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Background Prompt and targeted management of bacteremia is critical to improving outcomes in patients with sepsis. This study evaluates an artificial intelligence (AI) module for predicting antibiotic susceptibility of pathogens isolated from adult blood cultures—excluding coagulase-negative staphylococci (CoNS)—in private healthcare facilities in the Occitanie region, France.

Methods

AI Tools: **Predi-ATB V11.4.1**, an AI tool, was used to predict susceptibility to 12 commonly used antibiotics based on bacterial species, sample type, patient sex, age, and origin (community, hospital, nursing home, dialysis, etc.).

A total of 890 antibiograms from **adult blood cultures**—excluding coagulase-negative staphylococci (CoNS)—in **private healthcare facilities** in the Occitanie region of France.

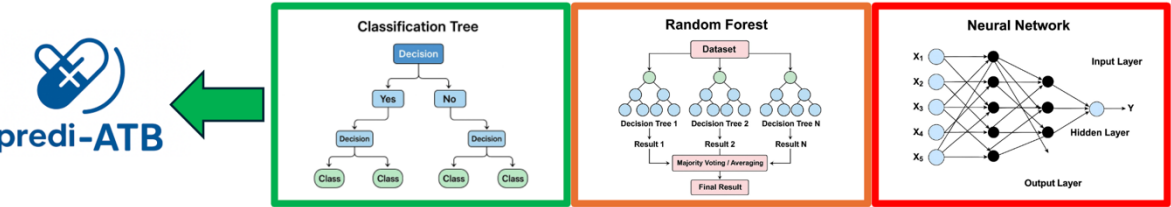
12 commonly used antibiotics for empirical or follow-up treatment: amoxicillin (AMOX) , piperacillin-tazobactam (TAZO), ceftriaxone (CEFTRI), cefepime (CEFEP), meropenem (MERO), gentamicin (GENTA), amikacin (AMIK), ciprofloxacin (CIPRO), levofloxacin (LEVO), daptomycin (DAPTO), vancomycin (VANCO), and cotrimoxazole (COTRIMO).

Pathogens : **Gram-negative bacilli (GNB):** *Escherichia coli* (n = 351), *Klebsiella pneumoniae* (n = 103), *Enterobacter spp.* (n = 37), *Klebsiella oxytoca* (n = 34), *Pseudomonas aeruginosa* (n = 61). **Gram-positive cocci (GPC):** *Staphylococcus aureus* (n = 172), *Enterococcus faecalis* (n = 102), *Enterococcus faecium* (n = 30)

Comparison of AI Models

Figure 1 : Predi-ATB V11.4.1 --> Classification tree vs Random Forest and Neural Net

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



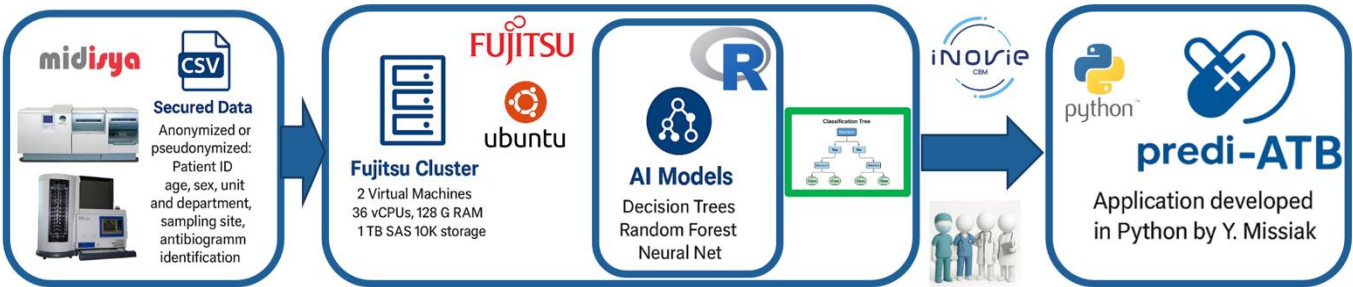
The **choice of a classification tree model** is natural, as its performance is comparable to or equal to that of Random Forest or Neural Networks, while being less complex and **more interpretable**, making it well-suited for medical applications.

Figure 2 : Classification tree prédiction Predi-ATB V11.4.1

N = 890	GNB	AMOX	TAZO	CEFTRI	CEFEP	MERO	AMIK	GENTA	CIPRO	LEVO	COTRIMO	VANCO	DAPTO
351	ECO	0,547	0,926	0,997	0,990	1	0,977	0,971	0,906	0,901	0,766	0	0
103	KP	0	0,893	1	0,949	1	0,971	0,861	0,748	0,764	0,767	0	0
61	PA	0	0,724	0	0,810	0,922	0,966		0,839	0,759	0	0	0
37	ENTB	0	0,583	0,568	0,703	1	0,919		0,757	0	0,784	0	0
34	KOX	0	0,853	1	0,967	1	1	0,941	0,882	0,906	0,882	0	0
	GPC	AMOX	TAZO	CEFTRI	CEFEP	MERO	AMIK	GENTA	CIPRO	LEVO	COTRIMO	VANCO	DAPTO
172	SAU	0,115	0,860	0,865	0,864	0,860	0,953	0,994	0,767	0,821	0,983	1	1
102	EFCA	1	1	0	0	1		0,909		0,950	0,931	1	1
30	EFCI	0,267	0,185	0	0	0,185		0,483		0,500	0,733	0,967	1

Results

A therapeutic option with predicted susceptibility >99% was always available. Meropenem showed the highest overall coverage (93.9%), especially when *E. faecalis* was considered susceptible. Among Gram-negative bacilli, cefepime (95.9%) outperformed ceftriaxone (86.7%) and piperacillin-tazobactam (89.7%), but remained less effective than meropenem (>99.9%), particularly against *P. aeruginosa* and *Enterobacter spp.*. No Gram-positive cocci were resistant to daptomycin; only one *E. faecium* isolate was resistant to vancomycin. The combination of carbapenem + daptomycin covered >99.9% of isolates, compared to 93.2% for piperacillin-tazobactam + daptomycin.



Conclusion

AI-based predictions aligned with current guidelines for severe infections and highlighted the potential for early optimization of empirical therapy. They also underscore the need for nuanced reassessment in cases involving *P. aeruginosa* and *E. faecium*. Integrating clinical data could further enhance personalized treatment strategies.

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