REMEDY-NOW

ANTIMICROBIAL STEWARDSHIP PLATFORM

SIH 2020 SOFTWARE ROUND
ORGANISATION: Amazon Web Services
PROBLEM STATEMENT: Antimicrobial Stewardship
Platform
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TEAM LEAD: SOMDEV BASU
COLLEGE CODE: 109

The Problem

Bacterial infections that don't respond to treatment are a growing concern. Currently antimicrobial resistant infections kill over 700,000 people per year, and by 2050 its estimated 10 million people will die from of antimicrobial resistant infections!
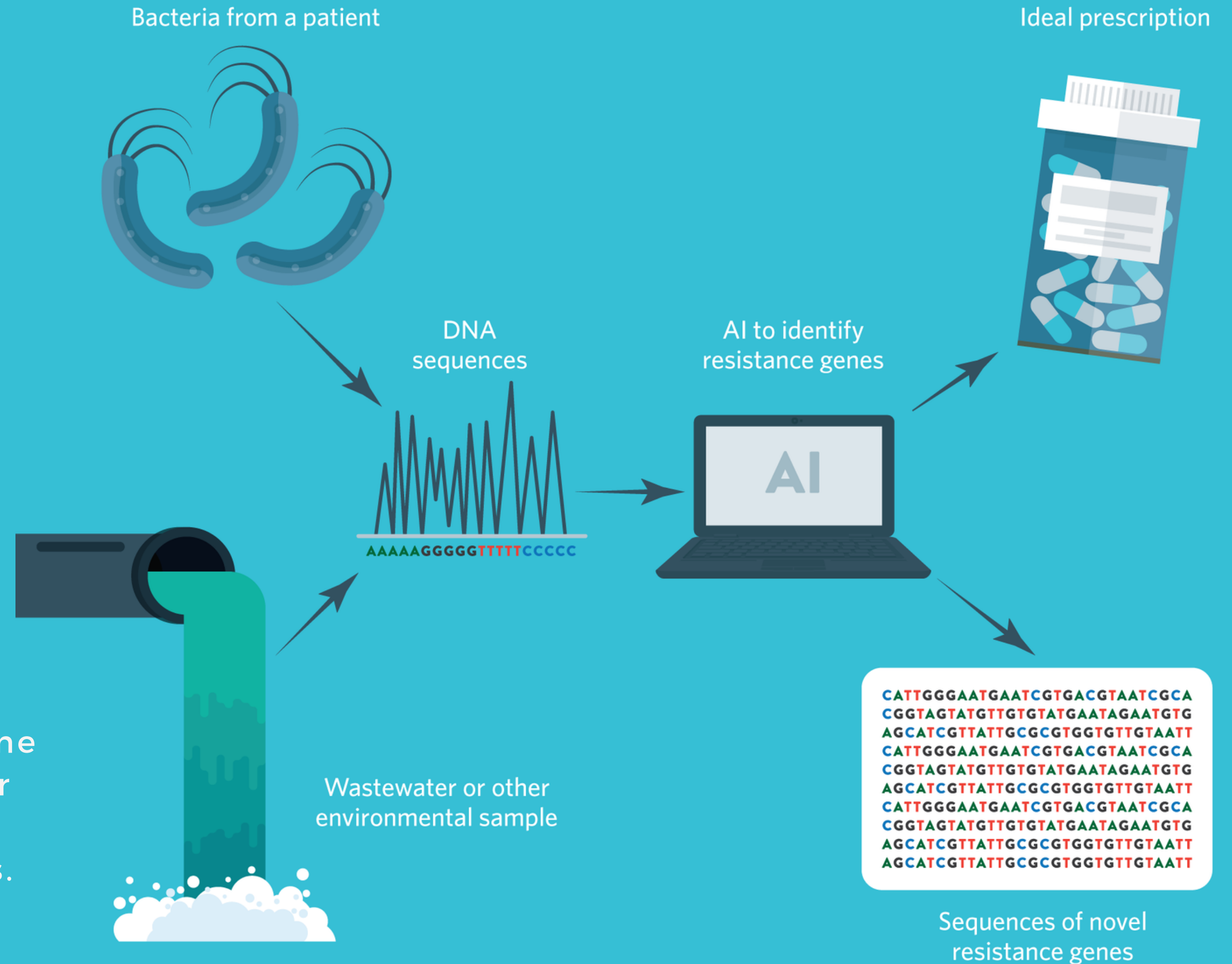
The solution

Many factors contribute to the resistance power that is developed by a microbe. This can be reduced by letting the regular users of the antibiotic know about the several issues associated with the misuse and patterns of the antibiotics associated with eradicating the microbe.

How it all works

Bacteria from a patient

DNA sequences

AAAAAGGGGGTTTTTCCCCC

AI to identify resistance genes

AI

Ideal prescription

Machine learning algorithms that predict antibiotic resistance from whole genome sequences could improve our ability to recognise and contain new resistant strains.
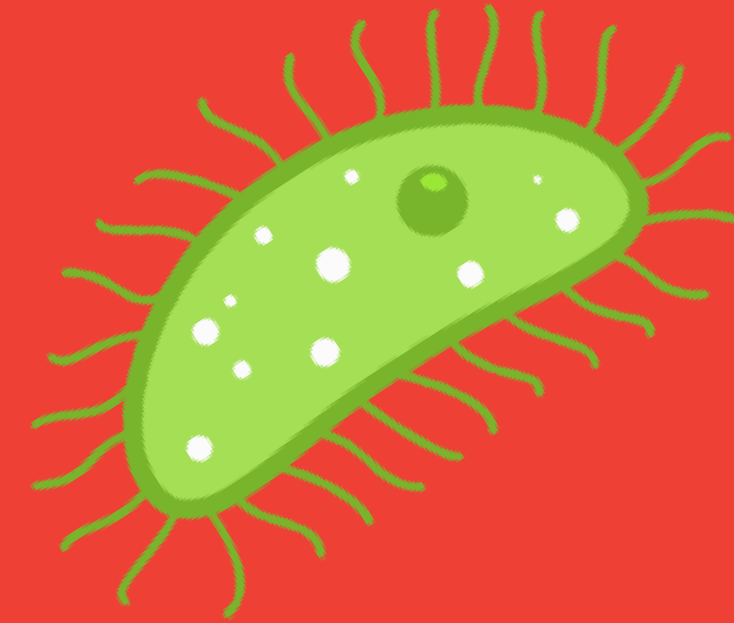
Wastewater or other environmental sample

CATTGGGAATGAATCGTGACGTAATCGCA
CGGTAGTATGTTGTGTATGAATAGAATGTG
AGCATCGTTATTGCGCGTGGTGTTGTAATT
CATTGGGAATGAATCGTGACGTAATCGCA
CGGTAGTATGTTGTGTATGAATAGAATGTG
AGCATCGTTATTGCGCGTGGTGTTGTAATT
CATTGGGAATGAATCGTGACGTAATCGCA
CGGTAGTATGTTGTGTATGAATAGAATGTG
AGCATCGTTATTGCGCGTGGTGTTGTAATT
AGCATCGTTATTGCGCGTGGTGTTGTAATT

Sequences of novel resistance genes

The stages building the platform...

Step 1

Collecting information about antibiotic usage and inculcate it in a dataset.

Step 2

Dataset analysis for information relating to resistance of the microbe to a particular antibiotic .

Step 3

Provide a user friendly, platform to show the drug usage patterns and allow the consumer to analyse and contribute to the product.
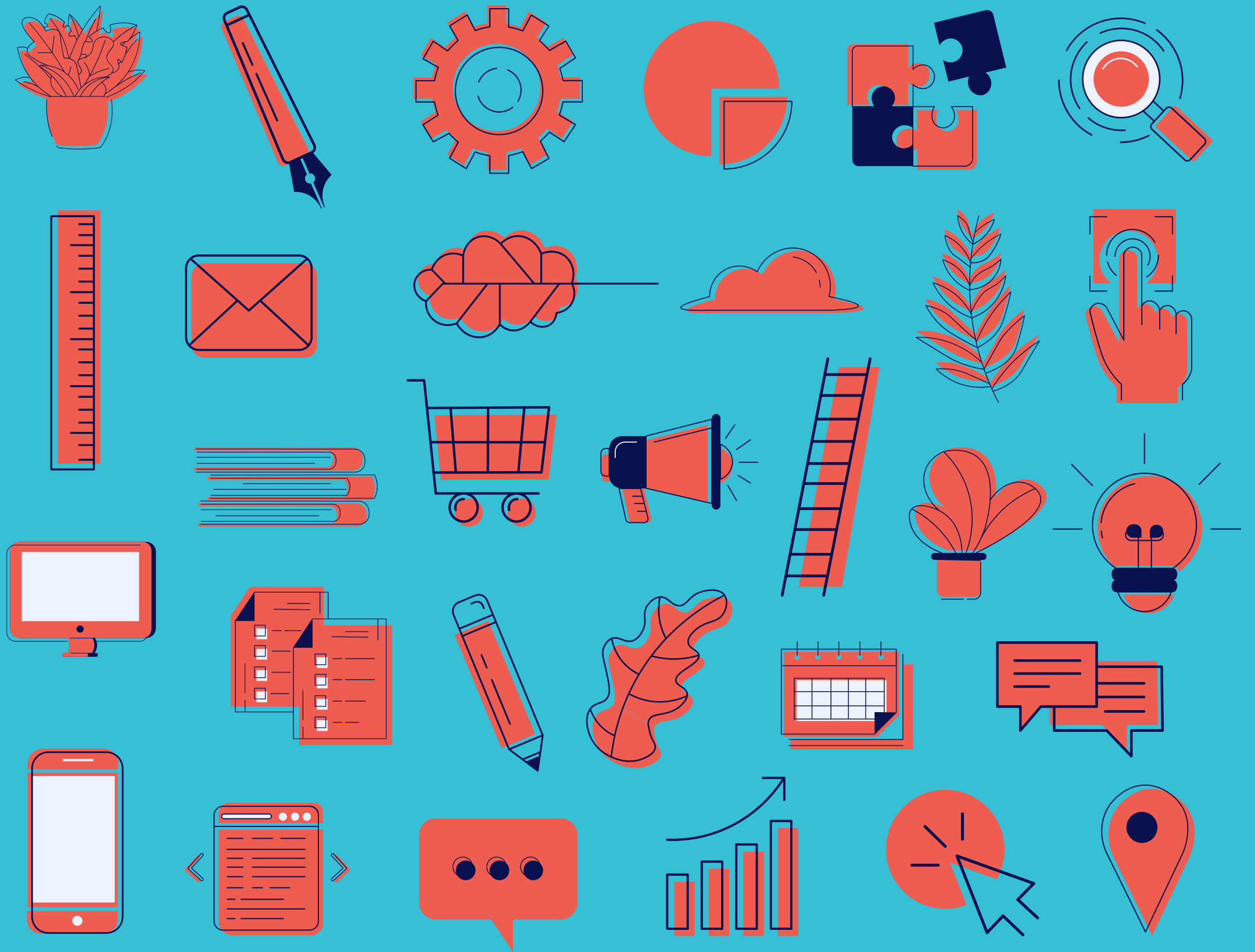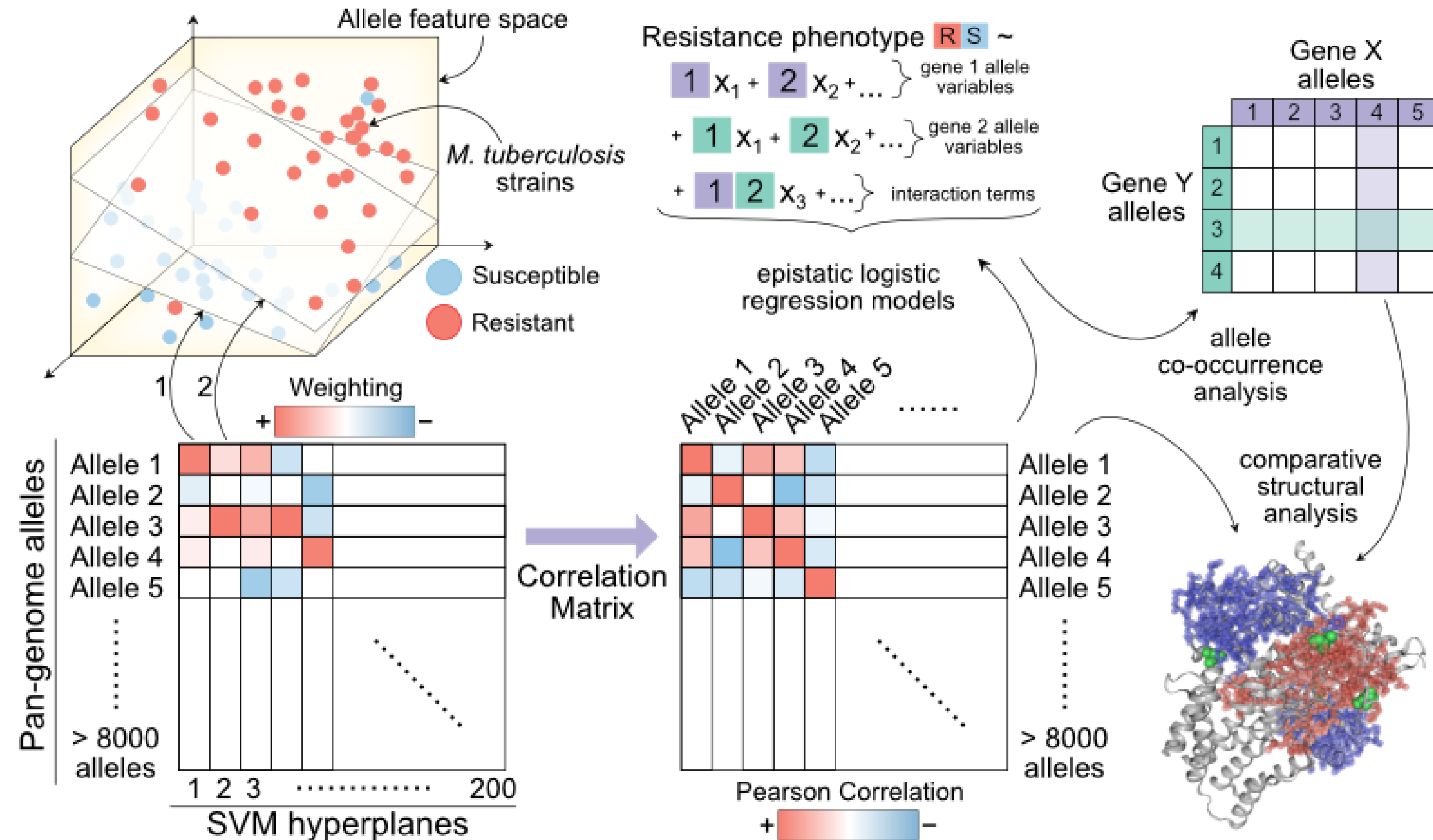
STEP 1

STUDYING THE INPUT DATA AND MAKING THE DATASET

The Input and the Dataset

The researchers used 1,595 M. tuberculosis genomes from the PATRIC database, whether each genome was from a strain resistant or susceptible to 13 different antibiotics.
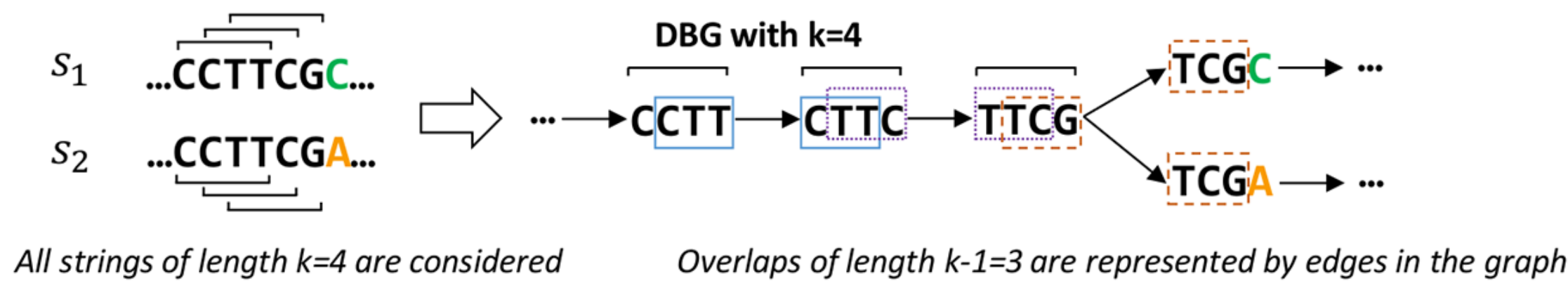
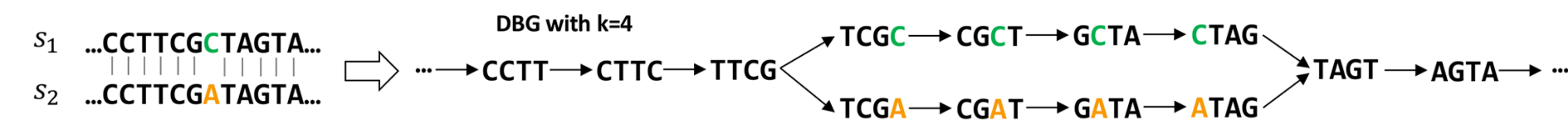# What we do here? Well, ask a biologist :)

Studying the DNA Strands of Tuberculosis

(A) DBG represents overlaps between strings

All strings of length k=4 are considered   Overlaps of length k-1=3 are represented by edges in the graph

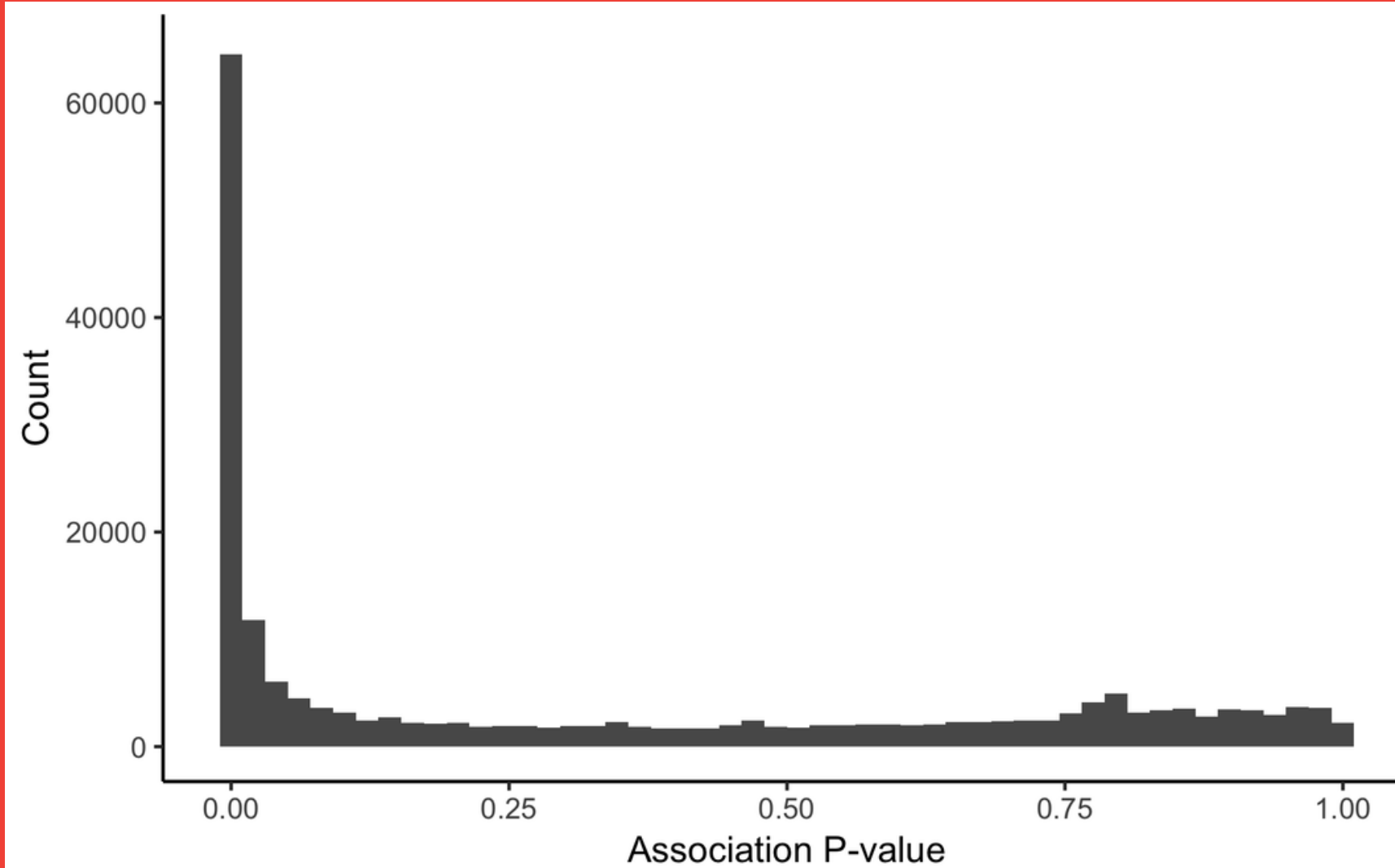(B) A point mutation is summarized as a bubble in the graph
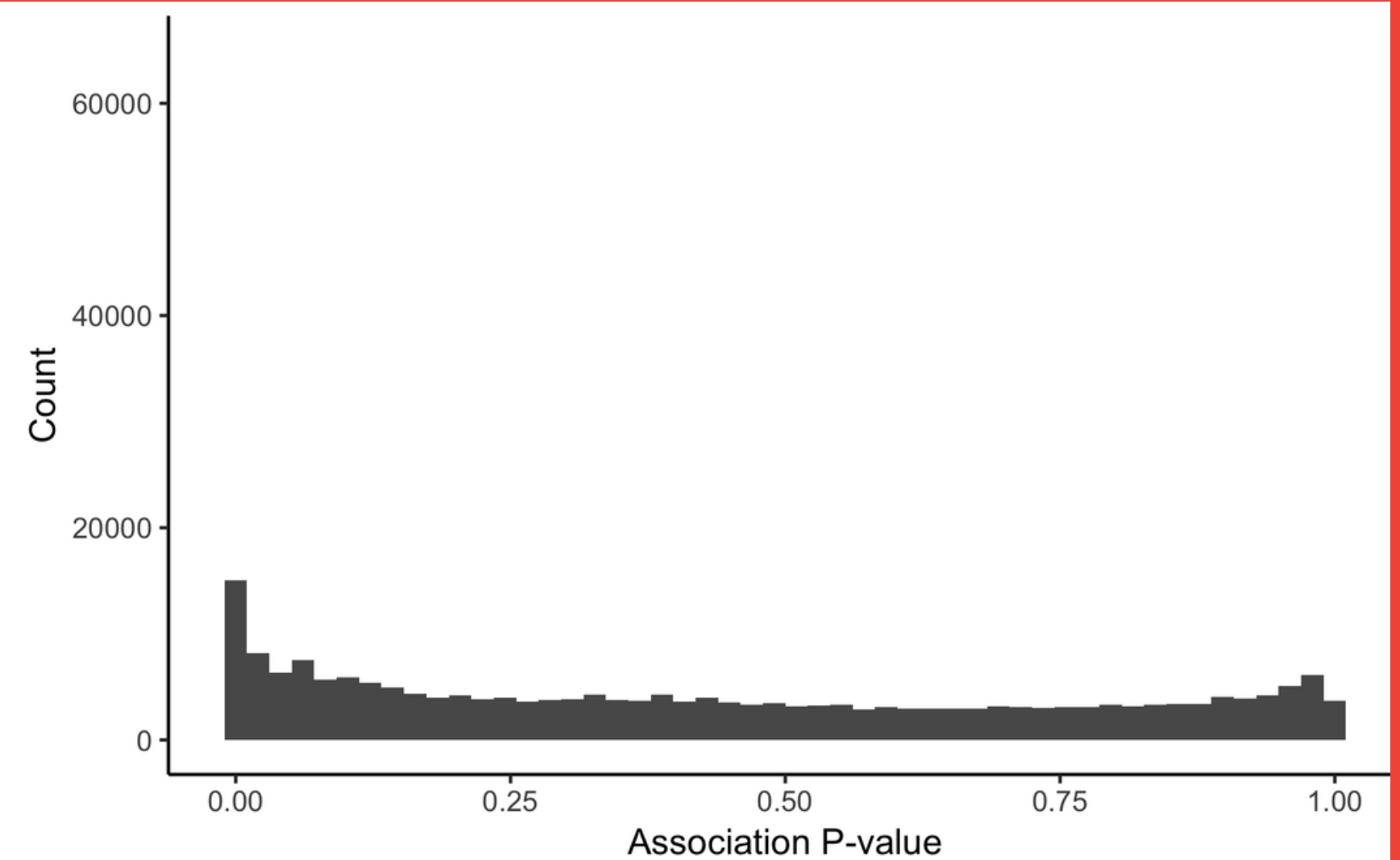
(C) DBG can be compacted

DON'T EVEN LOOK IF YOU AREN'T INTO GENETICS

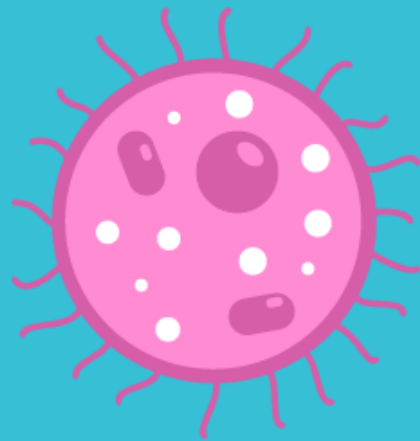# Ciprofloxacin Resistance unitigs

Azithromycin Resistance unitigs

Usually when working with unitigs, the number of variables may range between 0.5–5 million.But we apply a filter to that, the filtering resulted in 8,873 unitigs strongly associated with ciprofloxacin resistance and 515 unitigs significantly associated with azithromycin resistance, for a dataset containing 3,971 samples.
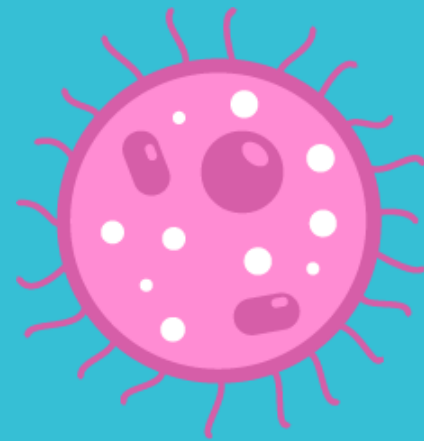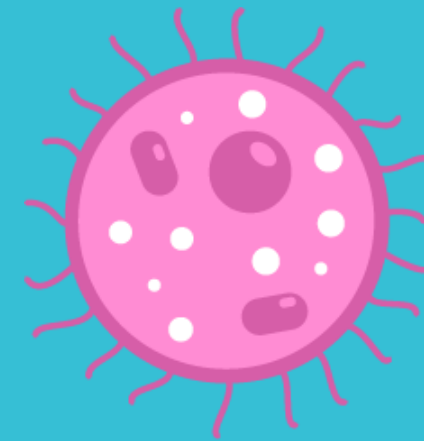
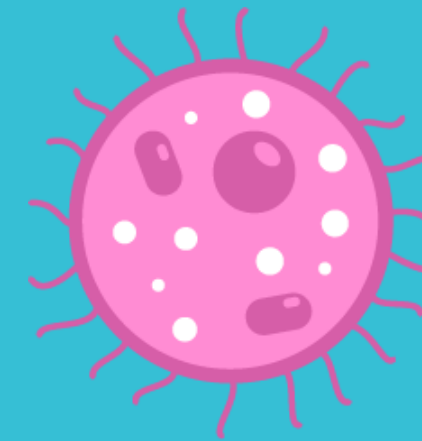# STEP 2

BUILDING THE MODEL

Types of Possible Models

Elastic Net Logistic Regression

Support Vector Machine

XGBoost

Random Forest
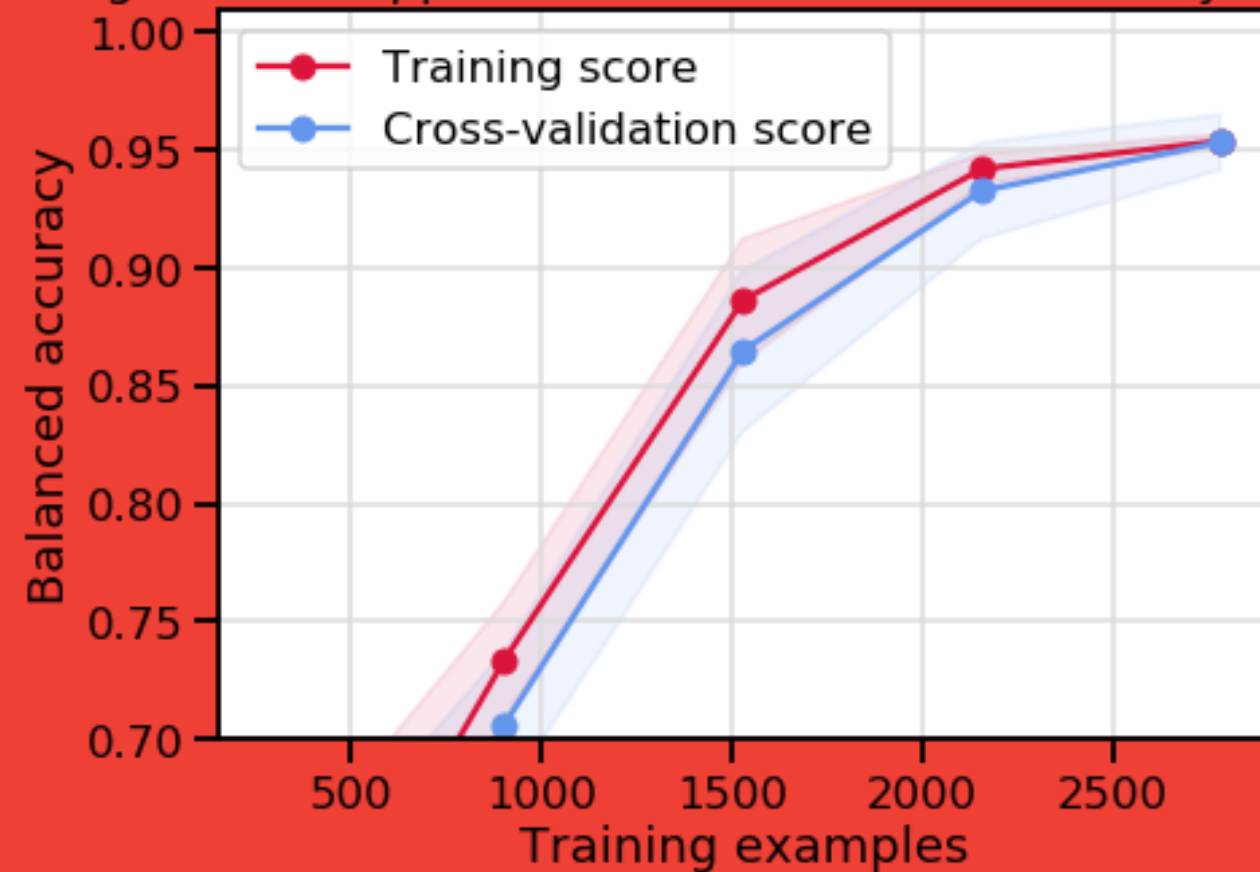
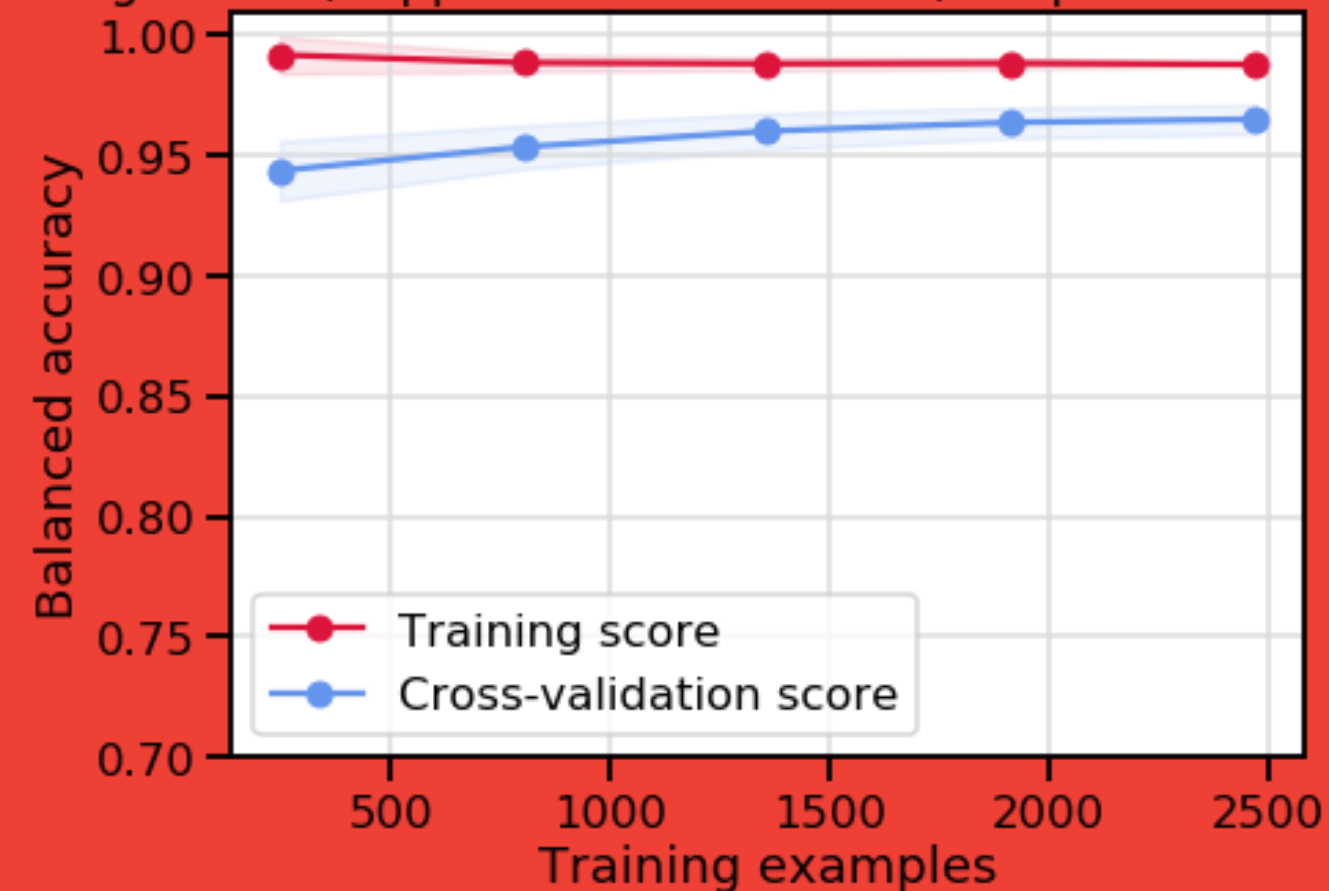# TWO AVAILABLE RESISTANCE PROFILES

Azithromycin resistance

Ciprofloxacin resistance

Learning Curve (Support vector machine) - Azithromycin

Learning Curve (Support Vector Machine) - Ciprofloxacin

- Our model split the data into five folds for cross-validation, and within each of those performed a grid search across possible hyper-parameters.
- The covariates in the prediction model include each individual patient's past microbiological test results, a rich set of personal characteristics such as gender, age, etc.
- Using this function we could compare the performances of the different model types across datasets.
- We finally find the SVM Model to be the most accurate of all.

Model Performance - Azithromycin Resistance

Model Training Times - Azithromycin Resistance
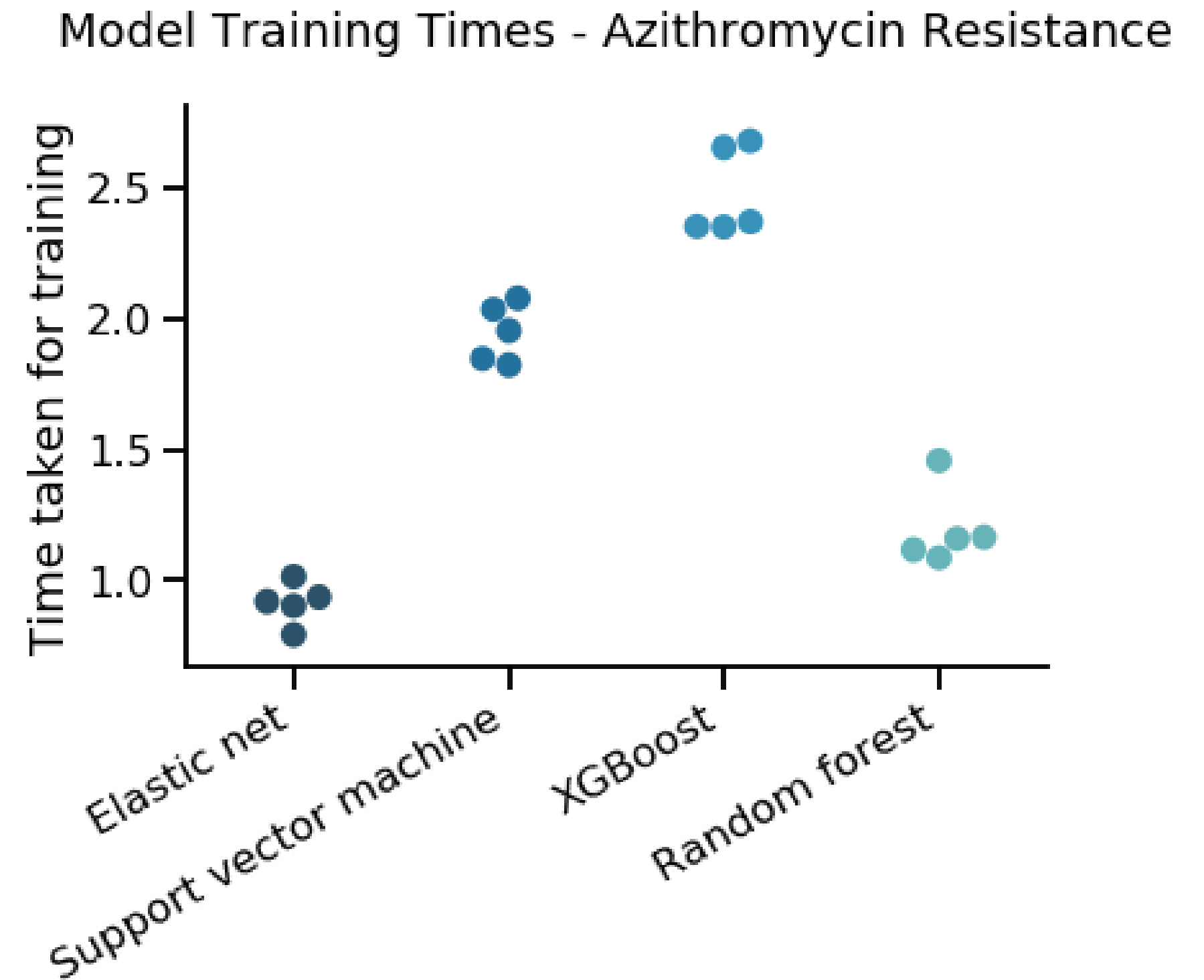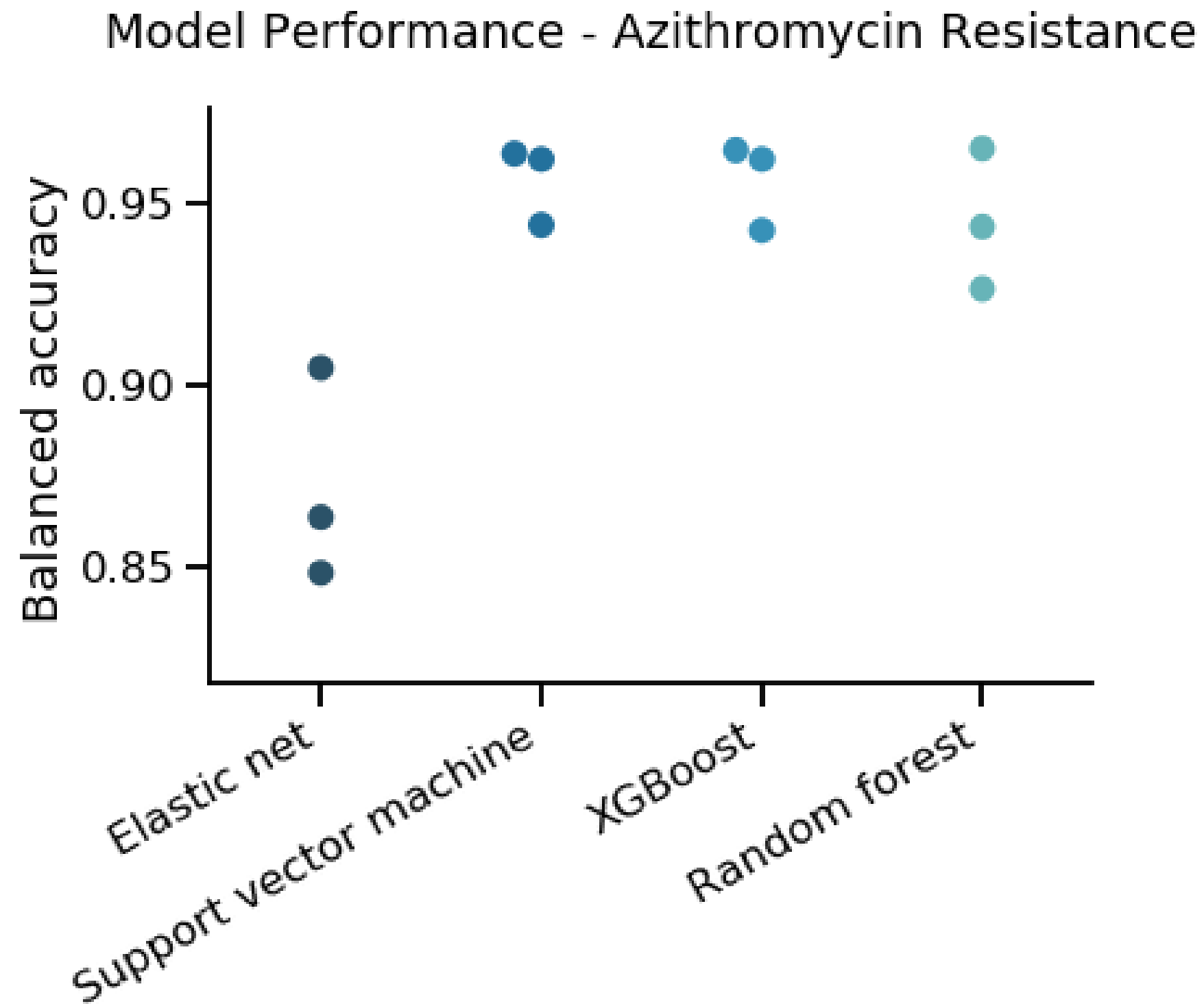
COMPARING THE VARIOUS MODELS, WE EVENTUALLY PLAN ON SUPPORT VECTOR MACHINE(SVM)

Support Vector Machine

A layman concept

This algorithm is designed to group similar data and draw boundaries between the groups. For the multidimensional matrix we created, it draws a multidimensional divider, called a hyperplane.

We also applied a technique called the L1-norm(used a small number of genes to draw the boundary).

Output
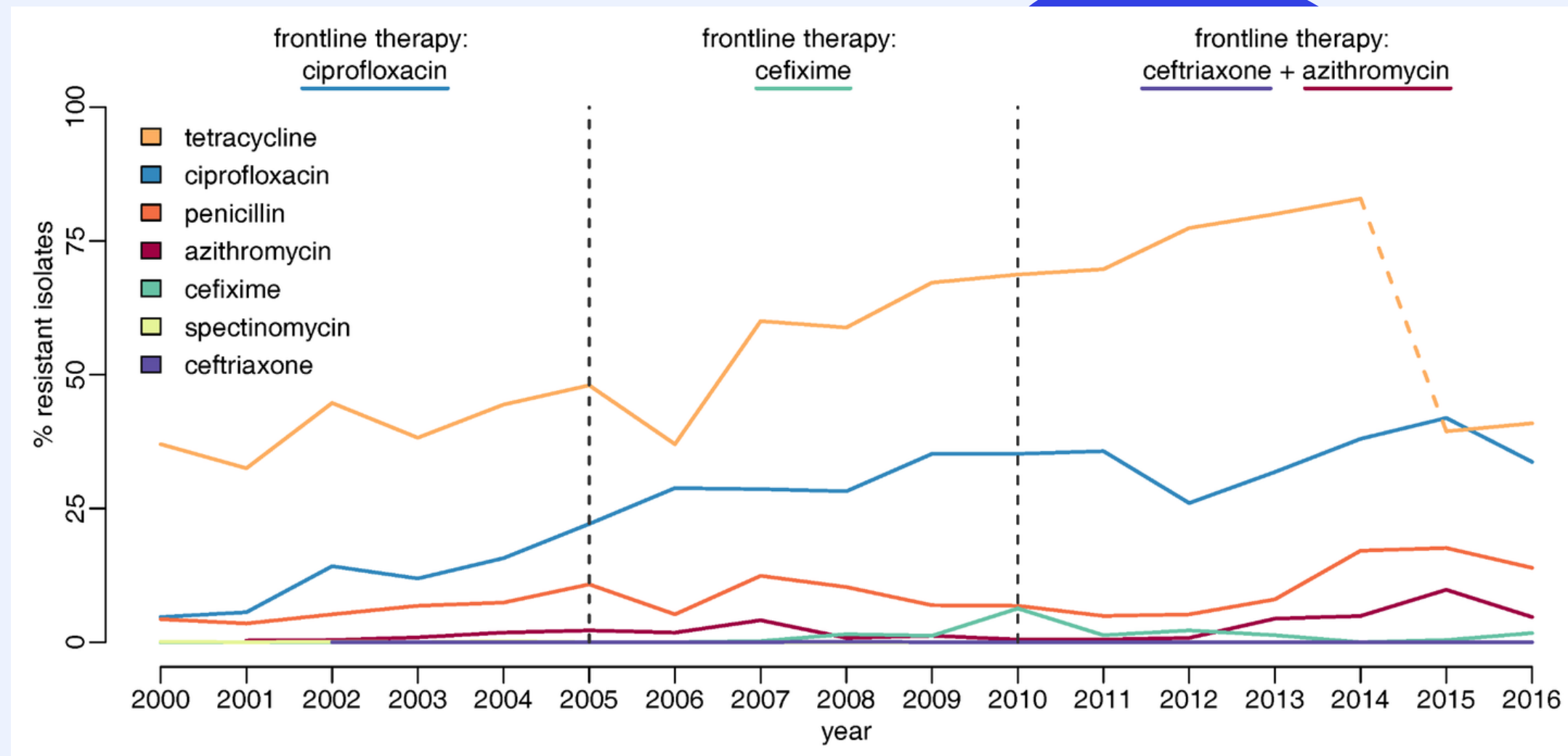
We made it!

The algorithm provides a list of genetic mutations involved in resistance to each drug. This information could help doctors choose the right drug for a patient with TB. We hope experimental biologists will pick up on our results and work out how those genes help neutralize antibiotics.

STEP 3

DESIGNING AND MAINTAINING THE PLATFORM

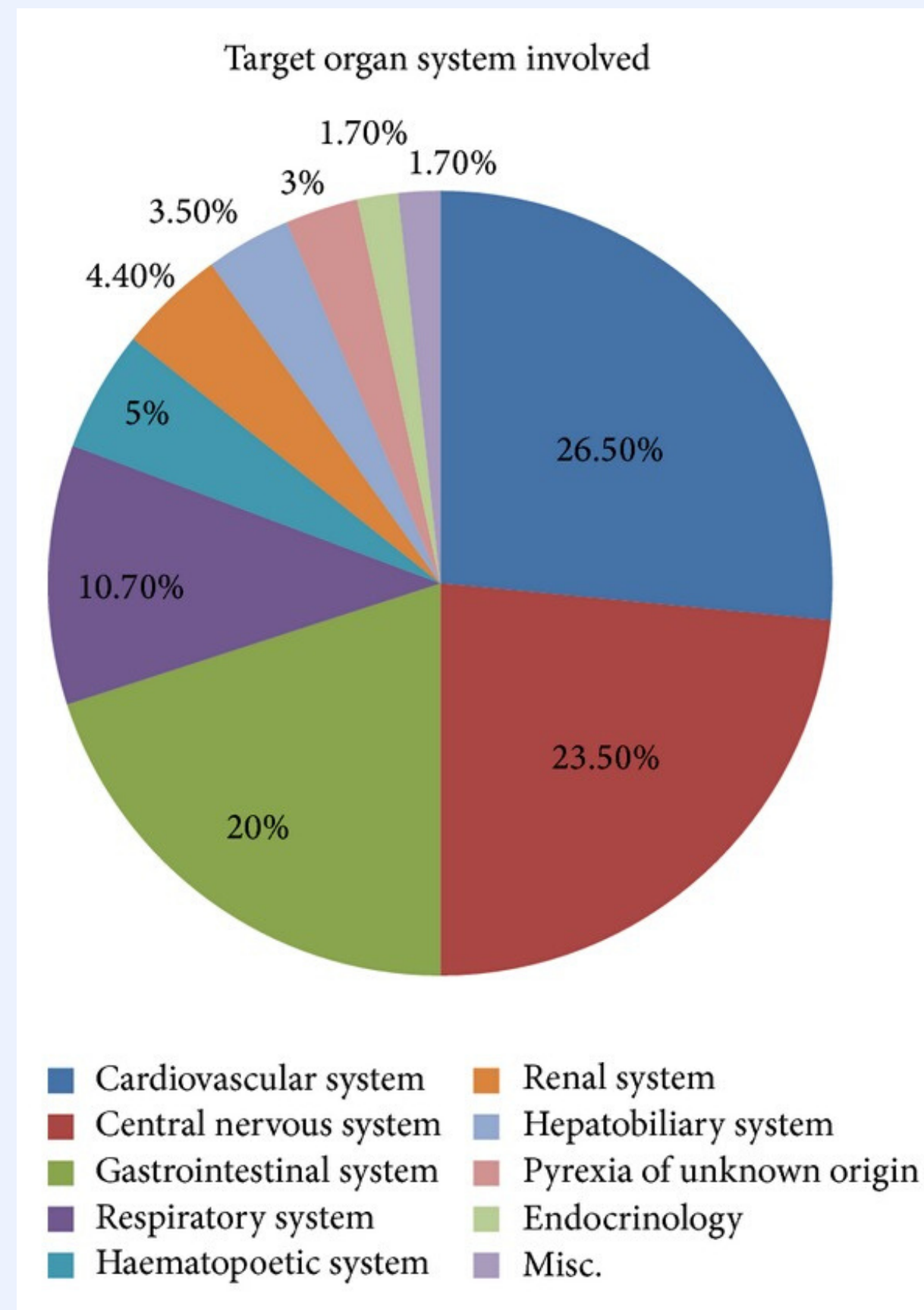India was the largest consumer of antibiotics in 2010 in the world. Evidence suggests that countries with high per-capita antibiotic consumption have higher rates of antibiotic resistance

Traction

Target organ system involved

1.70%
1.70%
3%
3.50%
4.40%
5%
10.70%
26.50%
23.50%
20%

- Cardiovascular system
- Central nervous system
- Gastrointestinal system
- Respiratory system
- Haematopoetic system
- Renal system
- Hepatobiliary system
- Pyrexia of unknown origin
- Endocrinology
- Misc.

Antibiotic consumption in India increased 103% between 2000 and 2015—the highest in low and middle-income countries, according to the study. The average amount of antibiotics consumed by 1,000 inhabitants in India everyday also increased 63% during this period, it showed.

Working of the Platform

✕ Step 1

In the initial stage, we'll have the data fed directly from according to the sources at NCBI.

✕ Step 2

We used IMS Health medicine sales data of antibiotic sales in the retail private sector in India. We thereby determine the ATC/DDD (dosage) index.
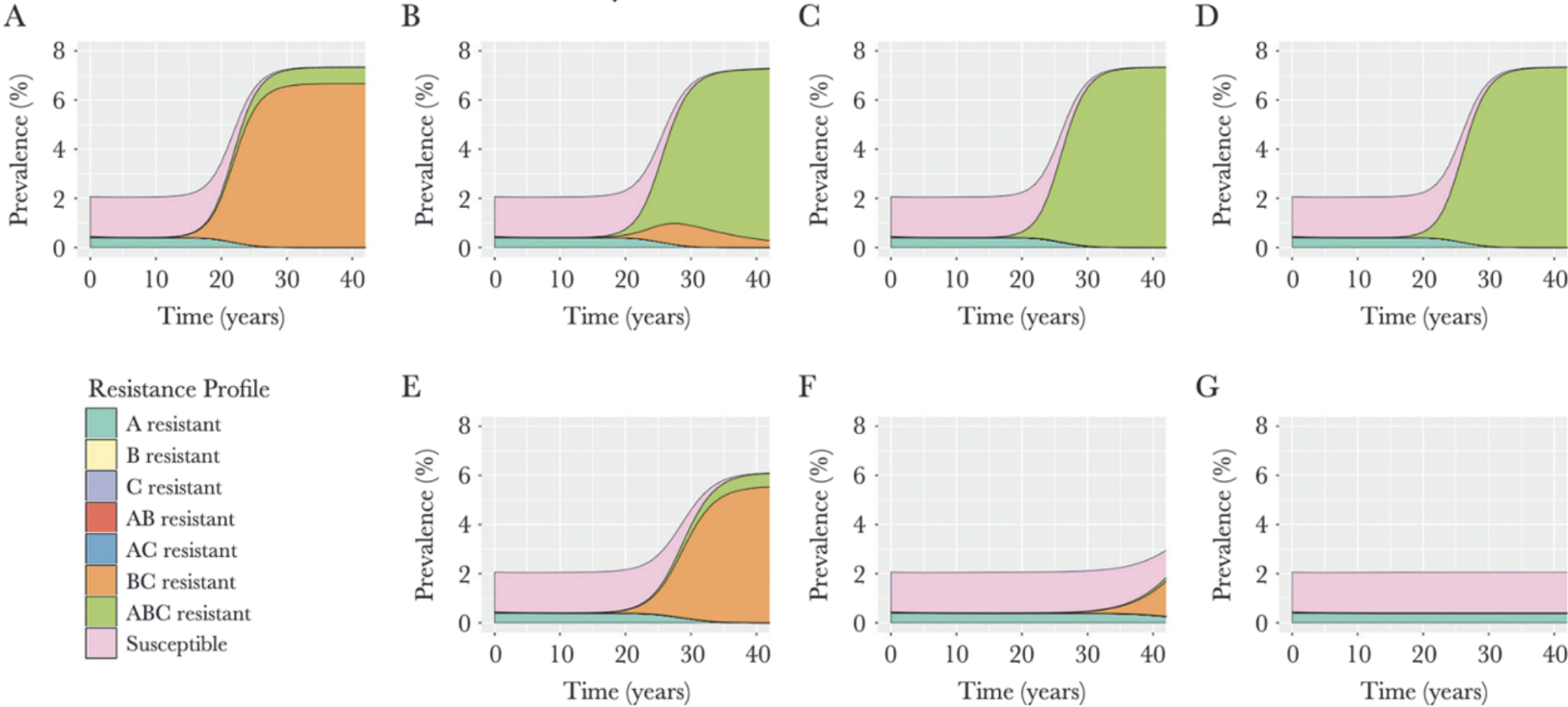
✕ Step 3

The platform would ask the user to register with their age, gender and currently suffering ailments (if any). The interface allows the user to upload data as well, thus the platform works with a crowdfunded approach.

✕ Step 4

Predict and show the overall time for the disease microbe to become resistant to the antibiotic, and suggest measures, replacement drugs.

If no testing is performed, resistance to the treatment rises

If testing for one drug is performed, resistance to all antibiotics rises

If testing for all drugs is performed, resistance is kept at bay

Resistance Profile
- A resistant
- B resistant
- C resistant
- AB resistant
- AC resistant
- BC resistant
- ABC resistant
- Susceptible

A lot of infection-causing microbes grow resistant to the antibiotic drugs, if it is the same drug used continuously. There's growing interest in testing for antibiotic resistance before a patient begins treatment.

The image shows the potential long-term impact of prescribing the right antibiotic the first time.

Implementing the ML Model and utilising the platform

Our predictions help develop policies to improve primary care, highlighting the relevance of physician expertise, policy implementation, and drug dosage pattern monitoring.
We find that our model can reduce antibiotic use by about 7.5 percent!

Tech Stack Used

Python, Web Server, Django, Scikit, Matplotlib, NumPy, Tensorflow, Pandas, Deep Learning Models, Logistic Regression with Elastic Net, XGBoost, Support Vector Machine, Random Forest, Flutter, MEAN/MERN Stack

Use cases of the model

PRETTY NEAT!

Drug Effectiveness Prediction: Using ML, we can predict the effectiveness of the antibiotic easily.

Patient Health Monitoring: Tt can continually be used to monitor the overall health of the patient.

Lowering the mortality rate in the country: Antimicrobial Stewardship would help in the large-scale reduction of deaths related to antibiotic resistance.

Our Dependencies

The entropy model that we use here is an elastic model, the drawback of this model is that when parent class inherits child class, the VM model's elasticity will increase. So, for further improvisations to this approach, we can go for Deep Learning approaches on Artificial Neural Networks instead.
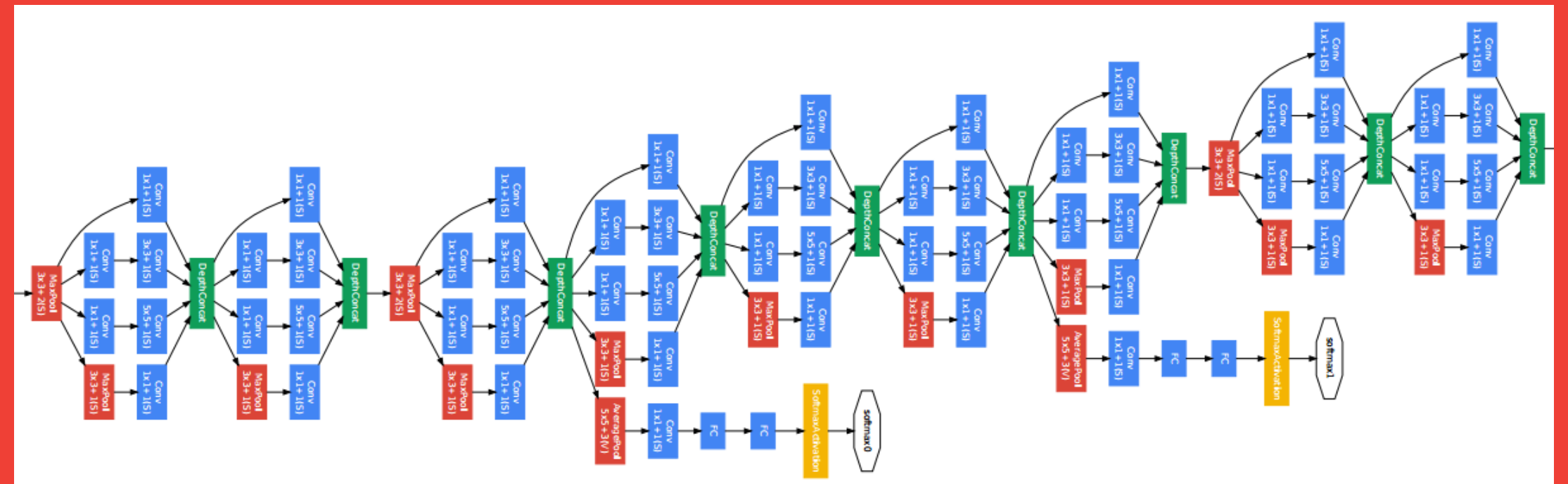
If by any means we are able to incorporate a Multilayer Perceptron Model with ANN at the presence of a huge dataset, the accuracy of the model will increase amazingly.

THANK YOU