

L'IA peut elle prédire l'antibiorésistance?

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**Groupe
Infectiologie
Digit@le**

Conflit d'intérêt



Open AI



Plan

Objectives: learn AI for collaboration with AI project

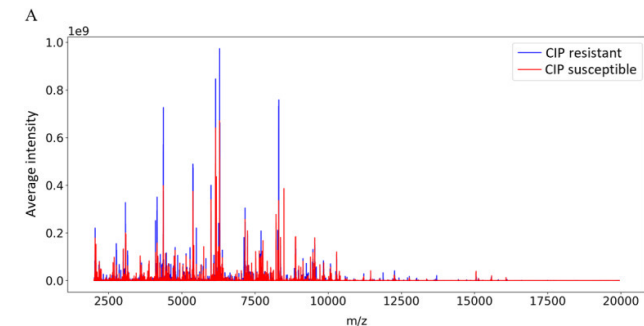
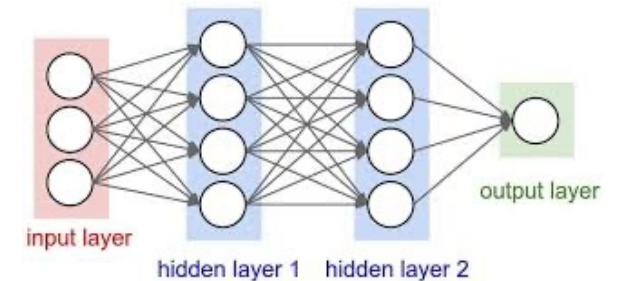
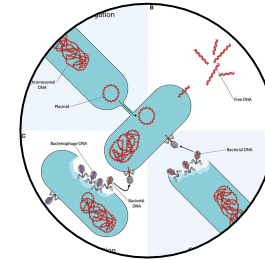
1. Antibioresistance:

- Mécanismes
- Déterminants
- Perspectives

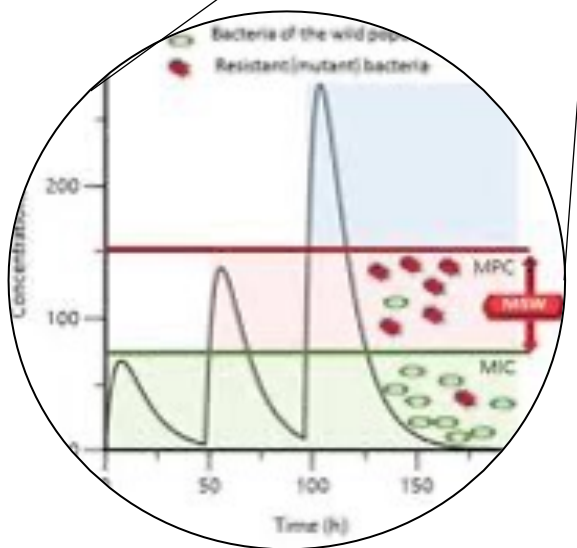
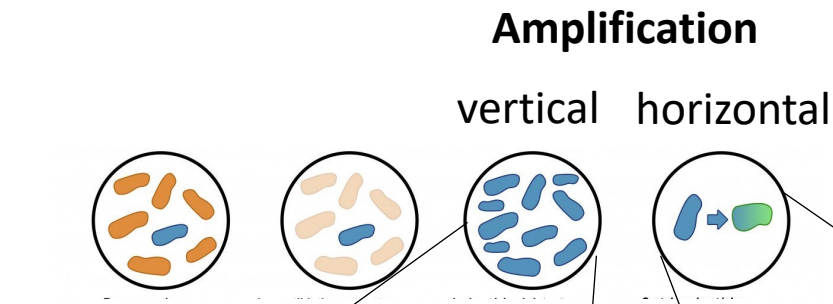
2. Intelligence artificielle

- Système expert vs Machine learning
- Machine learning traditionnel et deep learning
- Metrics

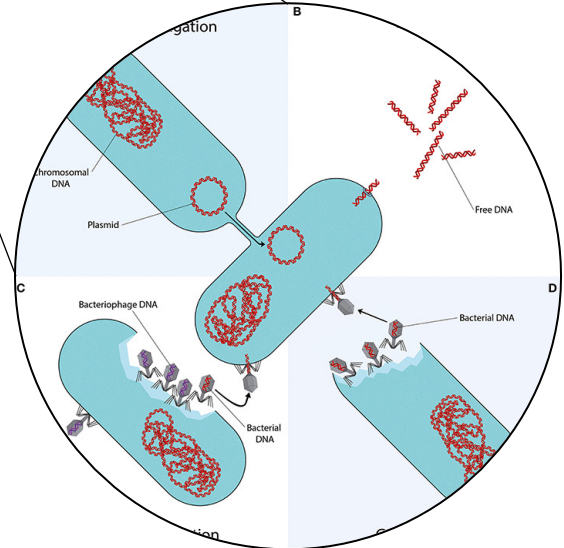
3. 4 exemples d'utilisation de l'IA pour prédiction de l'antibiorésistance



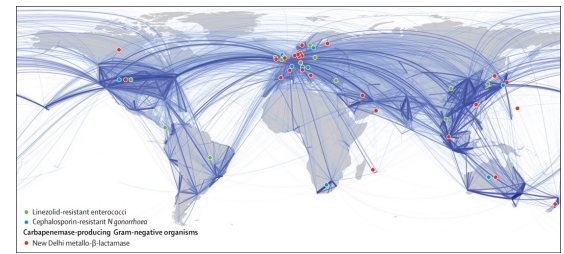
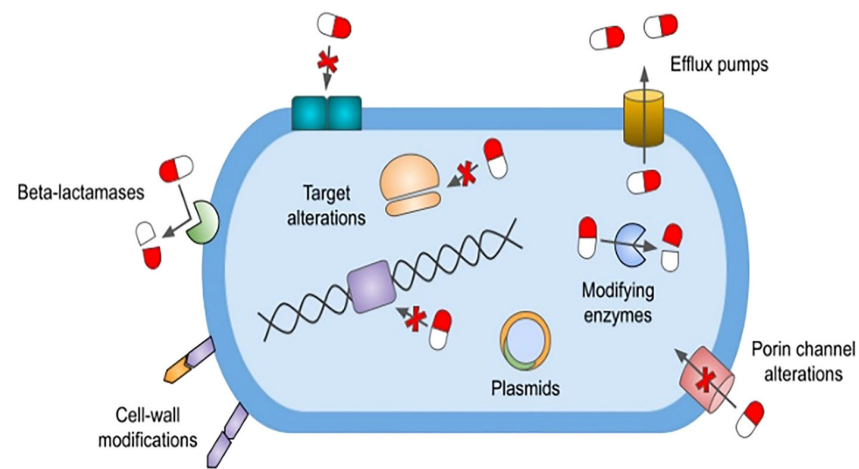
Mécanismes de l'antibiorésistance



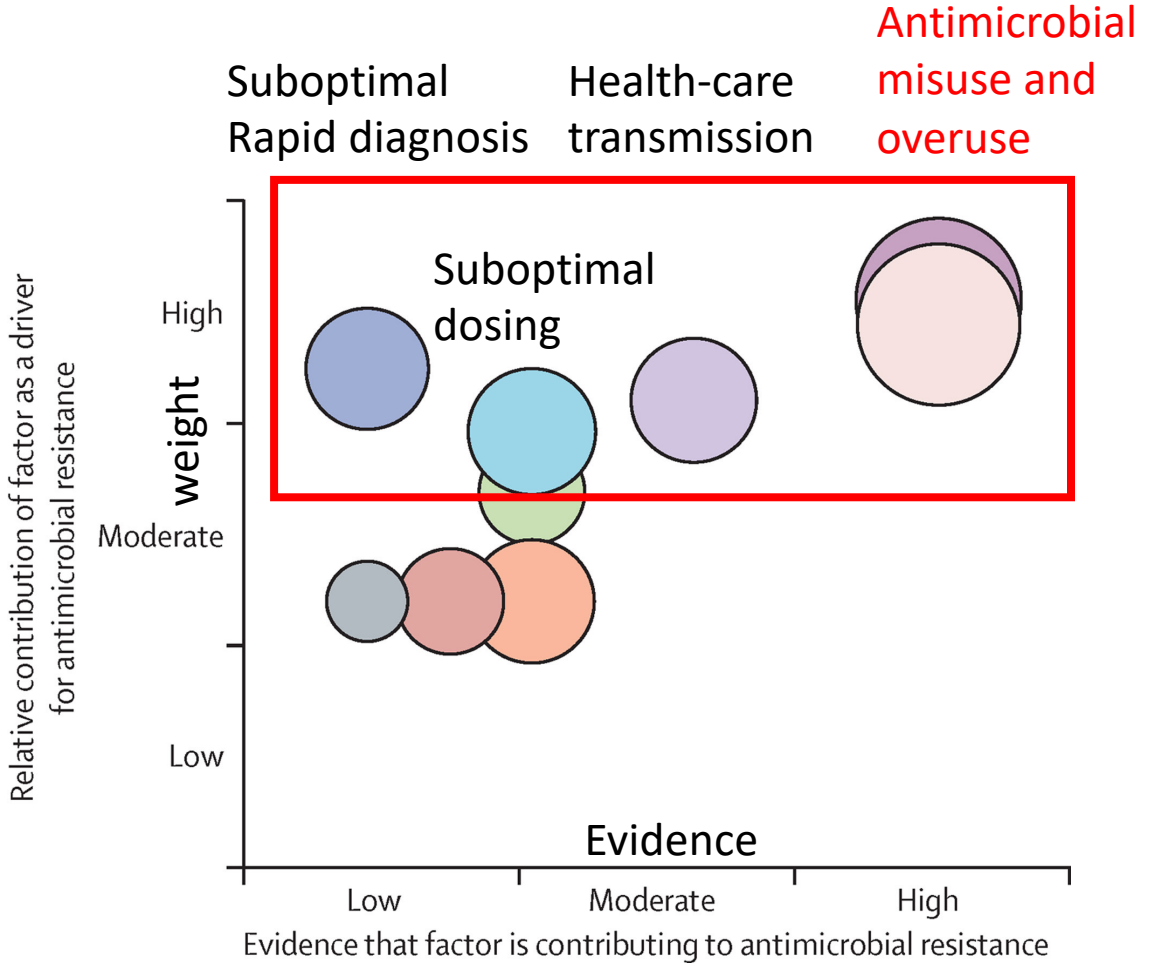
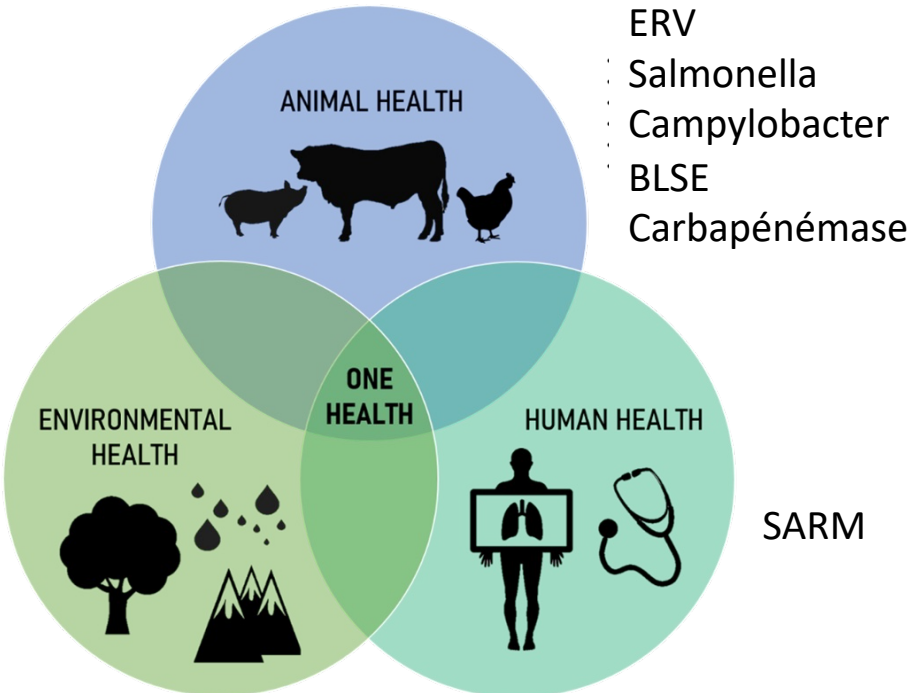
Mutant selective windows



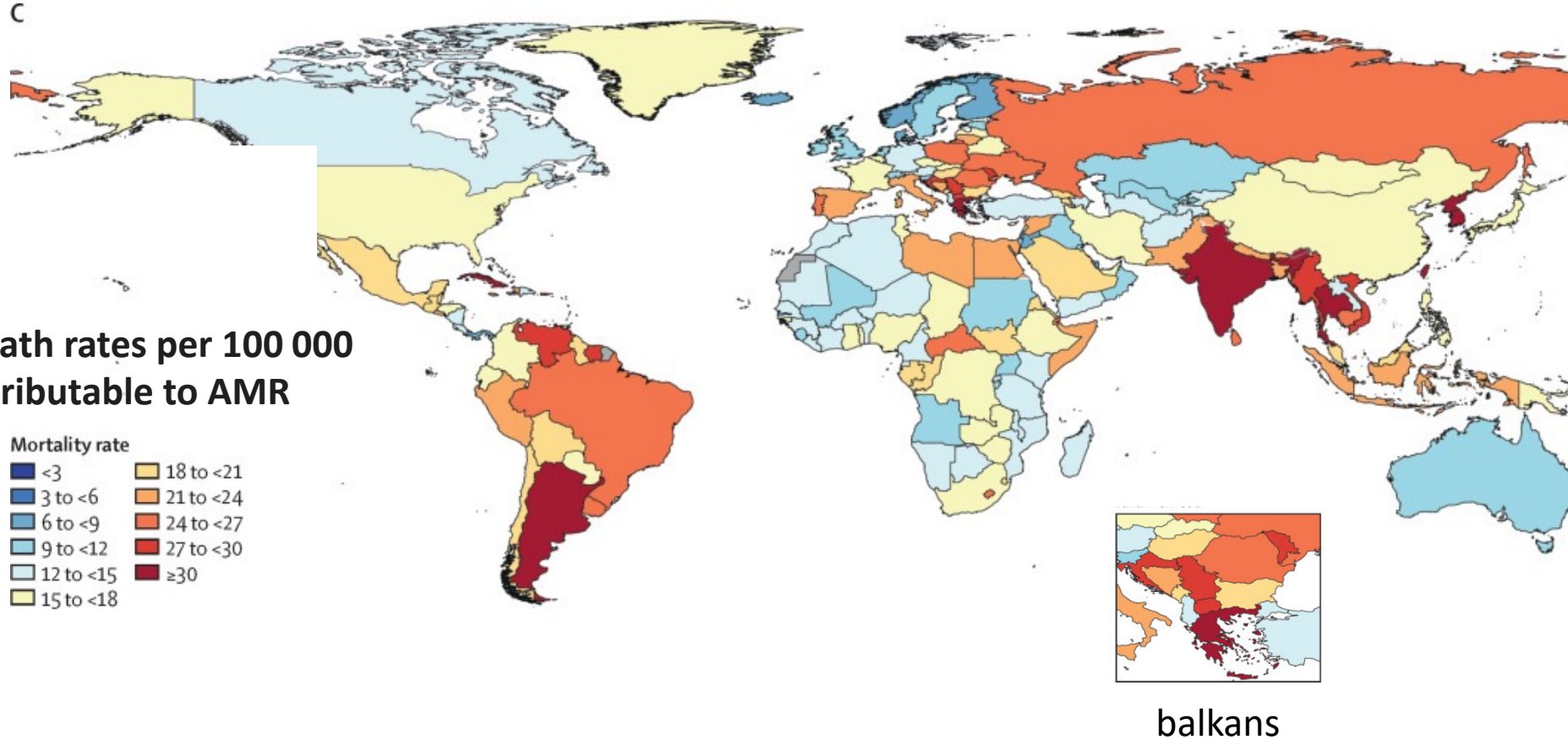
Horizontal gene transfer



Déterminants de l'antibiorésistance



92 millions de morts évitables d'ici 2050



Critical group



Enterobacterales
carbapenem-resistant



Enterobacterales
third-generation
cephalosporin-resistant



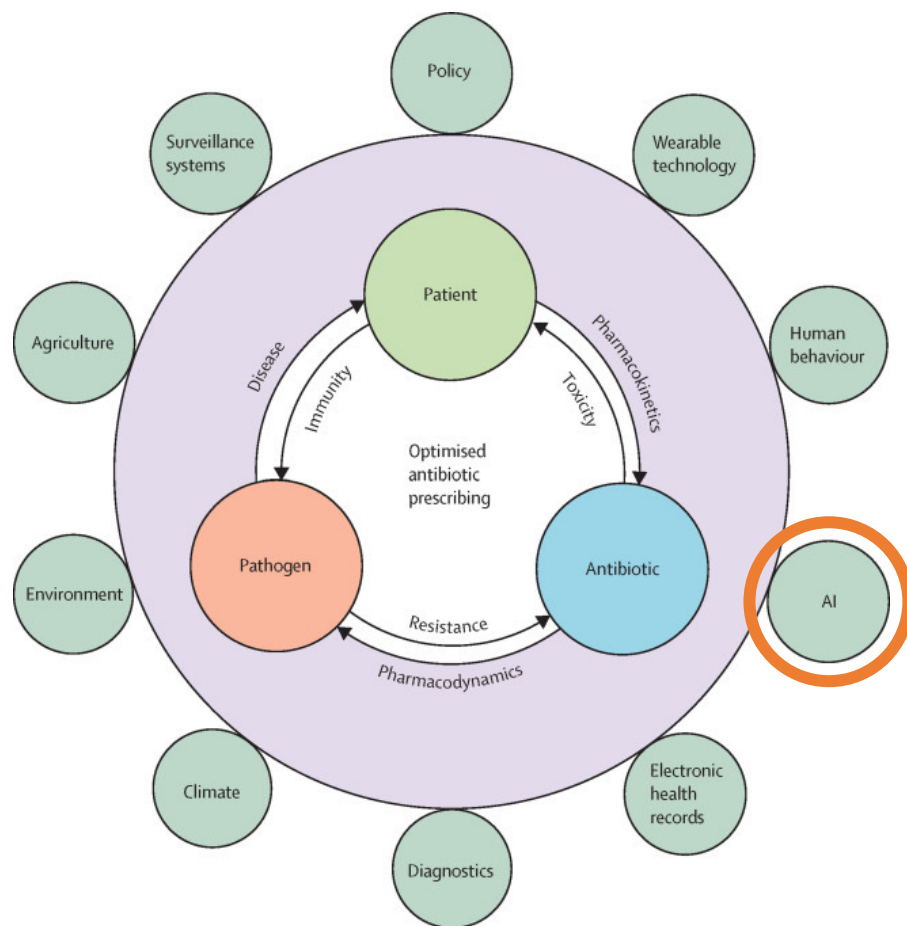
*Acinetobacter
baumannii*
carbapenem-resistant



*Mycobacterium
tuberculosis*,
rifampicin-resistant^a

^aRR-TB was included after an independent analysis with parallel criteria and subsequent application of an adapted MCDA matrix.

L'IA pour lutter contre l'antibiorésistance?



Drug discovery

Accelerating antimicrobial peptide design: Leveraging deep learning for rapid discovery

Ahmad M Al-Omari ¹, Yazan H Akkam ², Ala'a Zyout ¹, Shayma'a Younis ¹, Shefa M Tawalbeh ¹, Khaled Al-Sawalmeh ³, Amjed Al Fahoum ¹, Jonathan Arnold ⁴

Aide à prescription

> Clin Infect Dis. 2024 Apr 10;78(4):825-832. doi: 10.1093/cid/ciad632.

Can Chatbot Artificial Intelligence Replace Infectious Diseases Physicians in the Management of Bloodstream Infections? A Prospective Cohort Study

Alexis Maillard ¹, Giulia Micheli ^{1 2}, Leila Lefevre ¹, Cécile Guyonnet ^{3 4}, Claire Poyart ^{3 4}, Etienne Canoui ¹, Martin Belan ^{1 5}, Caroline Charlier ^{1 5 6 7}

Chatbot

> Nature. 2024 Jan;625(7996):643-644. doi: 10.1038/d41586-024-00099-4.

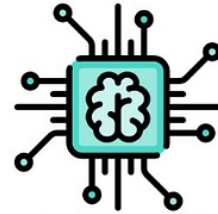
Google AI has better bedside manner than human doctors – and makes better diagnoses

Mariana Lenharo

PMID: 38216763 DOI: 10.1038/d41586-024-00099-4

Using digital health technologies to optimise antimicrobial use globally. The lancet digital health 2024

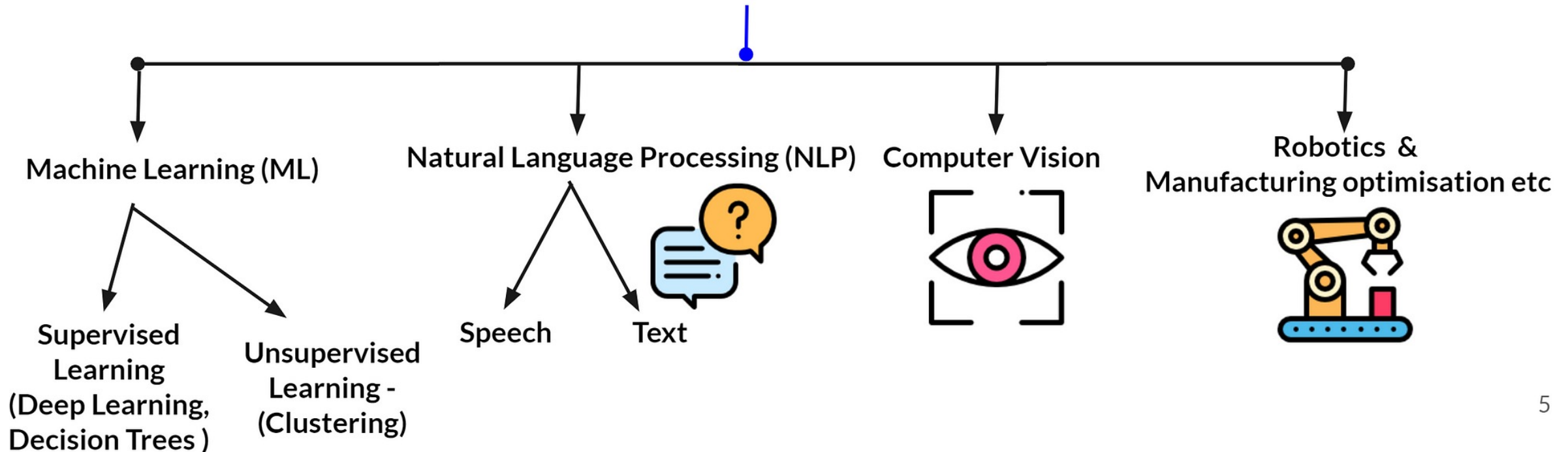
Artificial Intelligence (AI)



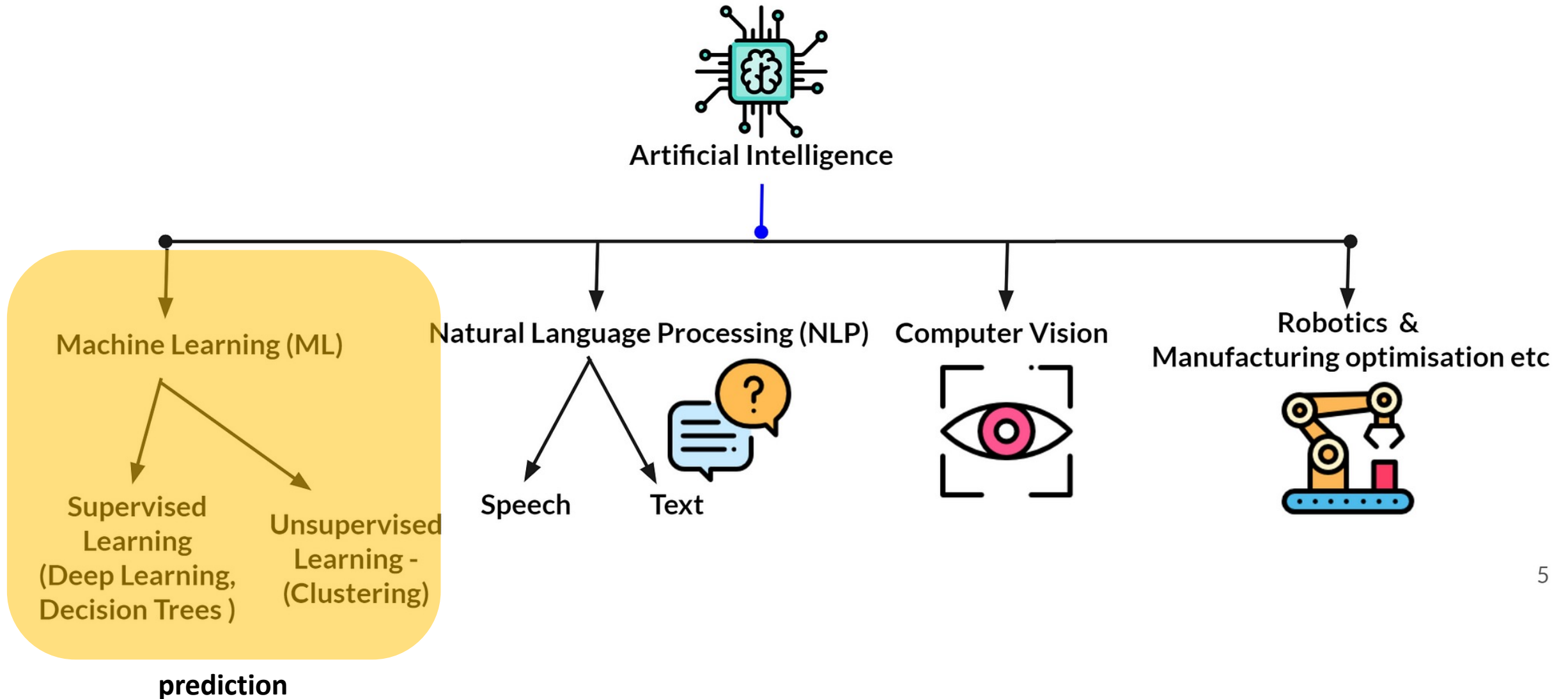
Artificial Intelligence

IA = branch of computer science that aims to create systems capable of performing tasks that typically require human intelligence »

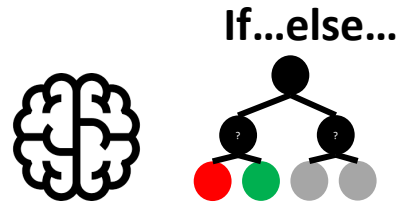
Applications : problem-solving, decision-making, perception, understanding natural language...



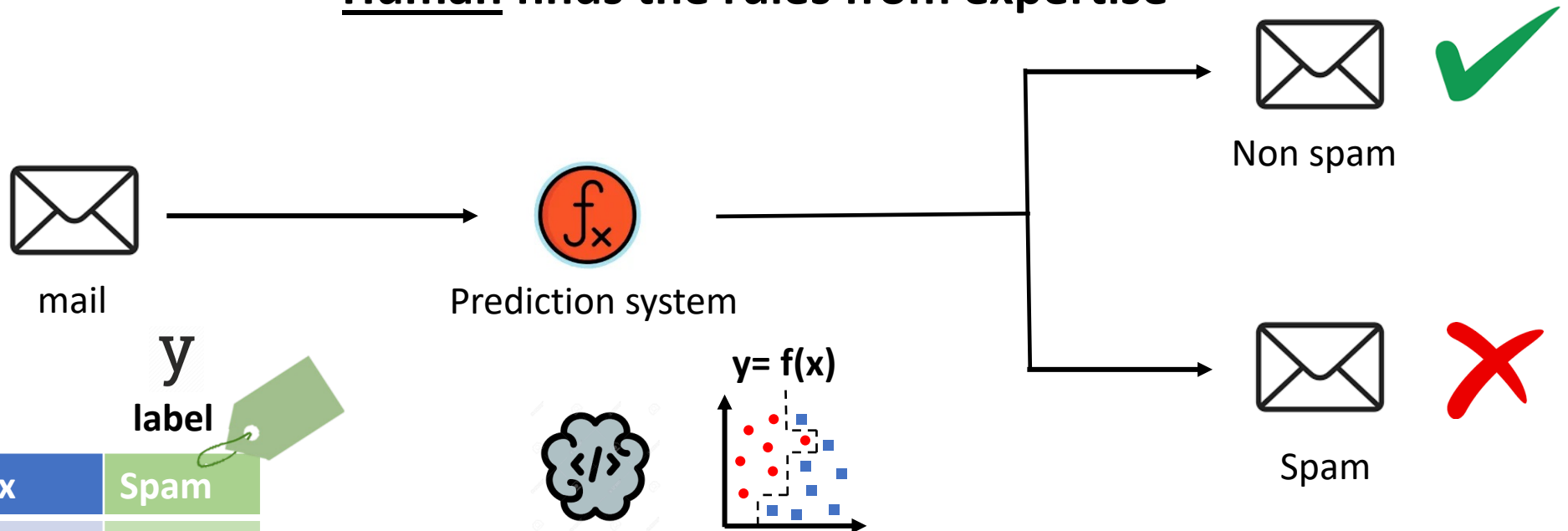
Artificial Intelligence (AI)



Expert system \neq Machine Learning



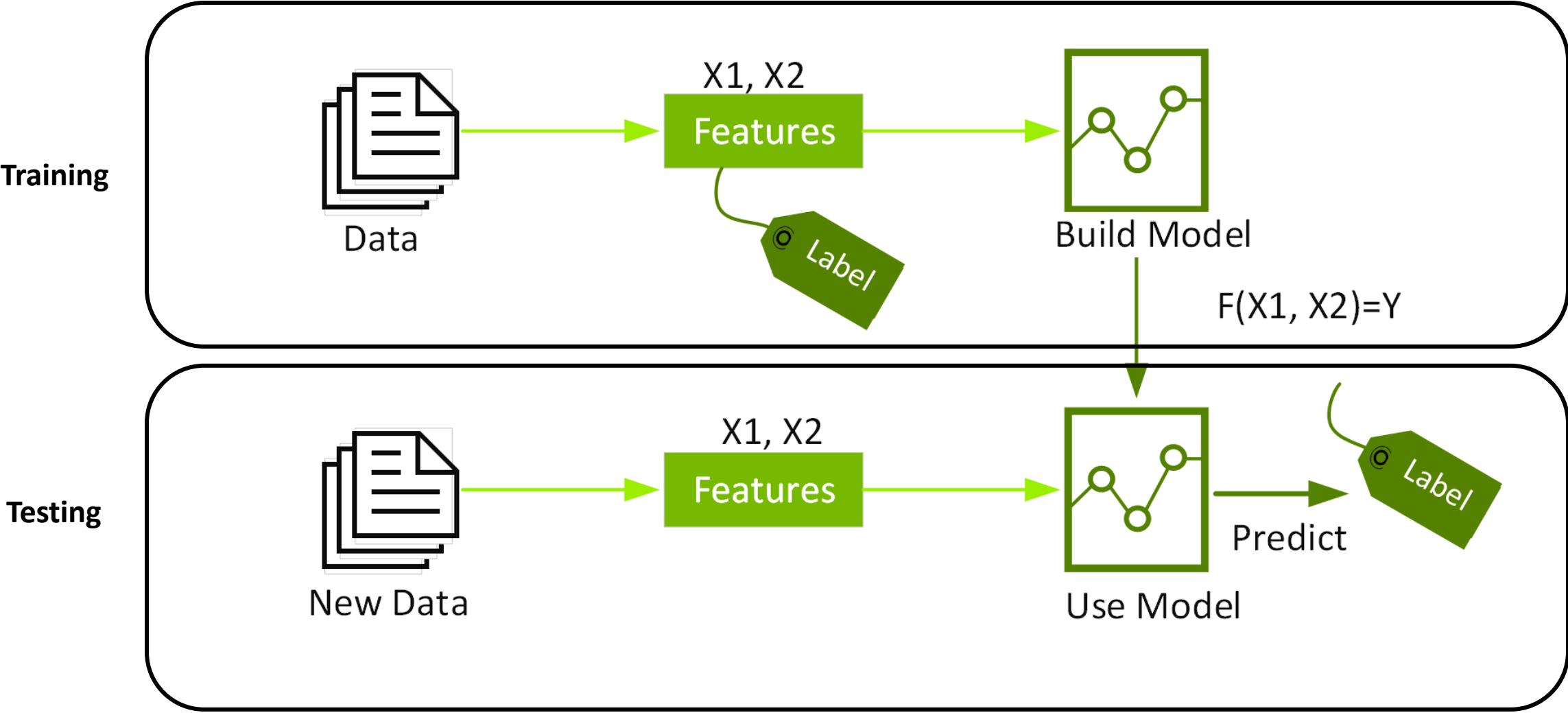
Human finds the rules from expertise



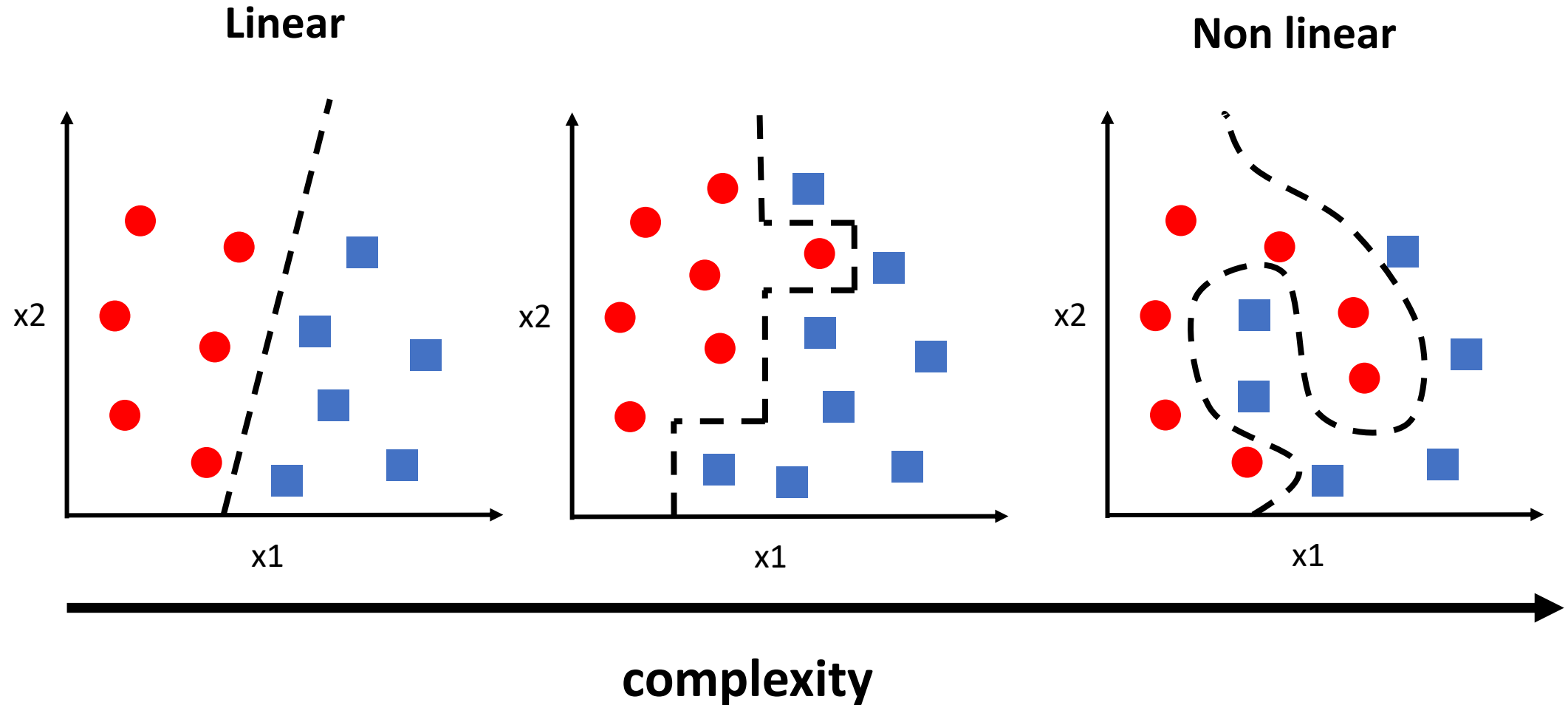
Machine Learn pattern from data

x features			y label
sender	ortho	sex	Spam
1	1	1	yes
0	0	0	no
1	0	1	yes

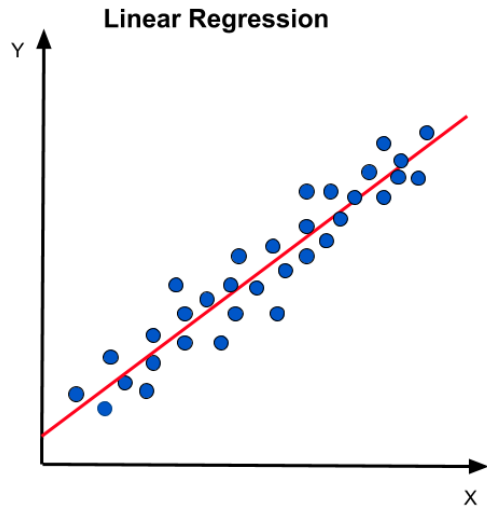
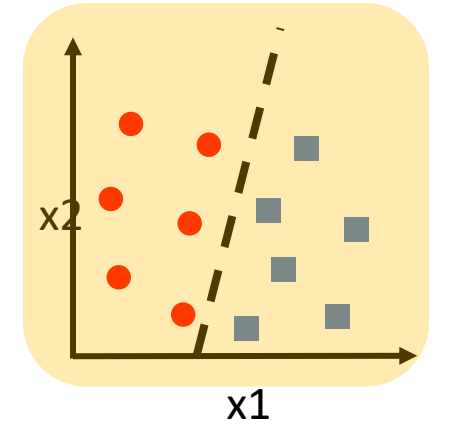
Machine learning: Training then Testing



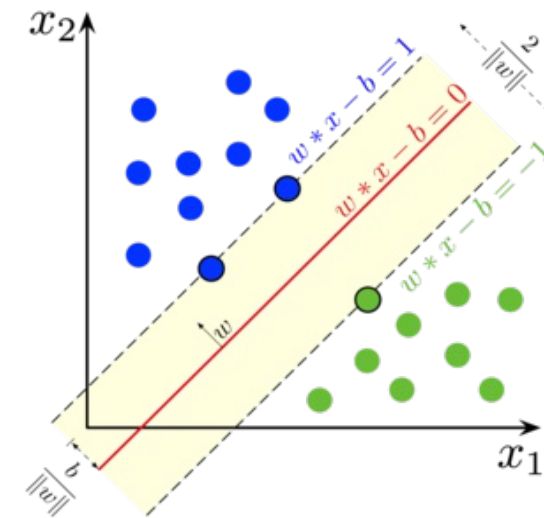
Prediction= finding a mathematical pattern



Traditional ML: linear algorithms

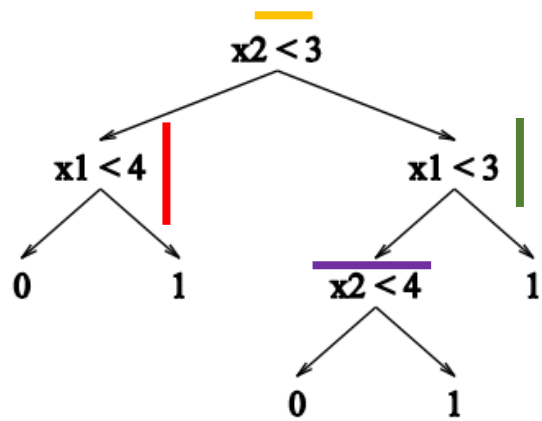


Linear/logistic regression

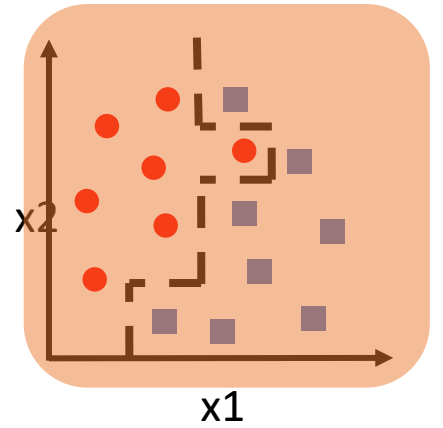
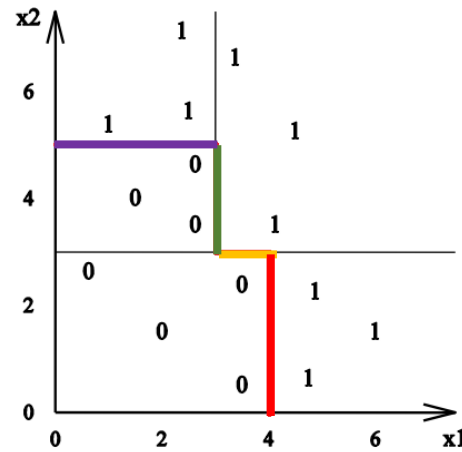


Support Vector Machine
SVM

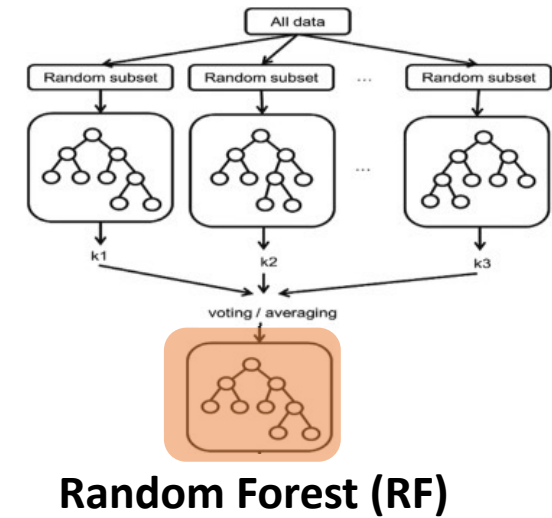
Traditionnall ML: Decision Tree



Decision tree

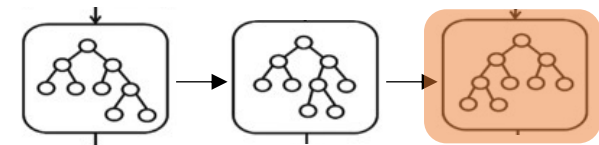


μ



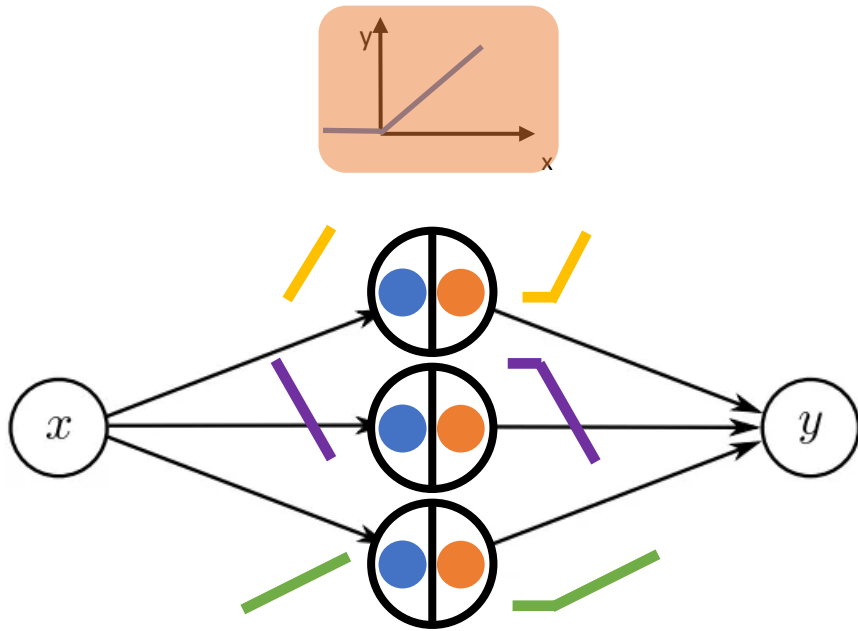
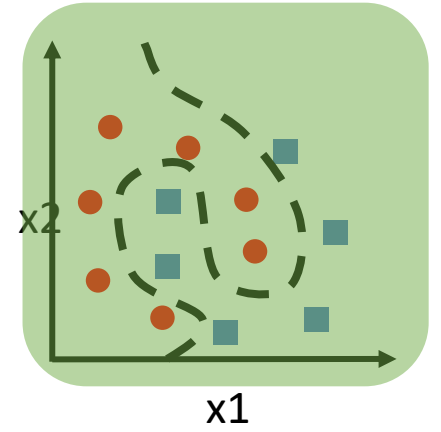
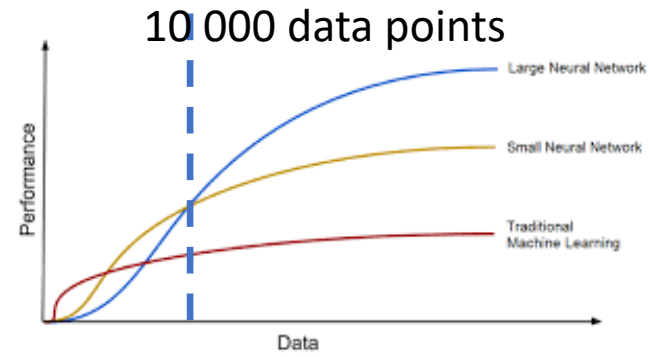
Random Forest (RF)

\nearrow

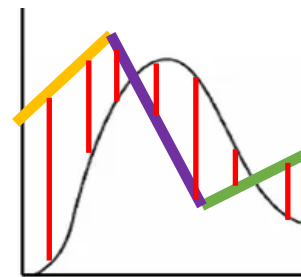


eXtrem Gradient Boosting (XGBoost)

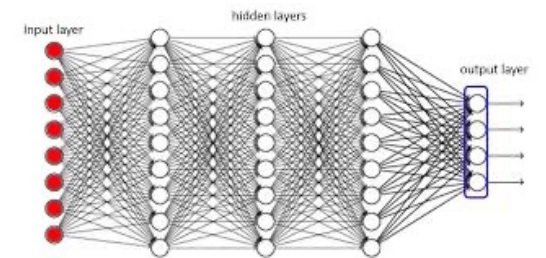
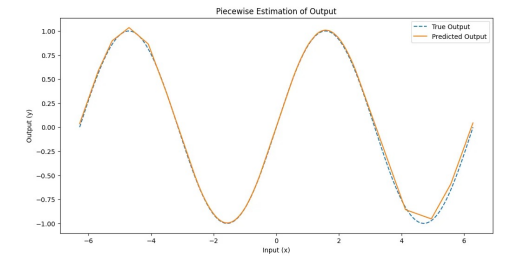
Deep Learning



Neural network



truth
prediction
errors



Large Language Model: « stochastic parrots »

User prompt

« Un, deux, trois ... »

System prompt= context

« tu es un mathématicien... »



LLM

« quatre, cinq, six »

P= 0.8


« partez! »

P= 0.15

« Soleil! »

P= 0.05

Comparing ML algo: Metrics

 Truth

	Resistant (+)	Sensible (-)
Predicton		
R (+)	True Positive	False positive
S (-)	False negative	True Negative

“How reliable is a positive/negative result?”

• **PPV (Precision)**

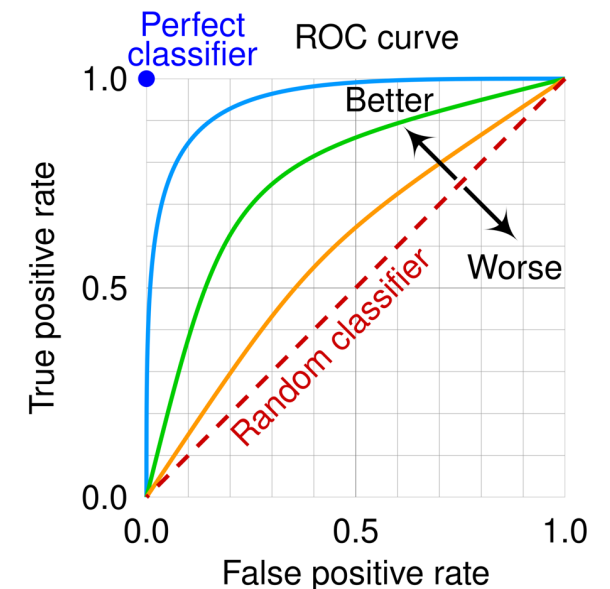
• **NPV**

• **Sensitivity(Recall):** • **Specificity**

• **Accuracy:** “overall prediction?”

• **F1 Score (harmonic mean of precision & recall):** >0.8: good

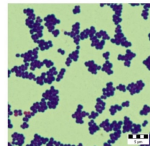
“balance resistant cases and false alarms?”



AMR prediction: 4 examples



<1d



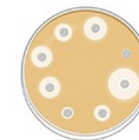
<5d



<1d

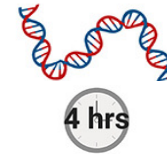


<48h

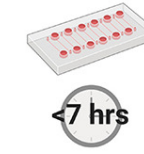


#4 AST

GeneXpert, BioFire
Betalactatest



Vitek, phoenix



Données épidémioclinico-bio

Liquide biologique

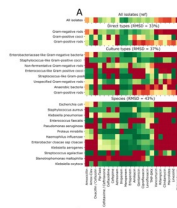
Examen direct

Cultures

Identification

Antibiogramme

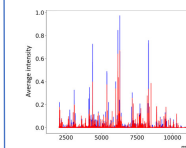
#1: Epidemio



#2 Imaging



#3 Maldi-TOF



Genomic surveillance

BK
acinetobacter
...

ML article reading guidelines

$$\mathbf{y} = \mathbf{f}(\mathbf{x})$$

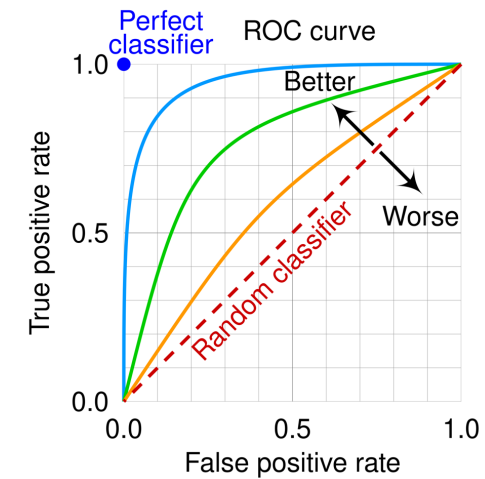
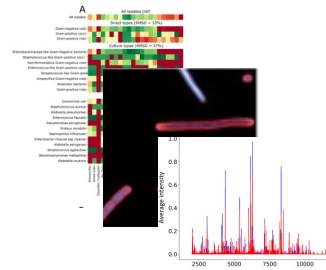
label = Features



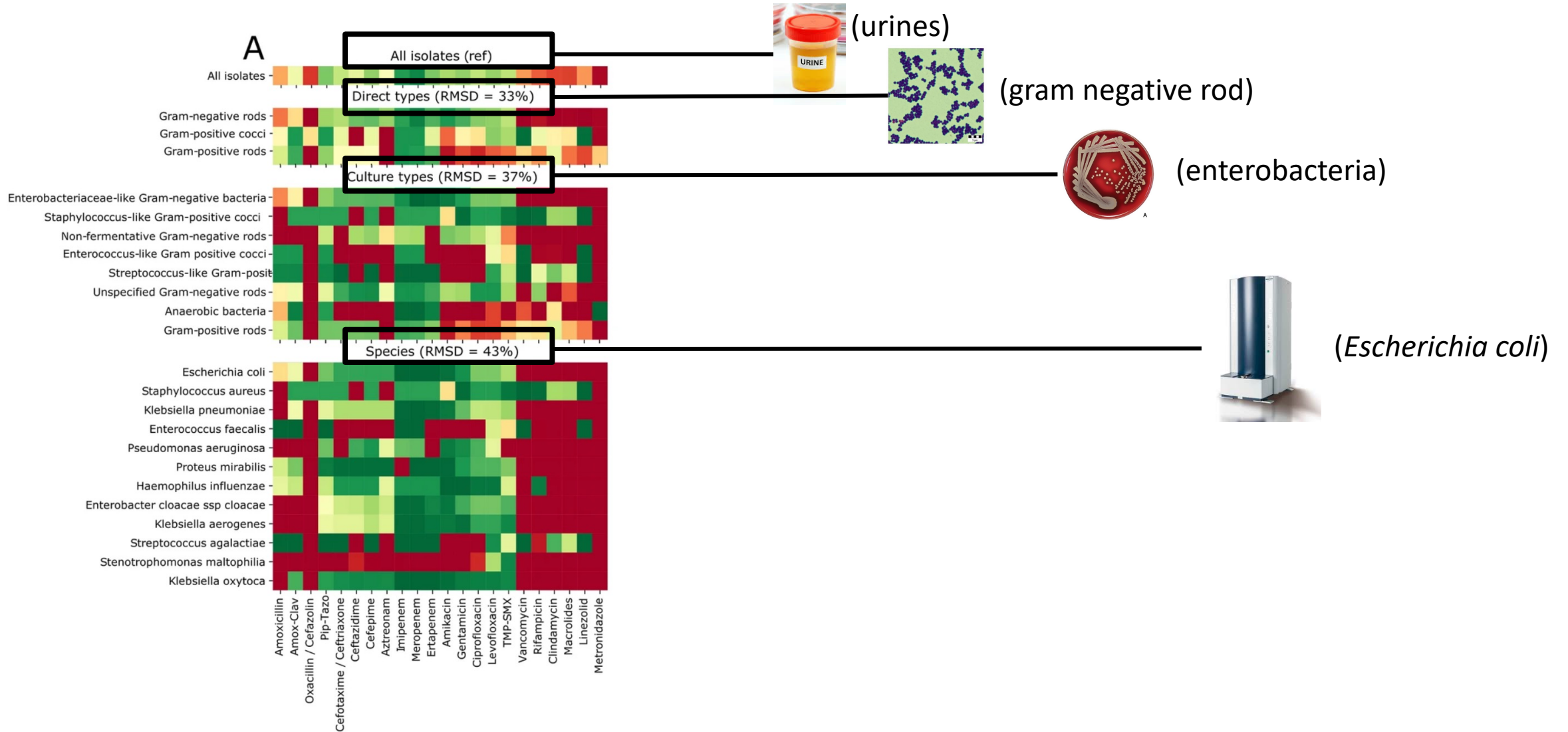
Key findings



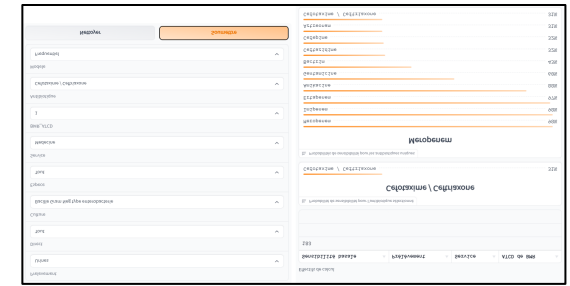
- Expert system
- ML
- deepLearning
- LLM



Exemple #1: Epidemiological data



#1 Objective & Methods

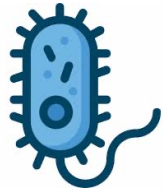


y

x

$f ()$

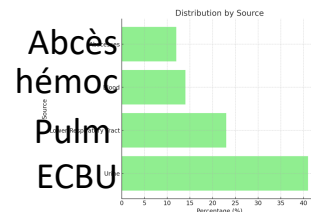
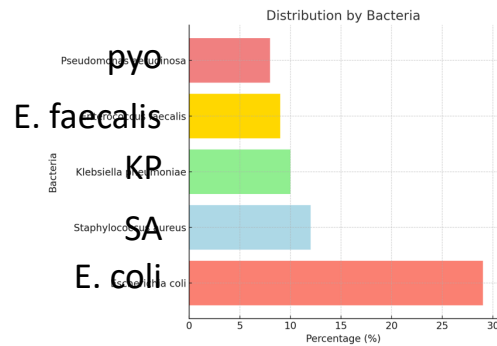
AMR prediction for:



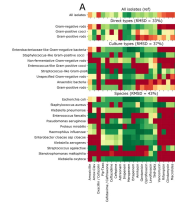
12 species



22 ATB



- 2014- 2020, Hôpital Européen Marseille
- 13,166 patients 30,975 antibiograms



- Historical bacterial ecology, Stage, Ward, BMR past history, period

Bayes/frequency based inference

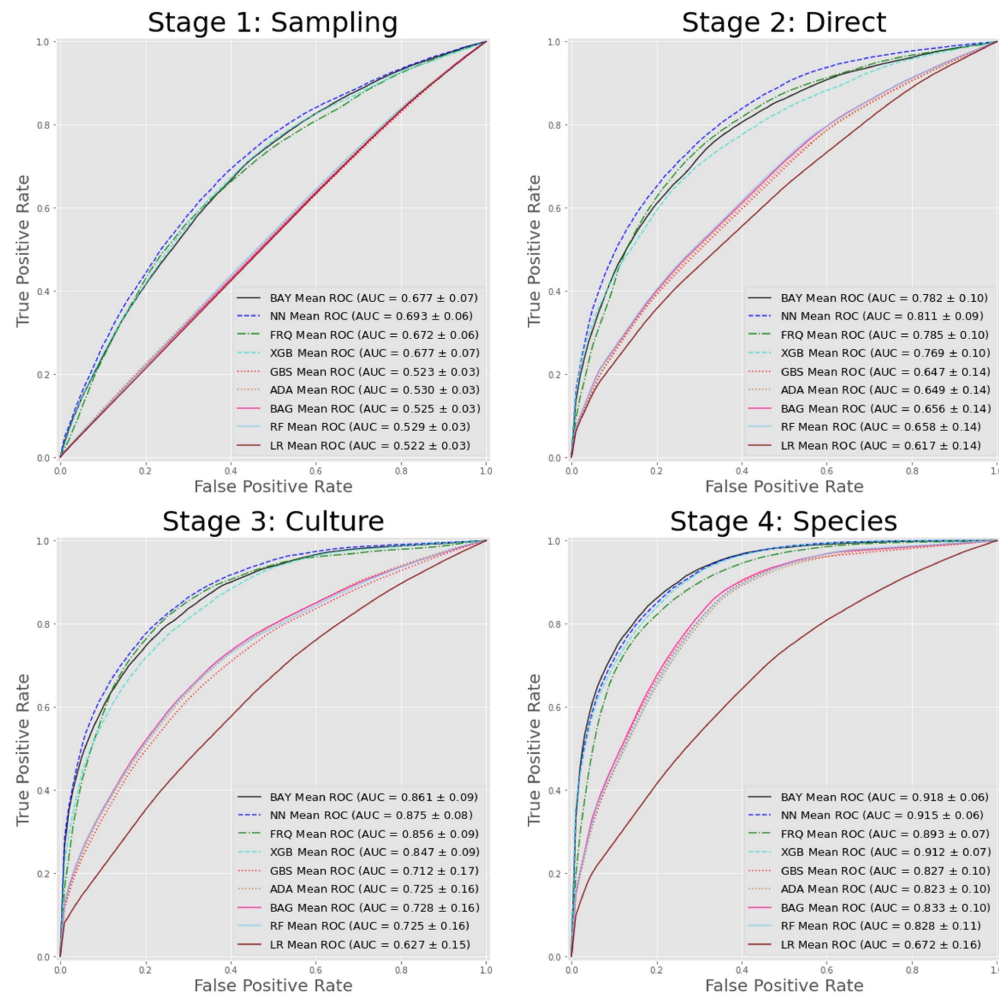
Logistic regression

Random forest
XGBoost
ADA, GBS

Neural network



#1 Key findings



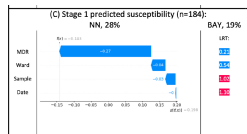
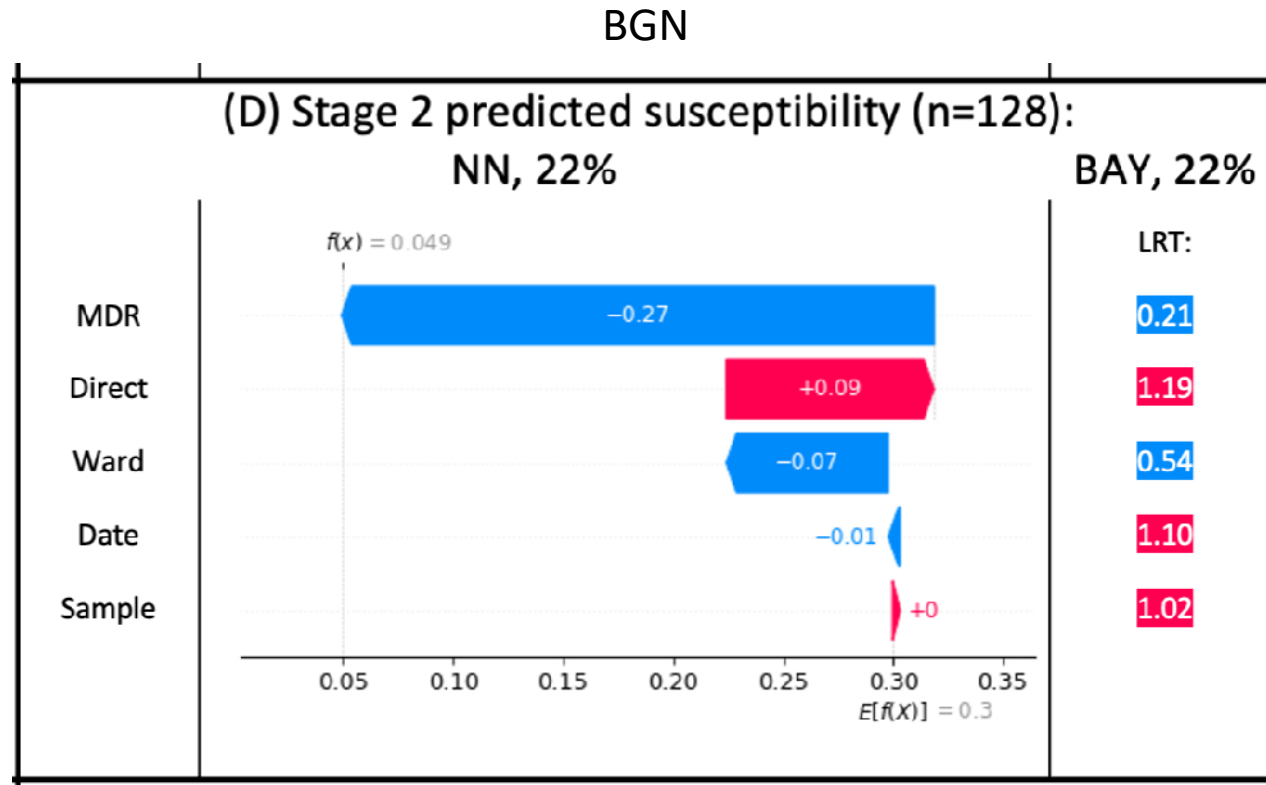
- Prediction quality improve with stage of analysis
- **Bayesian and neural net win the competition**

Model	Stage 1 "sampling"	Stage 2 "Direct"	Stage 3 "Culture"	Stage 4 "Species"	Overall mean
All isolates of the 2020 validation dataset					
BAY	0.677	0.782	0.861	0.918	0.809
NN	0.693	0.811	0.875	0.915	0.823
FRQ	0.672	0.785	0.856	0.893	0.802
XGB	0.677	0.769	0.847	0.912	0.801
GBS	0.523	0.647	0.712	0.827	0.677
ADA	0.530	0.649	0.725	0.823	0.682
BAG	0.525	0.656	0.728	0.833	0.686
RF	0.529	0.658	0.725	0.828	0.685
LR	0.522	0.617	0.627	0.672	0.610
Overall mean	0.594	0.708	0.773	0.847	0.731

#1 Explainable AI? C3G S prediction

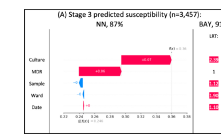


Récidive de PNA
avec portage
BLSE

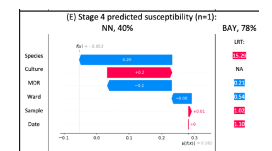


1.Sampling

2.Direct Examination

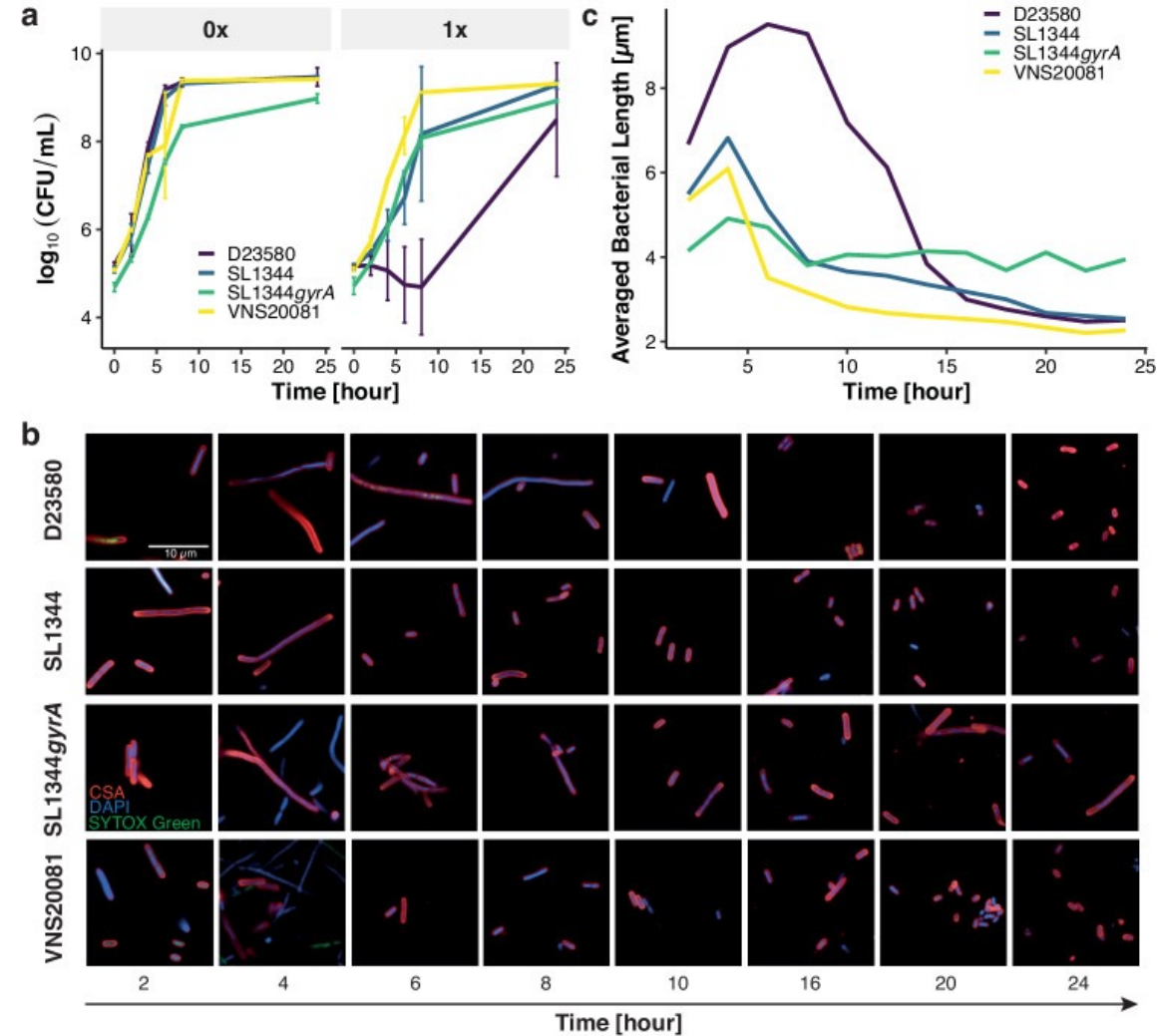


3.Cultures






4.MALDI_TOF

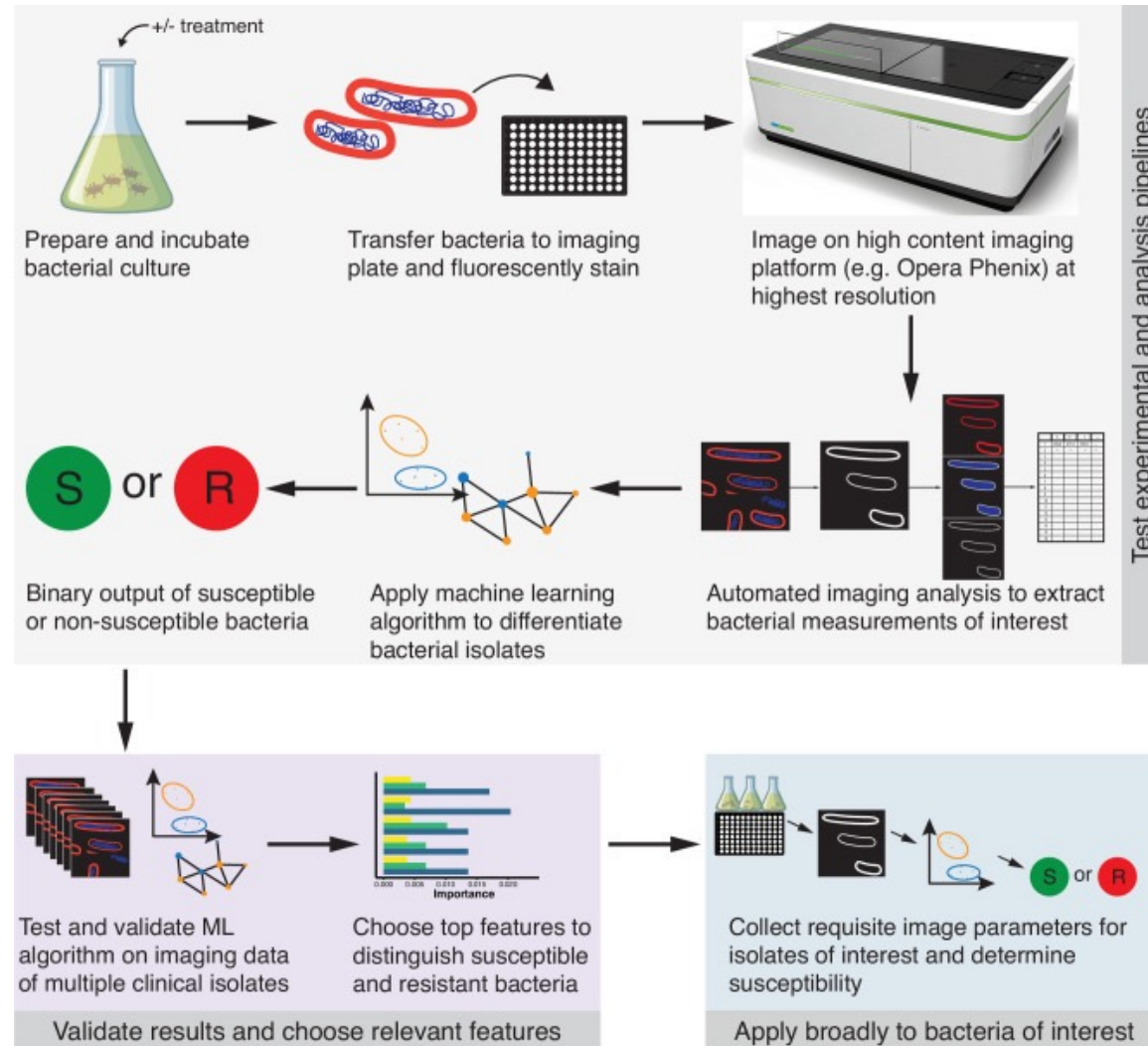
Exemple #2: Imaging data



#2: Objective & Methods

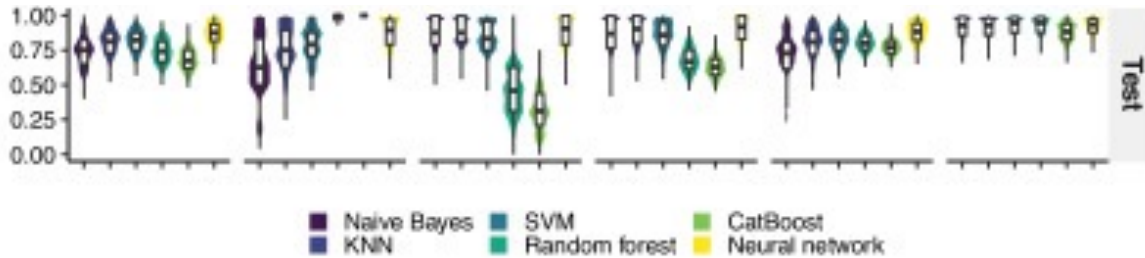
y	x	$f ()$
<p>AMR prediction for:</p>  <p><i>Salmonella typhi</i></p>  <p>Ciprofloxacin</p>	<p>4 S. Typhimurium isolates 4 C° of ciprofloxacin 24h 1681 High-content imaging (HCI) :</p>  <p>65 features: morphological, intensity, and texture features for each individual bacterial cell</p>	<p>Bayes</p> <p>KNN SVM Random Forest CatBoost</p> <p>Neural network</p>

#2: Workflow





#2 Key findings



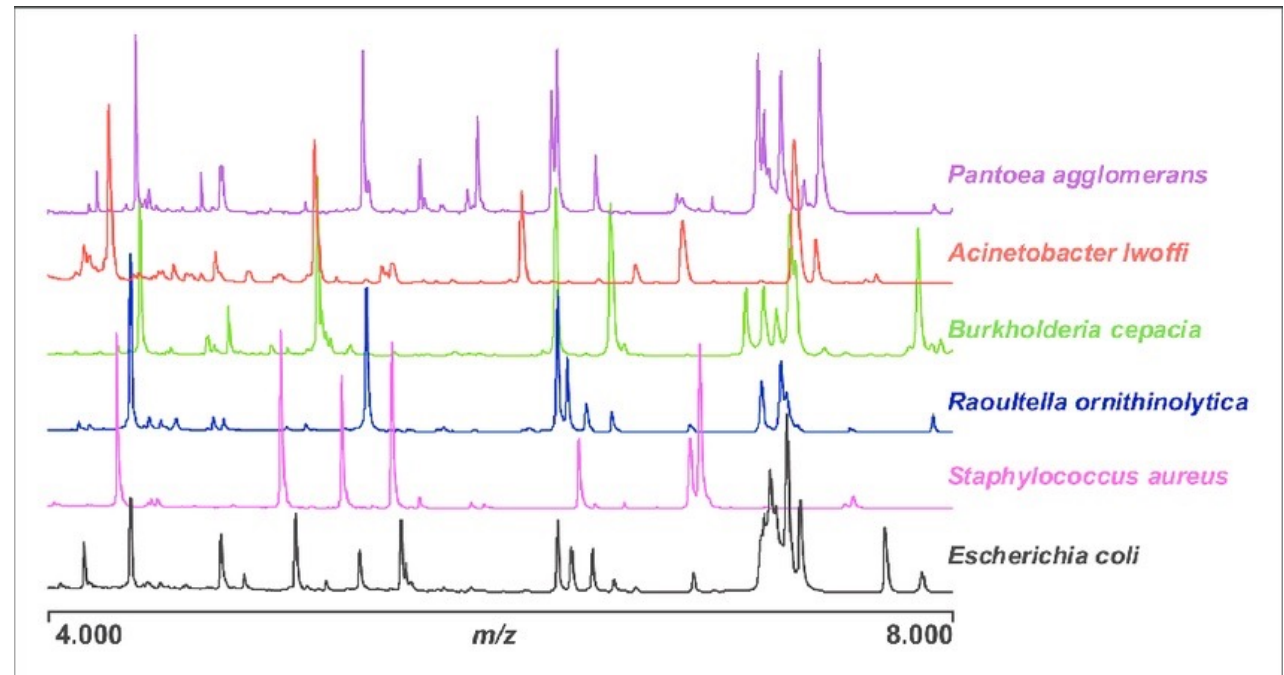
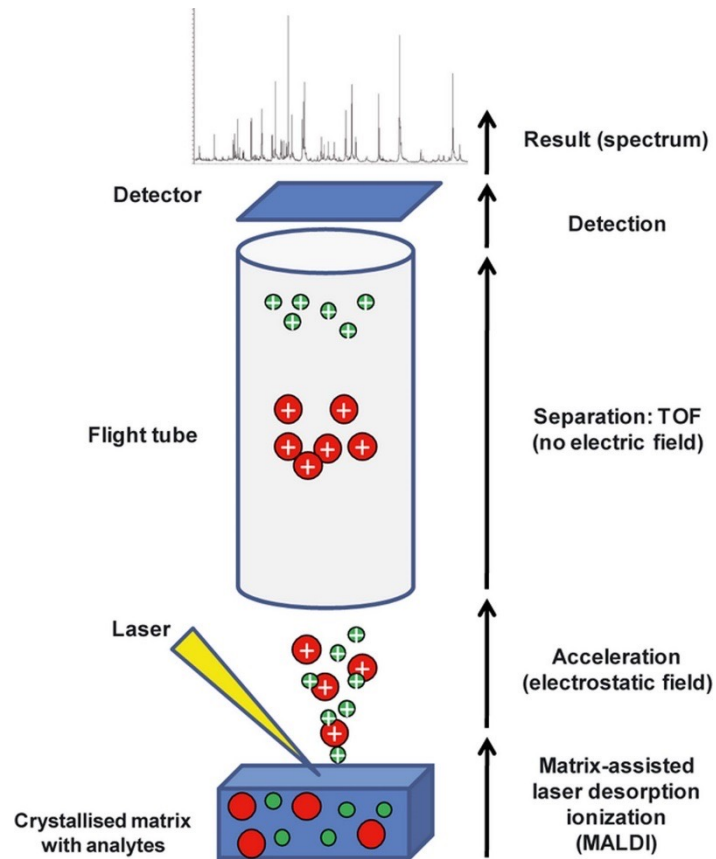
Method	Test set					
	Accuracy	Sensitivity	Specificity	Precision	F1 score	AUC
Naïve Bayes	0.74±0.13	0.63±0.24	0.87±0.15	0.85±0.15	0.69±0.20	0.91±0.10
KNN	0.81±0.11	0.74±0.20	0.88±0.11	0.88±0.12	0.78±0.15	0.91±0.08
SVM	0.81±0.09	0.78±0.14	0.84±0.12	0.85±0.11	0.81±0.11	0.92±0.09
Random forest	0.74±0.09	0.99±0.03	0.46±0.18	0.68±0.10	0.80±0.07	0.92±0.07
CatBoost	0.68±0.09	1.00±0.02	0.32±0.16	0.63±0.08	0.77±0.06	0.88±0.08
Neural network	0.87±0.08	0.87±0.12	0.88±0.12	0.90±0.10	0.87±0.08	0.91±0.07

- Machine learning classifiers can distinguish between ciprofloxacin susceptible and resistant isolates without ciprofloxacin exposure
- **Neural network win**

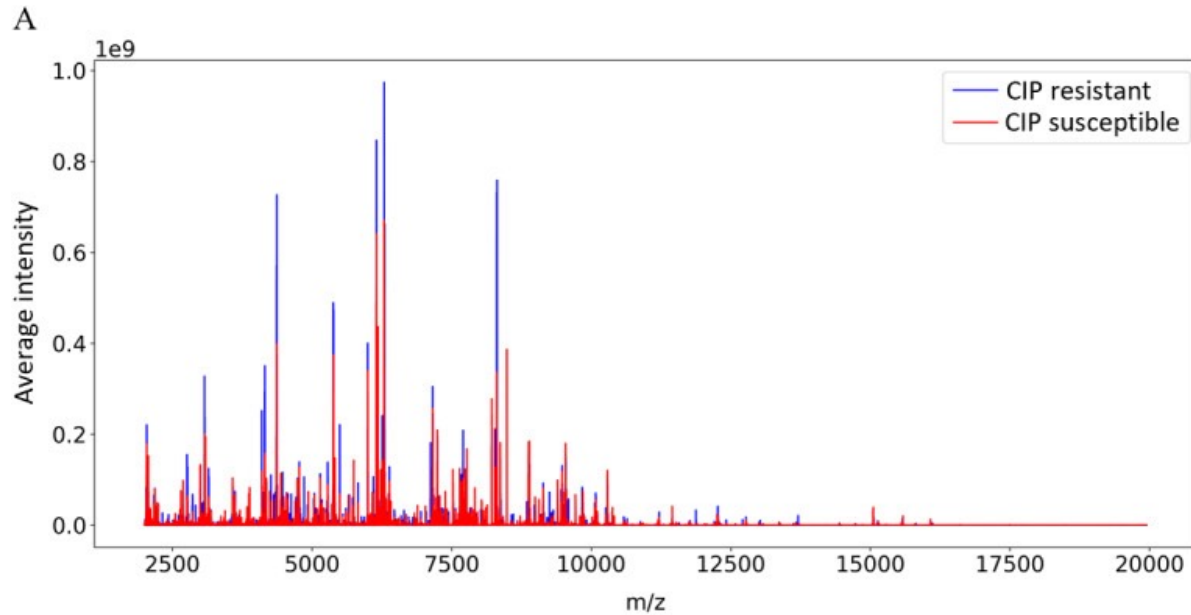
Mécanistic hypothesis:

DNA gyrase mutations may interact with other cellular pathways, which ultimately impact directly on cellular morphology.

Exemple #3: proteomic data from MALDI-TOF





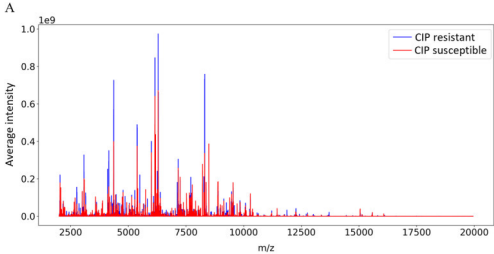
#3 MALDI_TOF & AMR prediction



Differential mass spectrometry profiles for CIP resistance in *Klebsiella pneumoniae*.

m/z: mass-to-charge

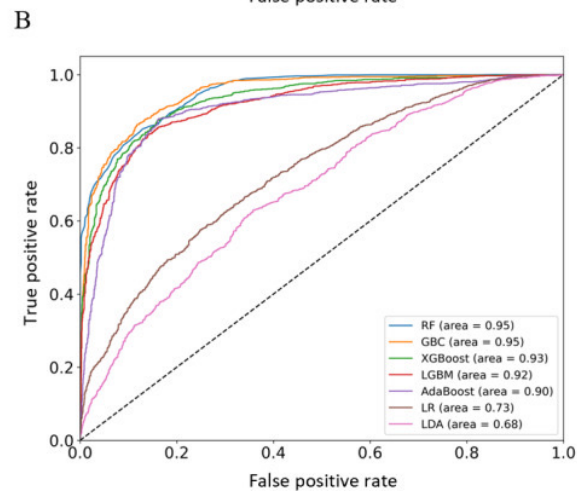
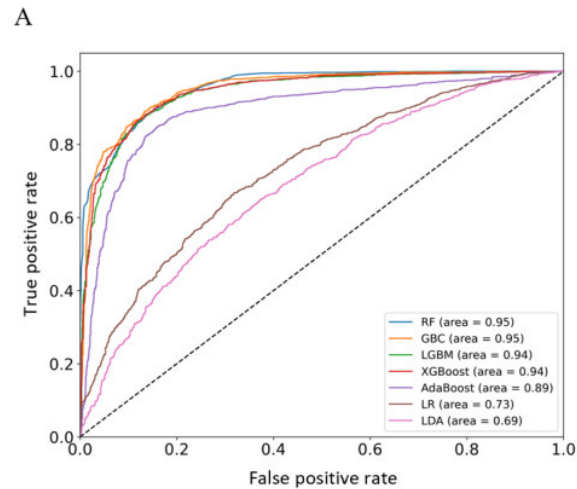
#3 Objective and Methods

y	x	$f ()$
<p>AMR Prediction for:</p>  <p><i>Klebsiella pneumoniae</i></p>  <p>Ciprofloxacin/Levo</p>	<p>January 2021 to December 2023 4 hospitals Taipei city 11,996 KP isolates.</p>  <p>MALDI-TOF Mass spectrometry profiles ~ 15 000 features</p>	<p>Logistic regression. LDA: linear discriminant analysis.</p> <p>Random forest. XGBoost GBC: gradient boosting classifier. LGBM: light gradient boosting machine.</p>



#3 Key findings

ROC curve



Levofloxacin resistance prediction

Models	Training AUC ^a	Testing AUC	Accuracy	Sensitivity	Specificity	PPV ^b	NPV ^c	F ₁ -score
RF ^d	0.99	0.95	0.86	0.89	0.82	0.86	0.86	0.87
GBC ^e	0.99	0.95	0.87	0.88	0.86	0.89	0.85	0.88
XGBoost	0.99	0.93	0.85	0.86	0.85	0.87	0.83	0.86
LGBM ^f	0.99	0.92	0.85	0.84	0.85	0.87	0.82	0.86
AdaBoost	0.99	0.90	0.85	0.85	0.84	0.87	0.83	0.86
LR ^g	0.77	0.73	0.66	0.74	0.57	0.68	0.64	0.70
LDA ^h	0.72	0.68	0.64	0.81	0.43	0.63	0.65	0.71

Random Forest and XGBoost achieved the best performances

#4 LLM & AST interpretation



Step 1: Generation of a GPT powered generative AI agent.



EUCAST GPT Expert
Expert on EUCAST standards and general antimicrobial susceptibility



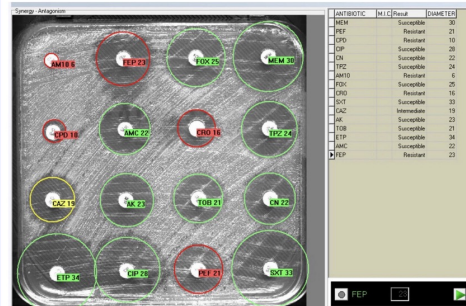
Step 2: Acquisition of knowledge.
Using document from EUCAST.org
- EUCAST breakpoint table v13.1
- Expert rules

Step 3: Within model testing.

Checked with few examples. Improving rules for obvious mistakes e.g. list of species with chromosomal AmpC.



Step 4: Input for prompt.



+ same image without measurement circles.
+ Table with measured inhibition zones

Step 5: Standardized prompting.

Ask for:
(i) Interpretation of image and table;
(ii) Provide output table with 4 categories: “None”, “ESBL”, “AmpC”, and “Carbapenemase”;
(iii) recommended confirmation;
(iv) and short argumentation text.



Step 5: Output analysis

EUCAST GPT Expert
Based on the information provided for Sample 2.S1 and the image analysis, here's the output for *Escherichia coli* considering the EUCAST guidelines:

Resistance Mechanism	Detected (Threshold)	Likelihood Analysis	Recommendation on Confirmation Tests
None	No	Unlikely	N/A
ESBL production	Yes	Very likely	Confirmatory tests recommended: double synergy test (DDST), combined disk test if or molecular tests (PCR)
AmpC production	No	Unlikely	N/A
Carbapenemase production	No	Very unlikely	N/A

Argumentation:

- None:** The resistance pattern does not support the absence of resistance mechanisms as there is resistance to several antibiotics including broad-spectrum cephalosporins.
- ESBL production:** Resistance to cephalosporins (CPO) and amoxicillin/clavulanic acid (AMC) while retaining susceptibility to meropenem (MEM) and ceftazidime (FOX) is indicative of ESBL production. ESBL-producing organisms typically show reduced susceptibility to cephalosporins but remain susceptible to carbapenems and ceftazidime.
- AmpC production:** Susceptibility to ceftazidime (FOX) indicates that AmpC production is unlikely, as organisms with AmpC typically have reduced susceptibility to ceftazidime.
- Carbapenemase production:** The pronounced susceptibility to meropenem (MEM) suggests that carbapenemase production is very unlikely, as resistance or reduced susceptibility to carbapenems would be expected if carbapenemase enzymes were present.

Confirmation Tests Recommendation:
Given the very likely presence of ESBL, confirmatory testing should be pursued. EUCAST recommends using phenotypic confirmatory tests like DDST or CDT to confirm ESBL production, or molecular tests like PCR for specific gene detection.

Output table

Argumentation

Step 6: Calculation of output performance e.g., sensitivity and specificity.

#4 LLM & AST interpretation

TABLE 1 Sensitivity and specificity of human experts and the customized EUCAST-GPT-expert

	Human experts ^a	EUCAST-GPT-expert ^b
ESBL		
Sensitivity	98.0% (91.8–100)	95.4% (94.5–96.3)
Specificity	99.1% (97.1–100)	69.2% (63.8–85.7)
AmpC		
Sensitivity	96.8% (93.3–100)	96.9% (87.5–96.9)
Specificity	97.1% (95.9–97.7)	86.3% (84.1–91.8)
Carbapenemases		
Sensitivity	95.5% (90.9–100)	100% (90.9–100)
Specificity	98.5% (98.5–98.5)	98.8% (98.8–98.8)



Pros & Cons

- #1: epidemio 4 stages
- #2: imaging
- #3: MALDI TOF
- #4 AST interpretation



	✓	✗
Quality	Data cleaning (#1)	No Clinical ATB data No Deep learning (#3)
Feasibility	#1, #3, #4	#2
Explainability	#1, #3, #4 (SHAP)	#2
Relevance	Fast prediction: #1>#2>#3 Number species/ATB (#1, #4)	#4>WGS (5d) Limited to species/ATB (#2, #3)

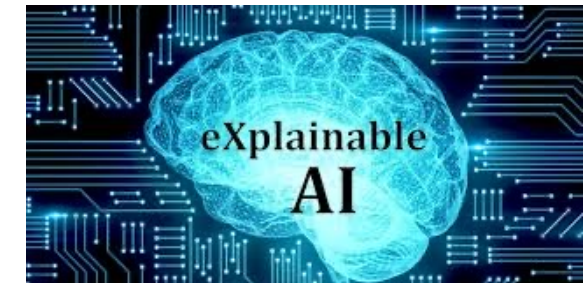
Artificial intelligence in antimicrobial stewardship: a systematic review and meta-analysis of predictive performance and diagnostic accuracy

	
<p>2000- 2024. Observational, cohort, or retrospective studies focusing on the application of AI/ML in AMS.</p> <p>3,458 retrieved articles 80 studies met the inclusion criteria.</p>	<ul style="list-style-type: none">• AUC [ES: 72.28 (70.42-74.14)]• accuracy [ES: 74.97 (73.35-76.58)]• sensitivity [ES: 76.89; (71.90-81.89)]• specificity [ES: 73.77; (67.87-79.67)]• NPV [ES:79.92 (76.54-83.31)]• PPV [ES: 69.41 (60.19-78.63)] <p>ES: mean pooled effect size (ES)</p>

Conclusion:

L'IA peut elle prédire l'antibiorésistance?

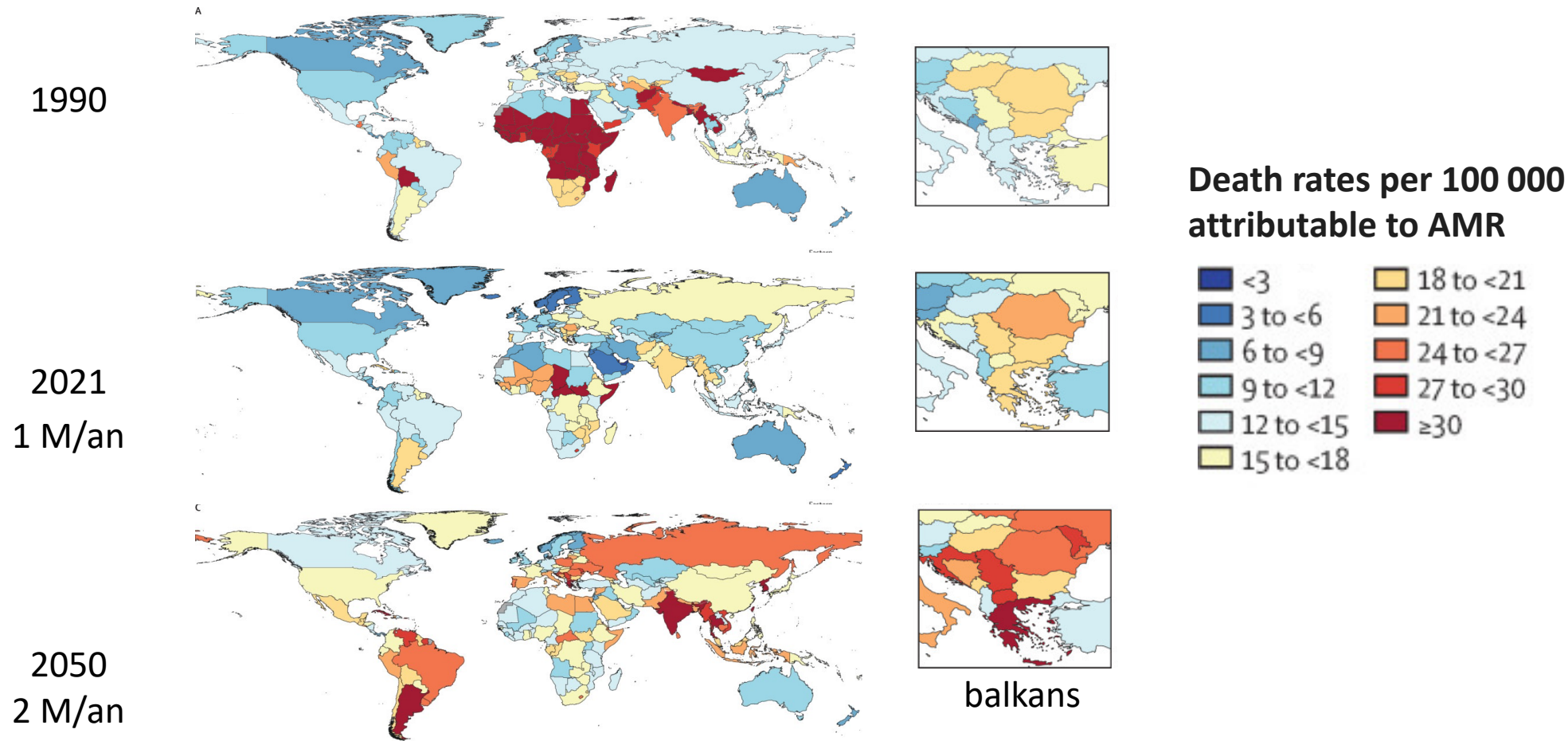
- L'IA peut tout prédire si accès à big data
- Pertinence?
 - Santé animale > humaine | Ville & Hôpital | aide à prescription > aide à prédiction
 - Timing % prescription d'antibiotique?
 - +++ si épargne prescription antibiotique
 - ++ si épargne large spectre
 - + si gain 24 heures désescalade
- Faisabilité:
 - Légale et politique: RGPD & DPI et accès données patients
 - Technique: « databases don't travel ». Combien de data scientist spécialisés en IA dans vos hôpitaux?
- Acceptabilité:
 - Effet black box IA



Bravo et Merci!



92 millions de morts évitables d'ici 2050



Critical group



Enterobacteriales
carbapenem-resistant



Enterobacteriales
third-generation
cephalosporin-resistant



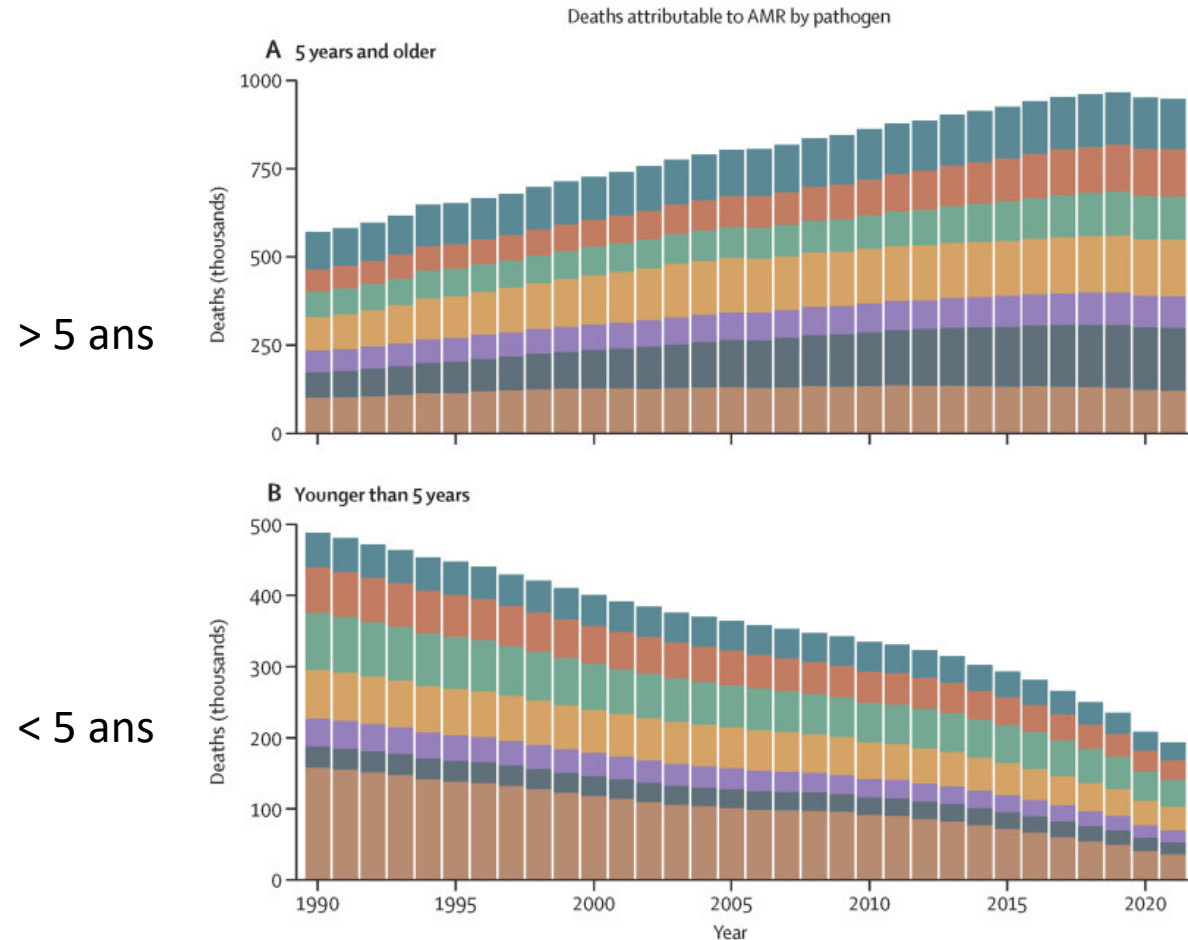
*Acinetobacter
baumannii*
carbapenem-resistant



*Mycobacterium
tuberculosis*,
rifampicin-
resistant^a

^aRR-TB was included after an independent analysis with parallel criteria and subsequent application of an adapted MCDA matrix.

Deaths attributable to AMR by pathogen, global, 1990–2021



> 5 ans

< 5 ans

Pathogen

Acinetobacter baumannii

Escherichia coli

Klebsiella pneumoniae

Other AMR bacteria

Pseudomonas aeruginosa

Staphylococcus aureus

Streptococcus pneumoniae

Critical group



Enterobacterales
carbapenem-resistant



Enterobacterales
third-generation
cephalosporin-resistant



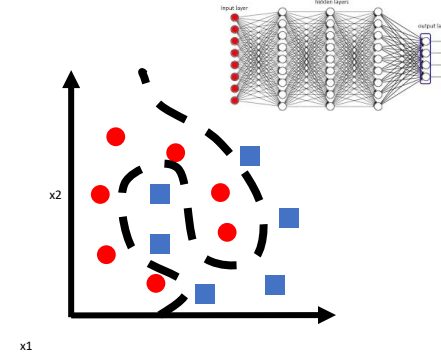
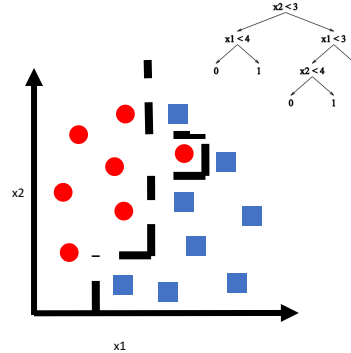
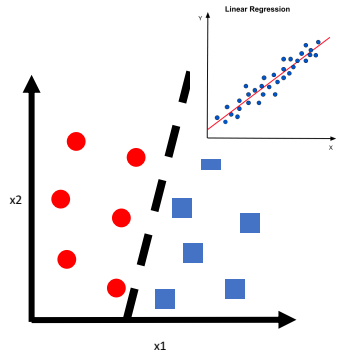
*Acinetobacter
baumannii*
carbapenem-resistant



*Mycobacterium
tuberculosis*,
rifampicin-
resistant*

*RR-TB was included after an independent analysis with parallel criteria and subsequent application of an adapted MCDA matrix.

Different ML flavours



	Regression	Decision tree	deep learning
Use case	Structured data	Structured data	Text, image, sound
Features extraction	Manual	Manual	Automated
Performance	+	++	+++
Explainability	+++	++	+
Data points	100	1000	10 000
Overfitting risk	+	++	+++

Overfitting concept

