

ISTANBUL TECHNICAL UNIVERSITY ★ GRADUATE SCHOOL

**AN ARTIFICIAL INTELLIGENCE APPROACH FOR BREAST CANCER
TREATMENT**



Ph.D. THESIS

Tuğçe BELDEK

Department of Management Engineering

Management Engineering Programme

APRIL 2024

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Thesis Advisor: Prof. Dr. Hatice CAMGÖZ AKDAĞ

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İSTANBUL TEKNİK ÜNİVERSİTESİ ★ LİSANSÜSTÜ EĞİTİM ENSTİTÜSÜ

MEME KANSERİ TEDAVİSİNDE YAPAY ZEKA YAKLAŞIMI

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To my family,



FOREWORD

Breast cancer, one of the most prevalent and life-threatening diseases affecting women worldwide, continues to be a significant health challenge. As researchers and healthcare professionals, it is our collective responsibility to advance our understanding of breast cancer risk factors, improve early detection methods, and develop effective preventive and treatment strategies. It is with great pride and enthusiasm that I present this thesis, which explores the relationship between women's properties and breast cancer occurrence through the application of machine learning techniques.

This thesis represents the culmination of extensive research, meticulous data collection, and rigorous analysis. It serves as a testament to the dedication and collaboration of numerous individuals who have contributed to the advancement of breast cancer research. It is my hope that this work will contribute meaningfully to the field, offering insights that can potentially impact the lives of countless women.

I extend my heartfelt appreciation to my family, friends, and loved ones who have provided unwavering support, understanding, and encouragement throughout this journey. Their belief in my abilities and their constant presence have been a constant source of strength and inspiration. Firstly, i want to thank to my advisor Prof. Dr. Hatice CAMGÖZ AKDAĞ for her valuable support since the beginning of my academic career. Many thanks to Assoc. Prof. Tuncay ÖZCAN that i learnt so much from his knowledge and experience. I want to thank to my colleague and best friend Aziz Kemal KONYALIOĞLU for his support for many years in every aspect of my life. I want to thank to my colleague Oğuz YÜCEL for his worthless effort by supporting me during the this thesis process. Another thank to my colleagues and friends from Istanbul Technical University for their friendship and support. It is very clear that today being an adult, in this level of my life is provided by my family by their strong belief and support behind me since i was a child. Many thanks to my mother and father, and my brother for their unrequited love. Lastly i want to thank to my fiancée that he always believed to me more than myself. I appreciate for your being in my life.

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With great excitement and anticipation, I present this thesis to the academic and scientific community, hopeful that it will inspire further advancements in breast cancer research and ultimately lead to a world where the burden of this disease is significantly reduced.

March 2024

Tuğçe BELDEK
(Textile Enginner & Manufacturing Engineer)





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ABBREVIATIONS

AI	: Artificial Intelligence
ANN	: Artificial Neural Network
CART	: Classification and Regression Tree
DT	: Decision Tree
LR	: Logistic Regression
ML	: Machine Learning
NN	: Neural Network
ROC	: Receiver Operating Characteristic
SMOTE	: The Synthetic Minority Oversampling Technique
SVM	: Support Vector Machine



SYMBOLS

θ	: Model Parameters to be Estimated
$\mathcal{T}$	: Decision Tree





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AN ARTIFICIAL INTELLIGENCE APPROACH FOR BREAST CANCER TREATMENT

SUMMARY

Breast cancer is a pressing health concern that demands comprehensive research to understand its risk factors and improve patient outcomes. In this thesis, we undertake a multidimensional analysis to explore the relationship between women's properties and breast cancer occurrence. Leveraging a dataset collected from a reputable clinic, we employ advanced machine learning techniques to identify significant risk factors and develop predictive models. The ultimate goal is to enhance our understanding of breast cancer etiology and contribute to the development of targeted interventions.

The thesis begins with a thorough review of existing literature on breast cancer risk factors, epidemiology, and the application of machine learning in the field. This review provides a theoretical foundation for our research and identifies gaps in knowledge, setting the stage for our investigation.

We start by collecting a comprehensive dataset from the clinic, comprising anonymized patient records. The dataset encompasses a wide range of variables, including demographic information, lifestyle factors, genetic markers, and medical history. Proper data preprocessing and feature engineering techniques are applied to ensure the integrity and quality of the analysis.

Next, we employ advanced machine learning algorithms such as logistic regression, decision trees and neural networks to develop predictive models. These models utilize the dataset to identify patterns and accurately predict the likelihood of breast cancer occurrence.

To interpret the results and assess the significance of women's properties, we conduct in-depth analyses and comparisons with existing knowledge. The findings shed light on the influential risk factors associated with breast cancer occurrence, providing valuable insights for preventive strategies, early detection, and targeted interventions.

In addition to the analysis of breast cancer risk factors, we incorporate a case study on value stream mapping in a radiology department. Value stream mapping, a lean management technique, is applied to identify bottlenecks, eliminate waste, and optimize processes in the radiology department. The case study highlights the practical application of value stream mapping in improving efficiency and patient flow, ultimately enhancing the overall quality of care in the radiology department.

Through this comprehensive research, we aim to advance our understanding of breast cancer etiology, improve risk assessment models, and facilitate the development of personalized prevention and treatment approaches. Furthermore, by incorporating a case study on value stream mapping, we demonstrate the practical applicability of lean management techniques in healthcare settings.

The insights gained from this thesis have implications for breast cancer research, clinical practice, and healthcare management. The identification of significant risk

factors can inform targeted screening programs, early detection strategies, and personalized interventions. Additionally, the application of value stream mapping techniques can enhance operational efficiency, optimize resource allocation, and improve patient care in radiology departments and other healthcare settings.

In conclusion, this thesis represents a comprehensive investigation into the relationship between women's properties and breast cancer occurrence. Through the utilization of machine learning techniques and the inclusion of a value stream mapping case study, we contribute to the growing body of knowledge in breast cancer research and healthcare management. It is our hope that this work will make a meaningful impact in the fight against breast cancer and drive advancements in patient care and outcomes.



MEME KANSERİ TEDAVİSİNDE YAPAY ZEKA YAKLAŞIMI

ÖZET

Meme kanseri, hasta sonuçlarını iyileştirme ve risk faktörlerini kavrama gereksinimi nedeniyle önemli bir sağlık meselesidir. Bu tez, kadın özellikleri ile meme kanseri arasındaki bağlantıyı çok yönlü bir analizle incelemektedir. Saygın bir klinikten elde edilen veri seti, önemli risk faktörlerini tanımlamak ve prediktif modeller geliştirmek amacıyla gelişmiş makine öğrenimi yöntemleri kullanılarak işlenmiştir. Asıl hedef, meme kanseri etiyolojisine dair anlayışı derinleştirmek ve hedeflenen müdahalelere katkı sağlamaktır.

Bu çalışma, meme kanseri risk faktörleri, epidemiyolojisi ve makine öğreniminin bu alandaki kullanımı üzerine kapsamlı bir literatür incelemesi ile başlar. Bu inceleme, araştırmanın teorik zeminini oluşturur ve bilgi açıklarını tanımlayarak incelemeye yön verir.

Araştırmada, klinikten toplanan, anonim hasta kayıtlarını içeren geniş bir veri yelpazesini barındıran kapsamlı bir veri seti kullanılmıştır. Analiz bütünlüğü ve kalitesini sağlamak için veri ön işleme ve özellik mühendisliği teknikleri uygulanmıştır.

Araştırmada, veri setini kullanarak desenleri tanımlayıp meme kanseri oluşum olasılığını doğru bir şekilde tahmin etmeyi amaçlayan lojistik regresyon, karar ağaçları ve yapay sinir ağları gibi ileri düzey makine öğrenimi algoritmaları kullanılmıştır.

Bu çalışmada, meme kanserini tahmin etmek için logistic regression modeli kullanılmıştır. Model, kadın özellikleri gibi bağımsız değişkenleri kullanarak hastalığın olasılığını hesaplar. Bu modelin seçilmesinin nedeni, çıktının olasılık olarak yorumlanabilmesi ve sonuçların tıbbi karar verme süreçlerinde doğrudan kullanılabilir olmasıdır. Model, çeşitli testlerle değerlendirilmiş ve kalibrasyonu için gereken ayarlamalar yapılmıştır. Ayrıca, modelin duyarlılık ve özgüllük oranları gibi performans metrikleri de detaylı olarak incelenmiştir.

Karar ağaçları, veri setindeki karmaşık yapıları basit karar düğümleriyle ifade edebilme avantajına sahiptir. Bu yöntem, özellikle heterojen popülasyonları analiz etmek ve önemli prediktörleri görsel olarak sunmak için kullanılmıştır. Ağaç yapısı, hastaların risk faktörlerine göre nasıl gruplandırıldığını açıkça göstermektedir, bu da klinisyenlere risk faktörlerini daha iyi anlama konusunda yardımcı olmaktadır. Bu modelin hassasiyeti ve ağaç derinliği gibi parametreler optimizasyon sürecinde detaylı bir şekilde ayarlanmıştır.

Yapay sinir ağları, bu tezde karmaşık ve non-lineer ilişkileri modellemek için kullanılmıştır. Çalışmada, çok katmanlı perceptron (MLP) mimarisi tercih edilmiş, bu sayede model, daha yüksek derecede doğrulukla tahmin yapabilme yeteneğine kavuşmuştur. Modelin eğitim süreci, kullanılan katman sayısı, nöron sayısı ve aktivasyon fonksiyonları gibi teknik detayları, modelin nasıl optimize edildiğini ve sonuçların doğruluğunu artırmak için yapılan çalışmaları anlatmaktadır.

Kadın özelliklerinin etkilerini değerlendirmek ve sonuçları yorumlamak amacıyla, bulgular derinlemesine analiz edilmiş ve mevcut bilgilerle karşılaştırılmıştır. Bu analiz, meme kanseri oluşumuyla ilişkili risk faktörlerini belirleyerek, erken teşhis, önleyici stratejiler ve hedefe yönelik müdahaleler için kıymetli içgörüler sunmaktadır. Her bir modelin bulguları, memen kanseri oluşumuyla ilişkili risk faktörlerini belirlemede nasıl bir rol oynadığı açıklanmaktadır. Örneğin, logistic regression modeli tarafından belirlenen en güçlü prediktörler, karar ağaçları ile teyit edilmiş ve ANN modeli ile daha da derinlemesine incelenmiştir. Bu bölüm, farklı modellerin bulgularının nasıl birbirini tamamladığını ve genel sonuçları nasıl güçlendirdiğini göstermektedir.

Karar Ağacı modelleri, tüm üç veri setinde %90 civarında tutarlı bir doğruluk seviyesi sergilemektedir. Ancak, bu modellerin hassasiyet ve hatırlama oranlarındaki performansları değişkenlik göstermekte olup, özellikle Veri Seti-1’de en düşük F1 puanı olan 0.333 ile dikkat çekmektedir. Bu durum, modelin gerçek pozitifler ile bu pozitif tahminlerin doğruluğu arasında mütevazı bir denge olduğunu göstermekte, modelin negatif vakaları pozitif olarak yanlış sınıflandırma eğilimi olabileceğine işaret etmektedir. Ayrıca, bu modeller temel olarak yaş ve kanser geçmişi değişkenlerinin, risk tahmininde daha önemli olduğu sonucuna ulaşmıştır.

Lojistik Regresyon modelleri, veri setleri boyunca hatırlama oranında dikkate değer bir artış göstermekte ve sürekli olarak 0.978’in üzerinde puan almaktadır. Bu yüksek hatırlama oranı, Lojistik Regresyon modellerinin gerçek pozitif vakaları tanıma konusunda olağanüstü yetenekli olduğunu göstermektedir. Ancak, Lojistik Regresyon modellerinin hassasiyeti, hatırlama oranlarıyla eşleşmemekte, bu da az sayıda yanlış pozitif olduğunu göstermektedir. Yine de Lojistik Regresyon modellerinin F1 puanları, özellikle Veri Seti2 LR ve Veri Seti3 LR’de, Karar Ağacı modellerine kıyasla hassasiyet ve hatırlama oranları arasında üstün bir dengeyi yansıtmaktadır. Bu modeller de özellikle yaş ve kanser geçmişi gibi değişkenlerin, hastalığın tahmininde kritik rol oynadığını belirtmektedir.

Yapay Sinir Ağı modelleri, özellikle Veri Seti3 ANN’de, tüm metriklerde neredeyse mükemmel puanlara yaklaşan olağanüstü genel performanslarıyla öne çıkmaktadır. Hassasiyet ve hatırlama oranları 0.988’in üzerinde olan ANN modelleri, yanlış pozitif ve negatifleri en aza indirirken pozitif vakaları doğru bir şekilde sınıflandırma konusunda olağanüstü bir yetenek sergilemektedir, bu da F1 puanlarının 1’e yakın olduğunu göstermektedir.

Sonuç olarak, her model farklı alanlarda güçlü yönler sergilemekle birlikte, sunulan metriklere göre Yapay Sinir Ağları en dengeli ve en yüksek genel performansı göstermektedir. Bu özel uygulama için, veri setleri boyunca genelleme yapabilme ve hatayı en aza indirme yeteneği nedeniyle ANN’nin tercih edilen model olabileceği önerilmektedir. Ancak, model seçimi sadece performans metrikleriyle değil, aynı zamanda modellerin yorumlanabilirliği, hesaplama verimliliği ve uygulanan alanda yanlış sınıflandırmaların özel maliyeti gibi faktörler göz önünde bulundurularak yapılmalıdır.

Radyoloji departmanında yapılan bir vaka çalışmasıyla birlikte, meme kanseri risk faktörlerinin analizi de bu teze dâhil edilmiştir. Değer akışı haritalama, radyoloji departmanındaki süreçleri optimize etmek, israfı azaltmak ve verimliliği artırmak için kullanılan stratejik bir yönetim tekniğidir. Bu vaka çalışması, değer akışı haritalama tekniklerinin sağlık hizmetlerinde nasıl uygulanabileceğini ve radyoloji departmanında hasta akışını ve genel bakım kalitesini nasıl iyileştirebileceğini vurgulamaktadır.

Bu araştırmanın genel amacı, meme kanseri etiyolojisini iletirmek, risk değerlendirme modellerini iyileştirmek ve kişiselleştirilmiş önleme ve tedavi yöntemlerinin geliştirilmesine yardımcı olmaktır. Ayrıca, değer akışı haritalama vaka çalışmasıyla, sağlık hizmetlerinde operasyonel verimliliğin nasıl artırılabilir ve kaynak tahsisinin nasıl optimize edilebileceğini göstermekteyiz.

Bu tez, meme kanseri araştırmaları, klinik pratiği ve sağlık hizmeti yönetimine değerli katkılar sağlar. Tanımlanan risk faktörleri, hedefli tarama programları, erken teşhis stratejileri ve kişiselleştirilmiş müdahaleler için önemli bilgiler sunar. Değer akışı haritalama tekniklerinin kullanılması, operasyonel verimliliği artırabilir ve radyoloji departmanları ile diğer sağlık hizmeti alanlarında hasta bakımını iyileştirebilir.

Sonuç olarak, bu çalışma, kadın özellikleri ile meme kanseri arasındaki ilişkiyi inceleyen kapsamlı bir araştırmadır. Makine öğrenimi tekniklerinin ve radyoloji departmanındaki değer akışı haritalama çalışmasının dahil edilmesiyle, meme kanseri araştırmaları ve sağlık yönetimi alanında bilgi birikimine önemli bir katkı sağlamıştır. Bu çalışmanın, meme kanseriyle mücadelede anlamlı bir etki yaratacağı ve hasta bakımı ve sonuçları üzerindeki gelişmeleri destekleyeceği umulmaktadır.



1. INTRODUCTION

Management of healthcare systems becomes more valuable given the fact that many researchers are trying to find new methods in order to facilitate the cure of diseases but trying to dig out a cure of disease or delaying it, is not always sufficient to save a life. Now, it is crucial to move rapidly to give a chance to the patient. By developing technology, there might be possibilities to use some special decision support systems, to decide which treatment to give to the patient as soon as possible.

Breast cancer is the most common cancer among women. It can strike regardless of age or background, but some factors can increase your risk of developing breast cancer. These include things like being overweight or obese, having a family history of breast cancer, and being exposed to certain chemicals and toxins. Many women don't know that their diet and lifestyle choices are also breast cancer risk factors.

Breast cancer continues to pose a significant health challenge, affecting millions of women worldwide and contributing to substantial morbidity and mortality rates. The complexity of this disease necessitates comprehensive investigations into its risk factors and underlying mechanisms. In recent years, the advent of machine learning techniques has offered promising avenues for analyzing large-scale clinical data and identifying patterns that may assist in understanding the determinants of breast cancer occurrence.

This thesis aims to explore the relationship between women's properties and breast cancer occurrence through the application of advanced machine learning tools. By leveraging a dataset collected from a reputable clinic, encompassing a wide range of variables related to patients' demographics, lifestyle factors, genetic markers, and medical history, this study endeavors to shed light on the factors that contribute to breast cancer development.

The objectives of this research are threefold: first, to identify relevant features from the dataset that exhibit significant associations with breast cancer occurrence; second,

to train machine learning models on the curated data to accurately predict the likelihood of breast cancer; and finally, to interpret the results and discern the properties of women that exert the most influence on breast cancer occurrence.

To accomplish these goals, a comprehensive review of existing literature on breast cancer risk factors, epidemiology, and machine learning applications in the field has been conducted. This literature review not only provides a theoretical foundation for the study but also helps identify gaps in knowledge and research opportunities.

The dataset collected from the clinic, comprising anonymized patient records, represents a valuable resource for investigating breast cancer. However, proper data preprocessing and feature engineering are crucial steps in ensuring the quality and integrity of the analysis. This includes handling missing values, outliers, and normalization to standardize the data for optimal performance of the machine learning algorithms.

Following data preparation, various machine learning algorithms will be applied to the dataset, including logistic regression, decision trees, random forests, support vector machines (SVM), and neural networks. These algorithms have demonstrated effectiveness in classification tasks and will be utilized to develop predictive models that can discern patterns and make accurate predictions regarding breast cancer occurrence.

The results obtained from these models will then be thoroughly analyzed, interpreting the importance of features and assessing the significance of various women's properties in relation to breast cancer occurrence. By drawing comparisons with existing knowledge and validating the findings, this study aims to contribute to the growing body of research on breast cancer risk factors, ultimately providing insights that can inform preventive strategies, early detection, and targeted interventions.

In conclusion, this thesis endeavors to leverage machine learning techniques to explore the relationship between women's properties and breast cancer occurrence. By analyzing a comprehensive dataset and employing state-of-the-art algorithms, the study aims to unravel the complex interactions between various factors and provide valuable insights for the prevention and management of breast cancer. The subsequent chapters will delve into the methodology, results, and discussions that shape this

investigation, with the ultimate goal of advancing our understanding of breast cancer etiology and improving patient outcomes.

1.1 Significance of Thesis

In Turkey, there is not an effective healthcare record and interfering system. Examples from the literature shows that new artificial intelligence (AI) based models are being used at healthcare systems to increase quality. It is very important to collect and analyze the data at the early stage of a breast cancer disease.

Breast cancer is a significant public health concern worldwide, affecting women of all ages and ethnic backgrounds. Understanding the risk factors and underlying mechanisms associated with breast cancer occurrence is crucial for developing effective preventive strategies, improving early detection, and guiding personalized treatment approaches. The application of machine learning techniques to analyze extensive clinical data has the potential to uncover valuable insights that can contribute to these goals. This thesis holds several key implications and significance:

Identification of Key Risk Factors: By exploring the relationship between women's properties and breast cancer occurrence, this thesis aims to identify specific risk factors that play a significant role in the development of the disease. The findings may reveal previously unrecognized associations between certain demographic, lifestyle, genetic, or medical history factors and breast cancer. This knowledge can help in identifying high-risk populations, implementing targeted screening programs, and developing personalized interventions for individuals at heightened risk.

Enhancement of Breast Cancer Prediction: The development of accurate machine learning models trained on a comprehensive dataset can contribute to improved breast cancer prediction. These models can utilize a wide range of patient characteristics to assess an individual's likelihood of developing breast cancer, thereby aiding clinicians in making informed decisions regarding screening frequency, diagnostic testing, and prevention strategies. Accurate prediction models can help optimize healthcare resource allocation and minimize unnecessary interventions for low-risk individuals.

Advancement in Precision Medicine: The integration of machine learning techniques with comprehensive patient data has the potential to advance the field of precision medicine in breast cancer. By identifying specific properties of women that influence

breast cancer occurrence, clinicians can tailor prevention, screening, and treatment approaches based on individual risk profiles. This move toward personalized medicine has the potential to improve patient outcomes, minimize adverse effects, and optimize resource allocation in the management of breast cancer.

Contribution to Breast Cancer Research: This thesis contributes to the expanding body of knowledge on breast cancer etiology by utilizing advanced machine learning tools. The insights gained from this research can inform and guide future studies, helping to refine risk assessment models, investigate underlying mechanisms, and identify novel biomarkers or therapeutic targets. Additionally, the methodology and approach employed in this thesis can serve as a reference for researchers interested in applying machine learning techniques to analyze large-scale clinical datasets in the context of breast cancer or other related diseases.

In conclusion, this thesis holds significant implications for breast cancer research and clinical practice. By unraveling the relationship between women's properties and breast cancer occurrence through the application of machine learning, it aims to contribute to risk assessment, early detection, and personalized management strategies. The findings have the potential to improve patient outcomes, inform public health policies, and pave the way for further advancements in the field of breast cancer research and precision medicine.

1.2 Purpose and Scope of Thesis

The purpose of this thesis is to investigate the relationship between women's properties and breast cancer occurrence using machine learning techniques. The study aims to identify the specific properties or characteristics of women that significantly influence the likelihood of developing breast cancer. By analyzing a comprehensive dataset collected from a clinic, this research seeks to provide insights into the risk factors associated with breast cancer, enhance prediction models, and contribute to the growing body of knowledge in the field.

The scope of this thesis encompasses the following key aspects:

Data Collection: The research relies on a dataset obtained from a reputable clinic, consisting of anonymized patient records. The data includes a wide range of variables related to demographics, lifestyle factors, genetic markers, and medical history. The

analysis will be conducted on this specific dataset to explore the relationship between women's properties and breast cancer occurrence.

Machine Learning Analysis: The thesis employs advanced machine learning techniques to analyze the collected data. Various algorithms, such as logistic regression, decision trees and neural networks, will be utilized to develop predictive models and identify relevant features associated with breast cancer occurrence.

Interpretation of Results: The results obtained from the machine learning analysis will be thoroughly interpreted and analyzed. The significance and impact of different women's properties on breast cancer occurrence will be examined. Comparisons with existing knowledge and validation of the findings will be conducted to ensure the reliability and relevance of the results.

Implications and Recommendations: The thesis will discuss the implications of the findings in the context of breast cancer research and clinical practice. The identified risk factors and properties associated with breast cancer occurrence will be discussed, and recommendations for preventive strategies, early detection, and personalized management approaches will be proposed. The thesis will also identify potential avenues for future research in the field.



2. LITERATURE REVIEW

2.1 Breast Cancer

Among women, breast cancer is the most frequent cancer type that nearly 2 million women are affected each year. Approximately 600,000 women died from breast cancer in 2018 (URL-1). Breast cancer arises in the lining cells (epithelium) of the ducts (85%) or lobules (15%) in the glandular tissue of the breast. Initially, the cancerous growth is confined to the duct or lobule (“in situ”) where it generally causes no symptoms and has minimal potential for spread (metastasis). Over time, these in situ (stage 0) cancers may progress and invade the surrounding breast tissue (invasive breast cancer) then spread to the nearby lymph nodes (regional metastasis) or to other organs in the body (distant metastasis). If a woman dies from breast cancer, it is because of widespread metastasis. Breast cancer treatment can be highly effective, especially when the disease is identified early. Treatment of breast cancer often consists of a combination of surgical removal, radiation therapy and medication (hormonal therapy, chemotherapy and/or targeted biological therapy) to treat the microscopic cancer that has spread from the breast tumor through the blood. Such treatment, which can prevent cancer growth and spread, thereby saves lives (URL-2). Figure 2.1 shows main two groups of breast cancer below.

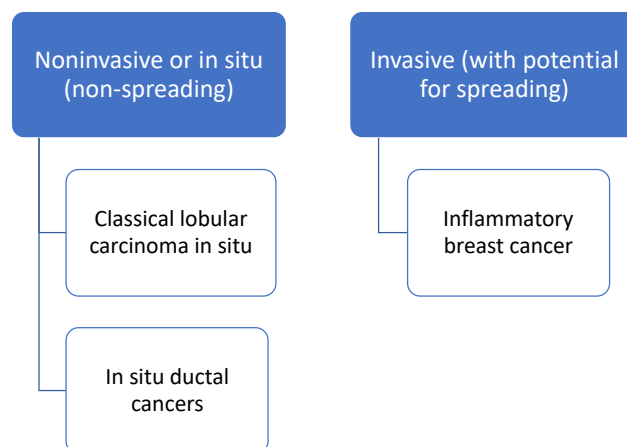


Figure 2.1 : Breast cancer types.

Everyone has some risk of developing breast cancer. In the United States, 1 in 8 women will be diagnosed with invasive breast cancer over the course of her lifetime. This means the average woman's breast cancer risk is 12-13%. A man's lifetime risk is much lower, 1 in 833. Being a woman and aging are the two biggest risk factors, but there are many other things that can increase or decrease a person's breast cancer risk. Understanding your own personal risk factors can help empower you to take action to keep your breast cancer risk as low as possible (URL-3). Some of the factors associated with breast cancer risk can't be changed, such as age and genetics. Other factors, such as lack of exercise, smoking, and eating unhealthy food can be changed by choosing healthier lifestyle options. Learn more about breast cancer risk factors and steps you can take to help protect your breast health. Established risks: Being a Woman, Age, Family History, Genetics, Personal History of Breast Cancer, Prior Radiation to Chest or Face, Certain Breast Changes, Race/Ethnicity, Being Overweight, Pregnancy History, Breastfeeding History, Menstrual History, Using HRT (Hormone Replacement History), Drinking Alcohol, Dense Breasts, Lack of Exercise and Smoking (URL-3). There are different risk factors that effect the probability of come down with breast cancer. The main factors are shown in Figure 2.2.

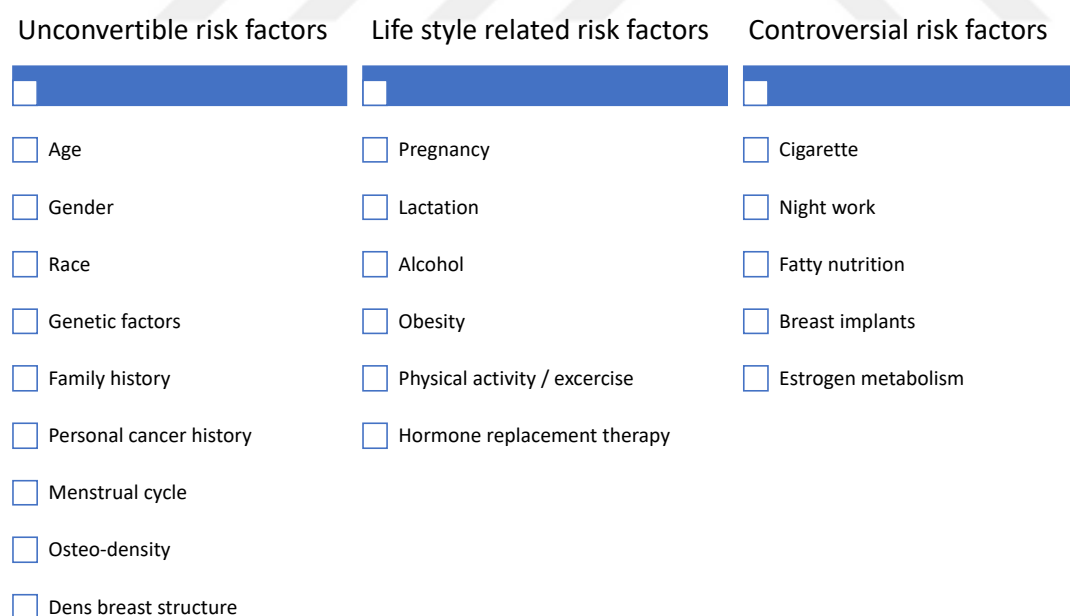


Figure 2.2 : Breast cancer risk factors.

There are different medical applications in the 8onitör8re that are used for different aims. The family disease record of three generations are collected on 48 conditions

and allows the doctors to see family disease history by providing a recommendation report including some pilot type of cancer such as breast, ovarian, colon and thrombosis by decision support mentality. The family health systems are mainly provided by all adults who are English speakers, non-adopted and patients scheduled by an appointment. The medical reports are formed based on the documents that are available on the database provided by medical record. During implementation, stakeholders pilot the components for optimizing integration. The main results of this process is 9onitör genetically intermitted thrombophilia and to 9onitör breast cancer, colon cancer and overian cancer just one year after. Patient surveys, some charts can be use after second step of results are obtained by the implementation measures related to the benefits and damages including the impact on clinic workflow and risks. The decision support's validity is taken into consideration by changes in true screening, rates of reclassification and comparison of the recommendations (Orlando et al., 2011). Generic electronic patient recording systems including DocuLive and Melior softwares are the types of software systems which are beneficial 9onitör breast cancer therapy. Reliable cases are recorded in order to assess advanced clinical quality while they are not providing a strong support on decisive therapy scheduling and method (Scherrer et al., 2015). Sequential Decision Making approaches cannot be suitable for every types of cancer since the existing situation shows that cancer decision makings are very hard because of some differences in communication style and type of information. It can be also said that cancer rates change based on the ethnicity, the patients' living places and mainly the other important factors out of the patient (Mead et al., 2013). Furthermore, it is not certain if the patient is aware of the first treatment decision depending on disease stage and the physician knowledge on this topic including treatment choices and side effects of this disease have an effect on the treatment decision. Being aware of results of SDMs can increase the options of the care of cancer patients (Lee et al., 2010).

Key et al. Studied epidemiology of breast cancer (2001). Breast cancer is the commonest cause of cancer death in women worldwide. Rates vary about five-fold around the 9onit, but they are increasing in regions that until recently had low rates of the disease. Many of the established risk factors are linked to oestrogens. Risk is increased by early menarche, late menopause, and obesity in postmenopausal women, and prospective studies have shown that high concentrations of endogenous oestradiol

are associated with an increase in risk. Childbearing reduces risk, with greater protection for early first birth and a larger number of births; breastfeeding probably has a protective effect. Both oral contraceptives and hormonal therapy for menopause cause a small increase in breast-cancer risk, which appears to diminish once use stops. Alcohol increases risk, whereas physical activity is probably protective. Mutations in certain genes greatly increase breast cancer risk, but these account for a minority of cases. Studies of the epidemiology of breast cancer have established that hormonal factors have a key role in the causation of this disease. Factors that increase exposure to oestrogens increase risk, and studies in postmenopausal women have shown a direct association between high oestradiol concentrations and breast-cancer risk. The low rates of breast cancer in some populations are to a substantial extent to conditions that are not realistic or desirable for more developed countries – late menarche, young age at first birth, and high parity. Feasible changes in risk factors, such as obesity, alcohol consumption, breastfeeding, and physical activity, could yield important reductions in breast cancer risk. Further progress may come from the identification of new, modifiable lifestyle (especially dietary) risk factors. Trials such as those of tamoxifen and other selective oestrogen-receptor modulators may result in effective methods for chemoprevention of breast cancer (Key et al., 2001).

Li et al. Made a statistical analysis of different types of breast cancer according to their sample (2005). Breast cancer is a heterogeneous disease, though little is known about some of its rarer forms, including certain histologic types. Using Surveillance, Epidemiology, and End Results Program data on 135157 invasive breast cancer cases diagnosed from 1992 to 2001, relationships between nine histologic types of breast cancer and various tumor characteristics were assessed. Among women aged 50–89 years at diagnosis, lobular and ductal/lobular carcinoma cases were more likely to be diagnosed with stage III/IV, ≥ 5.0 cm, and node-positive tumors compared to ductal carcinoma cases. Mucinous, comedo, tubular, and medullary carcinomas were less likely to present at an advanced stage. Lobular, ductal/lobular, mucinous, tubular, and papillary carcinomas were less likely, and comedo, medullary, and inflammatory carcinomas were more likely to be oestrogen receptor (ER) negative/progesterone receptor (PR) negative and high grade (notably, 68.2% of medullary carcinomas were ER-/PR- vs 19.3% of ductal carcinomas). In general, similar differences were observed among women diagnosed at age 30–49 years. Inflammatory carcinomas are associated

with more aggressive tumour phenotypes, and mucinous, tubular, and papillary tumors are associated with less aggressive phenotypes. The histologic types of breast cancer studied here differ greatly in their clinical presentations, and the differences in their hormone receptor profiles and grades point to their likely different aetiologies (Li et al., 2005). Another study is done by Dent et al., to compare triple-negative and other breast cancer types (2007). To compare the clinical features, natural history, and outcomes for women with “triple-negative” breast cancer with women with other types of breast cancer. They studied a cohort of 1,601 patients with breast cancer, diagnosed between January 1987 and December 1997 at Women’s College Hospital in Toronto. Triple negative breast cancers were defined as those that were estrogen receptor negative, progesterone receptor negative, and HER2neu negative. The prognostic significance of triple-negative breast cancer was explored. The median follow-up time of the 1,601 women was 8.1 years. One hundred and eighty of 1,601 patients (11.2%) had triple-negative breast cancer. Compared with other women with breast cancer, those with triple-negative breast cancer had an increased likelihood of distant recurrence (hazard ratio, 2.6; 95% confidence interval, 2.0-3.5; $P < 0.0001$) and death (hazard ratio, 3.2; 95% confidence interval, 2.3-4.5; $P < 0.001$) within 5 years of diagnosis but not thereafter. The pattern of recurrence was also qualitatively different; among the triple-negative group, the risk of distant recurrence peaked at 3 years and declined rapidly thereafter. Among the “other” group, the recurrence risk seemed to be constant over the period of follow-up. Triple-negative breast cancers have a more aggressive clinical course than other forms of breast cancer, but the adverse effect is transient (Dent et al., 2007).

2.2 Lean Management in Healthcare

Lean manufacturing, which is also called the “Toyota Production System (TPS)” was a new process-driven production system in the industry, founded by Japanese leaders (Abdulmalek and Rajgopal, 2007). The main aim of lean manufacturing is to eliminate the “waste” while increasing the quality of the product (Sundar et al., 2014). Waste types can be classified in eight different ways: producing more than the need, inventory, defects, waiting, transportation, extra motions, non-value added activities and the unused human ability. These waste cost nearly 95 percent of the whole production cost which is mentioned by Taiichi Ohno who is one of the leaders

of TPS (Kilpatrick, 2003). Main action of TPS is to eliminate different types of waste, such as defective products, inventory, transportation, waiting, movement and overproduction (Ohno, 1988). Lean principles mainly aim to make a sustainable production line while eliminating nonvalue added activities. This line has to work with customer orders which mean a pull system (Sundar et al., 2014). In August 1997, a non-profit organization “Lean Enterprise Institute, Inc.” Was founded by James P. Womack. He aimed to explain lean thinking in accordance with the Toyota system which is being used by many different sectors spread wide (Lean Enterprise Institute, 2000). In a production line, lean manufacturing aims to create a high-quality product and an on-time shipment to the customer. In Canada, these lean principles are concerned for healthcare systems because of the excess patient amount (Ng et al., 2010). Recovery of the patient is the total of the value created in the medical service. 12onitör12 reason, as mentioned for production line, also in healthcare sector, the process has to be customer based, that means patient based at a hospital (Kujala et al., 2006). In a healthcare system, to reach a “perfect” medical experience, delays, waiting times in a queue, unnecessary repeating actions and false applications should be eliminated or at least minimized. When lean principles are adapted to healthcare systems to create value, some issues have to be considered such as patients, taxpayers and service providers’ equality and the legal issues for costing while reaching the required pleasant level for patients. Even though every process in a production line is known by its standards, in a service line especially at a hospital, patients’ road is not clear due to different examination results. This uncertainty causes more complicated systems to be analyzed (Young et al., 2004). Waste definition differs from sector to sector so that when healthcare systems are considered, mostly documentation causes “waste.” Also the whole process flows and the hardware of the hospital can yield non-value added activities (Campbell, 2009).

2.3 Artificial Intelligence (AI) in Cancer Treatment

In this section, artificial intelligence applications about cancer treatment and cancer studies are presented chronologically. Firstly, in 2021, Bhinder et al. (2021) discussed the AI application effects in cancer care nowadays and implied the characterization of predictions and treatments for tumours. Cirillo et al. (2021) reviewed artificial intelligence techniques for being used in cancer researches and proposed a solution for

AI applications in heterogeneous parts and data granularity in cancer research. Yu and Helwig (2021) performed a systematic literature review for understanding the role of AI in gastric cancer and stomach cancer. In cancer biopsies, Ström et al. (2020) explained artificial intelligence importance in a population-based approach in order to investigate diagnosis and grading in prostate cancers. Also, in 2020, Pantanowitz et al. (2020) assessed prostate core needle biopsies' developments by computer aided approaches, especially AI techniques, by an AI detection algorithm. In the same area, another population-based study in prostate cancer in biopsies, has been done by Zlotta and Sadeghian (2020) criticizing the diagnostic studies by the aid of AI applications. As a late study, not only Madabhushi et al. (2020) used AI application, especially deep learning algorithms, for detection of cancer morphology for Gleason scoring in tumour issues but also Thomas (2020) compared AI and deep learning applications in automated Gleason grading of prostate tumors. Patel et al. (2020) overviewed the latest studies about AI application in lung breast and liver cancers' diagnosis. Troyanskaya et al. (2020) have discussed the future opportunities of AI applications in cancer diagnosis and cure in the literature which transforms the current methods to different methods by the help of AI. In the same year, Huang et al. (2020) tried to understand the developments in AI in order to assist cancer diagnosis, prognosis and contribution the AI applications to human health. Another study in 2020, done by Ho (2020), investigated machine learning, artificial intelligence and neural network applications and practices in cancer therapy. Furthermore, Coccia (2020) evaluated deep learning applications in cancer imaging and care by Amara's law and their radical changes in curing and diagnostics. As one of the latest studies, Liang et al. (2020) presented a study about artificial intelligence applications for drug therapy for cancer and mainly concluded that AI can improve the detection of tumours. Jin et al. (2020) reviewed the studies about artificial intelligence applications in gastric cancer in order to observe the limitations and directions for future. One of different cancer types, which is oral cancer, has been studied by Ilhan et al. (2020) investigating AI application and techniques for imaging modalities and applicability in oral cancer by a literature review. Another literature review study has been performed by Niu et al. (2020) for AI applications via gastric cancer in recent years' studies. Moreover, for oesophageal cancer types, AI aided applications in diagnostic, therapeutic parts of curing by a literature review have been done by Zhang et al. (2020). Ikeda et al. (2020) used convolutional neural networks, an artificial intelligence technique, for

classifying tumour lesions images and normal tissues for bladder cancer. Akazawa and Hashimoto (2020) used artificial intelligence for ovarian tumors in order to estimate the pathological diagnosis and integrated it by machine learning algorithms. Furthermore, Shimizu and Nakayama (2020) have tried to systematically review AI applications in oncology area and investigated the important perspective in the studies for cancer research. Another application of convolutional neural networks has been done for pharyngeal cancer detection by Tamashiro et al (2020) for evaluation of prognosis and diagnosis. For laryngopharyngeal cancer type, an artificial intelligence technique for detection has been used by Inaba et al. (2020) by a newly model of AI in a narrow-band imaging by integrating AI with deep-learning.

For lung cancer application of AI, Wang et al. (2019) analyzed pathology imaging by AI methods' studies in the literature for understanding the effect of AI on lung cancer imaging. Horie et al. (2019) used AI for oesophageal cancer detection and diagnosis in Japan for three types of tumours including carcinoma, adenocarcinoma and squamous cells. Harmon et al. (2019) assessed pathological grading in prostate cancer by AI applications in detection and curing by a literature review. At the same year, in gastrointestinal cancer area, Luo et al. (2019) used artificial intelligence for detection and diagnosis for upper gastrointestinal cancers. In breast cancer area, Sheth and Giger (2019) evaluated AI application in imaging process, also named as computer aided detection, for prognosis and tumoral phenotypes and its integration in clinical genotype and risk prediction. Moreover, Liu et al. (2019) integrated AI application and black-box simulation for breast cancer nodal metastasis detection and evaluated clinical implementation of deep learning based artificial intelligence techniques. Talari et al. (2019) evaluated machine learning applications and artificial intelligence techniques integrating with Raman Spectroscopy for obtaining a better medical diagnosis in breast cancer. Different study about breast cancer detection by mammography and AI applications has been done by Rodriguez-Ruiz et al. (2019) by multi-case study with 101 radiologists. In skin cancer detection application via AI, Hekler et al. (2019) described artificial intelligence techniques for skin cancer patterns and the combination of human effect and AI effect accuracy, which is up to 92,95%. In the same area of skin cancer, Brinker et al. (2019) published a study that German dermatologists compared artificial intelligence techniques for melanoma types of skin cancer by imageable and non-imageable types by questionnaire. Nagarajan et al. (2019)

integrated computational biology and artificial intelligence for cancer precision drug discovery studies by a systematic review. Another AI study in cancer treatment and diagnosis by AI application has been done by Goldenberg et al. (2019) for prostate cancer implying increasing power of AI and machine learning in cancer treatment and diagnosis. Again, in BC, Houssami et al. (2019) investigated whether AI application in oncology department can be accurate for detection of breast cancer in a large-scale population or not. Lamy et al. (2019) used Case-Based reasoning classification with a black-box algorithm for breast cancer detection and management the process. Linda Bi et al. (2018) reviewed the current studies about cancer imaging by the aid of Artificial Intelligence methods and techniques for radiographic detection and management. In 2018, Hirasawa et al. (2018) used artificial intelligence techniques and neural networks in gastric cancer detection by endoscopic images and developed a convolutional neural network model for detection.

On the other hand, for cell lung cancers, Rabbani et al. (2018) reviewed artificial intelligence and machine learning applications in lung cancer studies for current applications in diagnostics and cure. Misawa et al. (2018) expressed artificial intelligence techniques for polyp detection for adenoma by colonoscopy. Another study in breast cancer detection, Rodriguez-Ruiz et al. (2018) investigated artificial intelligence efficiency in breast cancer detection with mammography by a statistical analysis. Houssami et al. (2017) evaluated breast cancer detection by AI techniques compared to mammography. Golden (2017) used deep learning algorithm for lymph cancer metastases from breast cancer detection by a computer aided approach. Hu et al. (2013) presented the studies artificial neural network application in prostate cancer management and diagnosis in the 15onitör15re. A different study is presented by Abbod (2007) reviewing the aid of artificial intelligence including Bayesian belief networks and neuro fuzzy modelling systems in urological cancers. Catto et al. (2003) compared artificial intelligence models by a statistical analysis and concluded that neuro-fuzzy models for bladder cancer is the mostly used one.

2.4 Machine Learning Applications in Breast Cancer

El Naqa and Murphy studied machine learning in cancer treatment (2015). Machine learning is a rapidly developing field of computational algorithms that aim to replicate human intelligence by acquiring knowledge from the surrounding environment. In the

era of big data, machine learning techniques have become indispensable and have found successful applications in various domains such as pattern recognition, computer vision, spacecraft engineering, finance, entertainment, computational biology, as well as biomedical and medical fields. In cancer treatment, more than half of the patients undergo radiotherapy, which is a primary modality for advanced stages of local disease. Radiotherapy involves a complex set of processes that encompass not only the consultation and treatment stages but also extend to ensure accurate delivery of the prescribed radiation dose and patient response assessment. These processes involve intricate human-machine interactions and decision-making, making it conducive to leveraging machine learning algorithms for optimization and automation. These algorithms can be applied to various aspects of radiotherapy, including radiation physics quality assurance, contouring and treatment planning, image-guided radiotherapy, respiratory motion management, treatment response modeling, and outcomes prediction. By utilizing machine learning algorithms, there is potential to enhance the safety and effectiveness of radiotherapy practice, ultimately leading to improved patient outcomes (El Naqa and Murphy, 2015).

Shinde and Shah conducted a paper using deep learning techniques (2018). Machine learning is a prominent field in modern computing, with extensive research focused on imbuing machines with intelligence. Learning, a fundamental human behavior, has been integrated into machines as well, with various techniques developed for this purpose. Traditional machine learning algorithms have been widely applied across different domains, and researchers have made significant efforts to enhance their accuracy. Furthermore, the emergence of deep learning, a subset of machine learning, has opened up new possibilities. Although deep learning is still in its early stages, it shows great potential in addressing challenges across various application domains and sub-domains. This paper provides a review of past and future applications of machine learning and deep learning, exploring their diverse application areas and sub-domains (Shinde and Shah, 2018).

Another study is conducted by Mahesh in terms of machine learning algorithms (2020). Machine learning (ML) is a field of study that focuses on algorithms and statistical models used by computer systems to perform specific tasks without explicit programming. Learning algorithms are utilized in various everyday applications, such as web search engines like Google, which effectively rank web pages through learned

algorithms. Machine learning algorithms find applications in diverse areas, including data mining, image processing, predictive analytics, and more. One of the key advantages of machine learning is its ability to automate tasks once an algorithm has learned how to handle the associated data. This paper provides a concise overview and **prospects** of the extensive range of applications for machine learning algorithms (Mahesh, 2020). Figure 2.3 shows the classification of machine learning algorithms (Mahesh, 2020).

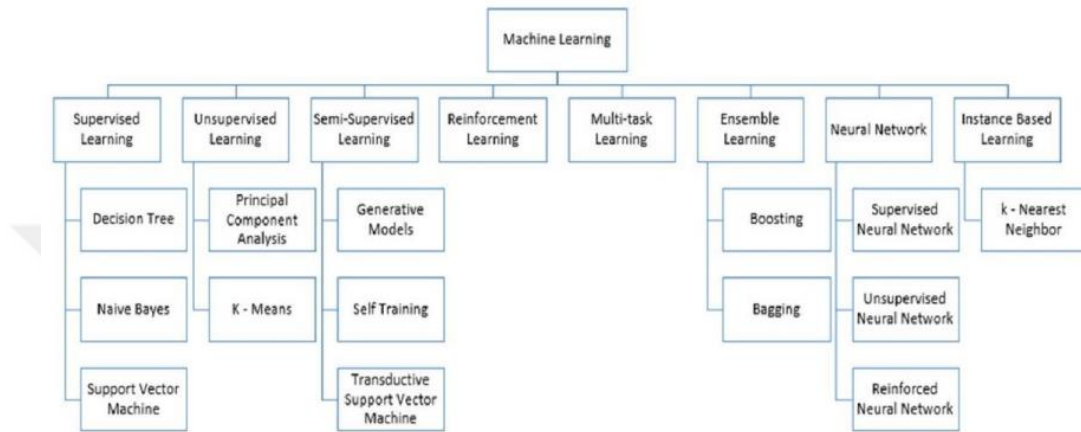


Figure 2.3 : Machine learning classification.

The quantity and size of medical databases are growing rapidly, yet much of this data remains unexplored in terms of discovering valuable and hidden knowledge. Advanced data mining techniques offer the potential to uncover hidden patterns and relationships within these datasets. The utilization of predictive models developed from these techniques can assist medical practitioners in making informed decisions. In this particular study, data mining techniques were employed to develop predictive models for breast cancer recurrence among patients who were followed up for a two-year period. The patients included in the study were registered in the Iranian Center for Breast Cancer (ICBC) program between 1997 and 2008. The dataset consisted of 1189 records, with 22 predictor variables and one outcome variable. Machine learning techniques, specifically Decision Tree (C4.5), Support Vector Machine (SVM), and Artificial Neural Network (ANN), were implemented to develop the predictive models. The primary objective of this paper is to compare the performance of these three well-known algorithms using sensitivity, specificity, and accuracy metrics on our dataset. The analysis revealed that the accuracy values for DT, ANN, and SVM were 0.936, 0.947, and 0.957, respectively. The SVM classification model demonstrated the

highest accuracy and the lowest error rate in predicting breast cancer recurrence, while the DT model had the lowest predicted accuracy. To ensure unbiased prediction accuracy, 10-fold cross-validation was employed in measuring the performance of each model (Ahmad et al., 2013).

Breast cancer (BC) is a prevalent form of cancer among women worldwide and accounts for a significant proportion of new cancer cases and cancer-related deaths. It poses a significant public health challenge in today's society. Timely diagnosis of BC plays a crucial role in improving patient prognosis and survival rates by enabling prompt clinical intervention. Additionally, accurate classification of benign tumors can help prevent unnecessary treatments. As a result, there is considerable research focused on achieving precise BC diagnosis and patient classification into malignant or benign groups. Machine learning (ML) is widely acknowledged as the preferred methodology for BC pattern classification and predictive modeling due to its unique ability to detect critical features from complex BC datasets. In this paper, our objective is to review various ML techniques and their applications in BC diagnosis and prognosis. We provide an overview of ML techniques such as artificial neural networks (ANNs), support vector machines (SVMs), decision trees (DTs), and k-nearest neighbors (k-NNs). Furthermore, we explore their specific applications in BC. To compare results obtained through different algorithms, we primarily utilize data from the Wisconsin breast cancer database (WBCD), which serves as a benchmark database. Lastly, we showcase a healthcare system model based on our recent work (Yue et al., 2018).

3. METHODOLOGY

3.1 Process Improvement

3.1.1 Process flow map

Process mapping is a visual representation accompanied by explanatory descriptions that depict how tasks are carried out. Its purpose is to help participants gain a clear understanding of the process and facilitate decision-making. By utilizing process mapping, individuals can identify the primary strengths and weaknesses within the current process, as well as recognize the significance of each individual step. Additionally, it aids in reducing the duration of cycles and the occurrence of defects, ultimately improving productivity. The key elements of a process map encompass the inputs, outputs, and the sequential steps involved. A well-executed process map should demonstrate the workflow and the interactions within the organization, employing commonly understood symbols to ensure clarity for all stakeholders. An ideal process map should provide thorough details concerning multiple paths, decision points, and instances of rework (URL-4). Flowchart symbols are given in Figure 3.1 (URL-5).

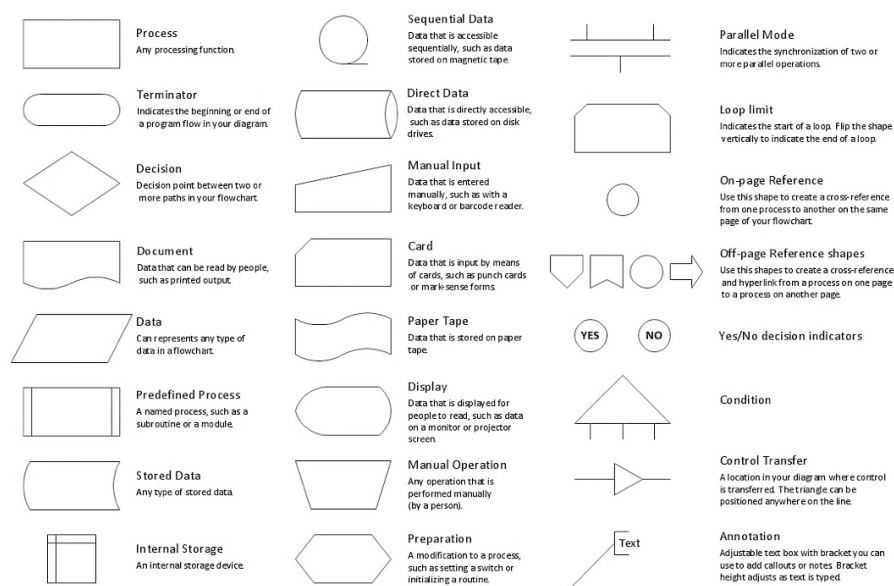


Figure 3.1 : Flowchart symbols.

3.1.2 Value stream mapping

Implementing lean principles starts with the analysis of current situation to classify value added and non-value added activities. VSM is one of the most efficient way to do this classification. The map shows the whole process of the production or service line with symbols. Its minimal structure is mainly related to “lean thinking.” The process drawn in the value stream map starts from the beginning that raw materials come from suppliers, and ends at the shipping department. The expert which draws the map, follows both the production steps and information flow at a random time and captures that moment. This map is called “current state map” (Gahagan, 2007). Current state map shows the bottlenecks on a one 20onitör. With lean principles, these problems which are classified as non-value added activities, should be eliminated or improved. After eliminating those “waste” improvement areas are shown in “future state map” (Rahani and Al-Ashraf, 2012). One of the key applications of lean management is VSM. It helps to identify each process step at an organization. This map makes all actors at the supply chain, to understand the production or service process line and with the elimination of non-value added activities to improve it. Workers from different actors should come together to study on VSM to improve the process via lean thinking. VSM should be very detailed 20onitör every kind of non-value added activities to make a big change in the whole 20onitör. These small activities have to be decided if they add any value to the patient in a hospital process or not. If the activity creates a value then it should remain in the process flow. After current state analysis, future maps are drawn to see the improvement and this step should be repeated to reach ideal state (Gellad and Day, 2016). VSM is being used in different areas also for healthcare systems. Hoffmann studied HIV services to observe medical processing time for each step in South Africa (Hoffmann et al., 2018). Ramaswamy studied at Kenya, for quality improvement of a healthcare system with the light of lean principles and VSM (Ramaswamy et al., 2017).

3.2 Breast Cancer Data Analysis

In this part of the thesis, our methodology including classification, regression trees, artificial neural networks (ANN) and logistic regression used in the thesis will be explained in detail. These algorithms have been compared for measuring the accuracy for each technique and determining the optimal forecasting and classification

algorithm. With the help of decision trees and logistic regression, attributes effecting breast cancer occurrence will be ranked due to their weights. Also ANN will be trained and tested with these attributes to be able to find out a patient with high risk of breast cancer.

In general, classification and regression trees serve as machine-learning techniques employed to generate predictive models from given datasets. These models are crafted through iterative partitioning of the dataset and subsequent fitting of basic prediction models within each partition (Loh, 2011). This iterative process culminates in the graphical representation of partitioning known as a decision tree. Classification trees are tailored for dependent variables characterized by a finite number of unordered values, where prediction accuracy is gauged by the cost associated with misclassification. Conversely, regression trees are geared towards dependent variables exhibiting continuous or ordered discrete values, wherein prediction accuracy is conventionally assessed through the squared disparity between observed and predicted values. (Loh, 2014).

On the other hand, the artificial neural network (ANN), commonly referred to as a neural network, represents a machine learning paradigm inspired by the structure and functioning of the human brain (Zou et al., 2009). With the proliferation of data in contemporary drug discovery endeavours, there exists a pressing need for sophisticated analytical techniques to elucidate intricate causal connections between individual or multiple responses and an extensive array of properties (Hassoun, 1995). Priddy and Keller (2005) stated that the ANN stands out among various adaptable methodologies, addressing this demand within the realm of drug discovery modelling. Contrasted with conventional regression methodologies, the ANN excels in capturing intricate nonlinear associations. Moreover, the ANN demonstrates remarkable fault tolerance and boasts rapid processing capabilities, further augmented by its inherent scalability through parallel processing architectures (Graupe, 2013). Now, in this section, we provide a general overview of each method employed in our thesis.

3.2.1 The synthetic minority oversampling technique (SMOTE)

Imbalance in data classification frequently emerges in various practical scenarios within medical pattern recognition and data mining. Many prevailing cutting-edge classification methodologies are primarily designed under the assumption of a

uniformly distributed training dataset (Wang et al., 2006). However, Gu et al. (2008) stated that to assess the classification efficacy of imbalanced datasets, traditional accuracy metrics are unsuitable since they prioritize the majority class and may not adequately reflect the performance on the minority class due to its lesser impact on overall accuracy.

In existing literature, the predominant focus has been on addressing this issue by enhancing classification performance on imbalanced datasets. Many researchers have employed Synthetic Minority Over-sampling Technique (SMOTE), presented firstly by Chawla et al. (2002), as a means to rebalance the data distribution (Jeatrakul et al., 2010; Torgo et al., 2013). SMOTE, categorized as an over-sampling technique, functions by augmenting the number of minority class instances through an interpolation method. It identifies clusters of minority class instances in proximity to one another and employs them to generate new instances for the minority class. By creating synthetic instances instead of simply replicating existing minority class instances, SMOTE mitigates the risk of overfitting (Jeatrakul et al., 2010; Wang et al., 2021; Jiang et al., 2016).

Many scholars in ML field state that in medical data, the quantity of information contained within minority samples typically falls short in comparison to the abundance of information present in majority samples. Consequently, the information from minority samples becomes overshadowed by the dominance of majority samples, leading to a substantial incidence of misclassification (Polat, 2018; Xu et al., 2021; Giraldo-Forero et al., 2013). In that sense, Dietterich (2000) concluded that misclassifying a patient as a healthy individual in disease diagnosis incurs significantly higher costs compared to misclassifying a healthy individual as a patient.

Moreover, within medical data analysis, SMOTE has gained widespread acceptance owing to its efficacy in achieving high accuracy when dealing with imbalanced datasets (Xu et al., 2021). Primarily, the SMOTE algorithm identifies boundary samples within the minority class to linearly interpolate, thereby generating synthetic samples that facilitate more effective learning. The underlying hypothesis of SMOTE is that points situated between two closely located negative class points still belong to the negative class. Therefore, SMOTE endeavours to synthesize new negative samples by interpolating among neighbouring negative class samples (Xue and Zhang, 2021).

As per SMOTE methodology, the generation of new synthetic negative class samples follows these steps (Chawla et al., 2002).

1. Determining the sample rate, denoted as m .
2. For each negative class sample, presented as x_i , calculating its k nearest neighbours
3. Randomly selecting m nearest neighbours denoted as y_{ij} , where $j = 1, 2, \dots, m$
4. Finally, synthesising new points denoted as p_j as given in the Equation 3.1.

$$p_j = x_i + rand(0,1)x(y_{ij} - x_i) \quad (3.1)$$

By integrating the newly generated synthetic negative class samples with the original dataset, a re-sampled training set is obtained, thereby substantially improving the degree of imbalance present in the original dataset (Xue and Zhang, 2012).

A graphical illustration about SMOTE technique can be seen as given in Figure 3.2 (Xu et al., 2021).

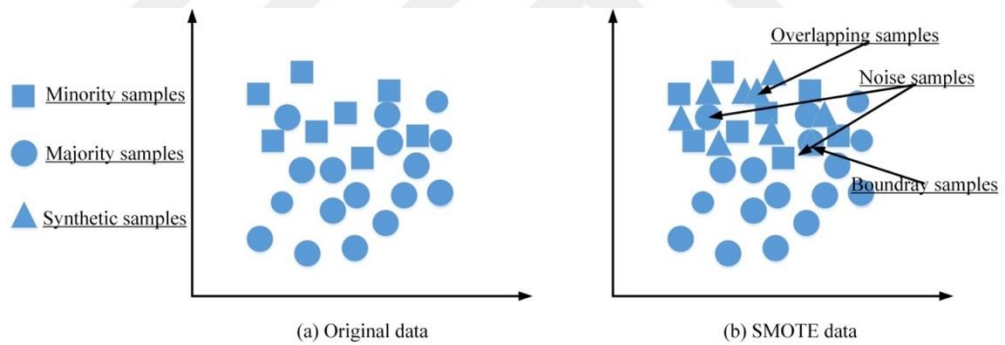


Figure 3.2 : Illustration about balancing the data by SMOTE.

3.2.2 Classification Algorithms and Regression Trees

When we advocate to use Classification and Regression Trees (CaRTs) in our thesis, the specific reason why CaRTs are suitable to determine the accuracy of forecasting breast cancer patterns is stated in the literature widely. Speybroech (2012) stated in medical area that CaRTs represent powerful analytical tools for exploring complex relationships. They facilitate analysis of both categorical (leading to classification trees) and continuous health outcomes (resulting in regression trees). For instance, a classification tree (CT) may be employed to predict a binary health outcome, such as disease status (diseased or healthy). The construction of a CT commences with a parent node encompassing all individuals in the dataset. Subsequently, the dataset is

partitioned at a designated value along a variable's range, thereby generating two child nodes characterized by enhanced homogeneity (purity) compared to the parent node.

Another pertinent example is found in the study conducted by Kurt et al. (2008), where they undertook a comparative analysis of classification techniques to predict the presence of coronary artery disease (CAD). As another example, in their comprehensive study, Khemphila and Boonjing (2010) conducted an exhaustive analysis to predict the likelihood of patients developing heart disease by comparing the performance of various classification techniques. The retrospective analysis encompassed 303 subjects and scrutinized the efficacy of logistic regression (LR), decision trees (DTs), and Artificial Neural Networks (ANNs). The variables considered in the analysis included medical profiles such as age, sex, chest pain type, blood pressure, cholesterol levels, fasting blood sugar, resting electrocardiogram (ECG) results, maximum heart rate, presence of induced angina, ST depression induced by exercise relative to rest (ST depression), slope of the peak exercise ST segment, number of major vessels colored by fluoroscopy (number of colored vessels), Thalassemia type (Thal), and the concept class. Through meticulous examination of these variables, the study aimed to shed light on the most effective approach for predicting heart disease, offering valuable insights for clinical decision-making in cardiovascular health. In this context, Amiri and Armano (2013) employed Classification and Regression Trees to develop a heart sounds diagnostic system aimed at assisting physicians in patient auscultation. The system's objective was to decrease the incidence of unnecessary echocardiograms and prevent the premature discharge of newborns affected by heart disease. Furthermore, Maghooli et al. (2016) endeavored to utilize the Classification and Regression Tree (CART) methodology to predict the differential diagnosis of Esophageal Squamous Dysplasia (ESD). Schilling et al. (2016) conducted a robust analysis utilizing Classification and Regression Trees (CART) to dissect the prescribing patterns of Australian general practitioners (GPs) concerning primary prevention strategies for cardiovascular disease (CVD). Their study aimed at discerning whether GPs exhibit a preference for absolute risk (AR) guidelines over individual risk factors when making critical prescribing decisions regarding lipid-lowering medications. By leveraging CART, renowned for its ability to unveil intricate relationships within complex datasets, their research offers valuable insights into the decision-making processes of healthcare professionals in the realm of

CVD prevention. As one of the latest researches related to medical forecasting and classification algorithms, Ozcan and Peker (2023) utilized the Classification and Regression Tree (CART) algorithm, a supervised machine learning method, to predict heart disease and elucidate decision rules, thereby illuminating the relationships between input and output variables. Furthermore, the study's outcomes delineated the importance of features influencing heart disease through ranking analysis.

Now, we'll introduce preliminaries related to classification algorithms and regression trees by the study of Dobra (2002) and Breiman et al. (1984) for our thesis.

3.2.2.1 Classification Algorithms

Let $X_1, \dots, X_m, C$ be random variables where X_i having a domain $\text{Dom}(X_i)$. The random variable C having $\text{Dom}(C) = \{1, \dots, J\}$. Let $X_1 \dots X_m$ be predictor attributes and C the class label that these variables represent predictor attributes (m is the number of predictor attributes) and the class label, respectively. (Dobra, 2002)

A classifier $\mathcal{C}$ is a function $\mathcal{C}: \text{Dom}(X_1) \times \dots \times \text{Dom}(X_m) \mapsto \text{Dom}(C)$. The set of events is denoted by $\Omega = \text{Dom}(X_1) \times \dots \times \text{Dom}(X_m) \times \text{Dom}(C)$

If we consider classifier $\mathcal{C}$ and a probability measure denoted as P over Ω 25onitör redefine functional $R_P(\mathcal{C}) = P[\mathcal{C}(X_1, \dots, X_n) \neq C]$ called as the misclassification rate of the classifier $\mathcal{C}$.

Classifier Construction Problem is stated as given a training dataset D of N independent identically distributed samples from Ω , sampled according to probability distribution P , find a function $\mathcal{C}$ that minimizes the functional $R_P(\mathcal{C})$, where P is the probability distribution used to generate D (Dobra, 2002)

A decision tree is a type of classifier represented as a directed acyclic graph $\mathcal{T}$. The root of the tree (denoted by $\text{Root}(\mathcal{T})$) does not have any incoming edges. Each external node is labelled exactly one incoming edge and may have 0,2 or more outgoing edges. We call a node T without outgoing edges a leaf node, otherwise T is called an internal node. Each leaf node is labeled with one class label; each internal node T is labeled with one predictor attribute $X_T, X_T \in \{X_1, \dots, X_m\}$ called the split attribute. We denote the label of node T by $\text{Label}(T)$ (Dobra, 2002).

Each edge (T, T') from an internal node T to one of its children T' has a predicate $q_{(T, T')}$ associated with it where $q_{(T, T')}$ involves only the splitting attribute X_T of node

n . The set of predicates Q_Y on the outgoing edges of an internal node T must be non-overlapping and exhaustive. A set of predicates Q is non-overlapping if the conjunction of any two predicates in Q evaluates to false. A set of predicates Q is exhaustive if the disjunction of all predicates in Q evaluates to true. We will call the set of predicates Q_T on the outgoing edges of an internal node T the splitting predicates of T ; the combined information of splitting attribute and splitting predicates is called the splitting criteria of T and is denoted by $\text{crit}(T)$.

Given a decision tree $\mathcal{T}$, we define the associated classifier recursively as given in (3.2) and (3.3).

$$\mathcal{C}(x_1, \dots, x_m, T) = \begin{cases} \text{Label}(T) & \text{if } T \text{ is a leaf node} \\ \mathcal{C}(x_1, \dots, x_m, T_j) & \text{if } T \text{ is an internal node, } X_i \text{ is label of } T, \text{ and} \\ & q_{(T, T_j)}(x_i) = \text{true} \end{cases} \quad (3.2)$$

$$\mathcal{D}_{\mathcal{T}}(x_1, \dots, x_m) = \mathcal{C}(x_1, \dots, x_m, \text{Root}(\mathcal{T})) \quad (3.3)$$

With precision and clarity, we designate the constructed function $\mathcal{D}_{\mathcal{T}}(\cdot)$ as a classifier, which we term a decision tree classifier, or simply, a classification tree. With this foundation, we proceed to formally delineate the problem of classification tree construction:

Classification Tree Construction Problem: Given a dataset $D = \{\omega_1, \dots, \omega_N\}$ where the ω_i are independent identically distributed random samples from a probability distribution P over Ω , find a classification tree $\mathcal{T}$ such that the misclassification rate functional $R_P(\mathcal{D}_{\mathcal{T}})$ is minimized.

Input: node T , data-partition D , split selection method $\mathcal{V}$

Output: classification tree $\mathcal{T}$ for D rooted at T

Top-Down Classification Tree Induction Schema:

BuildTree (Node T , data-partition D , split attribute selection method $\mathcal{V}$) (Dobra, 2002).

3.2.2.2 Regression Trees

Trees elucidate the variation of a single response variable through one or more explanatory variables. The response variable typically falls into one of two categories: categorical (for classification trees) or numeric (for regression trees), while the explanatory variables can encompass both categorical and numeric attributes (De'ath

and Fabricius,2000) Construction of the tree involves iterative data splitting, guided by simple rules based on individual explanatory variables. At each split, the dataset is divided into two distinct groups, each aiming for maximum homogeneity (Sutton, 2005). This splitting process is subsequently applied independently to each subgroup. The primary objective is twofold: to partition the response variable into homogeneous groups while maintaining the tree's size within reasonable bounds (Wilkinson, 2004). The size of the tree corresponds to the number of final groups. The splitting continues until an excessively large tree is generated, which is then pruned to achieve the desired size. Each group is typically characterized by its distribution (for categorical response) or mean value (for numeric response) of the response variable, along with group size and the values of explanatory variables defining it (Berk, 2008)

Trees stand as powerful tools for dynamic exploration, offering adept descriptions and predictions of patterns and processes. Their advantages are manifold (De'ath and Fabricius,2000):

1. **Adaptability:** Trees exhibit remarkable flexibility, accommodating a diverse spectrum of response types, from numeric to categorical, ratings, and even survival data.
2. **Robustness:** They maintain their integrity even in the face of monotonic transformations of explanatory variables, ensuring reliable performance across varied data landscapes.
3. **Simplicity and Efficiency:** Constructing trees is characterized by ease and robustness, making them accessible even to users with limited statistical expertise.
4. **Interpretability:** The intuitive nature of trees facilitates straightforward interpretation, enabling stakeholders to glean actionable insights effortlessly.
5. **Handling Missing Values:** Their innate capability to handle missing values in both response and explanatory variables adds to their allure, ensuring comprehensive data utilization (Berk, 2008).

In essence, trees emerge as not just complementary but formidable contenders against traditional statistical techniques like multiple regression, analysis of variance, logistic regression, log-linear models, linear discriminant analysis, and survival models. They offer a compelling alternative, marrying versatility with interpretability, thereby empowering analysts to extract profound insights from complex datasets (Berk, 2008).

The primary advantage of employing a hierarchical tree structure for classification decisions is its transparency, rendering it simpler to interpret compared to artificial neural networks (ANNs). To induce the decision tree (DT) from a dataset, an evaluation measure of each of the evidential features is utilized to maximize the inter-node heterogeneity (Rodriguez-Galiano et al., 2015; Breiman, 2017).

Two distinct methodologies are discernible within decision trees (DT): classification trees and regression trees (RT) (Yang et al., 2017). To induce the DT, recursive partitioning and multiple regressions are conducted on the dataset. Starting from the root node, the process of data splitting at each internal node of the tree proceeds according to a set of rules until a predetermined stop condition is met. Each terminal node, or leaf, is associated with a simple regression model applicable only within that node. Upon completion of the tree's induction process, pruning may be employed to enhance the tree's generalization ability by reducing its structural complexity. The number of cases in nodes can serve as a pruning criterion (Kern et al., 2019)

As outlined by Breiman et al. (1984), the induction of decision trees (DT) begins with the selection of optimal splitting criteria. Initially, the process entails partitioning the dependent feature, or the parent node (root), into binary segments, wherein the child nodes exhibit greater 'purity' than the parent node. Throughout this iterative procedure, decision trees explore all potential splits to identify the optimal split, denoted as s^* , which maximizes the 'purity' of the resultant tree. This purity is defined by the largest decrease in impurity, ultimately guiding the construction of an effective decision tree model. Equation 3.4 shows the general equation defined by Breiman et al. (1984) for regression trees.

$$\Delta i(s, t) = i(t) - p_L i(t_L) - p_R i(t_R) \quad (3.4)$$

In this equation, s represents split at node t , and the node t is partitioned by s into the left child node t_L with a proportion of p_L , and right child node t_R with a proportion of p_R . $i(t)$ denotes the measure of impurity before splitting, $i(t_L)$ and $i(t_R)$ are measures of impurity after splitting, and $\Delta i(s, t)$ measures the decrease in impurity from split s (Kern et al., 2019).

Numerous methodologies exist for gauging impurity within decision trees, each offering its unique approach to quantifying uncertainty. Among these, prominent techniques such as the gain-ratio (Quinlan, 1993), Gini index (Breiman et al., 1984),

and Chi-square (Mingers, 1989) stand out. However, it is the Gini index that reigns supreme as the go-to measure in many studies. In this research, the Gini index emerges as the cornerstone for evaluating impurity, denoted as $i(t)$ as and epitomizes the quintessential metric for assessing classification accuracy and purity within decision trees. Equation 3.5 shows the main equation for this classification.

$$I_G(t_{X(x_i)}) = 1 - \sum_{j=1}^m f(t_{X(x_i)}, j)^2 \quad (3.5)$$

In this context, $f(t_{X(x_i)}, j)$ denotes the proportion of samples with the value x_i belonging to leave j as node t . The decision tree's splitting criterion hinges on selecting the attribute with the minimal Gini impurity index (I_G). His strategic approach underscores the paramount importance of maximizing classification purity and optimizing predictive accuracy within the decision tree framework.

3.2.3 Logistic Regression

The method of modeling the probability of a discrete result given an input variable is known as logistic regression. The most frequent logistic regression models have a binary outcome, which might be true or false, 29onitö no, and so forth. Multinomial logistic regression can be used to model situations with more than two discrete outcomes. Logistic regression is a handy analysis tool for determining if a fresh sample fits best into a category in classification tasks. Because components of cyber security, such as threat detection, are classification problems, logistic regression is a valuable analytic tool (Edgar and Manz, 2017). Figure 3.3 shows a logistic regression model output vs. probability graph (URL-6).

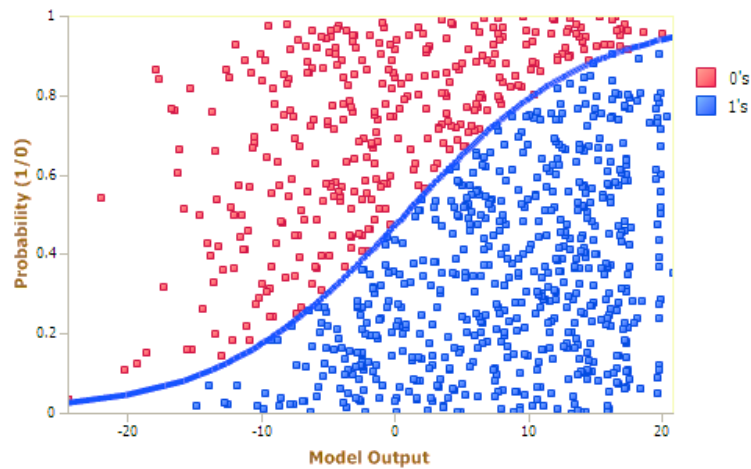


Figure 3.3 : Logistic regression model output vs. probability graph.

Logistic regression is like a regression problem where the dependent variable is a categorical variable. It is widely used in linear classification problems. Although it is called regression, there is a classification here (URL-6).

Logistic regression is a statistical method used to analyze a dataset with one or more independent variables that determine an outcome. The outcome is measured with a binary variable. It is 1 (TRUE, success, pregnant, etc.) or 0 (FALSE, error, non-pregnant, etc.).

The goal of logistic regression is to find the most appropriate model to describe the relationship between a two-way characteristic (dependent variable = response or outcome variable) and a set of independent (predictive or explanatory) variables. Logistic regression generates the coefficients (and their standard errors and significance levels) of a formula to estimate the probability of the existence of characteristics of interest by logit transform given in Equation (3.6).

$$\text{logit}(p) = b_0 + b_1X_1 + b_2X_2 + b_3X_3 + \dots + b_kX_k \quad (3.6)$$

Where p is the probability of existence of the characteristic shown in Equation (3.7) and (3.8).

$$\text{odds} = \frac{p}{1-p} = \frac{\text{probability of presence of characteristic}}{\text{probability of absence of characteristic}} \quad (3.7)$$

$$\text{logit}(p) = \ln\left(\frac{p}{1-p}\right) \quad (3.8)$$

Rather than choosing parameters that minimize the sum of square root errors (like ordinary regression), estimation in logistic regression chooses parameters that maximize the probability of observation of sample values.

To summarize logistic regression;

Events are independent

Does not assume a linear relationship between the dependent variable and the independent variables, but assumes a linear relationship between the logits of the explanatory variables and the response

The arguments can even be power terms or some other nonlinear transformation of the original arguments.

The dependent variable does NOT have 31onitör a normal distribution, but typically assumes a distribution from an exponential family (eg, binomial, Poisson, multiterm, normal, ...); Assuming the binomial distribution of the binary logistic regression response

Variance homogeneity need not be satisfied

Errors need to be independent, but not normally distributed

It uses maximum probability estimation (MLE) instead of ordinary least squares (OLS) to estimate parameters and therefore relies on large sample approaches

Goodness-of-fit measures are based on sufficiently large samples where less than 20% of the heuristic's cell counts are below 5.

When there are continuous markers, G2 and X2 are not the best statistics to evaluate the overall fit of the model, often some data needs to be grouped.

Logistic regression is the appropriate regression analysis to be conducted when the dependent variable is binary. As with all regression analysis, logistic regression is a predictive analysis. Logistic regression is used to describe data and explain the relationship between a dependent binary variable 31onitör or more nominal, inter-row, interval, or ratio-level independent variables. "How does the probability (31onitö no) of lung cancer change for weight and for each pack of cigarettes smoked per day?" may be the question that logistic regression may find the answer.

There are some assumptions for logistic regression. The result must be discrete, otherwise, as described, the dependent variable must be bidirectional in 31onitö (31onitö no). There should be no outliers in the data that could be evaluated by converting the continuous predictors to standard or z-scores and removing values below -3.29 or above 3.29. There should not be high interplay between the variables (multicollinearity). This can be evaluated with the correlation matrix between the estimators.

Logistic regression assumes that the dependent variable is a stochastic event. For example, if we analyze the pesticide kill rate, the result would be kills or no kills. Even one of the most persistent mistakes can only be one of these two situations; logistic regression considers the probability of killing insects. If the insect kill probability is >0.5 , it is considered dead, if <0.5 it is considered alive (URL-6).

The outcome variable – must be coded as 0 and 1 – is placed in the first box labeled Dependent, while all predictors are entered in the Covariates box (Categorical variables must be model coded accordingly). Sometimes a probit model is used instead of the logit model for logistic regression. Figure 4 shows difference between a logit and probit model for different values (-4.4). Both models are widely used in logistic regression and in most cases one model is equipped with both functions and the function with the better fit is chosen. However, probit assumes the normal distribution of the probability of the logit event assuming the log distribution. Thus the difference between logit and probit is often seen in small samples. Difference between a logit and probit model for different values shown in Figure 3.4 (URL-5).

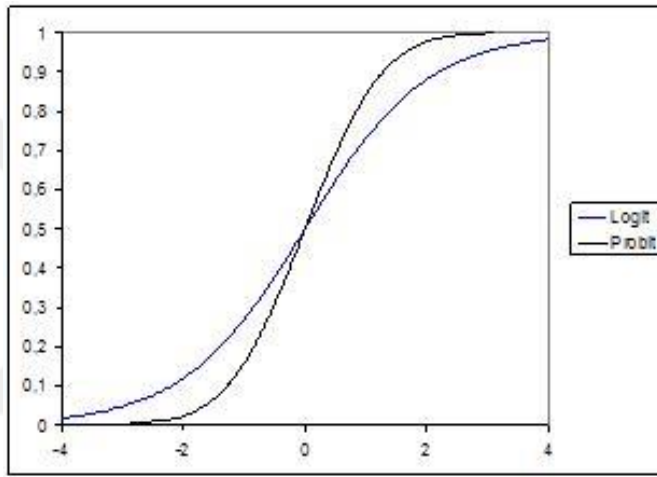


Figure 3.4 : Difference between a logit and probit model for different values.

At the heart of logistic regression analysis is the task of estimating the log rate of an event. Mathematically, logistic regression estimates the multiple linear regression function defined as (Eq. 3.9):

$$\text{logit}(p) = \log\left(\frac{p(y=1)}{1-p(y=1)}\right) = \beta_0 + \beta_1 x_{i2} + \beta_2 x_{i2} + \cdots + \beta_p x_{im} \quad (3.9)$$

for $i = 1 \dots n$

Another important consideration when choosing a model for logistic regression analysis is model fit. Adding independent variables to a logistic regression model always increases its statistical validity because it will explain slightly more variance (usually expressed as R^2) of log rates. However, adding more variables to the model makes this inefficient and overfitting occurs. However, many people want an equivalent way of describing how good a particular model is, and many pseudo- R^2

values have been developed. These should be interpreted with extreme caution as they have numerical calculations that cause artificially high or low (URL-6).

3.2.4 Artificial neural networks (ANN)

Before starting our methodology to be used in our thesis, the main reason why we chose to use ANN application can be stated as the fact that artificial neural networks (ANNs) represent a contemporary computational approach that has garnered widespread adoption in tackling multifaceted real-world challenges. The appeal of ANNs lies in their exceptional information processing capabilities, which are primarily characterized by nonlinearity, extensive parallelism, resilience to faults and noise, as well as robust learning and generalization abilities (Basheer and Hajmeer, 2000).

In that sense, Patel and Goyal (2007) highlighted that ANNs serve as digitized counterparts to the biological brain, adept at discerning intricate nonlinear associations among both dependent and independent variables within datasets where human cognition may falter. Presently, ANNs find pervasive utility across diverse medical domains, particularly within cardiology, oncology and radiology. Their application extends to diagnosis, electronic signal analysis, medical image interpretation, and radiology. Numerous researchers have leveraged ANNs for modelling in medical and clinical research, with burgeoning usage observed in pharmacoepidemiology and medical data analysis. Another illustrative case is provided by Brause (2001), who highlights that showcased instances of success across various applications reinforce a compelling observation: neural diagnostic systems notably outperform human diagnostic capacities. Moreover, Haglin et al. (2019) provide a compelling rationale for incorporating the Artificial Neural Network (ANN) technique in our thesis, highlighting the pronounced increase in the significance of artificial neural networks in recent decades due to technological advancements. A plethora of studies corroborate that artificial neural networks play a pivotal role not only in the diagnosis, prognosis, and treatment of 33onit diseases but also in advancing environmental and community initiatives.

An artificial neural network (ANN) stands as a computational powerhouse designed to mirror the intricate parallelism observed in the human brain (Al-Shayea, 2011). Comprising a web of interconnected processing units, or neurons, operating simultaneously, ANNs draw inspiration from the complex workings of biological

nervous systems (Suzuki et al., 2003).. Just as in 34onitö, the efficacy of an ANN heavily hinges on the intricate connections between these neural elements (Anwar, 2018). Each assembly of processing units forms a layer within the network, with the input layer kickstarting the information flow and the output layer yielding the final result. Spanning between the input and output layers, additional hidden layers—shrouded from direct observation—play a pivotal role in shaping the network’s computational prowess. Illustrated in Figure 3.2, the architecture of a neural network epitomizes its multifaceted 34onitö. To harness the full potential of an ANN, one must embark on the arduous journey of training, a process entailing the meticulous adjustment of connection weights between neurons. Through this iterative fine-tuning, the neural network is sculpted to masterfully execute a predefined function, paving the way for groundbreaking advancements in artificial intelligence (Al-Shayea, 2011). Figure 3.5 shows a standard neural network (Al-Shayea, 2011).

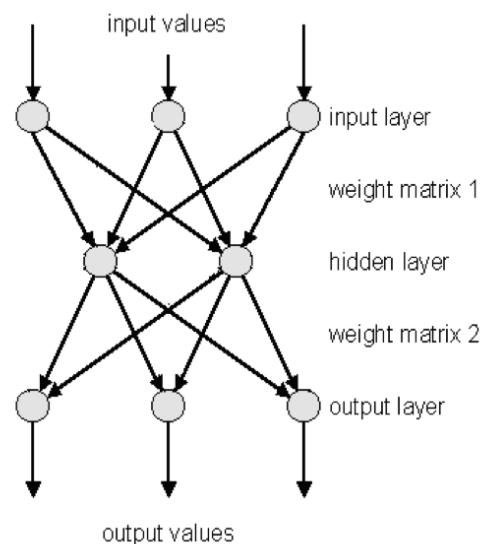


Figure 3.5 : A standard neural network.

Furthermore, Feed-forward neural networks are extensively utilized and proven models for tasks such as classification, forecasting, and problem-solving. A conventional feed-forward backpropagation neural network is suggested for disease diagnosis. It comprises three layers: the input layer, a hidden layer, and the output layer (Al-Shayea, 2011). Figure 3.6 and Figure 3.7 show an example of nephritis diagnosis and heart disease diagnosis via ANN (Al-Shayea, 2011).

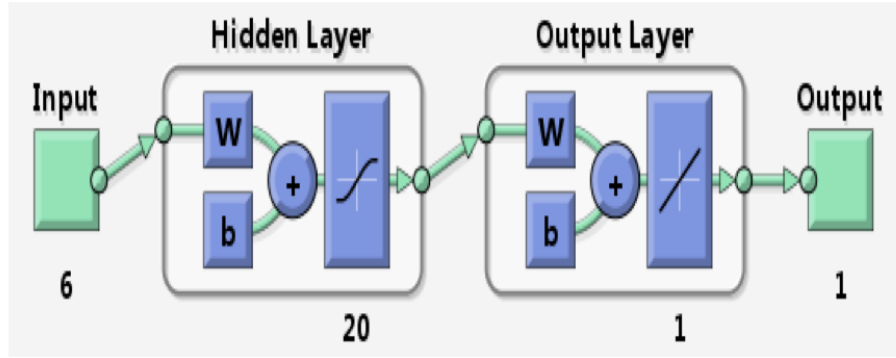


Figure 3.6 : Nephritis diagnosis structure via ANN.

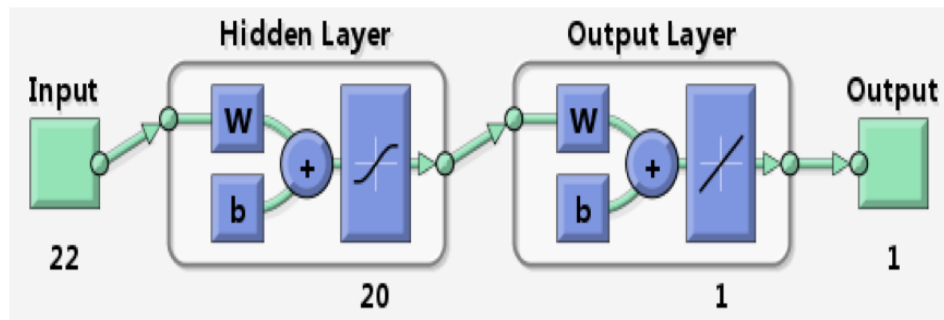


Figure 3.7 : Heart disease diagnosis structure via ANN.

3.2.4.1 L1 and L2 regularisation

L1 regularization is a widely adopted technique for feature selection, renowned for its ability to achieve superior generalization performance in supervised settings characterized by numerous irrelevant features. Ng's investigation (Ng, 2004) delves into the behavior of the two standard regularization methods, L1 and L2, in supervised learning scenarios where there exists a plethora of input features, yet only a small subset of these features holds relevance for the learning process. Similarly, as Goodman's work (Goodman, 2004) demonstrates that, in conditional maximum entropy models, employing an exponential distribution as a prior aligns more closely with the actual parameter distribution compared to other techniques, such as Gaussian prior, thereby enhancing accuracy and simplifying the learning algorithm. Both studies focus on distinct regularization terms when applied within a supervised framework, featuring a large feature vector wherein not all features contribute significantly to the learning process. Recent research endeavours have aimed at optimizing methods tailored for L1-regularization approaches (Cortes et al., 2012; Moore and DeNero, 2011) or refining L1-based normalization solutions like $L(1, \infty)$ (Vogt and Roth, 2010).

In that sense, the authors explained future label paradigm to further investigate L1 and L2 regularisation (Demir-Kavuk et al., 2011; He et al., 2012; Yang et al., 2023).

Instance labelling approaches demand a robust input comprising a set defined as $\mathcal{L} = \{x_i, y_i\}_{i=1}^l$ of l labeled documents and a set $\mathcal{U} = \{x_j\}_{j=l+1}^n$ of $n - l$ unlabelled documents sampled from a distribution $\mathcal{D}$. Emerge as the vanguard in inducing text classification models from labeled documents. GLMs represent a formidable family of statistical models, encompassing revered methodologies such as linear regression, logistic regression, and Poisson regression, all of which can be meticulously derived from the abstract model by crafting a precise link function (Mazilu and Iria, 2011). The link function $g(\cdot)$ stands as the cornerstone, empowering the expected value of a label y_i to intricately hinge upon the m -dimensional feature vector x_i , thus fortifying the predictive prowess of the model given in the Equation (3.10) (Cortes et al., 2012; He et al., 2012).

$$g(E[y_i]) = \mu + \sum_{k=1}^m \theta_k x_{ik} \quad (3.10)$$

where θ represents the model parameters to be estimated. A commonly utilized link function is $g = \ln(p/(1-p))$ (the logit function), which engenders the logistic regression probabilistic model as provided in the Equation 3.11 (Cortes et al., 2012; He et al., 2012).

$$p(y = 1 | x_i; \theta) = \frac{1}{1 + \exp(-\mu - \sum_{k=1}^m \theta_k x_{ik})} \quad (3.11)$$

Estimating the model parameters θ can be conceptualized as solving the optimization problem, devoid of a regularization term, then we obtain the Equation (3.12) (Cortes et al., 2012; He et al., 2012).

$$\text{Arg max}_{\theta} \sum_{i=1}^l \log p(y_i | x_i; \theta) \quad (3.12)$$

3.2.4.2 Dropout training in ML approaches

Dropout training, pioneered by Hinton et al. (2012), emerged as a strategy to mitigate overfitting by stochastically excluding subsets of features during each iteration of the training process. Despite its remarkable effectiveness, the precise theoretical underpinnings behind the success of dropout remain elusive (Wager et al., 2013; Wang

and Manning, 2013). Dropout training falls within the broader spectrum of learning methodologies that introduce artificial perturbations to training data in order to enhance prediction stability (Maaten et al., 2013; Baldi and Sadowski, 2013; Wang and Manning, 2013; Simard et al., 2017; Wager et al., 2013). There exists a well-established association between artificial feature corruption and regularization (Rifai et al., 2011; Ba and Frey, 2013; Wu and Gu, 2015).. For instance, Bishop (1995) demonstrated that training with features corrupted by additive Gaussian noise yields an effect akin to a form of L2-type regularization in scenarios characterized by low noise levels. In this study, we take a significant stride towards unraveling the mechanics of dropout training by scrutinizing its role as a regularizer. The investigation is centered on generalized linear models (GLMs), a class of models wherein feature dropout manifests as a variant of adaptive model regularization (Wager et al., 2013).

Within this framework, Wager et al. (2013) posited that dropout training equates to first-order equivalence with L2-regularization subsequent to transforming the input via $\text{diag}(\hat{J})^{-1/2}$ where $\hat{J}$ represents an estimate of the Fisher information matrix. This transformation effectively renders the objective's level curves more spherical, thereby harmonizing the regularization applied to disparate features. In the realm of logistic regression, dropout can be construed as a variant of adaptive L2-regularization that exhibits a predilection for rare yet valuable features (Wager et al., 2013). Furthermore, Wang and Manning (2013) deliberated on the challenge of learning from rare yet valuable features, a topic previously explored in the domain of online learning by Duchi et al. (2011). The latter demonstrated that their AdaGrad adaptive descent algorithm achieves superior regret bounds compared to regular stochastic gradient descent (SGD) in this context.

3.2.4.3 Activation functions

The activation function is a crucial component in the training process of neural networks. It serves to introduce the requisite non-linearity into the model, enabling it to acquire and comprehend complex representations (Rasamoelina et al., 2020). Activation functions are integral to artificial neural networks, serving to transform an input signal into an output signal. This transformed output is subsequently passed as input to the next layer in the network. In the context of an artificial neural network, the

process entails computing the sum of products of inputs and their corresponding weights, followed by the application of an activation function. This activation function facilitates the generation of the output for a given layer, which is then forwarded as input to the subsequent layer in the network stack (Sharma et al., 2017; Sibi et al., 2013).

Figure 3.8 has been adapted from Rasamoelina et al. (2020) to introduce certain activation functions in our thesis.

Name	Equation	Derivative	Range	Order of Continuity	Monotonic derivative
Sigmoid	$\frac{1}{1+e^{-x}}$	$\frac{e^{-x}}{(1+e^{-x})^2}$	$(-\infty, +\infty)$	C^∞	Yes
Hyperbolic Tangent	$\frac{2}{1+e^{-2x}} - 1$	$\frac{1}{\cosh^2 x}$	$(-1, 1)$	C^∞	Yes
ReLU	$\max(0, x)$	$\begin{cases} 0, & \text{if } x \leq 0 \\ 1, & \text{if } x > 0 \end{cases}$	$[0, \infty)$	C^0	Yes
Leaky ReLU	$\max(0, x) + \alpha \min(0, x)$	$\begin{cases} 1, & \text{if } x \geq 0 \\ \alpha, & \text{otherwise} \end{cases}$	$(-\infty, +\infty)$	C^0	Yes
PReLU	$\max(0, x) + \alpha \times \min(0, x)$	$\begin{cases} 1, & \text{if } x \geq 0 \\ \alpha, & \text{otherwise} \end{cases}$	$(-\infty, +\infty)$	C^0	Yes
ReLU6	$\min(\max(0, x), 6)$	$\begin{cases} 0, & \text{if } x < 0 \text{ or } x > 6 \\ 1, & \text{if } 6 \geq x \geq 0 \end{cases}$	$[0, 6)$	C^0	Yes
ELU	$\max(0, x) + \min(0, \alpha(e^x - 1))$	$\begin{cases} \alpha e^x, & \text{if } x < 0 \\ 1, & \text{if } x \geq 0 \end{cases}$	$(-\alpha, +\infty)$	$\begin{cases} C^1, & \text{if } \alpha 1 \\ C^0, & \text{if } \alpha \neq 1 \end{cases}$	Yes if $\alpha \geq 1$
SELU	$\gamma(\max(0, x) + \min(0, \alpha(e^x - 1)))$	$\gamma \begin{cases} \alpha e^x, & \text{if } x < 0 \\ 1, & \text{if } x \geq 0 \end{cases}$	$(-\gamma\alpha, +\infty)$	C^0	Yes
Swish	$\frac{x}{1+e^{-x}}$	$\frac{e^x(x+e^x+1)}{(e^x+1)^2}$	$(\approx -0.2784, +\infty)$	C^∞	No
Mish	$x \tanh(\log(1 + e^x))$	$\frac{e^x(4e^x x + 4x + 6e^x + 4e^{2x} + e^{3x} + 4)}{(2e^x + e^{2x} + 2)^2}$	$(\approx -0.3088, +\infty)$	C^∞	No

Figure 3.8 : An overview of activation functions.

3.2.4.4 Learning rate

The learning rate stands out as the most critical hyper-parameter to fine-tune when training deep neural networks (Smith, 2017). Practitioners utilizing this machine learning and neural network methods are tasked with specifying initial parameters, including the initial learning rate. This step is particularly crucial as an improper learning rate selection can result in suboptimal local solutions, where the loss function's value fails to improve compared to other local solutions. Consequently, a notable drawback of these methods is their reliance on sensitive hyperparameters, which pose challenges in achieving appropriate tuning (Takase et al., 2018). Furthermore, such algorithms commonly incorporate a learning rate parameter, dictating the extent to which weights can adjust in response to observed errors on the training set. The selection of this learning rate holds significant sway over both generalization accuracy and training speed. However, determining the optimal learning rate poses a challenge, as it varies depending on the specific task at hand

resulted in the fact that users of these training algorithms often grapple with the dilemma of choosing the appropriate learning rate, as there is limited guidance on selecting the ideal value (Wilson and Martinez, 2001).





4. APPLICATION

4.1 Process Improvement

In this study, it is aimed to decrease diagnosis time of the breast cancer by using models for oncologists, especially breast oncologists, to facilitate the diagnosis and cure methods of breast cancer based on the triggering factors of breast cancer. The process flow map is drawn according to the steps of the breast patient at Istanbul Breast Center. The process flow map of a patient is given in Figure 4.1.

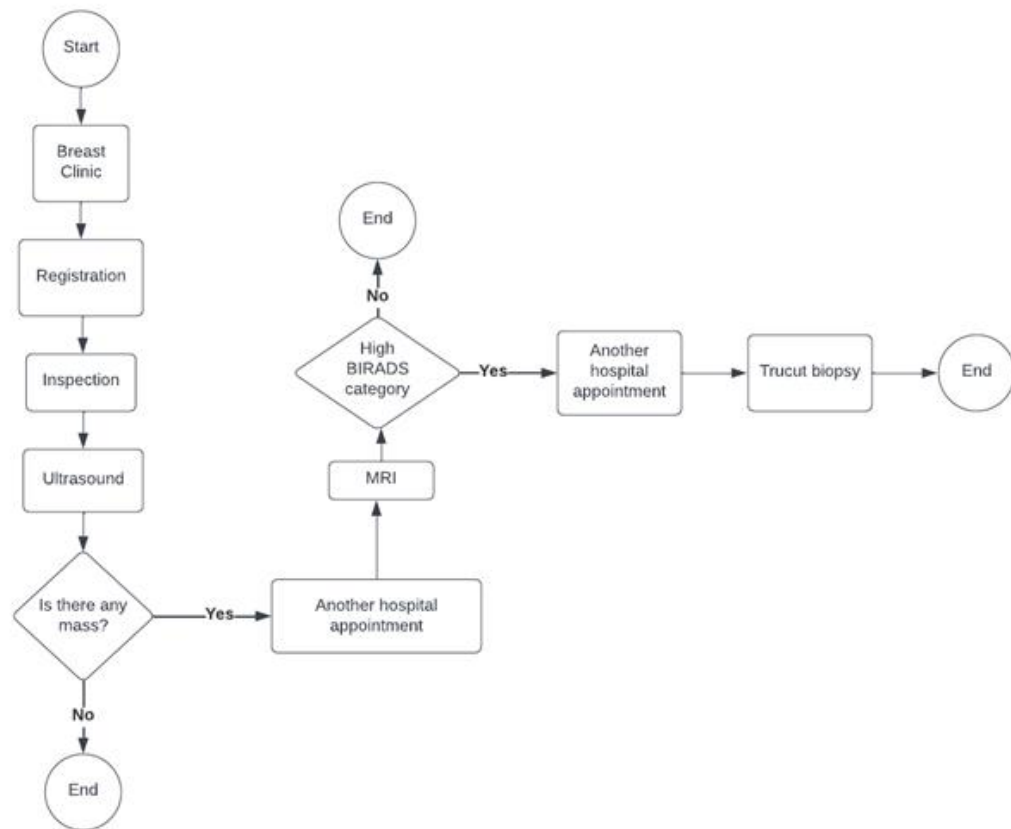


Figure 4.1 : Process flow map of a patient.

The journey of a patient starts with the appointment step for the breast cancer clinic. They are coming when the date is come, and start the registration process at the welcoming desk. The registration process includes two steps. The medical personnel asks if the patient has older radiologic results and if the answer is yes, they start downloading the images to their own system. On the other hand, they want a three pages patient information form to be filled by the patient. They gather every demographic and historic information about the patient. The properties are those which constitutes the breast cancer risk such as birth age, the cancer history of the patients' family, other diseases occurred, daily routines etc. After all, the doctor makes the first inspection by hand also by using ultrasound device. If there is a risk and a mass found by the first inspection, then the doctor requests further imaging, Breast Magnetic resonance imaging (MRI). MRI results gives different categories according to the type of the mass at the breast. The category is named as BIRADS and it is between 0-6. When it gets higher, it means that it is much more risky that the mass probably is malignant. The doctor decides to make a trucut biopsy to find out the tumor malignancy in the last step if the previous inspections shows high risk. This process is long, due to finding an appropriate day for the inspection or the radiological tests. Also the patients are waiting in the waiting hall for the medical personnel, because of registration and hygiene processes. These waiting times are non-value added steps for a diagnosis that expands the time and this is very dangerous 42onitör patient with a breast cancer. The early the diagnosis is, the high survival rate.

In this case, the first step at the clinic is tried to be shortened. If the patient information and the previous radiological results may be gathered before the doctor inspection, maybe the other tests will be requested earlier. The time reduction in the breast cancer diagnosis is vital so that lean thinking will help in terms of eliminating time waste. The following radiological steps takes much longer time due to the crowded hospitals, exceeded demand. If the patient come with more than one test result, according to his/her breast cancer risk, than the disease treatment process will start earlier. The improved process flow chart is shown in Figure 4.2.



Figure 4.2 : The improved process flow chart.

As seen in Figure 4, when the steps are shortened, when the time waste is eliminated, the whole clinic process ends with the inspection and the ultrasound control. Which means, the doctor will see other radiological results and give the treatment decision when the patient is at the clinic. The treatment process differs for each patient that means for each case. Sometimes a neo-adjuvant chemotherapy is the first step to be able to shrink the tumor, or sometimes the patient is directly rushed into surgery. This decision is very important to be given in the earliest stage of the breast cancer.

4.2 Case Study of a Radiology Department

Lean management aims to eliminate actions which do not add any value to the process that are defined as “waste.” Elimination of non-value added steps, shortens the lead time of the process which means to reach customer more quickly. The current state of the hospitals’ departments can be provided by some lean management tools. With the help of the value stream mapping (VSM), the big 43onitör of a whole process can be seen. This 43onitör shows every step that the patient will follow and it also tells about the cycle time for each service. If any of the service steps are not necessary, it is tried to be eliminated such as walking between too many doors, waiting 43onitör reports, waiting for registration, etc. In this case study, data are taken from the paper which gives details about the radiology department’s current situation at Şişli Hamidiye Etfal

Hospital in Istanbul, Turkey (Camgöz-Akdağ et al., 2017). The radiology department is considered with its mammography and ultrasound units.

There are two mammography devices at the radiology department of the hospital but one of them is not in use. Also the mammography room closes its doors less than six hours as working time. For ultrasound process, there are four radiologists 44onitör assistant but they are not only checking for breast cancer but also some other diseases. This hospital evaluates nearly 550 patients in average per month via mammography. There are wrong treatment results at the hospital such as recalls or making unnecessary tests. The whole process starts with the polyclinic examination. The doctor will refer to mammography and the patient will get an appointment. Mammography appointment may be a few days later and when the patient comes, she has to wait in a queue. After mammography screening the patient has to wait 44onitör report to see her doctor again. If the doctor decides for another test then an ultrasound process will start (Camgöz-Akdağ et al., 2017). The current state of the radiology department of Şişli Etfal Hospital is visualized by the value stream map. This method captures a random moment to see the value added and non-value added activities on a single 44onitör. The current state value stream map is given in Figure 4.3. The timeline shows both value added and non-value added activities' durations. Bottom lines between processes show non-value added activities, mostly waiting activity 44onitör patient. The biggest bottleneck is waiting 44onitör mammography appointment date, the report and the ultrasound appointment date. These durations are close to each other which are three to four days on average. The value-added activities are only presents the steps to get the result from the doctor in the end. This time is totally 67.3 min, nearly 1 h. But the whole process continues totally for 17367.95 min, nearly 12 days. This big difference is caused by the “waste” which decreases patients' satisfaction.

The patient process starts with registration desk after taking an appointment. Examination process will be the next one that includes again registry operations. After taking the report result, doctor will see the patient and may request a ultrasound scanning. The detailes steps and cycle times of the related processes can be seen in detail in Table 4.1.

Table 4.1 : Cycle times of the process steps in the current state.

Process name	Cycle time (minutes)
Registration desk	0.5
Examination	5.1
Mammography desk	3.0
Registration desk	2.5
Intern	0.7
Preparation	4.0
Test	7.0
Dressing up	3.0
Report	7.0
Report result	5.0
Doctor	3.0
Medication	3.0
Ultrasound date	5.0
Registration desk	2.0
Registraion desk	3.5
Test	8.0
Doctor	5.0

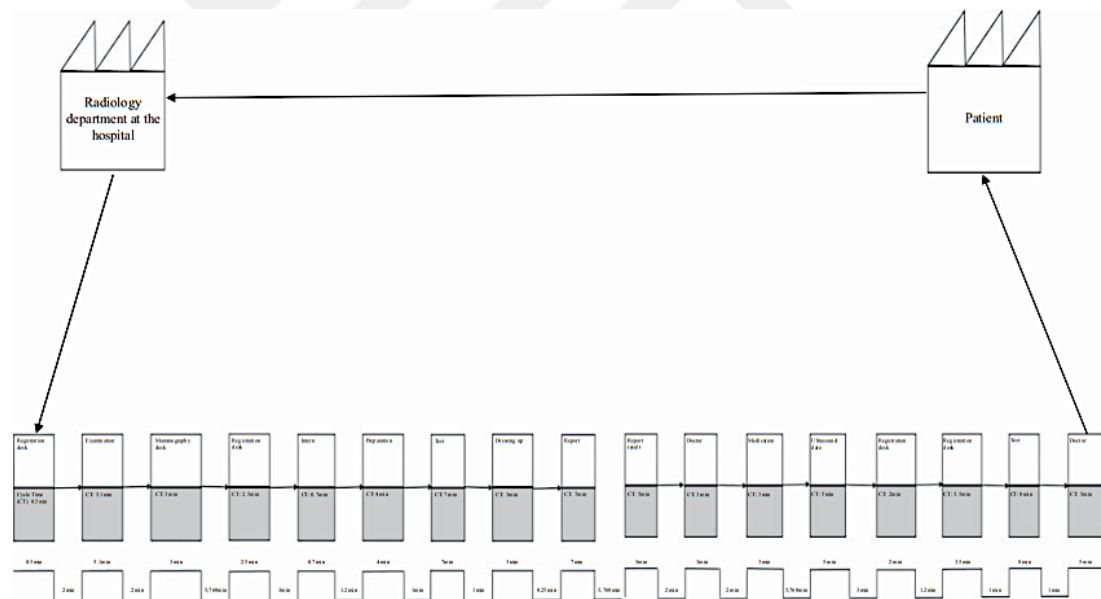


Figure 4.3 : Current state value stream map.

Improvement areas are shown in future map (Figure 4.4). As it is seen, total lead time of the patients' road, which starts from the beginning of the radiology department and ends after the doctors' reporting, decreased nearly 9 days which means a big improvement. As it is seen from the future map, preparation, test, dressing up, report and report result process cycle times are decreased by some technological and physical

changes in the hospital. Cycle times of the radiology department process steps in the future 46onitör given in Table 4.2.

Table 4.2 : Cycle times of the process steps in the future state.

Process name	Cycle time (minutes)
Registration desk	0.5
Examination	5.1
Mammography desk	3.0
Registration desk	2.5
Intern	0.7
Preparation	4.0
Test	7.0
Dressing up	3.0
Report	7.0
Report result	5.0
Doctor	3.0
Medication	3.0
Ultrasound date	5.0
Registration desk	2.0
Registraion desk	3.5
Test	8.0
Doctor	5.0

With more than one dressing room, patients will not have to wait for other patients to enter the mammography room. Another improvement area is technologically developed computers and systems. With the simultaneous voice transformers doctor can dictate the result and the nurse can directly take out the report. After the improvement, maximum one day later, the report can be delivered to the patient. Waiting a mammography result is nearly 4 days at the current situation that means extending the treatment process. With the correct arrangement of appointments and the required test plan, patients will come on time and will not wait for long queues. In front of the mammography and ultrasound rooms there may be electronic screens 46onitör the coming appointment. This will also improve satisfaction at a less crowded hospital isle. Another very important issue is training. Healthcare personnel must know the whole radiology process that they are responsible of. Due to these small changes the whole process will be finished nearly 4 days earlier.



Figure 4.4 : Future state value stream map.

4.3 Data Analysis of Breast Cancer Clinic

Data has been collated and formatted for analysis from the Istanbul Breast Clinic's real-world records. Of the approximately 500 entries logged, 418 possess meaningful completeness. The ratio of individuals with breast cancer to those without, among the clinic attendees represented in this dataset, was found to be nearly equal. Given the global breast cancer statistics, which suggest that one out of every eight women in the United States is expected to receive a breast cancer diagnosis during her lifetime (URL-7), a process of elimination was conducted, reducing the raw data count to a total of 248 cases. Out of these, 31 have been diagnosed with breast cancer, while 217 are categorized as healthy individuals. Within this dataset, there are 13 independent variables 47onitör dependent variable.

Incomplete entries within the raw data have been addressed through data imputation techniques. Individuals diagnosed with cancer and those without were segregated into their respective groups, with missing values in existing features being supplanted by the median value of the total data. The data underwent classification, and regression analyses employing decision tree, logistic regression, and artificial neural networks algorithms to amass outcomes.

Owing to the limited 47onitö of raw data, the Synthetic Minority Over-sampling Technique (SMOTE), as previously mentioned in the methodology section, has been utilized to augment the dataset. Initially, the dataset was expanded to encompass 1000 individuals, with the probability of having breast cancer adjusted to 12.5%, in

accordance with the 48onitör48re. Post analysis with the 1000-record dataset using all algorithms, SMOTE was once again employed to further amplify the dataset to 10,000 records. The outcomes 48onitör specified algorithms were compiled 48onitör 10,000 individuals, and the results have been compared within the study. The datasets of 248, 1000, and 10,000 records have been denoted as “Data Set-1”, “Data Set-2”, and “Data Set-3” respectively. “All analyses were conducted using Python language within the Google Colab environment.

4.3.1 Classification and Regression Trees (CART) Algorithm

In this study, the data obtained were initially analyzed using the Classification and Regression Tree (CART) algorithm. As a result of this algorithm, it was determined to what extent the independent variables present within the data influenced the dependent variable, breast cancer. The impact ratio varies for each variable. Accordingly, graphs depicting the importance rankings of the variables have been provided for all three datasets in Figures 4.5, 4.6 and 4.7.

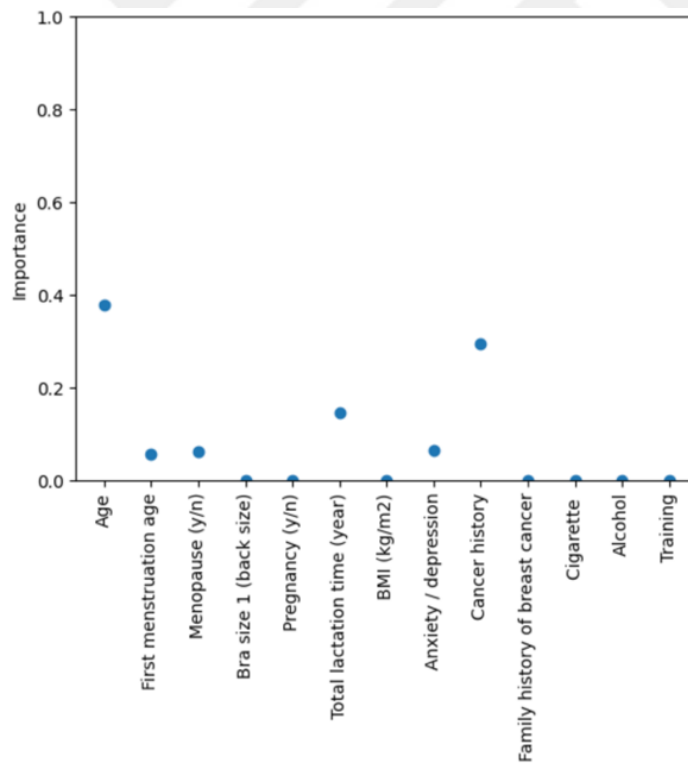


Figure 4.5 : Importance graph for data set-1.

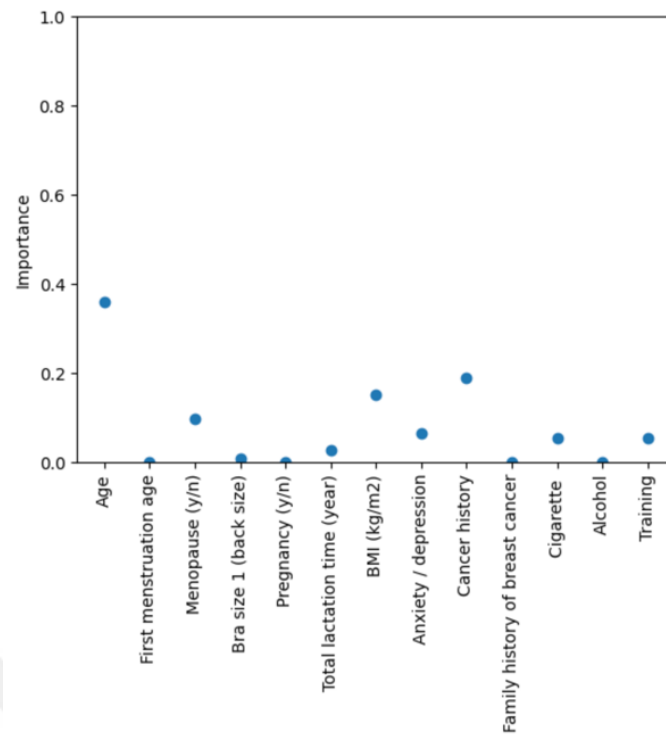


Figure 4.6 : Importance graph for data set-2.

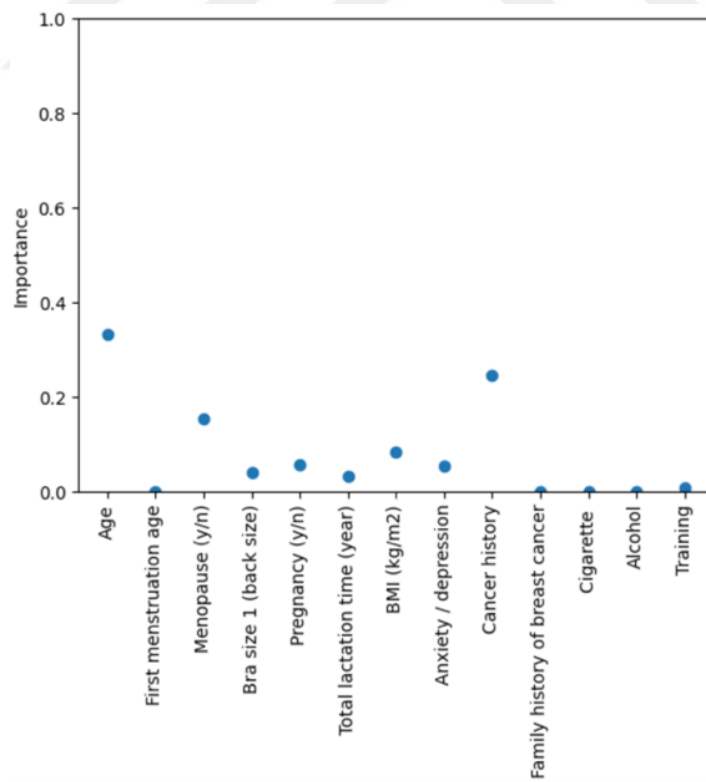


Figure 4.7 : Importance graph for data set-3.

As can be observed from the provided graphs, the importance coefficients of the attributes have yielded similar values across the different datasets. Age has emerged as the most significant factor, followed by a history of cancer as the next critical determinant. The influence of the total duration of lactation evident in the raw data has diminished as the dataset increased in size. Similarly, the significance of smoking and regular exercise, which gained prominence in the second dataset, has waned with the expansion to 10,000 records. With the growth of the dataset, menopausal status and a history of pregnancy have also gained importance. Body mass index and anxiety are among the attributes that influence the likelihood of developing breast cancer. The accuracy results obtained on the three datasets have been provided in Table 4.3.

Table 4.3 : Comparison of accuracy values for each data set.

	Training Accuracy	Testing Accuracy
Data Set-1	0.960	0.907
Data Set-2	0.914	0.930
Data Set-3	0.914	0.910

As the number of data points increased, the training accuracy decreased. For Data Set-1, the smaller number of observations may have led the model to generalize the results more readily compared to the others, resulting in higher training accuracy. Additionally, the larger gap between the training and testing accuracies in the first model indicates a higher propensity for overfitting. As the sample size increased, the training accuracies converged, which is another indicator that the characteristics of the smoothed data are similar. Moreover, as the sample size grew, the difference between the training and testing accuracies diminished, helping to mitigate overfitting.

The outcome of the Classification and Regression Trees (CART) algorithm has determined the extent to which various attributes influence the probability of breast cancer. One of the parameters of the analysis, the max depth, was set at 5. Results for scenarios with both lower max depth values and unlimited max depth have also been obtained. However, in the case of unlimited max depth, while the training accuracy approached approximately 1, the testing accuracy was around 0.8, indicating a significant gap that suggests the presence of overfitting.

In addition to numerical data, a visual representation of the decision tree has also been obtained. The decision tree corresponding to Data Set-1 is provided in Figure 4.8. As can be discerned from the branching of the tree, a max depth of 5 was selected, and

the attribute of age emerged with the highest weight. The findings related to the age attribute can be explained as follows:

Gini: The Gini impurity is a measure of how often a randomly chosen element from the set would be incorrectly labeled if it was randomly labeled according to the distribution of labels in the subset. A Gini score of 0.222 suggests some degree of mixture of classes in this group, but it's relatively low, indicating that most of the samples in this node belong to the same class.

Samples: This indicates the number of observations in the dataset that reach this node. There are 173 individuals whose data are being considered at this point in the tree.

Value: The array [151, 22] tells you the distribution of the two classes among these samples. Assuming class 0 is for individuals who do not have breast cancer and class 1 is for individuals who do, this would mean that of the 173 individuals who are 69.5 years or younger, 151 do not have breast cancer and 22 do.

Class: This tells us that the majority class among the samples in this node is class 0. If a prediction was to be made at this point without further splitting, the model would predict the most common class, which is class 0 in this case.

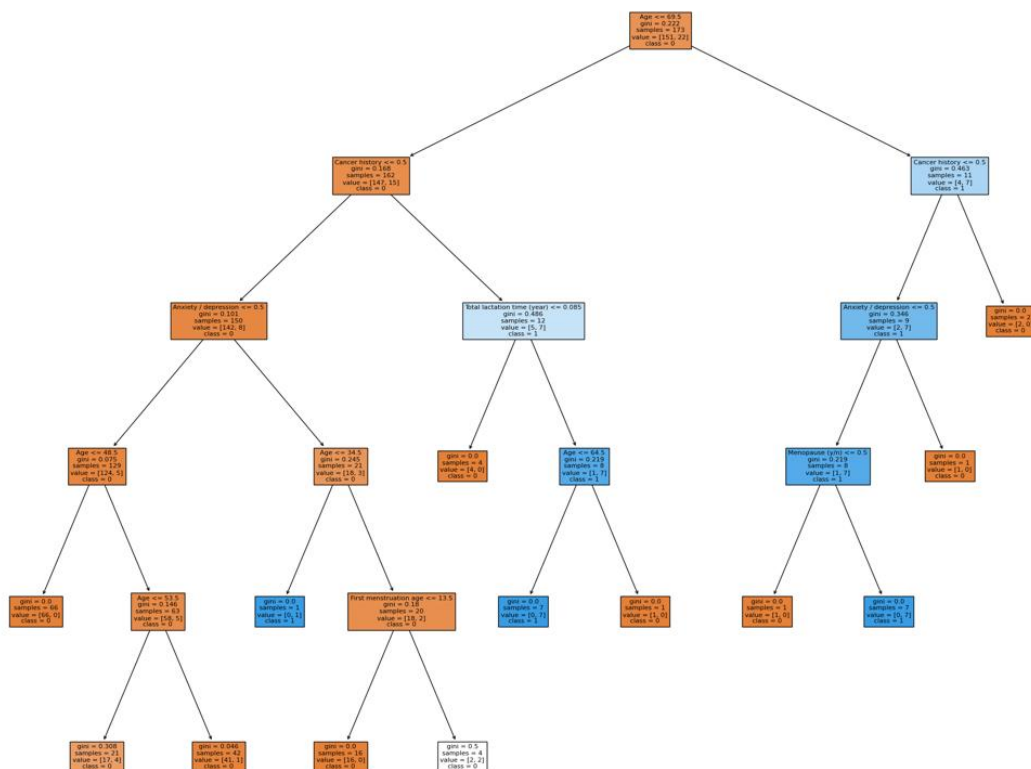


Figure 4.8 : Decision tree of data set-1.

Another comparative metric involves the accuracy, precision, recall, and F1 score values, which can be observed through the confusion matrix. The confusion matrix for Data Set 1 is presented in Figure 4.9, while the metrics for all datasets are provided in Table 4.4.

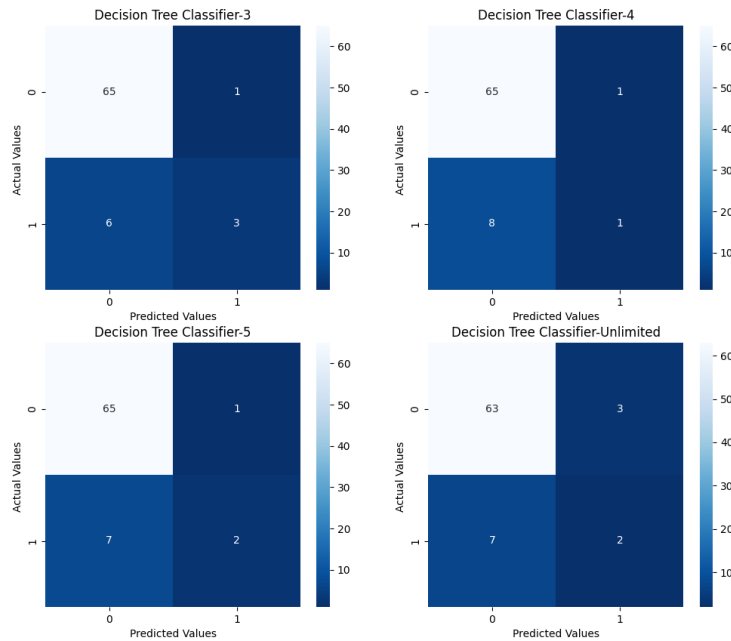


Figure 4.9 : Confusion matrix for data set-1.

As shown in the given 52onitö, analyses have been conducted with max depth values of 3, 4, 5, and unlimited, and the accuracy values have been calculated accordingly. 52onitör decision tree algorithm with a max depth of 5, it correctly predicted 65 of the true values labeled as 0 and incorrectly predicted 1. Conversely, it incorrectly predicted 7 of the true values labeled as 1 and correctly predicted 2.

Table 4.4 : Comparison metrics between data sets' decision tree results.

	Accuracy	Precision	Recall	F1-Score
Data Set-1	0.906667	0.666667	0.222222	0.333333
Data Set-2	0.923333	0.714286	0.344828	0.465116
Data Set-3	0.909667	1.000000	0.277333	0.434238

Accuracy is the ratio of correctly predicted instances to the total instances in the dataset. It gives a general sense of how often the model is correct. Data set 2 gave better performance in terms of accuracy. Precision measures the ratio of correctly

predicted positive observations to the total predicted positive observations. High precision relates to the low false positive rate. In first analysis 66.67% precision suggests that of all instances predicted as positive, around 67% were actually positive. Data set 2 gave 71.43% precision that indicates an improvement in the model's ability to not label a negative sample as positive. The last analysis with 10000 data gave 100% precision that means there were no false positives; every instance predicted as positive was indeed positive.

Recall, or sensitivity, measures the ratio of correctly predicted positive observations to all observations in the actual class. High recall indicates the model is good at detecting the positives. The highest recall rate is 34.48% by data set 2 in this analysis. F1-Score is the harmonic mean of Precision and Recall. An F1-Score takes both false positives and false negatives into account and is a more reliable measure when there are uneven class distributions. First F1-Score of 33.33% indicates a rather poor balance between precision and recall, skewed towards precision. Second F1-Score of 46.51% suggests a better balance than Data Set-1, but still indicates room for improvement. The last F1-Score of 43.42% is lower than Data Set-2, which is interesting given the perfect precision, but is due to the lower recall rate.

The table suggests that while Data Set-2 has the highest accuracy and F1-Score, indicating a generally better model performance across all aspects, Data Set-3 has the best precision, suggesting no false positives in the predictions made by the model. However, Data Set-3 suffers in recall, meaning it misses a higher number of actual positive instances. The balance between these metrics can inform which dataset/model might be best for a particular application depending on whether false positives or false negatives carry a higher cost.

The results of the analysis for Data Set-3 are represented in the Receiver Operating Characteristic (ROC) curve, which is provided in Figure 4.10.

A Receiver Operating Characteristic (ROC) curve is a graphical plot that illustrates the diagnostic ability of a binary classifier system as its discrimination threshold is varied. The curve is created by plotting the true positive rate (TPR, also known as recall or sensitivity) against the false positive rate (FPR, also known as 1-specificity) at various threshold settings.

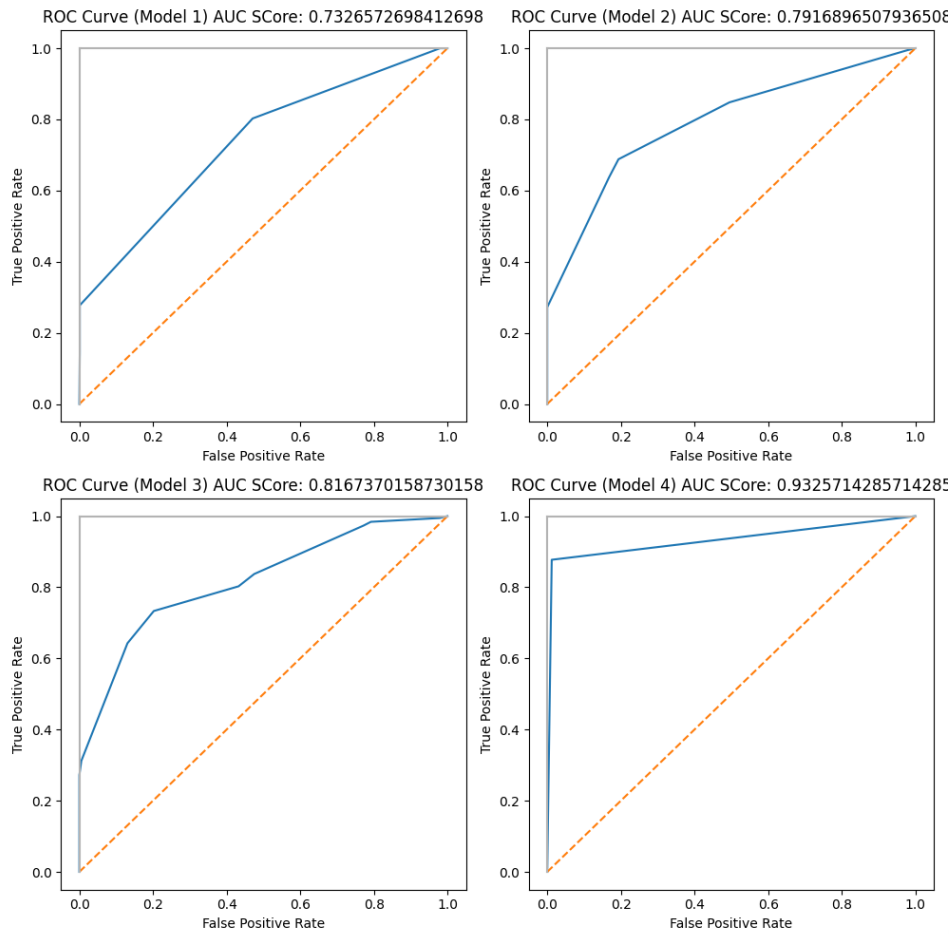


Figure 4.10 : ROC curves for data set-3 analysis.

The ROC curve is generated by evaluating the model at different thresholds. A threshold is a point of decision-making like the patient is breast cancer or not. True Positive Rate is the proportion of actual positives that are correctly identified by the model.

False Positive Rate is the proportion of actual negatives that are incorrectly identified as positives. The 45-Degree Line represents the strategy of random guessing. A classifier with no discriminative power will have points lying along this line. Area Under the Curve (AUC) is the most important aspects of the ROC curve. This is a single scalar value that summarizes the performance of the classifier. An AUC of 0.5 suggests no discrimination and an AUC of 1.0 indicates perfect discrimination, where the classifier is able to perfectly differentiate between the classes without any error. A curve that is closer to the top-left corner indicates a better performance. The steeper the curve, the better the model is at achieving a high TPR while maintaining a low FPR.

The ROC curve is particularly useful for evaluating classifiers on imbalanced datasets where the number of negatives vastly exceeds the number of positives or vice versa. It helps in determining the optimal cutoff point for maximum sensitivity and specificity and comparing the performance of different classifiers. ROC curves gave the best performance with Data Set-3.

4.3.2 Logistic Regression

Logistic Regression is a statistical method utilized for binary classification tasks, particularly prevalent in machine learning and statistical modeling. It aims to predict the probability of a binary outcome based on one or more predictor variables. In logistic regression, the output variable (also known as the dependent variable or target variable) is binary, taking values such as 0 or 1, true or false, success or failure, etc.

The logistic regression function is expressed as the logistic or sigmoid function, which transforms any real-valued input into a value between 0 and 1. This function is crucial as it maps the predicted values to probabilities, enabling the classification of instances into one of the two categories based on a threshold.

In logistic regression, the key parameters include:

1. **Intercept (Bias):** The intercept term represents the value of the predicted output when all predictor variables are zero. It is a constant term that shifts the logistic function along the y-axis.
2. **Coefficients (Weights):** Coefficients are the weights assigned to each predictor variable in the logistic regression equation. These coefficients determine the impact of each predictor on the predicted outcome. A positive coefficient indicates that an increase in the predictor variable's value increases the log-odds of the event happening, while a negative coefficient implies the opposite.
3. **Regularization Parameters (optional):** Regularization parameters, such as L1 and L2 regularization coefficients, can be applied to logistic regression to prevent overfitting. Regularization penalizes large coefficient values, thereby promoting simpler models and reducing the risk of overfitting to the training data.
4. **Solver:** The solver refers to the optimization algorithm used to estimate the coefficients of the logistic regression model. Common solvers include 'liblinear', 'lbfgs', 'newton-cg', 'sag', and 'saga', each with its advantages and limitations.

5. **Penalty:** In some implementations, logistic regression allows for specifying the penalty term associated with regularization. The penalty term is added to the loss function during training to control the complexity of the model.
6. **Maximum Iterations:** Logistic regression models often require iterative optimization procedures to converge to a solution. The maximum iterations parameter specifies the maximum number of iterations allowed for the solver to converge or reach a stopping criterion.
7. **C (Regularization Strength):** C is the inverse of the regularization strength, where smaller values specify stronger regularization. It controls the trade-off between fitting the training data well and keeping the model simple to avoid overfitting. Higher values of C imply less regularization, potentially leading to a model that closely fits the training data but might overfit.
8. **Tolerance (tol):** Tolerance is a stopping criterion for the optimization algorithm. It determines the tolerance for the optimization process to converge to a solution. If the change in the coefficients between successive iterations is less than the tolerance value, the optimization process is considered converged. Increasing the tolerance may reduce computation time but could potentially lead to suboptimal solutions.
9. **Class Weight:** Class weight is a parameter used to handle class imbalance in the dataset. It assigns different weights to different classes, effectively adjusting the importance of each class during model training. This is particularly useful when one class is significantly underrepresented compared to the other class in binary classification tasks.
10. **Multi-Class Handling:** Logistic regression can also be extended to handle multi-class classification problems through strategies such as one-vs-rest (OvR) or multinomial logistic regression. Parameters related to multi-class handling may include the strategy for handling multiple classes and how the probabilities are computed for each class.
11. **Warm Start:** Warm start allows the optimization process to start from the previous solution rather than starting from scratch. This can be beneficial when training multiple logistic regression models with similar data, as warm starting can speed up convergence.

12. Random State: Random state is a parameter used to control the random number generator's seed value. It ensures reproducibility of results across different runs by initializing the random number generator to the same state before model fitting.

13. Dual: The “dual” parameter specifies whether to solve the primal or dual optimization problem. In scikit-learn's logistic regression implementation, when the number of samples (n_{samples}) is greater than the number of features (n_{features}), the algorithm solves the primal optimization problem by default. However, when the number of samples is smaller than the number of features, setting “dual=True” allows the algorithm to solve the dual optimization problem. The choice between primal and dual optimization depends on the problem size and characteristics. In general, the primal form is preferred for large datasets with more samples than features, while the dual form may be more suitable for smaller datasets or when using certain optimization methods. Including the “dual” parameter provides additional flexibility in configuring logistic regression models, especially when dealing with datasets of varying sizes and characteristics. Proper selection of the “dual” parameter can improve the efficiency and effectiveness of the logistic regression model, particularly in scenarios where the number of samples and features differ significantly.

These parameters play a crucial role in fitting the logistic regression model to the training data and subsequently making predictions on new data. Proper selection and tuning of these parameters are essential for achieving optimal model performance, generalization, and robustness.

Table 4.5 : Logistic regression parameters.

Option-Parameter	L2 Regularization	Tolerance(tol)	Solver	Regularization Strength ©
Option 1	0.1	0.0001	lbfgs	0.1
Option 2	1	0.001	saga	1
Option 3	10	0.01	liblinear	10

In the logistic regression analysis conducted in the thesis, 81 different scenarios were examined for each dataset by selecting three different values for parameters L2 regularization, tolerance, solver, and regularization strength. Training and testing accuracies were computed for each scenario, aiming to identify the most optimal model with the significant parameters for classification. Except for default values

in logistic regression, which are L2 regularization with a default value of 1 and L2 regularization, also known as Ridge regularization, penalizes the squared of coefficients. It is commonly used to prevent overfitting by discouraging overly complex models. The parameter represents the regularization strength, with higher values indicating stronger regularization. Tolerance specifies the convergence criterion of optimization algorithm. It determines the minimum change in coefficients between iterations of optimization process to be considered converged. Lower tolerance values require stricter convergence criteria, potentially leading to longer computation times but finer convergence. Tolerance with a default value of 0.0001, Solver refers to the algorithm used to optimize the logistic regression objective function. Different solvers have different computational complexities and are suitable for different types of problems. For example, 'lbfgs' is a quasi-Newton optimization algorithm that works well for small to medium-sized datasets and solver with a default value of 'lbfgs', and Regularization strength, represented by the parameter C, controls the trade-off between fitting the training data well and keeping the model simple to avoid overfitting. Higher values of C indicate less regularization, potentially leading to a model that closely fits the training data but might overfit. Lower values of C increase the regularization strength, resulting in a simpler model that generalizes better to unseen data, regularization strength with a default value of 1, two alternative options were chosen for each parameter. The provided Table 4.5 includes the different values for each parameter.

Table 4.6 : Training and testing accuracy comparison.

Dataset	Training Accuracy	Testing Accuracy
Data Set-1	0,879	0,880
Data Set-2	0,881	0,913
Data Set-3	0,898	0,891

The findings presented in Table 4.6 compare the training and test accuracies of a model trained on three different datasets. The results demonstrate that Dataset2 achieved the highest test accuracy (0.913) compared to the other datasets. In contrast, Dataset1 exhibited the lowest test accuracy (0.88), distinguishing it from the other datasets. The lower training and test accuracies of Dataset1, relative to the other datasets, indicate that the model inadequately grasped the information in this dataset and had a weak

generalization capability. This suggests that the model failed to sufficiently learn the patterns and relationships specific to Dataset1 and could not generalize to different datasets. The higher training and test accuracies of Dataset2 compared to Dataset1 indicate that the model better grasped the information in this dataset and had a stronger generalization capability. The findings reveal that the model more effectively learned the patterns and relationships in Dataset2 and was more successful in generalizing this knowledge to different datasets. While the training accuracy of Dataset3 was close to that of Dataset2, the test accuracy was lower than both datasets. This indicates that the model did not grasp the information in Dataset3 as well as Dataset2 and had a weaker generalization capability than Dataset2. Although the high training accuracy suggests that the model was able to learn the patterns specific to Dataset3 to some extent, the low test accuracy reveals that its generalization capability was insufficient. The findings clearly demonstrate that Dataset2 was the dataset on which the model performed best. The low accuracy values for Dataset1 indicate that the model did not fully comprehend the information in this dataset and had a weak generalization capability. Although the training accuracy of Dataset3 was close to that of Dataset2, the lower test accuracy of Dataset3 compared to both datasets indicates that the model's generalization capability was weak.

Table 4.7 : Comparison of the performance metrics.

Dataset	Accuracy	Precision	Recall	F1-Score
Data Set-1	0,880	0,877	0,985	0,928
Data Set-2	0,913	0,923	0,985	0,953
Data Set-3	0,891	0,906	0,978	0,940

The findings presented in Table 4.7 compare the performance of a model trained on three different datasets. The model's performance on each dataset was evaluated using various metrics such as accuracy, precision, recall, and F1-score.

The accuracy value of 0.88 is relatively high, indicating that the model generally predicted the data in Dataset1 well. The precision value of 0.877 suggests that the model's ability to correctly predict positive instances is slightly lower. The recall value of 0.985 shows that the model largely predicted all positive instances correctly. The F1-score of 0.928 confirms that the model's overall performance is good for Dataset1. Dataset2 is the dataset with the highest performance in terms of all metrics. The

accuracy value of 0.913 indicates that the model predicts the data in Dataset2 with a considerably high accuracy. The precision and recall values also increase to 0.923 and 0.985, respectively, demonstrating the model's improved ability to distinguish between positive and negative instances. The F1-score of 0.953 confirms that the model exhibits an extremely successful performance on Dataset2. Dataset3 shows a lower performance compared to Dataset2. The accuracy value of 0.891 indicates that the model does not predict the data in Dataset3 as well as Dataset2. The precision and recall values are also lower compared to Dataset2. The F1-score of 0.940 confirms that the model performs lower on Dataset3 compared to Dataset1 and Dataset2. The obtained results clearly demonstrate that Dataset2 is the dataset on which the model performs best. Although Dataset1 and Dataset3 also show acceptable performance, Dataset2's possession of the highest values in all metrics indicates that the model is more successful on this dataset.

Table 4.8 : Logistic regression results.

Independent variables \ coefficients	Data set-1	Data set-2	Data set-3
Age	0.021383	0.026065*	3.103240*
First menstruation age	-0.092976	0.060900	-0.09450*
Menopause (y/n)	0.658631	1.481768*	1.660768*
Bra size (back size)	0.013819	0.004197	1.650328*
Pregnancy (y/n)	-0.508821	-0.747948*	-0.95840*
Total lactation time (year)	0.069955	0.020615	-0.59015*
BMI (kg/m ²)	0.051696	0.087283*	1.304820*
Anxiety /depression (y/n)	-0.440907	1.394822*	1.500942*
Cancer history (y/n)	2.291776*	3.138459*	5.125479*
Family history of breast cancer (y/n)	-0.671425	1.515248*	1.625243*
Cigarette (y/n)	-0.297029	1.087255*	1.230885*
Alcohol (y/n)	-19.423004	-19.655272	10.098846
Training (y/n)	0.919835	-1.480927*	-1.56077*

*p<0.05-statistically significant

Table 4.8 shows the coefficients of the independent variables according to the logistic regression results. The higher amount of data means higher significance as seen in the results. The coefficients are rounded up to 6 decimal places to provide a common idea about the effects of the independent variables on breast cancer occurrence. As stated by World Health Organization the most effective characteristics are gender and age. In our thesis all patients were women so the gender variable was ignored. But one of the highest coefficient belongs to age may be approved by the analysis. The other most effective variable is cancer history which is also seen under decision tree results.

Age, menopause, bra size, BMI, depression, cancer history, family history, cigarette and alcohol usage are affecting breast cancer occurrence positively. Reversely, first menstruation age, pregnancy, total lactation time and training are affecting breast cancer occurrence negatively.

4.3.3 Artificial Neural Network (ANN)

Artificial neural networks, utilizing mathematical models, are predominantly employed techniques in the field of artificial intelligence, notably in supervised and reinforcement learning paradigms. This thesis aims to develop a model predicting whether patients are susceptible to breast cancer, based on 13 different attributes available in the dataset. Given the plethora of parameters inherent in artificial neural networks, hyperparameter optimization was conducted in this study by exploring various values for different parameters. Python, one of the most widely used programming languages in data science, along with the Keras library, was utilized for modeling artificial neural networks.

In artificial neural networks, prior to executing the model, it is essential to standardize variables to ensure the optimization of weights between nodes. Standardization aims to mitigate the discrepancies arising from variables measured in different units, thereby preventing the model from being improperly trained or encountering overfitting issues. Following the completion of label encoding for categorical variables, data standardization was performed using the standardization available within Python.

The optimization process in training artificial neural networks holds significant importance in achieving desirable performance metrics. Among various optimization algorithms, Adam is favored due to its adaptive learning rate and momentum properties. Similarly, the binary cross-entropy loss function is commonly employed in binary classification tasks, offering a means to quantify the dissimilarity between predicted and actual class labels. Given its efficacy in binary classification, the sigmoid activation function was selected for the output layer, while parameters such as batch size and epoch number were kept constant at 32 and 100, respectively, across all models.

For hyperparameter optimization, the study explored three different values for each parameter, including learning rate, activation function, hidden nodes, drop-out rates,

L1 regularization coefficient, and L2 regularization coefficient. A total of 2187 distinct scenarios were executed for three different hidden layers, with the training and testing accuracy values computed for each scenario. The model exhibiting the highest classification accuracy was scrutinized among these scenarios.

Artificial Neural Networks (ANNs) are intricate systems characterized by numerous parameters, each playing a crucial role in the network's performance and behavior. Among these parameters, the learning rate, activation function, number of hidden nodes, dropout rates, L1 regularization coefficient, and L2 regularization coefficient stand out for their significant impact on the training, convergence, and generalization capabilities of the network.

Parameters which are conducted in hyperparameter optimization are as follows:

1. **Learning Rate:** The learning rate governs the step size at which the weights are updated during the training process. Choosing an appropriate learning rate is essential to ensure efficient convergence without overshooting or getting stuck in local minima. Generally, a higher learning rate accelerates convergence but may lead to instability, while a lower learning rate ensures stability but may slow down convergence. Adaptive learning rate techniques, such as those employed in the Adam optimizer, dynamically adjust the learning rate based on the gradient magnitudes, providing a balance between convergence speed and stability.

2. **Activation Function:** Activation functions introduce non-linearity into the network, enabling it to approximate complex functions. Common activation functions include sigmoid, tanh, ReLU, and their variants. The choice of activation function depends on the nature of the problem and the characteristics of the data. ReLU and its variants, such as Leaky ReLU and Parametric ReLU, are popular choices due to their ability to mitigate the vanishing gradient problem and accelerate convergence, especially in deep networks.

3. **Number of Hidden Nodes:** The number of hidden nodes determines the capacity of the network to learn and represent complex patterns in the data. A smaller number of hidden nodes may lead to underfitting, where the network fails to capture the underlying structure of the data. Conversely, an excessive number of hidden nodes can result in overfitting, where the network learns noise in the training data, leading to

poor generalization performance on unseen data. The optimal number of hidden nodes often requires experimentation and validation on a validation dataset.

4. Dropout Rates: Dropout is a regularization technique used to prevent overfitting by randomly deactivating a fraction of neurons during training. This helps in promoting robustness and generalization by forcing the network to learn redundant representations. The dropout rate determines the probability of dropping out a neuron during each training iteration. Typically, dropout rates between 0.2 and 0.5 are found to be effective in preventing overfitting, but the optimal dropout rate may vary depending on the complexity of the network and the size of the dataset.

5. L1 and L2 Regularization Coefficients: L1 and L2 regularization techniques penalize the magnitude of the weights to prevent overfitting and encourage simpler models. L1 regularization adds the absolute values of the weights to the loss function, promoting sparsity and feature selection. On the other hand, L2 regularization adds the squared magnitudes of the weights, leading to smaller but non-zero weights. The choice between L1 and L2 regularization depends on the desired characteristics of the model. Higher regularization coefficients increase the penalty on the weights, leading to more regularized models with potentially better generalization performance.

In practice, determining the optimal values for these parameters often involves experimentation through techniques like grid search or random search, combined with cross-validation to assess the model's performance across different parameter configurations. Additionally, techniques such as early stopping can be employed to prevent overfitting and determine the appropriate number of training epochs. Ultimately, the selection of these parameters should be guided by the specific characteristics of the dataset and the objectives of the modeling task.

Table 4.9 : Training and testing accuracy for data sets

Dataset	Training Accuracy	Testing Accuracy
Data Set-1	0.954	0.933
Data Set-2	0.944	0.953
Data Set-3	0.987	0.981

Table 4.9 shows training and testing accuracies for different data sets. Comparing the training and testing accuracies across the three datasets reveals some interesting

insights into the model's performance and generalization capabilities. Here's a comparative analysis of the provided data:

Data Set 1 demonstrates a high training accuracy of 95.4%, indicating that the model performs well on the data it was trained on. However, there is a noticeable drop in testing accuracy to 93.3%, suggesting that the model may be overfitting to some extent. Overfitting occurs when the model learns noise or random fluctuations in the training data, leading to reduced performance on unseen data. Data Set 2 also exhibits high training accuracy at 94.4%, but interestingly, the testing accuracy is slightly higher at 95.3%. This suggests that the model generalizes better to unseen data compared to Data Set 1. The smaller disparity between training and testing accuracies implies that overfitting may be less of an issue in this dataset. Data Set 3 stands out with remarkably high training and testing accuracies of 98.7% and 98.1%, respectively. The minimal difference between training and testing accuracies indicates that the model generalizes exceptionally well to unseen data. This suggests that Data Set 3 contains clear and distinguishable patterns that the model can effectively learn and apply to new instances.

In summary, while all three datasets yield high training and testing accuracies, there are notable differences in their generalization performance. Data Set 3 emerges as the most favorable dataset, with the smallest disparity between training and testing accuracies, indicating superior generalization capabilities. Data Set 2 also demonstrates strong generalization, while Data Set 1 shows some signs of overfitting. These findings underscore the importance of evaluating both training and testing accuracies to assess the robustness and generalization performance of machine learning models.

The performance evaluation of the three datasets employed confusion matrix metrics, the results of which are presented in Table 4.10.

Table 4.10 : Performance metrics for data sets.

Dataset	Accuracy	Precision	Recall	F1-Score
Data Set-1	0,933	0,968	0,953	0,961
Data Set-2	0,953	0,956	0,981	0,969
Data Set-3	0,981	0,988	0,992	0,990

The provided table presents various performance metrics, including accuracy, precision, recall, and F1 score, for three distinct datasets labeled as Data Set 1, Data Set 2, and Data Set 3. These metrics offer comprehensive insights into the model's predictive capabilities, highlighting its ability to correctly classify instances, detect relevant cases, and balance between precision and recall. Below is a detailed comparative analysis of these metrics across the datasets:

Accuracy measures the overall correctness of the model's predictions, reflecting the proportion of correctly classified instances among all instances in the dataset. Data Set 3 exhibits the highest accuracy, indicating that the model correctly predicts the class labels for a significant majority of instances in this dataset. Data Set 2 follows with slightly lower accuracy, while Data Set 1 demonstrates the lowest accuracy among the three datasets. Precision quantifies the proportion of true positive predictions among all positive predictions made by the model. It represents the model's ability to avoid false positives. Data Set 3 stands out with the highest precision, indicating that it has the lowest rate of false positive predictions, followed by Data Set 1 and Data Set 2. Recall measures the model's ability to correctly identify all relevant instances, reflecting the proportion of true positive predictions among all actual positive instances in the dataset. Data Set 3 demonstrates the highest recall, indicating that it has the lowest rate of false negatives, followed by Data Set 2 and Data Set 1. The F1 score is the harmonic mean of precision and recall, providing a balanced measure of a model's performance. It takes into account both false positives and false negatives, making it particularly useful for imbalanced datasets. Data Set 3 exhibits the highest F1 score, indicating excellent balance between precision and recall, followed by Data Set 2 and Data Set 1.

In summary, while all three datasets yield high performance across various metrics, Data Set 3 consistently outperforms the others in terms of accuracy, precision, recall, and F1 score. This suggests that Data Set 3 contains clearer patterns and is more easily learnable by the model. However, further analysis of the datasets' characteristics and the specific context of the classification task is necessary to fully interpret these findings and draw actionable insights.



5. COMPARISON OF THE ANALYSIS RESULTS

Table 5.1 presents a comparative evaluation of three distinct predictive modeling techniques—Decision Trees (DT), Logistic Regression (LR), and Artificial Neural Networks (ANN)—across three datasets, using four metrics: accuracy, precision, recall, and F1-score.

Table 5.1 : Comparison of all algorithms' performance metrics.

Dataset, algorithm	Accuracy	Precision	Recall	F1-Score
Data Set-1 DT	0.907	0.667	0.222	0.333
Data Set-2 DT	0.923	0.714	0.345	0.465
Data Set-3 DT	0.910	1.000	0.277	0.434
Data Set-1 LR	0,880	0,877	0,985	0,928
Data Set-2 LR	0,913	0,923	0,985	0,953
Data Set-3 LR	0,891	0,906	0,978	0,940
Data Set-1 ANN	0,933	0,968	0,953	0,961
Data Set-2 ANN	0,953	0,956	0,981	0,969
Data Set-3 ANN	0,981	0,988	0,992	0,990

The Decision Tree models exhibit a commendable level of accuracy, remaining consistent around 90% across all three datasets. However, these models demonstrate a varied performance in terms of precision and recall, which is particularly evident in Data Set-1 with the lowest F1-score of 0.333. This suggests a modest balance between the rate of true positives and the precision of those positive predictions, which may indicate a tendency for the model to misclassify negative cases as positive (false positives).

Logistic Regression models show a notable enhancement in recall across the datasets, consistently scoring above 0.978. This high recall indicates that the Logistic Regression models are exceptionally adept at identifying true positive cases. However, the precision of the Logistic Regression models does not match their recall, indicating a small number of false positives. Nevertheless, the F1-scores of Logistic Regression models are robust, particularly in Dataset2 LR and Dataset3 LR, reflecting a superior balance between precision and recall compared to the Decision Tree models.

The Artificial Neural Network models stand out with outstanding overall performance, particularly in Data Set3 ANN, where the model approaches near-perfect scores in all metrics. With precision and recall both exceeding 0.988, the ANN models exhibit an exceptional ability to correctly classify positive cases while minimizing both false positives and negatives, as evidenced by F1-scores close to 1.

In conclusion, while each model demonstrates strengths in different areas, the Artificial Neural Networks show the most balanced and highest overall performance according to the provided metrics. This suggests that for this specific application, ANN might be the preferred model due to its ability to generalize and minimize error across the datasets. It is worth noting, however, that model selection should be informed not only by performance metrics but also by considerations of the models' interpretability, computational efficiency, and the specific cost of misclassifications in the applied domain.

6. CONCLUSIONS AND RECOMMENDATIONS

In conclusion, this thesis has undertaken a multidimensional analysis to explore the relationship between women's properties and breast cancer occurrence, recognizing the pressing need for comprehensive research in this field. By leveraging a reputable clinic's dataset and employing advanced machine learning techniques, we have identified significant risk factors and developed predictive models with the ultimate goal of enhancing our understanding of breast cancer etiology and contributing to the development of targeted interventions.

The thorough review of existing literature provided a solid theoretical foundation and highlighted gaps in knowledge, setting the stage for our investigation. Through the collection and preprocessing of a comprehensive dataset, we ensured the integrity and quality of our analysis, encompassing various variables such as demographic information, lifestyle factors, genetic markers, and medical history.

The utilization of advanced machine learning algorithms facilitated the development of predictive models that accurately determined the likelihood of breast cancer occurrence. Through in-depth analyses and comparisons with existing knowledge, we interpreted the results and identified influential risk factors, providing valuable insights for preventive strategies, early detection, and targeted interventions.

Furthermore, the incorporation of a case study on value stream mapping in a radiology department showcased the practical application of lean management techniques in improving efficiency and patient flow. This highlights the broader applicability of our research findings and contributes to the enhancement of overall quality of care in healthcare settings.

By advancing our understanding of breast cancer etiology, improving risk assessment models, and showcasing the practical applicability of lean management techniques, this thesis aims to drive advancements in patient care and outcomes. The identification of significant risk factors can inform targeted screening programs, early detection strategies, and personalized interventions, while the application of value stream

mapping techniques can optimize resource allocation, enhance operational efficiency, and improve patient care.

Overall, this comprehensive research contributes to the growing body of knowledge in breast cancer research, clinical practice, and healthcare management. It is our hope that the insights gained from this thesis will have a meaningful impact in the fight against breast cancer, leading to advancements in personalized prevention and treatment approaches, and ultimately improving patient outcomes.

The primary contributions of this thesis can be delineated in two points:

1. The study collaborates with a breast clinic in Turkey that boasts a 100% survival rate and serves the largest population of breast cancer patients in the region. These rates surpass the breast cancer statistics reported in the literature. Therefore, analyzing local data from Turkey constitutes a significant contribution, reflecting superior outcomes in breast cancer management.
2. The implementation of lean approaches for process improvement and the transition to a digital format will expedite data entry, eliminating time wastage. In the context of breast cancer, where early diagnosis is crucial, saving time is of utmost importance. The use of machine learning algorithms to quickly assess the likelihood of a patient being diseased will complement the doctor's examination, enabling rapid preliminary assessment. This will facilitate earlier requests for necessary medical tests and, if needed, expedite the commencement of treatment.

Future studies could gather real data sets electronically to achieve larger volumes, allowing the algorithms used in this study to be applied to more extensive data sets. Generalizing these algorithms across Turkey could lead to the development of a mobile application, enabling medical personnel or patients to input data and assess the likelihood of breast cancer, with the potential to monitor the entire treatment process as it progresses.

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APPENDICES

APPENDIX A: Pseudo Code for Hyperparameter Optimization

APPENDIX B: Decision Trees for Different Data Sets

APPENDIX C: Examples from Scenerio Analyis Results for Different Data Sets



APPENDIX A : Pseudo Code for Hyperparameter Optimization

```
data = load_data_from_excel()
X, y = separate_independent_dependent_variables(data)
X_train, X_test, y_train, y_test = split_data(X, y)

# Model creation and training process
results_df = create_empty_results_dataframe()

for lr in learning_rates:
    for activation_func in activation_functions:
        for nodes in hidden_nodes:
            for dropout_rate in dropout_rates:
                for l1_reg in l1_regs:
                    for l2_reg in l2_regs:
                        model_name = create_model_name(lr, activation_func, nodes,
dropout_rate, l1_reg, l2_reg)
                        model = create_model(lr, activation_func, nodes, dropout_rate, l1_reg,
l2_reg)
                        train_model(model, X_train, y_train)
                        train_accuracy = evaluate_model_accuracy(model, X_train, y_train)
                        test_accuracy = evaluate_model_accuracy(model, X_test, y_test)
                        results_df.append([model_name, lr, activation_func, nodes,
dropout_rate, l1_reg, l2_reg, train_accuracy, test_accuracy])

print(results_df)
```

APPENDIX B : Decision Trees for Different Data Sets

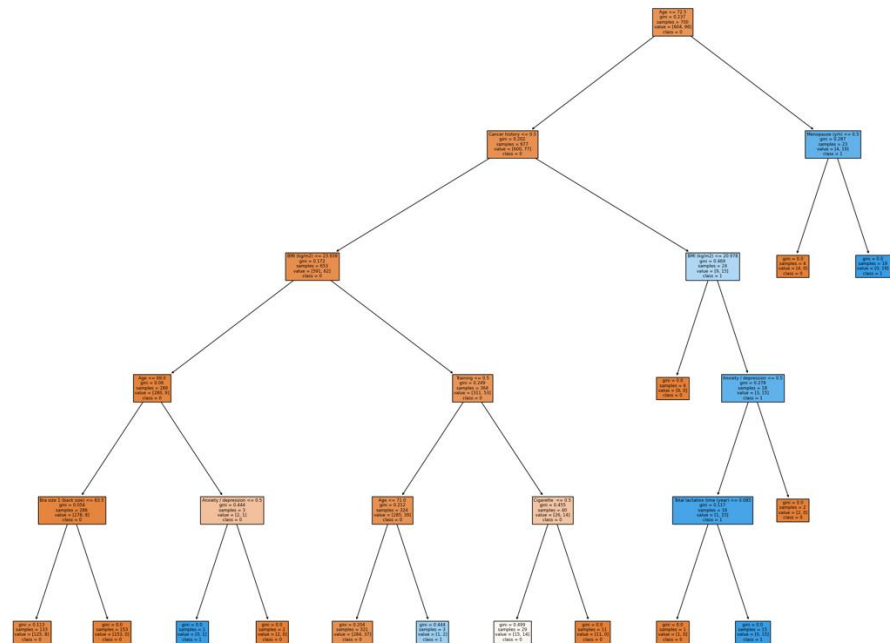


Figure B.1 : Decision tree of data set-2.

Figure B.2 : Decision tree of data set-3.

APPENDIX C : Examples from Scenerio Analysis Results for Different Data Sets

Model_Name	Learning_Rate	Activation_Function	Hidden_Nodes	Hidden_Layer	Dropout_Rate	L1_Regularization	L2_Regularization	Training_Accuracy	Testing_Accuracy
LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.0_L2_0.0_HL_2	0.001	tanh	10	1	0	0	0	0.913294792	0.839999974
LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.0_L2_0.001_HL_2	0.001	tanh	10	1	0	0	0.001	0.919075131	0.879999995
LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.0_L2_0.01_HL_2	0.001	tanh	10	1	0	0	0.01	0.913294792	0.839999974
LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.001_L2_0.0_HL_2	0.001	tanh	10	1	0	0.001	0	0.907514453	0.853333354
LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.001_L2_0.001_HL_2	0.001	tanh	10	1	0	0.001	0.001	0.895953774	0.853333354
LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.001_L2_0.01_HL_2	0.001	tanh	10	1	0	0.001	0.01	0.907514453	0.853333354
LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.01_L2_0.0_HL_2	0.001	tanh	10	1	0	0.01	0	0.890173435	0.853333354
LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.01_L2_0.001_HL_2	0.001	tanh	10	1	0	0.01	0.001	0.884393036	0.853333354
LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.01_L2_0.01_HL_2	0.001	tanh	10	1	0	0.01	0.01	0.878612697	0.839999974
LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.0_L2_0.0_HL_2	0.001	tanh	10	1	0.1	0	0	0.924855471	0.866666675
LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.0_L2_0.001_HL_2	0.001	tanh	10	1	0.1	0	0.001	0.913294792	0.853333354
LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.0_L2_0.01_HL_2	0.001	tanh	10	1	0.1	0	0.01	0.907514453	0.853333354
LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.001_L2_0.0_HL_2	0.001	tanh	10	1	0.1	0.001	0	0.901734114	0.866666675
LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.001_L2_0.001_HL_2	0.001	tanh	10	1	0.1	0.001	0.001	0.901734114	0.866666675
LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.001_L2_0.01_HL_2	0.001	tanh	10	1	0.1	0.001	0.01	0.913294792	0.866666675
LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.01_L2_0.0_HL_2	0.001	tanh	10	1	0.1	0.01	0	0.890173435	0.866666675
LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.01_L2_0.001_HL_2	0.001	tanh	10	1	0.1	0.01	0.001	0.890173435	0.866666675
LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.01_L2_0.01_HL_2	0.001	tanh	10	1	0.1	0.01	0.01	0.895953774	0.879999995
LR_0.001_AF_tanh_HN_10_Dropout_0.2_L1_0.0_L2_0.0_HL_2	0.001	tanh	10	1	0.2	0	0	0.895953774	0.866666675
LR_0.001_AF_tanh_HN_10_Dropout_0.2_L1_0.0_L2_0.001_HL_2	0.001	tanh	10	1	0.2	0	0.001	0.919075131	0.839999974
LR_0.001_AF_tanh_HN_10_Dropout_0.2_L1_0.0_L2_0.01_HL_2	0.001	tanh	10	1	0.2	0	0.01	0.901734114	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_L1_0.0_L2_0.0_HL_2	0.001	sigmoid	10	1	0	0	0	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_L1_0.0_L2_0.001_HL_2	0.001	sigmoid	10	1	0	0	0.001	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_L1_0.0_L2_0.01_HL_2	0.001	sigmoid	10	1	0	0	0.01	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_L1_0.001_L2_0.0_HL_2	0.001	sigmoid	10	1	0	0.001	0	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_L1_0.001_L2_0.001_HL_2	0.001	sigmoid	10	1	0	0.001	0.001	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_L1_0.001_L2_0.01_HL_2	0.001	sigmoid	10	1	0	0.001	0.01	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_L1_0.01_L2_0.0_HL_2	0.001	sigmoid	10	1	0	0.01	0	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_L1_0.01_L2_0.001_HL_2	0.001	sigmoid	10	1	0	0.01	0.001	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_L1_0.0_L2_0.0_HL_2	0.001	sigmoid	10	1	0.1	0	0	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_L1_0.0_L2_0.001_HL_2	0.001	sigmoid	10	1	0.1	0	0.001	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_L1_0.0_L2_0.01_HL_2	0.001	sigmoid	10	1	0.1	0	0.01	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_L1_0.01_L2_0.0_HL_2	0.001	sigmoid	10	1	0.1	0.01	0	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_L1_0.01_L2_0.001_HL_2	0.001	sigmoid	10	1	0.1	0.01	0.001	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_L1_0.01_L2_0.01_HL_2	0.001	sigmoid	10	1	0.1	0.01	0.01	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_L1_0.0_L2_0.0_HL_2	0.001	sigmoid	10	1	0.2	0	0	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_L1_0.0_L2_0.001_HL_2	0.001	sigmoid	10	1	0.2	0	0.001	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_L1_0.0_L2_0.01_HL_2	0.001	sigmoid	10	1	0.2	0	0.01	0.895953774	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_L1_0.001_L2_0.0_HL_2	0.001	sigmoid	10	1	0.2	0.001	0	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_L1_0.001_L2_0.001_HL_2	0.001	sigmoid	10	1	0.2	0.001	0.001	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_L1_0.001_L2_0.01_HL_2	0.001	sigmoid	10	1	0.2	0.001	0.01	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_L1_0.01_L2_0.0_HL_2	0.001	sigmoid	10	1	0.2	0.01	0	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_L1_0.01_L2_0.001_HL_2	0.001	sigmoid	10	1	0.2	0.01	0.001	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_20_Dropout_0.0_L1_0.0_L2_0.0_HL_2	0.001	sigmoid	20	1	0	0	0	0.895953774	0.839999974
LR_0.001_AF_sigmoid_HN_20_Dropout_0.0_L1_0.0_L2_0.001_HL_2	0.001	sigmoid	20	1	0	0	0.001	0.895953774	0.839999974
LR_0.001_AF_sigmoid_HN_20_Dropout_0.0_L1_0.0_L2_0.01_HL_2	0.001	sigmoid	20	1	0	0.001	0	0.895953774	0.839999974
LR_0.001_AF_sigmoid_HN_20_Dropout_0.0_L1_0.001_L2_0.0_HL_2	0.001	sigmoid	20	1	0	0.001	0.001	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_20_Dropout_0.0_L1_0.001_L2_0.001_HL_2	0.001	sigmoid	20	1	0	0.001	0.01	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_20_Dropout_0.0_L1_0.01_L2_0.0_HL_2	0.001	sigmoid	20	1	0	0.01	0	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_20_Dropout_0.0_L1_0.01_L2_0.001_HL_2	0.001	sigmoid	20	1	0	0.01	0.001	0.890173435	0.839999974
LR_0.001_AF_sigmoid_HN_20_Dropout_0.0_L1_0.01_L2_0.01_HL_2	0.001	sigmoid	20	1	0	0.01	0.01	0.890173435	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.0_L1_0.0_L2_0.0_HL_2	0.001	relu	10	1	0.1	0	0	0.895953774	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.0_L1_0.0_L2_0.001_HL_2	0.001	relu	10	1	0	0	0	0.907514453	0.866666675
LR_0.001_AF_relu_HN_10_Dropout_0.0_L1_0.0_L2_0.001_HL_2	0.001	relu	10	1	0	0	0.001	0.913294792	0.826666653
LR_0.001_AF_relu_HN_10_Dropout_0.0_L1_0.0_L2_0.01_HL_2	0.001	relu	10	1	0	0	0.01	0.919075131	0.853333354
LR_0.001_AF_relu_HN_10_Dropout_0.0_L1_0.001_L2_0.0_HL_2	0.001	relu	10	1	0	0.001	0	0.901734114	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.0_L1_0.001_L2_0.001_HL_2	0.001	relu	10	1	0	0.001	0.001	0.913294792	0.826666653
LR_0.001_AF_relu_HN_10_Dropout_0.0_L1_0.001_L2_0.01_HL_2	0.001	relu	10	1	0	0.001	0.01	0.895953774	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.0_L1_0.01_L2_0.0_HL_2	0.001	relu	10	1	0	0.01	0	0.913294792	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.0_L1_0.01_L2_0.001_HL_2	0.001	relu	10	1	0	0.01	0.001	0.901734114	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.0_L1_0.01_L2_0.01_HL_2	0.001	relu	10	1	0	0.01	0.01	0.901734114	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.1_L1_0.0_L2_0.0_HL_2	0.001	relu	10	1	0.1	0	0	0.901734114	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.1_L1_0.0_L2_0.001_HL_2	0.001	relu	10	1	0.1	0	0.001	0.901734114	0.866666675
LR_0.001_AF_relu_HN_10_Dropout_0.1_L1_0.0_L2_0.01_HL_2	0.001	relu	10	1	0.1	0	0.01	0.907514453	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.1_L1_0.001_L2_0.0_HL_2	0.001	relu	10	1	0.1	0.001	0	0.907514453	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.1_L1_0.001_L2_0.001_HL_2	0.001	relu	10	1	0.1	0.001	0.001	0.919075131	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.1_L1_0.001_L2_0.01_HL_2	0.001	relu	10	1	0.1	0.001	0.01	0.93063581	0.853333354
LR_0.001_AF_relu_HN_10_Dropout_0.1_L1_0.01_L2_0.0_HL_2	0.001	relu	10	1	0.1	0.01	0	0.907514453	0.853333354
LR_0.001_AF_relu_HN_10_Dropout_0.1_L1_0.01_L2_0.001_HL_2	0.001	relu	10	1	0.1	0.01	0.001	0.890173435	0.879999995
LR_0.001_AF_relu_HN_10_Dropout_0.1_L1_0.01_L2_0.01_HL_2	0.001	relu	10	1	0.1	0.01	0.01	0.890173435	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.2_L1_0.0_L2_0.0_HL_2	0.001	relu	10	1	0.2	0	0	0.890173435	0.853333354
LR_0.001_AF_relu_HN_10_Dropout_0.2_L1_0.0_L2_0.001_HL_2	0.001	relu	10	1	0.2	0	0.001	0.884393036	0.853333354
LR_0.001_AF_relu_HN_10_Dropout_0.2_L1_0.0_L2_0.01_HL_2	0.001	relu	10	1	0.2	0	0.01	0.872832358	0.853333354
LR_0.001_AF_relu_HN_10_Dropout_0.2_L1_0.001_L2_0.0_HL_2	0.001	relu	10	1	0.2	0.001	0	0.901734114	0.853333354
LR_0.001_AF_relu_HN_10_Dropout_0.2_L1_0.001_L2_0.001_HL_2	0.001	relu	10	1	0.2	0.001	0.001	0.884393036	0.853333354
LR_0.001_AF_relu_HN_10_Dropout_0.2_L1_0.001_L2_0.01_HL_2	0.001	relu	10	1	0.2	0.001	0.01	0.907514453	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.2_L1_0.01_L2_0.0_HL_2	0.001	relu	10	1	0.2	0.01	0	0.890173435	0.839999974
LR_0.001_AF_relu_HN_10_Dropout_0.2_L1_0.01_L2_0.001_HL_2	0.001	relu	10	1	0.2	0.01	0.001	0.895953774	0.853333354

Figure C.1 : Examples from scenerio analysis results for data set-1.

Model Name	Learning_Rate	Activation_Function	Hidden_Nodes	Hidden_Layer	Dropout_Rate	L1_Regularization	L2_Regularization	Training_Accuracy	Testing_Accuracy
LR_0.001_AF_tanh_HN_10_Dropout_0.0_1_1.0_0.0_L2_0.0_HL_2	0.001	tanh	10	1	0	0	0	0.9342857	0.92000017
LR_0.001_AF_tanh_HN_10_Dropout_0.0_1_1.0_0.0_L2_0.001_HL_2	0.001	tanh	10	1	0	0	0.001	0.93142852	0.90666696
LR_0.001_AF_tanh_HN_10_Dropout_0.0_1_1.0_0.0_L2_0.01_HL_2	0.001	tanh	10	1	0	0	0.01	0.922857165	0.89999976
LR_0.001_AF_tanh_HN_10_Dropout_0.0_1_1.0_0.001_L2_0.0_HL_2	0.001	tanh	10	1	0	0.001	0	0.920000017	0.89999976
LR_0.001_AF_tanh_HN_10_Dropout_0.0_1_1.0_0.001_L2_0.001_HL_2	0.001	tanh	10	1	0	0.001	0.001	0.92428571	0.910000026
LR_0.001_AF_tanh_HN_10_Dropout_0.0_1_1.0_0.001_L2_0.01_HL_2	0.001	tanh	10	1	0	0.001	0.01	0.920000017	0.90666696
LR_0.001_AF_tanh_HN_10_Dropout_0.0_1_1.0_0.01_L2_0.0_HL_2	0.001	tanh	10	1	0	0.01	0	0.90142858	0.879999995
LR_0.001_AF_tanh_HN_10_Dropout_0.0_1_1.0_0.01_L2_0.001_HL_2	0.001	tanh	10	1	0	0.01	0.001	0.902857125	0.883333325
LR_0.001_AF_tanh_HN_10_Dropout_0.0_1_1.0_0.01_L2_0.01_HL_2	0.001	tanh	10	1	0	0.01	0.01	0.895714283	0.879999995
LR_0.001_AF_tanh_HN_10_Dropout_0.1_1_1.0_0.0_L2_0.0_HL_2	0.001	tanh	10	1	0.1	0	0	0.925714314	0.91666687
LR_0.001_AF_tanh_HN_10_Dropout_0.1_1_1.0_0.0_L2_0.001_HL_2	0.001	tanh	10	1	0.1	0	0.001	0.918571413	0.90666696
LR_0.001_AF_tanh_HN_10_Dropout_0.1_1_1.0_0.0_L2_0.01_HL_2	0.001	tanh	10	1	0.1	0	0.01	0.917142868	0.889999986
LR_0.001_AF_tanh_HN_10_Dropout_0.1_1_1.0_0.001_L2_0.0_HL_2	0.001	tanh	10	1	0.1	0.001	0	0.921428561	0.899999976
LR_0.001_AF_tanh_HN_10_Dropout_0.1_1_1.0_0.001_L2_0.001_HL_2	0.001	tanh	10	1	0.1	0.001	0.001	0.912857115	0.903333306
LR_0.001_AF_tanh_HN_10_Dropout_0.1_1_1.0_0.001_L2_0.01_HL_2	0.001	tanh	10	1	0.1	0.001	0.01	0.921428561	0.899999976
LR_0.001_AF_tanh_HN_10_Dropout_0.1_1_1.0_0.01_L2_0.0_HL_2	0.001	tanh	10	1	0.1	0.01	0	0.892857134	0.876666665
LR_0.001_AF_tanh_HN_10_Dropout_0.1_1_1.0_0.01_L2_0.001_HL_2	0.001	tanh	10	1	0.1	0.01	0.001	0.887142837	0.876666665
LR_0.001_AF_tanh_HN_10_Dropout_0.1_1_1.0_0.01_L2_0.01_HL_2	0.001	tanh	10	1	0.1	0.01	0.01	0.895714283	0.876666665
LR_0.001_AF_tanh_HN_10_Dropout_0.2_1_1.0_0.0_L2_0.0_HL_2	0.001	tanh	10	1	0.2	0	0	0.917142868	0.90666696
LR_0.001_AF_tanh_HN_10_Dropout_0.2_1_1.0_0.0_L2_0.001_HL_2	0.001	tanh	10	1	0.2	0	0.001	0.915714264	0.913333356
LR_0.001_AF_tanh_HN_10_Dropout_0.2_1_1.0_0.0_L2_0.01_HL_2	0.001	tanh	10	1	0.2	0	0.01	0.911428571	0.903333306
LR_0.001_AF_tanh_HN_10_Dropout_0.2_1_1.0_0.001_L2_0.0_HL_2	0.001	tanh	10	1	0.2	0.001	0	0.905714273	0.903333306
LR_0.001_AF_tanh_HN_10_Dropout_0.2_1_1.0_0.001_L2_0.001_HL_2	0.001	tanh	10	1	0.2	0.001	0.001	0.914285719	0.896666646
LR_0.001_AF_tanh_HN_10_Dropout_0.2_1_1.0_0.001_L2_0.01_HL_2	0.001	tanh	10	1	0.2	0.001	0.01	0.918571413	0.90666696
LR_0.001_AF_tanh_HN_10_Dropout_0.2_1_1.0_0.01_L2_0.0_HL_2	0.001	tanh	10	1	0.2	0.01	0	0.894285738	0.876666665
LR_0.001_AF_tanh_HN_10_Dropout_0.2_1_1.0_0.01_L2_0.001_HL_2	0.001	tanh	10	1	0.2	0.01	0.001	0.892857134	0.876666665
LR_0.001_AF_tanh_HN_20_Dropout_0.0_1_1.0_0.0_L2_0.0_HL_2	0.001	tanh	20	1	0	0	0	0.937142849	0.920000017
LR_0.001_AF_tanh_HN_20_Dropout_0.0_1_1.0_0.0_L2_0.001_HL_2	0.001	tanh	20	1	0	0	0.001	0.937142849	0.923333347
LR_0.001_AF_tanh_HN_20_Dropout_0.0_1_1.0_0.0_L2_0.01_HL_2	0.001	tanh	20	1	0	0	0.01	0.932857156	0.91666687
LR_0.001_AF_tanh_HN_20_Dropout_0.0_1_1.0_0.001_L2_0.0_HL_2	0.001	tanh	20	1	0	0.001	0	0.92428571	0.90666696
LR_0.001_AF_tanh_HN_20_Dropout_0.0_1_1.0_0.001_L2_0.001_HL_2	0.001	tanh	20	1	0	0.001	0.001	0.930000007	0.90666696
LR_0.001_AF_tanh_HN_20_Dropout_0.0_1_1.0_0.001_L2_0.01_HL_2	0.001	tanh	20	1	0	0.001	0.01	0.931428561	0.913333356
LR_0.001_AF_tanh_HN_20_Dropout_0.0_1_1.0_0.01_L2_0.0_HL_2	0.001	tanh	20	1	0	0.01	0	0.894285738	0.876666665
LR_0.001_AF_tanh_HN_20_Dropout_0.0_1_1.0_0.01_L2_0.001_HL_2	0.001	tanh	20	1	0	0.01	0.001	0.892857134	0.876666665
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.0_L2_0.0_HL_2	0.001	tanh	20	1	0.1	0	0	0.937142849	0.920000017
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.0_L2_0.001_HL_2	0.001	tanh	20	1	0.1	0	0.001	0.937142849	0.923333347
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.0_L2_0.01_HL_2	0.001	tanh	20	1	0.1	0	0.01	0.932857156	0.91666687
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.001_L2_0.0_HL_2	0.001	tanh	20	1	0.1	0.001	0	0.92428571	0.90666696
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.001_L2_0.001_HL_2	0.001	tanh	20	1	0.1	0.001	0.001	0.930000007	0.90666696
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.001_L2_0.01_HL_2	0.001	tanh	20	1	0.1	0.001	0.01	0.931428561	0.913333356
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.01_L2_0.0_HL_2	0.001	tanh	20	1	0.1	0.01	0	0.894285738	0.876666665
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.01_L2_0.001_HL_2	0.001	tanh	20	1	0.1	0.01	0.001	0.894285738	0.879999995
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.01_L2_0.01_HL_2	0.001	tanh	20	1	0.1	0.01	0.01	0.894285738	0.876666665
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.01_L2_0.001_HL_2	0.001	tanh	20	1	0.1	0.01	0.001	0.892857134	0.876666665
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.01_L2_0.01_HL_2	0.001	tanh	20	1	0.1	0.01	0.01	0.920000017	0.903333306
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.01_L2_0.0_HL_2	0.001	tanh	20	1	0.1	0.01	0	0.892857134	0.876666665
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.01_L2_0.001_HL_2	0.001	tanh	20	1	0.1	0.01	0.001	0.889999986	0.876666665
LR_0.001_AF_tanh_HN_20_Dropout_0.1_1_1.0_0.01_L2_0.01_HL_2	0.001	tanh	20	1	0.1	0.01	0.01	0.898571432	0.879999995
LR_0.001_AF_tanh_HN_20_Dropout_0.2_1_1.0_0.0_L2_0.0_HL_2	0.001	tanh	20	1	0.2	0	0	0.925714314	0.913333356
LR_0.001_AF_tanh_HN_20_Dropout_0.2_1_1.0_0.0_L2_0.001_HL_2	0.001	tanh	20	1	0.2	0	0.001	0.921428561	0.910000026
LR_0.001_AF_tanh_HN_20_Dropout_0.2_1_1.0_0.0_L2_0.01_HL_2	0.001	tanh	20	1	0.2	0	0.01	0.912857115	0.910000026
LR_0.001_AF_tanh_HN_20_Dropout_0.2_1_1.0_0.001_L2_0.0_HL_2	0.001	tanh	20	1	0.2	0.001	0	0.917142868	0.899999976
LR_0.001_AF_tanh_HN_20_Dropout_0.2_1_1.0_0.001_L2_0.001_HL_2	0.001	tanh	20	1	0.2	0.001	0.001	0.910000026	0.899999976
LR_0.001_AF_tanh_HN_20_Dropout_0.2_1_1.0_0.001_L2_0.01_HL_2	0.001	tanh	20	1	0.2	0.001	0.01	0.911428571	0.90666696
LR_0.001_AF_tanh_HN_20_Dropout_0.2_1_1.0_0.01_L2_0.0_HL_2	0.001	tanh	20	1	0.2	0.01	0	0.89142859	0.876666665
LR_0.001_AF_tanh_HN_20_Dropout_0.2_1_1.0_0.01_L2_0.001_HL_2	0.001	tanh	20	1	0.2	0.01	0.001	0.898571432	0.879999995
LR_0.001_AF_tanh_HN_20_Dropout_0.2_1_1.0_0.01_L2_0.01_HL_2	0.001	tanh	20	1	0.2	0.01	0.01	0.892857134	0.879999995
LR_0.001_AF_tanh_HN_30_Dropout_0.0_1_1.0_0.0_L2_0.0_HL_2	0.001	tanh	30	1	0	0	0	0.939999998	0.913333356
LR_0.001_AF_tanh_HN_30_Dropout_0.0_1_1.0_0.0_L2_0.001_HL_2	0.001	tanh	30	1	0	0	0.001	0.938571453	0.923333347
LR_0.001_AF_tanh_HN_30_Dropout_0.0_1_1.0_0.0_L2_0.01_HL_2	0.001	tanh	30	1	0	0	0.01	0.938571453	0.91666687
LR_0.001_AF_tanh_HN_30_Dropout_0.0_1_1.0_0.001_L2_0.0_HL_2	0.001	tanh	30	1	0	0.001	0	0.927142859	0.910000026
LR_0.001_AF_tanh_HN_30_Dropout_0.0_1_1.0_0.001_L2_0.001_HL_2	0.001	tanh	30	1	0	0.001	0.001	0.927142859	0.910000026
LR_0.001_AF_tanh_HN_30_Dropout_0.0_1_1.0_0.001_L2_0.01_HL_2	0.001	tanh	30	1	0	0.001	0.01	0.92428571	0.90666696
LR_0.001_AF_tanh_HN_30_Dropout_0.0_1_1.0_0.01_L2_0.0_HL_2	0.001	tanh	30	1	0	0.01	0	0.892857134	0.879999995
LR_0.001_AF_tanh_HN_30_Dropout_0.0_1_1.0_0.01_L2_0.001_HL_2	0.001	tanh	30	1	0	0.01	0.001	0.897142828	0.879999995
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_1_1.0_0.0_L2_0.0_HL_2	0.001	sigmoid	10	1	0	0	0	0.911428571	0.893333316
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_1_1.0_0.0_L2_0.001_HL_2	0.001	sigmoid	10	1	0	0	0.001	0.910000026	0.899999976
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_1_1.0_0.0_L2_0.01_HL_2	0.001	sigmoid	10	1	0	0	0.01	0.902857125	0.879999995
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_1_1.0_0.001_L2_0.0_HL_2	0.001	sigmoid	10	1	0	0.001	0	0.897142828	0.879999995
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_1_1.0_0.001_L2_0.001_HL_2	0.001	sigmoid	10	1	0	0.001	0.001	0.898571432	0.879999995
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_1_1.0_0.001_L2_0.01_HL_2	0.001	sigmoid	10	1	0	0.001	0.01	0.899999976	0.879999995
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_1_1.0_0.01_L2_0.0_HL_2	0.001	sigmoid	10	1	0	0.01	0	0.897871451	0.866666675
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_1_1.0_0.01_L2_0.001_HL_2	0.001	sigmoid	10	1	0	0.01	0.001	0.878571451	0.866666675
LR_0.001_AF_sigmoid_HN_10_Dropout_0.0_1_1.0_0.01_L2_0.01_HL_2	0.001	sigmoid	10	1	0	0.01	0.01	0.878571451	0.866666675
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_1_1.0_0.0_L2_0.0_HL_2	0.001	sigmoid	10	1	0.1	0	0	0.902857125	0.889999986
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_1_1.0_0.0_L2_0.001_HL_2	0.001	sigmoid	10	1	0.1	0	0.001	0.899999976	0.886666656
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_1_1.0_0.0_L2_0.01_HL_2	0.001	sigmoid	10	1	0.1	0	0.01	0.902857125	0.879999995
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_1_1.0_0.001_L2_0.0_HL_2	0.001	sigmoid	10	1	0.1	0.001	0	0.899999986	0.876666665
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_1_1.0_0.001_L2_0.001_HL_2	0.001	sigmoid	10	1	0.1	0.001	0.001	0.895714283	0.879999995
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_1_1.0_0.001_L2_0.01_HL_2	0.001	sigmoid	10	1	0.1	0.001	0.01	0.899999976	0.876666665
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_1_1.0_0.01_L2_0.0_HL_2	0.001	sigmoid	10	1	0.1	0.01	0	0.878571451	0.866666675
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_1_1.0_0.01_L2_0.001_HL_2	0.001	sigmoid	10	1	0.1	0.01	0.001	0.878571451	0.866666675
LR_0.001_AF_sigmoid_HN_10_Dropout_0.1_1_1.0_0.01_L2_0.01_HL_2	0.001	sigmoid	10	1	0.1	0.01	0.01	0.878571451	0.866666675
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_1_1.0_0.0_L2_0.0_HL_2	0.001	sigmoid	10	1	0.2	0	0	0.905714273	0.883333325
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_1_1.0_0.0_L2_0.001_HL_2	0.001	sigmoid	10	1	0.2	0	0.001	0.887142837	0.873333335
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_1_1.0_0.0_L2_0.01_HL_2	0.001	sigmoid	10	1	0.2	0	0.01	0.897142828	0.883333325
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_1_1.0_0.001_L2_0.0_HL_2	0.001	sigmoid	10	1	0.2	0.001	0	0.884285688	0.863333344
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_1_1.0_0.001_L2_0.001_HL_2	0.001	sigmoid	10	1	0.2	0.001	0.001	0.895714283	0.870000005
LR_0.001_AF_sigmoid_HN_10_Dropout_0.2_1_1.0_0.001_L2_0.01_HL_2	0.001	sigmoid	10</						

	Model Name	Learning Rate	Activation Function	Hidden Nodes	Dropout Rate	L1 Regularization	L2 Regularization	Training Accuracy	Testing Accuracy
0	LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.0_L2_0.0_HL_2	0.001	tanh	10	0	0	0	0.961142838	0.958999991
1	LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.0_L2_0.001_HL_2	0.001	tanh	10	0	0	0.001	0.954714298	0.955999997
2	LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.0_L2_0.01_HL_2	0.001	tanh	10	0	0	0.01	0.948000014	0.947666645
3	LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.001_L2_0.0_HL_2	0.001	tanh	10	0	0.001	0	0.936428547	0.944000006
4	LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.001_L2_0.001_HL_2	0.001	tanh	10	0	0.001	0.001	0.941999972	0.944333315
5	LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.001_L2_0.01_HL_2	0.001	tanh	10	0	0.001	0.01	0.9342857	0.93933332
6	LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.01_L2_0.0_HL_2	0.001	tanh	10	0	0.01	0	0.912	0.916333318
7	LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.01_L2_0.001_HL_2	0.001	tanh	10	0	0.01	0.001	0.885428548	0.897666693
8	LR_0.001_AF_tanh_HN_10_Dropout_0.0_L1_0.01_L2_0.01_HL_2	0.001	tanh	10	0	0.01	0.01	0.883571446	0.894999981
9	LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.0_L2_0.0_HL_2	0.001	tanh	10	0.1	0	0	0.930428565	0.94599998
10	LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.0_L2_0.001_HL_2	0.001	tanh	10	0.1	0	0.001	0.922714293	0.935000002
11	LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.0_L2_0.01_HL_2	0.001	tanh	10	0.1	0	0.01	0.925571442	0.94266665
12	LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.001_L2_0.0_HL_2	0.001	tanh	10	0.1	0.001	0	0.913857162	0.920666695
13	LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.001_L2_0.001_HL_2	0.001	tanh	10	0.1	0.001	0.001	0.912	0.924000025
14	LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.001_L2_0.01_HL_2	0.001	tanh	10	0.1	0.001	0.01	0.913571417	0.922999978
15	LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.01_L2_0.0_HL_2	0.001	tanh	10	0.1	0.01	0	0.880714297	0.889333308
16	LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.01_L2_0.001_HL_2	0.001	tanh	10	0.1	0.01	0.001	0.885142863	0.891333342
17	LR_0.001_AF_tanh_HN_10_Dropout_0.1_L1_0.01_L2_0.01_HL_2	0.001	tanh	10	0.1	0.01	0.01	0.882000029	0.888666689
18	LR_0.001_AF_tanh_HN_10_Dropout_0.2_L1_0.0_L2_0.0_HL_2	0.001	tanh	10	0.2	0	0	0.913857162	0.930333316
19	LR_0.001_AF_tanh_HN_10_Dropout_0.2_L1_0.0_L2_0.001_HL_2	0.001	tanh	10	0.2	0	0.001	0.915285707	0.925000012
20	LR_0.001_AF_tanh_HN_10_Dropout_0.2_L1_0.0_L2_0.01_HL_2	0.001	tanh	10	0.2	0	0.01	0.913428545	0.927666664
21	LR_0.001_AF_tanh_HN_10_Dropout_0.2_L1_0.001_L2_0.0_HL_2	0.001	tanh	10	0.2	0.001	0	0.901714265	0.916333318
22	LR_0.001_AF_tanh_HN_10_Dropout_0.2_L1_0.001_L2_0.001_HL_2	0.001	tanh	10	0.2	0.001	0.001	0.900571406	0.918666661
23	LR_0.001_AF_tanh_HN_10_Dropout_0.2_L1_0.001_L2_0.01_HL_2	0.001	tanh	10	0.2	0.001	0.01	0.898857117	0.912999988
24	LR_0.001_AF_tanh_HN_10_Dropout_0.2_L1_0.01_L2_0.0_HL_2	0.001	tanh	10	0.2	0.01	0	0.880999982	0.884666681
25	LR_0.001_AF_tanh_HN_10_Dropout_0.2_L1_0.01_L2_0.001_HL_2	0.001	tanh	10	0.2	0.01	0.001	0.87914288	0.885666668
26	LR_0.001_AF_tanh_HN_10_Dropout_0.2_L1_0.01_L2_0.01_HL_2	0.001	tanh	10	0.2	0.01	0.01	0.881428599	0.889666677
123	LR_0.001_AF_sigmoid_HN_20_Dropout_0.1_L1_0.01_L2_0.0_HL_2	0.001	sigmoid	20	0.1	0.01	0	0.873285711	0.879000008
124	LR_0.001_AF_sigmoid_HN_20_Dropout_0.1_L1_0.01_L2_0.001_HL_2	0.001	sigmoid	20	0.1	0.01	0.001	0.873285711	0.879000008
125	LR_0.001_AF_sigmoid_HN_20_Dropout_0.1_L1_0.01_L2_0.01_HL_2	0.001	sigmoid	20	0.1	0.01	0.01	0.873285711	0.879000008
126	LR_0.001_AF_sigmoid_HN_20_Dropout_0.2_L1_0.0_L2_0.0_HL_2	0.001	sigmoid	20	0.2	0	0	0.919857144	0.930000007
127	LR_0.001_AF_sigmoid_HN_20_Dropout_0.2_L1_0.0_L2_0.001_HL_2	0.001	sigmoid	20	0.2	0	0.001	0.914714277	0.927666664
128	LR_0.001_AF_sigmoid_HN_20_Dropout_0.2_L1_0.0_L2_0.01_HL_2	0.001	sigmoid	20	0.2	0	0.01	0.919428587	0.927999973
129	LR_0.001_AF_sigmoid_HN_20_Dropout_0.2_L1_0.001_L2_0.0_HL_2	0.001	sigmoid	20	0.2	0.001	0	0.873285711	0.879000008
130	LR_0.001_AF_sigmoid_HN_20_Dropout_0.2_L1_0.001_L2_0.001_HL_2	0.001	sigmoid	20	0.2	0.001	0.001	0.873285711	0.879000008
131	LR_0.001_AF_sigmoid_HN_20_Dropout_0.2_L1_0.001_L2_0.01_HL_2	0.001	sigmoid	20	0.2	0.001	0.01	0.873285711	0.879000008
132	LR_0.001_AF_sigmoid_HN_20_Dropout_0.2_L1_0.01_L2_0.0_HL_2	0.001	sigmoid	20	0.2	0.01	0	0.873285711	0.879000008
133	LR_0.001_AF_sigmoid_HN_20_Dropout_0.2_L1_0.01_L2_0.001_HL_2	0.001	sigmoid	20	0.2	0.01	0.001	0.873285711	0.879000008
134	LR_0.001_AF_sigmoid_HN_20_Dropout_0.2_L1_0.01_L2_0.01_HL_2	0.001	sigmoid	20	0.2	0.01	0.01	0.873285711	0.879000008
135	LR_0.001_AF_sigmoid_HN_30_Dropout_0.0_L1_0.0_L2_0.0_HL_2	0.001	sigmoid	30	0	0	0	0.950857162	0.952666664
136	LR_0.001_AF_sigmoid_HN_30_Dropout_0.0_L1_0.0_L2_0.001_HL_2	0.001	sigmoid	30	0	0	0.001	0.948714256	0.952666664
137	LR_0.001_AF_sigmoid_HN_30_Dropout_0.0_L1_0.0_L2_0.01_HL_2	0.001	sigmoid	30	0	0	0.01	0.944142878	0.944999988
138	LR_0.001_AF_sigmoid_HN_30_Dropout_0.0_L1_0.001_L2_0.0_HL_2	0.001	sigmoid	30	0	0.001	0	0.873285711	0.879000008
139	LR_0.001_AF_sigmoid_HN_30_Dropout_0.0_L1_0.001_L2_0.001_HL_2	0.001	sigmoid	30	0	0.001	0.001	0.873285711	0.879000008
140	LR_0.001_AF_sigmoid_HN_30_Dropout_0.0_L1_0.001_L2_0.01_HL_2	0.001	sigmoid	30	0	0.001	0.01	0.873285711	0.879000008
141	LR_0.001_AF_sigmoid_HN_30_Dropout_0.0_L1_0.01_L2_0.0_HL_2	0.001	sigmoid	30	0	0.01	0	0.873285711	0.879000008
142	LR_0.001_AF_sigmoid_HN_30_Dropout_0.0_L1_0.01_L2_0.001_HL_2	0.001	sigmoid	30	0	0.01	0.001	0.873285711	0.879000008
143	LR_0.001_AF_sigmoid_HN_30_Dropout_0.0_L1_0.01_L2_0.01_HL_2	0.001	sigmoid	30	0	0.01	0.01	0.873285711	0.879000008
144	LR_0.001_AF_sigmoid_HN_30_Dropout_0.1_L1_0.0_L2_0.0_HL_2	0.001	sigmoid	30	0.1	0	0	0.928857148	0.935666668
145	LR_0.001_AF_sigmoid_HN_30_Dropout_0.1_L1_0.0_L2_0.001_HL_2	0.001	sigmoid	30	0.1	0	0.001	0.929285705	0.935333312
146	LR_0.001_AF_sigmoid_HN_30_Dropout_0.1_L1_0.0_L2_0.01_HL_2	0.001	sigmoid	30	0.1	0	0.01	0.92957145	0.939999998
147	LR_0.001_AF_sigmoid_HN_30_Dropout_0.1_L1_0.001_L2_0.0_HL_2	0.001	sigmoid	30	0.1	0.001	0	0.873285711	0.879000008
148	LR_0.001_AF_sigmoid_HN_30_Dropout_0.1_L1_0.001_L2_0.001_HL_2	0.001	sigmoid	30	0.1	0.001	0.001	0.873285711	0.879000008
149	LR_0.001_AF_sigmoid_HN_30_Dropout_0.1_L1_0.001_L2_0.01_HL_2	0.001	sigmoid	30	0.1	0.001	0.01	0.873285711	0.879000008
150	LR_0.001_AF_sigmoid_HN_30_Dropout_0.1_L1_0.01_L2_0.0_HL_2	0.001	sigmoid	30	0.1	0.01	0	0.873285711	0.879000008
151	LR_0.001_AF_sigmoid_HN_30_Dropout_0.1_L1_0.01_L2_0.001_HL_2	0.001	sigmoid	30	0.1	0.01	0.001	0.873285711	0.879000008
152	LR_0.001_AF_sigmoid_HN_30_Dropout_0.1_L1_0.01_L2_0.01_HL_2	0.001	sigmoid	30	0.1	0.01	0.01	0.873285711	0.879000008
153	LR_0.001_AF_sigmoid_HN_30_Dropout_0.2_L1_0.0_L2_0.0_HL_2	0.001	sigmoid	30	0.2	0	0	0.925571442	0.930999994
154	LR_0.001_AF_sigmoid_HN_30_Dropout_0.2_L1_0.0_L2_0.001_HL_2	0.001	sigmoid	30	0.2	0	0.001	0.920142829	0.927999973
186	LR_0.001_AF_relu_HN_10_Dropout_0.2_L1_0.01_L2_0.0_HL_2	0.001	relu	10	0.2	0.01	0	0.873285711	0.879000008
187	LR_0.001_AF_relu_HN_10_Dropout_0.2_L1_0.01_L2_0.001_HL_2	0.001	relu	10	0.2	0.01	0.001	0.873285711	0.879000008
188	LR_0.001_AF_relu_HN_10_Dropout_0.2_L1_0.01_L2_0.01_HL_2	0.001	relu	10	0.2	0.01	0.01	0.873285711	0.879000008
189	LR_0.001_AF_relu_HN_20_Dropout_0.0_L1_0.0_L2_0.0_HL_2	0.001	relu	20	0	0	0	0.982142866	0.971000016
190	LR_0.001_AF_relu_HN_20_Dropout_0.0_L1_0.0_L2_0.001_HL_2	0.001	relu	20	0	0	0.001	0.980857134	0.974666655
191	LR_0.001_AF_relu_HN_20_Dropout_0.0_L1_0.0_L2_0.01_HL_2	0.001	relu	20	0	0	0.01	0.982285738	0.976666689
192	LR_0.001_AF_relu_HN_20_Dropout_0.0_L1_0.001_L2_0.0_HL_2	0.001	relu	20	0	0.001	0	0.967857122	0.963333309
193	LR_0.001_AF_relu_HN_20_Dropout_0.0_L1_0.001_L2_0.001_HL_2	0.001	relu	20	0	0.001	0.001	0.966714263	0.959666669
194	LR_0.001_AF_relu_HN_20_Dropout_0.0_L1_0.001_L2_0.01_HL_2	0.001	relu	20	0	0.001	0.01	0.965714276	0.961000025
195	LR_0.001_AF_relu_HN_20_Dropout_0.0_L1_0.01_L2_0.0_HL_2	0.001	relu	20	0	0.01	0	0.916142881	0.917333305
196	LR_0.001_AF_relu_HN_20_Dropout_0.0_L1_0.01_L2_0.001_HL_2	0.001	relu	20	0	0.01	0.001	0.883857131	0.889999986
197	LR_0.001_AF_relu_HN_20_Dropout_0.0_L1_0.01_L2_0.01_HL_2	0.001	relu	20	0	0.01	0.01	0.914285719	0.913333356
198	LR_0.001_AF_relu_HN_20_Dropout_0.1_L1_0.0_L2_0.0_HL_2	0.001	relu	20	0.1	0	0	0.956285715	0.968666673
199	LR_0.001_AF_relu_HN_20_Dropout_0.1_L1_0.0_L2_0.001_HL_2	0.001	relu	20	0.1	0	0.001	0.954999983	0.967333317
200	LR_0.001_AF_relu_HN_20_Dropout_0.1_L1_0.0_L2_0.01_HL_2	0.001	relu	20	0.1	0	0.01	0.958285689	0.968333304
201	LR_0.001_AF_relu_HN_20_Dropout_0.1_L1_0.001_L2_0.0_HL_2	0.001	relu	20	0.1	0.001	0	0.936857164	0.942666665
202	LR_0.001_AF_relu_HN_20_Dropout_0.1_L1_0.001_L2_0.001_HL_2	0.001	relu	20	0.1	0.001	0.001	0.938714266	0.953666687
203	LR_0.001_AF_relu_HN_20_Dropout_0.1_L1_0.001_L2_0.01_HL_2	0.001	relu	20	0.1	0.001	0.01	0.929714262	0.940333307
204	LR_0.001_AF_relu_HN_20_Dropout_0.1_L1_0.01_L2_0.0_HL_2	0.001	relu	20	0.1	0.01	0	0.873285711	0.879000008
205	LR_0.001_AF_relu_HN_20_Dropout_0.1_L1_0.01_L2_0.001_HL_2	0.001	relu	20	0.1	0.01	0.001	0.873285711	0.879000008
206	LR_0.001_AF_relu_HN_20_Dropout_0.1_L1_0.01_L2_0.01_HL_2	0.001	relu	20	0.1	0.01	0.01	0.873285711	0.879000008
207	LR_0.001_AF_relu_HN_20_Dropout_0.2_L1_0.0_L2_0.0_HL_2	0.001	relu	20	0.2	0	0	0.946857154	0.959333336
208	LR_0.001_AF_relu_HN_20_Dropout_0.2_L1_0.0_L2_0.001_HL_2	0.001	relu	20	0.2	0	0.001	0.946428597	0.96633333
209	LR_0.001_AF_relu_HN_20_Dropout_0.2_L1_0.0_L2_0.01_HL_2	0.001	relu	20	0.2	0	0.01	0.941999972	0.953333318
210	LR_0.001_AF_relu_HN_20_Dropout_0.2_L1_0.001_L2_0.0_HL_2	0.001	relu	20	0.2	0.001	0	0.931999981	0.944999993
211	LR_0.001_AF_relu_HN_20_Dropout_0.2_L1_0.001_L2_0.001_HL_2	0.001	relu	20	0.2	0.001	0.001	0.923571408	0.930000007
212	LR_0.001_AF_relu_HN_20_Dropout_0.2_L1_0.001_L2_0.01_HL_2	0.001	relu	20	0.2	0.001	0.01	0.926142871	0.941333354
213	LR_0.001_AF_relu_HN_20_Dropout_0.2_L1_0.01_L2_0.0_HL_2	0.001	relu	20	0.2	0.01	0	0.873285711	0.879000008
214	LR_0.001_AF_relu_HN_20_Dropout_0.2_L1_0.01_L2_0.001_HL_2	0.001	relu	20	0.2	0.01	0.001	0.873285711	0.879000008
215	LR_0.001_AF_relu_HN_20_Dropout_0.2_L1_0.01_L2_0.01_HL_2	0.001	relu	20	0.2	0.01	0.01	0.873285711	0.879000008
216	LR_0.001_AF_relu_HN_30_Dropout_0.0_L1_0.0_L2_0.0_HL_2	0.001	relu	30	0	0	0	0.984571457	0.976000011
217									



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