



Universität  
Zürich<sup>UZH</sup>

Institute for Medical Microbiology

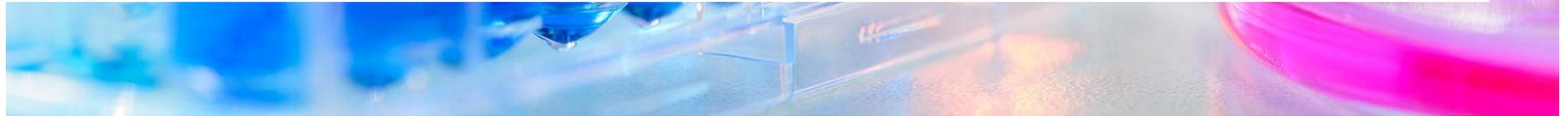


# Artificial Intelligence in Antimicrobial Susceptibility Testing

Prof. Adrian Egli; MD PhD, FAMH, ESCMID fellow

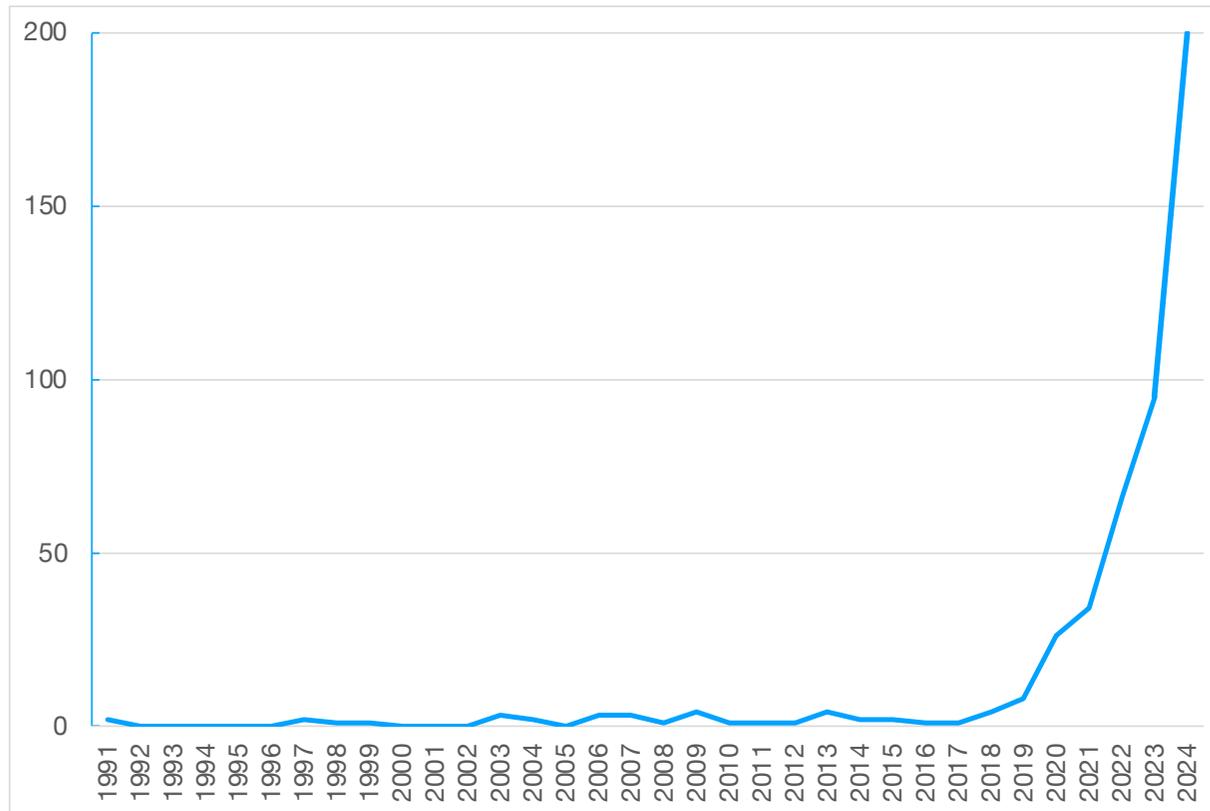
Director, Institute of Medical Microbiology

27 May 2025



Universität  
Zürich<sup>UZH</sup>

## A rapid increase of the literature: “Artificial intelligence” AND “antibiotic”



Pubmed Search 24.05.2025

Exponential increase of the literature in the past 4 years.

Clearly, there is a huge hype around AI:

**Bill Gates Predicts AI Will Replace Doctors and Teachers Within a Decade**

27. March 2025 **Medium**

# Early thoughts on digitalization and AI started in 1966

Original Article

## Human meaning of medical informatics: Reflections on its future and trends

F. Grémy

Pages 1-11 | Received 01 Sep 1988, Published online: 12 Jul 2009

Cite this article <https://doi.org/10.3109/14639238909010875>



Medical Informatics >

Volume 14, 1989 - [Issue 1](#)

[Journal homepage](#)

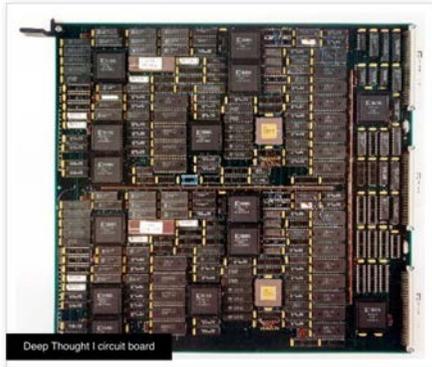
The philosophy underlying medical informatics, and indeed information systems in general, is discussed. The need for integrating concepts is considered, and particular emphasis is placed on the avoidance of fragmentation and overspecialization. Human and artificial intelligence are compared and contrasted. It is shown that human intellectual activity cannot be reduced to a set of formal computations. The main emphasis of this paper is that **the unique properties of human intelligence should not be devalued or ignored in attempts to promote machine systems in inappropriate areas.**



Francois Grémy (1929-2014) – 1966 explains the need to join medicine and informatics as a new discipline.

Grémy F, Medical Informatics 1989

## What else happened in 1989...

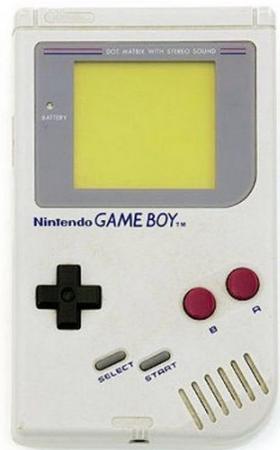


### Computer defeats master chess player

• *AI & Robotics*

David Levy is the first master chess player to be defeated by a computer. The program Deep Thought defeats Levy who had beaten all other previous computer counterparts since 1968.

**AND...**

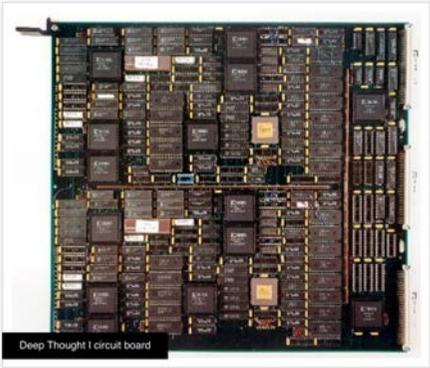


8 Bit  
Clock frequency: 4.19 MHz  
RAM: 8 Kbytes



Apple's first laptop

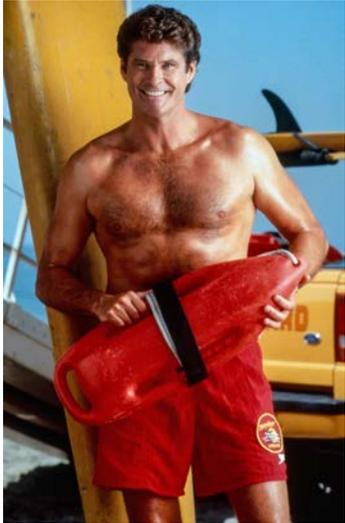
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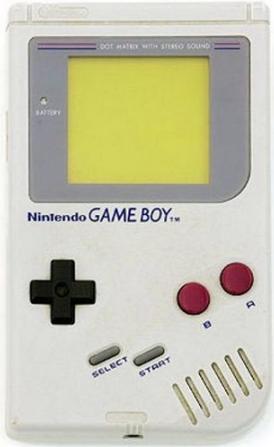
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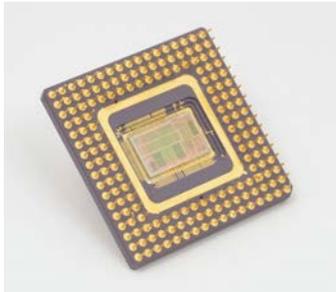


Apple's first laptop



The Wall felt...

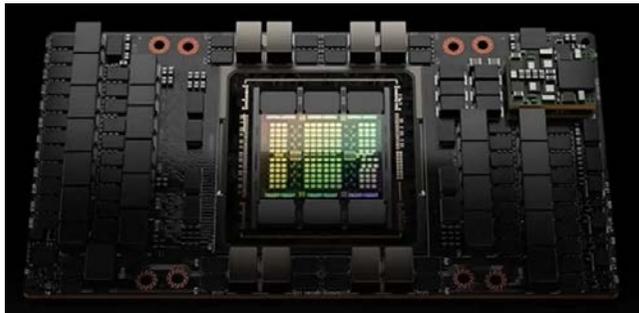
# (Hyper)rapid evolution of computer chips and AI



1989, Intel 486; 6-8 x10e6 FLOPs

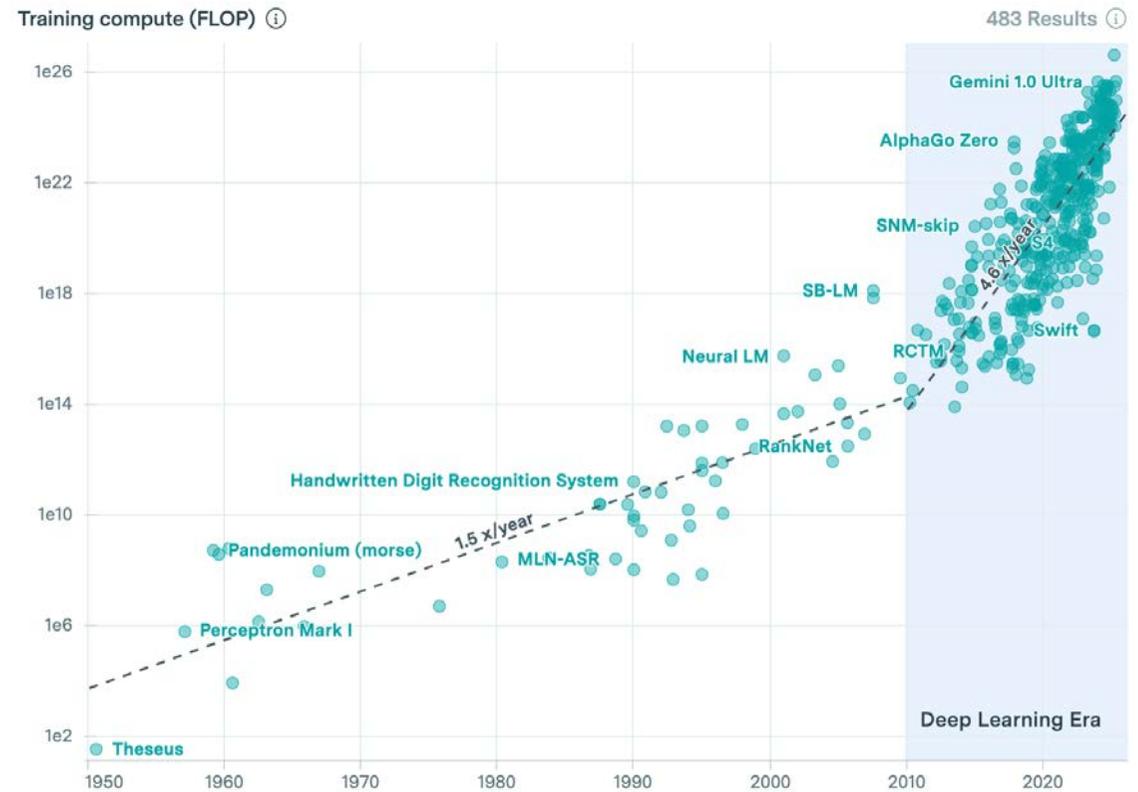


About 250'000'000(!) x faster



2025, Nvidia H100; up to 2x 10e15 FLOPs

<https://epoch.ai/blog/compute-trends>



Performance of super computers have doubled every 9 months.  
High performance AI systems require 10e5+ H100s.

# What can we do with AI?

## Input



Black box (a.k.a. AI)

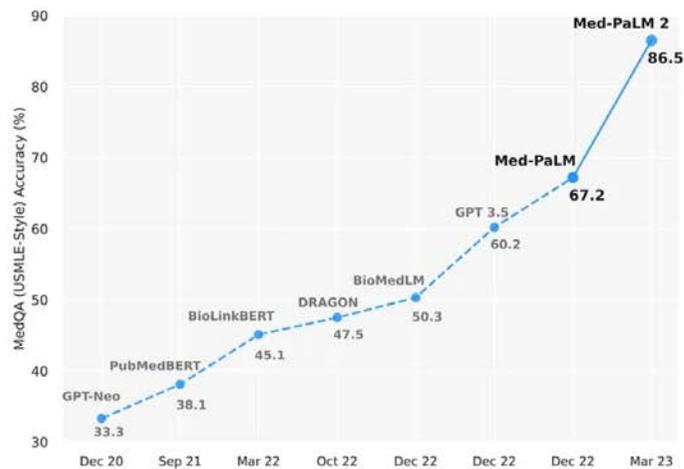


## Output



## Skill 1: categorisation!

# Accessing information! LLMs are very good in accessing and processing large amounts of information ( $\neq$ knowledge).



**Skill 2: information access!**

**Figure 1 | Med-PaLM 2 performance on MultiMedQA** Left: Med-PaLM 2 achieved an accuracy of 86.5% on USMLE-style questions in the MedQA dataset. Right: In a pairwise ranking study on 1066 consumer medical questions, Med-PaLM 2 answers were preferred over physician answers by a panel of physicians across eight of nine axes in our evaluation framework.

- Newst models with deep research capacity reach >98% in MedQA.
- **Domain level expertise** e.g. in public health and epidemiology is likely much lower.
- **Challenges:** Data scarcity. Medicine is per se a very heterogenous topic, little data interoperability.

Singhal K, Azizi S, Tu T et al. Nature 2023

## What is AI?

- **AI refers to** “the ability of computer systems to perform tasks that typically require human intelligence, such as learning, problem-solving, and decision-making” [1].
- **Machine learning** includes algorithms that can analysis data, recognition of patterns, make predictions without explicit programming. Trend towards explainable AI (XAI) – using specific methods to identify the weight of features in models e.g. SHapley Additive exPlanations.
- Different **benchmarks** such as MedQA are too easy to pass, therefore... “Humanity’s last exam” [2].

### Why AI and antimicrobial resistance?

- Machine learning works well with **highly structured, large data**, such as from clinical microbiology and laboratory medicine [3-6].

[1] AI definition from Google search, 08.05.2025; [2] Phan L, et al. arXiv:2501.14249, 2025; [3] Vihta KD et al. Commun Med 2024; [4] Egli A CID 2022; [5] Weis C et al. Nature Med 2023; [6] Acosta JN, Falcone GJ et al. Nature Medicine 2022;

# Classification of data types.

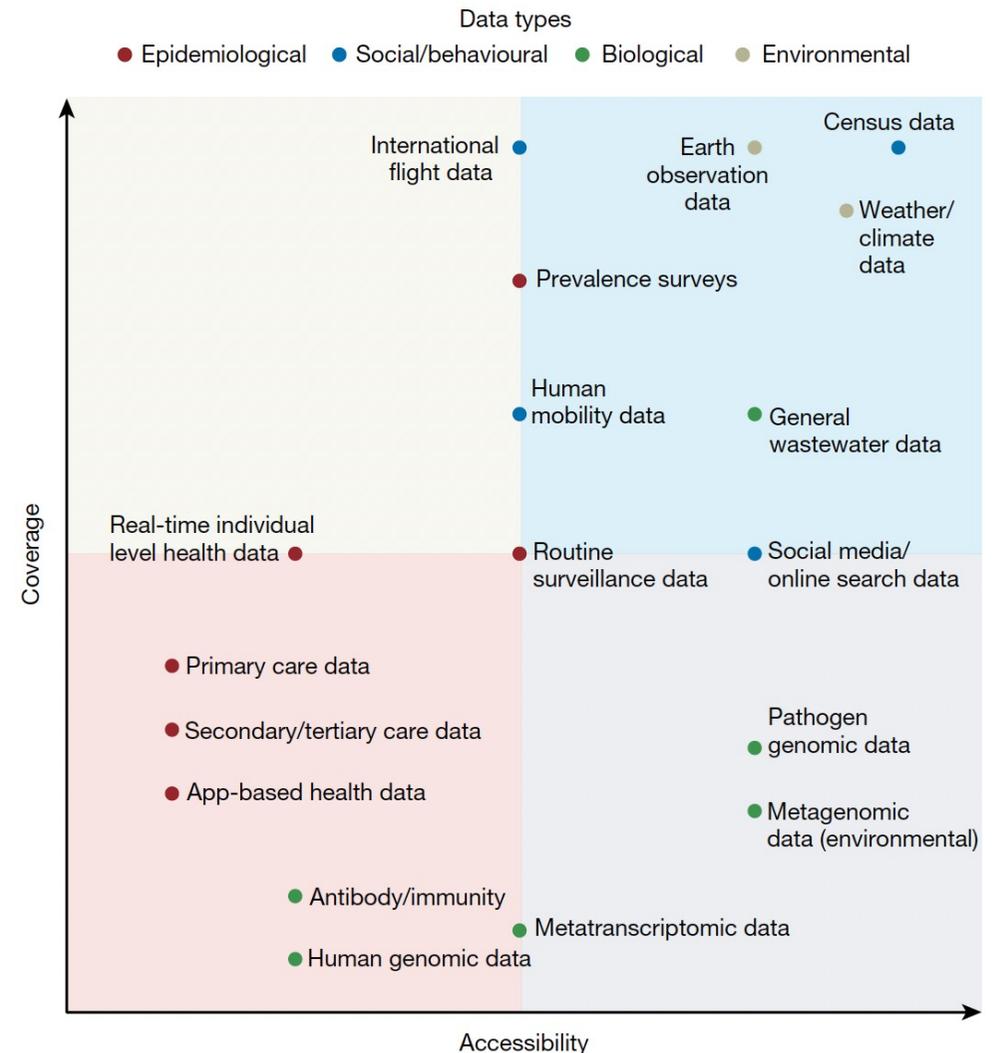
**Purpose:** Classify infectious disease data by accessibility and population coverage.

**Data Categories:** Epidemiological, environmental, social/Behavioral, biological.

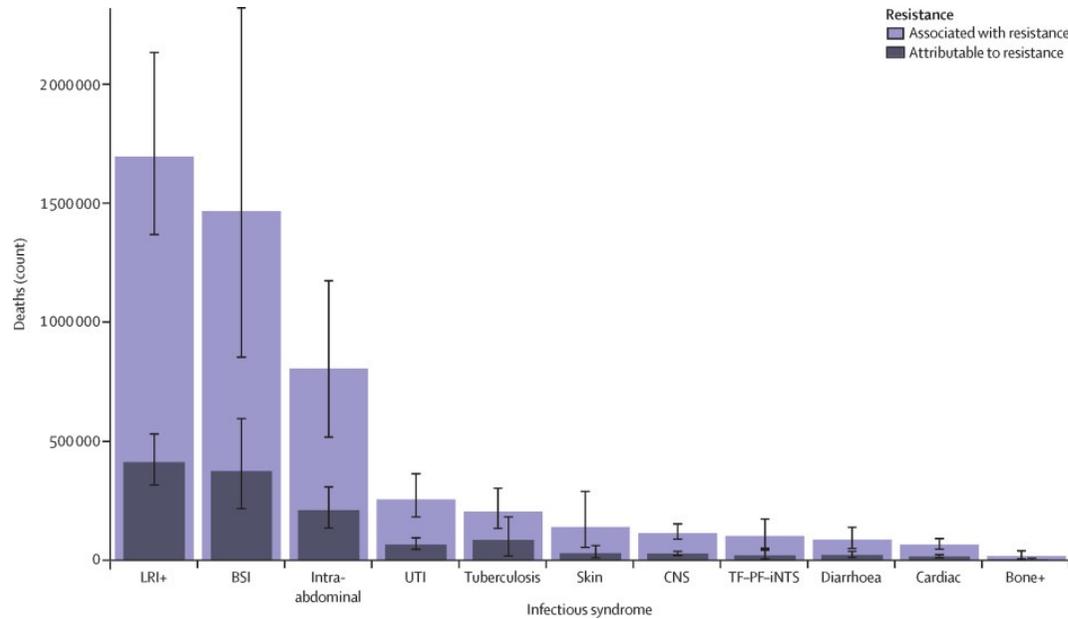
**High Coverage & Accessibility:** Census, weather, and wastewater data.

**Low Accessibility:** Individual-level health data, genomic and immunity data.

**Impact:** Identifies strengths and gaps in data for disease modelling and public health strategies.



# For AST there are problems: many different pathogens...

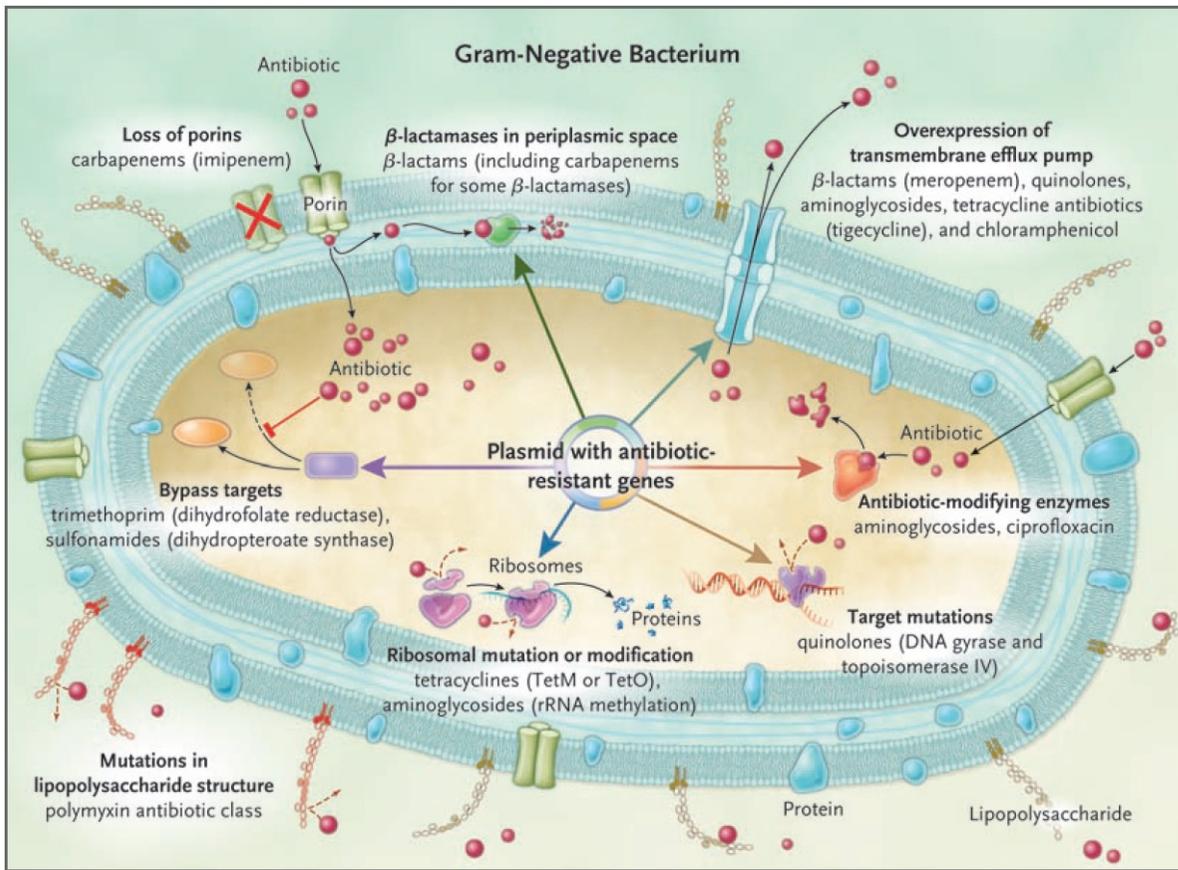


- Different lead pathogens.
- Different sample types.

Antimicrobial resistance collaborators, Lancet 2022

→ In 2019: Estimated 4,95 million people (95% CI 3,62–6,57) died with AMR, incl. 1,27 million people (95% CI 0,91–1,71) died due to AMR

## ... and many different molecular mechanisms for resistance



Peleg AY and Hooper DC, NEJM 2010

- Porin loss
- Efflux pump
- Target modification
- Cleaving enzymes

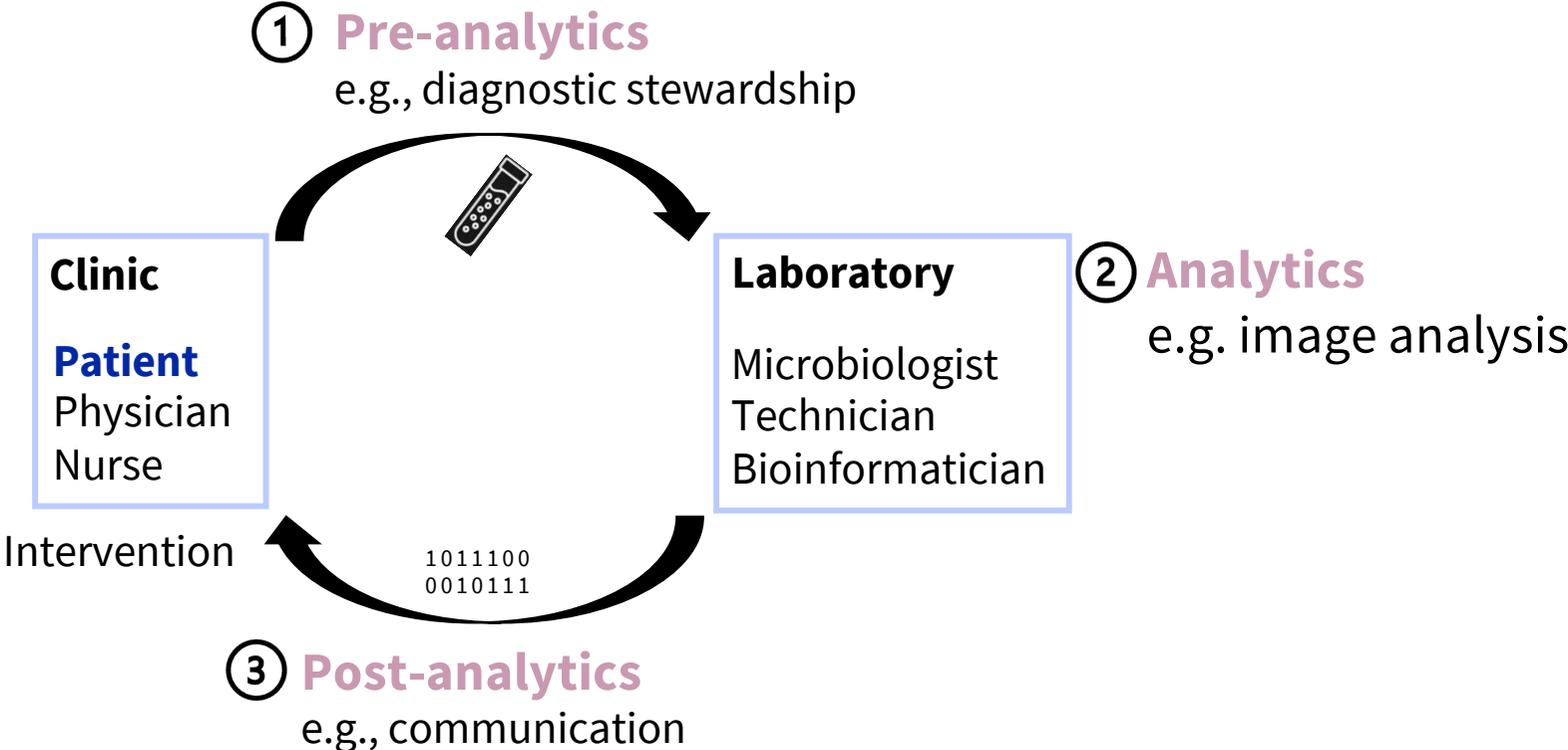
Many **diverse resistance mechanisms**:

- Many different assays with different readouts from pheno- to genotypic.
- Not all predictable from genomics.
- Minimal inhibitory concentration is a complex interplay of many things.

What do we aim to predict? Categorical resistance vs. minimal inhibitory concentration or inhibition zone?

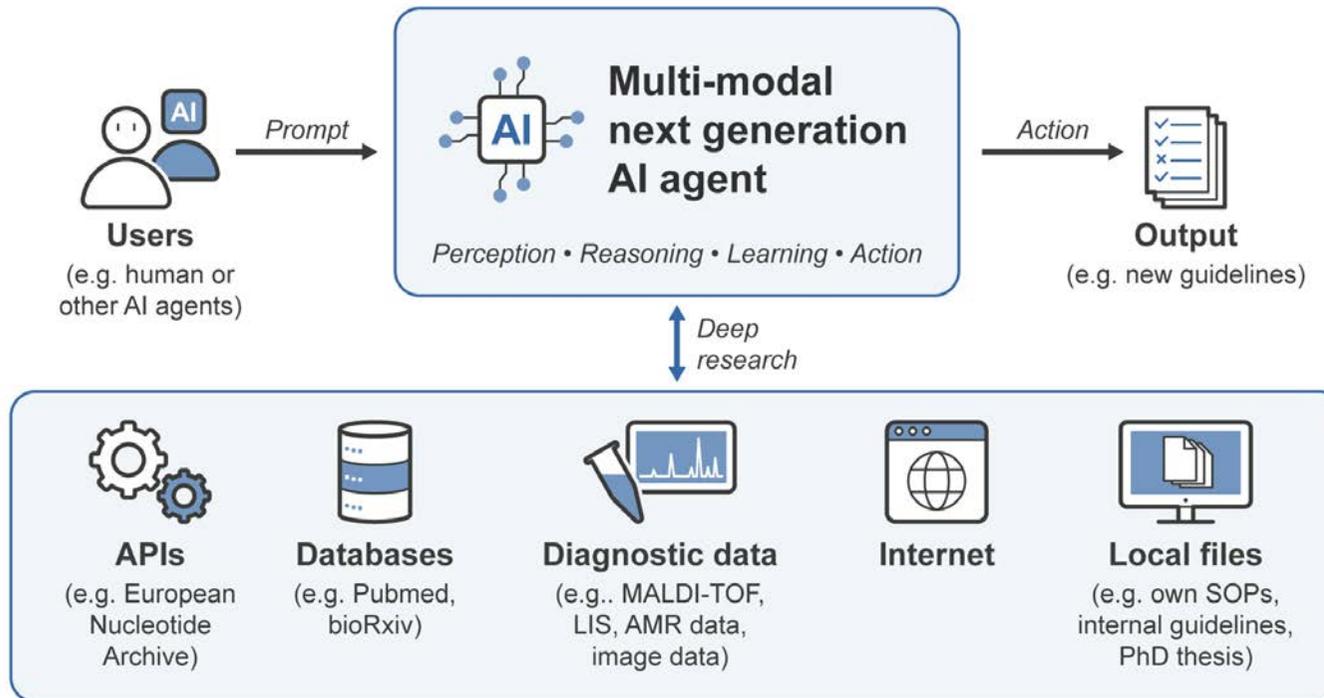
# Where can AI be implemented? [1]

aka “the brain-to-brain cycles”



[1] Egli A, Schrenzel J, Greub G, Clin Micro Infect 2020; [2] Egli A, Clin Infect Disease 2023

# From pre-trained ChatGPT 3.5 to AI agents within two years!



Potential applications of **deep research**:

- Real-time review on topics
- Real-time surveillance
- Real-time business intelligence

**AI agents** executes tasks for you e.g. accessing different healthcare datasets and summarizing findings [1].

## → AI agents with Deep Research and Codex capacities.

- Egli A et Howden B, in review; [1] Moritz M, Topol E, Rajpurkar P, Nature Biomedical Engineering April 2025

# Implementation of AI agents into practice



Currently no commercial, validated software in the domain space of AST available.

Most institutions do not have own, secured LLMs.

So if you use a commercial vendor make sure and be aware of the regulatory space in Europe:

- GDPR
- AI Act
- IVDR
- etc.

**Do not edit**  
How to change the design



**Have you ever used (in a professional situation) ChatGPT (or alike) to ask for diagnostic advice?**

① The Slido app must be installed on every computer you're presenting from

**slido**

# Preanalytics in the routine lab

→ How do different LLMs perform to provide pre-analytical advice?



Eline Meijer



Dr. M. Bressan

→ We formulated 30 typical pre-analytical questions, including sequencing.

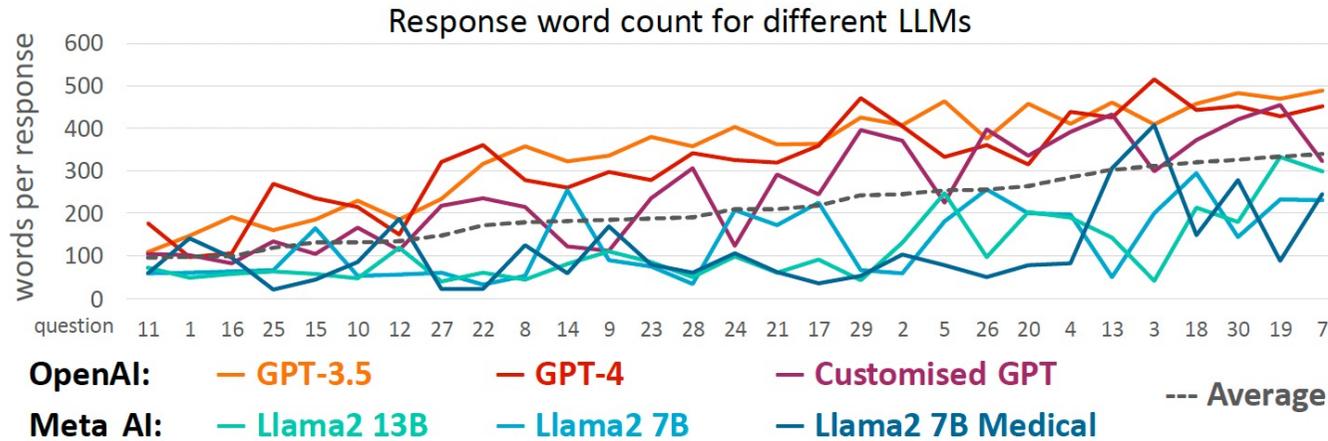
→ We established three LLMs at the Institute (Llama2 7B, Llama2 7B with medical info, and Llama2 13B) and accessed in addition ChatGPT, GPT4, customized GPT.

	OpenAI Models	Meta AI Models	
<b>General-purpose</b>	<b>GPT-3.5</b>	<b>Llama2 13B</b>	→ 180 outputs
	<b>GPT-4</b>	<b>Llama2 7B</b>	
<b>Domain-enhanced</b>	<b>Customised GPT-4</b> Topic specific documents uploaded for reference	<b>Llama2 7B Med.</b> Pre-trained on curated medical corpus	

Bressan M, Meijer E, ... et Egli A, unpublished

# Output against “textbook” response

**Figure 1.** OpenAI models mostly provided longer responses compared to Meta AI



**Table 1. Automated evaluation metrics:** OpenAI models achieved higher similarity scores to exemplary answers compared to Meta AI models.

	C. GPT	GPT-4	GPT-3.5	L2 Med.	L2 13B	L2 7B
BLEU & ROUGE*	0.120	0.117	0.105	0.103	0.101	0.091
BERT score	0.345	0.325	0.304	0.293	0.298	0.293
<b>Model ranking</b>	<b>1</b>	<b>2</b>	<b>3</b>	<b>4</b>	<b>4</b>	<b>5</b>

\* Evaluation metrics included: nltk bleu, sacre bleu, rouge-1, rouge-2 and rouge-l

Bressan M, Meijer E, ... et Egli A, unpublished

# How do humans assess the responses?



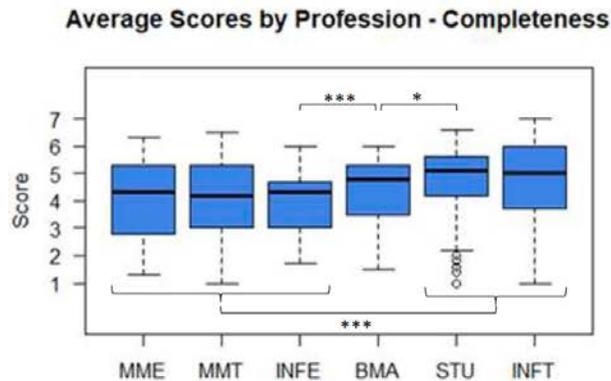
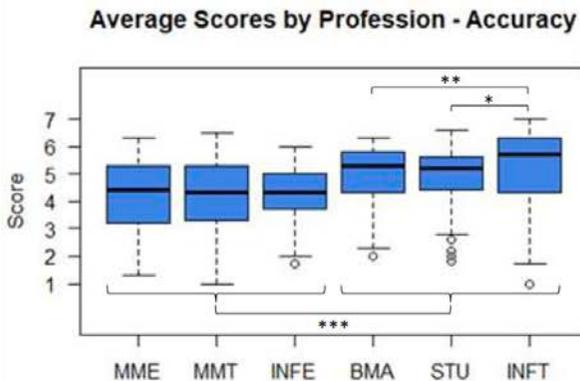
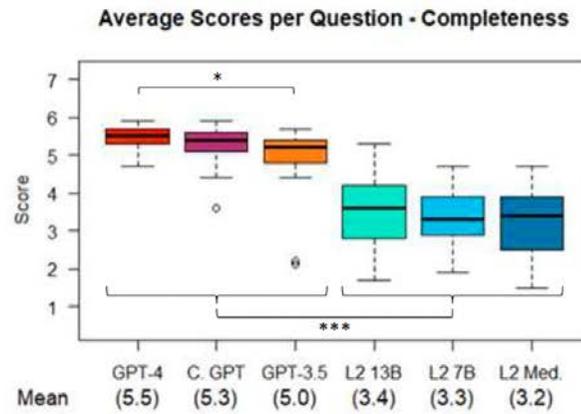
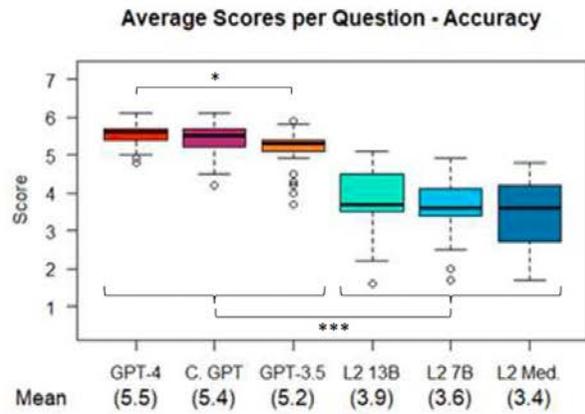
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## OpenAI wins!

... however, the development is fast.

See this is as a **blueprint** how to compare and validate the performance of **LLMs for diagnostic stewardship** in the future.

# Domain level expertise remains critical!



Bressan M, Meijer E, ... et Egli A, unpublished

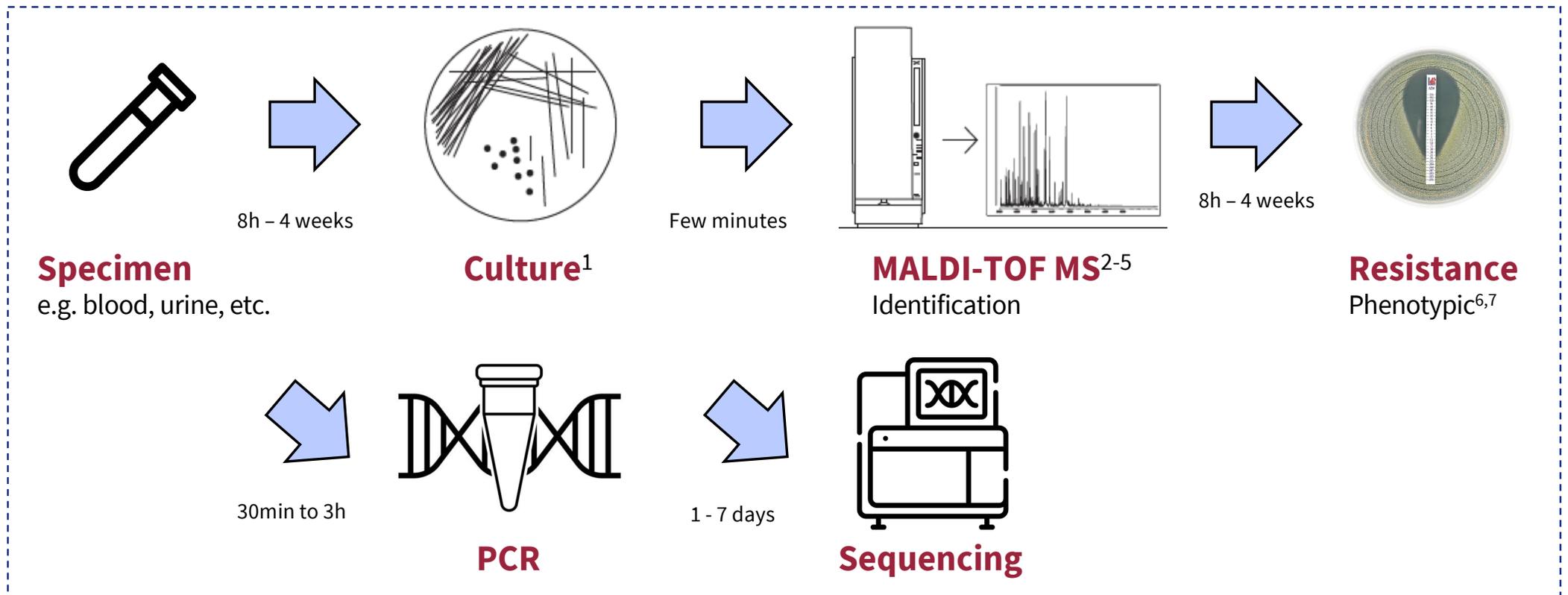
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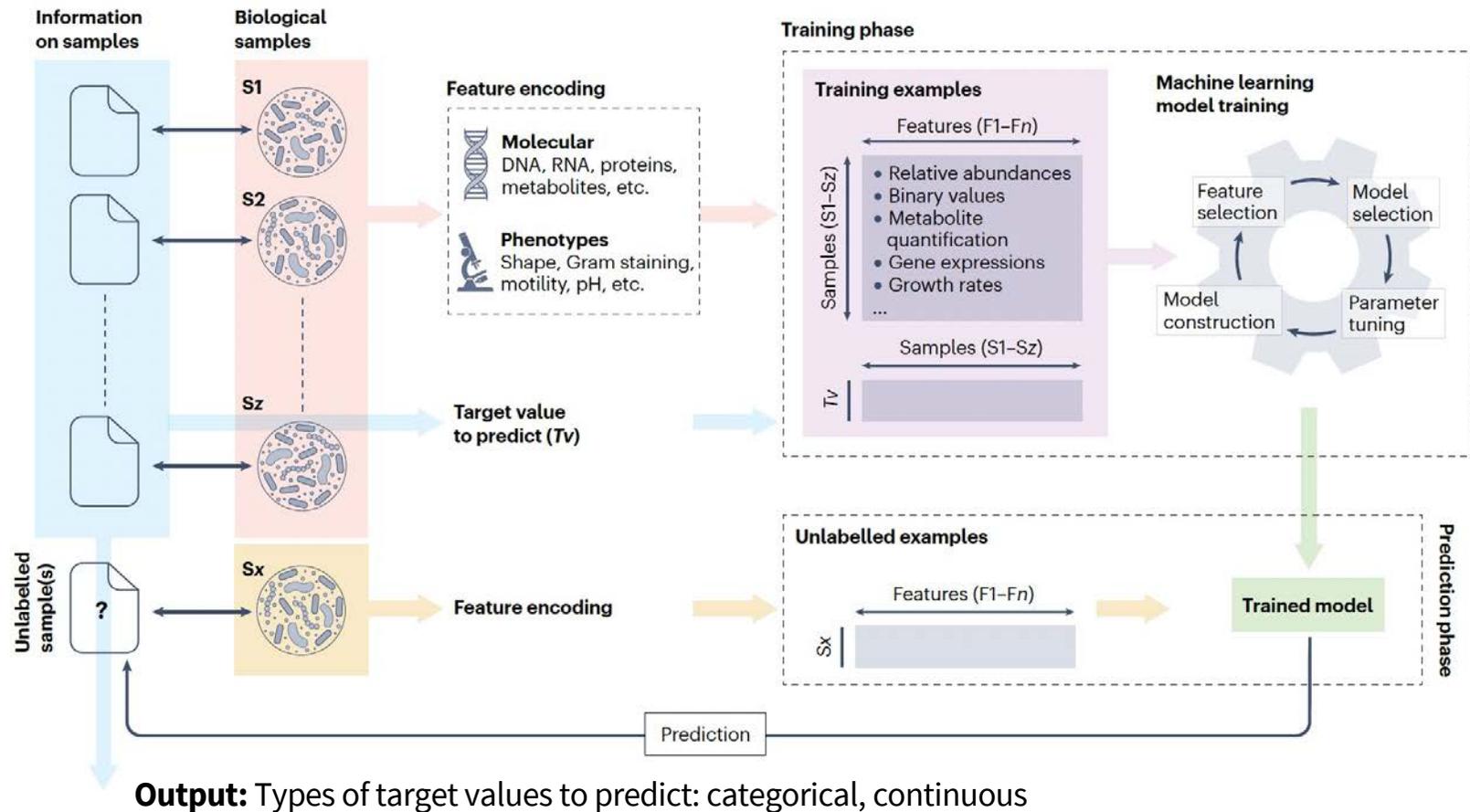
... but what is more interesting:  
 → The more away a healthcare expert from his domain expertise, the **less critical** the person is...

# Analytics in routine labs



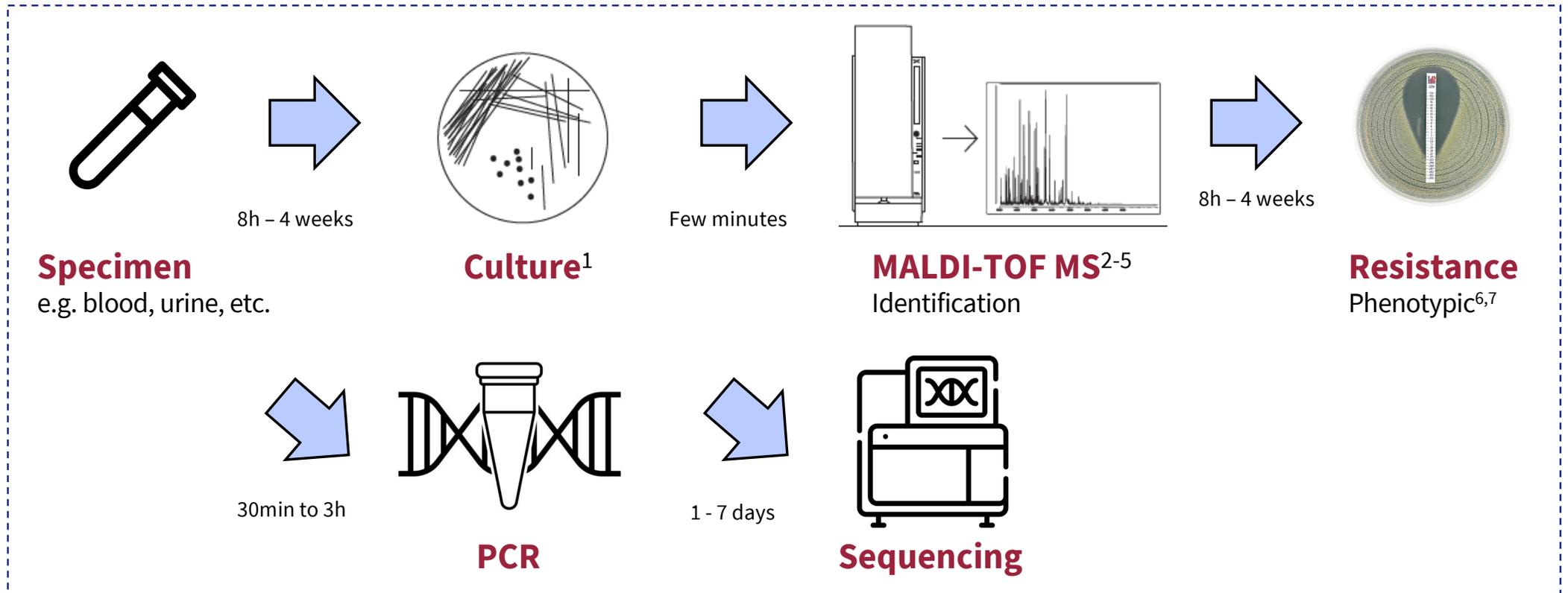
<sup>1</sup>Hinic V, Amrein I, ... et Egli A J Micro Met 2017; <sup>2</sup>Dierig A, Frei R, Egli A, Ped Infect Dis J 2015 <sup>3</sup>Egli A et al. Transpl Infect Dis 2015; <sup>4</sup>Osthoff M, ... et Egli, A. Clin Microbiol Infect 2017; <sup>5</sup>Weis C, ... Egli A, Borgwardt K, Bioinformatics 2020; <sup>6</sup>Egli A, Schmid H, et al. Clin Microbiol Infect 2017; <sup>7</sup>Hinic V, Reist J, Egli A J Microbiol Met 2018

# Basic concept of AI in medical microbiology



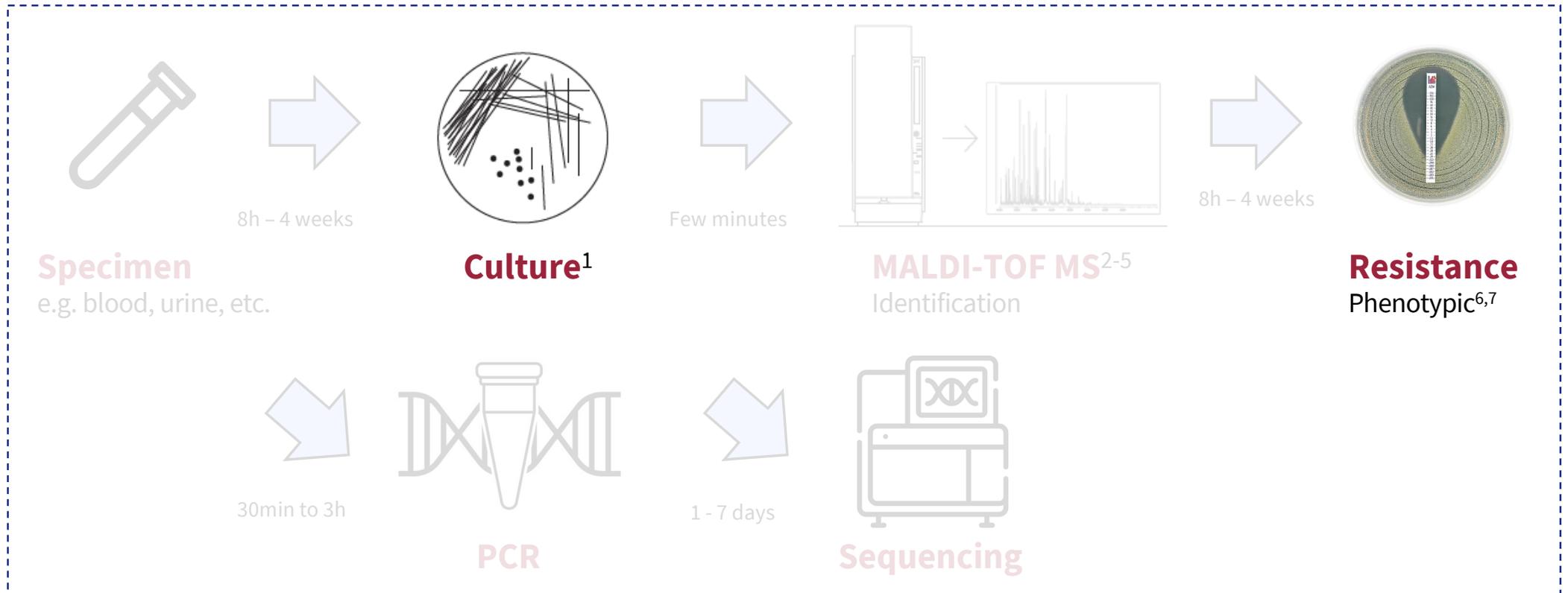
Asnicar F, Thomas AM, et al. Nature Rev Microbiology, 2024

# Analytics in routine labs



<sup>1</sup>Hinic V, Amrein I, ... et Egli A J Micro Met 2017; <sup>2</sup>Dierig A, Frei R, Egli A, Ped Infect Dis J 2015 <sup>3</sup>Egli A et al. Transpl Infect Dis 2015; <sup>4</sup>Osthoff M, ... et Egli, A. Clin Microbiol Infect 2017; <sup>5</sup>Weis C, ... Egli A, Borgwardt K, Bioinformatics 2020; <sup>6</sup>Egli A, Schmid H, et al. Clin Microbiol Infect 2017; <sup>7</sup>Hinic V, Reist J, Egli A J Microbiol Met 2018

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How to change the  
design

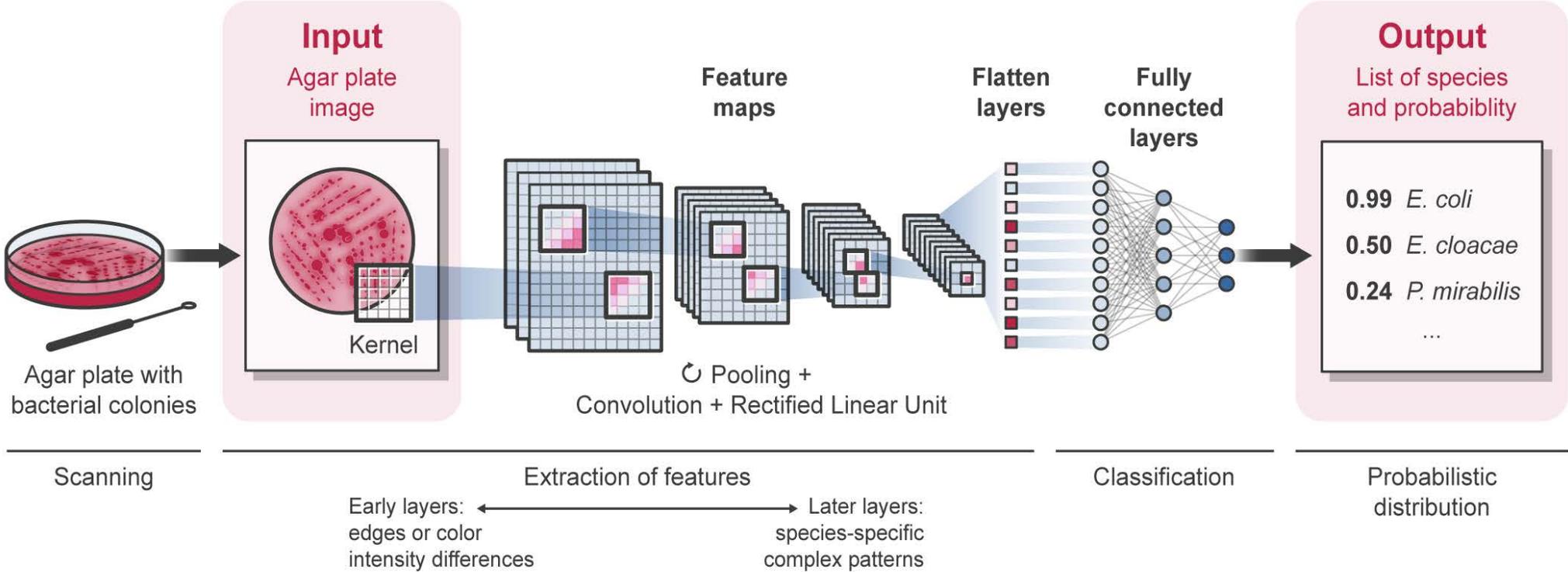


**What kind of bacterial species do you see here?**

① The Slido app must be installed on every computer you're presenting from

**slido**

# What is a convolutional neural network?



Weber L, ... et Egli A, in prepare

# Culture plates on total lab automation

## Detection of colonies

— positive vs. negative plates; Sensitivity 97-99%; specificity 94-99%. [1-2]

## Identification of bacterial species

— *Staphylococcus aureus*, *E. coli*, etc. with specificity of 94%-99%. [1-4]



Special thanks to  
Dr. Oliver Nolte  
for providing the images

[1] Croxatto A et al. Biomedical J 2017; [2] Glasson J et al JCM 2016; [3] Cherkaoui A, Renzi G et al. Front Cell Infect Microbiol 2019

[4] Signoroni A et al. Nat Commun 2023

# Automated reading of resistance

Automated measurement of inhibition zones: principles. [1-2]

“Lot of work remains to be done before achieving a smooth work-flow. Currently all results are approved by clinical microbiologists, but in the near future these instruments would automatically deliver S/I/R categories without requiring a human check.” [3]

*Pseudomonas aeruginosa*

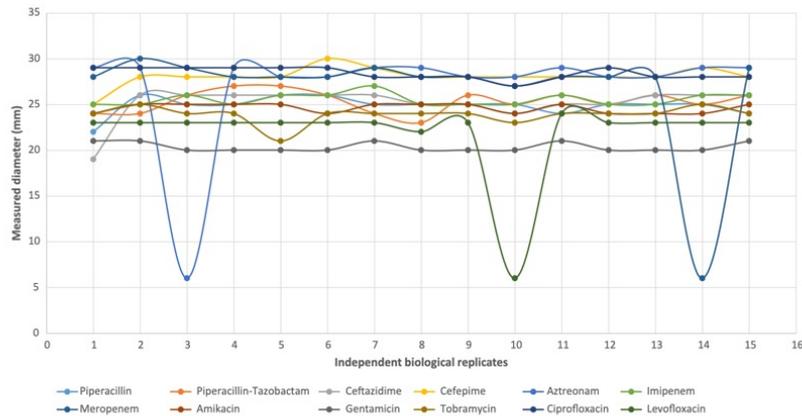


Fig. 1. Distribution of inhibition zone diameters on WASPLab using BioRad antibiotic discs for different antibiotics tested for 15 independent biological replicates of *Pseudomonas aeruginosa* ATCC 27853.

*E. coli*

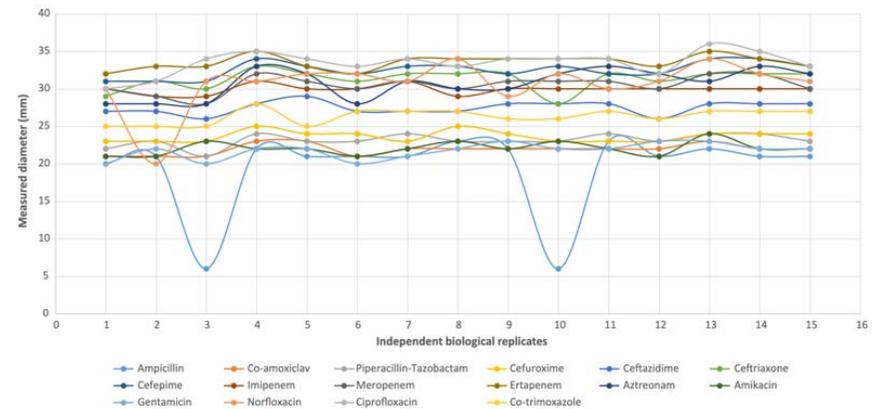


Fig. 3. Distribution of inhibition zone diameters on WASPLab using BioRad antibiotic discs for different antibiotics tested for 15 independent biological replicates of *Escherichia coli* ATCC 25922.

[1] Cherkaoui A, Renzi G, et al. CMI 2019; [2] Hombach M et al. JAC 2017; [3] Dauwalder O et Vandenesch F, CMI 2020

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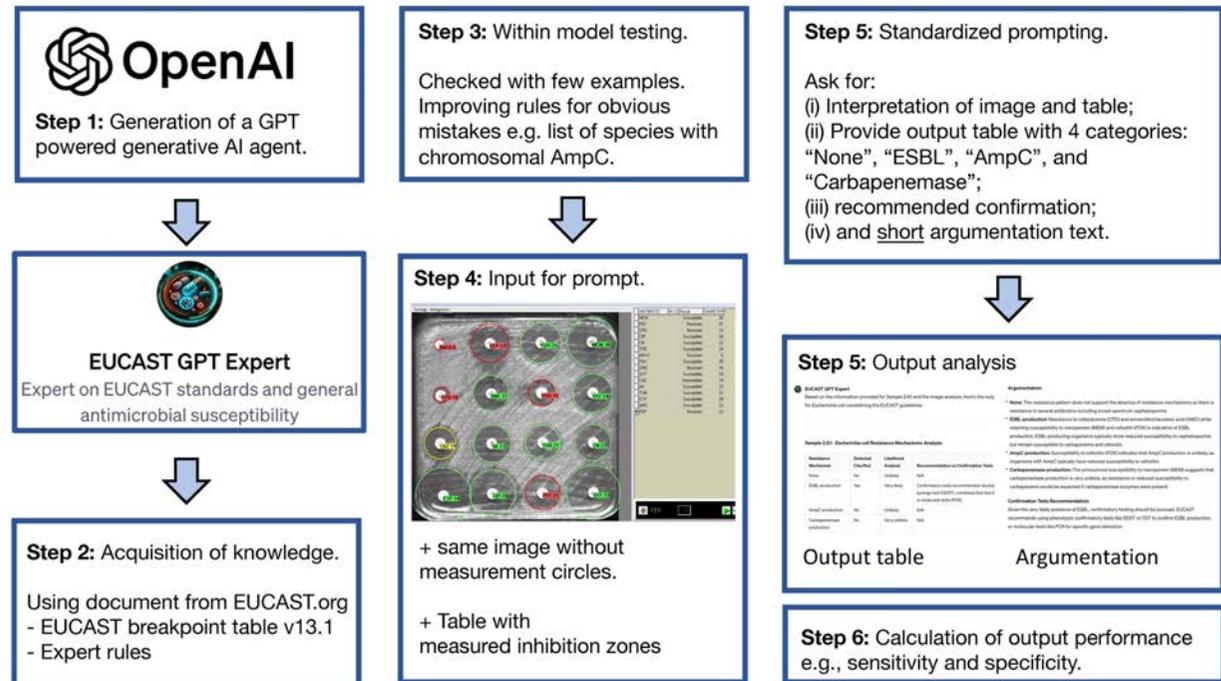
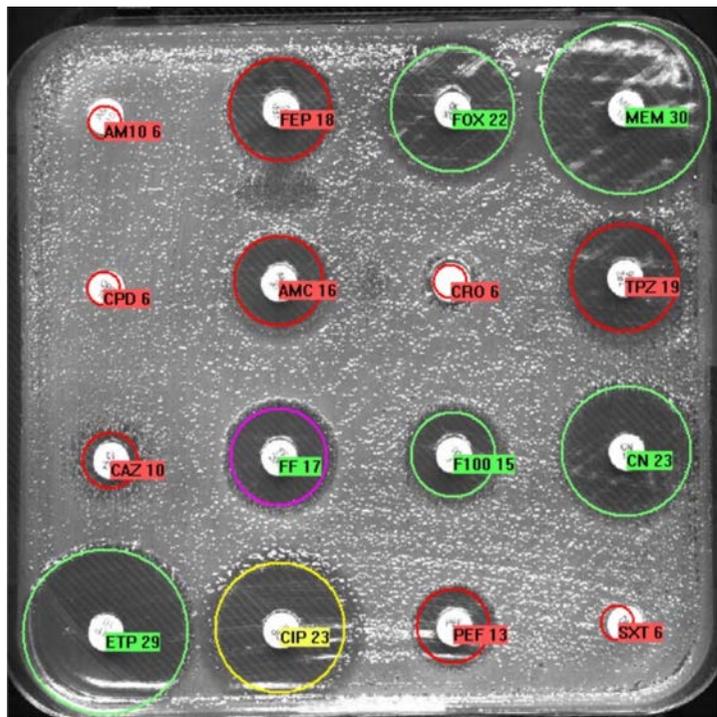
**slido**

# Customized GPT as an expert



Prof. Ch. Giske Dr. M. Bressan

**Leading question:** Can we use a multi-modal LLM to predict the underlying molecular resistance mechanism?



Giske Ch, Bressan M, ... Egli A, JCM 2024

## Human expert vs. custom GPT

		Human experts <sup>a</sup>	EUCAST-GPT-expert <sup>b</sup>
<b>ESBL</b>	Sensitivity	98.0% (91.8 – 100)	95.4% (94.5 – 96.3)
	Specificity	99.1% (97.1 – 100)	69.2% (63.8 – 85.7)
<b>AmpC</b>	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)
<b>Carbapenemases</b>	Sensitivity	95.5% (90.9 – 100)	100% (90.9 – 100)
	Specificity	98.5% (98.5 – 98.5)	98.8% (98.8 – 98.8)

Giske Ch, Bressan M, ... Egli A, JCM 2024

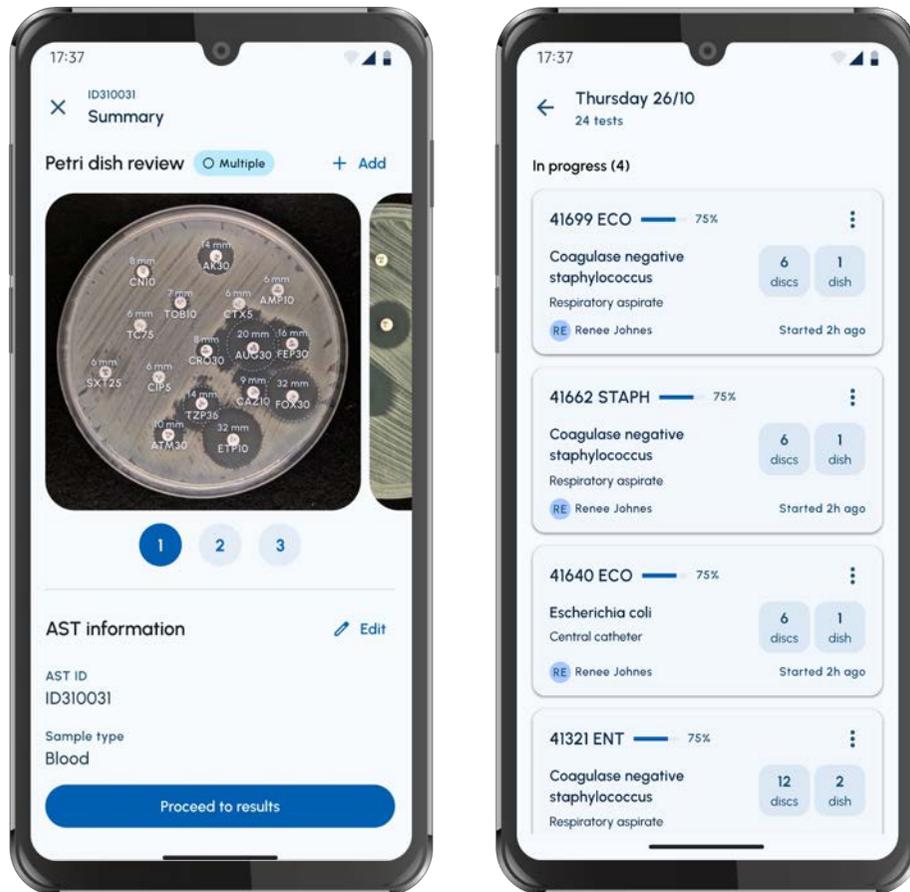
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	Specificity	98.5% (98.5 – 98.5)	98.8% (98.8 – 98.8)

- Customized GPT is necessary (domain level expertise), as GPT-4 cannot provide a useful output.
- **Specificity of human experts much better** than the AI.
- Prospective validation is necessary.

Giske Ch, Bressan M, ... Egli A, JCM 2024

# Antibiogo – a tool by Medecins sans frontieres



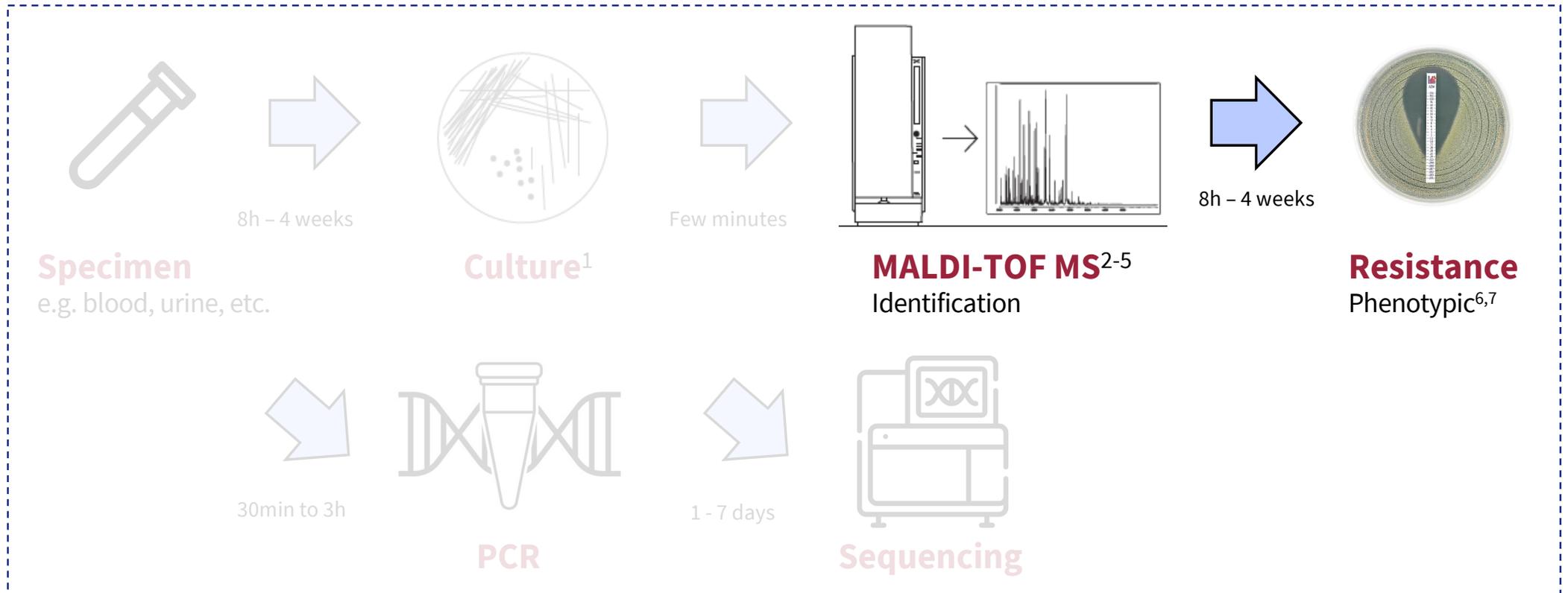
ASTapp is a **free, offline** application to help the non-expert staff in low resources setting laboratories with the **interpretation of antibiograms**.

CE approved.

Early (non-peer reviewed) validation:  
“For evaluation of the ES, 509 paired samples were read in parallel, and **agreement of the measured diameters was excellent** ( $R^2=0.95$ ). The ES correctly classified 474 (95.2%) of 498 interpretable samples (95% CI 92.9- 97.4), corresponding to a Krippendorff’s alpha value of 90.6% (95% CI 87%-94%).”<sup>1</sup>

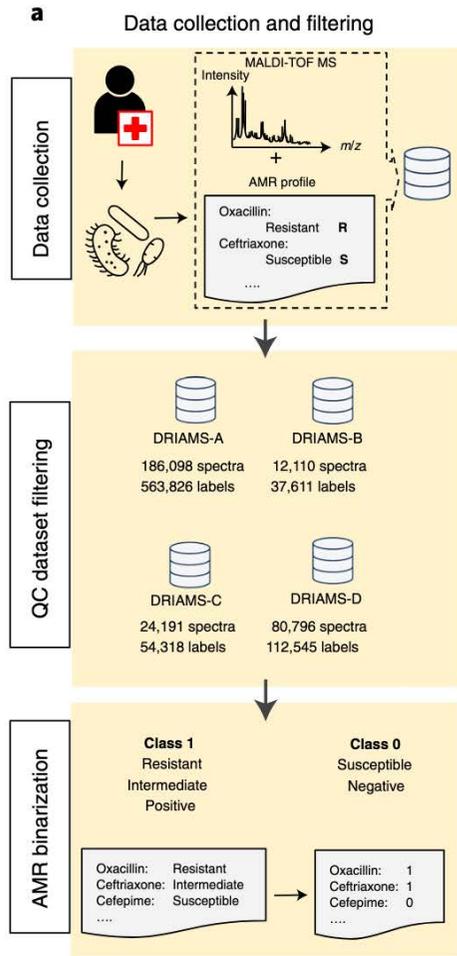
1 Malou N, Al Asmar M, et al. MSF Science Portal 2021

# Analytics in routine labs



<sup>1</sup>Hinic V, Amrein I, ... et Egli A J Micro Met 2017; <sup>2</sup>Dierig A, Frei R, Egli A, Ped Infect Dis J 2015; <sup>3</sup>Egli A et al. Transpl Infect Dis 2015; <sup>4</sup>Osthoff M, ... et Egli, A. Clin Microbiol Infect 2017; <sup>5</sup>Weis C, ... Egli A, Borgwardt K, Bioinformatics 2020; <sup>6</sup>Egli A, Schmid H, et al. Clin Microbiol Infect 2017; <sup>7</sup>Hinic V, Reist J, Egli A J Microbiol Met 2018

# Can we predict AMR profiles directly from MALDI-TOF?



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Basel**

Aline Cuénod, Michael Osthoff  
Kirstine K. Soegaard, Adrian Egli

**ETH zürich**

Caroline Weis, Bastian, Rieck,  
Karsten Borgwardt

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Claudia Lang, Olivier Dubuis

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Aarau

Michael Oberle

**Kantonsspital  
Baselland**

Susanne Graf

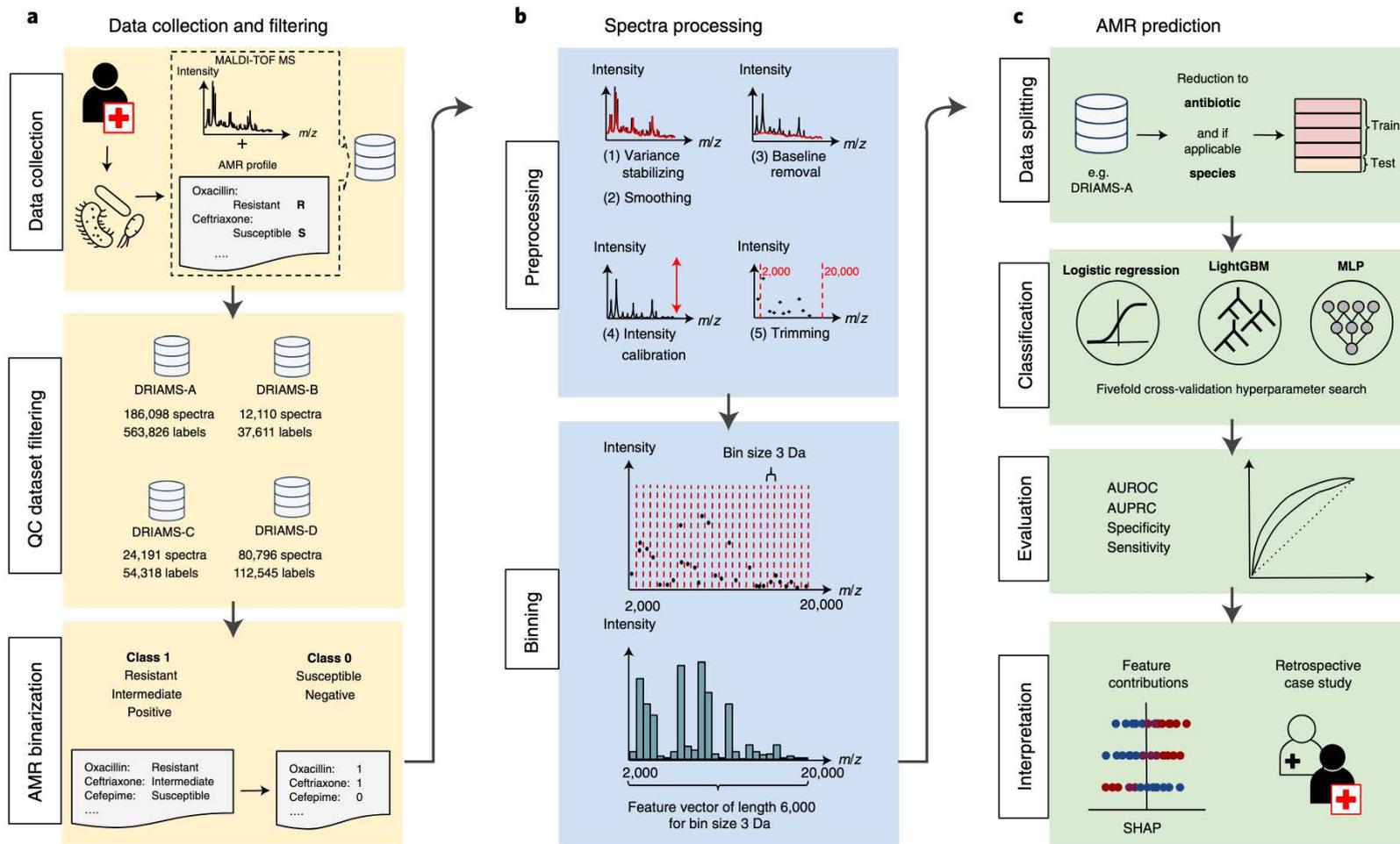


Dr. C. Weis



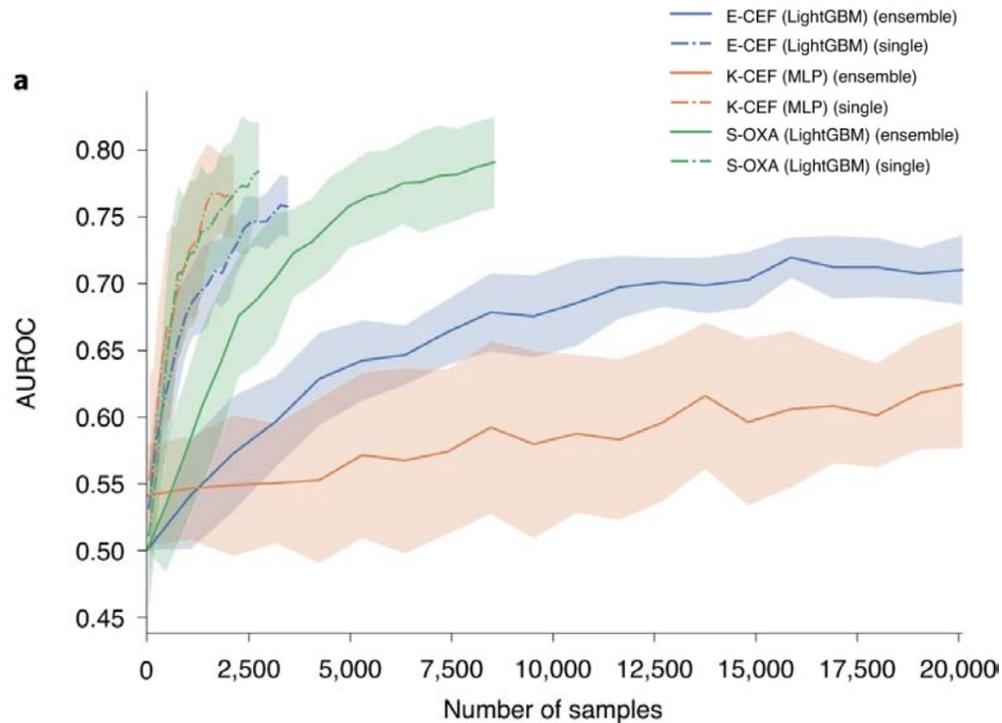
Dr. A. Cuénod

[1] Weis C, Cuénod A, ... et Egli A, Nature Med 2021; [2] Weis C, et al. Bioinformatics 2020



[1] Weis C, Cuénod A, ... et Egli A, Nature Med 2021; [2] Weis C, et al. Bioinformatics 2020

# Prediction of AMR phenotypes directly from MALDI-TOF MS



## Prediction of **susceptibility**

		AUROC
<i>S. aureus</i>	Oxacillin	0.8
<i>E. coli</i>	Ceftriaxon	0.74
<i>K. pneumoniae</i>	Ceftriaxon	0.74

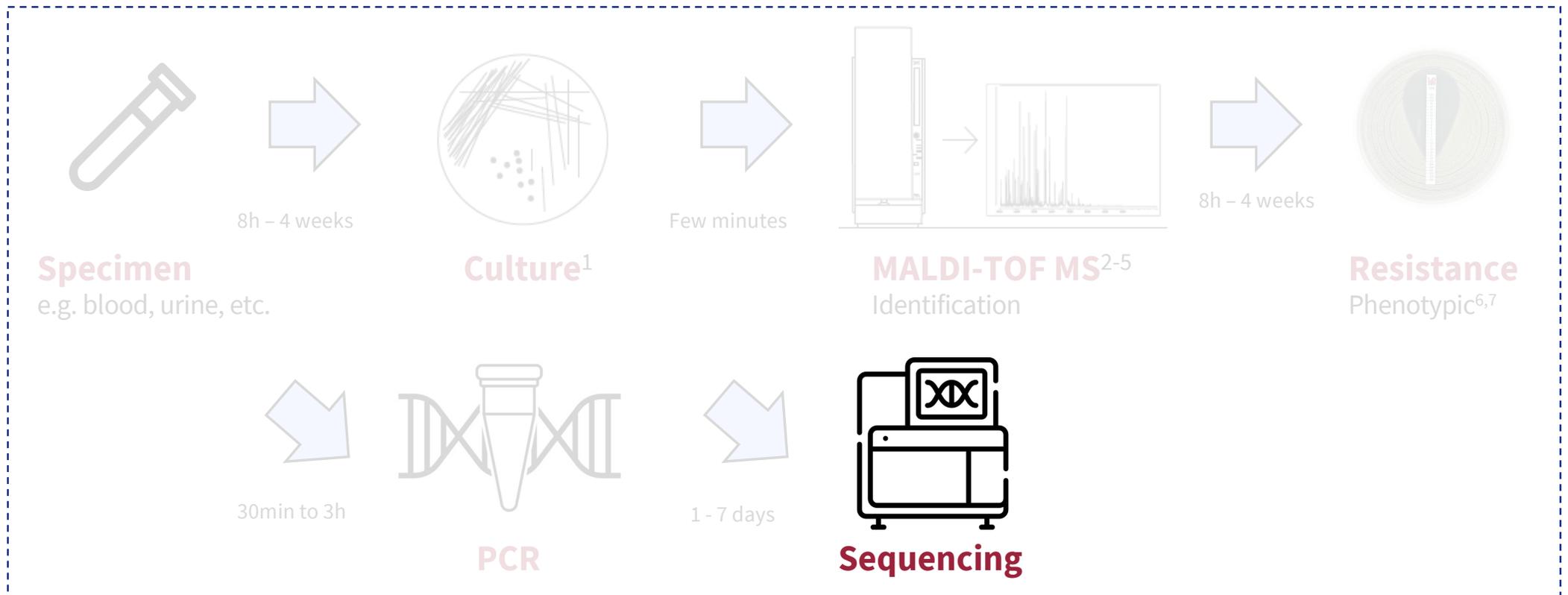
→ **Not perfect, but promising**

DRIAMS data set is public available.

Multiple studies confirmed findings [1-8]

[1] Weis C, Cuénod A, ... et Egli A. Nature Med 2021; [2] Ren M, Chen Q, et al. Scientific Reports, 2024; [3] Astudillo CA, Lopez-Cortes XA et al. Scientific Reports 2024; [4] Nguyen HA, Peleg AY, et al. mSystems 2024; [5] Lopez-Cortes XA, Mariquez-Trocoso JM et al. Int J Mol Sci 2025; [6] De Waele G, Menschaert G, et al. Elife 2024; [7] Wang WY, Chui CF, et al. Int J Antimicrob Agents 2024; [8] Yu J, Lin HH et al. Int J Antimicrob Agents 2023

# Analytics in routine labs



<sup>1</sup>Hinic V, Amrein I, ... et Egli A J Micro Met 2017; <sup>2</sup>Dierig A, Frei R, Egli A, Ped Infect Dis J 2015 <sup>3</sup>Egli A et al. Transpl Infect Dis 2015; <sup>4</sup>Osthoff M, ... et Egli, A. Clin Microbiol Infect 2017; <sup>5</sup>Weis C, ... Egli A, Borgwardt K, Bioinformatics 2020; <sup>6</sup>Egli A, Schmid H, et al. Clin Microbiol Infect 2017; <sup>7</sup>Hinic V, Reist J, Egli A J Microbiol Met 2018

# The holy grail: Direct genotype to phenotype prediction

- Databases e.g. CARD<sup>1</sup>, other databases <sup>12</sup>
- Pangenome gene feature selection<sup>2</sup>
- Plasmid prediction<sup>11</sup>

## Specific pathogens

- MTB<sup>4, 8</sup>

- ESKAPEE<sup>5, 6, 9, 10</sup>

- *H. pylori*<sup>7</sup>

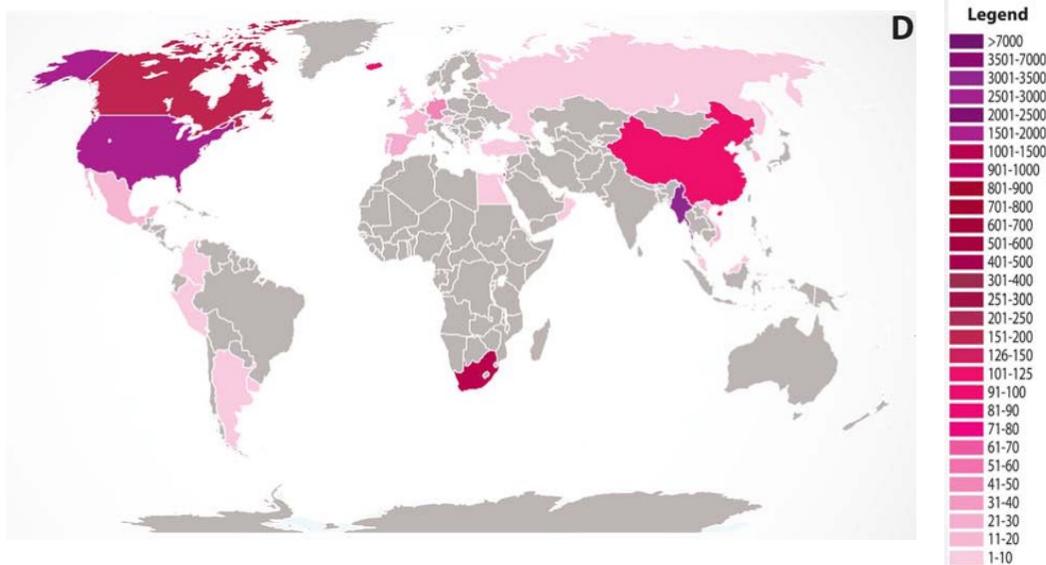
1 Alcock BP, et al. Nucleic Acids Research 2023; 2 Yang MR et Wu YW BMC Bioinformatics 2022; 4 Kuang X et al. Scientific Reports 2022; 5 Sharma R et al. J Biomed Health Inform 2024; 6 Nsubuga M et al. BMC Genmimics 2024; 7 Yu J et al Front Cell Infect Microbiol 2023; 8 Yurtseven A et al. BMC Microbiology 2023; 9 Btisti Biffignandi G et al. Microbial Genomics 2024; 10 Shaik S et al. mBio 2022; 11 van der Graaf-van Bloois L et al. Microb Genom 2021; 12 VanOeffelen M et al. Briefings in Bioinformatics 2021

# Using public data for machine learning

A broad range of papers. Few good ones – most are retrospective!

Good example:

Databases e.g. curated DB<sup>1</sup> with 67k+ genomes → open source, 4 species with >5k isolates: *M. tuberculosis*, *S. enterica*, *S. pneumoniae*, and *N. gonorrhoeae*, nevertheless strong sequencing bias!



Available genome sequences of *Streptococcus pneumoniae* are strongly biased!

<sup>1</sup> VanOeffelen M et al. Briefings in Bioinformatics 2021



## Many use cases, total hype

- **Pre- to post-analytics** e.g. LLMs to communicate
- **Image analysis**
  - measurement of inhibition zone and categorical interpretation
  - multi-modal large language for determination of molecular resistance mechanism
- **MALDI-TOF MS**
  - Direct prediction of resistance from spectra
- **Whole genome sequencing**
  - Aiming for the minimal inhibitory concentration

**Do not edit**  
How to change the  
design

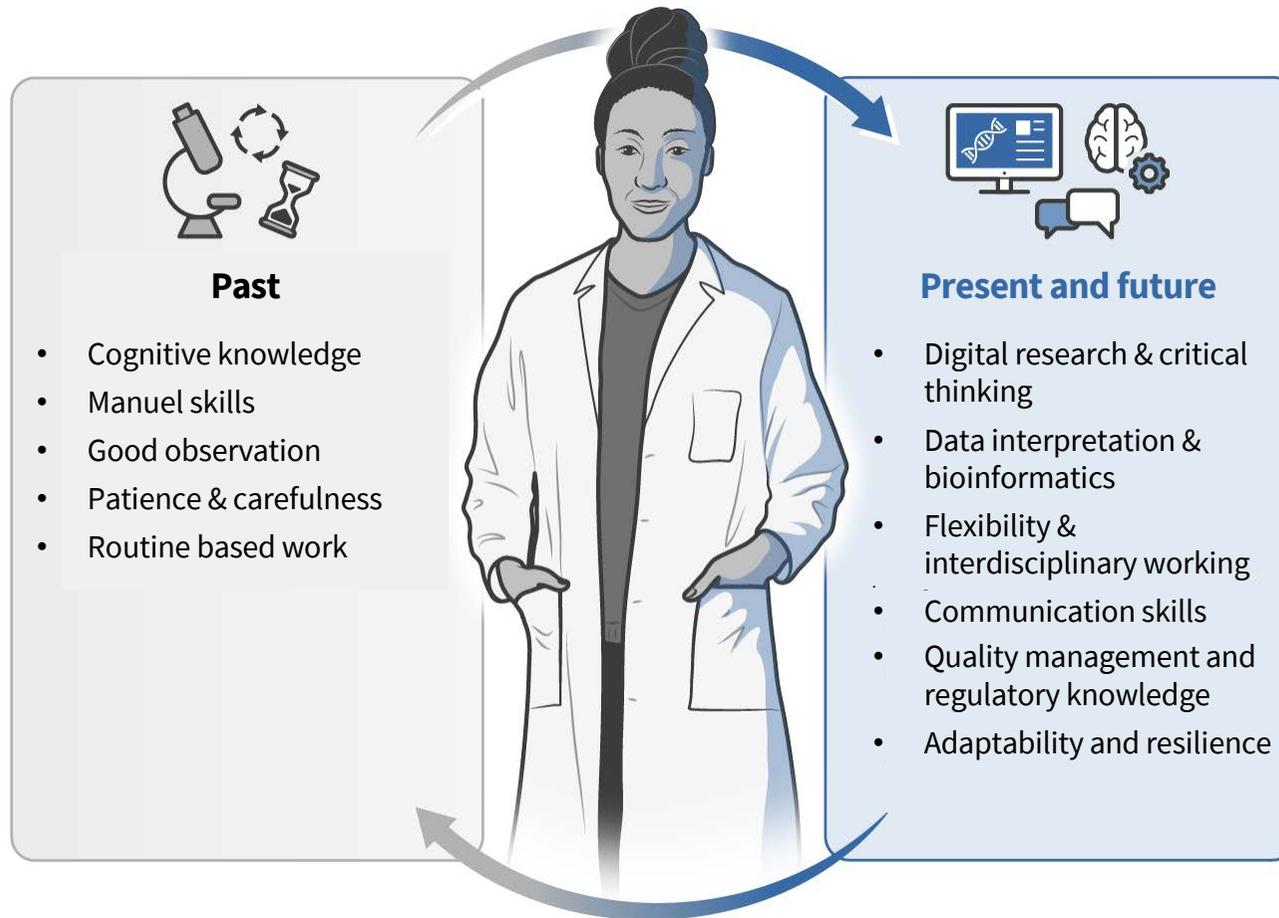


**Does this sound too good to be true?**

① The Slido app must be installed on every computer you're presenting from

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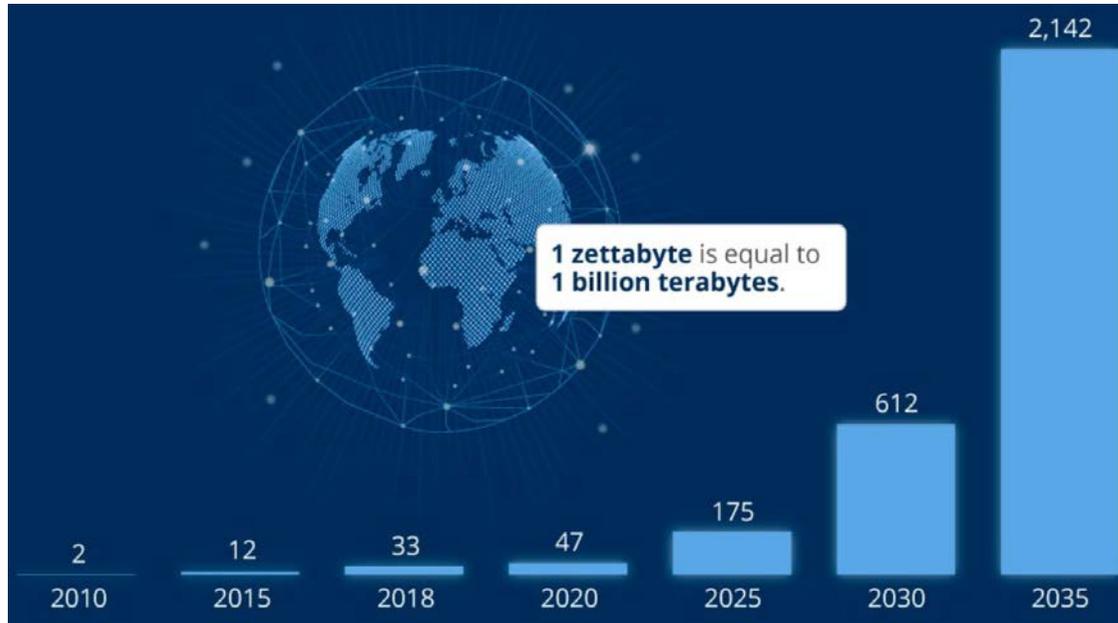
# Education is key! How to keep up with the development



- Regular and continuous education is critical.
- Adaptation of curricula for lab technicians and microbiologists
  
- It is very likely that in 10 years, we cannot define ourselves via knowledge.

Egli Andrea & Egli Adrian, LabMag 2025, in press

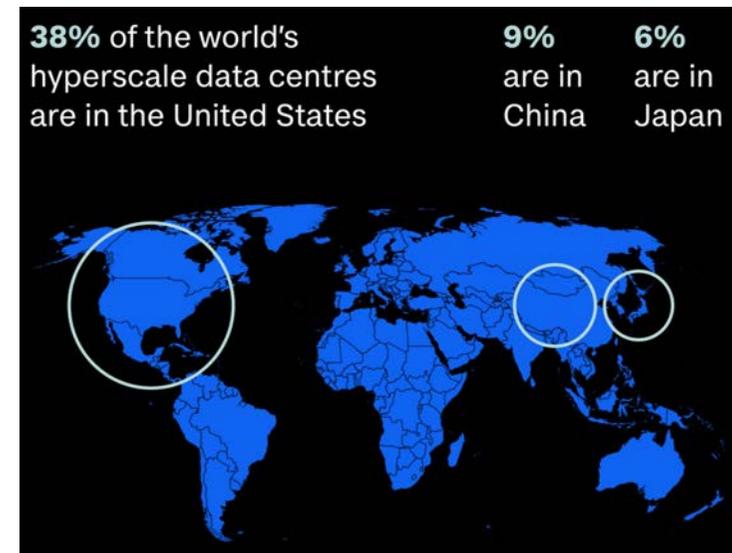
## Critical aspects: Data storage & bias



- 541 hyperscale data centers. 41.5% at Amazon!
- Shared data is heavily biased.
- Open data is absolutely critical for public health.
- Follow FAIR data criteria.

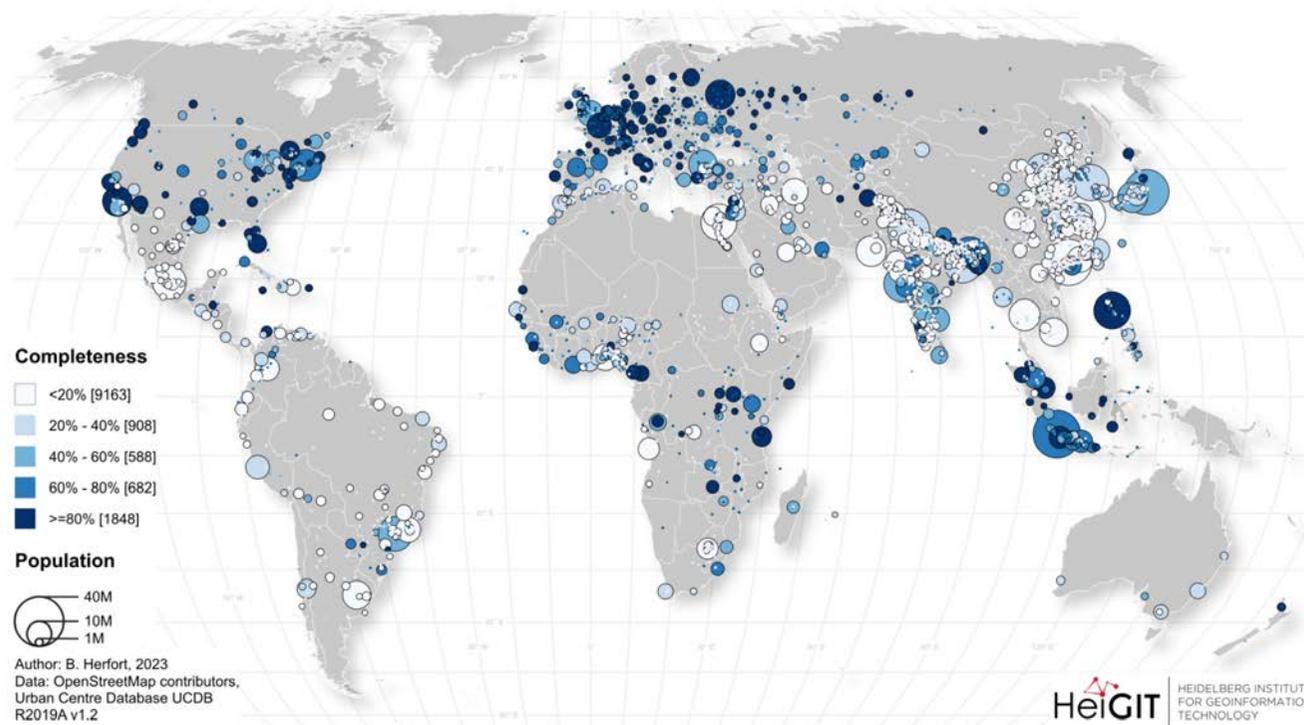
IDC Global DataSphere, Nov 2018; Statista.com

- **Massive expansion of data** stored in gigantic data centers. Rapid decline of storage costs (about 1000-fold lower in the past 20 years). 30% real data, 70% synthetic data e.g. simulations, modelling, etc.
- First 19-sec Youtube Video “Me at the Zoo” 23. April 2005, 361M views.
- 1 billion hours of Youtube videos are consumed per day. 82 years of content is uploaded every day.

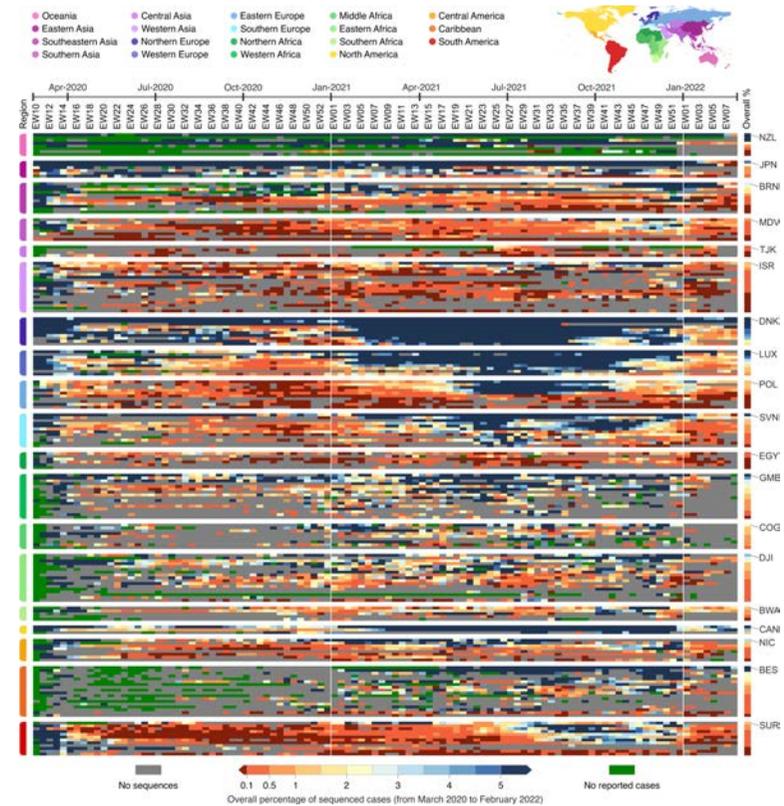


# LMICs are clearly under-represented but have the highest public health burden of disease

## Streep Map contributions

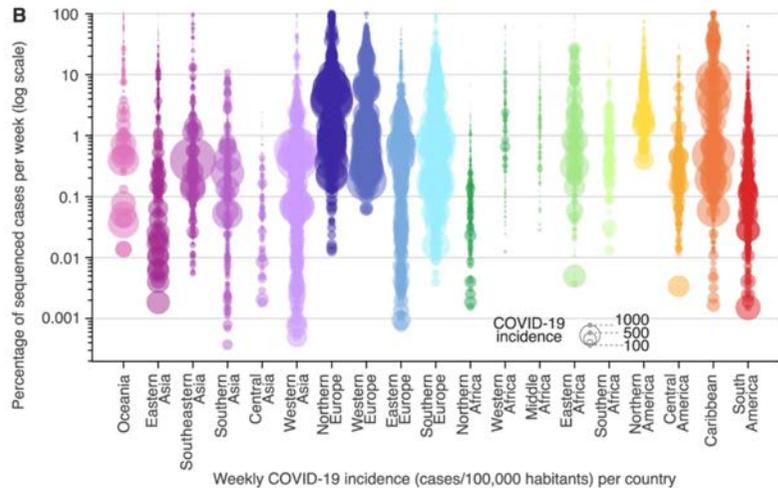


## COVID 19 Sequencing



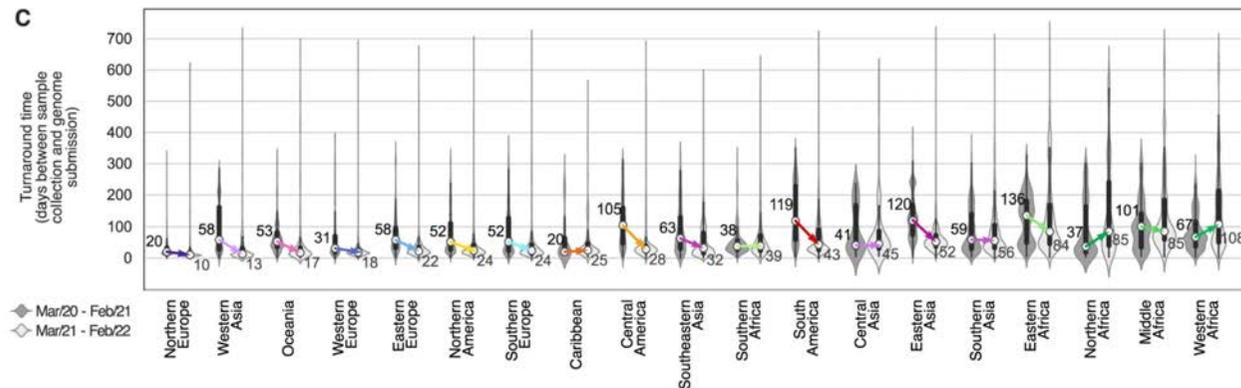
Herfort B, Lautenbach S, et al. Nat Commun 14, 3985, 2023; Brito AF, Semenova E, et al. Nat Commun 7003, 2022

# Percentage of sequenced cases and turnaround time in high- vs. LMICs



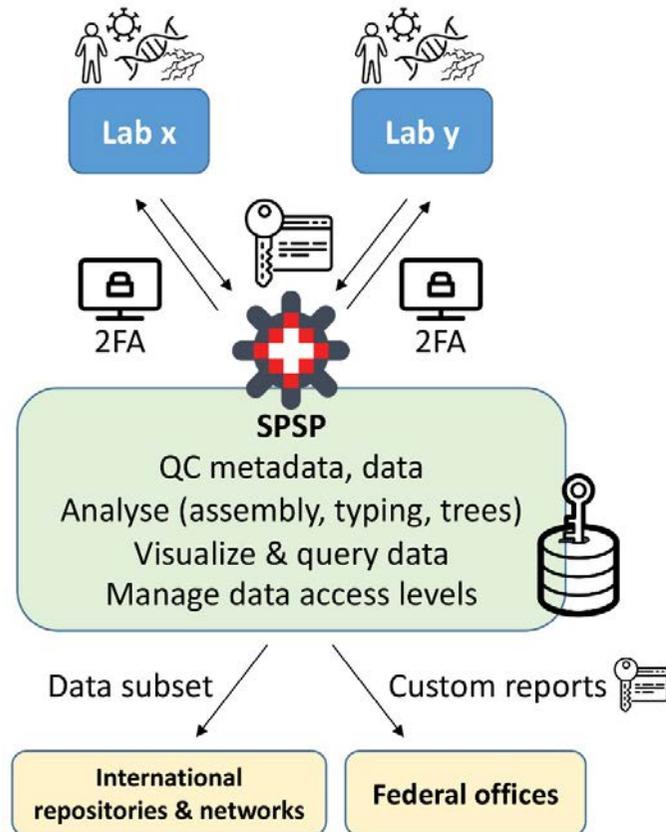
## Significant variation:

- Much more cases sequenced.
- Turnaround time was prolonged in some LMICs.
- How much sequencing is necessary?
- Switzerland sequenced 3.6% of all cases – also with 35% of all sequenced cases introduction of new variants would not have been substantially delayed <sup>(1)</sup>
- Some countries have not shared their sequences!



Brito AF, Semenova E, et al. Nat Commun 7003, 2022; <sup>(1)</sup> Wegner F, Cabrera-Gil B, et al. Microbiol Spectr 2024

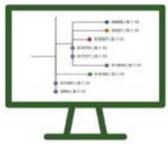
# National data sharing incentives for public health: Swiss Pathogen Surveillance Platform and AusTrakka.





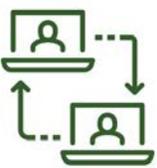
**PLATFORM ARCHITECTURE**

- Secure platform stored on Cloud (Microsoft Azure and Active Directory)
- Role-based authorisation (e.g. uploader, viewer, admin)
- Uploads of sequence and corresponding epidemiological data
- On-demand running of containerized bioinformatic pipelines (Docker)



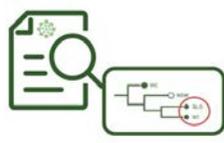
**PLATFORM FUNCTIONS**

- Quality control and validation of uploaded data
- Perform species-specific *in silico* genotyping and other assays
- Interactive phylogenetic tree with epidemiological annotations
- Real-time updates triggered by new data
- Identification of potential outbreak clusters



**TEAM FUNCTIONS**

- Ensure appropriate governance and data sharing processes
- Assess and investigate outbreaks and clusters
- Respond to requests for genomic investigation
- Teaching and training
- Continuous improvement process



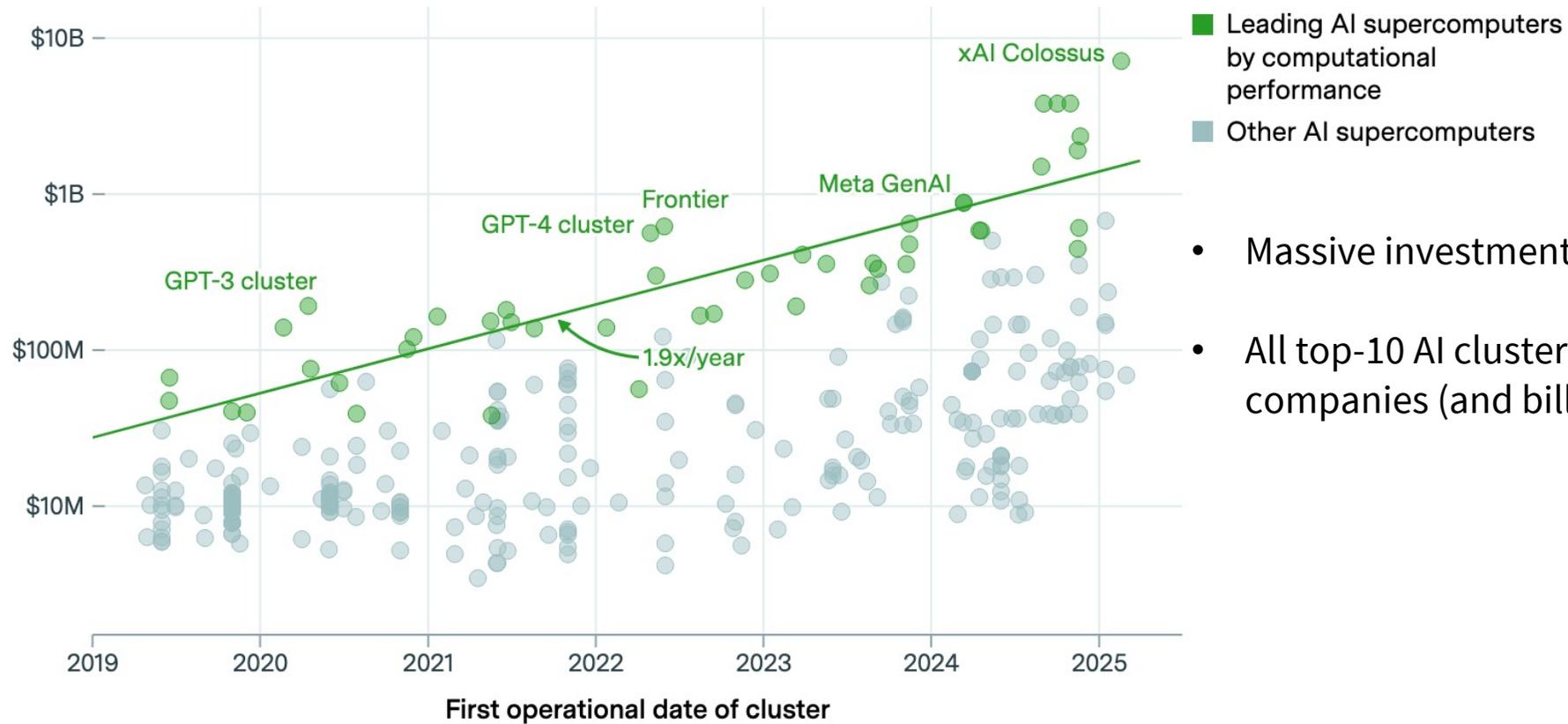
**OUTPUTS**

- Interactive phylogenetic tree with epidemiological annotations
- Detailed genomic content report (genotype, AMR, virulence, lineage)
  - Systematic detection of SARS-CoV-2 Variants of Concern
  - Surveillance of primers and probes for SARS-CoV-2 diagnostics
- Integrated genomic surveillance reports to health authorities
- Multi-jurisdictional outbreak reports

Neves A, Walther D, et al. Microbial Genomics 2023;9:001001; Huang T, Goncalves da Silva A, et al. Nat Communications 2022, 13:865

# Critical aspects: Commercial dependency

Hardware cost (USD)



- Leading AI supercomputers by computational performance
- Other AI supercomputers

- Massive investments are necessary.
- All top-10 AI clusters are owned by companies (and billionaires).

<https://epoch.ai/blog/compute-trends>

**Do not edit**  
How to change the  
design



**How often do you use modern  
Chatbots like ChatGPT (and alike)  
per day?**

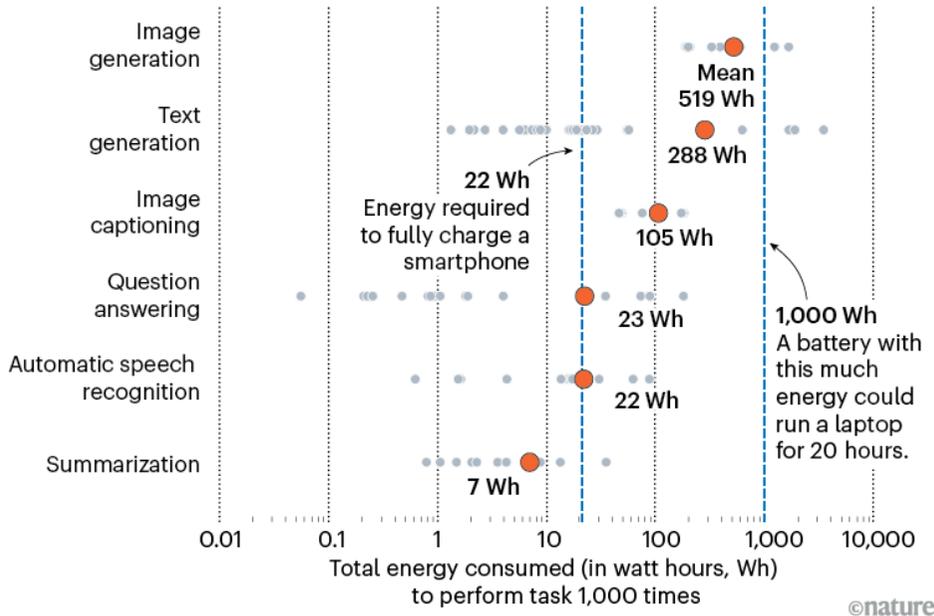
① The Slido app must be installed on every computer you're presenting from

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# Critical aspects: Infinite energy hunger

## HOW MUCH ENERGY DOES AI USE?

The AI Energy Score project tested dozens of artificial-intelligence models to estimate how much energy they consume when performing various tasks. Plotting the energy required to perform a task 1,000 times shows that energy use varies greatly depending on the task and the model.



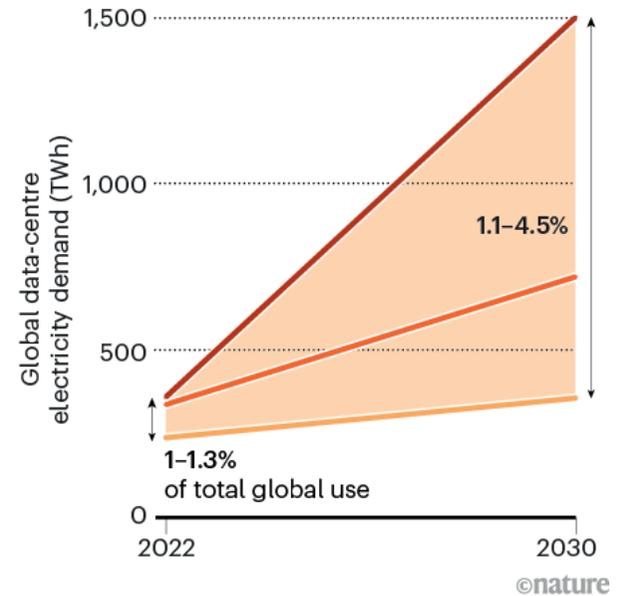
## DATA CENTRES' MODEST GLOBAL IMPACT

Data centres currently use 1–1.3% of the world's electricity. But as more are built to supply artificial-intelligence models, they are expected to use up to 4.5% by 2030. The wide range shows the uncertainty in projections.

### Data source

- SemiAnalysis 2024 (base case)
- IEA 2024 (high projection)
- IEA 2024 (low projection)

\*IEA: International Energy Agency, *World Energy Outlook 2024*. The agency says it will release new figures in April 2025.



AI power demand in U.S. from 7 TWh in 2025 to 652 TWh in 2030 (Wells Fargo Securities). In 2023, the US produced 4178 TWh (491b\$, 1.8% of GDP). 1 nuclear plant produces approximate 1 TWh (1 billion kWh). In the U.S. 54 power plants – contributing to 20% of energy.

Chen S, Nature, 05. March 2025; International Energy Agency. *World Energy Outlook 2024* (IEA, 2024)

## Key messages

- ① **Integration of AI into AMR is complex.**
- ② **At each step, high quality and careful evaluation are required. Bias!**
- ③ **The diagnostic lab is good to start due to high regulation (burden)...**
- ④ **Huge promise: From image analysis to sequencing data.**
- ⑤ **Stay critical... And educate yourself!**

“The age of AI has started” Bill Gates 2022

# Acknowledgment

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Website: [www.appliedmicrobiologyresearch.ch](http://www.appliedmicrobiologyresearch.ch)

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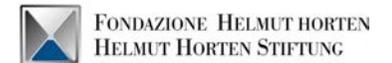
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**Max Planck Institute Munich:** Karsten Borgwardt



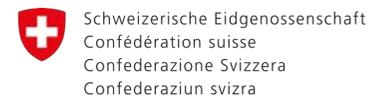
Contact me if you want to collaborate!

## Funding



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Education

# Artificial Intelligence and Machine Learning in Medical Microbiology Diagnostics



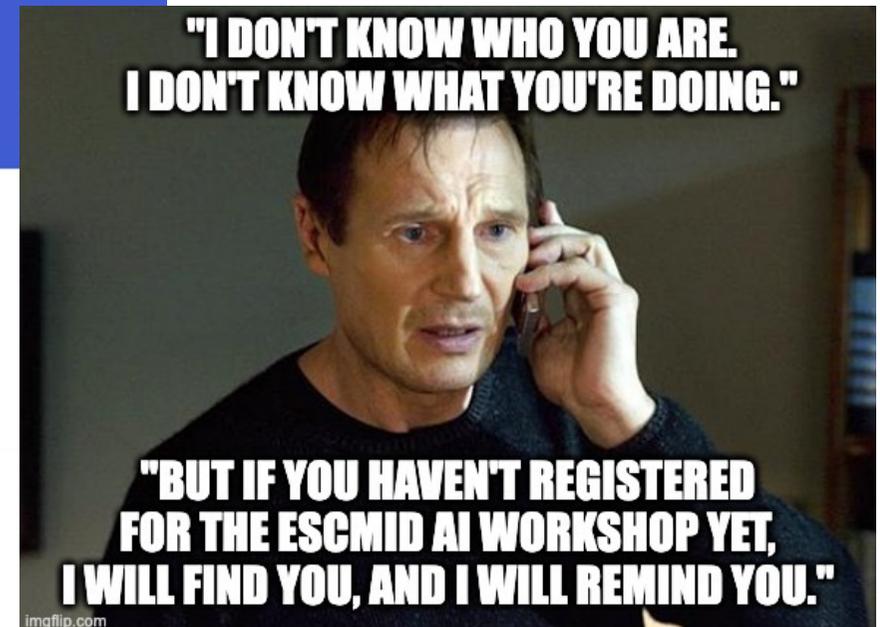
Universität  
Zürich<sup>UZH</sup>

## Event Description

📅 02 - 05 June 2025 📍 Zurich, Switzerland 🔄 Hybrid

**Register now!** It closes very soon...

University of Zurich | Public Health Microbiology in the Digital Era





# AI for modelling epidemics: time series data

**Objective:** Use foundation models (transformer-based) for epidemic time-series analysis.

**Input:** Case incidence data with potential gaps or missing points.

**Model Training:** Transformer architecture trained on empirical and simulated epidemic data.

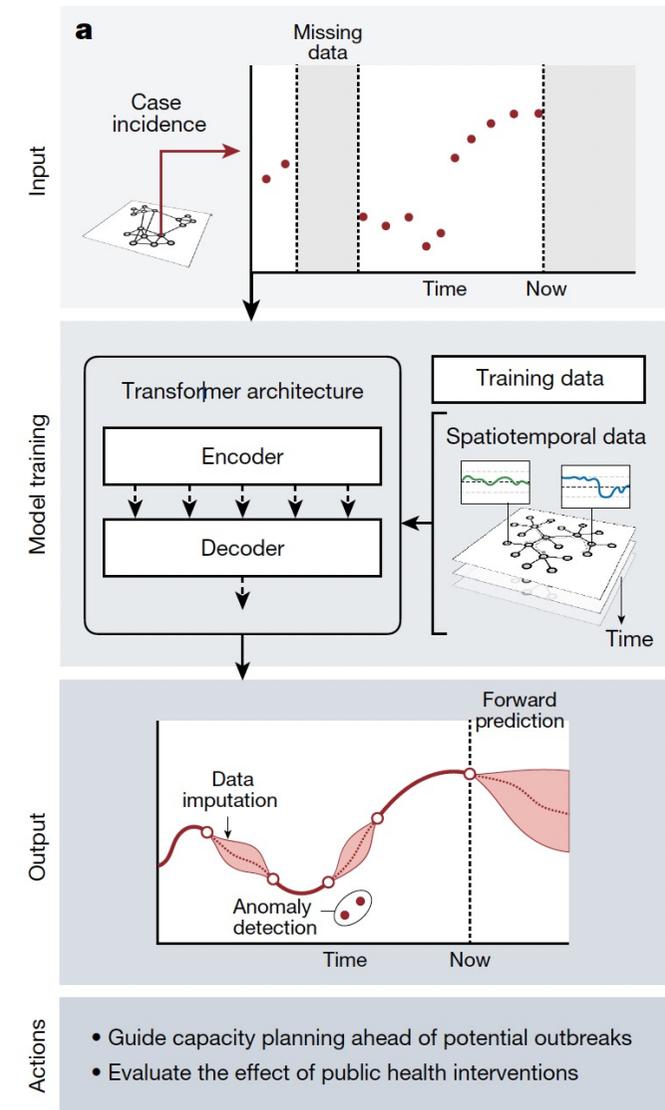
**Output:** Provides data imputation, forward predictions, and anomaly detection.

**Public Health Applications:** Guides resource allocation and evaluates intervention effectiveness.

Foundation models. A large-scale AI model trained on vast datasets, capable of generalizing across tasks, such as analyzing epidemic data, detecting anomalies, and forecasting outbreaks.

Kraemer MUG, Tsui JLH et al. Nature 2025

University of Zurich | Artificial Intelligence in Antimicrobial Susceptibility Testing



# AI for modelling epidemics: GNNs

**Method:** Graph neural networks (GNNs) analyze infectious disease spread.

**Data Structure:** Nodes represent locations/individuals; edges represent transmission pathways.

**Features:** Include disease cases, demographics, healthcare capacity.

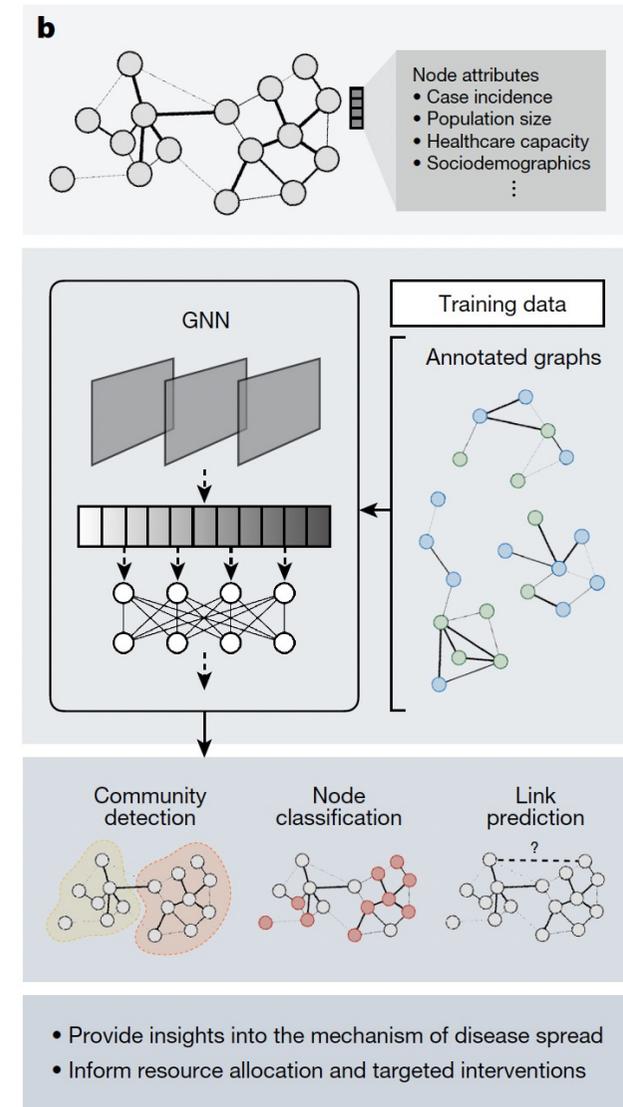
**GNN Capabilities:** Node classification, community detection, and identifying hidden transmission routes.

**Public Health Impact:** Clarifies disease spread dynamics, aiding targeted interventions and resource allocation.

Graph neural networks. AI models analyzing data structured as graphs (nodes and edges) to identify infection clusters, transmission links, and predict disease spread.

Kraemer MUG, Tsui JLH et al. Nature 2025

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# AI for modelling epidemics: protein prediction

**Goal:** Predict immune-escape mutations using deep learning.

**Method:** Uses structural prediction tools (AlphaFold, ESMFold) to analyze viral genomes.

**Application:** Identifies mutations disrupting antibody binding, indicating potential vaccine resistance.

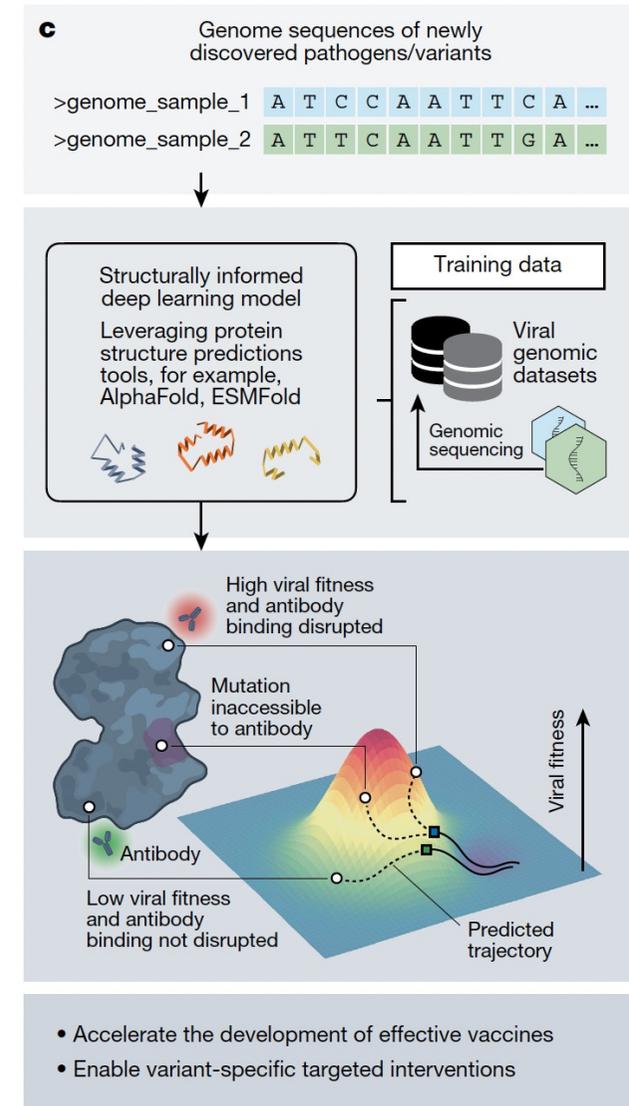
**Impact:** Accelerates next-generation vaccine development.

**Public Health Action:** Enables targeted interventions against emerging pathogen variants.

Deep learning models. Models using structural biology (e.g., AlphaFold) predict pathogen mutations that evade immunity, enabling faster vaccine development and targeted containment.

Kraemer MUG, Tsui JLH et al. Nature 2025

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