**Written responses to remaining audience questions of the webinar 'Using artificial intelligence to analyse and predict susceptibility to antimicrobials' by Adrian Egli & Javier Fernandez Dominguez.**
**Originally broadcast on 28 October 2025. See webinar recording here: [https://revive.gardp.org/using-artificial-intelligence-to-analyse-and-predict-susceptibility-to-antimicrobials/](https://revive.gardp.org/using-artificial-intelligence-to-analyse-and-predict-susceptibility-to-antimicrobials/)**

| **Question asked** | **Response from the speakers** |
|---|---|
| Thanks for the informative talk. My question is, "Do you think AI-based prediction of antimicrobial resistance from MALDI-TOF MS data could help identify regions or animal populations where vaccine interventions, such as those targeting *Leptospira hardjo*, would have the greatest impact in reducing antibiotic use?" | Thank you for your question.<br>MALDI-TOF MS based prediction of AMR is still a research tool and does not provide valid results – the AUROC is between 0.70 – 0.90.<br>I believe what you are asking if MALDI-TOF MS for species identification to screen for the prevalence of certain species. And then yes, you could perhaps compare rates before and after a vaccine study and see the rate of this specific pathogens, which should go down. |
| In conflict and crisis zones, where surveillance and laboratory capacity are limited, how can genomic tools like resistome and mobilome analysis be realistically applied to track the spread of AMR pathogens such as *Staphylococcus aureus*? | I do not think that genomic tools (which require infrastructure: lab, sequencer, DNA extraction, high performance computer) are accessible in conflict and crisis zones. An option could be a very portable sequencer like Oxford Nanopore Technology, but the flowcells need a cooling chain and the sequencing is very expensive. For MRSA and other MDR pathogens I would rather focus on rapid antigen lateral flow assays. |
| Great talks thanks. Regarding implementation of iAST what is the effort to anticipate to train the model to local epidemiology ? And did you identify specific epidemiological variables challenging the model outcomes? | The training process usually takes between 2 and 4 weeks, depending on the volume of available data. The data we use to adapt the model to local epidemiology are mainly antibiograms, complemented by a few additional variables such as basic demographic information and the hospital service where the patient is treated, among others. |
| Thanks so much for this mind blowing presentation. Can we have a practical hands-on of the iAST demonstration? | Sure, please feel free to send me an email to javier.fernandez@pragmatech.ai, and we'll be happy to arrange a hands-on demonstration of iAST. |
| Javier: What type of models/algorithms are you using to predict bacteria profiles? | I'm sorry, but the specific algorithm we use is protected under industrial secrecy, so I can't share detailed information about it. What I can say is that it's based on machine learning techniques specifically designed for antimicrobial resistance prediction. |

Audience questions from the webinar 'Using artificial intelligence to analyse and predict susceptibility to antimicrobials' by Adrian Egli & Javier Fernández Domínguez moderated by Margo Diricks, originally broadcast on 28 October 2025.

| Question asked | Response from the speakers |
|---|---|
| In your opinion, how can we demonstrate that the use of artificial intelligence can be productive for underdeveloped countries, or for the world and how can the margin of error of artificial intelligence can be minimized. | You need to define a use case for a suitable tool and then validate it and monitor the outcome. Example: if you have a digital microscope or an automated detection of resistance you should document the impact – this could be a clinical or economic output.<br>The quality of AI largely depends on the quality and amount of training data. |
| Adrian: What is your opinion on using open source models instead of closed source like openAI? | Very often open source models are weaker in performance as the training of commercial solutions is much deeper (and much more expensive).<br>A solution is cost-effective models and then train it with domain specific knowledge. Open source models have the advantage that you can control them and there are less privacy data issues. |
| Adrian: Any opinion about small agentic models vs large models?" | It really depends on the use case you have which model to take. A small model is often optimized for very specific tasks. |
| In LMICs, microbiology data are often incomplete, inconsistent, or not digitized. How can AI models be trained effectively on such limited or fragmented datasets? | I think quality is essential – you first need to take the effort to digitalize the data. Think about “garbage in, garbage out”. With images and text this is more feasible. |
| Great presentations. Is there a unique AI prediction model for Mycobacterium tuberculosis resistance? | Yes, there is an automated microscope which scans slides of e.g. sputum and can detect fluorescent bacteria. |
| Thank you for this excellent webinar. My question is for both speakers. From what I understand, the use of AI still heavily depends on the availability and quality of data used to train the models. How can we make this a feasible reality in LMICs? | You are right – in high income countries there was heavy investments into data infrastructure over the past years. Clearly a program needs to be developed to invest into data infrastructure and you need to build the expertise. |
| The output of the AI tool is not exactly the same (after three enquiries, as you mentioned), is there any hint to choose an objective and accurate output? | Clearly it depends on the model you use. There is variability – as ML are basically fancy statistical models. Therefore it needs proper validation and evaluation. Especially if you use AI models which were trained with different cohorts. |

Audience questions from the webinar ‘Using artificial intelligence to analyse and predict susceptibility to antimicrobials’ by Adrian Egli & Javier Fernández Domínguez moderated by Margo Diricks, originally broadcast on 28 October 2025.

| Question asked | Response from the speakers |
|---|---|
| For both speakers, do AI models treat horizontally and vertically transmitted drug resistance the same? | No. These are different types of resistances – it depends on the balance of the data. Also different models are usually required for these.<br>E.g. in vertically – so called graph neural networks are used. |
| Which is the latest tool in AI prediction of antimicrobial susceptibility | There is not the single best tool. Check reviews on these topics as the field is very rapidly evolving. It also depends on if you want to make genotype -> phenotype prediction or if you want to analyse images with inhibition zones. |
| What are the major challenges in AI based diagnosis? | Data quality, validation of prospective cohorts, and commercial software. |
| Adrian: Can AI based predication can also be used for genomic surveillances accuracy and confidence. | Yes, there is an excellent review in Nature about this topic.<br>See: https://www.nature.com/articles/s41467-024-55461-x<br>See: https://pmc.ncbi.nlm.nih.gov/articles/PMC11987553/ |
| Adrian: Can you suggest some AI tools | Large Language Models: open evidence (https://www.openevidence.com/)<br>In the lab: software linked to full lab automation e.g. PhenoMatrix |
| The antibiotic susceptibility is very local & varies so a software made globally may not be suitable for all the Hospital? | Most likely yes – it is very important that if you use a software trained on different data that you re-validate it. |
| I feel prediction cannot replace the final susceptibility results. Especially in developing countries? | Yes, this is right – AI is still at the beginning and there is a huge hype. I would clearly focus on classical phenotypic testing before investing into AI. |
| Can you please give some ideas on block chain technology in pharmaceutical supply chain? | This is a great idea – as it increases the security of the workflow. This would also be valuable in e.g. study management. But I am not aware of a commercial tool. |
| Adrian: What are the different molecular mechanisms for resistance? | 4 basic mechanisms: (i) target site modification e.g. mutations affecting amino acid sequence and then the binding affinity (Kd); (ii) efflux pumps – pumping drugs out of the bacterial cells; (iii) porin loss – reducing the influx of drugs into the cells; (iv) bacterial enzymes cleaving the drugs. |
| Adrian: Has it been validated to carry out AMR studies using AI?" | I am not sure what this question means – there are indeed many studies (many retrospective) that validated e.g. genotype -> phenotype prediction. |

Audience questions from the webinar 'Using artificial intelligence to analyse and predict susceptibility to antimicrobials' by Adrian Egli & Javier Fernández Domínguez moderated by Margo Diricks, originally broadcast on 28 October 2025.

| Question asked | Response from the speakers |
|---|---|
| Javier: Are there research laboratories in the USA institutions that are currently using the AI approach in AMR research? | No, we're not currently working with a U.S. research laboratory, but we'd love to establish a collaboration with an American institution in the coming months. If any U.S. groups are interested in partnering or hosting a pilot, please contact me at javier.fernandez@pragmatech.ai |
| Could you share examples of how iAST has improved antimicrobial stewardship in clinical practice? | Not yet, since we haven't been able to commercialize or deploy the tool beyond our pilot site before obtaining CE marking, we don't yet have real-world clinical data. However, we expect to have those results soon, as upcoming implementations will allow us to measure the real impact of iAST on antimicrobial stewardship in practice. |
| Hi! my question from Respected Prof. Adrian is can AI help identify emerging resistance mechanisms that are not yet clinically recognized? | It depends on the way the AI is setup – theoretically one can train an AI to also react or recognize unknown resistance e.g. new mutations. But if there is a completely new mechanisms e.g. a new gene then it would be difficult I feel. |
| "One of the main challenges with AI models is their "black-box" nature, which makes it difficult to understand how decisions are made. What would you recommend as an effective approach to address this issue? | Use models which provide certain explanations e.g. SHAP, Lime etc.<br>See https://www.edps.europa.eu/system/files/2023-11/23-11-16_techdispatch_xai_en.pdf |
| I'm curious about the integration of genomic data alongside phenotypic data in determining ASTs and also potentially in training AI models. Can WGS and transcriptomics potentially help guide correct assessment of ASTs? | Yes, there are plenty of papers doing this. Please see PubMed… |
| Different mechanisms are involved in conferring resistance to a particular antibiotic. Whether AI will consider all possible mechanisms in predicting the resistance. Can MALDI-TOF incorporate all the mechanisms for prediction? | AI cannot incorporate all at the same time as they work differently – so likely different AI needs to be trained. Same is for MALDI-TOF. Efflux pump activity is difficult. |

Audience questions from the webinar 'Using artificial intelligence to analyse and predict susceptibility to antimicrobials' by Adrian Egli & Javier Fernández Domínguez moderated by Margo Diricks, originally broadcast on 28 October 2025.

| Question asked | Response from the speakers |
| --- | --- |
| Do the AI models recommend different antibiotic therapies based on the different bacteria (E.coli/Staph) isolated from the same source of infection (e.g. UTI) | It depends on what antibiotics you added. |
| Hi Dr Vishal Shete from India. I would like to know the legal and ethical issues of feeding the data, especially CLSI/EUCAST guidelines, to open platforms like ChatGPT? | I do not see an issue with open information. If you share data check the license. |