جـــامـعـة الـــشرق الأوسـط
MIDDLE EAST UNIVERSITY
Amman - Jordan

Predictive Modeling of Antimicrobial Resistance in Jordan: A Machine Learning Approach Using National Surveillance Data based on Electronic Health Records

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نموذج تنبؤي لمقاومة مضادات الميكروبات في الأردن : نهج تعلم الآلة باستخدام بيانات المراقبة الوطنية المستندة إلى السجلات الصحية الإلكترونية

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قُدمت هذه الرسالة استكمالاً لمتطلبات الحصول على درجة الماجستير في العلوم الصيدلانية

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This thesis, titled **"Predictive Modeling of Antimicrobial Resistance in Jordan: A Machine Learning Approach Using National Surveillance Data based on Electronic Health Records"** by researcher **Banan Khalif Odha Alawidha** and was successfully defended and approved on 21/01/2026.

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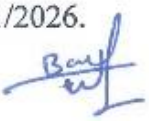
Signature: 

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Dedication

This work is dedicated to the soul of my late father, the absent yet ever-present in our lives. His love, guidance, and sacrifices continue to accompany me in every step. His memory remains a source of strength and inspiration. May his soul rest in peace.

I dedicate this work to my beloved mother for her endless love, patience, and constant support. She has always been my true support, and through her encouragement and belief in me, I was able to continue and achieve this milestone.

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Banan Khalif Odha Alawidha

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List of Abbreviation

Abbreviation	Meaning
AI	Artificial Intelligence
AMR	Antimicrobial Resistance
AUC-ROC	Area Under the Receiver Operating Characteristic
BSI	Bloodstream Infection
CDC	Centers for Disease Control and Prevention
EARS-Net	European Antimicrobial Resistance Surveillance Network
ECDC	European Centre for Disease Prevention and Control
E.coli	*Escherichia coli*
EME	Emergency Medicine Department
F	Female
HDA	Health Data Analytics
ICU	Intensive Care Unit
IN	Inpatient
M	Male
MDR	Multidrug-Resistant
ML	Machine learning
MOH	Ministry of Health
MRSA	Methicillin-Resistant *Staphylococcus aureus*
NormMCC	Normalized Matthews Correlation Coefficient
OUT	Outpatient
PDR	Pan Drug-Resistant
SHAP	Shapley Additive Explanations
UTI	Urinary Tract Infection
VRE	Vancomycin-Resistant Enterococcus
WHO	World Health Organization
XDR	Extensively Drug-Resistant

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Abstract

Background: Antimicrobial resistance (AMR) is one of the most significant global public health threats of the 21st century. It happens when bacteria, viruses, fungi, and parasites become resistance to antimicrobial agents, making infections difficult to treat. As a result, AMR leads to increased morbidity, mortality, and healthcare costs, and is expected to become a main cause of death globally by 2050 if not effectively addressed.

Objectives: The main objective of this study is to develop and evaluate machine learning models for predicting antimicrobial resistance in Jordan using electronic health records. In addition, to analyze current patient data to identify factors associated with antibiotic resistance, describe antimicrobial resistance patterns in Jordan through descriptive analysis, and evaluation the performance of the developed machine learning models using standard evaluation metrics

Method: This study is an observational study was carried out in a Jordanian governmental hospitals between 2020 and 2024. Clinical data were taken from the Health Data Analytics System, which is derived from the Hakeem Electronic Health Record (EHR) system. The final dataset consisted of 835,735 records with 19 variables. Data analysis was initially performed using Excel pivot tables to define the major features, including age, sex, microbial species, and antibiotic types, in order to identify patterns of antimicrobial resistance. Descriptive analyses were used to investigate the distribution and pattern of antibiotic resistance among these factors. Antimicrobial resistance prediction models were developed using four ensemble machine learning techniques: Random Forest, AdaBoost, Stacking, and voting. The model's performance was assessed

using standard classification metrics. In addition, SHAP (SHapley Additive ExPlanations) analysis was used to determine the most influential factors contributing to antibiotic resistance.

Results: Between 2020 and 2024, the prevalence of antimicrobial resistance varied from 35% to 39%, with 2021 showing the greatest rate. Males were more resistant to antibiotics than females .The elderly population (≥65 years) showed the highest resistance rate, followed by newborns aged 0–1 years. *Escherichia coli* was the predominant pathogen, accounting for 45.71% of all isolates. *Acinetobacter baumannii* had the highest resistance rate at 69.18%, followed by coagulase-negative *Staphylococcus* at 41.83% and *Pseudomonas* species at 39.64%. Nosocomial infections have been associated with increased incidence of antibiotic resistance compared to community-acquired infections. The Stacking classifier had the greatest overall performance among the machine learning models tested, with an accuracy of 0.764 and a F1 score of 0.738. The voting classifier had the greatest area under the ROC curve (AUC). AdaBoost had the lowest overall performance, whereas Random Forest and Voting classifiers performed moderately well. Using SHAP (Shapley Additive Explanations) analysis, the antibiotic name was found to be the most important feature in all ensemble models, regardless of machine learning method, and had a significant impact on antimicrobial resistance outcomes.

Conclusion: The results of this study show that antibiotic resistance is a major public health issue in Jordan, with a high prevalence that is predicted to rise further if existing practices are maintained. These findings highlight the critical need for greater regulations that restrict antibiotic prescribing and use. Furthermore, integrating machine-learning methods into clinical practice can aid in clinical decision-making, optimize antibiotic therapy, and help to reduce the prevalence of antimicrobial resistance.

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الملخص

الخلفية: تُعد مقاومة مضادات الميكروبات (AMR) واحدة من أخطر التهديدات العالمية للصحة العامة في القرن الحادي والعشرين. تحدث هذه الظاهرة عندما تتوقف البكتيريا والفيروسات والفطريات والطفيليات عن الاستجابة للعوامل المضادة للميكروبات، مما يجعل علاج العدوى أكثر صعوبة. ونتيجة لذلك، تسهم مقاومة مضادات الميكروبات في زيادة معدلات المراضة والوفيات وارتفاع تكاليف الرعاية الصحية، ومن المتوقع أن تصبح أحد الأسباب الرئيسية للوفاة عالميًا بحلول عام 2050 إذا لم يتم التصدي لها بفعالية.

الأهداف: يهدف هذا البحث إلى تطوير وتقييم نماذج تعلم آلي للتنبؤ بمقاومة مضادات الميكروبات في الأردن باستخدام السجلات الصحية الإلكترونية. كما يسعى إلى تحليل بيانات المرضى الحالية لتحديد العوامل المرتبطة بمقاومة المضادات الحيوية، ووصف أنماط مقاومة مضادات الميكروبات في الأردن من خلال التحليل الوصفي، وتقييم أداء نماذج التعلم الآلي المطورة باستخدام مقاييس التقييم القياسية.

المنهجية: هذه دراسة رصدية أُجريت في المستشفيات الأردنية خلال الفترة من 2020 إلى 2024. تم الحصول على البيانات السريرية من نظام تحليلات البيانات الصحية، المستمد من نظام السجلات الصحية الإلكترونية «حكيم». تألفت مجموعة البيانات النهائية من 835,735 سجلًا للمرضى، تضمنت 19 متغيرًا شملت بيانات عددية وفئوية.تم إجراء التحليل الأولي للبيانات باستخدام الجداول المحورية (Pivot Tables) في برنامج Excel لاستكشاف الخصائص الرئيسية مثل العمر، والجنس، وأنواع الكائنات الدقيقة، وأنواع المضادات الحيوية، بهدف تحديد أنماط مقاومة مضادات الميكروبات. كما أُجريت تحليلات وصفية لدراسة توزيع واتجاهات مقاومة المضادات الحيوية عبر هذه المتغيرات.تم تطبيق أربع تقنيات خاضعة للإشراف في التعلم الآلي، وهي: الغابة

العشوائية(Random Forest) ، وأدا بوست(AdaBoost) ، والتكديس(Stacking) ، والتصويت (Voting)، لتطوير نماذج تنبؤية لمقاومة مضادات الميكروبات. وتم تقييم أداء النماذج باستخدام مقاييس تصنيف قياسية. بالإضافة إلى ذلك، تم استخدام تحليل SHAP (Shapley Additive Explanations)لتحديد أكثر الخصائص تأثيرًا في مقاومة مضادات الميكروبات.

النتائج: تراوحت النسبة السنوية لانتشار مقاومة مضادات الميكروبات خلال الفترة من 2020 إلى 2024 بين 35% و39%، مع تسجيل أعلى نسبة في عام 2021. وكانت مقاومة المضادات الحيوية أعلى لدى الذكور مقارنة بالإناث. كما أظهرت الفئة العمرية من كبار السن (≤65 سنة) أعلى معدلات المقاومة، تلتها فئة الرضع بعمر 0–1 سنة.كانت بكتيريا الإشريكية القولونية (*Escherichia coli*)الأكثر شيوعًا، حيث شكّلت 45.71% من إجمالي العزلات. وأظهرت بكتيريا الأسينيتوباكتر بوماني (*Acinetobacter baumannii*) أعلى معدل مقاومة (69.18%)، تلتها المكورات العنقودية سالبة التخثر (41.83%) وأنواع الزائفة (*Pseudomonas*) بنسبة 39.64% ، أرتبطت العدوى المكتسبة داخل المستشفيات بمعدلات أعلى من مقاومة مضادات الميكروبات مقارنة بالعدوى المكتسبة من المجتمع. ومن بين نماذج التعلم الآلي التي تم تقييمها، أظهر نموذج التكديس (Stacking) أفضل أداء عام، حيث حقق دقة (Precision) بلغت 0.764 وقيمة F1-score مقدارها 0.738. بينما حقق نموذج التصويت (Voting) أعلى قيمة للمساحة تحت منحنى ROC (AUC). في المقابل، أظهر نموذج AdaBoost أضعف أداء، في حين أظهرت نماذج الغابة العشوائية والتصويت أداءً تنبؤيًا متوسطًا. وباستخدام تحليلSHAP ، تبيّن أن اسم المضاد الحيوي هو العامل الأكثر تأثيرًا عبر جميع نماذج التجميع، بغض النظر عن خوارزمية التعلم الآلي المستخدمة، وكان له تأثير كبير على نتائج مقاومة مضادات الميكروبات.

الخلاصة: تشير نتائج هذه الدراسة إلى أن مقاومة مضادات الميكروبات تمثل تهديدًا كبيرًا للصحة العامة في الأردن، مع معدل انتشار مرتفع من المتوقع أن يزداد في حال استمرار الممارسات الحالية. وتؤكد هذه النتائج الحاجة الملحّة إلى تعزيز وتطبيق السياسات المنظمة لوصف واستخدام المضادات الحيوية. كما أن دمج تقنيات التعلم الآلي في الممارسة السريرية قد يسهم في دعم اتخاذ القرار الطبي، وتحسين العلاج بالمضادات الحيوية، والمساعدة في تقليل عبء مقاومة مضادات الميكروبات

Chapter One
Background and Problem Statement

1.1 Introduction

Antimicrobial resistance (AMR) is one of the most significant international public health risks of the 21st century. When bacteria, viruses, fungi and parasites stop responding to antimicrobial treatments, it is referred to AMR. Management of infections becomes more challenging, increasing morbidity, mortality, and healthcare costs (WHO, 2021; Prestinaci et al., 2015).

AMR can develop spontaneously through genetic mutations and adaptive mechanisms but is mainly accelerated by human activity. Improper and excessive use of antimicrobials in health, agriculture, and veterinary scenarios are the main resistance factors (WHO, 2021). Inadequate use of antibiotics for non-bacterial infections, failure to complete prescribed courses, and the use of broad-spectrum agents when narrow spectrum options are available, all contribute to the selection pressure that favors resistant strains (Prestinaci et al., 2015). In 2018, Albaz examined the knowledge of Palestinian refugees who came to UNRWA health centers in Jordan with regarding the use of antibiotics. She noticed that 63% of patients shared antibiotics at home and 60% bought antibiotics without a prescription from the pharmacy (Al Baz, 2018). Despite the fact that COVID-19 is a viral illness that does not usually necessitate antibiotic therapy, around 70% of COVID-19 patients in Asia get antibiotics during treatment (Rawson et al., 2020).

Global antibiotic consumption increased by approximately 65% between 2000 and 2015. In 2000, the highest rates of consumption were reported in countries such as New Zealand, Spain, Hong Kong, the United States, and France. By 2015, however, the highest consumption levels were observed in Turkey, Tunisia, Libya, and Romania. Among antibiotic classes, penicillin were the most commonly used, with global consumption rising by 36% during this period. Between 2000 and 2015, the overall consumption of antibiotics in countries with high incomes increased by 6%. On the other hand, antibiotic use increased by 114% during the same duration in countries with low or middle incomes (Klein et al., 2018). The most recent study by Klein et al.(2024) demonstrated that the global consumption of antibiotics increased by 16.3% between 2016 and 2023, rising from 29.5 to 34.3 billion defined daily doses. Despite the COVID-19 pandemic reduced

antibiotic use, particularly in high-income countries. If the current patterns of antibiotics consumption are not changed, the use of antibiotics will likely increase by more than 50 % by 2030 (Klein et al., 2024).

In the United States, it has been stated that around 80 % of antibiotics are used in animal production, where they are often added to animal feed (Bartlett, 2013), and in 2010, an estimated 63.2 tons were used in animal production internationally. Antibiotics are commonly added in animal feed to prevent disease and enhance growth (Bartlett et al., 2013); for example, colistin is often used in pig farming to increase growth (Lekagul et al., 2019).

The Centers for Disease Control and Prevention (CDC) estimates that more than 2 million people in the United States become infected with antibiotic-resistant pathogens each year, resulting in at least 23,000 deaths (CDC; 2013). Multidrug-resistant bacteria led to 400,000 diseases and 25,000 deaths in Europe in 2007 (Prestinaci et al., 2015).

Four million nine hundred fifty thousand fatalities globally were related to bacterial AMR in 2019, of which 1.27 million were caused directly by resistant infections ("Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis," 2022). AMR may become the main cause of mortality globally by 2050 if precautions fail to be implemented, with death expected to reach over 10 million annually by 2050 (O'Neill, 2016).

The financial burden of AMR is immense. Antibiotic resistance is expected to cost the United States $55 billion annually, combining $20 billion in direct health care costs and $35 billion in indirect costs (Ahmad & Khan, 2019). Resistance often necessitates the use of more expensive second- or third-line treatments, extended hospitalizations, complex diagnostics procedures, and strict infection control measures (Shrestha et al., 2018). Indirect costs further include loss of patient productivity due to prolonged illness or premature death, which that could disrupt the socio-economic balance (Shrestha et al., 2018).

Studies on the prevalence of antimicrobial resistance in Jordan are limited. However, the ministry of health in Jordan has established the national antimicrobial resistance surveillance system in collaboration with national and international partners in 2019 to monitor periodic infections and assess the prevalence of antibiotic resistance with the aim to guide national policy. For the purpose to improve data collecting and reporting and providing accurate and reliable findings, the number of monitoring sites increased from 8 in 2018 to 42 in 2023. Using data from 2017 to 2023, it has been discovered that 35% of *E. coli* isolates and 45% of

Klebsiella pneumoniae isolates developed MDR in 2017. In 2018, 2019, and 2020, there was a decrease, but the values remained within a similar range. The prevalence rates of *Klebsiella pneumoniae* (44%) and *E. coli* (40%) in 2023 were consistent to those in other years. The MDR rate for *Pseudomonas aeruginosa* was 20% in 2023 and 21% in 2017. In 2017 and 2023, *Acinetobacter baumannii* showed 80% and 74%, respectively. In 2023, among all bacterial isolates (n = 64,333), 39.8% were classified as MDR, 17.2% as Extensively Drug-Resistant (XDR) , and 1% as Pan Drug Resistance (PDR) , representing an overall high percentage (Jordan Ministry of Health, 2024).

AMR is an international threat that needs urgent action. Global efforts are now focusing to reduce the prevalence of AMR by reducing unnecessarily antibiotic consumption and developing effective strategy to combat resistance. This strategy includes establish antimicrobial stewardship programs across countries, and promoting the rational use of antibiotic. In addition, machine-learning techniques are being utilized to predict antimicrobial resistant patterns, support personalized treatment approaches, and aid clinicians making best clinical decisions for optimal patient care.

Machine learning (ML) is a type of artificial intelligence (AI) that has grown significantly in recent years, especially for the processing of huge amounts of data. The primary objective is to teach the computer to understand standards and make decisions without knowing what to do each time. Machine learning can be classified into three basic categories: supervised, unsupervised, and reinforcement learning. If the data is labeled, we already know the correct answers, and this is referred to as supervised learning. Unsupervised learning occurs when a computer tries to find patterns on its own if the data is not labeled. Reinforcement, on the other side, works more like trial and error, teaching the system what to do with rewards or punishments, similar to how you train a pet with treats (Sarker, 2021). AI has a significant impact on the healthcare sector in many ways, including diagnosis, treatment, and drug discovery, and is increasingly integrated throughout the system. The adoption of artificial intelligence in the healthcare sector began with the transition from paper knowledge and documentation to digital health records, which became the cornerstone for the integration of artificial intelligence in healthcare (Feretzakis et al., 2020).

Data derivation techniques are often based on two approaches: one uses clinical and demographic data as well as antibiotic susceptibility results (Feretzakis et al., 2020; Mintz

et al., 2023; Moran et al., 2020), while the other uses whole genome sequencing data (Nguyen et al., 2020). These methods are used to identify antimicrobial resistance patterns. The current research has demonstrated that huge data sets, including patient demographics, clinical information, and microbiological susceptibility results can aid in the development of decision-making systems for accurately determining bacterial resistance patterns. However, whole genome sequencing is not as frequently utilized for large-scale investigations as more targeted demographic and clinical data since it is costly and time demanding(Helmy et al., 2016).

Due to the limited data available on AMR patterns in Jordan and the growing global threat of AMR, there is an urgent need to support efforts aimed at reducing its prevalence both locally and internationally. Therefore, this study aims to analyze AMR patterns in Jordan over recent years between 2020 to 2024 and apply machine-learning techniques to predict the resistant pattern

Objectives:

1.1 The primary goal of this research to create and assess machine-learning models that can predict antimicrobial resistance in Jordan using electronic health records.

1.2 To examine present patient data in order to find factors associated with antibiotic resistance.

1.3 To describe the patterns of antimicrobial resistance in Jordan using descriptive analysis.

1.4 To evaluate the performance of the machine learning model using metrics.

Chapter Two

Theoretical Framework and Previous Studies

2.1 Antimicrobial resistance worldwide

Antimicrobial resistance has long been acknowledged as a worldwide public health issue. Scientific research continues to expand to improve understanding of antibiotic resistance and its interactions with epidemiological factors, risk drivers, and clinical impacts. As a result, numerous studies have investigated antibiotic resistance patterns, risk factors, and prevalence in different countries. The following section provides an extensive review of significant research on this issue.

Early studies assessing antibiotic resistance in hospital settings identified age as a significant risk factor, particularly between elderly patients. In the study by Claudia M. Denkinger (2013) titled “Increase in Multidrug Resistance Upon Admission to the Hospital: A 12-Year Surveillance Study,” the authors conducted long-term monitoring in a 620-bed tertiary-care hospital in Boston with approximately 39,000 admissions per year. The analysis covered the years 1989 to 2009, during which the hospital recorded an average of 39,197 admissions per year and collected an average of 6,534 positive bacterial isolates annually. Patients were categorized into two age groups: those younger than 65 years and those 65 years and older. The study demonstrated that the prevalence of MDROs on admission was significantly higher in the elderly, with MDRO rates approximately twofold higher for MRSA and VRE, and threefold higher for multidrug-resistant Gram-negative organisms compared to the younger age group(Denkinger et al., 2013).which is consistent with the study by Li Huang and colleagues, titled "Etiological profile of urinary tract infection and antibiotic resistance patterns among different age groups”, which reported that older age groups bear the highest burden of multidrug-resistant and extensively drug-resistant infections, which may be related to weakened immunity, chronic diseases, and increased exposure to the healthcare environment Among the pathogens, *E. coli* was the most prevalent one in the pediatric, adult, and geriatric groups, while *Enterococcus faecium* was the most prevalent organism within neonates. MDR *E. coli* increased significantly with age, from 26% in neonates to 68% in geriatric patients .Additionally, a high prevalence of *Enterococcus faecium* in neonates has been associated with nosocomial transmission. Overall, the study concluded that age plays an important role in influencing antibiotic resistance patterns (Huang et al., 2021).

In addition to a study conducted among pediatric patients, by Carmen Duicu and colleagues' (2021), aimed to evaluate antibiotic resistance patterns in pediatric UTI cases. The results showed that the most dominant pathogen was *E. coli* (72.2%), followed by *Klebsiella* spp., *Proteus* spp. *and Pseudomonas aeruginosa*. Children less than 1 year of age represented the largest age group, suggesting that infants are the population at highest risk for UTI. *E. coli* has shown high resistance to ampicillin, amoxicillin, trimethoprim-sulfamethoxazole, cefuroxime and ciprofloxacin. Additionally, 34.13% of the isolates were identified as MDR and 56.3% of these MDR pathogens were found in children with urinary tract abnormalities. Overall, the study concluded that the most affected group is infants under 1 year of age, who carry a higher risk of UTI and associated antimicrobial resistance (Duicu et al., 2021).

One of the most important studies related to antimicrobial resistance globally is the study conducted by the Global Burden of Disease AMR Collaborators and published in The Lancet (Murray et al., 2022). This study analyzed 471 million records across 204 countries and territories, including 23 bacterial pathogens and 88 pathogens–drug combinations. Using predictive statistical modeling, the authors aimed to determine the number of deaths and disability-adjusted life years (DALYs) attributable to and associated with bacterial AMR in 2019. The analysis accounted for infection-related deaths, pathogen-specific mortality, resistance prevalence, and the excess risk of death linked to resistant infections, providing one of the most comprehensive global assessments to date. The results showed that bacterial AMR was associated with 4.95 million deaths globally, including 1.27 million deaths directly related to resistant infections. The highest AMR-related mortality was reported in western sub-Saharan Africa (27.3 deaths per 100,000 population), while Australasia had the lowest rate (6.5 deaths per 100,000). The most common pathogens associated with AMR-related deaths were *Escherichia coli, Staphylococcus aureus, Klebsiella pneumoniae, Streptococcus pneumoniae, Acinetobacter baumannii, and Pseudomonas aeruginosa*. In addition, methicillin-resistant *Staphylococcus aureus* (MRSA) was identified as a major pathogen–drug combination responsible for more than 100,000 deaths ("Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis," 2022).

Regional studies have examined antimicrobial resistance with different research objectives. In the study conducted in five tertiary hospitals in Mecca, Saudi Arabia by

Omar B. Ahmed, Atif H. Asghar, and Majid Bamaga (2023), the authors aimed to characterize aminoglycoside resistance genes in multidrug-resistant *Klebsiella pneumoniae* isolates. The results showed that *Klebsiella pneumoniae* was the most common pathogen isolated. Among *K. pneumoniae* isolates, 57.3% were multidrug-resistant (MDR). Within these MDR isolates, amikacin resistance was 100%, gentamicin resistance was 98%, and tobramycin resistance was 98%. In addition, these isolates showed 100% resistance to amoxicillin-clavulanate, ciprofloxacin, cefotaxime, and aztreonam. The findings indicate a very high level of aminoglycoside resistance in MDR *Klebsiella pneumoniae* and highlight a significant clinical challenge in managing these infections (Ahmed et al., 2023).Further regional evidence on amniglycoside resistance has been reported from Iran . In the study by Niloofar Saeli and colleagues (2024), titled "Prevalence and Mechanisms of Aminoglycoside Resistance Between Drug-Resistant *Pseudomonas Aeruginosa* Clinical Isolates in Iran", the authors aimed to determine the prevalence of aminoglycoside resistance in Pseudomonas aeruginosa, including the mechanism of aminoglycoside resistance, in addition to identifying the mechanism of aminoglycoside resistance. The results showed that 48% of the isolates were resistant to at least one aminoglycoside. Resistance rates were 45.5% for tobramycin, 43% for amikacin, and 39% for netilmicin. Multidrug resistance was prevalent, with 94.7% of aminoglycoside resistant isolates classified as MDR. When comparing amikacin resistance globally, the study reported that amikacin resistance in Iran averaged 50.6%, which is much higher than rates showed in the United States (6%) and Europe (12.9%), indicating substantial geographic variation in aminoglycoside resistance patterns (Saeli et al., 2024).In addition to resistance patterns associated with particular antibiotic classes , other regional investigations have examined demographic factors related to antimicrobial resistance , in the study done by Amir M., Malik A.H., and Salim M.R., a cross-sectional design was used at the Combined Military Hospital in Bannu, Pakistan, between January 2023 and April 2024, with the aim of comparing age, gender, and bacterial isolates from urine cultures with their antibiotic-resistance patterns. The study demonstrated that the most common pathogen was *E. coli* (69.6%), followed by *Pseudomonas aeruginosa* (17.4%), *Klebsiella pneumoniae*, and *Enterobacter species, with E. coli* being the most prevalent organism across all age groups and sexes. The highest antibiotic resistance was observed against ampicillin (88.2%), followed by amoxicillin-clavulanic acid (85.7%), ciprofloxacin (74.2%), ceftriaxone (69.2%), levofloxacin (66.7%) and co-trimoxazole

(65.6%). Lower resistance rates were noted for cefepime (36%), gentamicin (33.3%), meropenem (27%), piperacillin-tazobactam (14.3%), fosfomycin (13.8%), amikacin (10.5%) and nitrofurantoin (7.5%). The study found no statistically significant differences between males and females in terms of antibiotic resistance, although the distribution of culture-positive cases was 58.7% in males and 41.3% in females. Similarly, there was no statistically significant association between age groups and resistance patterns, although E. coli remained the leading cause of UTI in all age groups. The authors concluded that urinary tract infections showed high resistance to many first-line antibiotics, which posed a challenge for empiric treatment, and highlighted the absence of a strong association between gender or age and resistance. (Amir et al., 2024).

However, different findings were mentioned by Khanal, and colleagues (2024), who examined multidrug-resistant (MDR) and antimicrobial-resistant *E. coli* urinary isolates among males and females in Australia. The study reported that E. *coli* was more common in men than in women in both community and hospital settings. In the community, MDR rates were 6.4% in men and 5.2% in women, while in hospitals, MDR rates were 16.5% in men and 12.8% in women. Higher resistance in men was showed especially for commonly used antibiotics such as amoxicillin, amoxicillin-clavulanate, cephalexin and norfloxacin. The study approved that men were more likely than women to get MDR *E. coli* infections (Khanal et al., 2024). In addition to studies examining antimicrobial resistance based on demographic factors and antibiotic classes, pathogen related studies have also been conducted. For example, study conducted by Masoumeh Beig and colleagues (2024), who evaluated the global burden of antimicrobial resistance in hyper virulent *Klebsiella pneumoniae* strains. The study reported that ampicillin had the highest rate of resistance (95.5%), followed by ampicillin-sulbactam (45.1%). Among cephalosporins, resistance rates were notable for cefazolin (36.4%), cefuroxime (25.7%), cefotaxime (64.2%), ceftazidime (55.9%), and cefepime (50.1%). Resistance to carbapenems was also high, including imipenem (44.8%), meropenem (51.4%) and ertapenem (42.6%), while resistance to aztreonam reached 53.9%. Within the aminoglycoside group, resistance rates were reported for gentamicin (36.3%), amikacin (41.2%) and tobramycin (35.6%). High resistance was observed for tetracycline (59.4%), doxycycline (46%) and minocycline (75.2%). Other antibiotics showed the following resistance rates: Chloramphenicol (39.1%), ciprofloxacin (46.3%), levofloxacin (35.3%), azithromycin (76.3%), tigecycline (19.3%), trimethoprim–sulfamethoxazole (39.3%), colistin (15.3%), fosfomycin (51.1%), and nitrofurantoin (39.2%). The study further

demonstrated a significant impact of the COVID-19 pandemic on antimicrobial resistance patterns. When comparing the pre-pandemic period (2014–2021) with the pandemic period (2022–2023), resistance rates increased markedly. For example, resistance to aztreonam increased from 33.3% to 69.1%, amikacin from 21.4% to 56.4%, cefepime from 33% to 64.4%, ceftazidime from 35.2% to 69.7%, ciprofloxacin from 29% to 64.1%, , levofloxacin from 22.7% to 59.3%, piperacillin–tazobactam from 37.9% to 71.6%, and trimethoprim–sulfamethoxazole from 26.1% to 53.8% (Beig et al., 2024).In addition to the study conducted by Ben Wali and colleagues (2025) ,who aimed to study the pattern of antimicrobial resistance among common pathogens isolated from adult bloodstream and urinary tract infections in Malawi (2020–2024),the study reported that *E. coli* (37.6%) and *K. pneumoniae* (8.3%) were the most common pathogens. Among gram-negative bacteria, resistance to third-generation cephalosporins was high, resistance to ceftriaxone ranged from 63% to 72.4%, and resistance to ceftazidime reached up to 74.6%. Resistance to ampicillin was always greater than 88% and resistance to amoxicillin–clavulanate was always greater than 95%. The range of co-trimoxazole resistance was 72.7% to 89.7%. Ciprofloxacin resistance increased from 66.7% to 81.0%. Resistance to gentamicin ranged from 48.4% to 67.0%, while resistance to amikacin was lower, ranging from 18.4% to 26.3%. Resistance to meropenem remained low, below 21%. Resistance to nitrofurantoin ranged from 0% to 95.2% in 2022. Resistance to piperacillin–tazobactam was 0% in 2020–2022, rising to 35.8% in 2024. For gram-positive bacteria, resistance to co-trimoxazole ranged from 83.53% to 71.53% 100% of the time. Ciprofloxacin resistance remained consistently high. The number of people who were resistant to vancomycin increased from 20% to 31%. Resistance to ceftriaxone reached up to 100% in the first years. Ampicillin resistance ranged from 21% to 55% and clindamycin resistance from 25% to 80% in 2020(Bwanali et al., 2025).Similarly , a study by by DebBarmy et al. (2025) titled “Phenotypic characterization and prevalence of carbapenem-resistant Enterobacterales in a tertiary care center in Bihar, India”, the authors focused on determining the prevalence of carbapenem-resistant Enterobacterales, the distribution of carbapenemase classes and differences between hospitalized and ambulatory isolates. The research showed that 32.97% *of* Enterobacterales showed resistance to carbapenems. Resistance was significantly higher in inpatients (47.7%) compared to outpatients (14%). Respiratory samples had the most carbapenem-resistant Enterobacterales, followed by pus, blood, and then urine, which had the least. *E. coli* and *Klebsiella pneumoniae* were the most common organisms found alone. The study found that all the bacteria were resistant to several

antibiotics such as ceftazidime, cefotaxime, piperacillin-tazobactam and aztreonam. This means that there are very few treatment options. Colistin, on the other hand, has remained effective, with very little resistance reported (DebBarma et al., 2025). While most pathogen related studies have focused on bacterial resistance, antifungal has also been reported. In the research paper "Twenty-year course of antifungal resistance in *Candida albicans*" by İlker Kilbaş et al. (2025), the authors sought to evaluate global trends in antifungal resistance over two decades, focusing specifically on fluconazole, other azole antifungals, and other antifungal classes. This study was a systematic review and meta-analysis, included the years 2000 to 2023, and examined resistance patterns to azole agents, polyenes, and echinocandins. The analysis involves both *Candida albicans* and non-albicans *Candida* species, including *C. tropicalis*, in different geographic regions, namely Europe, North America, Asia, Africa and the Middle East. The results showed that Turkey and a number of low- and middle-income countries had the highest rates of resistance to fluconazole, with *Candida albicans* reaching about 45-50%. On the other hand, Europe (0.7–2%) and North America (1–6%) had lower rates of resistance. In some areas, resistance to the azole group was more than 20-25%. At the same time, amphotericin B resistance remained low, between 0% and 8.5%, and echinocandin resistance remained low worldwide, usually below 5% (Kilbas et al., 2025).

Recent studies have highlighted the role of demographic factors in antimicrobial resistance, for example, In the study titled “Gender Differences in Global Antimicrobial Resistance” by Salehi, Laitinen, Bhanushali, and colleagues (2025) to investigate how antibiotic resistance genes differ between women and men in countries with different sociodemographic and economic characteristics. The results showed that women had a higher antibiotic resistance gene (ARG) load compared to men, especially in high-income countries, where women showed a 9% higher ARG load. However, in low- and middle-income countries, the situation was different: men had a 5% higher ARG burden than women. In terms of age, infants had the highest burden of ARGs. This burden decreased during childhood and then steadily increased from adolescence to older adulthood, with females showing higher values in adulthood. Gender differences in ARG load did not emerge in early childhood but became evident in adulthood. The study also found that the composition of the resistome, or overall distribution of antibiotic resistance genes, was the same in both sexes. This accounted for only 0.28% of the variation. Gender played a small role compared to larger factors such as region, age and antibiotic use. Regional differences were significant, with Asia showing the highest ARG load and diversity,

while other regions had lower values. The study found that age, gender, economic region and antibiotic use play a big role in how patterns of antimicrobial resistance change. Overall, women had systematically higher burden and diversity of ARGs in high-income countries, although gender differences were small compared to larger influencing factors (Salehi et al., 2025).In addition , a study titled "Combining Demographic Shifts with Age-Based Resistance Prevalence to Estimate Future Antimicrobial Resistance Burden in Europe and Implications for Targets" conducted by Naomi Waterlow, and colleagues (2025) employed a large-scale modeling methodology to project the evolution of antimicrobial resistance in bloodstream infections (BSIs) in Europe from 2030 to 2050. The study used 12,807,473 bloodstream infection susceptibility tests collected from 2010 to 2019 across 25 European countries, gathering data from the European Antimicrobial Resistance Surveillance Network (EARS-Net). The study included eight major bacterial pathogens and used six specific incidence categories to project antimicrobial resistance in BSI cases from 2020 to 2050. The main results showed that age has a large effect on AMR burden. Elderly patients, particularly those aged 74 years and older, are expected to see the greatest increase in resistant bloodstream infections. On the other hand, younger age groups are expected to have a stable or declining incidence of these infections. The study also found that men were likely to have more resistant cases of BSI, particularly to six of the eight bacteria examined. Also, by 2050, 89% of bacteria and antibiotic combinations are expected to be more resistant, and this will vary widely from country to country, even for the same pathogen. Overall, the study concluded that Europe will face a substantial increase in the burden of AMR, particularly in older patients, and that men will be at higher risk of resistant infections. She also emphasized that there will be significant differences between countries in the magnitude of the increase in resistance (Waterlow et al., 2025). Furthermore, a study conducted at Düzce University Hospital NICU by Mukaddes Kılıç Sağlam and Mine Yanoğlu (2025), aimed to assess antibiotc resistant between neonates aged 0–28 days. The results indicated that *Escherichia coli* was the most common pathogen, comprising 50% of the multidrug-resistant isolates. In total, 45.1% of all isolates were Multi drug resistance (MDR). According on these result, the study approved that neonates has a high-risk cohort for multidrug-resistant infections (Sağlam et al., 2025).

Among global studies, WHO reports provide the most comprehensive assessments of antimicrobial resistance. The Global Antibiotic Resistance Surveillance Report 2025

finds that globally one in six bacterial infections is resistant to antibiotics, with the highest burden in South-East Asia and the Eastern Mediterranean (around 31%) and the lowest in the Western Pacific (about 9%) and Europe (about 10%). Urinary tract infections are the most resistant type of infection, with about one in three being resistant. Bloodstream infections are next, with one in six being resistant, followed by gastrointestinal infections (one in 15) and gonorrhoeal infections (one in 125). *E. coli* has a 44.8% resistance to third-generation cephalosporins, while *Klebsiella pneumoniae* has a 55.2% resistance. In South-East Asia, *Acinetobacter* spp. is 54.3% resistant to carbapenem, and *K. pneumoniae* is 41.2% resistant. The global rate of MRSA among Gram-positive pathogens is 27.1%, but in the Eastern Mediterranean, it rises to 50.3%. *Shigella* species exhibit 29.7% resistance to fluoroquinolones, increasing to 75% in Southeast Asia; non-typhoidal *Salmonella* demonstrates 18% resistance to ciprofloxacin. *Neisseria gonorrhoeae* is resistant to ciprofloxacin in 75% of cases, and ceftriaxone resistance—though low globally at 0.3%—reaches 2.5% in the Eastern Mediterranean. The resistance rates for *Shigella* with ciprofloxacin (27%), *K. pneumoniae* with imipenem (15%), *Salmonella* with ciprofloxacin (14%), *E. coli* with imipenem (12.5%), and *Acinetobacter* with imipenem (5%) are all going up each year. On the other hand, the rates for MRSA (–2.5%) and penicillin-resistant *S. pneumoniae* (–11%) are going down. The results indicate that reduced surveillance coverage correlates with elevated AMR levels, and that fragile health systems endure increased resistance burdens (WHO,2025).

2.2 Antimicrobial resistance in Jordan

At the national level , one of the available studies was conducted at the King Hussein Medical Center in Amman by Amani Batarseh and colleges (2015), to investigate the antimicrobial resistance profile and the prevalence of *Acinetobacter baumannii* isolates. The findings revealed high resistance rates to various antibiotics, including ceftriaxone (100%), ceftazidime (98.3%) quinolones (94.8%), imipenem (97.4%), and piperacillin–tazobactam (96.6%). On the other hand, reduced resistance rates were identified for minocycline (26.7%) and colistin (1.7%). Overall, the study concluded that Acinetobacter baumannii showed broad resistance to most of the antibiotics tested, with only limited susceptibility observed for minocycline and colistin (Batarseh et al., 2015). In addition, study conducted by Sallam et al. (2019) at the University of Jordan reported antimicrobial susceptibility pattern of *Streptococcus pneumoniae*. The findings showed that

Streptococcus pneumoniae was highly susceptible to vancomycin and ceftriaxone, while resistance increased to erythromycin, clindamycin and levofloxacin. MDR increased from 1.6% to 14.6% at the end of the study, indicating an increasing trend of antimicrobial resistance and MDR (Sallam et al., 2019). At the same institution, the University of Jordan Hospital, Khaoula Abu Hammour, and colleagues (2023) examined the prevalence of carbapenem-resistant Gram-negative pathogens from November 2021 to June 2022. The results found that *Escherichia coli*, was the most prevalent pathogen, which accounted for 34.6% of all samples. *Acinetobacter baumannii* had the highest rate of carbapenem resistance (93.3%), followed by *Klebsiella pneumoniae* (59.2%)and *Pseudomonas aeruginosa* (41. 9%).one other hand, *E. coli*, was less resistant (6.9%). The study found that carbapenem resistance is a major risk to public health and that a 41% resistance rate is very high Hammour et al. (2023). Similarly, a study conducted by Amin A. Aqel et al. (2024), to investigate antibiotic resistance patterns using samples obtained in 2022 from the Al-Karak Government Hospital in Jordan. using data from the hospital's National Electronic Health Record System. The results showed that the bacteria varied in suitability to antibiotics. The most significant finding was the identification of prevalence drug-resistant (XDR) and pan-drug-resistant (PDR) strains, particularly in *Pseudomonas aeruginosa*, *Klebsiella pneumoniae* and *Escherichia coli*, underscoring a significant public health problem (Aqel et al., 2024).

These studies show that antimicrobial resistance is becoming more common in Jordan. There is therefore an urgent need for strong policies and a national strategy to combat antimicrobial resistance, as well as further research to understand resistance patterns in Jordan.

2.3 Machine learning and antimicrobial resistance

Machine learning is one of the methods used to identify antimicrobial resistance by analyzing complex datasets, including demographic, clinical information, and microbiological susceptibility tests, in order to develop a system that can help identify bacterial resistance patterns and supporting clinical decision-making in antimicrobial treatment. Several studies have demonstrated the potential of machine learning to support AMR prediction. One of the early studies in this filed was conducted by Lewin-Epstein et al. (2020), who aimed to design and apply machine learning models to predict antibiotic resistance, based on previous electronic medical health records. They used 16,000

antibiotic resistance results from bacterial cultures of hospitalized patients, as well as electronic medical records. With 85% of the data used for training and 15% for testing. The study focused on five antibiotics: ceftazidim, gentamicin, imipenem, fluoroquinolones and sulfametoxazole-trimetoprim. They applied techniques such as logistics regression, neural networks and increased gradient. These methods have been combined to increase accuracy and improve performance. The study found that the area under the recipient's operational characteristic (AUC) ranged from 0.73 to 0.79 to different antibiotics when bacterial species were excluded. However, when bacterial species were included, AUC improved, reaching 0.80 to 0.88, showing the effect of bacterial species on data. However, there is a limitation because the data does not include critical information.

Similarly, Feretazkis et al. (2020) conducted a study to use machine learning techniques to predict antimicrobial resistance and support empirical antibiotic treatment decisions. The researchers utilized 5509 samples from a Greek tertiary hospital , focusing on basic patient demographics , sample type , gram stain results ,and susceptibility data results , applying Five machine learning models :J48 , random forest , logistic regression , K-Nearest Neighbors(KNN), multilayer perceptron (MLP) , Their findings indicated that the best performance was achieved by logistic regression with an AUC of 0,758 ,and KNN achieved the highest F-measure of 0.724, indicating good predictive power. The study highlighted that ML models can be useful even with a moderate-sized dataset. Nonetheless, the research had certain limitations, including limited to basic lab and demographic data without detailed clinical data which may impact prediction performance and generalizability.

Using different machine learning approach, Moran et al. (2020) aim to evaluate the precision of the open-source machine-learning algorithm (XGBoost) in forecasting antibiotic resistance. The dataset of 9352 patients with 15695 hospitalizations in Birmingham, UK from January 2010 to October 2019 was utilized to study the effects of co-amoxiclav and piperacillin/tazobactam on Gram-negative bacteria. The dataset includes blood and urine cultures, demographics, and prescription information. The authors found that the model worked better with urine cultures than with blood cultures. AUC values for piperacillin/tazobactam and co-amoxiclav in urine cultures were 0.70 and 0.71, respectively. In blood cultures, the values were 0.66 and 0.67. The study approves

that using XGBoost can reduce the abuse of broad-spectrum antibiotics by up to 40%, allowing doctors to choose more accurate therapies and enhance antibiotic stewardship. The researcher tested the model on Gram-negative infections, so it may not valid for Gram-positive bacteria. In addition to general resistance prediction, numerous studies have focused on high-risk setting in hospitals such as Intensive care units (ICUs). In this context, Çağlayan et al. (2022) developed machine-learning techniques to detect ICU patients colonized with multidrug-resistant organisms (MDROs) on admission. This study is a retrospective cohort design, based on electronic clinical records, and included 4,670 ICU admissions gather between 2017 and 2018. The study looked at three main types of MDROs: vancomycin-resistant *Enterococci* (VRE), carbapenem-resistant *Enterobacteriaceae*, and aphylocillin-resistant *Enterobacteriacea*e (MRSA). Using three supervised machine-learning models: regularized logistic regression, random forest, and extreme gradient boosting (XGBoost). They divided the dataset into 80% for training and 20% for testing. The results showed that logistic regression had a sensitivity of 80% and a specificity of 66% for VRE. For CRE, the best model was XGBoost with 73% sensitivity and 77% specificity. The random forest model had 67% sensitivity and 59% specificity for MRSA. When predicting any MDRO as a combined outcome, the random forest model showed the strongest performance with 82% sensitivity and 83% specificity. An interpretability analysis of the model showed that important factors that increase the likelihood of someone getting MDRO colonization are having a previous stay in a long-term care facility, having been placed in isolation before, having skin and soft tissue infections, being diagnosed with an infectious and parasitic disease, and having been in the ICU before. These findings highlight the effectiveness of ensemble machine learning models in identifying MDRO risk at ICU admission and support their potential role in infection management and antimicrobial surveillance strategies. In addition to ICU-focused studies, Viet Tran Q. et al. (2023) developed machine learning models to predict antibiotic resistance in ICU patients a, using electronic medical records (EMR) gathered from two Vietnamese hospitals from January 2020 to June 2022. The positive bacterial cultures for adult ICU patients (18years or older) were included. The total number of data was 1,296 patients and 2,432 bacterial isolates obtained from various sample sources, including urine, respiratory samples, wounds, and catheters. Two datasets were used for model development. The first dataset included demographic information, clinical characteristics, antimicrobial susceptibility testing (AST) results, and complete blood

count (CBC) data. The second dataset added biochemical laboratory parameters to the first dataset. Five supervised machine learning models: XGBoost, LightGBM, Random Forest, AdaBoost, and Ridge Logistic Regression were used. They split the data into 80% for training and 20% for testing. They used several classification metrics to measure the model performance, such as accuracy, precision, sensitivity (recall), specificity, F1-score, AUROC, precision-recall curve, and the normalized Matthews correlation coefficient (normMCC) to deal with class imbalance. The results have been explained using SHapley Additive Explanations (SHAP). The results showed that XGBoost had the best overall performance with accuracy, F1, AUROC and normMCC scores between 0.94 and 1.00. Random Forest and LightGBM also performed very well, with Random Forest having a higher specificity by adding biochemical laboratory data, the model performed much better for all algorithms. The SHAP analysis showed that the most important predictors of antimicrobial resistance were the type of organism causing the infection, class of antibiotic, previous susceptibility results, CBC and biochemical laboratory markers, and clinical diagnosis on admission. This study shows that ensemble machine learning models, especially XGBoost, LightGBM, and Random Forest, can accurately predict ICU antimicrobial resistance using routine EMR data. This supports early clinical decision-making and antimicrobial stewardship.

Despite broad global study, few studies have used machine learning techniques to predict antimicrobial resistance in Jordan. One of the limited existing investigations was carried out by Al-Khlifeh and Hassanat (2024), the primary goal was to predict antimicrobial-resistant patterns in bacterial pathogens isolated from patients in a Salt city, Jordan, using machine learning techniques. The researchers analyzed 2,893 microbiology reports from Al Hussein Salt Hospital between October 2020 and December 2022. 489 samples were used to train and test machine learning models. The datasets of the study included demographic data (Age and sex), bacterial species, source of infection, and susceptibility tests obtained using the VITEK 2 system. Two classification models, random forests (RFs) and categorization regression trees (CARTs) were used to predict resistance to different antibiotics. The results showed that *E. coli* was the most prevalent organism, and Random Forest achieved superior predictive accuracy ranging from 0.64 to 0.99 across antibiotics. Age was considered significant predictors for certain antibiotic resistance, such as trimethoprim, sulfamethoxazole, and ciprofloxacin. Despite this strength, the study had several limitations, including small sample size for machine

learning subsets, absence of clinical status information, and limited geographic coverage, as data were collected from a single hospital not representative of all Jordan.

In contrast to single-center studies, larger multicenter investigations have also been conducted. Haredasht et al. (2024) executed a retrospective cohort study entitled "Enhancing Antibiotic Stewardship: A Machine Learning Approach to Predicting Antibiotic Resistance in Inpatient Care," aimed at creating machine learning models to tailor antibiotic decision-making at the individual patient level. The study was conducted at Stanford University Hospital and nearby community hospitals. It included adult patients (18 years or older) over a long period of time, from 2009 to 2023. The data set had 49,572 patient encounters and included blood, urine, respiratory and other clinical cultures, as well as other types of samples. The authors focused on the prognosis of resistance to five commonly prescribed antibiotics: cefazolin, ceftriaxone, cefepime, piperacillin–tazobactam and ciprofloxacin. The main machine learning method was the LightGBM gradient boosting model, and logistic regression was used as the basis. They divide the data by time, using records from 2009 to 2021 to train the model and records from 2022 to 2023 to test it. This ensured that the model could be tested in a real environment. We used AUROC, accuracy, sensitivity, specificity, and F1 scores to measure how well the model performed. Predictive features included many structured electronic health record variables such as demographic information, prior antibiotic use, prior resistant culture results, patient comorbidities, prior hospitalizations, local institutional antibiogram data, and limited laboratory and vital signs performed within the first 24 hours of admission. The authors used SHAP to find the most important factors that influence antimicrobial resistance. The results approved that the AUROC values for the five antibiotics ranged from 0.74 to 0.78, with the cefazolin model having the highest ability to discriminate between them (AUROC = 0.78). The piperacillin-tazobactam model had the best overall accuracy, indicating that it can make good predictions. Prior antibiotic exposure and history of antibiotic-resistant infections were the most important predictors across all models.

Recently, machine learning approaches have been applied to support clinical decision making in antimicrobial resistance. In this context, Ferrari et al. (2024) conducted a study entitled "Using interpretable machine learning to predict bloodstream infection and antimicrobial resistance in patients admitted to the ICU", The study aimed to predict

bloodstream infection (BSI) and antimicrobial resistance (AMR) in the first hours of ICU admission by using of machine learning models applied to electronic health record (EHR) data. This was a retrospective cohort study done in the intensive care units of Guy's Hospital and St Thomas' NHS Foundation Trust in the United Kingdom. The dataset contained 1,142 ICU patients collected over an eight-year period. Demographics (such as age), laboratory values, vital signs, medical history, current treatment (such as antibiotic use), and parts of the APACHE score were used to construct the model, using many different classical and ensemble machine learning models such as logistic regression, decision tree, random forest, gradient boosting, XGBoost, LightGBM, AdaBoost and Extra Trees classifiers. Standard evaluation metrics such as AUROC, accuracy, precision, recall, and F1 score were used to measure the model performance. A small, balanced training dataset was used to correct the imbalance data. The results showed that the proposed interpretable machine learning method performed well in making predictions. The model that performed best had an AUROC of 0.86 and an F1-score of 0.44 for the prediction of antimicrobial resistance. These results show that interpretable ensemble machine learning models could help find BSI and AMR in the early stages of the ICU and help guide antimicrobial stewardship interventions.

The most recent evidence was provided by Almalki et al. (2025), who conducted a study entitled "Predicting Antimicrobial Resistance Using Machine Learning on Electronic Health Records: A Comparative Study of Ensemble Models." The study aimed to use supervised machine learning models to predict antimicrobial resistance to help clinicians make decisions and manage antimicrobial use. The study included 1,000 patients divided into 500 resistant cases and 500 susceptible cases. The dataset contained many different types of information, such as demographic information, microbiological culture results, antibiotic susceptibility profiles, laboratory values, medication history, and comorbidities. We looked at a number of file models such as XGBoost, LightGBM, Random Forest and HistGradientBoostingClassifier. The authors split the dataset into 80% for training and 20% for testing. then used precision, recall, F1 score, and ROC-AUC to measure how well the model performed. SHAP was also used to make the results easier to understand and to appreciate the correct features. The results showed that XGBoost had the best AUC (0.902) and the best recall (88%) for resistant infections. LightGBM and HistGradientBoostingClassifier had the best accuracy (80%), reducing false positive resistance predictions. Random Forest did not perform as well as other

models, but maintain stable results. The SHAP analysis found that antibiotic type, bacteria type, and laboratory-related variables were the most important factors.

As observed, the world is moving towards using machine learning as a tool to predict bacterial resistance to antibiotics as shown by previous studies. These studies have shown increased efficiency and accuracy in identifying resistant bacteria. However, the use of machine learning to predict antimicrobial resistance remains limited in Jordan and other middle-income countries. In this study, we focus on the application of machine learning to investigate bacterial resistance patterns using local dataset and to support clinical decision -making related to antimicrobial resistance.

Chapter Three

Methodology (Methods and Procedures)

3.1 Data Source and Study Design and Inclusion - Exclusion criteria

This study is a retrospective observational study focusing on Jordanian hospitals between 2020 and 2024. Clinical data was collected from the Health Data Analytics (HDA) system derived from the Hakim Electronic Health Medical Records, where antimicrobial-resistant cases from various patients are centralized for data collection. Data was obtained from all Ministry of Health hospitals across the Kingdom. The collected dataset includes multiple variables for each patient, such as laboratory test results, demographic information, diagnostic notes, medication use, treatment response, and microbiological reports. Hakim Health Information System is the center for the collected dataset in this study. Hakim is a platform that allows physicians to access patient records and perform operations such as adding, deleting, updating, and others. The dataset was collected from Hakim, which contains 19 fields and 839,735 patient records as entries. These records include a mix of numerical and categorical variables.

3.1.1 Inclusion Criteria

Records were included in the study if they met the following criteria:

3.1.1.1 Data derived from the Hakim Electronic Health Medical Records through the Health Data Analytics (HDA) system.

3.1.1.2 Records obtained from Ministry of Health hospitals in Jordan.

3.1.1.3 Records collected during the period 2020–2024.

3.1.1.4 Records containing essential variables, including: Age , Sex (gender) , Laboratory records with microbiological reports and antibiotic susceptibility results., Antibiotic name, Antibiotic susceptibility outcome (resistant, susceptible, intermediate)

3.1.1.5 Records that passed data validation checks and were suitable for descriptive and machine learning analysis.

3.1.2 Exclusion Criteria

Records were excluded from the study if they met any of the following conditions:

3.1.2.1 Duplicate records identified through full or partial matching of patient ID and features.

3.1.2.2 Records with missing or incomplete essential variables.

3.1.2.3 Records with more than 5% missing data across total features.

3.1.2.4 Records that failed data validation (incorrect data type or inconsistent values).

3.2 Method of Descriptive Analysis

A descriptive analysis was performed to characterize the study population and assess the dataset before machine learning model. This analysis aimed to provide an overview of patient demographics, patterns of antibiotic resistance, and bacterial distribution.

3.2.1 Data cleaning and preparation

Prior to analysis, the data was cleaned to ensure the quality of data. The process involved the following steps:

3.2.1.1 Remove duplicate records

All data was selected in Microsoft Excel. Then, remove duplicate data by using the remove duplicates feature on the data tab. All columns were selected to ensure the removal of all duplicate records.

3.2.1.2 Processing the missing data

To identify Blank cells, all data was selected and the Go to Special → Blanks function in Microsoft Excel was used, Records with missing values were evaluated. Blank dates of admission or discharge were left only for patients who had cultures collected in outpatient or emergency departments where admission data were unavailable.

3.2.1.3 Data validation

Data validation was performed to confirm data consistency and accuracy. Boolean and Excel functions such as ISNUMBER, ISTEXT and conditional formulas (TRUE/FALSE) were used to verify that numeric fields contained numbers and

categorical fields contained text. Validation ensured that each variable had the correct format required for later machine learning.

3.2.1.4 Age group categorization

Age values were recorded in days, weeks, months, and years. An IF conditional formula was applied to categories age into groups. Age values recorded in days, weeks, or months were classified into 0–1-year group .As result, age was grouped into the following categories: 0–1 year, 1–18 years, 19–64 years, ≥65 years.

3.2.1.5 Antibiotic drug class classification

A drug classification table has been created to simplify antibiotic-related analysis. This table includes the antibiotic names alongside their respective medication classes, including fluoroquinolones, penicillins, macrolides, cephalosporins, and carbapenems. The VLOOKUP tool in Microsoft Excel was utilized to automatically classify each antibiotic in the primary dataset. This method facilitated accurate alignment between antibiotic names and the related pharmacological categories with exact matching.

3.2.2 Descriptive analysis Using PivotTables

The dataset included 839,728 laboratory records with numerous variables such as patient ID, age, gender, antibiotic type, organism, resistance status, ward type, source of infection, and year of isolation. Descriptive analysis was done by Microsoft Excel Pivot Tables to analyze antimicrobial resistance across different variables. For each variable of interest, a PivotTable was created using the patient ID in the Values field to calculate counts and the variable of interest (e.g., sex, age group, ward type, pathogen, antibiotic class, or year) in the Rows section. A Resistance Status variable (resistant, susceptible, and intermediate) was added in the Columns section. The value field was set to Count to get the total number of records in each category. To facilitate comparison, the results were presented as percentages of row totals, allowing for an assessment of resistance distribution among groups. Visualization was performed using 100% stacked column charts created from PivotTable results. The x-axis showed the categories of the chosen variable, and the y-axis represented the proportion of isolates. Appropriate data labels and axis names were added to improve clarity and interpretation.

3.3 Method of Machine learning

3.3.1 Data cleaning and preparation

3.3.1.1 Duplicate removal:

This step is very important for producing a consistent dataset, as the dataset contains many duplicate records for the same patient. Therefore, removing duplicates makes the dataset cleaner and more focused, with no redundant records. The matching process to identify duplicate records was applied in two ways: the first used full matching and the second used partial matching. When half of the features were identical for the same patient ID, one of the records was removed, keeping only a single entry in the dataset. After applying duplicate removal, the number of records in the dataset was reduced to 501,321 distinct records.

3.3.1.2 Handling missing values:

In the dataset, some records had missing values in their features. To fill these values, it would require returning to the patient case in the hospital. Therefore, records with missing information in more than 5% of the total number of features were removed. For records with less than 5% missing information, the missing values were calculated and filled. The filling was performed using one of the following methods: mean or median imputation, advanced imputation techniques, or multiple imputation via chained equations (MICE). The most appropriate method was selected based on the available information in each record.

3.3.1.3 Merging spreadsheets:

The dataset collected from Hakim was distributed across three separate Excel files. To consolidate these files into a single file for the next processes, a merging procedure was performed by matching their features based on the patient ID and applying an inner join operation. Duplicate records were also removed after the consolidation process. After merging the three files and removing duplicates, the number of records was reduced to 21,277 unique patient records.

3.3.1.4 Feature selection:

Feature selection from the cleaned dataset plays a very important role in the results. Using all features can negatively impact the prediction performance. The cleaned dataset

contained 19 features, but not all of them were suitable for the prediction classifier model. During feature selection, six variables were excluded from the dataset. Patient ID was removed because it is an identifier and does not provide predictive value for antimicrobial resistance. Admission date and discharge date were excluded because these variables were not available for all patients, and the analysis focused on the period since admission rather than exact dates. Date of birth was excluded because age variable was used instead. Laboratory reference was removed as it represents a test identifier and does not contain clinical or predictive information. Laboratory test parameters were also excluded because they were not available for all patients and could not be reliably matched with admission records. The final relevant features selected were 13. In the next prediction steps, SHAP can help determine which features have a greater effect than others on the prediction outcomes.

3.3.1.5 Scaling and normalization:

This process is very significant for converting the dataset into numerical values. Ensemble learning methods can only read numerical data; therefore, the records must be converted to numerical form by applying a scaling method and then applying normalization to ensure that all values fall between 0 and 1. Categorical variables were encoded to convert the labels into numerical values. The encoding method identifies unique labels and assigns corresponding numeric values. For example, the *diagnosis* attribute included 352 different category values, so a wider encoding approach was needed. The simple Min–Max normalization method was applied to each feature to generate normalized values across all records in the cleaned dataset. Min–Max normalization was used because it scales all features to a fixed range (0–1) and is less affected by extreme values commonly found in clinical data. In contrast, Z-score standardization depends on the mean and standard deviation, which can be distorted by outliers, leading to unstable feature scaling. In this study, antimicrobial susceptibility outcomes were encoded as follows: 0 = Resistant, 1 = Sensitive, and 2 = Intermediate.

3.3.1.6 Handling imbalance in the dataset:

The classes were not evenly represented in the dataset, so class imbalance had to be addressed before training. SMOTE (Synthetic Minority Over-Sampling Technique) was used to generate additional examples for the minority class. SMOTE helps avoid bias during learning by balancing class proportions without simply duplicating existing

samples. In addition, controlled over-sampling and under-sampling were applied to maintain a balanced distribution. Overall, the machine learning analysis was conducted at the patient-based level rather than the laboratory-record level. The original dataset contained multiple repeated laboratory tests for the same patient; therefore, duplicate matching, exclusion of incomplete records, and dataset consolidation were applied to retain a single representative record per patient. This approach ensured data consistency and clinical relevance, resulting in a final dataset of 21,277 unique patient records suitable for machine learning model development and evaluation.

3.3.1.7 Training/testing split:

Determining the ratio for training and testing is very important in prediction methods. After preprocessing, the dataset is now cleaned, encoded, normalized, and balanced.The popular standard used for training–testing split is 80:20, where 80% of the dataset is used for training and 20% is reserved for testing the methods. The final cleaned dataset contains 13 selected features and consists of 21,277 records. Table 3.1 summarizes the 13 selected features with their categories. The dataset was divided into two splits. The training set consisted of 17,021 samples with 13 features, while the Testing set included 4,256 samples with 13 features.

Table 3.1: List of features in the cleaned dataset

No.	Feature Name	Number of Features
1	Antibiotic Name (English)	47
2	Topography Name (English)	281
3	Organism	64
4	Organism Type	3
5	Specimen Collection Date	-
6	Nosocomial Infection Indicator	2
7	Ward Type	4
8	Period Since Admission (Hours)	-
9	Age	-
10	Sex	2
11	Date Entered	-
12	Diagnosis	352
13	Reference Susceptibility Interpretation (Actual results)	3

3.3.2 Ensemble Learning Methods

Four ensemble learning models and SHAP, an explainable AI technique, were applied to produce trustworthy predictions of AMR diseases and to interpret which features influence the prediction results. The four ensemble methods—Random Forest, AdaBoost, stacking, and a voting classifier—were evaluated separately. For each model, SHAP was used to analyze the contributions of the 13 selected features. This approach was applied in line with previous studies (Haredasht et al., 2024; Viet Tran Q. et al., 2023; Ferrari et al., 2024; Almalki et al., 2025). Four ensemble methods are used in this study, and their characteristics and mathematical foundations are described in the following subsections.

3.3.2.1 Random forest

Random Forest is an ensemble learning technique that builds on decision tree models and uses a bagging approach. During the training process, many decision trees are generated, and their predictions are combined to produce a result – using majority voting for classification problems or averaging for regression tasks. This method works well when there are many features or complex relationships within the data (Sarker, 2021).

It helps maintain low bias while reducing overfitting and making outliers less problematic. The Random Forest method is considered a strong choice for prediction due to several reasons. Random Forest can efficiently handle high-dimensional data compared with other methods. It can highlight which features are important in the dataset during training. If there are missing values in some records, Random Forest can handle them effectively. Overfitting can also be avoided in the Random Forest method, which increases the accuracy of the prediction outcome (Sarker, 2021).

In this study, 100 decision trees were used in the Random Forest model, and each tree was restricted to a depth of 10 with a maximum of five splits.

3.3.2.2 AdaBoost

AdaBoost (Adaptive Boosting) is an ensemble method that depends on a sequential workflow when building the model. In each sequence, a weak learner is trained to identify the mistakes of the previous learner and correct them before moving to the next. AdaBoost operates in multiple rounds, and in each round, it assigns more attention to samples that were misclassified earlier. The main idea of AdaBoost is to boost the performance of weak learner models. Adjusting the weights of samples is the key process used to handle difficult cases in

the training method. The weight adjustment is based on classification errors to determine the appropriate weight for each sample in the classifier model (Sarker, 2021).

AdaBoost converges faster toward suitable weights. In addition, its sequential training structure makes implementation relatively simple. The classification accuracy improves by prioritizing difficult samples in each round (Sarker, 2021). In this study, the AdaBoost classifier was used with 50 estimators, employing simple decision stubs as base learners to keep the model computationally efficient. Furthermore, overfitting is avoided compared with training weak learners independently.

3.3.2.3 Stacking Classifier

Sacking, also called stacked generalization, is one of the ensembles learning models that depends on an integration mechanism. In this approach, several basic models are integrated to generate a final learner using a meta-learner. These base models work together to enhance prediction by adjusting their weights to reach a final decision. By overcoming the limitations of individual models and learning the correct weight contributions, stacking can find global patterns in the dataset, enabling the system to perform better than any single model (Lazzarini, Tianfield & Charissis, 2023).

Stacking has an advantage over other ensemble methods because it combines diverse learner models and adjusts their weights collectively. It can accommodate multiple combinations of base and meta learners and determine complex relationships reflected in the outputs of all learners. In this study, two basic models—Random Forest and Decision Tree—were used as the base learners, while Logistic Regression functioned as the meta-learner. This hybrid structure improves prediction accuracy while maintaining flexibility in the modeling process (Lazzarini, Tianfield & Charissis, 2023).

3.3.2.4 Voting Classifier

The idea behind a voting classifier model is to aggregate the outputs from different models through specific voting types. There are two voting strategies: hard voting and soft voting. In this aggregated model, various classifiers produce their predictions, and then the voting mechanism computes the projected probabilities from each model. The combination can be done by averaging the probabilities or selecting the majority class predicted by the models. As one of the ensembles learning approaches, voting can improve robustness and reduce variance. Although individual models may generate

mistakes on certain samples, applying a voting strategy can cancel out these errors and increase the prediction accuracy (Burka et al., 2022).

In this study, Random Forest, AdaBoost, and Decision Tree classifiers are used within a soft voting ensemble model to enhance prediction performance. The main advantages of soft voting include ease of interpretation, simple implementation, and reduction of forecasting variance by averaging the predictive distributions.

3.3.3 The SHAP method and SHAP metric

In explainable AI methods, SHAP has gained significant attention across various domains, including healthcare. It helps to explain and interpret which features have the greatest impact on prediction models and classification methods. To understand the key biomarkers that have a significant effect on diagnosis and strongly influence the prediction of patient outcomes, SHAP plays an important role. Clinicians and researchers can use SHAP to interpret and explain the features in a dataset. SHAP has been applied in many diseases, such as heart disease, diabetes, Alzheimer's disease, and various types of cancer, where it has been used extensively. SHAP provides both global and local interpretability for individual patients or groups of patients for a specific disease. It aids clinical decision-making and helps ensure the accuracy of results in research focused on prediction models and classifiers (Lundberg & Lee, 2020).

SHAP is a mathematical tool used to explain machine-learning models, such as prediction, classification, clustering, and others. It can be integrated with tree-based algorithms to support clinical data analysis and to understand the importance of each feature in a dataset. TreeExplainer, a method within SHAP, helps interpret models by calculating the contribution of each feature at the patient level and across the entire dataset. It provides insights into how variables—such as cognitive assessments, demographic factors, and genetic markers—affect the results and influence diagnostic predictions (Lundberg & Lee, 2020).

In practice, SHAP is applied to trained file models to generate complex explanations at two levels: local and global. This layered interpretability highlights the most compelling biomarkers for disease classification and assists in clinical validation. In addition, visualization methods such as summary and force plots improve clarity by mapping element interactions and strengthen confidence in the model's decision-making

process. The SHAP method provides key metrics that help interpret ensemble learning models. High absolute SHAP value indicates that a feature has a strong impact on the model's prediction. While Positive SHAP value indicates that a feature increases the predicted probability for classification tasks ,and a negative SHAP value indicates that The feature decreases the predicted probability (Lundberg & Lee, 2020) .

3.3.3.1 Evaluation Metrics and Validation Strategy

For model performance measurement, the following metrics were utilized (Rainio, Teuho, & Klén, 2024).

3.3.3.2 Accuracy: Judges the overall accuracy of the prediction.

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

3.3.3.3 Precision: Calculates the proportion of true positives among predicted positives.

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

3.3.34 Recall (Sensitivity): Calculates the ability of the model to detect positive cases.

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

3.3.3.5 F1 Score: Balances precision and recall.

$$\text{F1} = 2.\frac{\text{Precision.Recall}}{\text{Precision} + \text{Recall}}$$

3.3.3.6 AUC-ROC Curve: Judges the discriminative capacity of the classifier.

$$\text{AUC} = \int_0^1 \text{TPR}(\text{FPR})\text{d}(\text{FPR})$$

3.3.3.7 Specificity: Specificity measures the proportion of actual negative samples correctly identified:

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}}$$

3.3.3.8 Matthews Correlation Coefficient (MCC) MCC provides a balanced measure that accounts for all components of the confusion matrix:

$$\text{MCC} = \frac{\text{TP} \times \text{TN} - \text{FP} \times \text{FN}}{\sqrt{((\text{TP} + \text{FP})\ (\text{TP} + \text{FN})(\text{TN} + \text{FP})\ (\text{TN} + \text{FN})\ )}}$$

Where TP, TN, FP, and FN are true positives, true negatives, false positives, and false negatives, respectively.

Chapter Four

Results of the Study

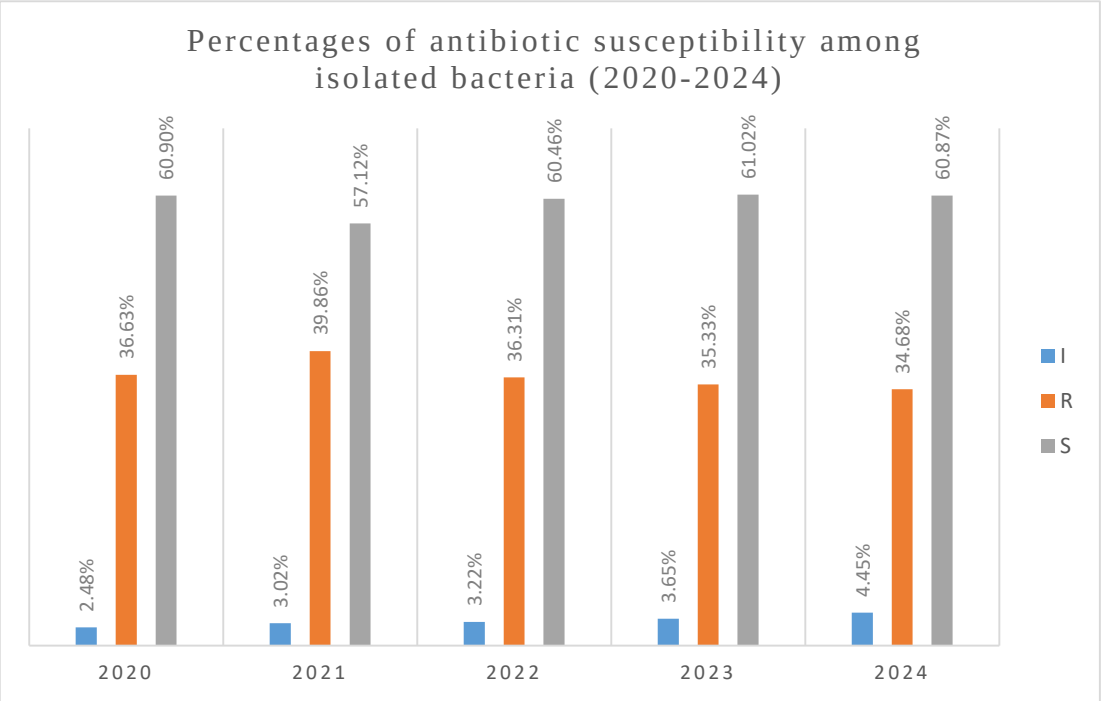
4.1 Descriptive analysis

4.1.1 Year of bacterial isolation and antibiotic susceptibility

The total number of bacterial isolates per year was presented in Table 4.1. For each year the total number of susceptible bacteria to any tested antibiotic was recorded. Figure 4.1 present the percentages of resistance, intermediate and sensitivity toward antibiotics, where the highest percentage of resistance bacteria detected was in 2021 with 59781 isolates (39.86%).

Table 4.1: Year of bacterial isolation, number of isolates and antibiotic susceptibility- resistance

Year of isolation	**Antibiotic susceptibility**			
	I	R	S	Total
2020	2938	43452	72242	118632
2021	4537	59781	85673	149991
2022	5704	64260	106997	176961
2023	7971	77060	133106	218137
2024	7828	61037	107142	176007
Total	28978	305590	505160	839728



I: intermediate, R: resistance, S: sensitive

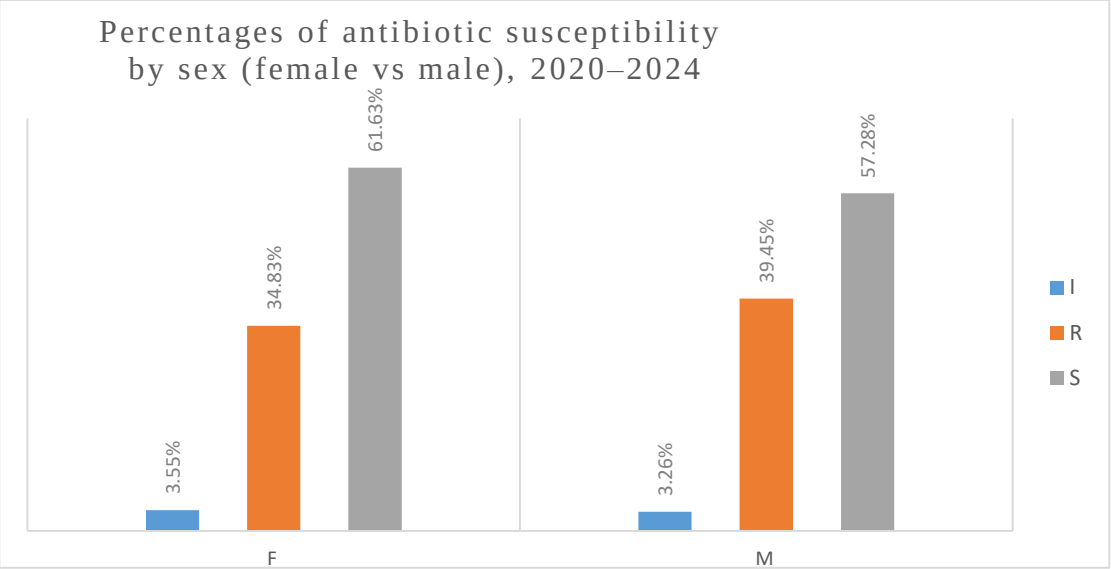
Figure 4.1: Percentages of antibiotic susceptibility for isolated bacteria (2020-2024)

4.1.2 Sex and antimicrobial resistance

During the study period males were more susceptible to infection with resistance bacteria than female with 39.45% of resistance bacteria were detected compared to female (34.83%). The total number of isolates for each sex were presented in Table 4.2 and the percentages of these bacteria were presented in Figure 4.2.

Table 4.2: Number of isolates by sex and antibiotic susceptibility

Number of Isolates(n)	**Antibiotic susceptibility**		
SEX	I	R	S
F	19719	193570	342514
M	9259	112020	162646
Total	28978	305590	505160



I: intermediate, R: resistance, S: sensitive

Figure 4.2 Comparison of antibiotic susceptibility percentage by sex

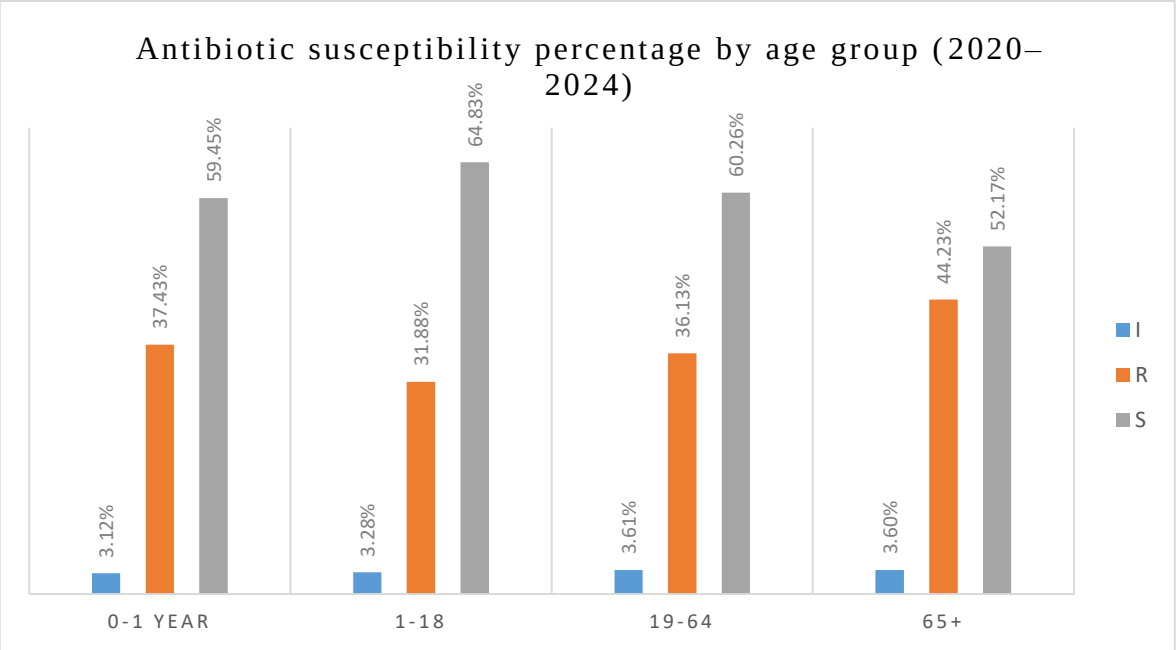
4.1.3 Age groups and antibiotic susceptibility

The patients included in this study were divided into groups based on age. The first group from 0–1-year, 1 -18 year was the second group, from 19-64 was the third group and more the 65 years was the fourth group. Table 4.3 showed the number of isolates per age group and the percentages of antibiotic susceptibility per age group was presented in Figure 4.3 the highest percentage of resistance bacteria was recorded in 65 years and more age group (44.23%) followed by the first age group (0-1 year) where the resistance percentage was 37.43%.

Table 4.3: Number of isolates by age group and their antibiotic susceptibility

Number of isolated bacteria with their antibiotic susceptibility			
Age Group	I	R	S
0-1 year	3850	46179	73354
1-18	7280	70677	143718
19-64	13393	133973	223487
65+	4455	54761	64601
Total	28978	305590	505160

I: intermediate, R: resistance, S: sensitive



I: intermediate, R: resistance, S: sensitive

Figure 4.3: Antibiotic susceptibility percentage by age group (2020-2024)

4.1.4 Antibiotic types and bacterial resistance

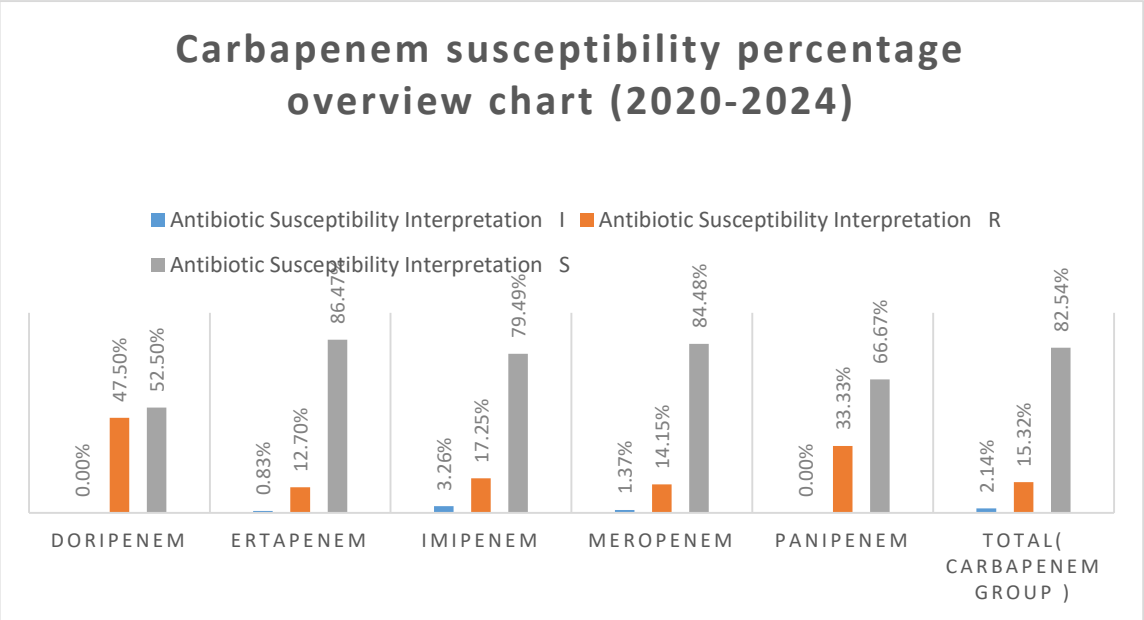
4.1.4.1 Carbapenem group

The resistance of doripnem against isolated bacteria was the highest percentage equals 47.5%. followed by panipenem were the resistance percentage equals 33.33%. the overall all resistance percentage among all the carbapenem group was equal to 15.32%. the lowest resistance percentage was recorded against ertapenem (12.7%). Table 4.4 presented the total number of isolates and carbapenem susceptibility, and Figure 4.4 presented the susceptibility percentages.

Table 4.4: Number of isolates and antibiotic susceptibility for carbapenem group (2020–2024)

	Number of bacterial isolates- antibiotic susceptibility			
Antibiotic	I	R	S	Total
Doripenem	0	19	21	40
Ertapenem	153	2347	15981	18481
Imipenem	1461	7730	35631	44822
Meropenem	463	4781	28540	33784
Panipenem	0	1	2	3
Total	2077	14878	80175	97130

I: intermediate, R: resistance, S: sensitive



I: intermediate, R: resistance, S: sensitive

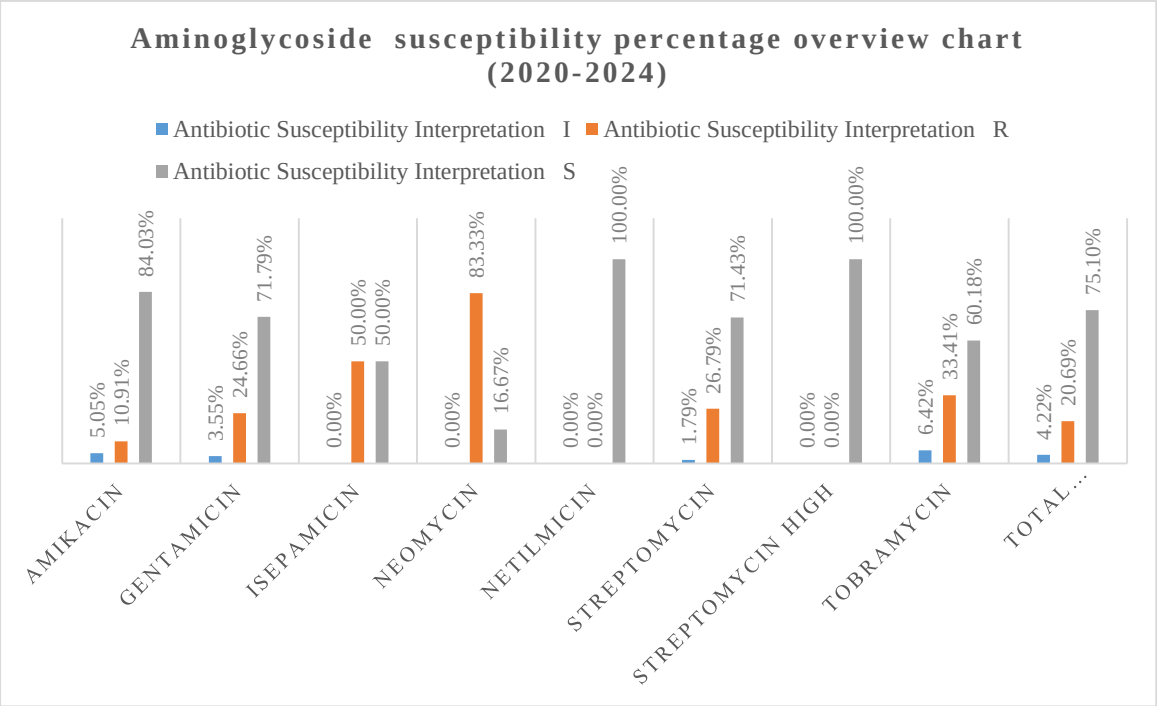
Figure 4.4: Percentage of antibiotic susceptibility for carbapenem group (2020–2024)

4.1.4.2 Aminoglycoside group

For aminoglycoside susceptibility against isolated bacteria the highest resistance was detected against neomycin 83.3% (for total 6 isolates), followed by 50% resistance against isepamicin (total of 2 isolates). No resistance was detected against streptomycin high. The number of isolates and aminoglycosides susceptibility were presented in Table 4.5, and the calculated percentages of susceptibility were presented in Figure 4.5.

Table 4.5: Number of isolates and antibiotic susceptibility for aminoglycoside group (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Total
Amikacin	1656	3576	27538	32770
Gentamicin	2171	15075	43884	61130
Isepamicin	0	1	1	2
Neomycin	0	5	1	6
Netilmicin	0	0	2	2
Streptomycin	1	15	40	56
Streptomycin High	0	0	3	3
Tobramycin	387	2014	3628	6029
Total (Aminoglycoside Group)	4215	20686	75097	99998



I: intermediate, R: resistance, S: sensitive

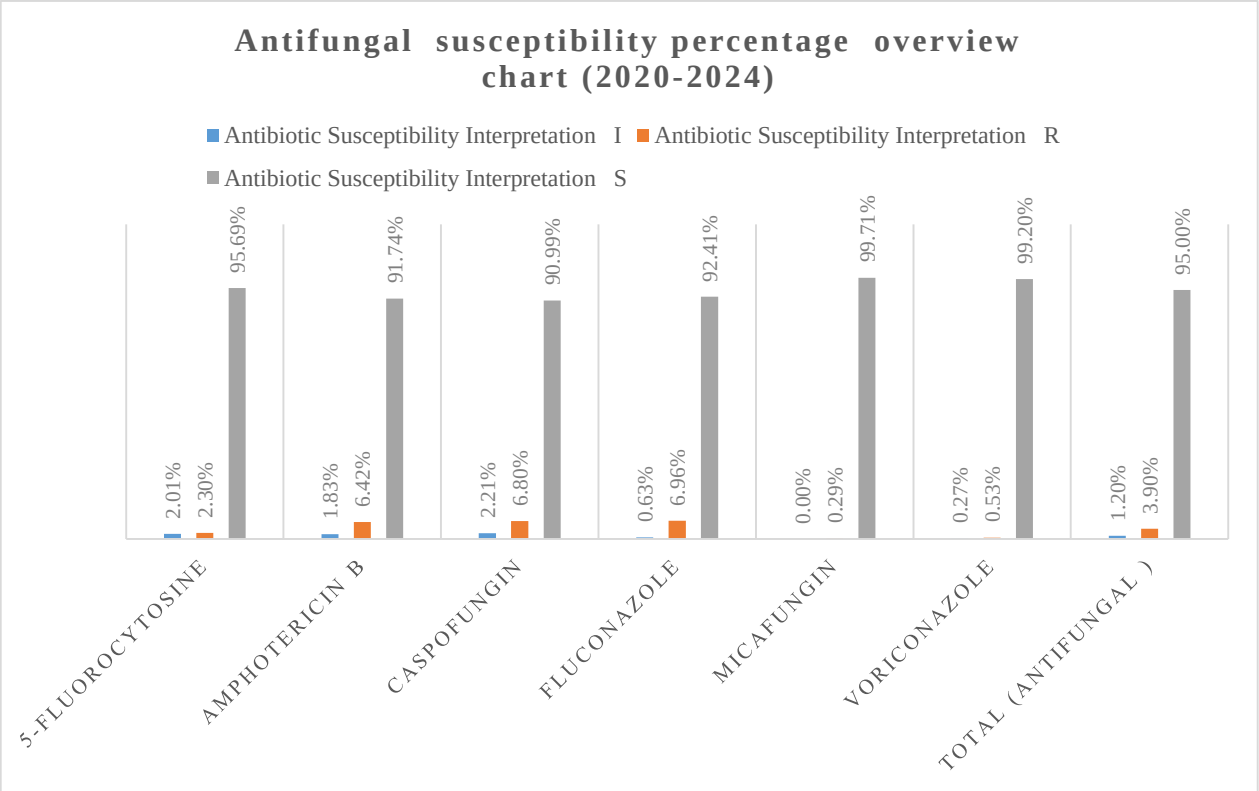
Figure 4.5: Percentage distribution of antibiotic susceptibility in aminoglycoside group (2020–2024)

4.1.4.3 Antifungal group

The highest antifungal resistance was recorded against fluconazole (6.96%). the lowest resistance was recorded against micafungin (0.29%). The number of isolates and antifungal susceptibility was presented in Table 4.6 and the susceptibility percentage was presented in Figure 4.6

Table 4.6: Number of isolates and antifungal susceptibility for antifungal group (2020–2024)

	Number of isolates- antifungal susceptibility			
Name of antifungal	I	R	S	Total
5-Fluorocytosine	7	8	333	348
Amphotericin B	2	7	100	109
Caspofungin	13	40	535	588
Fluconazole	2	22	292	316
Micafungin	0	1	339	340
Voriconazole	1	2	371	374
Total	25	80	1970	2075



I: intermediate, R: resistance, S: sensitive

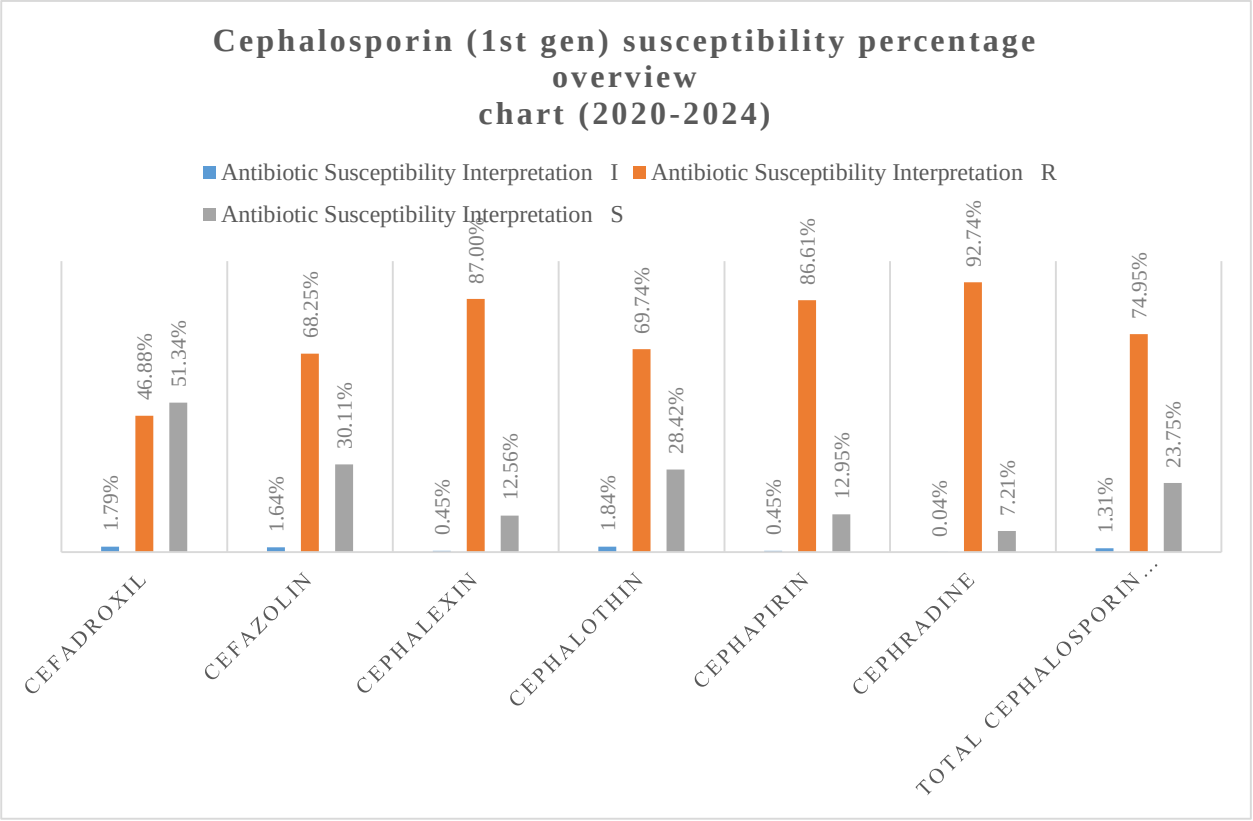
Figure 4.6: Percentages of antifungal susceptibility (2020–2024)

4.1.4.4 First generation of cephalosporin.

For the all first generation of cephalosporins 74.95 % was the resistance percentage and 23.75% was the sensitive percentage of bacteria for this group (for 19203 isolated bacteria). With the highest resistance was recorded against cephardine (92.74%). The number of isolates and antibiotic susceptibility presented in Table 4.7 and the calculated percentages in Figure 4.7

Table 4.7: Number of isolates and antibiotic susceptibility for the first generation of cephalosporin group (2020–2024).

	Number of isolates - antibiotic susceptibility			
Name of antibiotics	I	R	S	Total
Cefadroxil	8	210	230	448
Cefazolin	75	3121	1377	4573
Cephalexin	16	3124	451	3591
Cephalothin	150	5673	2312	8135
Cephapirin	1	194	29	224
Cephradine	1	2070	161	2232
Total	251	14392	4560	19203



I: intermediate, R: resistance, S: sensitive

Figure 4.7: Percentages of antibiotic susceptibility for the first generation of cephalosporin (2020–2024)

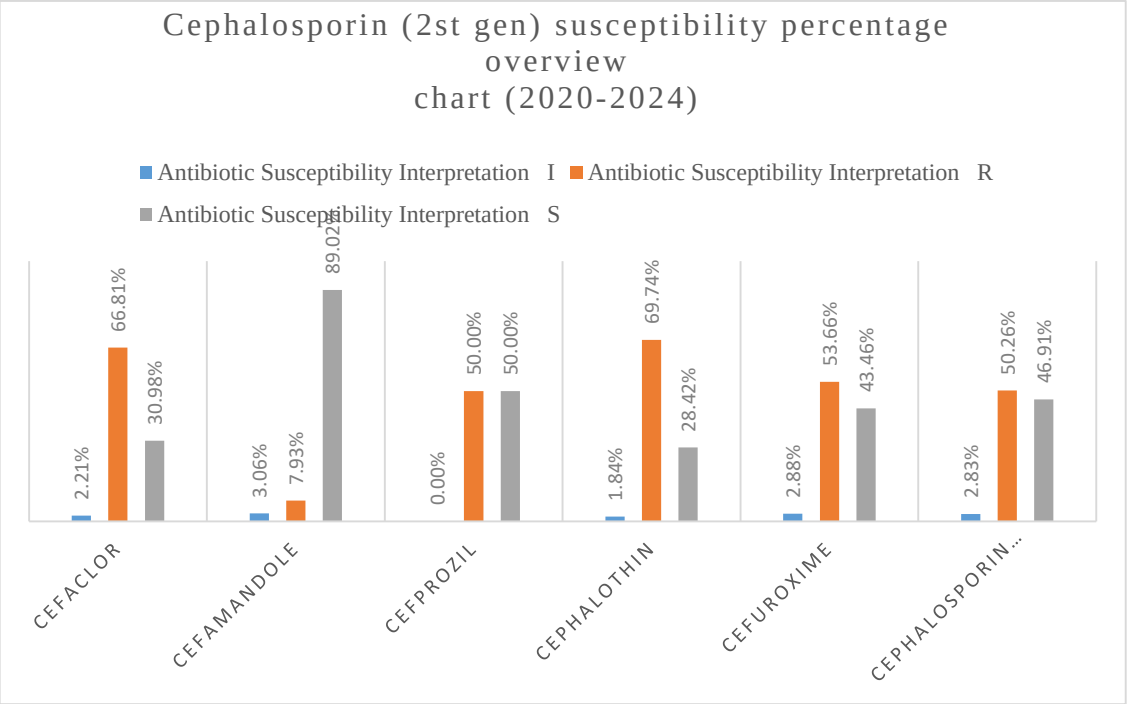
4.1.4.5 Second generation of cephalosporin

For the second generation of cephalosporin 50.2% (for 29392 isolates of bacteria) was the overall resistance against this group. The highest resistance percentage was recorded against cephalothin 69.74%, and the lowest resistance percentage was against cefamandole (7.93%). The number of isolates and antibiotic susceptibility presented in Table 4.8 and the calculated percentages in Figure 4.8

Table 4.8: Number of isolates and antibiotic susceptibility for the second generation of cephalosporin (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Total
Cefaclor	61	1844	855	2760
Cefamandole	91	236	2650	2977
Cefprozil	0	1	1	2
Cefuroxime	680	12692	10280	23652
Cephalosporin	832	14773	13786	29391

I: intermediate, R: resistance, S: sensitive



I: intermediate, R: resistance, S: sensitive

Figure 4.8: Percentage of antibiotic susceptibility for second generation of cephalosporin (2020–2024)

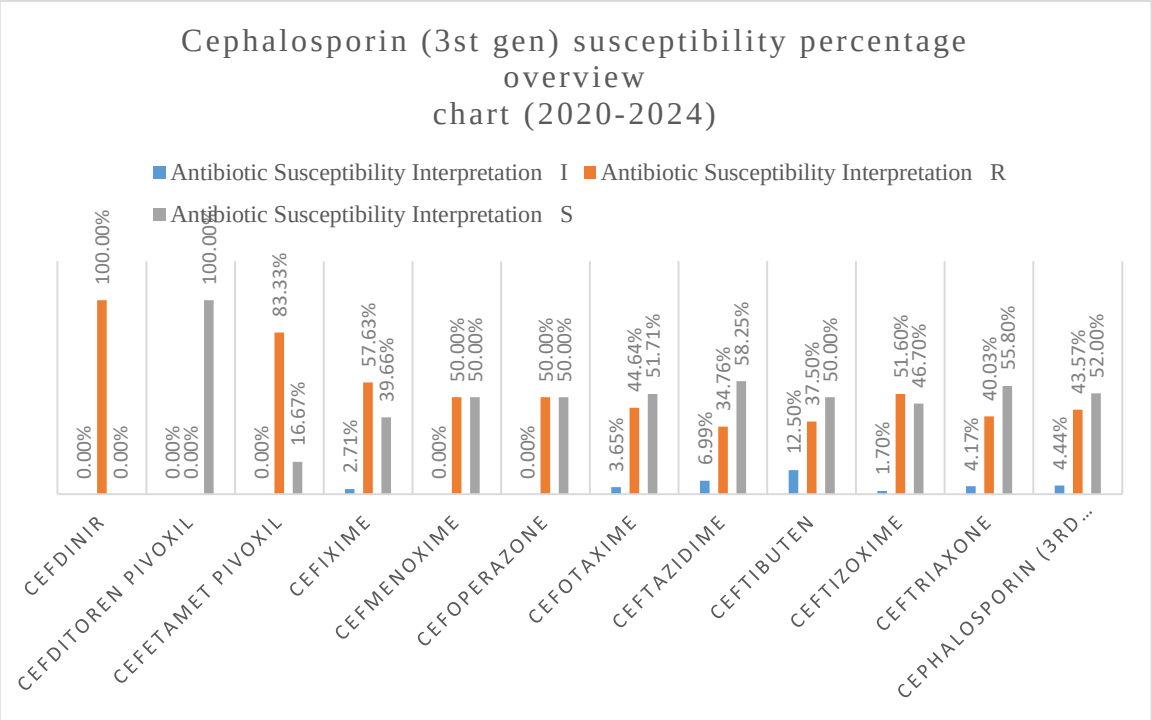
4.1.4.6 Third generation of cephalosporin

For the third generation of cephalosporin 43.57 % was the resistance percentage and 52.00% was sensitive percentage of bacteria for this group (for 10553 isolated bacteria). With the highest resistance was recorded against cefdinir (100 %) and the lowest resistance percentage was against Ceftazidime (34.7 %). The number of isolates and antibiotic susceptibility presented in Table 4.9 and the calculated percentages in Figure 4.9.

Table 4.9: Number of isolates and antibiotic susceptibility for the third generation cephalosporin (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Total
Cefdinir	0	4	0	4
Cefditoren Pivoxil	0	0	1	1
Cefetamet Pivoxil	0	5	1	6
Cefixime	570	12103	8330	21003
Cefmenoxime	0	3	3	6
Cefoperazone	0	5	5	10
Cefotaxime	1034	12651	14655	28340
Ceftazidime	1919	9547	15997	27463
Ceftibuten	1	3	4	8
Ceftizoxime	25	759	687	1471
Ceftriaxone	1134	10896	15189	27219
Cephalosporin (	4683	45976	54872	105531

I: intermediate, R: resistance, S: sensitive



I: intermediate, R: resistance, S: sensitive

Figure 4.9: Percentage of antibiotic susceptibility for the third generation of cephalosporin (2020–2024)

4.1.4.7 Fourth generation of cephalosporin

For the fourth generation of cephalosporin 34.61 % was the resistance percentage and 63.83 % was sensitive percentage of bacteria for this group (for 15575 isolated bacteria). With the highest resistance was recorded against cefirome (100 %) and the lowest resistance percentage was against cefepime (34.7 %). The number of isolates and antibiotic susceptibility presented in Table 4.10 and the calculated percentages in Figure 4.10

Table 4.10: Number of isolates and antibiotic susceptibility for the fourth generation of cephalosporin (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Grand Total
Cefepime	244	5389	9941	15574
Cefpirome	0	1	0	1
Cephalosporin	244	5390	9941	15575

I: intermediate, R: resistance, S: sensitive

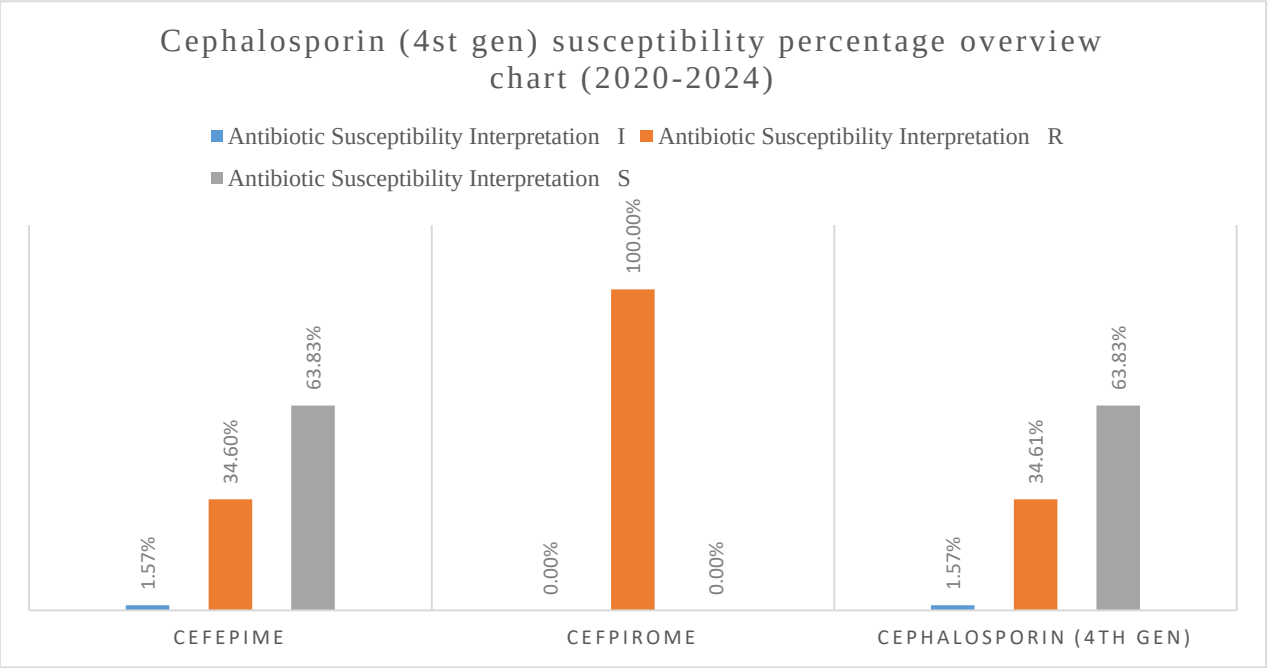


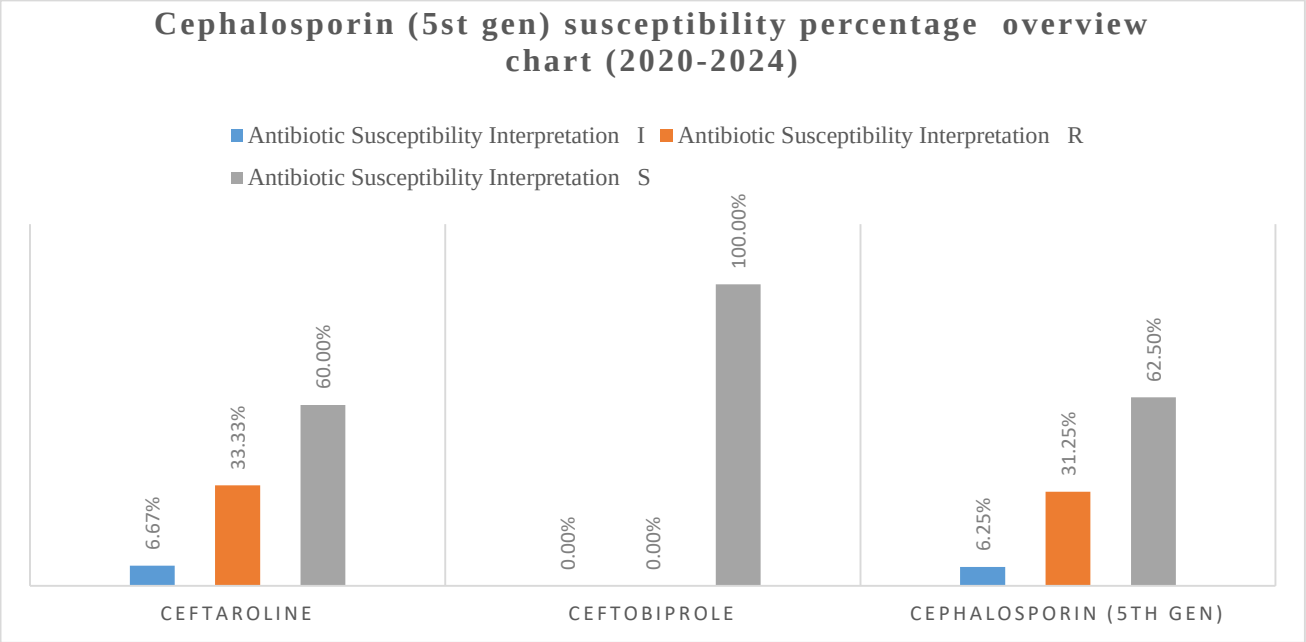
Figure 4.10 Percentage of antibiotic susceptibility to the fourth generation of cephalosporin (2020–2024)

4.1.4.8 Fifth generation of cephalosporin

For the fifth generation of cephalosporin 31.25 % was the resistance percentage and 62.50 % was sensitive percentage of bacteria for this group (for 16 isolated bacteria). With the highest resistance was recorded against ceftaroline (33.33 %), whereas no resistance was observed against Ceftobiprole. The number of isolates and antibiotic susceptibility presented in Table 4.11, and the calculated percentages in Figure 4.11

Table 4.11: Number of isolates and antibiotic susceptibility for the fifth cephalosporin generation (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Grand Total
Ceftaroline	1	5	9	15
Ceftobiprole	0	0	1	1
Cephalosporin (5th gen)	1	5	10	16



I: intermediate, R: resistance, S: sensitive

Figure 4.11: Percentage of antibiotic susceptibility for the fifth cephalosporin generation (5th gen) (2020–2024)

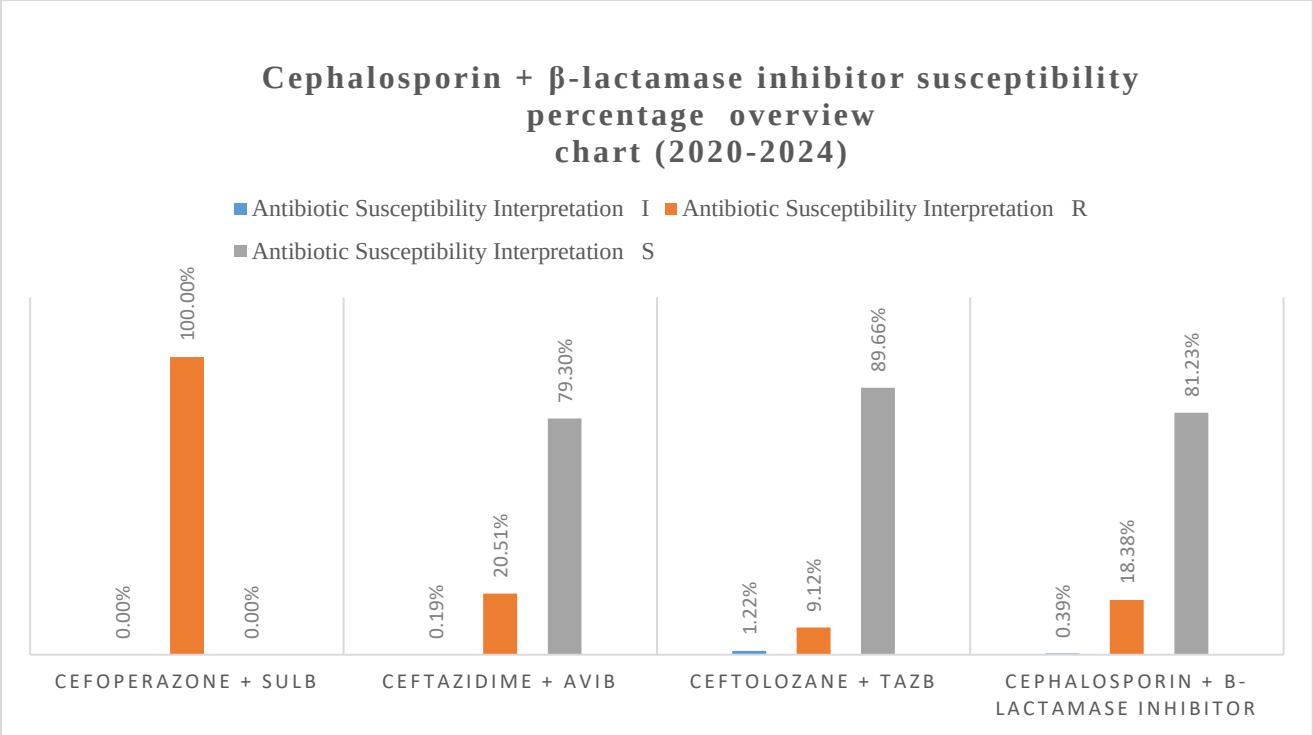
4.1.4.9 Cephalosporin + β-lactamase inhibitor group

For cephalosporin + β-lactamase inhibitor group susceptibility against isolated bacteria, 18.38% was the resistance percentage and 81.23% was the sensitive percentage of bacteria for this group (for 3890 isolated bacteria). With the highest resistance was detected against Cefoperazone + Sulbactam (100 %) and the lowest resistance percentage was against Ceftolozane + Tazbactam (9.12 %) The number of isolates and antibiotic susceptibility were presented in Table 4.12 ,and the calculated percentages of susceptibility was presented in Figure 4.12

Table 4.12: Number of isolates and antibiotic susceptibility cephalosporin + β-lactamase inhibitor group (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Grand Total
Cefoperazone + Sulbactam	0	1	0	1
Ceftazidime + Avibactam	6	647	2501	3154
Ceftolozane + Tazbactam	9	67	659	735
Cephalosporin + β-lactamase inhibitor	15	715	3160	3890

I: intermediate, R: resistance, S: sensitive



I: intermediate, R: resistance, S: sensitive

Figure 4.12: Percentage of antibiotic susceptibility to cephalosporin + β-lactamase inhibitor (2020–2024)

4.1.4.10 Fluoroquinolone group

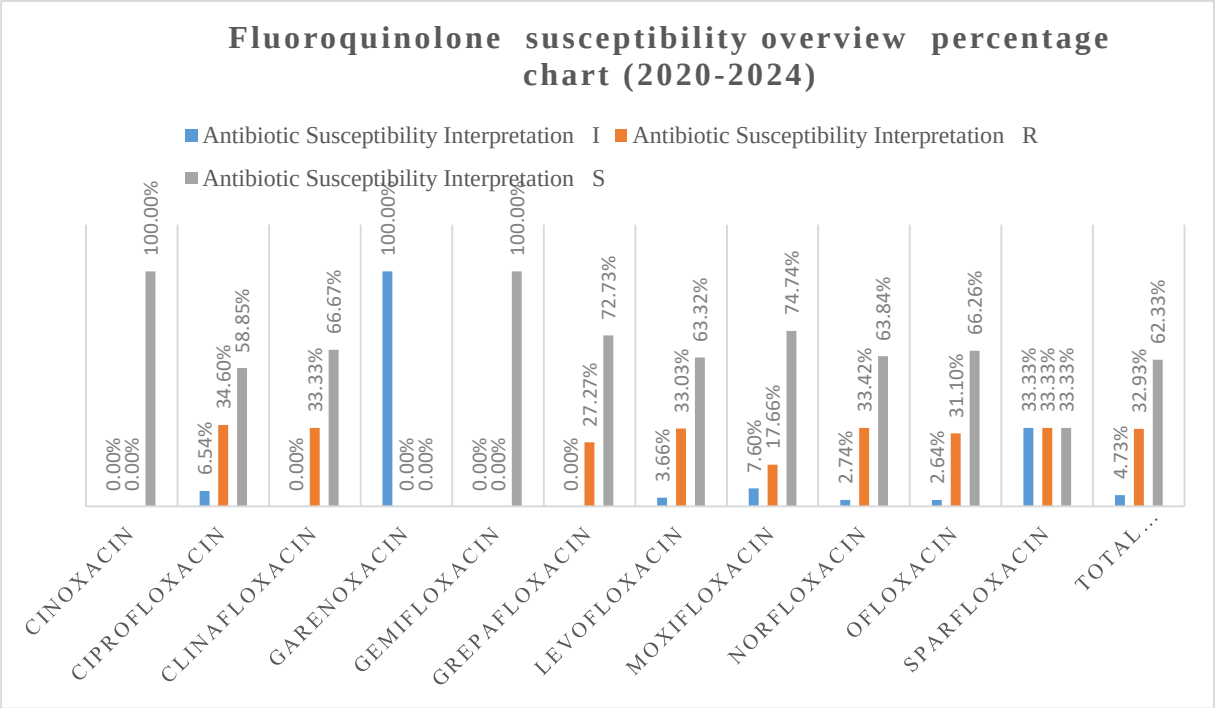
For fluoroquinolone group **32.93** % was the resistance percentage and 62.33% was the sensitive percentage of bacteria for this group (for 94724 isolated bacteria). With the highest resistance was recorded against ciprofloxacin (33.33 %), whereas no resistance was observed for cinoxacin, garenoxacin, and gemifloxacin. The number of isolates and antibiotic susceptibility presented in Table 4.13, and the calculated percentages in Figure 4.13

Table 4.13: Number of isolates and antibiotic susceptibility to fluoroquinolone group (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Total
Cinoxacin	0	0	1	1
Ciprofloxacin	2467	13045	22186	37698
Clinafloxacin	0	1	2	3
Garenoxacin	1	0	0	1
Gemifloxacin	0	0	2	2
Grepafloxacin	0	3	8	11

	Number of isolates- antibiotic susceptibility			
Levofloxacin	979	8837	16942	26758
Moxifloxacin	329	764	3234	4327
Norfloxacin	571	6977	13327	20875
Ofloxacin	133	1569	3343	5045
Sparfloxacin	1	1	1	3
Total	4481	31197	59046	94724

I: intermediate, R: resistance, S: sensitive

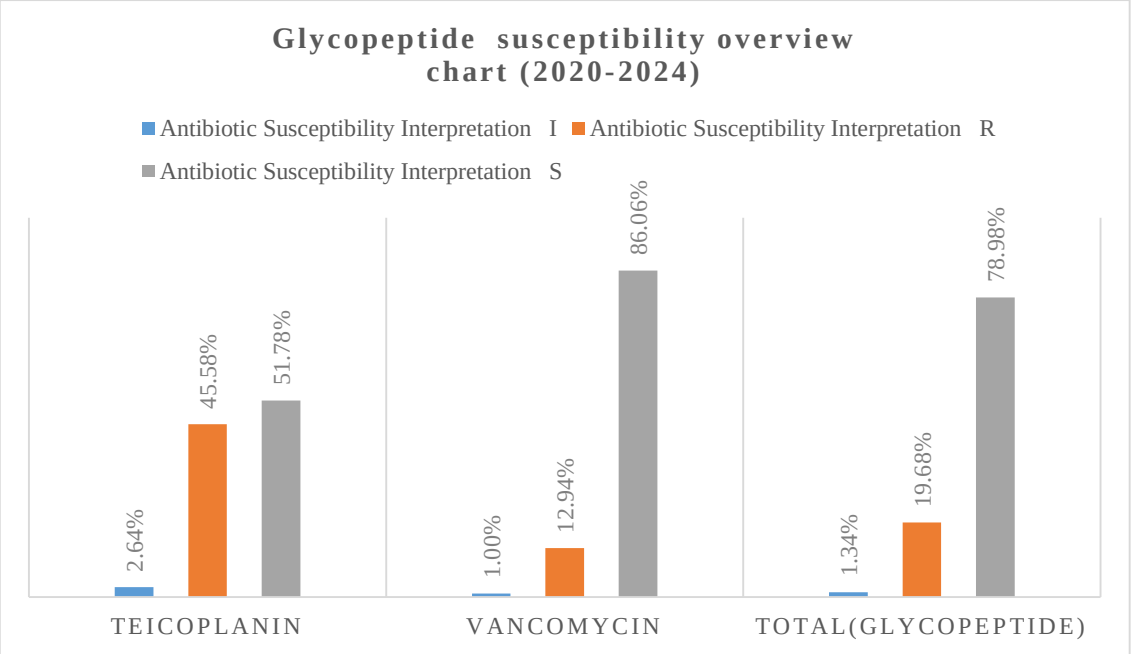


I: intermediate, R: resistance, S: sensitive

Figure 4.13: Percentage distribution of antibiotic susceptibility in fluoroquinolone group (2020–2024)

4.1.4.11 Glycopeptide group

For glycopeptide group 19.68 % was the resistance percentage and 78.98% was the sensitive percentage of bacteria for this group (for 29332 isolated bacteria). With the highest resistance was recorded against teicoplanin (45.58 %) and the lowest resistance was against vancomycin (12.94 %). The number of isolates and antibiotic susceptibility presented in Table 4.14 and the calculated percentages in Figure 4.14



I: intermediate, R: resistance, S: sensitive

Figure 4.14 Percentage of antibiotic susceptibility to glycopeptide group (2020–2024)

Table 4.14: Number of isolates and antibiotic susceptibility to glycopeptide group (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Total
Teicoplanin	160	2763	3139	6062
Vancomycin	232	3011	20027	23270
Total	392	5774	23166	29332

I: intermediate, R: resistance, S: sensitive

4.1.4.12 Lincosamide group

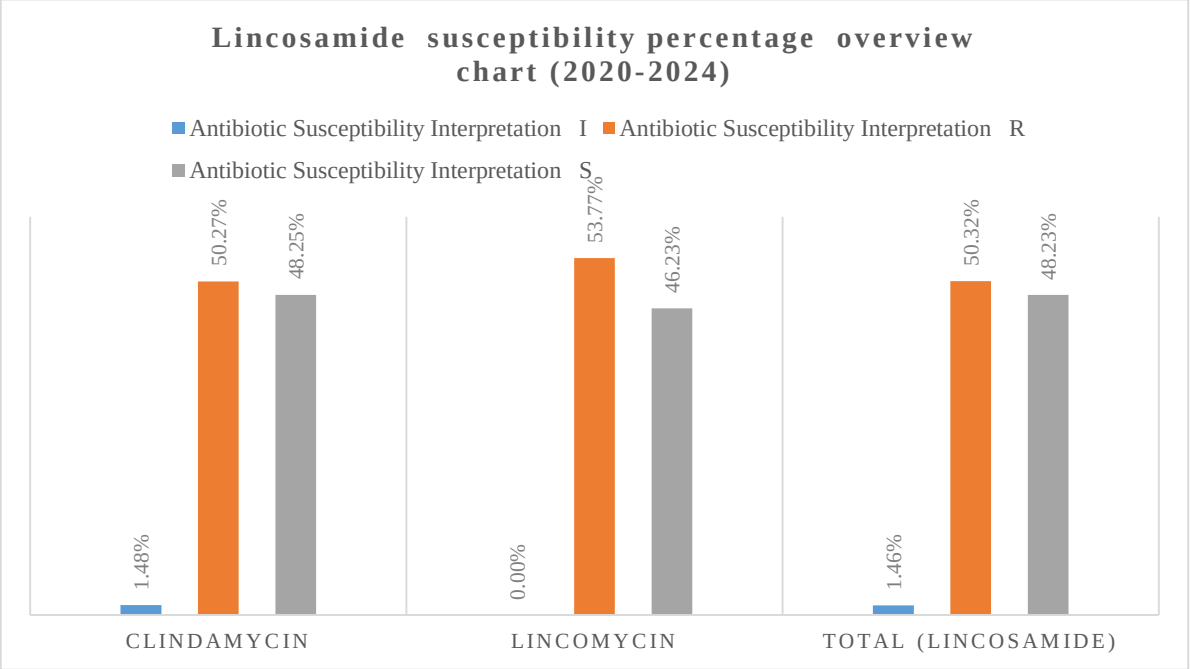
For lincosamide group 50.32 % was the resistance percentage and 48.23% was the sensitive percentage of bacteria for this group (for 15691 isolated bacteria). The number

of isolates and antibiotic susceptibility presented in Table 4.15, and the calculated percentages in Figure 4.15

Table 4.15: Number of isolates and antibiotic susceptibility in lincosamide group (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Total
Clindamycin	229	7788	7475	15492
Lincomycin	0	107	92	199
Total	229	7895	7567	15691

I: intermediate, R: resistance, S: sensitive



I: intermediate, R: resistance, S: sensitive

Figure 4.15 Percentage distribution of antibiotic susceptibility in lincosamide group (2020–2024)

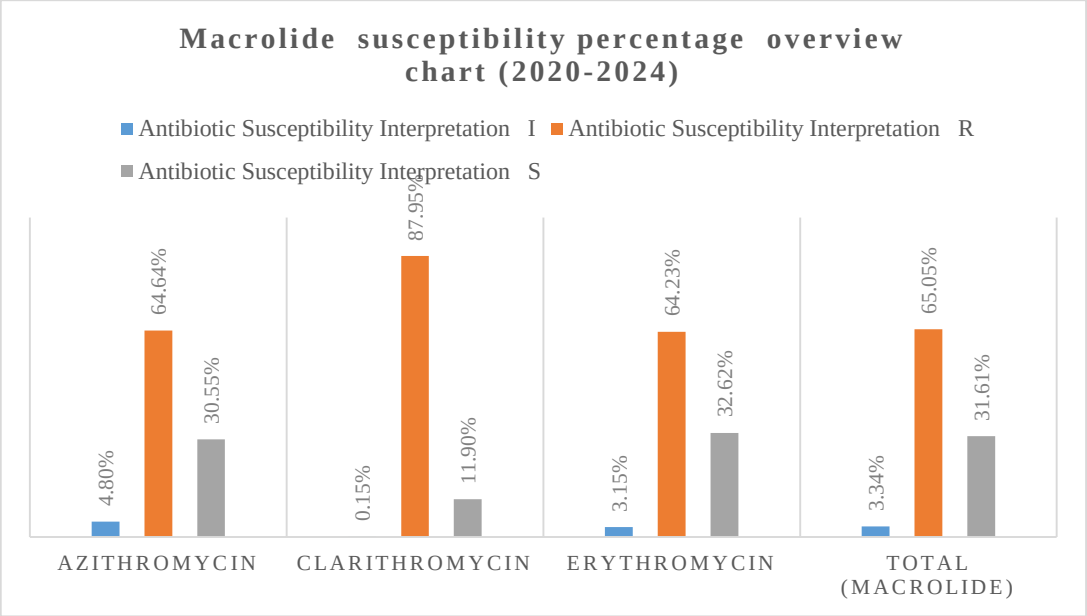
4.1.4.13 Macrolide group

Macrolide group susceptibility against isolated bacteria, 18.38% was the resistance percentage and 81.23% was the percentage of sensitive bacteria for this group (for 21100 isolated bacteria). With the highest resistance was detected against clarithromycin (87.95%) and the lowest resistance percentage was against erythromycin (64.23 %) The number of isolates and antibiotic susceptibility were presented in Table 4.16 and the calculated percentages of susceptibility was presented in Figure 4.16

Table 4.16: Number of isolates and antibiotic susceptibility in macrolide group (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Total
Azithromycin	175	2355	1113	3643
Clarithromycin	1	584	79	664
Erythromycin	529	10786	5478	16793
Total	705	13725	6670	21100

I: intermediate, R: resistance, S: sensitive



I: intermediate, R: resistance, S: sensitive

Figure 4.16 Percentage of antibiotic susceptibility for macrolide group (2020–2024)

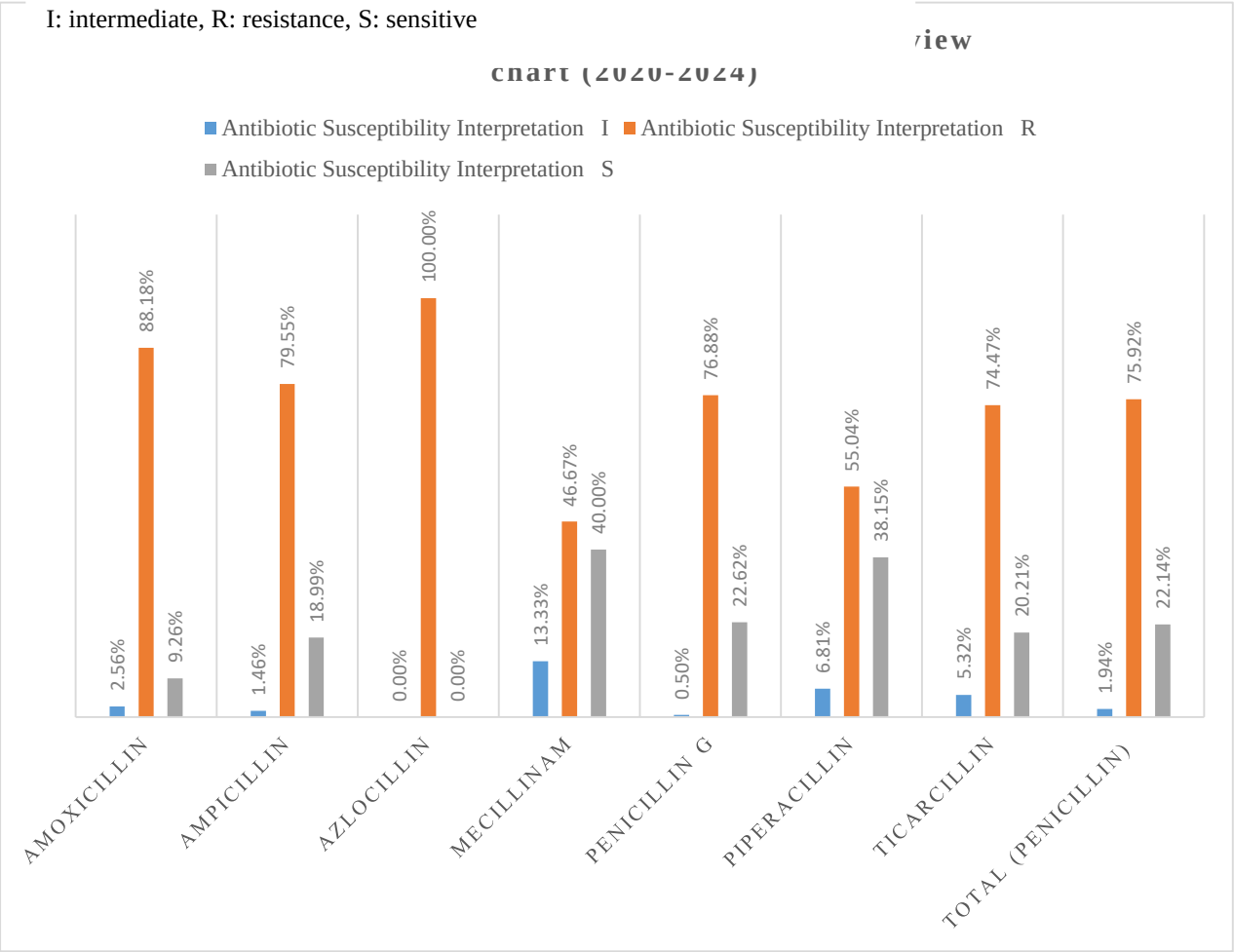
4.1.4.14 Penicillin group

For penicillin group susceptibility against isolated bacteria 75.92 % was the resistance percentage and 22.14 % was the percentage of sensitive bacteria for this group (for 44948 isolated bacteria). With the highest resistance was detected against azlocillin (100 %) and the lowest resistance percentage was against piperacillin (55.04 %) The number of isolates and antibiotic susceptibility were presented in Table 4.17 and the percentages of susceptibility was presented in Figure 4.17

Table 4.17: Number of isolates and antibiotic susceptibility in penicillin group (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Total
Amoxicillin	83	2858	300	3241
Ampicillin	293	15950	3807	20050
Azlocillin	0	1	0	1
Mecillinam	2	7	6	15
Penicillin G	77	11894	3500	15471
Piperacillin	414	3344	2318	6076
Ticarcillin	5	70	19	94
Total (penicillin)	874	34124	9950	44948

I: intermediate, R: resistance, S: sensitive



I: intermediate, R: resistance, S: sensitive

Figure 4.17: Percentage of antibiotic susceptibility to penicillin group (2020–2024)

4.1.4.15 Penicillin- β-lactamase inhibitor group

For penicillin- β-lactamase inhibitor group susceptibility against isolated bacteria 28.91 % was the resistance percentage and 64.06 % was sensitive percentage of bacteria for this group (for 68950 isolated bacteria). With the highest resistance was detected against ticaracillin +clavulanate (77.27 %) and the lowest resistance percentage was against piperacillin + tazobactam (18.14 %) The number of isolates and antibiotic susceptibility were presented in Table 4.18 and the calculated percentages of susceptibility was presented in Figure 4.18

Table 4.18: Number of isolates and antibiotic susceptibility in penicillin + β-lactamase inhibitor group (2020–2024

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Grand Total
Amoxicillin + Clavulanate	2470	10870	13505	26845
Ampicillin + Sulbactam	741	2120	1270	4131
Piperacillin + Sulbactam	5	42	24	71
Piperacillin + Tazobactam	1636	6866	29357	37859
Ticarcillin + Clavulanate	0	34	10	44
Total(Penicillin + β-lactamase inhibitor)	4852	19932	44166	68950

I: intermediate, R: resistance, S: sensitive

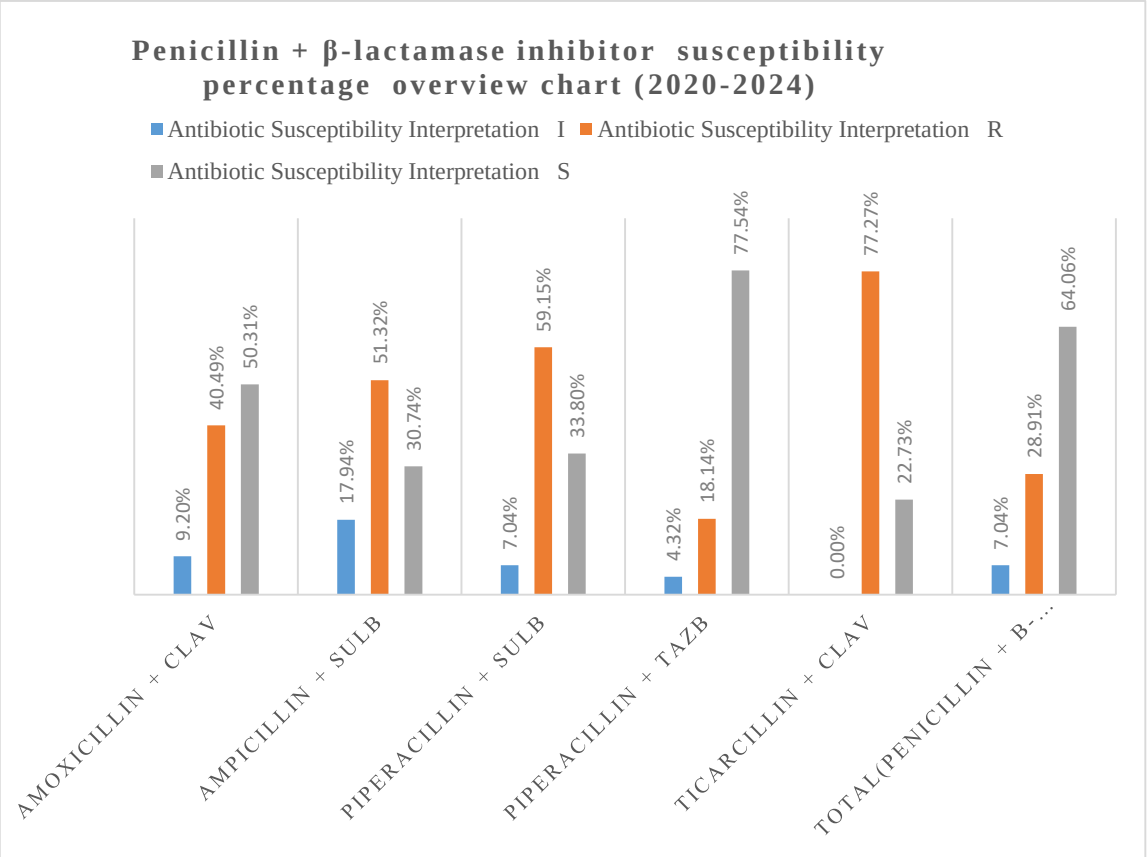


Figure 4.18: Percentage of antibiotic susceptibility for penicillin- β-lactamase inhibitor group (2020–2024)

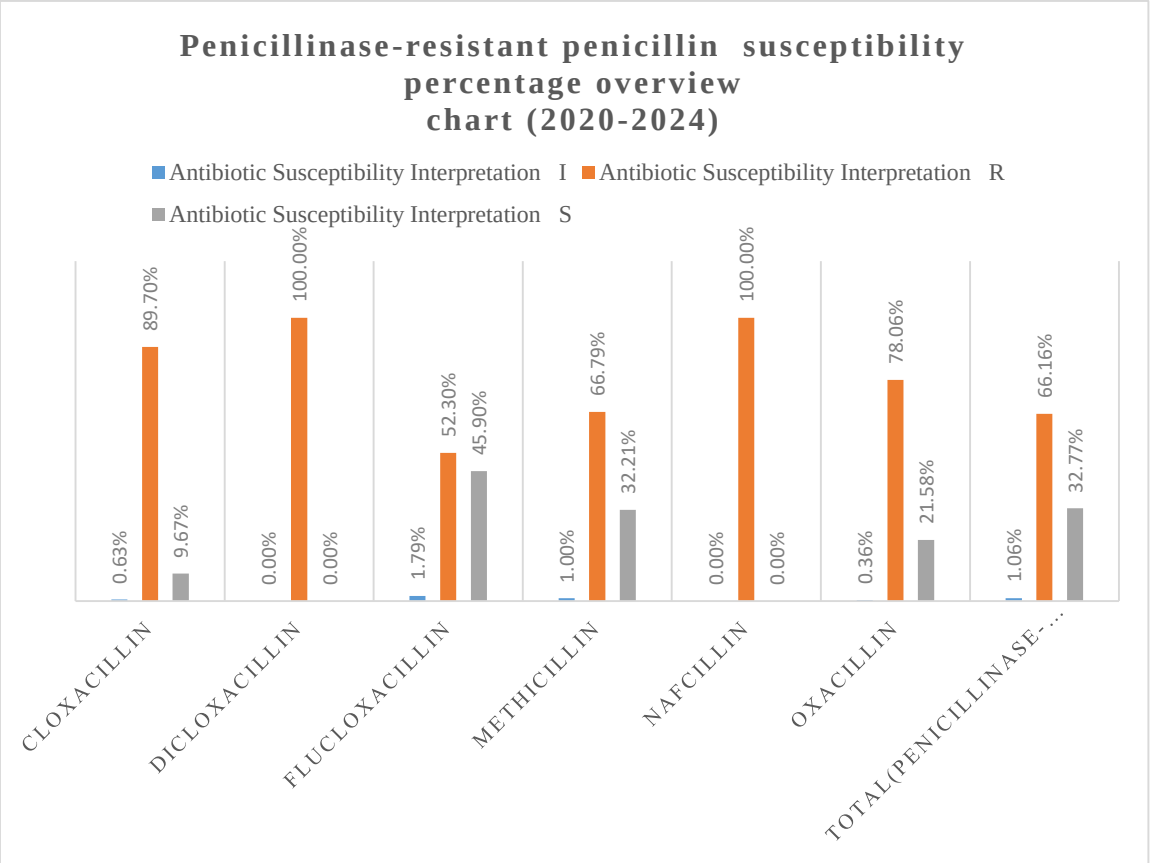
4.1.4.16 Penicillin- penicillinase resistant

For Penicillinase-resistant against isolated bacteria 66.16 % was the resistance percentage and 32.77 % was sensitive percentage of bacteria for this group (for 29309 isolated bacteria). The number of isolates and Penicillinase-resistant were presented in Table 4.19 and the calculated percentages of susceptibility was presented in Figure 4.19

Table 4.19: Number of isolates and antibiotic susceptibility in penicillinase-resistant penicillin group (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Total
Cloxacillin	9	1289	139	1437
Dicloxacillin	0	1	0	1
Flucloxacillin	248	7240	6354	13842
Methicillin	8	537	259	804
Nafcillin	0	2	0	2
Oxacillin	47	10322	2854	13223
Penicillinase-resistant	312	19391	9606	29309

I: intermediate, R: resistance, S: sensitive



I: intermediate, R: resistance, S: sensitive

Figure 4.19: Percentage of antibiotic susceptibility in penicillinase-resistant penicillin group (2020–2024)

4.1.4.17 Polymyxin group

For polymixin group 14.82 % was the resistance percentage and 81.32 % was sensitive percentage of bacteria for this group (for 5433 isolated bacteria). The number of isolates and polymixin susceptibility were presented in Table 4.20 and the calculated percentages of susceptibility was presented in Figure 4.20

Table 4.20: Number of isolates and antibiotic susceptibility in polymyxin group (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Total
Colistin	28	463	2354	2845
Polymyxin B	182	342	2064	2588
Total	210	805	4418	5433

I: intermediate, R: resistance, S: sensitive

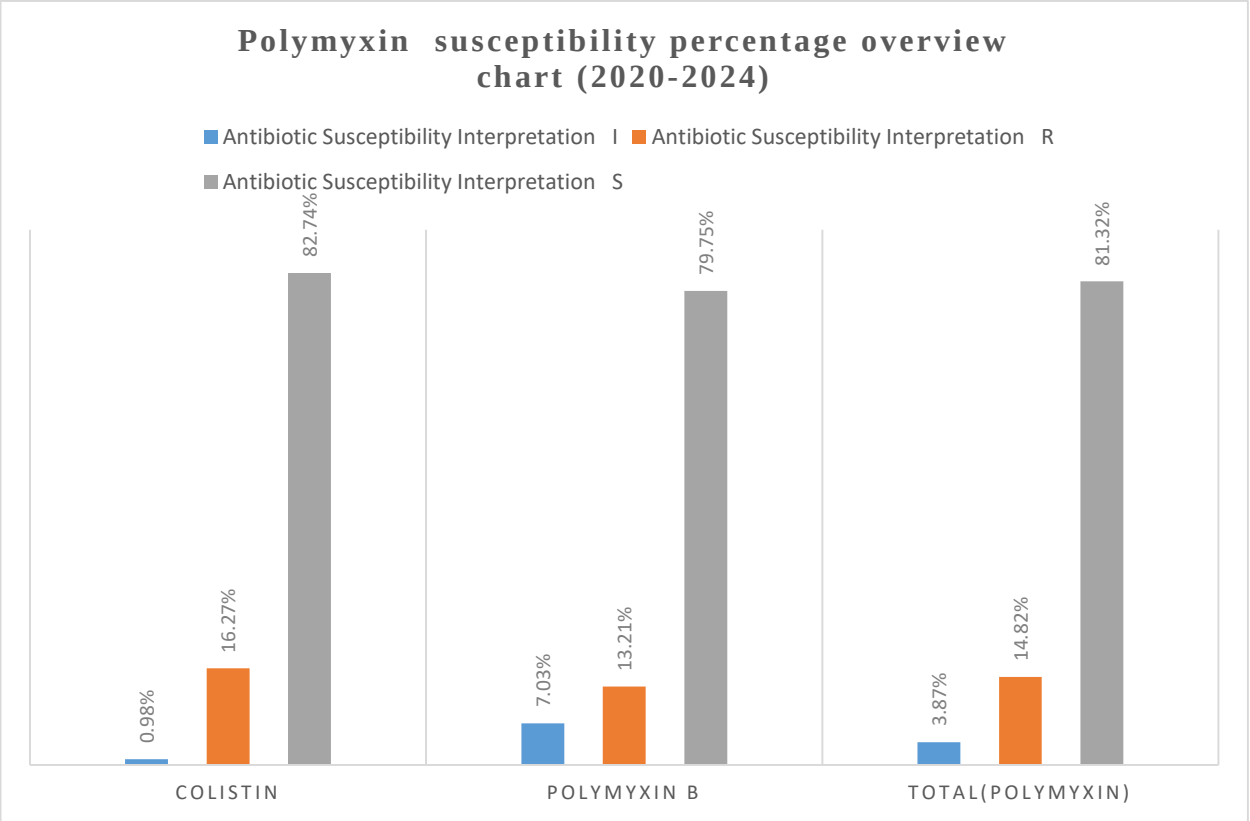


Figure 4.20: Percentage of antibiotic susceptibility to polymyxin group (2020–2024)

4.1.4.18 Tetracycline group

For tetracycline group susceptibility, 52.53 % was the resistance percentage and 45.83 % was sensitive percentage of bacteria for this group (for 12157 isolated bacteria). With the highest resistance was detected against doxycycline (77.27 %) and the lowest resistance percentage was against minocycline (36.15 %). The number of isolates and tetracycline susceptibility were presented in Table 4.21 and the calculated percentages of susceptibility was presented in Figure 4.21

Table 4.21: Number of isolates and antibiotic susceptibility in tetracycline group (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Grand Total
Doxycycline	46	2038	1028	3112
Minocycline	56	107	133	296
Tetracycline	97	4241	4411	8749
Total (Tetracycline)	199	6386	5572	12157

I: intermediate, R: resistance, S: sensitive

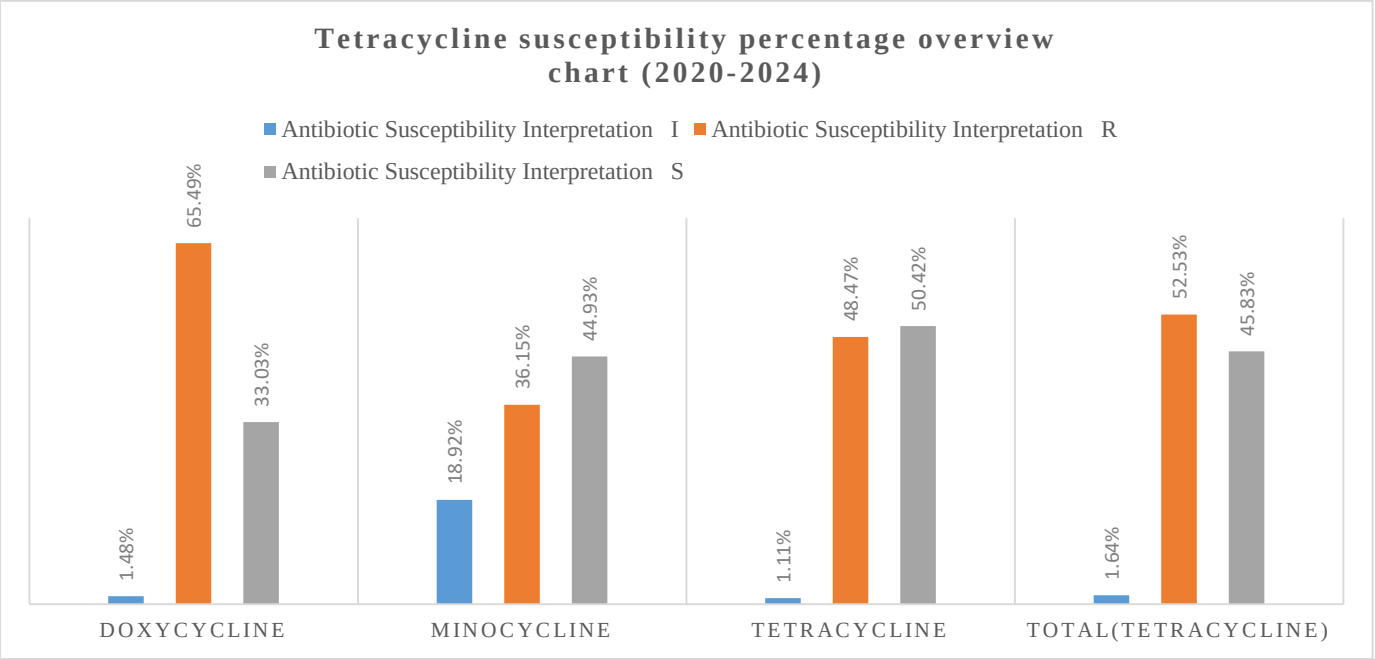


Figure 4.21 Percentage of antibiotic susceptibility to tetracycline group (2020–2024)

4.1.4.19 Remaining Antibiotics

For the remaining antibiotics, resistance rates were as follows: linezolid 0.78%, metronidazole 84.81%, nitrofurantoin 16.55%, trimethoprim–sulfamethoxazole 51.25%, and fosfomycin 12.71%. These antibiotics represent some of the most commonly used agents. Table 4.22 presents the number of isolates and their susceptibility patterns to the remaining antibiotics. Table 4.23 shows the calculated percentages of susceptibility to selected antibiotics. Figure 4.22 illustrates the calculated susceptibility percentages.

Table 4.22: Number of isolates and antibiotic susceptibility for selected antibiotics (2020–2024)

	Number of isolates- antibiotic susceptibility			
Antibiotics	I	R	S	Total
Aztreonam	210	3877	4162	8249
Bacitracin	1	132	30	163
Carumonam	12	1459	372	1843
Cefmetazole	0	1	0	1
Cefotetan	0	8	5	13
Chloramphenicol	58	1095	1547	2700
Dalbavancin	0	2		2
Faropenem	0	1	0	1
Fosfomycin	27	1119	7656	8802

	Number of isolates- antibiotic susceptibility			
Fusidic Acid	1	17	3	21
Iclaprim	0	0	1	1
Linezolid	5	54	6902	6961
Meropenem + Vaborb	1	26	60	87
Metronidazole	2	1630	290	1922
Moxalactam	1	8	22	31
Nalidixic Acid	224	5517	3252	8993
Nitrofurantoin	3248	6021	27109	36378
Novobiocin	2	38	189	229
Oritavancin	0	0	4	4
Pipemidic Acid	1	6	21	28
Quinupristin + Dalfopristin	10	23	1139	1172
Rifampin	39	877	4799	5715
Spectinomycin	0	8	10	18
Sulfisoxazole	0	489	121	610
Sulfonamides	0	1	0	1
Tigecycline	179	205	8988	9372
Trimethoprim	0	6	13	19
Trimethoprim + Sulfamethoxazole	357	26336	24692	51385
Trospectomycin	0	1	0	1

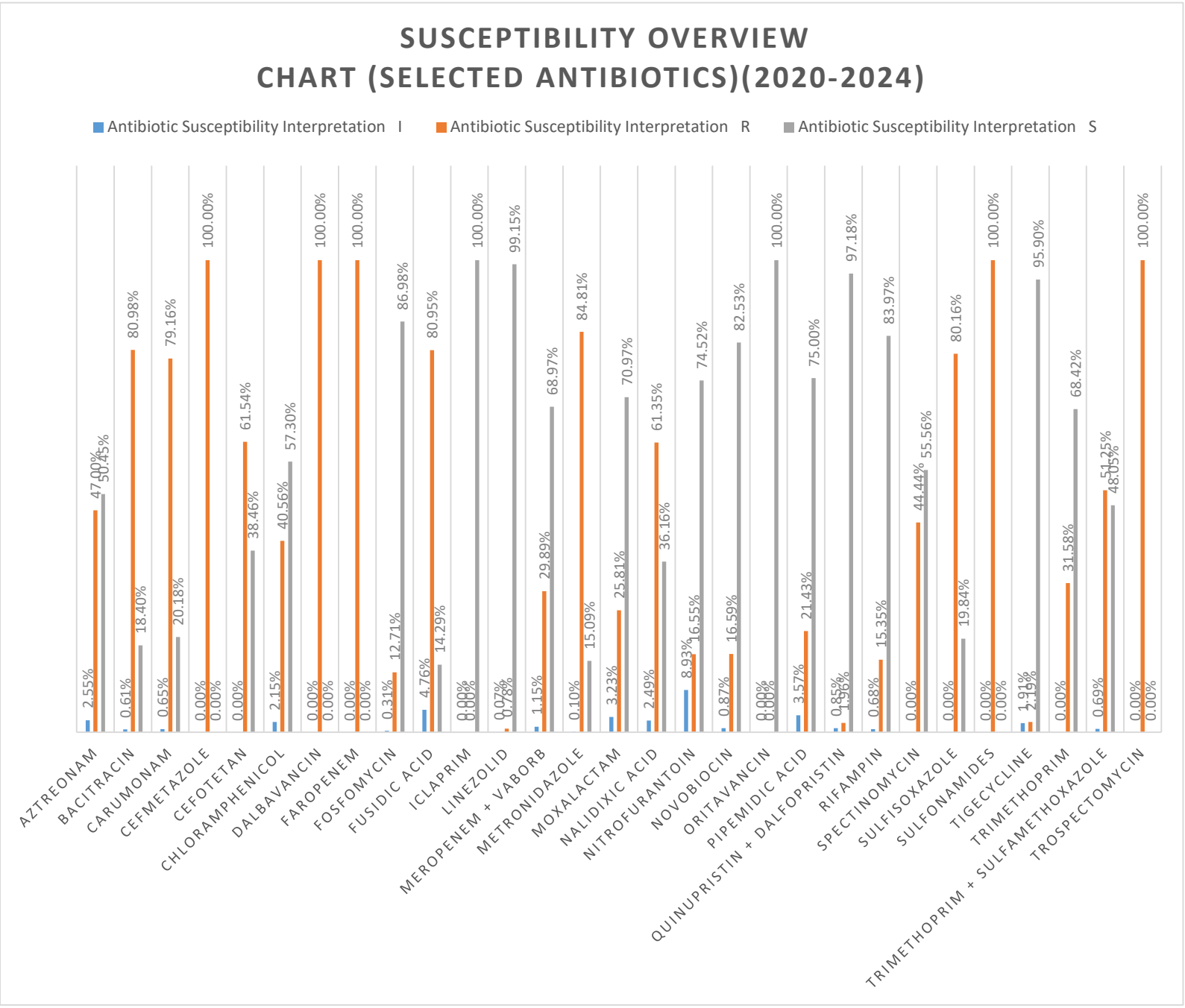
I: intermediate, R: resistance, S: sensitive

Table 4.23: Percentage of antibiotic susceptibility for selected antibiotics (2020–2024)

	Antibiotic Susceptibility Percentages		
Antibiotic	I	R	S
Aztreonam	2.55%	47.00%	50.45%
Bacitracin	0.61%	80.98%	18.40%
Carumonam	0.65%	79.16%	20.18%
Cefmetazole	0.00%	100.00%	0.00%
Cefotetan	0.00%	61.54%	38.46%
Chloramphenicol	2.15%	40.56%	57.30%
Dalbavancin	0.00%	100.00%	0.00%
Faropenem	0.00%	100.00%	0.00%

	Antibiotic Susceptibility Percentages		
Fosfomycin	0.31%	12.71%	86.98%
Fusidic Acid	4.76%	80.95%	14.29%
Iclaprim	0.00%	0.00%	100.00%
Linezolid	0.07%	0.78%	99.15%
Meropenem + Vaborb	1.15%	29.89%	68.97%
Metronidazole	0.10%	84.81%	15.09%
Moxalactam	3.23%	25.81%	70.97%
Nalidixic Acid	2.49%	61.35%	36.16%
Nitrofurantoin	8.93%	16.55%	74.52%
Novobiocin	0.87%	16.59%	82.53%
Oritavancin	0.00%	0.00%	100.00%
Pipemidic Acid	3.57%	21.43%	75.00%
Quinupristin + Dalfopristin	0.85%	1.96%	97.18%
Rifampin	0.68%	15.35%	83.97%
Spectinomycin	0.00%	44.44%	55.56%
Sulfisoxazole	0.00%	80.16%	19.84%
Sulfonamides	0.00%	100.00%	0.00%
Tigecycline	1.91%	2.19%	95.90%
Trimethoprim	0.00%	31.58%	68.42%
Trimethoprim + Sulfamethoxazole	0.69%	51.25%	48.05%
Trospectomycin	0.00%	100.00%	0.00%

I: intermediate, R: resistance, S: sensitive



I: intermediate, R: resistance, S: sensitive

Figure 4.22: Percentage of antibiotic susceptibility to selected antibiotics (2020–2024)

4.1.5 Analysis of microbe type and resistance

Among the isolated microbes, *Escherichia coli* showed the highest prevalence, accounting for 45.7% of isolates, while *Acinetobacter baumannii* demonstrated a high resistance rate of 69.18%. Table 4.24 presents the number of isolates of the top ten most prevalent bacterial species. Table 4.25 shows the percentages of the top ten most prevalent bacterial species. Table 4.26 illustrates the number of isolates and antibiotic susceptibility patterns of the selected microbes. Figure 4.23 shows the percentage of antibacterial susceptibility among selected bacterial species.

Table 4.24: Number of isolates of top 10 most prevalent bacterial species (2020-2024)

Isolated bacteria	Count
Acinetobacter baumannii	15447
Enterobacter cloacae	24163
***Enterococcus* spp.**	13755
Escherichia coli	384075
Klebsiella pneumonia	89178
Pseudomonas aeruginosa	26813
***Pseudomonas* spp.**	15619
***Staphylococcus* (coagulase-negative)**	86649
Staphylococcus aureus	85156
***Streptococcus* spp. (Group Viridans α-hemolysis)**	18390
Total	759245

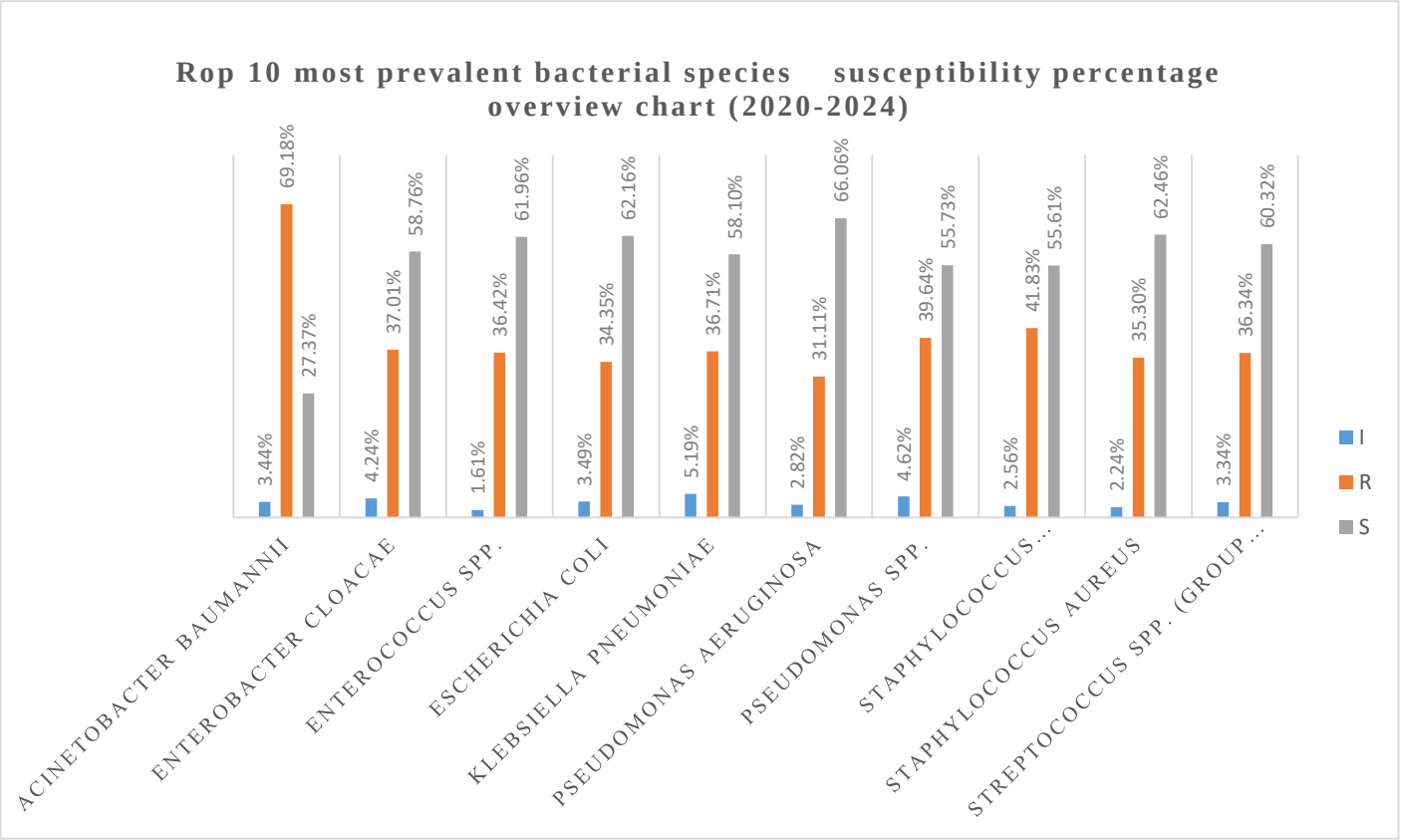
Table 4.25: Percentage of top 10 most prevalent bacterial species (2020-2024)

Name of bacterial species	Percentage (%)
Acinetobacter baumannii	1.84%
Enterobacter cloacae	2.88%
Enterococcus spp.	1.64%
Escherichia coli	45.72%
Klebsiella pneumonia	10.62%
Pseudomonas aeruginosa	3.19%
Pseudomonas spp.	1.86%
Staphylococcus (coagulase-negative)	10.32%
Staphylococcus aureus	10.14%
Streptococcus spp. (Group Viridans α-hemolysis*)*	2.19%
Total	90.45%

Table 4.26: Number of isolates and antibiotic susceptibility in selected bacterial species (2020–2024)

	Number of isolates- antibiotic susceptibility			
Isolated bacteria	I	R	S	**Total**
Acinetobacter baumannii	532	10687	4228	**15447**
Enterobacter cloacae	1024	8942	14197	**24163**
***Enterococcus* spp.**	222	5010	8523	**13755**
Escherichia coli	13420	131928	238727	**384075**
Klebsiella pneumonia	4628	32737	51813	**89178**
Pseudomonas aeruginosa	757	8342	17714	**26813**
***Pseudomonas* spp.**	722	6192	8705	**15619**
***Staphylococcus* (coagulase-negative)**	2218	36244	48187	**86649**
Staphylococcus aureus	1910	30060	53186	**85156**
Streptococcus spp.* (Group Viridans α-hemolysis*)	615	6683	11092	**18390**
Total	**26048**	**276825**	**456372**	**759245**

I: intermediate, R: resistance, S: sensitive



I: intermediate, R: resistance, S: sensitive

Figure 4.23: Percentage of antibiotic susceptibility in selected bacterial species (2020–2024)

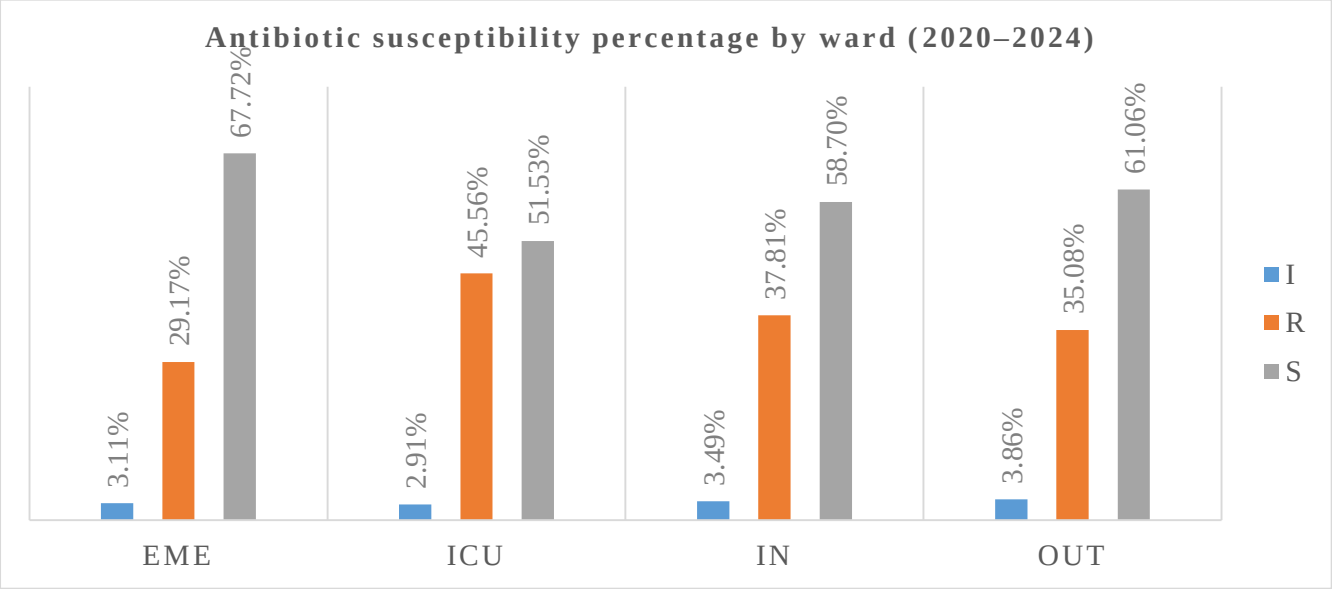
4.1.6 Analysis of ward type and resistance

Regarding ward type and its relationship with antimicrobial resistance, the intensive care unit (ICU) showed the highest resistance rate (45.56%), whereas the emergency department exhibited the lowest resistance rate (29.17%). Table 4.27 presents the number of isolates by ward type and antibiotic susceptibility counts, while Figure 4.24 illustrates the calculated percentages of antibiotic susceptibility according to ward type.

Table 4.27: Number of isolates by ward type and antibiotic susceptibility

	Number of isolates -antibiotic susceptibility		
Ward Type	I	R	S
Emergency	5230	49051	113891
ICU	4103	64133	72532
In patient	7931	85989	133496
Out patient	11714	106417	185241
Total	28978	305590	505160

I: intermediate, R: resistance, S: sensitive



I: intermediate, R: resistance, S: sensitive

Figure 4.24: Comparison of antibiotic susceptibility percentage by ward type

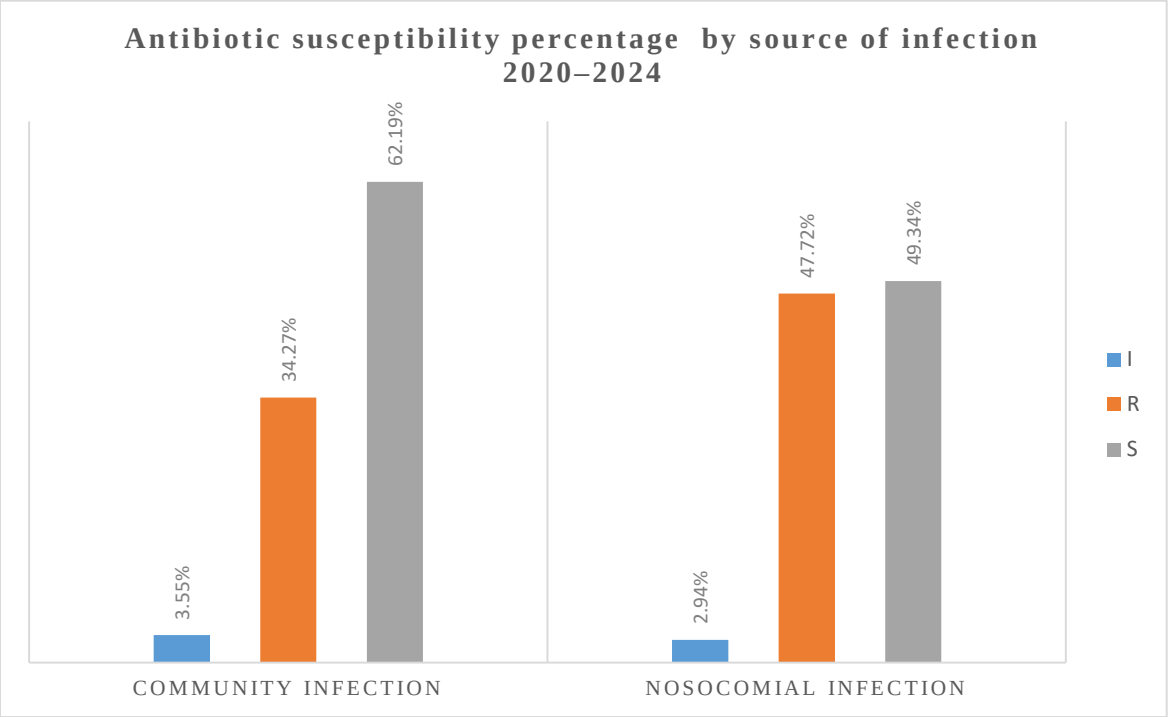
4.1.7 Analysis of infection source and resistance

Regarding the source of infection and its relationship with antimicrobial resistance patterns, nosocomial infections accounted for a higher resistance rate (47.72%), whereas community-acquired infections showed a lower resistance rate (34.27%). Table 4.28 presents the number of isolates by source of infection and antibiotic susceptibility counts. Figure 4.25 illustrates a comparison of antibiotic susceptibility percentages according to the source of infection**.**

Table 4.28: Number of isolates by source of infection and antibiotic susceptibility

	Number of isolates -antibiotic susceptibility			
Source Of Infection	I	R	S	Total
Community acquired infection	25081	242268	439686	707035
Nosocomial acquired infection	3897	63322	65474	132693
Total	28978	305590	505160	839728

I: intermediate, R: resistance, S: sensitive



I: intermediate, R: resistance, S: sensitive

Figure 4.25: Comparison of antibiotic susceptibility percentage by source of infection

4.2 The Result of Machine learning

4.2.1 Ensemble Methods Performance

Ensemble learning methods were evaluated on a dataset containing 21,277 records with 12 features and 3 target classes. The dataset was divided into training (80%, 17,021 records) and test (20%, 4,256 records) sets. Table 4.29 presents comprehensive performance metrics for all four ensemble methods across different evaluation metric.

The Stacking classifier had the best performing model with the highest accuracy (0.7648) and F1 score (0.7380). The voting classifier achieved the best AUC-ROC score (0.7820), indicating superior discrimination ability.

The performance comparison in Figure 4. 26 provides a comprehensive evaluation of the four ensemble learning models used in this study. The permutation matrices show that all models classify most samples into class 2, indicating a persistent class imbalance in the data set.

Table 4.29: Performance comparison of ensemble learning methods

Metric	Random Forest	AdaBoost	Stacking	Voting
Accuracy	0.7585	0.7072	**0.7648**	0.7603
Precision	0.709	0.6377	**0.7626**	0.7575
Recall	0.7585	0.7072	**0.7678**	0.7603
F1-Score	0.7237	0.6561	**0.738**	0.733
Specificity	0.7626	0.7057	**0.7799**	0.7761
MCC	0.3502	0.1617	**0.3852**	0.3721
AUC-ROC	**0.7819**	0.705	0.7808	**0.782**

Table 4.30: Best performing models by metric

Metric	Best Model	Score
Accuracy	Stacking	0.7648
F1-Score	Stacking	0.738
AUC-ROC	Voting	0.782

Among the models, Random Forest and Stacking show higher discriminative power, producing fewer misclassifications in class 1 compared to AdaBoost and Voting. The ROC curves further support these findings: Class 1 achieves the highest AUC values

across all models, indicating that the models capture their decision boundary more effectively than class 0. Stacking and Random Forest achieve the strongest overall performance, with AUC values close to 0.81 for class 1 and 0.78 for class 2. In contrast, AdaBoost shows lower AUC values in all classes, confirming its weaker predictive power for this task. Overall, AdaBoost, Stacking and voting classifiers visualization highlights that Stacking and Random Forest offer the most balanced and reliable performance across all classes, making them the most suitable ensemble methods for antimicrobial resistance prediction.

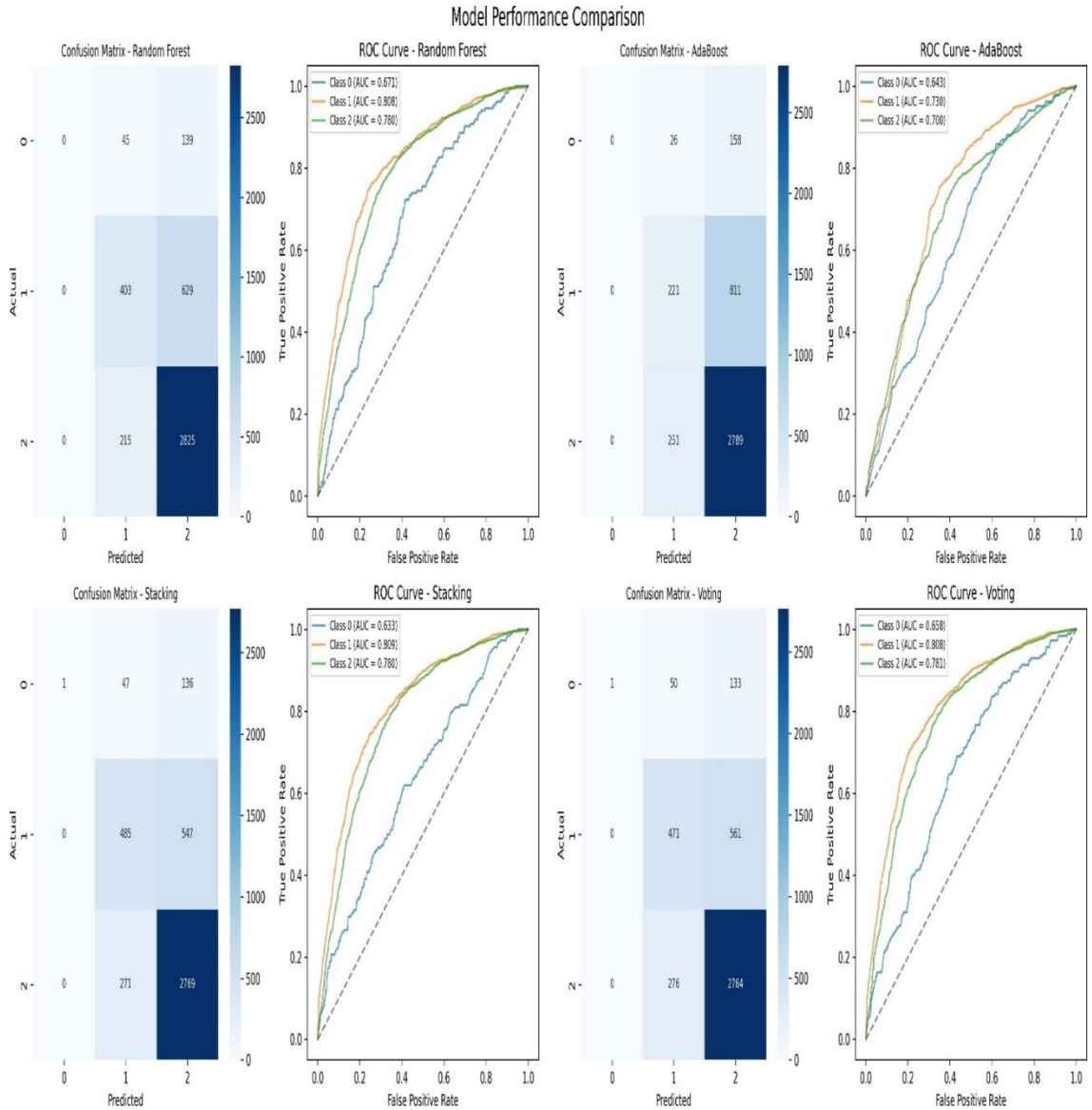


Figure 4.26: Comparison of Confusion Matrices and ROC Curves for RandomForest, AdaBoost, Stacking, and Voting Classifiers

4.2.2 Explainable AI Analysis using SHAP

SHAP analysis was used to assess the model predictions and identify the most important features in all ensemble methods. A comprehensive analysis of feature importance revealed similar patterns across all ensemble models. Table 4.31 presents the normalized importance scores for the main features

Table 4.31: Feature of important scores from SHAP analysis

Feature	Random Forest	AdaBoost	Stacking	Voting	Overall Impact
AntibioticNameEn	1.000	1.000	1.000	1.000	1.000
org type	0.256	0.137	0.338	0.351	0.271
Organism	0.149	0.094	0.384	0.396	0.256
period since admission	0.164	0.317	0.085	0.061	0.157
spec date	0.11	0.152	0.102	0.073	0.109
date entered	0.056	0.087	0.092	0.056	0.073
Age	0.047	0	0.075	0.064	0.047
ward type	0.047	0.036	0.051	0.037	0.043
Topography Name	0.056	0	0.051	0.048	0.039
Diagnosis	0.025	0.006	0.08	0.042	0.038

The SHAP analysis found that the AntibioticNameEn was the most important feature across all ensemble methods, having a normalized total importance score of 1.0000. This feature demonstrated consistently high importance across all four ensemble models. Feature importance analysis revealed strong consistency across all ensemble methods, with antibiotic name consistently appearing as the most important feature in predicting antimicrobial susceptibility interpretations.

Table 4.32: Experimental setup and key results summary

Parameter	Value
Total Dataset Records	21,277
Number of Features	12
Target Classes	3
Training Set Size	17,021 records (80%)
Testing Set Size	4,256 records (20%)
Best Performing Model	Stacking Classifier
Best Model Accuracy	0.7648
Most Important Feature	AntibioticNameEn
Overall Importance Score	1.000

The SHAP analysis shown in Figure 4.27 explains how the Random Forest classifier evaulates and prioritizes features during AMR prediction. The bar graph on the left shows the average absolute SHAP values, which represent the global contribution of each element across all samples. The most influential variable is AntibioticNameEn followed by ORGAN TYPE, HOURS SINCE ADMISSION and organism. Together, these variables have the strongest effect on model predictions, suggesting that antibiotic type and organism-related characteristics play a major role in resistance classification. Lower ranked variables such as ward type, sex, and diagnosis show minimal overall effect, indicating lower predictive weight within the ensemble learning structure.

The SHAP summary chart on the right shows how individual functions affect the sample. including their direction and magnitude . Positive SHAP values indicate feature conditions that increase the predicted probability of AMR, while negative values reduce it. The color gradient from blue to red reflects the low to high values of the elements, allowing for visual understanding of interactions and non-linear effects. For example, high values of AntibioticNameEn and ORG TYPE tend to drive predictions towards resistance, proving their critical role in classification results. Together, these visualizations emphasize both global and local interpretability, improve clinical reliability and transparency in the decision-making process.

The remaining ensemble-based methods—AdaBoost, Stacking, and Voting—were further evaluated using SHAP analysis to provide a complete explanation of how individual classifiers interpret and prioritize variables during AMR prediction. Figures 4.28, 4.29 and 4.30 represent the mean absolute SHAP values for these models,

demonstrating the global contribution of each element across all samples. Consistently across all classifiers, AntibioticNameEn appears to be the most important varible in determining model outputs. Figure 4.31 shows feature importance ratings across all models, demonstrating that AntibioticNameEn has the strongest predictive influence in the dataset. This consistency confirms a strong and stable effect on antimicrobial resistance prediction, regardless of file method.

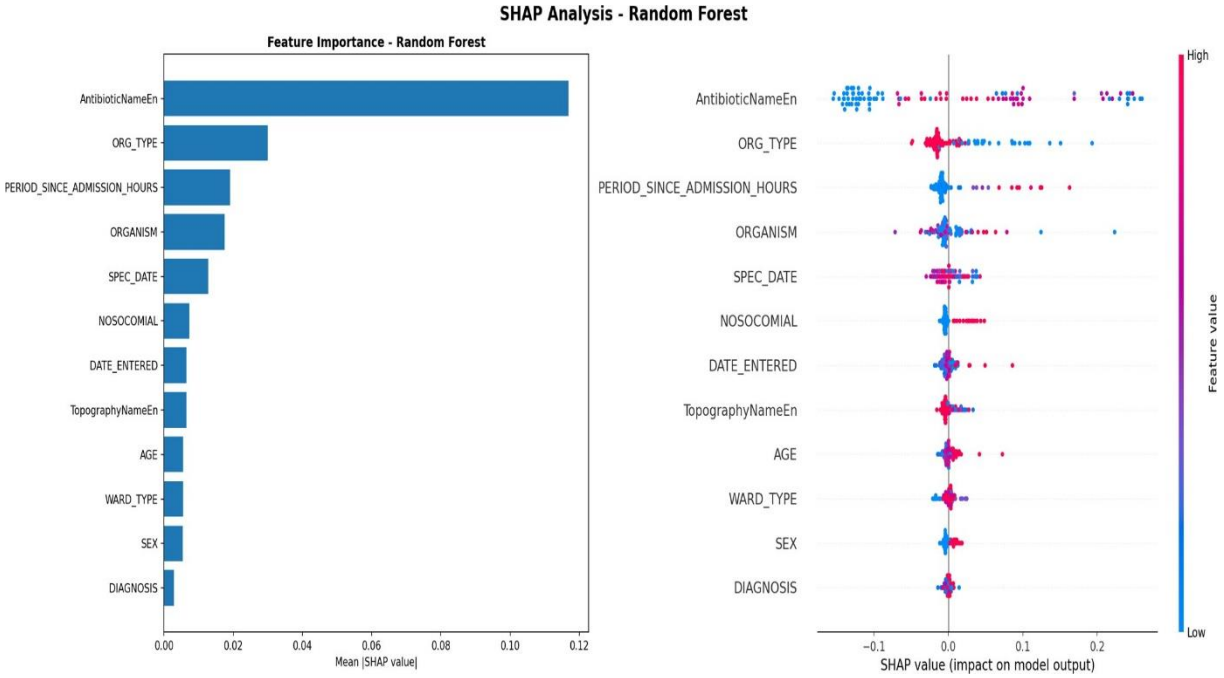


Figure 4.27 : SHAP feature importance (left) and shap summary plot (right) for the random forest classifier.

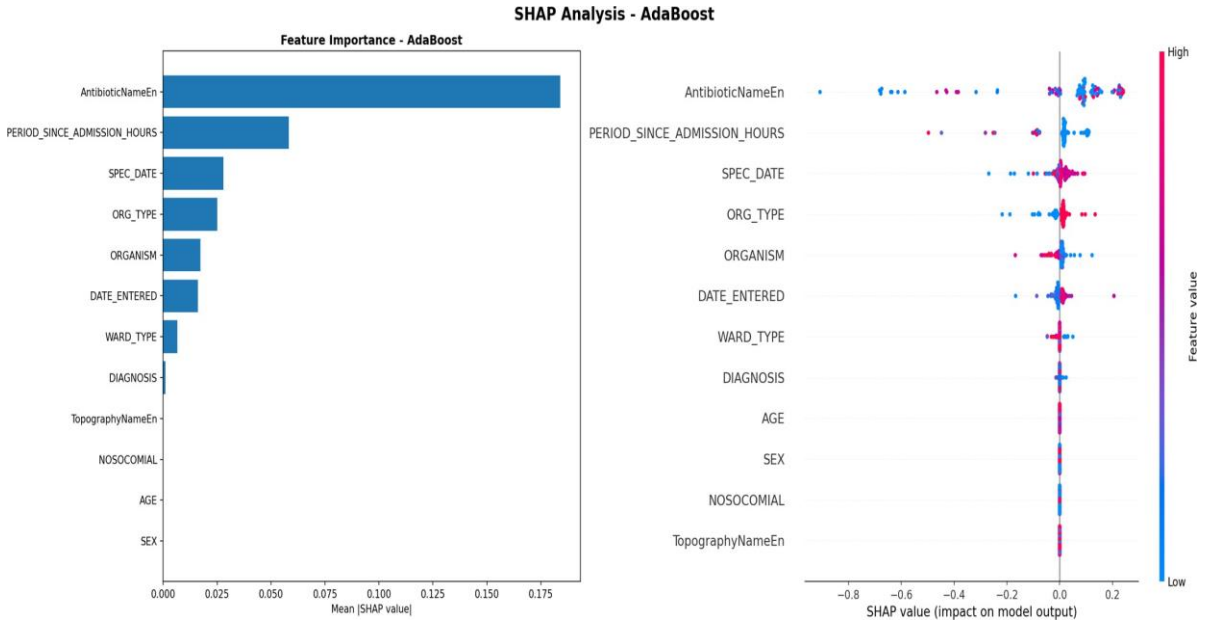


Figure 4.28: SHAP feature importance (left) and shap summary plot (right) for the adaboost classifier.

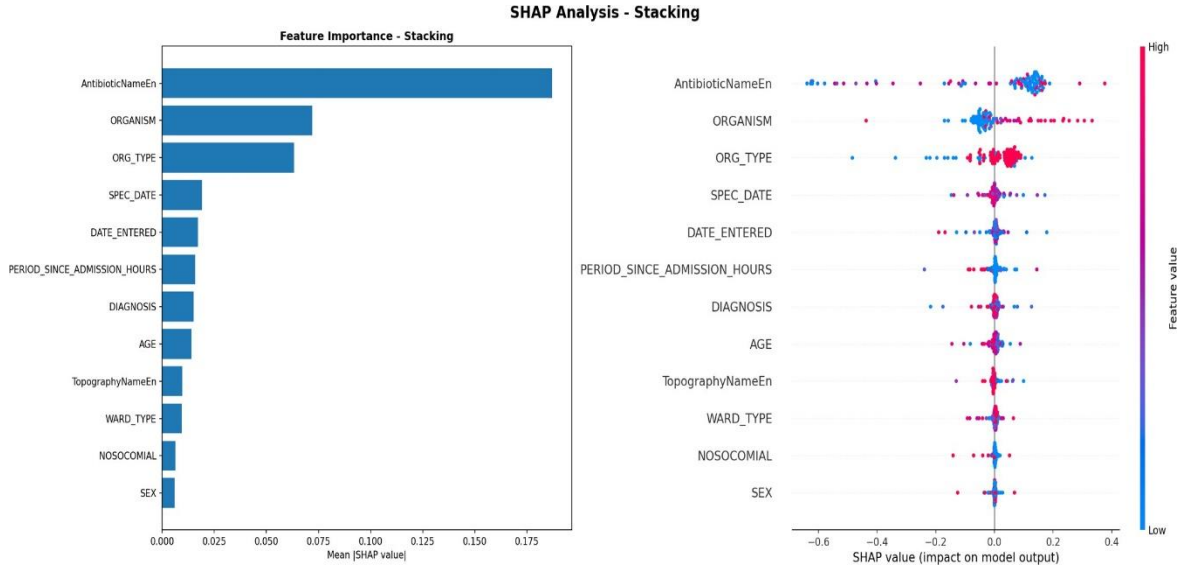


Figure 4.29: SHAP feature importance (left) and shap summary plot (right) for the stacking classifier.

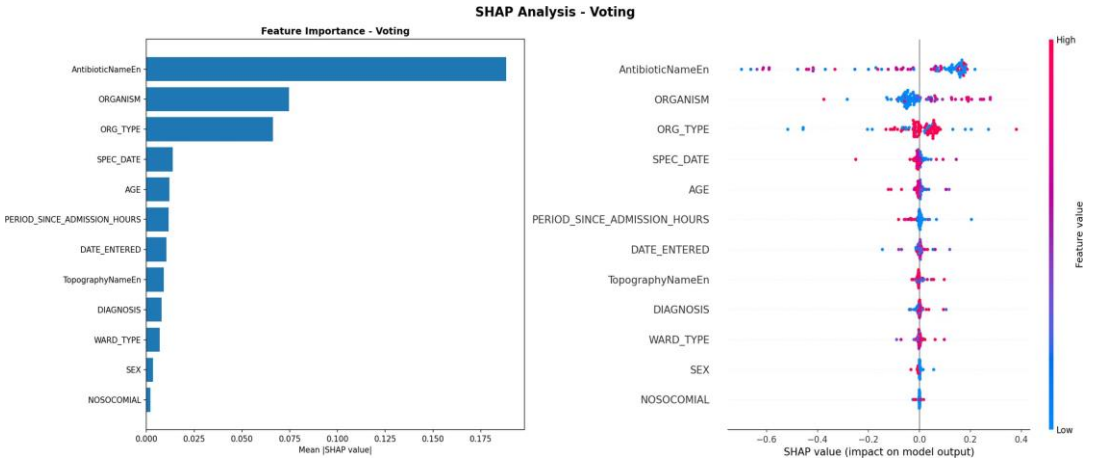


Figure 4.30: SHAP features importance (left) and SAHP summary plot (right) for the voting classifier.

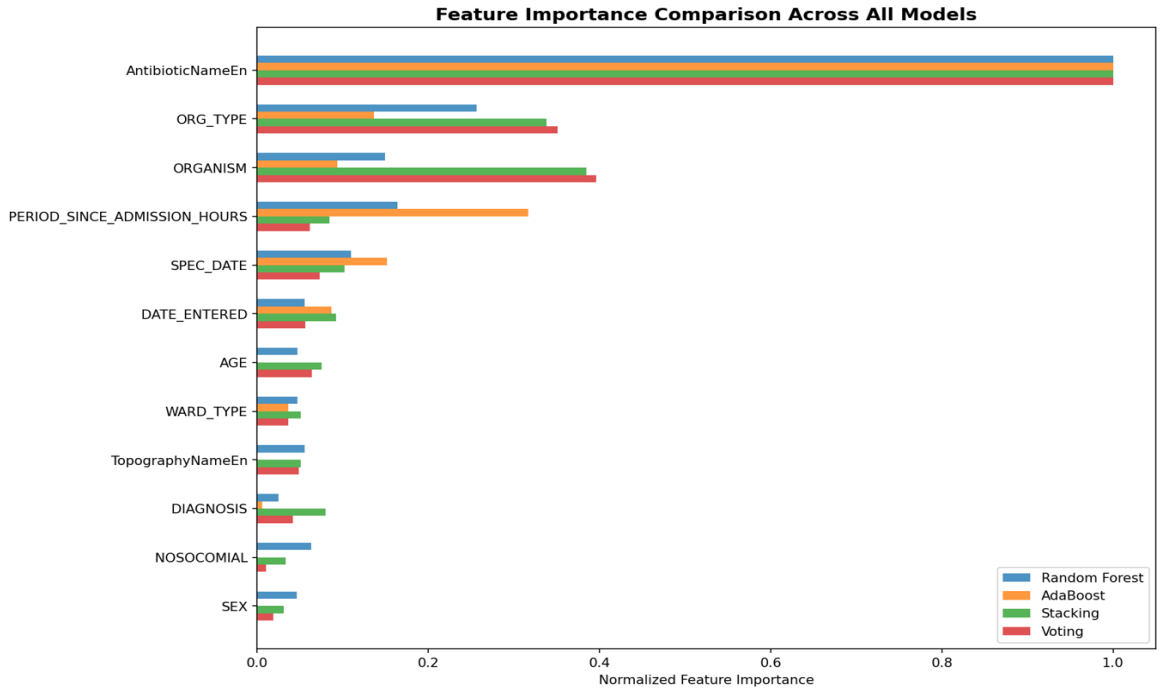


Figure 4.31: Feature importance comparison across all features

Chapter Five

Discussion of Findings and Recommendation

5.1 Descriptive analysis

5.1.1 Annual Patterns (2020–2024)

The annual pattern of antibiotic resistance in this study (2020–2024) showed only minor fluctuations and was generally stable. Resistance ranged between 34% and 39%, with the highest value recorded in 2021. Sensitivity ranged between 57% and 61%, with the highest sensitivity observed in 2023, while intermediate values ranged from 2.48% to 4.55%. Overall, these findings indicate a relatively consistent national resistance profile across the five-year period.

When compared with global data, the burden in Jordan appears substantially higher. According to the World Health Organization (2025), one in six bacterial infections worldwide in 2023 was resistant to antibiotics (approximately 16–17%). Relative to this baseline, the resistance rate observed in Jordan is approximately double, suggesting a higher national risk of antimicrobial resistance.

The highest resistance rates were observed in 2020 and 2021, with 2021 representing the peak year. This rise may be related to increased antibiotic use during the COVID-19 pandemic, when empiric and broad-spectrum antibiotics were frequently prescribed. Al-Azzam et al. (2021) reported that consumption of Watch-group antibiotics in Jordan increased by 26% between 2019 and 2020, with notable increases in specific broad-spectrum agents. Specifically, the use of third-generation cephalosporins and carbapenems increased by 19% and 52%, respectively, macrolides by 57%, and azithromycin by 74%, reflecting pandemic-associated shifts in prescribing.

Following the COVID-19 period, resistance declined, with the lowest rate recorded in 2024. This decrease may reflect improved antimicrobial stewardship efforts and the impact of the national antimicrobial resistance surveillance system established in 2019, which supports structured monitoring, reporting, and guidance of antibiotic prescribing practices in collaboration with national and international partners. Nevertheless, resistance levels remain higher than the global average, indicating the need for stronger

policies, sustained stewardship programs, and stricter prescribing regulations to achieve meaningful long-term reductions.

5.1.2 Sex Differences

This study found higher antibiotic resistance in males (39.45%) compared with females (34.83%). Similar patterns were reported by Khanal et al. (2024), who showed that MDR rates were higher in males and concluded that males are at greater risk of MDR *E. coli* infection. In contrast, Amir et al. (2024) reported no significant effect of gender on antimicrobial resistance.

Global evidence also suggests that sex-based differences may vary by economic context. Salehi et al. (2025), in "Gender Differences in Global Antimicrobial Resistance," reported that antibiotic-resistance gene (ARG) load is higher in women than men in high-income countries; however, in low- and middle-income countries—similar to the setting of this study—men had a 5% higher ARG load. This aligns with the present findings.

Sex differences in resistance likely reflect a combination of biological, behavioral, and healthcare-related factors. In low- and middle-income countries, men may experience higher resistance due to higher hospitalization rates, occupational exposures, trauma, and chronic comorbidities, increasing the risk of healthcare-associated infections and exposure to resistant organisms (Salehi et al., 2025).

In addition, the European Association of Urology Guidelines on Urological Infections (2024) (Kranz et al., 2024) classify UTIs in men as complicated infections, often requiring empiric broad-spectrum antibiotics and longer treatment durations, particularly when prostatic involvement cannot be excluded. Because *Escherichia coli* remains the most common uropathogen, repeated and prolonged exposure to broad-spectrum therapy in male patients may increase selective pressure and contribute to higher observed resistance.

5.1.3 Age Differences

In this study, antibiotic resistance varied across age groups. The highest resistance occurred in the ≥65-year group (44.23%), followed by infants aged 0–1 year (37.43%), while the lowest resistance was observed in the 1–18-year group (31.88%). These findings are consistent with multiple studies showing that older age is associated with

increased risk of multidrug resistance due to immunosenescence, frequent healthcare exposure, and repeated antibiotic use (Denkinger et al., 2013; Theodorakis et al., 2024). Huang et al. (2021) similarly reported that increasing age is a significant risk factor for both MDR and XDR infections.

Waterlow et al. (2025) also emphasized that increasing age is a major risk factor for rising multidrug resistance and may worsen the overall AMR burden in Europe. In addition, infants have repeatedly been identified as a high-risk group: Duicu et al. (2021) and Sağlam et al. (2025) both reported that the 0–1 year age group shows elevated AMR risk, which aligns with the present results. However, Amir et al. (2024) reported that age did not have a statistically significant effect on antimicrobial resistance. Despite such differences, a substantial body of evidence supports the conclusion that older age (≥65 years) is associated with higher resistance risk.

5.1.4 Antibiotic-Resistance Pattern

5.1.4.1 Carbapenem Group

The overall carbapenem resistance rate was 15.23%, indicating that carbapenems remain relatively effective in this setting. Doripenem showed the highest resistance (47.5%), followed by panipenem (33.33%), while ertapenem showed the lowest resistance (12.7%).

Hammour et al. (2023) reported a higher carbapenem resistance rate of 41.2% compared with the present study. These differences may reflect variation in sample size, patient demographics, antibiotic exposure patterns, and pathogen distribution. DebBarma et al. (2025) similarly reported carbapenem-resistant Enterobacterales prevalence of 32.97% in India, largely associated with hospital-acquired pathogens such as *E. coli* and *K. pneumoniae*.

Globally, Beig et al. reported resistance rates of 44.8% for imipenem, 51.4% for meropenem, and 42.6% for ertapenem. Relative to these estimates, the present study demonstrates lower carbapenem resistance across agents, suggesting that carbapenem resistance remains comparatively lower locally, potentially due to reduced carbapenem use, stewardship measures, or differences in circulating organisms.

5.1.4.2 Aminoglycosides

The total resistance rate in the aminoglycoside group was 20.69%. Neomycin showed the highest resistance (83.33%), followed by isepamicin (50%). The analysis focused primarily on amikacin and gentamicin due to their clinical relevance and frequent testing. Gentamicin was tested on 61,130 isolates and amikacin on 32,770 isolates. Amikacin resistance was 10.91%, whereas gentamicin resistance was 24.66%.

Compared with Ahmed et al. (2023), aminoglycoside resistance in MDR *Klebsiella pneumoniae* was substantially higher (100% resistance to amikacin and 98% to gentamicin). Saeli et al. (2024) reported that 48% of *Pseudomonas aeruginosa* isolates were resistant to at least one aminoglycoside, with resistance rates of 45.5% for tobramycin, 43% for amikacin, and 39% for gentamicin—higher than the amikacin resistance observed in this study.

Beig et al. (2024) reported gentamicin resistance of 36.3%, higher than in this study. Tobramycin resistance was similar (35.6%). However, amikacin resistance in Beig et al. (2024) was 41.1%, markedly higher than the present results. Overall, the findings suggest that amikacin remains relatively effective locally compared with many global reports.

5.1.4.3 Antifungals

The total resistance rate among antifungals was 3.9%. Micafungin showed the lowest resistance (0.29%), while fluconazole showed the highest (6.96%).

Compared with Kilbas et al. (2025), fluconazole resistance (45–50%) was far higher than in the present study. Amphotericin B resistance was comparable: 6.42 % in this study versus 0–8.5% in Kilbas et al. (2025). Voriconazole resistance was higher in Kilbas et al. (2025) (4.37) than in this study (0.53). Both studies showed the same overall pattern: fluconazole had the highest resistance while echinocandins had the lowest resistance.

CDC (2023) estimates fluconazole resistance in the United States at 0.7%–6%, consistent with this study. ECDC estimates resistance at 0.7%–2%, which is lower than observed here. Echinocandins are recommended as first-line therapy for many invasive fungal infections due to low resistance and favorable outcomes (Arendrup and Patterson, 2017; Pappas et al., 2016). Overall, the antifungal group remains effective in Jordan, based on the low resistance levels observed.

5.1.4.4 First generation of cephalosporin

First-generation cephalosporins showed a high overall resistance rate of 74.95%. The highest resistance was observed with cephradine (92.74%), followed by cephalexin (87%) and cephapirin (86%), while cefadroxil showed comparatively lower resistance (46.88%).

Cephalothin had the highest number of tested isolates (8,135), followed by cefazolin (4,573). Despite differences in sample sizes, resistance rates were consistently high, indicating poor effectiveness for this group locally.

Beig et al. (2024) reported global cefazolin resistance of 36.4%, whereas in this study cefazolin resistance reached 68.25%, indicating substantially higher resistance locally. Clinically, these findings may reflect misuse/overuse of first-generation cephalosporins in community and hospital settings, with increased resistance particularly among Gram-negative bacteria. Continued reliance on these agents for empiric therapy increases the risk of treatment failure and delayed clinical response.

Therefore, first-generation cephalosporins should not be used as first-line therapy unless susceptibility is confirmed. Surgical prophylaxis protocols relying on cefazolin should also be reevaluated and updated based on local antibiogram patterns to ensure effectiveness and minimize postoperative infection risk.

5.1.4.5 Second generation of cephalosporin

The overall resistance rate of second-generation cephalosporins was 50.26%. Cephalothin showed the highest resistance (69.74%), while cefamandole showed the lowest (7.93%). Cefuroxime resistance was 53.66% and had the largest number of tested isolates (23,652).

In Beig et al. (2024), cefuroxime resistance was approximately 25.7%, lower than in this study, suggesting a higher local risk of resistance to second-generation cephalosporins. Because cefuroxime is commonly prescribed for respiratory and urinary tract infections and surgical prophylaxis, the observed resistance is clinically important and increases the probability of treatment failure when used empirically without microbiological confirmation.

Cefuroxime should therefore be used cautiously and supported by susceptibility testing whenever possible. These findings also reinforce the need to strengthen antimicrobial stewardship and incorporate local antibiogram data into treatment guidelines.

5.1.4.6 Third generation of cephalosporin

The overall resistance rate of third-generation cephalosporins was 43.57%. Cefdinir showed 100% resistance, while ceftazidime showed a low resistance (34.76%). No resistance was recorded in cefditoren pivoxil in single tested sample. Cefixime resistance was 57.63%. Ceftriaxone and cefotaxime were the most frequently prescribed in hospitals, with resistance rates of 40.03% and 44.64%, respectively.

Beig et al. (2024) reported higher resistance for cefotaxime (64.2%) and ceftazidime (55.9%) than observed in this study, suggesting a relatively better susceptibility profile locally. Bwanali et al. (2025) also reported much higher resistance (ceftriaxone 63%–72.4%; ceftazidime up to 74.6%) than found here. However, despite being lower than global/regional reports, resistance remains clinically significant and may increase if empiric prescribing continues without susceptibility guidance.

To preserve clinical usefulness, third-generation cephalosporins should be regulated through stewardship interventions and guided by local antibiogram data.

5.1.4.7 Fourth generation of cephalosporin

Fourth-generation cephalosporins showed an overall resistance rate of 34.61%. Resistance to cefepime was 34.6%, while cefpirome showed 100% resistance, although this was based on one isolate only. Nearly all isolates in this group were tested for cefepime.

Beig et al. reported pooled global cefepime resistance of 50.1%; therefore, the lower rate observed here suggests that cefepime remains relatively effective locally.

5.1.4.8 Fifth generation of cephalosporin

Fifth-generation cephalosporins were evaluated in only 16 isolates: 15 for ceftaroline and 1 for ceftobiprole. Resistance for the group was 31.25%; ceftaroline resistance was 33.33%, and ceftobiprole showed 100% susceptibility based on a single isolate.

Morroni et al. (2018) reported ceftobiprole resistance of 12% among MRSA isolates, which differs from this study largely due to the very small sample size here. Overall, the limited use suggests these drugs are reserved antibiotics locally for severe or multidrug-resistant infections.

5.1.4.9 Cephalosporin + β-lactamase inhibitor group

This group showed an overall resistance rate of 18.38%. Cefoperazone–sulbactam showed 100% resistance but was based on a single isolate. Ceftazidime–avibactam represented 3,154 samples with 20.51% resistance, while ceftolozane–tazobactam showed 9.12% resistance.

Valzano et al. (2024) reported 18.3% resistance to ceftazidime–avibactam, similar to this study (20.51%). For ceftolozane–tazobactam, Valzano et al. reported 20.8%, higher than the 9.12% observed here. These combinations remain effective locally, likely because they are used as reserve agents in serious MDR infections, reducing inappropriate use and preserving activity.

5.1.4.10 Fluoroquinolone group

The overall resistance rate to fluoroquinolones was 32.93%. Ciprofloxacin showed the highest resistance (34.16%). No resistance was detected for cinoxacin, garenoxacin, or gemifloxacin, while levofloxacin resistance was 33.03%.

Beig et al. (2024) reported global ciprofloxacin resistance of 46.3%, higher than observed here. Global levofloxacin resistance was 35.3%, similar to this study. Amer et al. (2024) in Pakistan reported substantially higher resistance (ciprofloxacin 74.2%; levofloxacin 66.7%), and Bwanali et al. (2025) reported ciprofloxacin resistance 66.7%–81%, also much higher than in this study.

Ciprofloxacin had a large number of tested isolates (n = 37,698), indicating extensive clinical use. Despite moderate resistance (34.16%), ciprofloxacin may still have a therapeutic role locally; however, misuse and overuse could accelerate resistance. Fluoroquinolones should therefore be reserved for severe infections and guided by stewardship measures.

5.1.4.11 Glycopeptide group

Overall glycopeptide resistance was 19.68%. Vancomycin had the largest number of tested isolates with resistance 12.94%, while teicoplanin resistance was 45.58%.

Compared with international reports, vancomycin resistance appears lower locally. Bwanali et al. (2025) reported vancomycin resistance 20%–31%. Higher rates have been reported in Australia (39.3%–46.8%) (O'Toole et al., 2023), and CDC reports approximately 30% resistance among healthcare-associated enterococcal infections in the United States. Collectively, these comparisons suggest vancomycin remains relatively effective locally against Gram-positive infections, though resistance remains clinically meaningful.

5.1.4.12 Lincosamide group

Lincosamide resistance was 50.32%. Clindamycin accounted for 15,492 of 15,691 isolates, with resistance 50.27%. Lincomycin resistance was 53.77%.

Bwanali et al. reported clindamycin resistance ranging widely (~25% to 80% in 2020). The present results fall within this range.

5.1.4.13 Macrolide group

Total macrolide resistance was 65.05%. Erythromycin had the largest number of tested isolates (16,793) with resistance 64.23; clarithromycin showed the highest resistance (87.95%), and azithromycin resistance was 64.64%.

Global data show comparable high macrolide resistance. Beig et al. (2024) reported azithromycin resistance 76.3% (higher than in this study), while erythromycin resistance ranged 64%–75%, similar to this study. WHO GLASS (2023) reported azithromycin resistance frequently exceeding 60%, and erythromycin resistance against Gram-positive bacteria >65%. Bwanali et al. (2025) reported erythromycin resistance 60%–80%, consistent with this study. ECDC surveillance (2024) reported erythromycin resistance 60%–75%, and clarithromycin resistance frequently exceeding 80%, consistent with the high resistance observed here.

The high macrolide resistance is plausibly linked to increased macrolide use during the COVID-19 period. Al-Azzam et al. (2021) reported macrolide consumption increased 57%, with azithromycin increasing 74%, contributing to selective pressure and the

development of resistance. Clinically, macrolides should be used cautiously—preferably guided by susceptibility testing—and supported by strengthened antimicrobial stewardship and local antibiograms.

5.1.4.14 Penicillin group

Penicillin group resistance was 75.92%. Mecillinam showed the lowest resistance (46.67%). Ampicillin had the highest number of tested isolates (20,050 out of 44,948) with resistance 79.55%. Amoxicillin resistance was 88.18%. Penicillin G (15,471 isolates) had resistance 76.88%. Piperacillin (6,076 isolates) had resistance 55.04%.

Bwanali et al. (2025) and Amir et al. (2024) reported ampicillin resistance around 88%, and Beig et al. (2024) reported 95.5%, consistent with the conclusion that ampicillin has limited utility. Overall, the high resistance suggests penicillins—especially ampicillin and amoxicillin—should not be used empirically in most cases and should be reserved for confirmed susceptible infections, guided by local antibiograms and stewardship policies.

5.1.4.15 Penicillin + β-lactamase inhibitor group

Overall resistance was 28.91%. Piperacillin–tazobactam had the largest number of tested isolates (37,859 of 68,950) with resistance 18.14%. Amoxicillin–clavulanate (26,845 isolates) had resistance 40.49%, while ticarcillin–clavulanate showed 77.27% resistance.

Ben Wali et al. (2025), Amir et al. (2024), and Ahmed et al. (2023) reported substantially higher amoxicillin–clavulanate resistance (95%, 85.7%, and 100% in MDR *K. pneumoniae*, respectively), higher than observed locally. For piperacillin–tazobactam, Beig et al. (2024) reported resistance 37.9%–71.6%, considerably higher than this study. Ben Wali et al. (2025) reported increases up to 35% in 2024, closer to but still higher than this study. Amir et al. (2024) reported 14.3%, similar to the present findings. Overall, piperacillin–tazobactam remains a viable local option for severe infections, while amoxicillin–clavulanate should be used cautiously and ideally guided by susceptibility testing.

5.1.4.16 Penicillinase-resistant Penicillin group

Overall resistance was 66.16%. Flucloxacillin was the most tested (13,842 out of 29,309) and showed resistance 52.30%, the lowest within this group. Oxacillin (13,223 isolates) showed resistance 78.06%, while dicloxacillin and nafcillin showed 100% resistance.

Rahimi et al. (2013) reported that 100% of MRSA isolates were resistant to oxacillin (MIC ≥ 4 μg/mL), similar to the present pattern, and Judi & Naser (2025) reported oxacillin resistance 57%–78%, consistent with this study. These findings indicate limited clinical utility for this group in settings with high MRSA prevalence, and these agents should not be used empirically without confirmed susceptibility testing.

5.1.4.17 Polymyxin group

Overall resistance was 14.82%. Colistin resistance was 16.27%, while polymyxin B resistance was 13.21%.

Beig et al. (2024) reported colistin resistance 15.3%, similar to this study. Sayehmiri et al. (2017) reported much lower resistance (~5% polymyxin; ~4% colistin against *A. baumannii*), while Adaleti et al. (2023) reported much higher resistance (colistin 40.7%, polymyxin B 34.0%). Locally, polymyxins remain relatively effective, likely because they are restricted reserve antibiotics used mainly in critically ill patients and guided by susceptibility testing and specialist oversight.

5.1.4.18 Tetracycline group

Overall resistance was 52.53%. Doxycycline showed the highest resistance (65.49%), followed by tetracycline (48.47%), while minocycline showed the lowest (36.50%). Tetracycline had the highest number of tested isolates (8,749).

Beig et al. (2024) reported tetracycline resistance 59.4%, doxycycline 46%, and minocycline 75.2%. Relative to those estimates, tetracycline and minocycline resistance were lower in this study, whereas doxycycline resistance was higher. WHO (2023) reported tetracycline resistance commonly between 40%–70%, doxycycline 30%–60%, and lower resistance for minocycline, which matches the overall pattern here. Bwanali et al. (2025) reported tetracycline resistance 55%–70% (higher than this study), and

doxycycline resistance >60%, consistent with this study. Overall, doxycycline should be used cautiously and preferably after susceptibility confirmation.

5.1.4.19 Remaining antibiotics

Among other agents, aztreonam resistance was 47.0% (8,249 isolates), and chloramphenicol resistance was 40.56% (2,700 isolates). Fosfomycin resistance was 12.71% (8,802 isolates). Linezolid resistance was 0.78% (6,961 isolates). Metronidazole resistance was 84.81% (1,922 isolates). Nalidixic acid resistance was 61.35% (8,993 isolates). Nitrofurantoin resistance was 16.55% (36,378 isolates). Rifampicin resistance was 15.35% (5,715 isolates). Tigecycline resistance was 2.19% (9,372 isolates). Trimethoprim–sulfamethoxazole resistance was 51.25% (51,385 isolates).

Beig et al. (2024) reported aztreonam resistance 53.9% (higher than this study) and noted pandemic-associated increases. Chloramphenicol resistance in Beig et al. (2024) was 39.1%, consistent with this study. Fosfomycin resistance in Amer et al. (2024) was 13.8%, similar to 12.71% here. For nitrofurantoin, Amer et al. reported 7.5% (lower), while Beig et al. reported 39.2% (higher), and Bwanali et al. (2025) reported a very wide range (0%–95.2%). Tigecycline resistance in Beig et al. was 19.3%, higher than here. For trimethoprim–sulfamethoxazole, Beig et al. reported 39.3% (lower), while Bwanali et al. reported 72.7%–89.7% (higher).

Overall, these mixed patterns reinforce the need for susceptibility-guided prescribing supported by stewardship and resistance surveillance.

5.1.5 Microbes

Escherichia coli was the most common pathogen (45.72%, n = 384,075), followed by *Klebsiella pneumoniae* (10.62%), coagulase-negative *Staphylococci* (10.32%), *Staphylococcus aureus* (10.14%), *Pseudomonas aeruginosa* (3.19%), and *Enterobacter cloacae* (2.88%).

In resistance patterns, *Acinetobacter baumannii* showed the highest resistance (69.18%), followed by coagulase-negative *Staphylococci* (41.83%) and *Pseudomonas* species (39.64%). Resistance in *K. pneumoniae* was 36.71%, and in *E. coli* was 34.35%.

The distribution aligns with previous research. Bwanali et al. (2025) reported *E. coli* and *K. pnemoniae* as the most common pathogens. Amir et al. (2024) similarly found *E.*

coli predominant (69.6%), followed by *P. aeruginosa*. Additional studies also report *E. coli* dominance across sexes and settings (Khanal et al., 2024; Sağlam et al., 2025; Duicu et al., 2021). Hammour et al. (2023) identified *E. coli* as the most common organism (34.64%), close to the present findings. WHO GLASS (2023) also reports *E. coli* as a leading cause of bloodstream infection globally (approximately 44.9% of isolates).

Regarding resistance magnitude, WHO GLASS (2025) reported lower resistance levels in *Acinetobacter* species (54.3 %) than observed in this study across several antibiotic groups, suggesting a higher burden locally. For *E. coli*, WHO GLASS (2025) resistance ranges for ceftriaxone (~43.5%) and cefotaxime (~39%–44.8%) were comparable to this study. For *K. pneumoniae*, WHO GLASS suggests higher resistance than *E. coli* (e.g., ~60% to ceftriaxone; ciprofloxacin 48.3%), compatible with the higher resistance observed in *K. pneumoniae* compared with *E. coli* here. For *S. aureus*, WHO GLASS (2025) reported MRSA prevalence of 27.1% in bloodstream infections, higher than the value reported in this study (10.14%).

Overall, while pathogen distribution is consistent with global patterns, the resistance burden—particularly for *A. baumannii*—appears elevated locally, supporting the need for targeted interventions and continuous surveillance.

5.1.6 Ward Type

Resistance was highest in ICU (45.56%), followed by inpatient wards (37.81%) and outpatient settings (35.08%), with the lowest resistance in the emergency department (29.17%). The largest number of isolates came from OUT (303,372).

These findings align with Debbarma et al. (2025), who reported higher resistance among inpatients (47.7%) compared with outpatients (14%), supporting the conclusion that hospitalization increases exposure to resistant organisms and antimicrobial selection pressure.

5.1.7 Infection Source

Hospital-acquired infections showed higher resistance (47.7%) than community-acquired infections (34.27%). This is consistent with the expected higher resistance in hospital settings due to greater antimicrobial consumption, invasive procedures, and prolonged admissions.

Debbarma et al. (2025) similarly reported higher resistance among nosocomial infections (47.7%) than community infections (14%). WHO GLASS (2025) also notes that AMR is consistently higher in hospital-acquired infections.

Therefore, strengthening infection prevention and control is critical, including routine surveillance (e.g., targeted screening and swab collection in high-risk areas), strict adherence to sterilization/disinfection protocols, and continuous improvement of infection-control practices in wards and operating rooms. These measures are essential to reduce transmission of MDR, XDR, and PDR organisms and improve patient safety.

5.2 Machine Learning

5.2.1 Machine Learning Model Performance

In this study, ensemble machine-learning approaches were applied to a dataset of 21,277 records with 12 features and three target classes. The dataset was split into a training set of 17,021 (80%) and a test set of 4,256 (20%). Random Forest, AdaBoost, Voting, and Stacking classifiers were evaluated.

The Stacking classifier achieved the highest overall performance, with precision 0.7649 and F1 score 0.7380, indicating a strong balance between precision and recall. Stacking also achieved the highest values across precision, recall, specificity, and Matthews correlation coefficient (MCC), supporting its robustness in classifying antimicrobial resistance.

The Voting classifier achieved the highest AUC-ROC (0.7892), indicating strong discriminative ability across thresholds. This suggests that while Voting may not maximize all accuracy-based metrics, it performs well for class separation and threshold-based evaluation.

Performance metrics were generally within narrow ranges: precision approximately 0.70–0.76, recall 0.70–0.76, F1 0.65–0.73, specificity 0.70–0.77, MCC 0.16–0.37, and AUC values approximately 0.70–0.78. AdaBoost showed the lowest overall performance, Random Forest and Voting were moderate, and Stacking performed best overall.

SHAP was used as an explainable AI layer to interpret model predictions and identify key predictors of resistance. Across all models, antibiotic name had the highest normalized SHAP value, indicating that the specific antibiotic tested strongly influences

resistance outcomes. This is clinically expected, as antimicrobial resistance is antibiotic-specific and shaped by mechanisms of action, spectrum, and usage patterns that determine selective pressure (Davies & Davies, 2010; Munita & Arias, 2016). Antibiotics used frequently or inappropriately typically exert stronger selective pressure, increasing resistance risk, whereas restricted/reserve agents often retain higher susceptibility.

Model-specific SHAP patterns also provided clinically coherent insights. In Random Forest, organism type was the second most important feature, followed by period since adoption and organism, suggesting sensitivity to microbiological and hospitalization-related factors. In AdaBoost, hospitalization-related features (e.g., time since administration) appeared more influential than organism-specific variables. In Stacking and Voting, the top predictors were antibiotic name, organism, and organism type, aligning with their comparable predictive performance and suggesting robust integration of microbiological identity and organism classification.

Overall, SHAP results were consistent across models, strengthening confidence in model interpretability and supporting the clinical relevance of the predictors identified.

When comparing these machine-learning results with previous studies, both similarities and differences were observed in performance and feature importance.

Al-Malki et al. (2025) reported higher recall (~80–88%) and AUC (0.90) using ensemble models (especially XGBoost), exceeding the performance observed here. This may reflect differences in dataset size and homogeneity. Importantly, interpretability findings were consistent: antibiotic type, bacterial organism, and laboratory variables were key predictors according to SHAP, aligning with this study.

Haredasht et al. (2024) reported AUC values 0.74–0.78 using LightGBM-based models, closely comparable to the AUC range in this study (~0.70–0.78). Their SHAP analysis highlighted the importance of prior antibiotic exposure and prior resistant infections, consistent with this study's observation that antibiotic-related features strongly influence predictions.

Ferrari et al. (2024) reported higher AUC (0.86) among ICU-only patients, likely due to a more homogeneous population that can improve model learning. However, their F1 scores (~0.44) were lower than those observed here (0.65–0.73), suggesting that while

discrimination was stronger, this study achieved a better balance between precision and recall—an important advantage in multi-class AMR prediction with class imbalance.

Tran Quoc et al. (2023) reported very high performance (accuracy, F1, AUC, MCC 0.90–1.00), likely due to smaller datasets and more homogeneous settings. Their SHAP findings (organism type, antibiotic class, prior susceptibility) were consistent with the feature importance patterns observed here.

Çağlayan et al. (2022) reported sensitivities and specificities broadly similar to those in this study for several ICU-focused MDRO predictions, supporting the validity of the present findings despite differences in scale and population.

In summary, while some studies report higher performance, these differences are likely driven by smaller sample sizes and more homogeneous populations. In contrast, this study used a large, diverse, multi-hospital dataset representing hospitals across the Hashemite Kingdom of Jordan and including different age groups and epidemiological characteristics. Notably, this work is presented as the first in Jordan to apply machine-learning techniques to a large and diverse population-based dataset.

Overall, the findings indicate that antimicrobial resistance is a significant public health threat in Jordan, with a high prevalence that may rise further if current practices continue. Therefore, it is strongly recommended to strengthen policies regulating antibiotic prescription in both community and hospital settings and to expand and optimize antimicrobial stewardship programs across hospitals, with emphasis on restricting certain antibiotic classes and reserving last-line agents for severe cases.

Finally, integrating machine-learning tools into clinical decision-making could support more appropriate antibiotic selection by incorporating epidemiological and clinical factors, improving decision accuracy and potentially enhancing patient outcomes.

5.3 Conclusion

This study provides a comprehensive national-level evaluation of antimicrobial resistance patterns in Jordan using electronic health record–based surveillance data and demonstrates the feasibility and clinical value of applying machine learning techniques to predict antimicrobial resistance outcomes. The findings reveal a consistently high burden of AMR across multiple antibiotic classes, pathogens, clinical settings, and patient groups during the period from 2020 to 2024, underscoring AMR as a major public health and clinical challenge in Jordan.

The descriptive analysis showed that overall resistance rates remained relatively stable over time, with peaks observed during the COVID-19 pandemic, reflecting changes in antibiotic prescribing practices and increased empiric use of broad-spectrum agents. Clinically important resistance patterns were identified across commonly prescribed antibiotic classes, including penicillins, cephalosporins, macrolides, and fluoroquinolones, many of which demonstrated resistance levels high enough to compromise their effectiveness as empiric therapies. In contrast, reserve antibiotics such as carbapenems, polymyxins, echinocandins, and linezolid generally maintained lower resistance rates, highlighting the clinical importance of restricted prescribing and stewardship-driven use.

Resistance was disproportionately higher among elderly patients, male patients, intensive care unit populations, and hospital-acquired infections, emphasizing the role of healthcare exposure, comorbidities, and prolonged antibiotic use in driving resistance. At the pathogen level, *Escherichia coli* remained the most frequently isolated organism, while *Acinetobacter baumannii* demonstrated the highest resistance burden, representing a critical threat in hospital settings. These findings have direct clinical implications for empiric therapy selection, infection control prioritization, and risk stratification of vulnerable patient populations.

Importantly, the machine learning component of this study demonstrated that ensemble models—particularly the stacking and voting classifiers—were capable of predicting antimicrobial resistance with moderate-to-good performance across multiple evaluation metrics. The integration of explainable artificial intelligence (SHAP) revealed that antibiotic-related factors, followed by pathogen identity and organism type, were the

most influential predictors of resistance, reinforcing the biological plausibility and clinical relevance of the models. These results indicate that machine learning approaches can complement traditional surveillance by providing decision-support insights that align with real-world clinical and microbiological drivers of AMR.

Overall, this thesis represents the first large-scale application of machine learning to national AMR surveillance data in Jordan and demonstrates that predictive modeling, when combined with robust descriptive epidemiology, can enhance understanding of resistance patterns and support more informed clinical and public health interventions.

5.4 Recommendations

Based on the findings of this study, the following recommendations are proposed to improve clinical practice, antimicrobial stewardship, and future research in Jordan:

5.4.1 Clinical Practice and Antibiotic Prescribing

- Empiric antibiotic therapy should be reconsidered and updated based on local resistance patterns, particularly for antibiotic classes that demonstrated high resistance rates, such as penicillins, first- and second-generation cephalosporins, macrolides, and fluoroquinolones.
- Increased reliance on antimicrobial susceptibility testing prior to antibiotic initiation is strongly recommended, especially in hospitalized patients, elderly populations, and intensive care units where resistance rates were highest.
- Reserve antibiotics, including carbapenems, polymyxins, echinocandins, and linezolid, should remain restricted to severe or multidrug-resistant infections, with prescribing guided by microbiological confirmation to preserve their effectiveness.

5.4.2 Antimicrobial Stewardship and Infection Control

- Antimicrobial stewardship programs should be strengthened and expanded across hospitals, with particular emphasis on intensive care units and wards associated with hospital-acquired infections.
- Local antibiograms should be regularly updated and actively integrated into clinical decision-making, treatment guidelines, and hospital protocols.
- Enhanced infection prevention and control measures—including surveillance, environmental disinfection, and adherence to hand hygiene and isolation

protocols—are essential to reduce transmission of resistant organisms, particularly *Acinetobacter baumannii*.

5.4.3 Integration of Machine Learning into Clinical Decision Support

- Machine learning–based predictive models should be explored as clinical decision-support tools to assist physicians in selecting appropriate empiric antibiotics, particularly in high-risk patients and settings.
- The use of explainable models, such as those employing SHAP analysis, is recommended to ensure transparency, clinician trust, and interpretability of predictions.
- Future implementation efforts should focus on integrating predictive models into hospital information systems while ensuring appropriate validation and clinical oversight.

5.4.4 Policy and Surveillance

- National policies regulating antibiotic prescription in both community and hospital settings should be strictly enforced, with monitoring mechanisms to limit inappropriate antibiotic use.
- Continued investment in the national antimicrobial resistance surveillance system is essential to ensure high-quality, real-time data that can inform clinical guidelines and public health strategies.

5.4.5 Future Research

- Future studies should incorporate additional clinical variables, such as comorbidities, prior antibiotic exposure, and treatment outcomes, to further enhance predictive performance.
- External validation of the developed machine learning models using independent datasets is recommended before clinical deployment.
- Longitudinal studies assessing the impact of stewardship interventions and predictive modeling on patient outcomes, resistance trends, and healthcare costs are warranted

5.5 Limitation

- Retrospective study design
- Incomplete clinical data (comorbidities, previous hospital admissions, prior antibiotic use, disease severity, treatment duration, and clinical outcomes)
- Reliance on electronic health records, which may include documentation errors and variability

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Appendices

Appendix (1): A study datasets

First dataset :

- Patient ID
- Laboratory reference
- Antibiotic name
- Topographical site (source of culture)
- Organism details
- Organism isolation time
- Species and species status
- Reference species entry
- Antimicrobial susceptibility results (sensitive, resistant, intermediate)
- Infection type (nosocomial or community-acquired)
- Etiology name
- Type and location: reward type; patient location (inpatient, ICU, outpatient, emergency)
- Admission date
- Discharge date
- Period since admission (hospitalization duration)
- Date of birth

- Age
- Sex
- Diagnosis

Second dataset :

- Diagnosis
- Complete blood count (CBC) parameters:

1. White blood cell (WBC) count
2. Red blood cell (RBC) count
3. Platelet count
4. Mean corpuscular volume (MCV)
5. Mean corpuscular hemoglobin (MCH)
6. corpuscular hemoglobin concentration (MCHC)

Appendix (2): A functional equation

1. An IF conditional formula was applied to categorize age into groups:

=IF(RIGHT(P2,1)="D","0–1 year",
IF(RIGHT(P2,1)="W","0–1 year",
IF(RIGHT(P2,1)="M","0–1 year",
IF(P2<=18,"1–18",
IF(P2<=64,"19–64","65+")))))

2. To automatically classify each antibiotic in the main dataset, a VLOOKUP formula was applied:=VLOOKUP(C2, Drug_class_Table!$A:$B, 2, FALSE)

where:
C2 = antibiotic name in the main dataset
Drug_class_Table!A:B = table holding antibiotic–class mapping
2 = returns the class (second column)
FALSE = exact match

Appendix (3): A Drug classification table

Antibiotic	**Class**
5-Fluorocytosine	Antifungal
Amikacin	Aminoglycoside
Amoxicillin	Penicillin (Aminopenicillin)
Amoxicillin + Clav	Penicillin + β-lactamase inhibitor
Amphotericin B	Antifungal
Ampicillin	Penicillin (Aminopenicillin)
Ampicillin + Sulb	Penicillin + β-lactamase inhibitor
Azithromycin	Macrolide
Azlocillin	Penicillin (Antipseudomonal)
Aztreonam	Monobactam
Bacitracin	Polypeptide Antibiotic
Carumonam	Monobactam
Caspofungin	Antifungal (Echinocandin)
Cefaclor	Cephalosporin (2nd gen)
Cefadroxil	Cephalosporin (1st gen)
Cefamandole	Cephalosporin (2nd gen)
Cefazolin	Cephalosporin (1st gen)
Cefdinir	Cephalosporin (3rd gen)
Cefditoren Pivoxil	Cephalosporin (3rd gen)
Cefepime	Cephalosporin (4th gen)
Cefetamet Pivoxil	Cephalosporin (3rd gen)
Cefixime	Cephalosporin (3rd gen)
Cefmenoxime	Cephalosporin (3rd gen)
Cefmetazole	Cephamycin (2nd gen related)
Cefoperazone	Cephalosporin (3rd gen)
Cefoperazone + Sulb	Cephalosporin + β-lactamase inhibitor
Cefotaxime	Cephalosporin (3rd gen)
Cefotetan	Cephamycin (2nd gen related)
Cefpirome	Cephalosporin (4th gen)
Cefprozil	Cephalosporin (2nd gen)
Ceftaroline	Cephalosporin (5th gen)
Ceftazidime	Cephalosporin (3rd gen)
Ceftazidime + Avib	Cephalosporin + β-lactamase inhibitor
Ceftibuten	Cephalosporin (3rd gen)
Ceftizoxime	Cephalosporin (3rd gen)
Ceftobiprole	Cephalosporin (5th gen)
Ceftolozane + Tazb	Cephalosporin + β-lactamase inhibitor
Ceftriaxone	Cephalosporin (3rd gen)
Cefuroxime	Cephalosporin (2nd gen)
Cephalexin	Cephalosporin (1st gen)
Cephalothin	Cephalosporin (1st gen)
Cephapirin	Cephalosporin (1st gen)

Cephradine	Cephalosporin (1st gen)
Chloramphenicol	Amphenicol
Cinoxacin	Fluoroquinolone
Ciprofloxacin	Fluoroquinolone
Clarithromycin	Macrolide
Clinafloxacin	Fluoroquinolone
Clindamycin	Lincosamide
Cloxacillin	Penicillinase-resistant Penicillin
Colistin	Polymyxin
Dalbavancin	Glycopeptide-like
Dicloxacillin	Penicillinase-resistant Penicillin
Doripenem	Carbapenem
Doxycycline	Tetracycline
Ertapenem	Carbapenem
Erythromycin	Macrolide
Faropenem	Penem
Flucloxacillin	Penicillinase-resistant Penicillin
Fluconazole	Antifungal
Fosfomycin	Fosfomycin
Fusidic Acid	Fusidanes
Garenoxacin	Fluoroquinolone
Gemifloxacin	Fluoroquinolone
Gentamicin	Aminoglycoside
Grepafloxacin	Fluoroquinolone
Iclaprim	Dihydrofolate Reductase inhibitor
Imipenem	Carbapenem
Isepamicin	Aminoglycoside
Levofloxacin	Fluoroquinolone
Lincomycin	Lincosamide
Linezolid	Oxazolidinone
Mecillinam	Penicillin (amidopenicillin)
Meropenem	Carbapenem
Meropenem + Vaborb	Carbapenem + β-lactamase inhibitor
Methicillin	Penicillinase-resistant Penicillin
Metronidazole	Nitroimidazole
Micafungin	Antifungal (Echinocandin)
Minocycline	Tetracycline
Moxalactam	Oxacephem (Cephalosporin-related)
Moxifloxacin	Fluoroquinolone
Nafcillin	Penicillinase-resistant Penicillin
Nalidixic Acid	Quinolone (1st gen)
Neomycin	Aminoglycoside
Netilmicin	Aminoglycoside
Nitrofurantoin	Nitrofurans

Norfloxacin	Fluoroquinolone
Novobiocin	Coumarin
Ofloxacin	Fluoroquinolone
Oritavancin	Glycopeptide-like
Oxacillin	Penicillinase-resistant Penicillin
Panipenem	Carbapenem
Penicillin G	Penicillin (Narrow-spectrum)
Pipemidic Acid	Quinolone
Piperacillin	Penicillin (Antipseudomonal)
Piperacillin + Sulb	Penicillin + β-lactamase inhibitor
Piperacillin + Tazb	Penicillin + β-lactamase inhibitor
Polymyxin B	Polymyxin
Quinupristin + Dalfopristin	Streptogramins
Rifampin	Rifamycin
Sparfloxacin	Fluoroquinolone
Spectinomycin	Aminocyclitol
Streptomycin	Aminoglycoside
Streptomycin High	Aminoglycoside
Sulfisoxazole	Sulfonamide
Sulfonamides	Sulfonamide
Teicoplanin	Glycopeptide
Tetracycline	Tetracycline
Ticarcillin	Penicillin (Antipseudomonal)
Ticarcillin + Clav	Penicillin + β-lactamase inhibitor
Tigecycline	Glycylcycline
Tobramycin	Aminoglycoside
Trimethoprim	DHFR inhibitor
Trimethoprim + Sulfamethoxazole	Combination Folate Pathway Inhibitors
Trospectomycin	Aminocyclitol
Vancomycin	Glycopeptide
Voriconazole	Antifungal