Studying the feature importance and interaction of how RF attains a higher accuracy in an interpretable manner (white box) can help us tune the Logistic Regression model based on the insights obtained by explaining the Random Forest accurate predictions as illustrated in 4.19.

| Feature | Importance | |
|---|---|---|
| 13 | Weight_Baby_Kg | 0.198178 |
| 18 | Hours_In_Labour | 0.113159 |
| 5 | Hemoglobin | 0.096827 |
| 3 | Height(cm) | 0.078727 |
| 11 | PreTerm | 0.073246 |
| 0 | Age_Of_Mother | 0.060493 |
| 1 | weight_before_preg | 0.057315 |
| 12 | FullTerm | 0.056798 |
| 4 | BMI | 0.047556 |
| 15 | Jaundice | 0.047427 |

Figure 4.19: Feature weights of RF feature importance

We began by assessing the feature importance to NICU admission prediction in the perspective of RF for easy understanding during interpretation. Figure 4.19 and Figure 4.20 justifies that the Weight of the baby, Hemoglobin and PreTerm birth risk history are the most influential factors of NICU admission.

### 4.3.2 Interpretable and Explainable Feature Learning.

#### SHapley Additive exPlanations (SHAP)

SHAP values show the impact of each feature whose comparative possession yields interpretation of predictions based on baseline values. The SHAP summary plot in Figure 4.21 provides comprehensive information about the impact of the features by merging feature importance with its effects. The color of the dots denotes the value of the feature (Blue: low value, red: Higher value). Features are well-organized depending on their importance during the interaction.

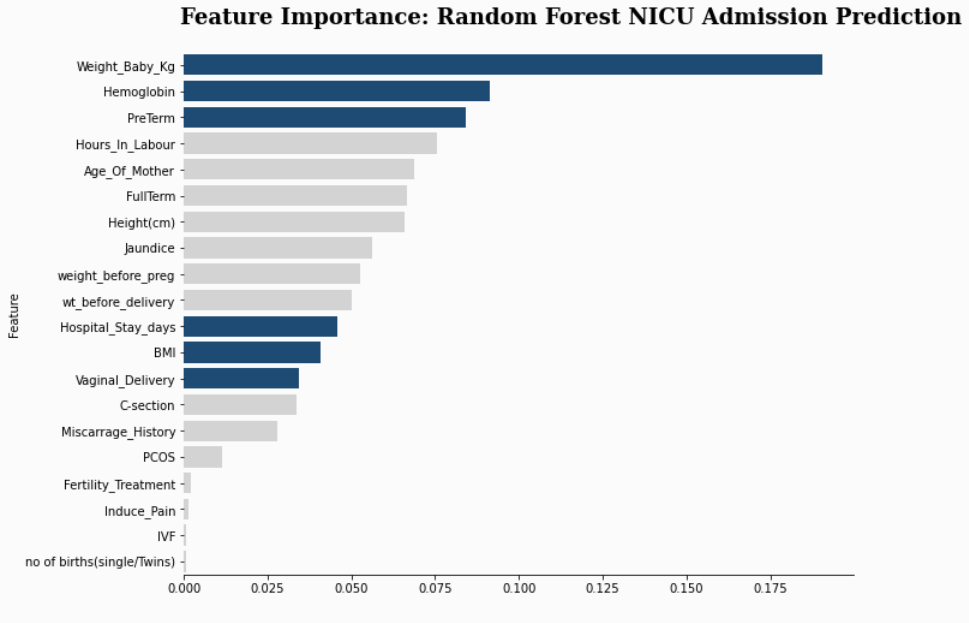


Figure 4.20: Random Forest NICU optimal feature importance

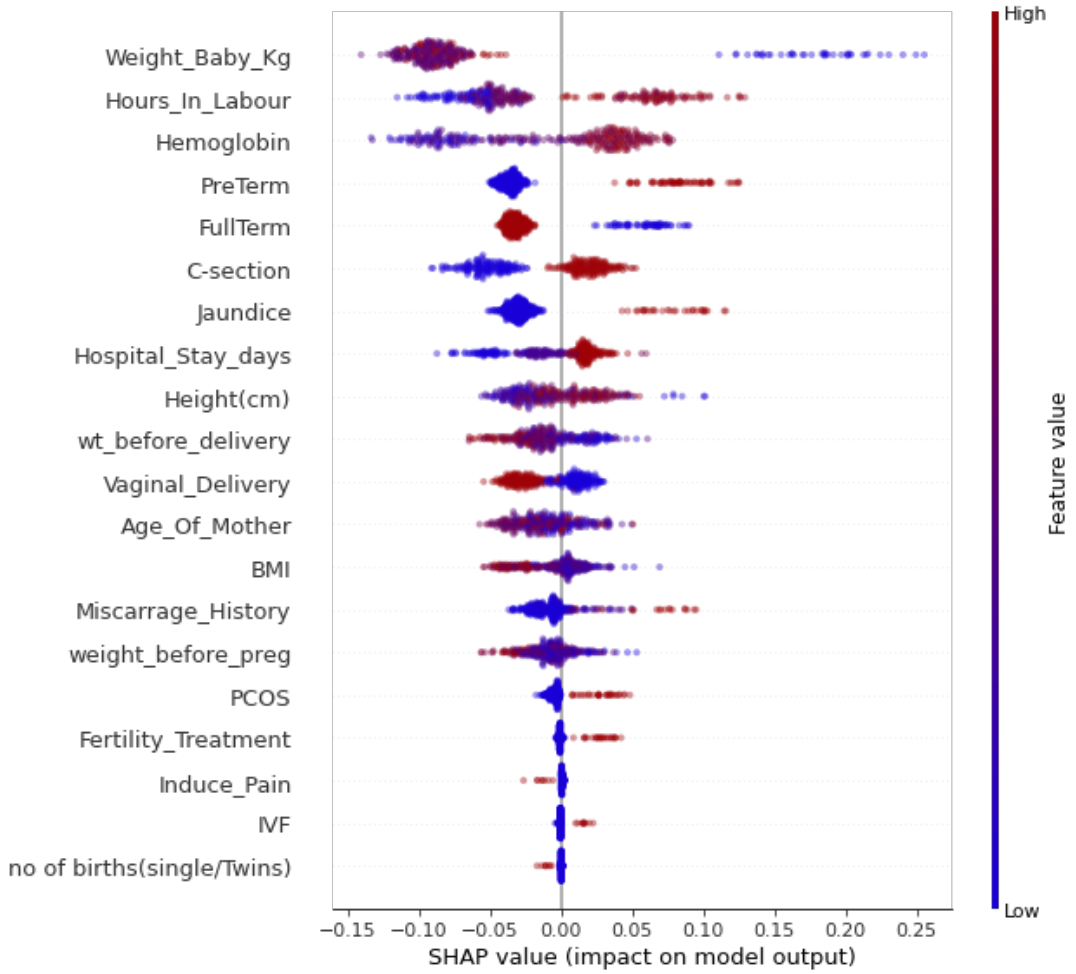


Figure 4.21: SHAP explanation for effects of data points (features) on NICU admission using RF

### Local Interpretable Model-agnostic Explanations (LIME)

By focusing on one example at a time, we used LIME to explain feature interaction in the LR model. Figure 4.22 demonstrates that the positivity changes of NICU admission are mainly influenced by Weight of the Baby, Number of Hospital Stay days and Preterm Birth History.

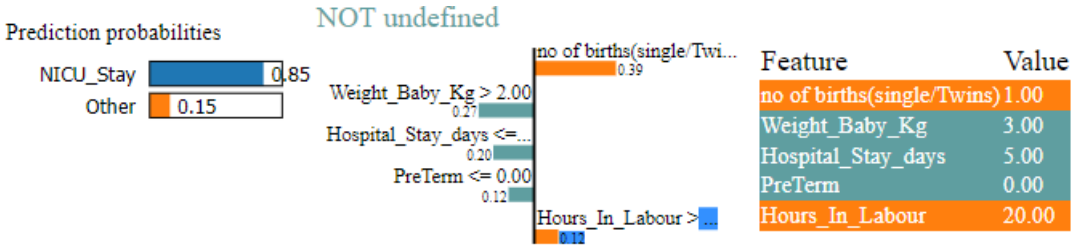


Figure 4.22: LIME unpacked explanation for LR NICU admission prediction

### Explain like I am 5 (ELI5)

ELI5 offers interpretability by displaying the coefficient for each variable, hence displaying what the LR ML model puts most value in. Figure 4.23 illustrates Hours in Labor, Number of Hospital Stay days and PreTerm birth history as the most influential factors that contribute to NICU admission.

| Weight[?] | Feature |
|---|---|
| +0.577 | Hours_In_Labour |
| +0.555 | Hospital_Stay_days |
| +0.334 | PreTerm |
| +0.292 | Jaundice |
| +0.243 | Height(cm) |
| +0.188 | IVF |
| +0.162 | PCOS |
| +0.142 | Miscarrage_History |
| +0.061 | <BIAS> |
| +0.041 | C-section |
| | *... 1 more positive ...* |
| -0.019 | Hemoglobin |
| -0.021 | Fertility_Treatment |
| -0.024 | Age_Of_Mother |
| -0.041 | Vaginal_Delivery |
| -0.082 | no of births(single/Twins) |
| -0.195 | Induce_Pain |
| -0.237 | wt_before_delivery |
| -0.263 | BMI |
| -0.334 | FullTerm |
| -0.560 | Weight_Baby_Kg |

Figure 4.23: ELI5 feature coefficient explanation of LR NICU admission prediction

Generally, the number of hospital stay days, preterm birth history and baby weight are the major influencers on NICU admission. They need strict monitoring and attention for effective NICU resource management and health policy making.

## 4.4 XAI-4-StemCell-Transplantation | LcMCH: II

In this section, we illustrate the results using various python libraries like numpy, matplotlib, seaborn among others. We obtained the predictive results for CatBoost, LightGBM and XBoost Models. The results include Confusion Matrices to demonstrate the predictive results of each of the Models, SHAP Feature Importance to demonstrate the most important metrics that determine pediatric patient survival upon stem cell transplantation, SHAP Summary Plots, SHAP Dependency Plots, SHAP Decision Plots, SHAP Waterfall Plots and SHAP Force Plots.

**Results for Hematologic Pediatric Patient Survival Prediction**

With a split ratio of 7:3 of Training to Testing Data, we obtained an overall pediatric survival predictive accuracy of 82%, 92% and 94% for CatBoost, LightGBM and XGBoost respectively. The summary of results is presented in table 4.3 with individual confusion matrices to illustrate the classical results of each model in Figure 4.24, Figure 4.26 and Figure 4.25.

| Algorithm | Accuracy | Recall | Auc | Precision |
|---|---|---|---|---|
| **CatBoost** | 0.8246 | 0.76 | 0.8175 | 0.8261 |
| **LightGBM** | 0.9211 | 0.875 | 0.9148 | 0.9543 |
| **XGBoost** | 0.9474 | 0.92 | 0.9444 | 0.9583 |

Table 4.3: Table of Results for Survival Prediction

Individual Confusion Matrices of the AI Models

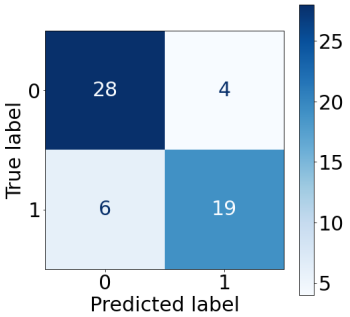


Figure 4.24: CatBoost Confusion Matrix

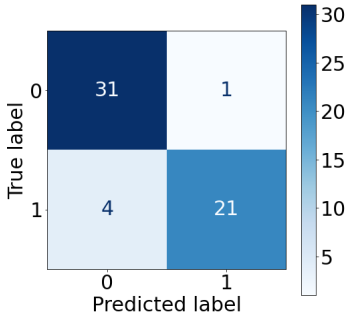


Figure 4.25: LightGBM Confusion Matrix

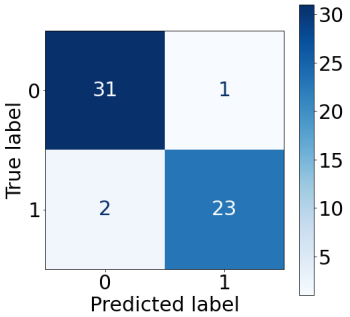


Figure 4.26: XGBoost Confusion Matrix

### 4.4.1 Feature Importance for Pediatric Patient Survival

Identification of the most important metrics that influence patient survival is extremely necessary for proactive stem transplantation interventions. It gives physicians an idea of the most influential factors that determine the success or failure of a transplantation medical procedure before the real bone marrow transplantation happens. This can greatly improve the survival rates of the children since were are

focused on predictive, preventive and personalized pediatric medicine to improve pediatric patient survival. In this subsection of our work, we illustrate the feature importance of the the three AI models.The Most Important Factors influencing Pediatric Patient survival upon stem cell transplantation are illustrated in Figure 4.27, Figure 4.28 and Figure 4.29.

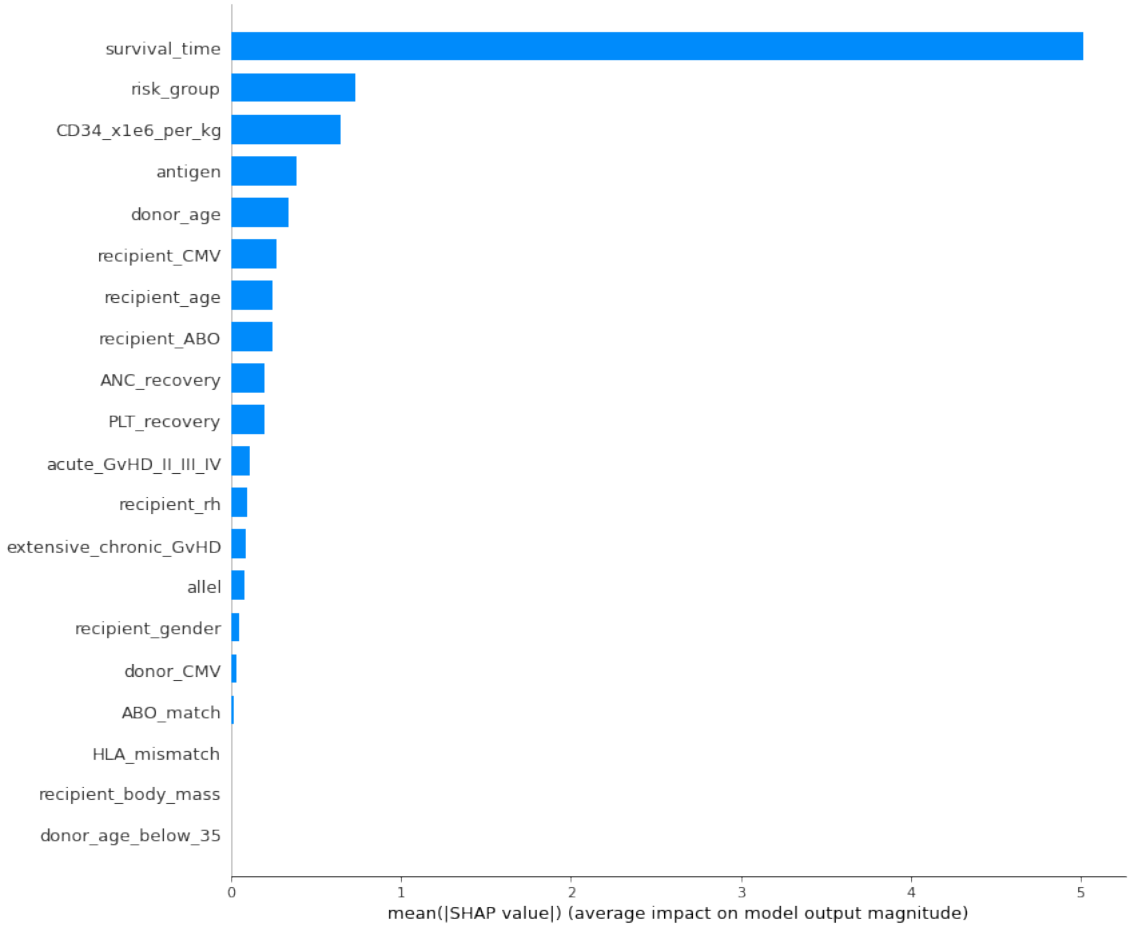


Figure 4.27: LightGBM Feature Importance

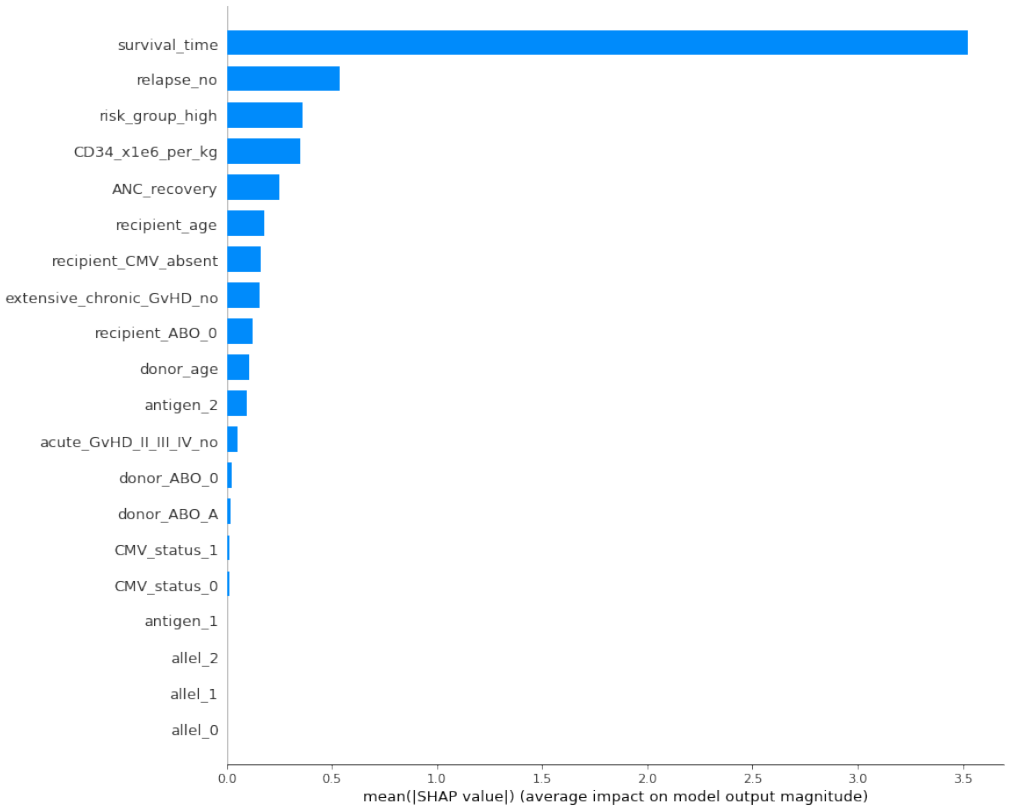


Figure 4.28: XBoost Feature Importance

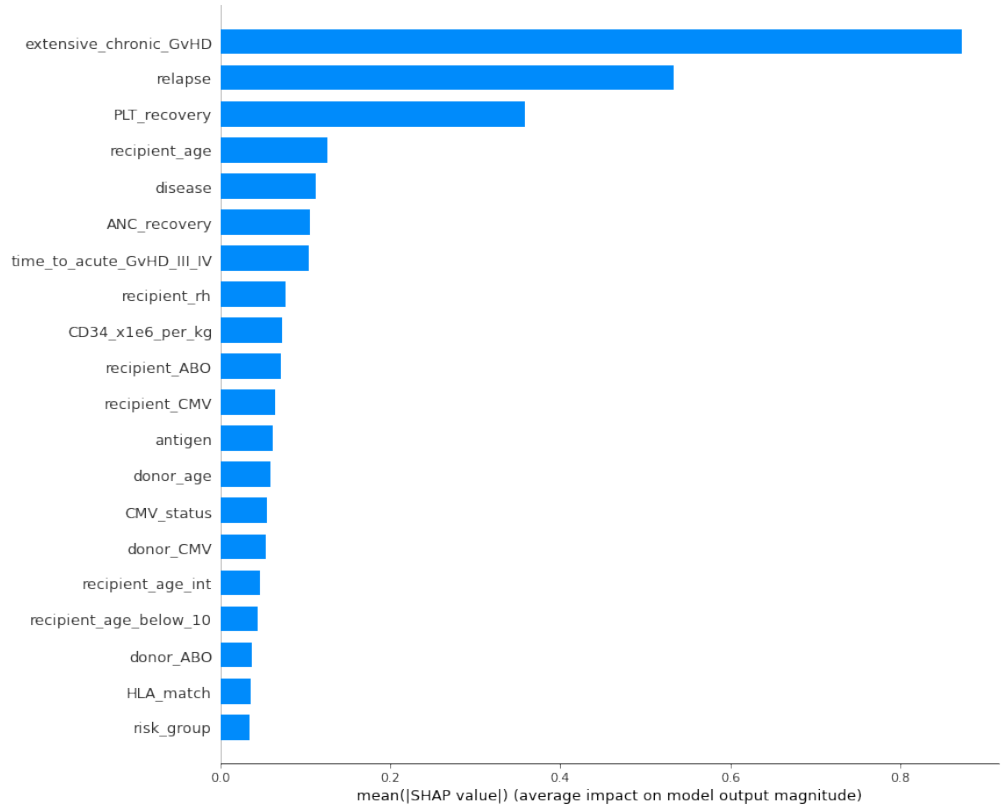


Figure 4.29: catboost Feature Importance

### 4.4.2 Feature Interaction for Pediatric Patient Survival

#### SHAP Summary Plots of Feature Interaction for Pediatric Patient Survival

The SHAP summary plot gives detailed information about the influence of the features (factors) by combining feature importance with its effects. The color of the dots represents the value of the feature (Blue: low value, red: Higher value). Features are ordered based on their importance during the interaction. We illustrated the summary plot of the three algorithms Thus; LightGBM in Figure 4.30, XBoost in Figure 4.31 and CatBoost in Figure 4.32.

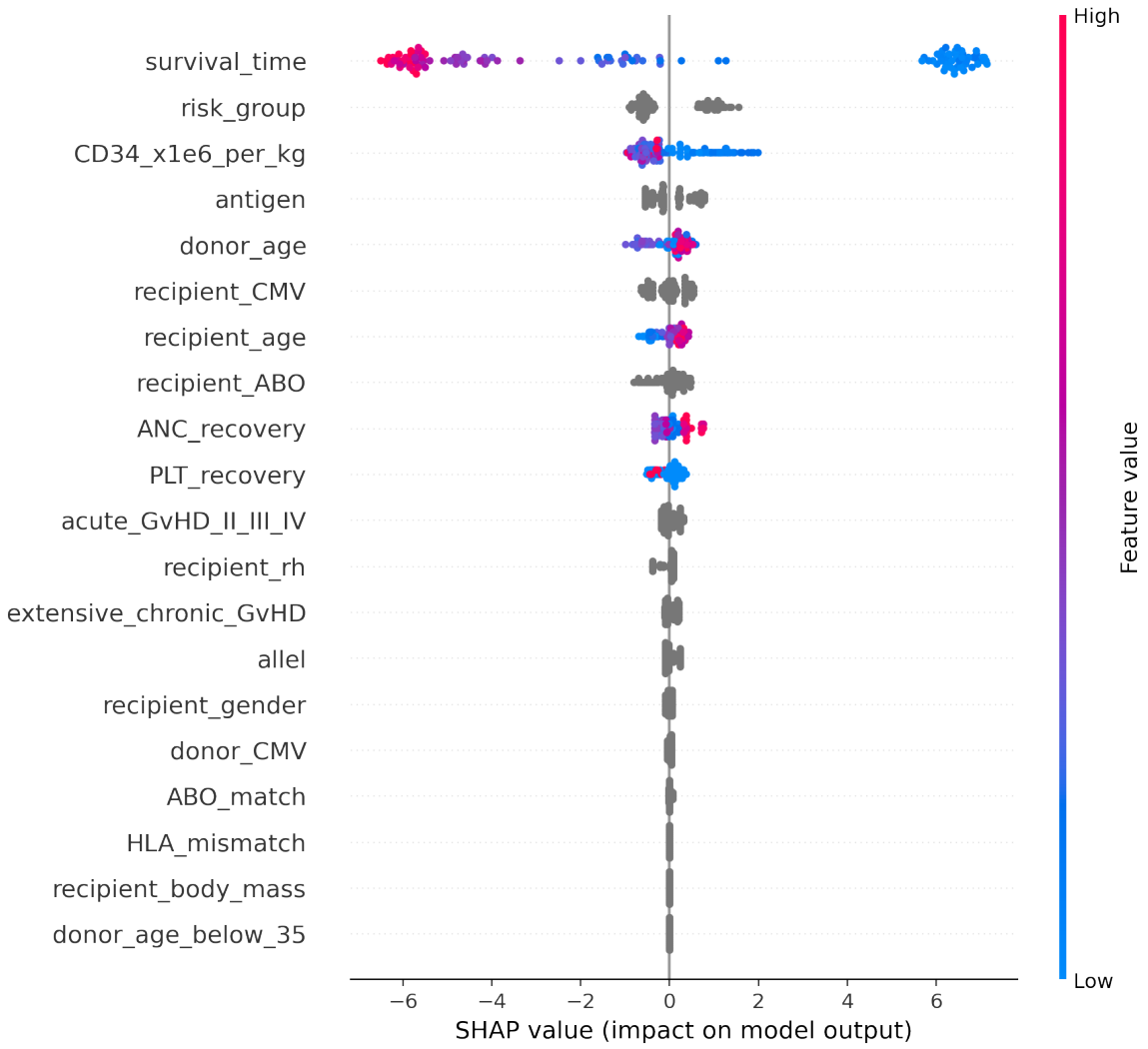


Figure 4.30: LightGBM Summary Plot

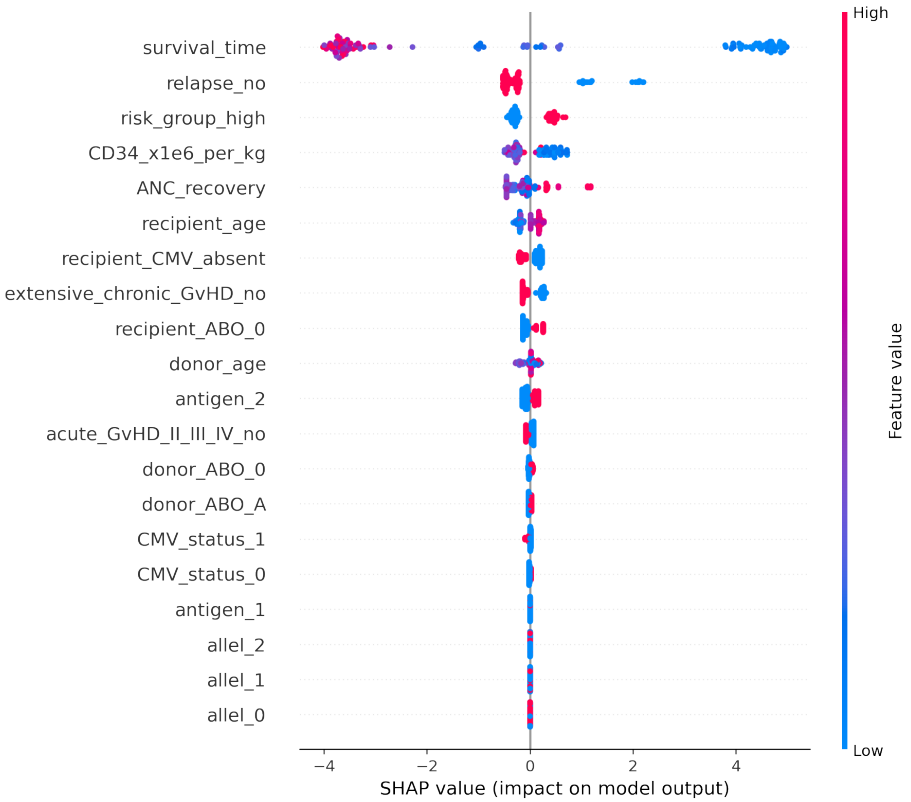


Figure 4.31: XGBoost Summary Plot

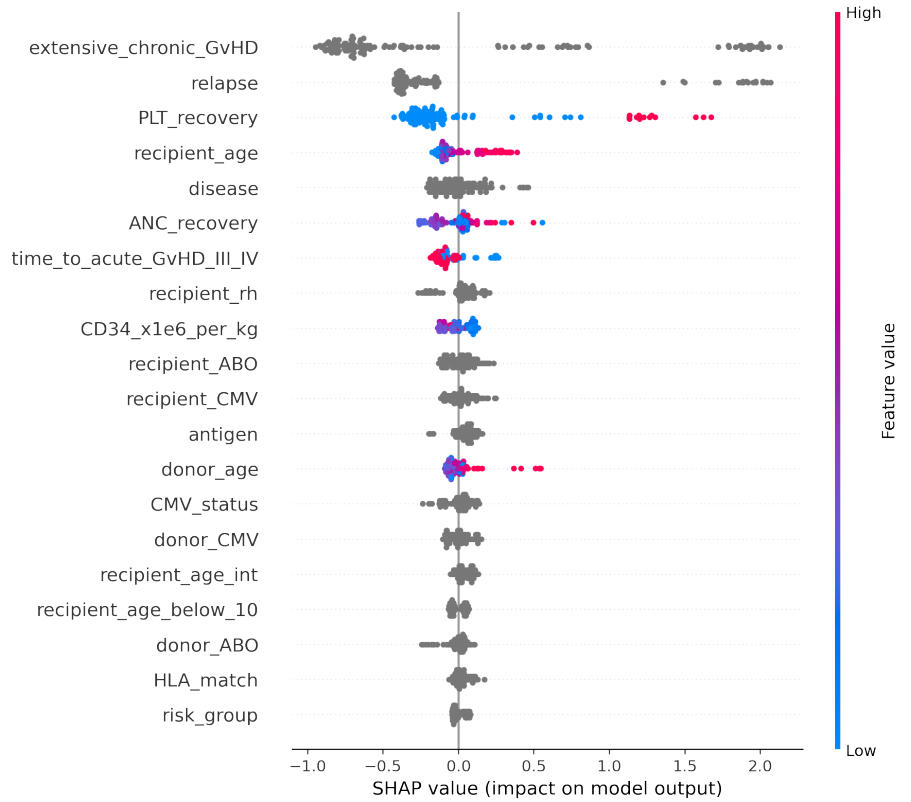


Figure 4.32: Catboost Summary Plot

### 4.4.3 SHAP Dependency and Decision Plots of AI Models during Pediatric Patient Survival Prediction.

From the simulations in Figure 4.30, Figure 4.31, Figure 4.28 and Figure 4.27, we can justify Kawłak's hypothesis that increasing the CD34+ cells /kg dosage generally prolongs survival time of patients. But we also observed that there are more influential factors that are important for patient survival for example the risk group and pediatric recipient's age. We therefore explainably explored the dependency of some of influential factors for pediatric patient survival as illustrated in Figure 4.33. We observe a strong positive dependency of CD34+ efficiency with increasing age of pediatric recipient's for survival.

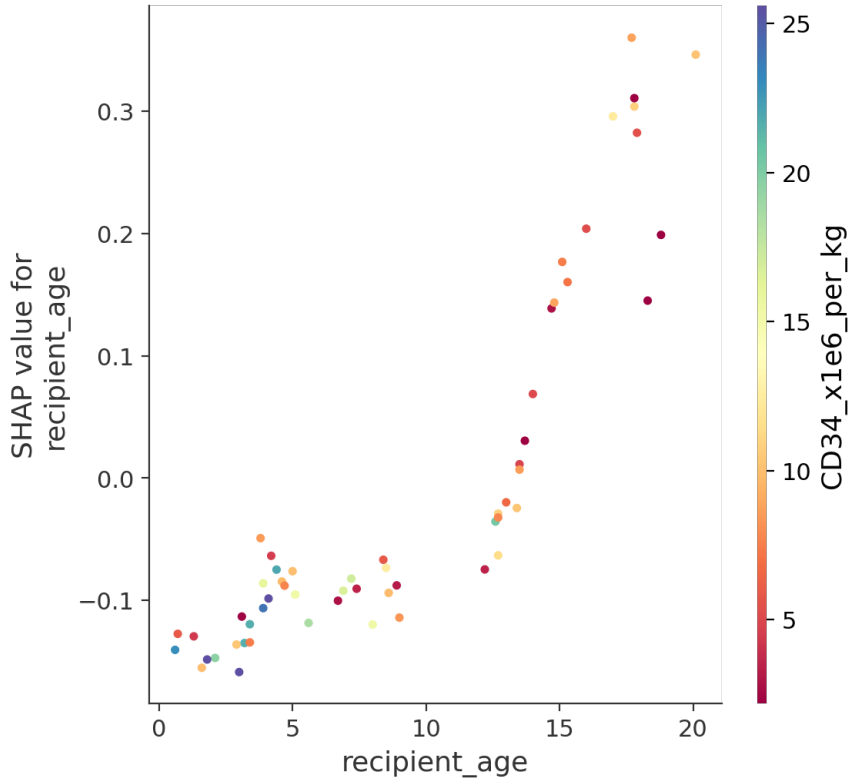


Figure 4.33: SHAP Dependency plot of CD3+ and Recepient's age for survival

We also demonstrate the decision plots of the first 15 pediatric patients in Figure 4.34 to show how the AI Models interacts with the hematologic Pediatric Patient feature to while predicting the survival of each patient before performing a stem cell transplantation procedure. We used the logit function to change log-odds numbers into probabilities or survival displayed at the top of the Decision Plot bar in Figure 4.34.

#### SHAP Force Plot of AI Model during Pediatric Patient Survival Prediction

From the plot in Figure 4.35, we observe the prediction probability value of 0.90. The base value of 0.4513 would be the predicted value if no feature of the current instance was known. That base value is the mean of the model output out of the training dataset. The feature value of this observation (instance) is given by the

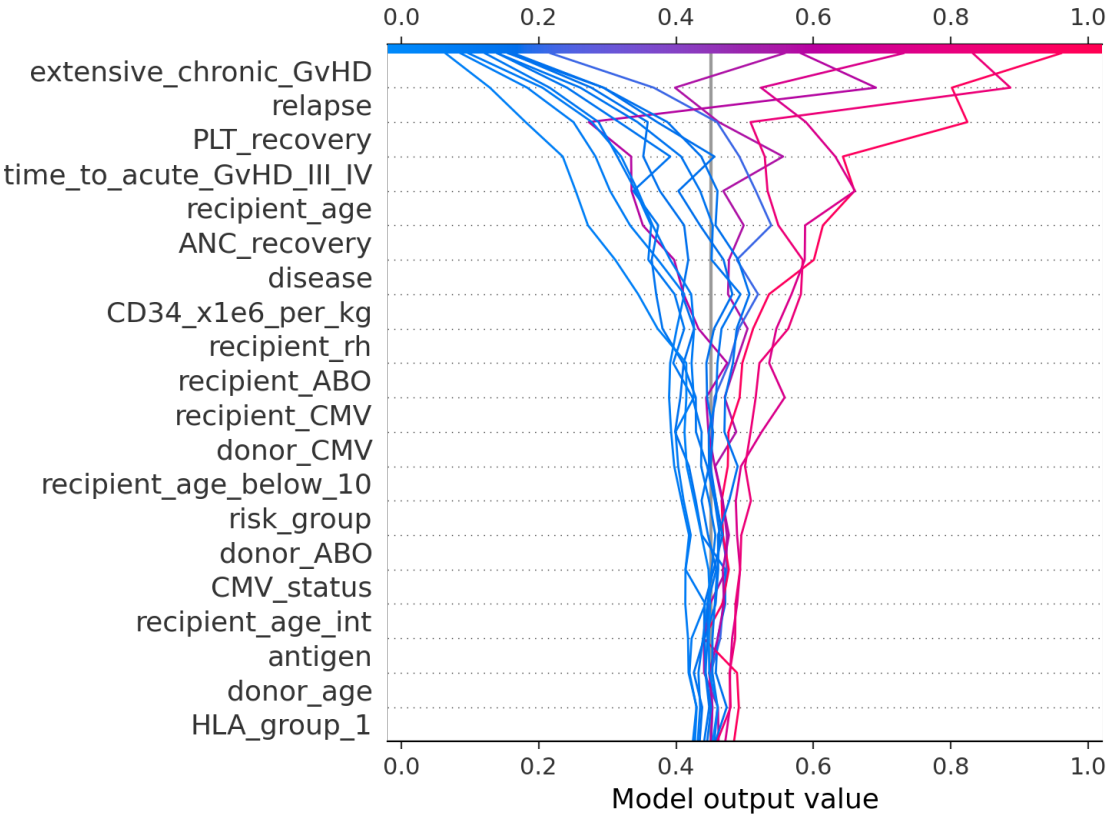


Figure 4.34: SHAP Decision plot of patient survival

Figure 4.35: CatBoost SHAP Focrceplot

numbers on the plot arrows. The features that pushed the model score higher are represented by the red color while blue represents the features that pushed the model score lower. The longer (bigger) the arrow, the larger the impact of the feature on the model output. The increase or decrease in impact is observed at the X-axis.

### 4.4.4 SHAP WaterPlot of AI Model during Pediatric Patient Survival Prediction

We display explanations for individual pediatric survival predictions using SHAP waterfall plots for a single row of objects as inputs. The base of a waterfall plot begins as the estimated value of the model output such that each row shows how the positive (red) or negative (blue) contribution of each feature moves the value from the expected model output over the hematologic pediatric dataset to the model output for pediatric survival prediction as illustrated in Figure 4.36, Figure 4.37 and Figure 4.38.

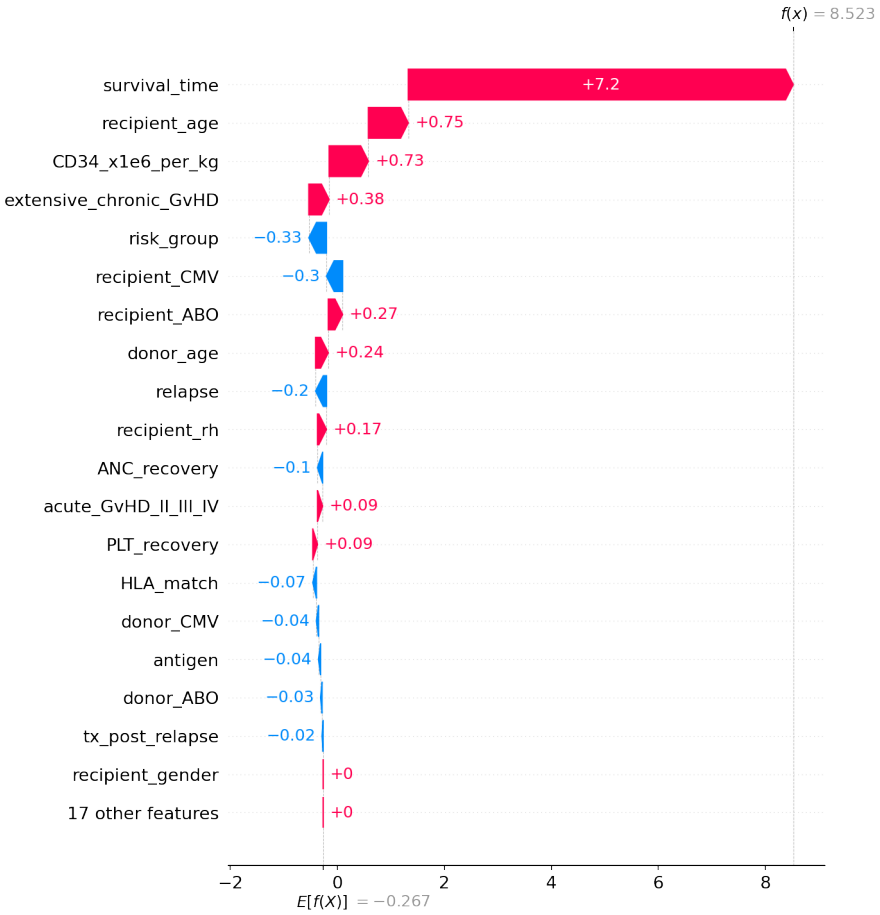


Figure 4.36: LightGBM SHAP Water Plot

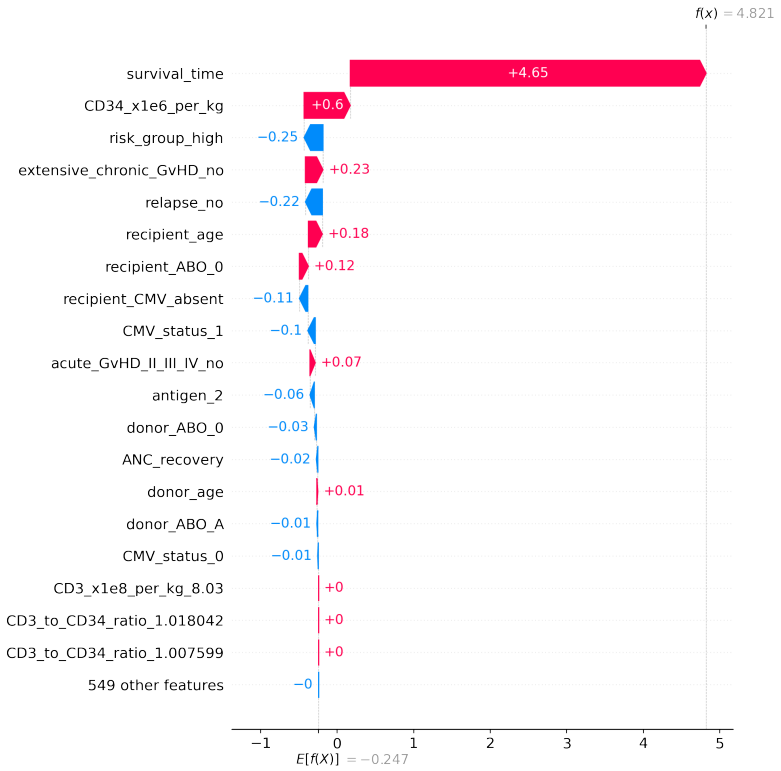


Figure 4.37: XGBM SHAP Water Plot

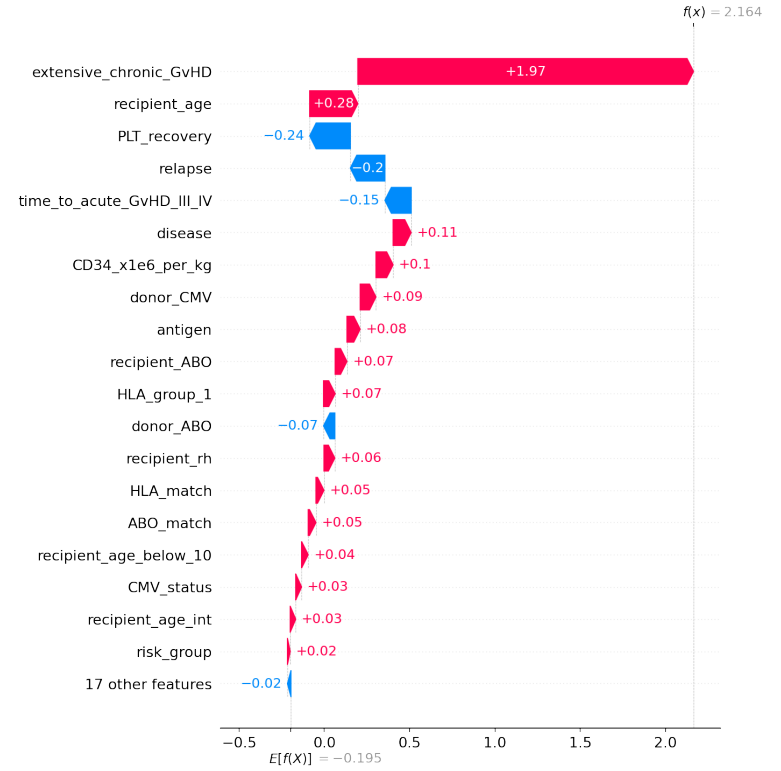


Figure 4.38: Cat SHAP Water Plot

## 4.5 XAI-4-Pulmonary-Health-Evaluation | LcMCH: III

### 4.5.1 Pulmonary Health Evaluation

We deployed pattern recognition and biomedical image processing to accurately classify the generated augmented images of pediatric chest X-ray images using a deep convolutional neural network which also acted as our base model for transfer learning into a specialized Inception network for validation and re-classification pattern recognized generated biomedical images in order to evaluate the health of the pediatric patient as illustrated in Figure 4.39.

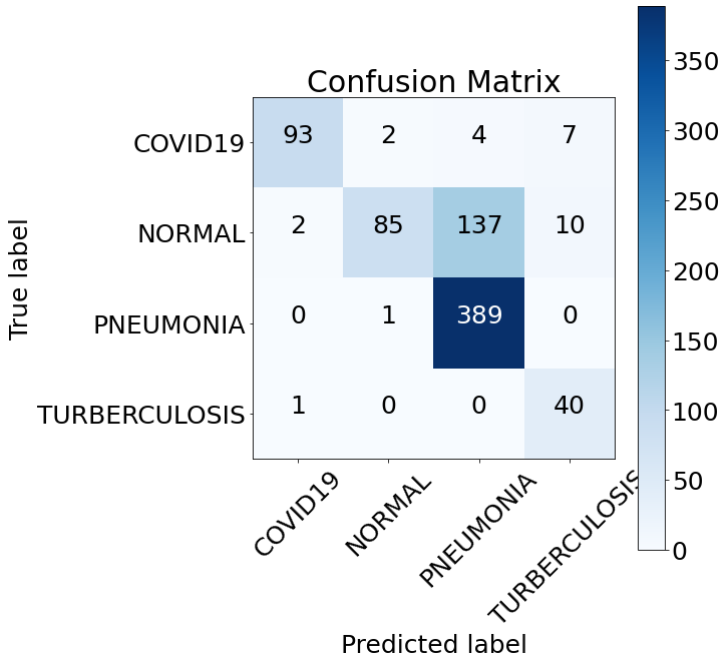


Figure 4.39: Confusion matrix after transfer learning

| Classification Report | | | | |
|---|---|---|---|---|
| | **precision** | **recall** | **f1-score** | **support** |
| **COVID19** | 0.97 | 0.88 | 0.92 | 106 |
| **NORMAL** | 0.97 | 0.36 | 0.53 | 234 |
| **PNEUMONIA** | 0.73 | 1.00 | 0.85 | 390 |
| **TURBERCULOSIS** | 0.70 | 0.98 | 0.82 | 41 |
| **accuracy** | | | 0.79 | 771 |
| **macro avg** | 0.84 | 0.80 | 0.78 | 771 |
| **weighted avg** | 0.83 | 0.79 | 0.76 | 771 |

Table 4.4: Pediatric pulmonary classification report of augmented chest X-ray images after transfer learning

We sampled the entire set up with 3 epochs first, then executed full with a maximum of 10 epochs for both networks. For both predictions, a total accuracy of 79% was attained as illustrated in Table 4.4.

### 4.5.2 Explainable AI with Layer-Wise Relevance Propagation (LRP).

We finally deployed Layer-Wise Relevance Propagation (LRP) as a transparent approach to explain the classification results by creating instance-level explanations for the neural networks. We used LRP to visualize the significance of individual pixels that contributed to the classification of each generated pediatric chest X-ray image during pulmonary health evaluation. With explainable AI for pediatric medicine, pediatricians can confidently diagnose and decide on the best treatment plans of the patient with comprehensible informed decisions. The safety and trustworthy of AI for pediatric medicine enables physicians to reliably recommend the better alternative treatment plan, further medical diagnosis or pediatric monitoring plans based on the interpreted pulmonary health evaluation metrics obtained. In our study, LRP exhibited the best and most interpretable explanation compared to other explainers like occlusion and smoothening gradient.
LRP is a machine learning explainable technique used to demystify black box neural networks and kernel machines [51]. It's applications have been demonstrated by number of authors including but not limited to [51][19][25][27][50][45] and [43] for decomposing nonlinear decision output functions in terms of their variable inputs to create vectors of feature inputs scores that make up their explanations.
LRP produces a decomposition;

$$R = (R_1, \ldots, R_d) \tag{4.1}$$

of that prediction on the input variables satisfying

$$\sum_{p=1}^{d} R_p = f(X) \tag{4.2}$$

where $X = (x_{1,\ldots,}x_d)$ is the input vector and $f(X)$ is prediction at the output of the neural network.
It is Important to note that LRP explains the output of the function rather than its local variation [41] unlike sensitivity analysis methods [5]. By uniformly applying backward propagation mechanisms on all neurons where;

$$a_j = p\left(\sum_i a_i w_{ij} + b_j\right) \tag{4.3}$$

Is the such neuron, $i$ and $j$ denotes the neuron indices at consecutive layers while $\Sigma i$, $\Sigma j$ denotes the summation over all neurons in these respective layers such that the propagation mechanism of LRP is defined as;

$$R_i = \sum_j \frac{Z_{ij}}{\sum_i Z_{ij}} R_j \tag{4.4}$$

where $Z_{ij}$is the contribution of neuron $i$ to the activation $a_j$, and normally depends on the activation $a_i$and the weight $W_{ij}$.
The backward propagation function is applied beginning from the neural network output $f(X)$ until the input features (pixels or variables) are reached. The output scores are then visualized as a heatmaps of the same dimensions as the input as illustrated in image 4.5. The explainability of LRP is justified when the propagation rules are illustrated as particular instances when embedded in the theoretical framework of deep Taylor decomposition [33]. LRP rules have also been designed for other machine learning models other than neural networks. These include LSTMs, Fisher Vector Models and Bag of words.
Figure 4.5 has six (6) rows. Row 1 illustrates raw Images of form the dataset labeled as Covid-19, Pneumonia and Tuberculosis respectively, Row 2 illustrates the synthesised augmented images according to the above listed pulmonary disease classes, row 3 illustrates the occlusion explanations of the classified augmented images, row 4 illustrates the smoothening gradient explanations of the images, row 5 and 4 illustrate the LRP explanations of the classified augmented images.

Occlusion Analysis is a type of perturbation analysis that repeatedly tests the effect of occluding patches or individual features in the input image on the neural network output. SmoothGrad.is a gradient-based explanation method where the function's gradient is averaged over a large number of locations corresponding to small random perturbations of the original data point. Like the method's name suggests, the averaging process 'smoothes' the explanation which in turn addresses the shattered gradient problem. The Layer-wise Relevance Propagation (LRP) method makes explicit use of the layered structure of the neural network and operates in an iterative manner to produce the explanation. LRP attributes relevance scores to the network model inputs or immediate neurons.

From Figure 4.5 row 3, we observe that Occlusion-based explanations are coarse and are representative of relevant regions instead of relevant pixel features. Figure 4.5 row 4, smooth Integrated Gradients produces very fine pixel-wise explanations with substantial evidence in favor of and against the prediction (red and blue pixels) while in Figure 4.5 row 5 and 6, LRP preserves the fine explanation structure but tends to produce less negative scores and attributes relevance to all features instead of individual pixels.

## 4.6 QLL-XAI-4-Fertility-Treatment | LcMCH: IV

### 4.6.1 Quantum Lattice Learning Implementation

We modeled a total of 61748 mathematical computational interactions for each simulation towards a convergent optimal result obtained and interpreted in lattice space. We examined the model best fitting the assigned ***'bic-criterion'***. Then we painted the simulated graph with Pearson correlation to display the signal flow through the Lattice Space as illustrated by a model of 4 inputs at in Figure 4.40.

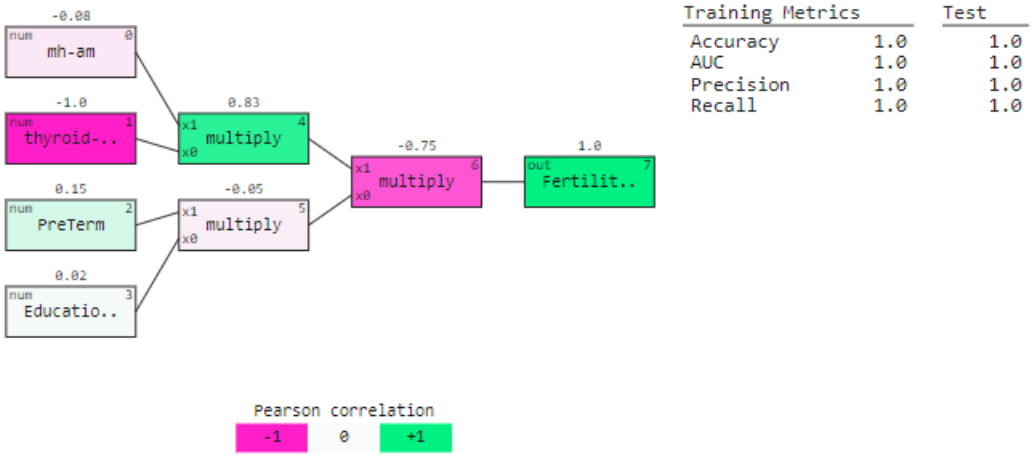


Figure 4.40: A 4 input Explainable Lattice Model Simulation.

Since each lattice model is a list of graphs sorted by accuracy, each model illustrates how the selected fertility health features (inputs) interact with others to attain an accurate fertility intervention predictive outcome (output) as illustrated in Figure 4.40, Figure 4.41, Figure 3.18 and Figure 3.19.

The most optimal Model is one that gives an accurate fertility intervention prediction with the least number of fertility health feature inputs. For this experiment, Figure 4.41 was the most optimal among all simulated models since it only required 2 inputs to give a correct fertility intervention predictive outcome.
Figure 4.41 illustrates the unbelievable performance accuracy of Lattice Models in Quantum Space. With only two fertility health features (Contraceptive_Type and thyroid-s), the mathematical lattice based model can accurately predict the outcome of any fertility health intervention fertility for a patient.

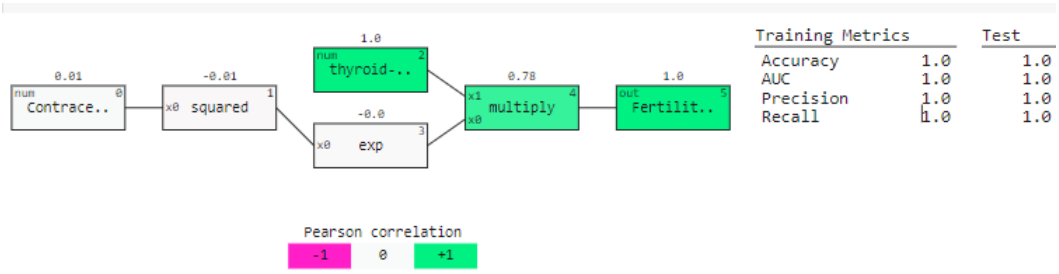


Figure 4.41: Summary of the Simulated Lattice Model

### 4.6.2 Results and Evaluation

We evaluated the training accuracy of the mathematical model as reflected in Figure 4.42.

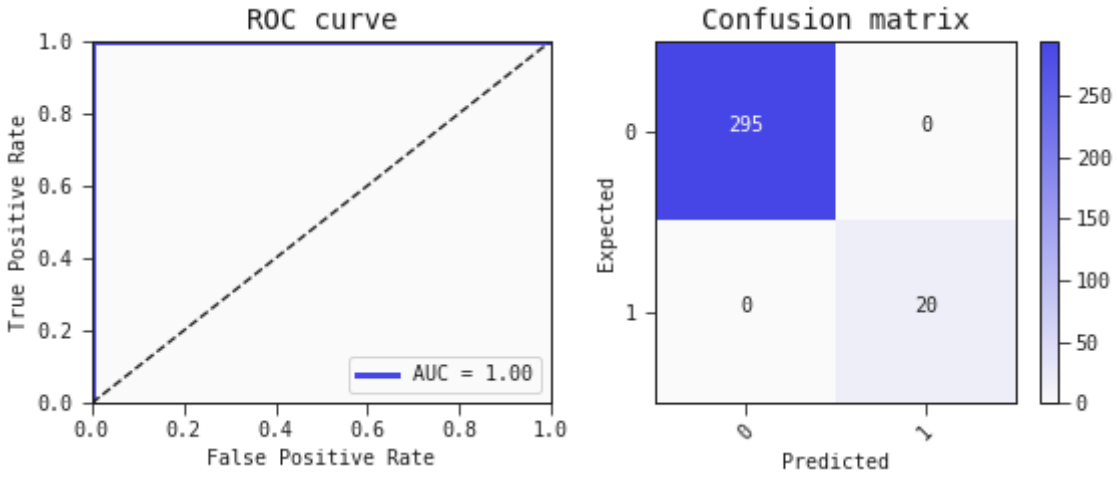


Figure 4.42: Training Metrics of Lattice Models

We tested and evaluated the most optimal lattice model illustrated in Figure 4.41. The model correctly predicted 127/127 of positive outcomes of fertility treatment and 8/8 of negative outcomes which is 100% accuracy, 100% recall and 100% precision as reflected in Figure 4.43.
We also evaluated the testing metrics used by the quantum lattice model for better diagnostic assessment for negative impacts like model fitting. The results obtained in Figure 4.43 justified the sufficiency of testing metrics with 100% recall, 100% precision on base of 135 data points.

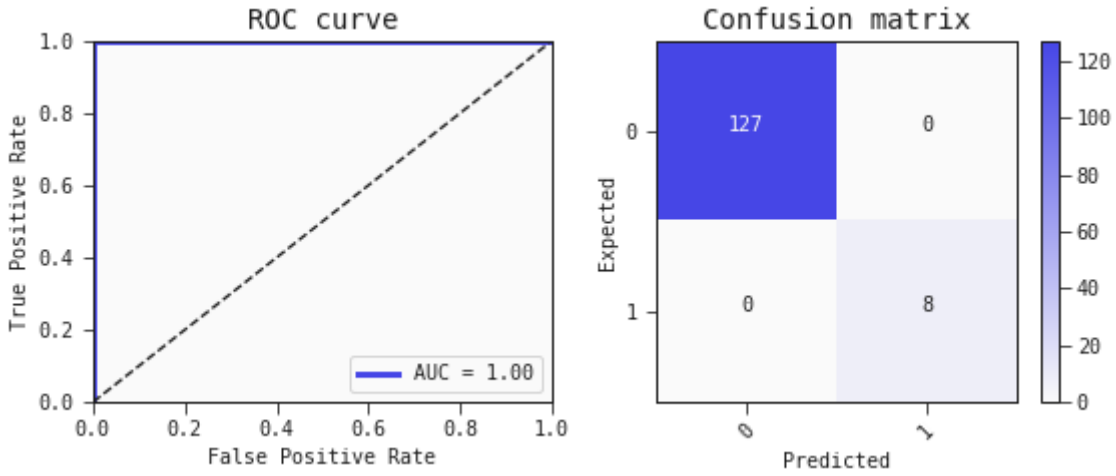


Figure 4.43: Testing Metrics of Optimal Lattice Model

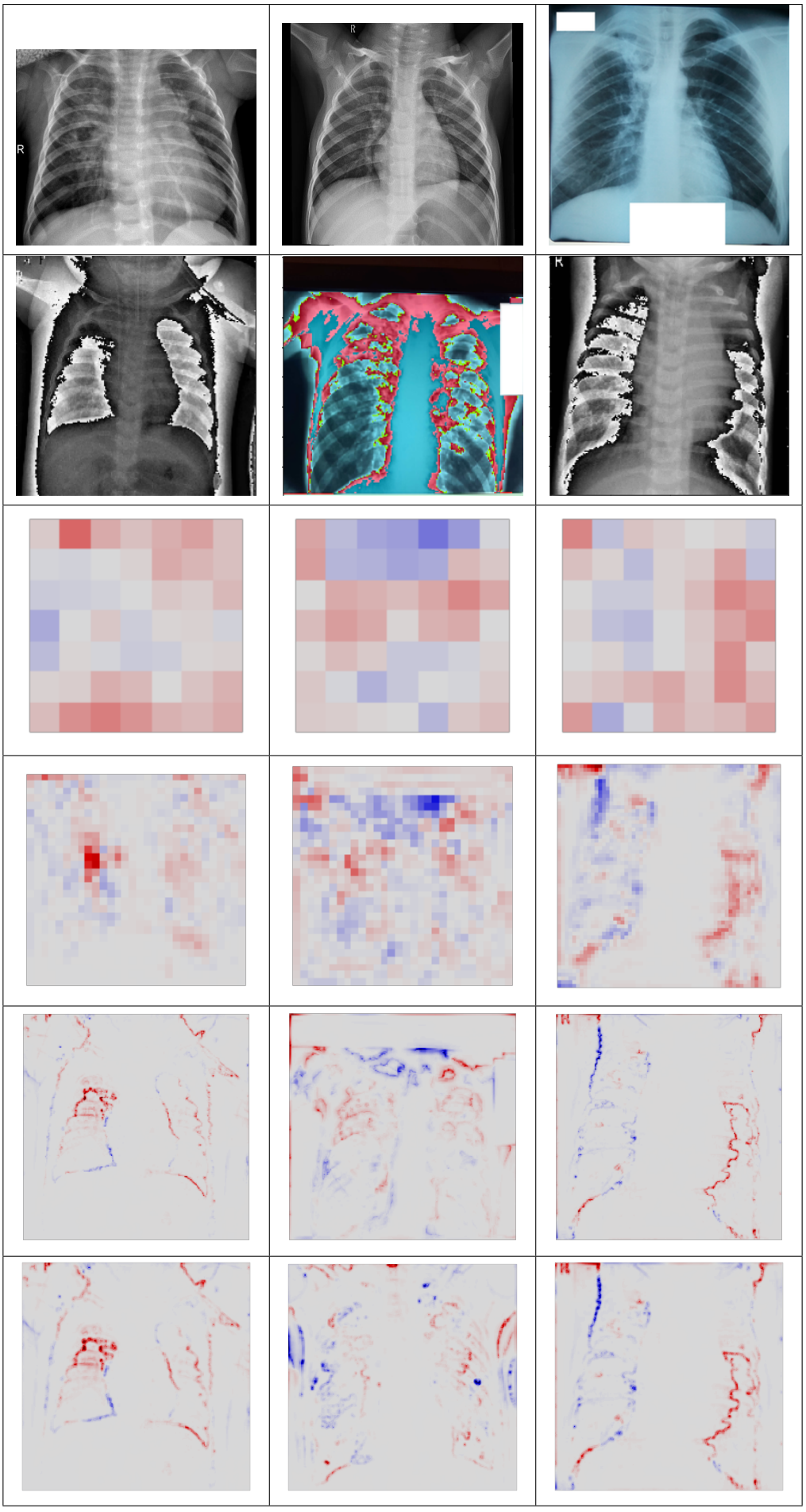

Table 4.5: Explained augmented chest X-ray images after transfer learning

# Chapter 5

# Conclusion

## 5.1 Summary of Major Observations and Lessons Learnt (How the Research paper Outcomes connect)

### 5.1.1 LcMCH: I | A Machine Learning Approach for Predicting Therapeutic Adherence to Osteoporosis Treatment

In this work, Nine Optimized Machine Learning (ML) models were presented to predict therapeutic Adherence of patients for strategic osteoporosis treatment and pharmacologic management. A combination of the optimized multi-category classification approaches proposed with the existing Biomakers can greatly improve the management of osteoporosis and overall monitoring of adherence with response to therapeutic medicine and development of suitable adherence-improving interventions.
Tree-based boosted algorithms performed better at classification of large amounts of data with little parameter tuning. Unfortunately, we could not really understand how any of the algorithms worked out the classification to obtain the good classical results. We therefore chose to use tree-based algorithms with the aim of investigating their thought process of attaining accurate classical results in Paper ID: 2.

### 5.1.2 LcMCH: I | Cardiotocogram Biomedical Signal Classification and Interpretation for Fetal Health Evaluation

In this work, we built ML models and extracted features to analyze and classify fetal cardiac biomedical signals with reduced ambiguity, high accuracy and easy Fetal Heart Rate (FHR) trace interpretations. It was observed that feature extraction greatly affected the accuracy of ML models, in fact it allows some individual ML models to perform better than Voting Ensemble ML model. Therefore, the best classification models can be confidently integrated or deployed for various fetal cardiac signal processing frameworks.

We paid extra attention to how the algorithms derived feature importance, each algorithm ranked important had different features leading to its accurate classical results. We therefore chose to focus on feature learning and feature importance derivation using multiple Explainable AI (XAI) techniques in Paper ID: 3.

### 5.1.3 LcMCH: II | Explainable Feature Learning for Predicting Neonatal Intensive Care Unit (NICU) Admissions

We explored maternal significant multidisiplinary features for NICU admission prediction. We observed that certain features, such as mother's height and hemoglobin initially looked to be good indicators for predicting NICU admissions. After extensive visualizations, we built and tested some ML predictive models like Random Forest, SVM, and Logistic Regression, tuned hyper-parameters of all models for predictive result improvement. Although Random Forest had the highest accuracy, the tuned Logistic Regression model exhibited the best recall and F1 score. We therefore chose the tuned Logistic Regression as our model for NICU admission prediction.
However, we tried to understand how Random Forest was using our data to get the highest accuracy score. We therefore deployed Explainable Machine Learning for Feature Learning where we explored feature importance for NICU admission prediction. We implemented SHAP to understand how the model made predictions, and also where they might be going wrong. Then we used LIME & ELI5 on our chosen Logistic Regression model to demonstrate feature interaction for the NICU admission prediction.
We observed that the various explainable techniques provided different tests (preferences) of feature importance. This was very noticeable with the SHAP plots display where we observed that Feature Importance display differed among the SHAP explanations. We therefore chose to focus on investigating SHAP explanations in detail for Paper ID: 4.

### 5.1.4 LcMCH: II | Explainable Artificial Intelligence for Hematologic Pediatric Patient Survival Prediction upon Stem Cell Transplantation

Having discovered that pediatric risk group and recipients' age are likely to be more influential determinants of prolonged survival as compared to CD34+ cell reception in Transplantation and Cellular Therapy, we strongly call for interdisciplinary research collaboration with special attention to the innovative application of Machine Learning (ML) and Artificial Intelligence (AI) in pediatric medicine. Besides validating Kawłak's hypothesis that increasing the CD34+ cells /kg dosage generally prolongs survival time of patients without synchronous occasion of unpleasant events affecting patients' quality of life (Kawłak et al., 2010), we demonstrated the potential of transparent Machine Learning and Artificial Intelligence at insightful precision medicine.
Extra attention was put on feature relevance for precision medicine. We observed that the importance of some features at precision medicine is greatly influenced by their availability and relevance in precision medicine. Some algorithms actually ar-

rived to the correct predictive results but dropped out some of the features which are important for the physicians to understand. Physicians also need to understand how the existence of some features shadows and skews the predictive results in precision medicine most especially in cases of limited data availability (limited features) for drawing medical decisions. We therefore focused on investigating feature relevance for precision medicine in case of data scarcity for extreme emergencies in Paper ID: 5.

### 5.1.5 LcMCH: III | Explainable Augmented Intelligence and Deep Transfer Learning for Pediatric Pulmonary Health Evaluation

Transfer learning can boost the application of biomedical instrumentation in both high and low resource settings for pediatric medicine regardless of scarcity of biomedical image data and high computational resources. Therefore augmented intelligence and deep transfer learning for Pediatric Pulmonology for digital healthcare is a great contributor to healthcare towards the 4th Industrial revolution.
Pediatric medical image processing can be made understandable, trustable, and comprehensible for pediatricians to assess connections and transparently analyze the most important features for precise predictive and preventive pediatric medicine using Explainable AI. Pixel wise pattern and feature interpretability analysis can allow clinicians like pediatricians to understandably trust, comprehensively assess connections and transparently analyze and use the features marked as important for precision pediatric medicine and pulmonary health evaluation hence a safe and trustable approach to preventive and precision medicine using Layer-Wise Relevance Propagation (LRP) explanation techniques.
We paid attention to feature relevance propagation and discovered how important it was in precision medicine. We therefore focused on building our own machine learning algorithm that could accurately predict the target outcome with strict tracking and traceability of relevant features as they interactively propagate towards the medical decision in Paper ID: 6.

### 5.1.6 LcMCH: IV | An Explainable Lattice based Fertility Treatment Outcome Prediction Model for TeleFertility

We introduced the concept of quantum lattice learning using Richard Feynman's technique and we developed lattice based Machine Learning models for explainable prediction of fertility treatment intervention outcomes. With Quantum Lattice Learning (QLL), we could implement principles of quantum physics in Computer Science and Data Engineering to trace the path of interactive features as they propagate towards the final medical decision. Despite the fact that explainable genetic programming can be of significant importance for healthcare quantum computing, the steps and procedures taken during data collection need extra attention since uncertainty caused by human cognitive bias during healthcare data collection can have a significant negative impact if the algorithm is executed on biased data.

## 5.2 Conclusion

Since we used the default kernel for all SVM applications these research methods, we hope to boost algorithmic performance and improve the accuracy by tuning SVM parameters like Gamma, Margin, Regularization and Kernel to deal with non-linearity and higher dimensions. We hope the research findings facilitate other researches in this domain to select classifiers and data preprocessing methods accordingly to build more generalizable ML predictive models.
Having developed Interpretable models and for predicting NICU admissions, we strongly recommend further research about the health center practices related to NICU admissions. That would help us understand if and determine any hidden patterns and features contributing to the increasing NICU to avoid unnecessary neonatal emergencies. Those investigations will greatly help in improving the robustness of the Explainable Machine Learning models for preventive maternal and neonatal medicine.
Since most pediatric pulmonary diseases have similar symptoms, more datasets are required with better annotation of bacterial, fungal or viral labels for better lethal pulmonary pattern recognition most especially in predictive and preventive medicine. A bigger contribution towards dataset access for pediatric patients is highly recommended to build better safer and trustable AI medical solutions for infants and children.
Generally, we strongly encourage and recommend further research and experimentation of machine learning and artificial intelligence explainability techniques in predictive, preventive and personalized medicine for maternal and child wellbeing.

## 5.3 Future Works

Future work will be focused on integration of the proposed models with in clinical decision making and pharmacologic tools for improved medical adherence. We hope to use the obtained results in developing a standardized Electronic Fetal Monitoring (EFM) Interpretation & Management Framework for fetal surveillance and evaluation in pregnant women to support new medication advancements and treatment procedures in maternal-fetal medicine. We also hope to use our findings towards developing a Standardized Explainable NICU Admission Evaluation and Management Framework for patients and neonatologists. We also hope to support researchers and innovators in developing better maternal and neonatal solutions for mother and child wellbeing. We shall work towards developing a Standardized Explainable Transplantation and Cellular Therapeutic Evaluation Framework for pediatric physicians to insightfully prescribe efficient treatment plans for their patients. Our future works shall also focus on supporting the improvement of robustness and lowering uncertainty of biomedical image processing applications in predictive and preventive medicine.
Generally, the obtained results shall guide us on advocating for the development of a Standardized Explainable Maternal and Child Health Evaluation and Management Framework for trustable and reliable Maternal and Neonatal Medicine for patients and physicians. We shall also support researchers and innovators in developing new medication advancements and treatment procedures in Maternal, Neonatal and Reproductive Medicine.

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# Appendix

## Detailed Simulations of the Research Papers

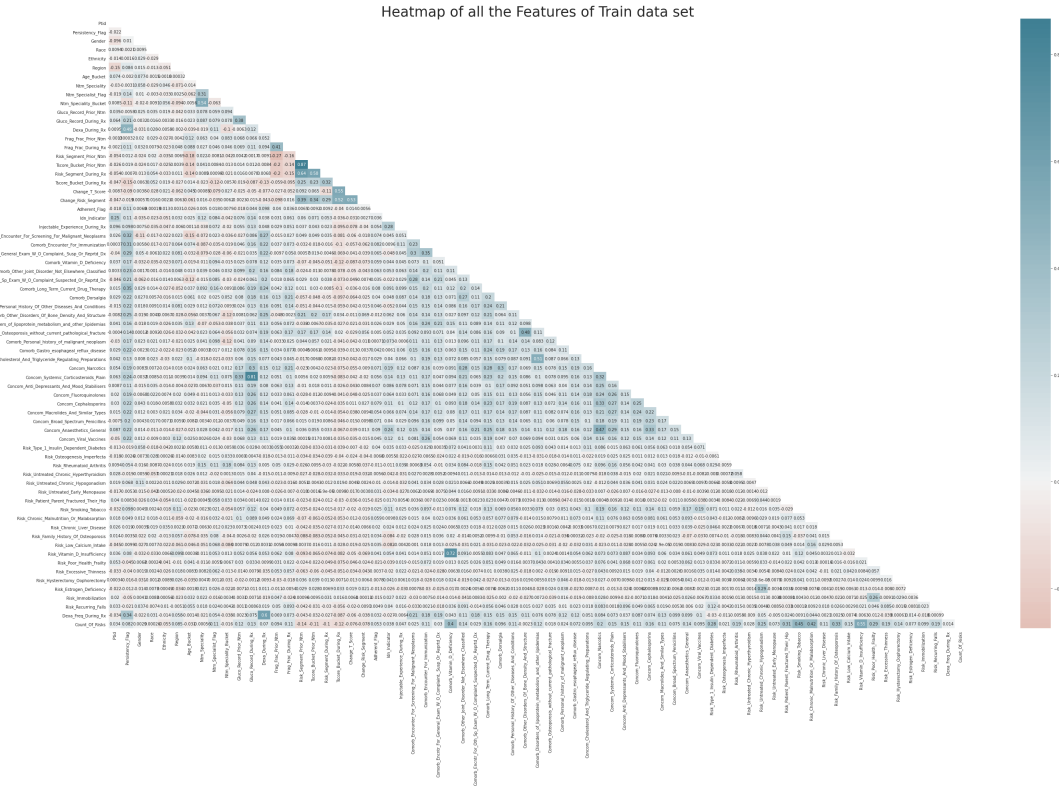


Figure 5.1: Full View of Correlation Heat map of features in train dataset

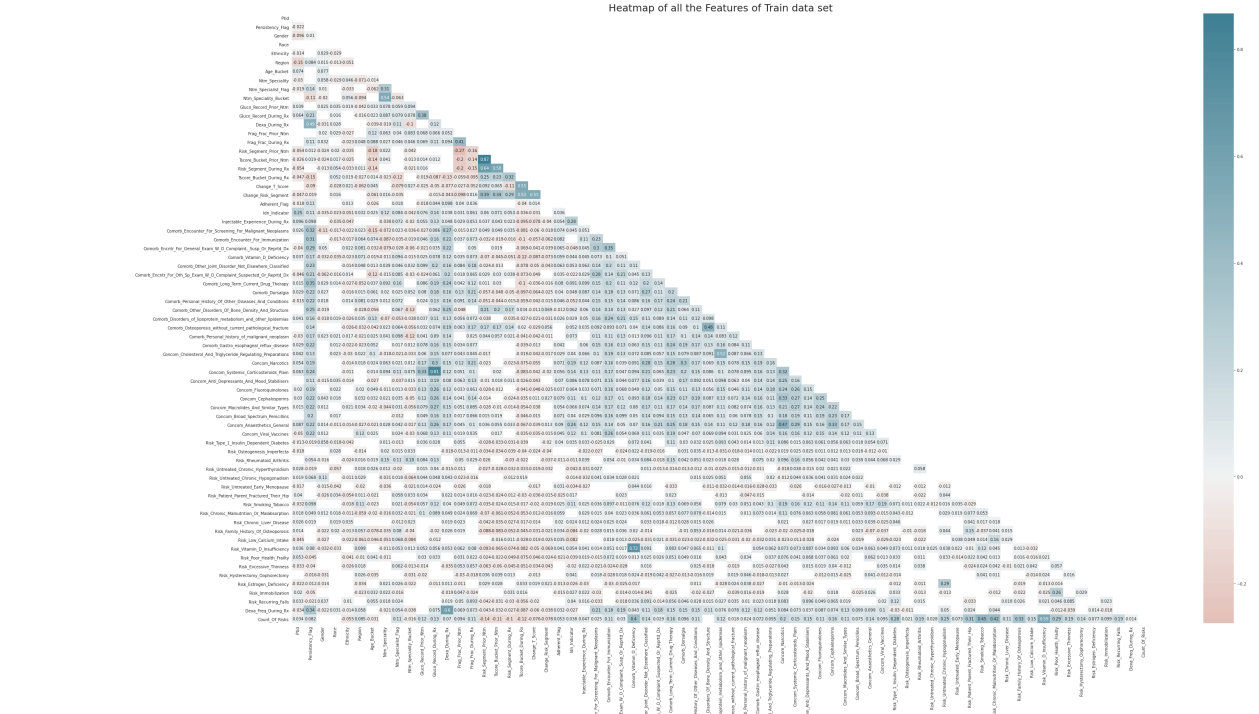


Figure 5.2: Full View of Correlation Heat map of features after restricting variables with low correlation results

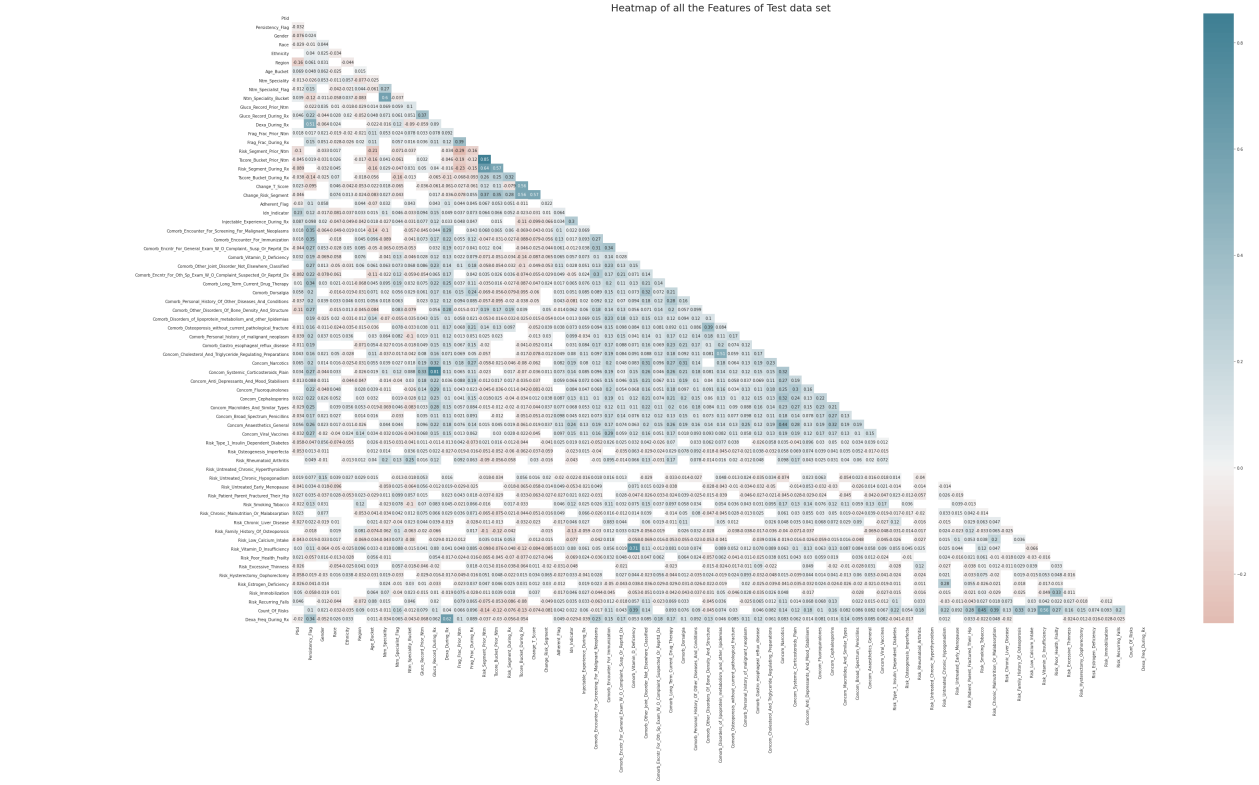


Figure 5.3: Full View of Correlation Heat map of features in test dataset

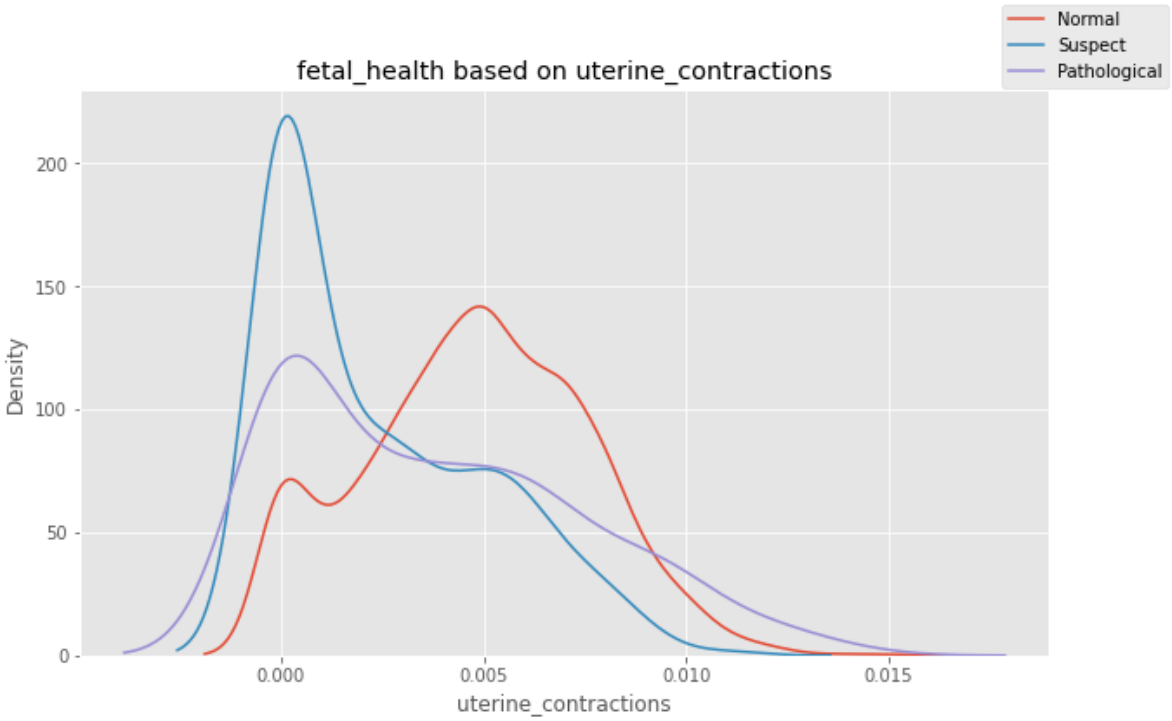


Figure 5.4: Fetal Health curves based on Uterine Contractions

Figure 5.5: Expanded Tree for Fetal Health CAT

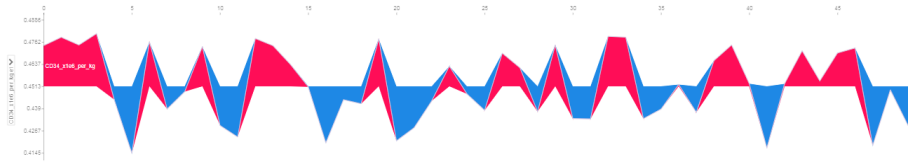

Figure 5.6: ForcePlot-of-first-50-patients

Figure 5.7: ForcePlot-of-patient-at-index-15

Figure 5.8: ForcePlot-of-patient-at-index-35

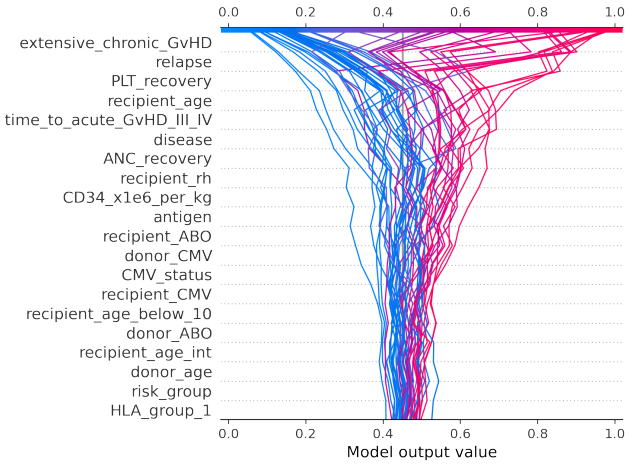


Figure 5.9: Shap-Decision-plot-of-first-50-patients

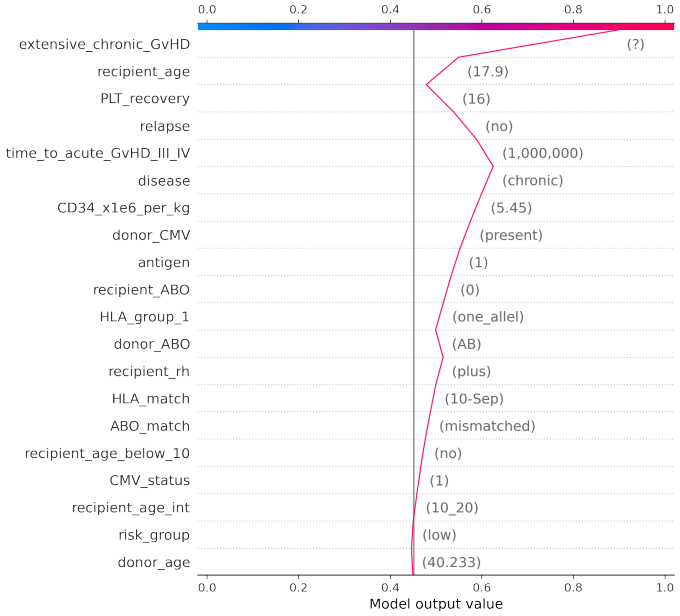


Figure 5.10: Shap Decision Plot of Patient at index-15

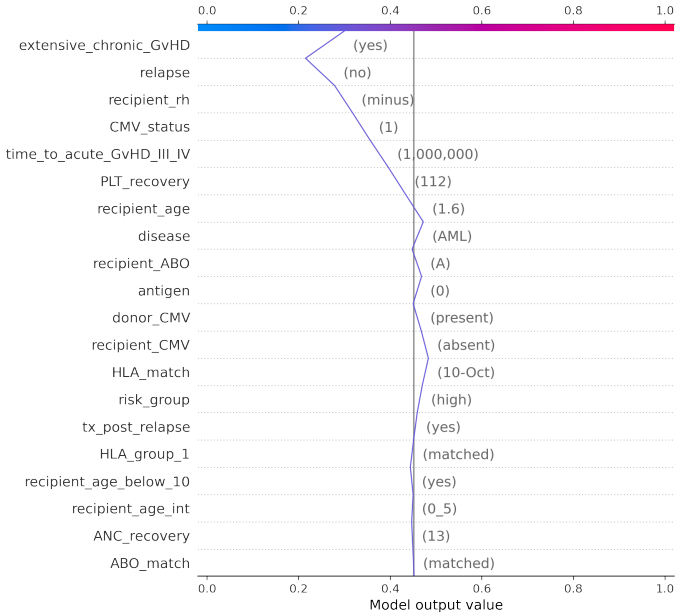


Figure 5.11: Shap Decision plot of patient at index-35

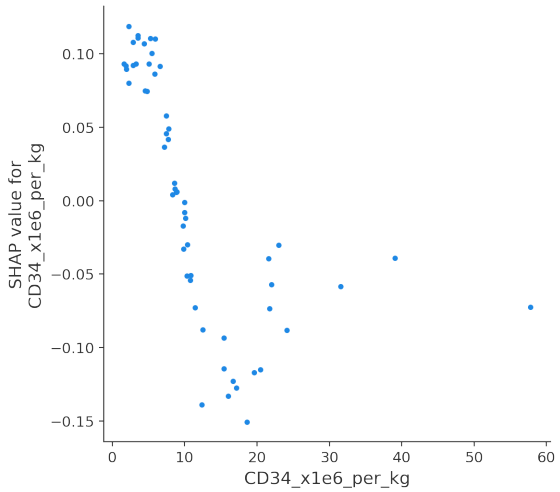


Figure 5.12: Shap dependency plot CD34_x1e6_per_Kg

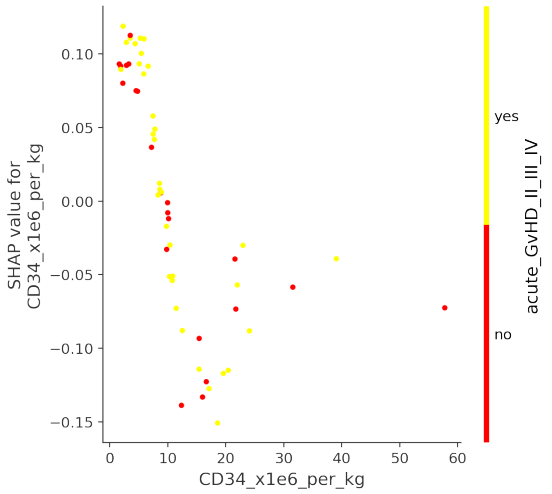


Figure 5.13: Shap Dependency Plot of CD34_x1e6_per_Kg and Survival

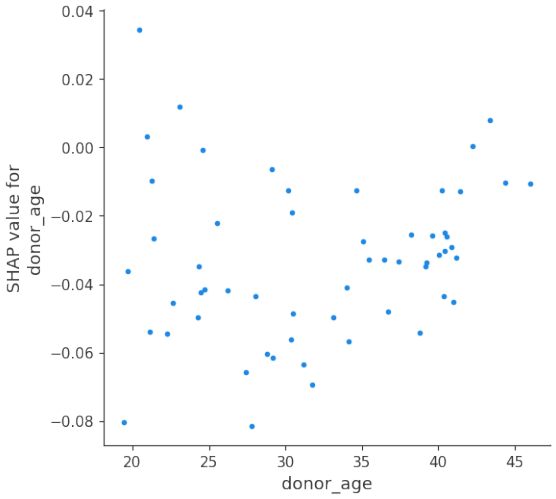


Figure 5.14: Shap Dependency plot of Donor Age

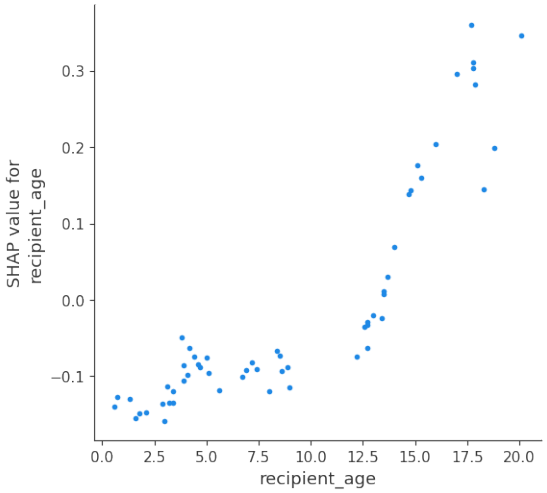


Figure 5.15: Shap Dependency Plot Recipient Age

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**Ggaliwango Marvin and Dr. Golam Rabiul Alam**
**2021 IEEE International Conference on Biomedical Engineering, Computer and Information Technology for Health (BECITHCON)**

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**Ggaliwango Marvin and Dr. Golam Rabiul Alam**
**2022 International Conference on Innovations in Science, Engineering and Technology (ICISET)**

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