RES-112

Artificial Intelligence Prediction of Antibiotic Susceptibility Using Machine Learning Techniques to Aid Empirical Antibiotic Therapy Decisions in France

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Background The objective of this study is to develop and evaluate machine learning (ML) techniques to predict bacterial resistance to specific antibiotics, based on bacterial identification, infection site, and patient demographic data. This approach aims to assist clinicians in selecting appropriate empirical antibiotic therapy, thereby improving treatment decisions and promoting the rational use of antibiotics to help reduce the impact of misuse on antimicrobial resistance.

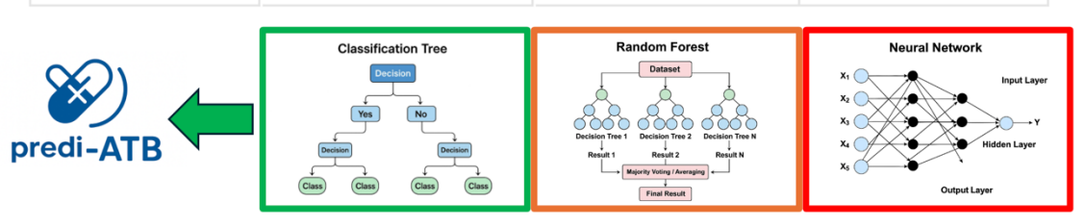
Methods

Based on 95,775 antibiograms, a total of 23,632 machine learning (ML) models including decision trees, random forests, and neural networks were developed to predict antibiotic susceptibility for 471 bacterial species and 66 antibiotics.

The models were trained using microbiology laboratory data, including patient demographics, culture results, and susceptibility profiles, without relying on clinical data. Model performance was evaluated using the Area Under the Curve (AUC) metric.

Figure 1 : **Comparison of AI Models**

Criteria	*Classification Tree*	*Random Forest*	*Neural Network*
Interpretability	++++	++	+
Performance	++	+++	+++
Robustness	++	+++	+++
Complexity	+	++	++++



The **choice of a classification tree model** is natural, as its performance is comparable to or equal to that of Random Forest or Neural Networks, while being less complex and **more interpretable**, making it well-suited for medical applications.

Predi-ATB V11.4.1

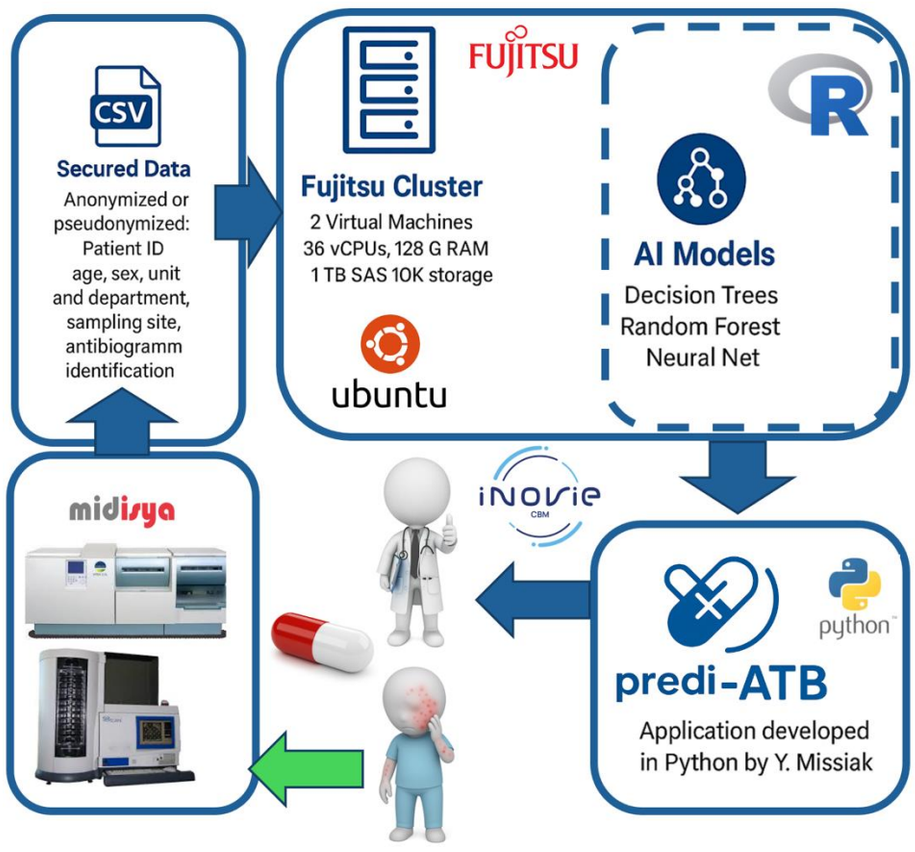


Figure 2 : **Example of AUC for classification tree prediction**

P.AERUGINOSA	AUC	n
MEROPENEME	0.98	2553
AMIKACINE	0.98	2901
COLISTINE	0.97	2547
TOBRAMYCINE	0.96	2905
AZTREONAM	0.93	2792
IMIPENEME	0.92	2894
CEFEPIME	0.92	2900
CEFTAZIDIME	0.90	2904
CIPROFLOXACINE	0.89	2902
PIPERA.TAZO	0.87	2884
CEFTRIAXONE	0.00	2875
ERTAPENEME	0.00	2905
COTRIMOXAZOLE	0.00	385

E.COLI	AUC	n
AZTREONAM	1.00	17211
MEROPENEME	1.00	47009
IMIPENEME	1.00	19096
ERTAPENEME	1.00	48029
FURANES	1.00	48019
AMIKACINE	0.99	48037
FOSFOMYCINE	0.98	44473
CEFOXITINE	0.98	47841
CEFEPIME	0.98	46421
CEFOTAXIME	0.97	13572
CEFTAZIDIME	0.97	47971
CEFTRIAXONE	0.96	47585
LEVOFLOXACINE	0.91	46061
CIPROFLOXACINE	0.90	48046
PIPERA.TAZO	0.87	44271

S.AUREUS	AUC	n
FURANES	1.00	5956
MINOCYCLINE	1.00	5733
TEICOPLANINE	1.00	5954
VANCOMYCINE	1.00	5920
TIGECYCLINE	1.00	5732
LINEZOLIDE	1.00	5947
PRISTINAMYCINE	1.00	5951
DAPTOMYCINE	1.00	4942
RIFAMPICINE	1.00	5954
OXA.CLOXA	0.89	5956
LEVOFLOXACINE	0.88	4950
CIPROFLOXACINE	0.82	5906

Results

The ML model accurately predicts antibiotic susceptibility across key pathogens.

For *E.coli*, predictions are influenced by sample type, clinical service, age, and sex.

S.aureus shows >99.9% accuracy for key antibiotics (vancomycin, daptomycin, linezolid) and >87% for methicillin resistance.

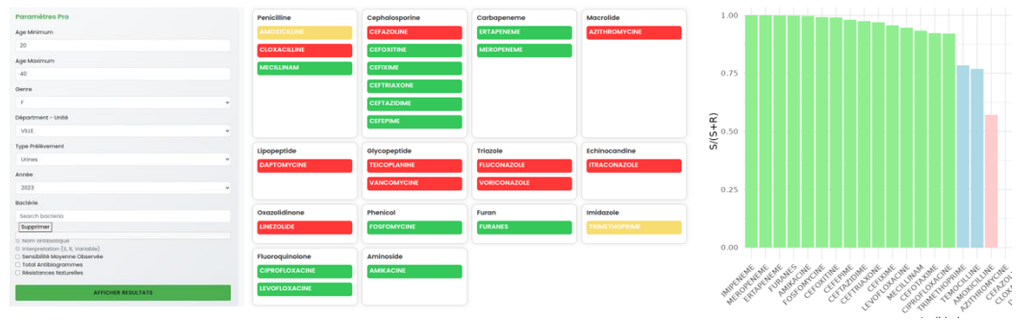
P.aeruginosa predictions exceed 85%, outperforming antibiogram timing.

S.agalactiae and *E.faecalis* show >99.9% accuracy, including cystitis treatment in women with amoxicilline or furadantine.

Conclusion

This study demonstrates the potential of ML to predict antibiotic susceptibility using only microbiological and demographic data. The approach is especially valuable in resource-limited settings. Decision tree models offer interpretable and accurate predictions, supporting better empirical antibiotic choices and enabling rapid treatment reassessment, even before or without antibiogram results.

Figure 3: **Api Web Application predi-ATB (UI Client, Data Server)**



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Data Privacy Method:
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Conflict of interests:
No conflict of interest