

## Group members :

Christian RWIBUTSO HAKIZINKA , Abdullah Amin , Shamsun Nahar , Abdelmola Albadwi

### 1. Project Idea:

The project aims to develop a predictive model for anticipating bacterial resistance to specific medications, addressing one of the most pressing challenges in global healthcare: Antimicrobial Resistance (AMR). AMR is a top public health threat, responsible for an estimated 1.27 million global deaths in 2019 and contributing to 4.95 million deaths worldwide. The misuse and overuse of antimicrobials in humans, animals, and plants accelerate the development of drug-resistant pathogens, posing significant risks to the gains of modern medicine. The economic impact is also alarming, with the World Bank estimating that AMR could lead to an additional US\$ 1 trillion in healthcare costs by 2050 and cause annual GDP losses ranging from US\$ 1 trillion to US\$ 3.4 trillion by 2030. This project will enable health institutions to anticipate outbreaks, pharmaceutical companies to develop new treatments proactively, and governments to strategize against the looming crisis, ultimately contributing to global efforts to combat AMR. click [here](#) for more info.

### 2. Relevance to Sustainable Development Goals (SDGs):

This project is directly aligned with SDG 3: Good Health and Well-Being, which aims to ensure healthy lives and promote well-being for all at all ages. Antibiotic resistance is a growing global health threat that compromises the effectiveness of treatments, leading to prolonged illnesses, higher healthcare costs, and increased mortality rates. By predicting when bacteria will develop resistance to medications, this project can contribute to preventing the spread of resistant strains, thereby preserving the efficacy of existing drugs. This proactive approach can improve patient outcomes, reduce the burden on healthcare systems, and support sustainable healthcare practices. Moreover, the project can indirectly contribute to SDG 9: Industry, Innovation, and Infrastructure, by encouraging pharmaceutical innovation and development of new medications.

### 3. Literature Examples:

#### 1. "Machine Learning in Predicting Antibiotic Resistance"

- **Summary:** This study explores the use of machine learning algorithms to predict antibiotic resistance in bacteria. The authors employed various models such as decision trees, random forests, and support vector machines (SVM) to analyze genetic data and predict resistance patterns. The study demonstrated that machine learning could effectively identify potential resistance traits, helping to guide treatment decisions and antibiotic usage. (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10044642/>)

#### 2. "Deep Learning for Antibiotic Resistance Prediction: A Comprehensive Review"

- **Summary:** This review paper examines the application of deep learning techniques in predicting antibiotic resistance. It discusses the use of neural networks and other advanced deep learning models to analyze large datasets, including genomic sequences, to forecast resistance trends. The paper also highlights the challenges and opportunities in integrating deep learning into healthcare for combating antibiotic resistance. (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9686762/>)

### 4. Describe Your Data:

For this project, we will utilize an Excel dataset containing detailed information about various drugs and their associated pathogens. The dataset includes key attributes such as drug identification, development timeline, clinical phases, routes of administration, and the pathogens they target.

### 5. Approach (Machine Learning or Deep Learning):

In our model, Gradient Boosting Machines (e.g., XGBoost, LightGBM) will be used to predict bacterial resistance by analyzing the intricate relationships between drug attributes, pathogen characteristics, and historical resistance patterns. The model will learn from the dataset's detailed information, such as drug identification, clinical phases, and routes of administration, to identify which drugs are most likely to be effective against specific pathogens. By iteratively improving the prediction accuracy through the boosting process, the model will provide healthcare professionals with precise recommendations for selecting the most effective medications based on a patient's history and the likelihood of resistance.