Speakers

Poster abstracts

Speakers

1. Resolving microbial genomes in complex communities at the single-cell level

Laura Carroll, Umeå University, laura.carroll@umu.se

Abstract: Single-cell metagenomic sequencing (scMetaG) can provide maximum-resolution insights into complex microbial communities. However, existing bioinformatic tools are not equipped to handle the large amounts of data generated by novel high-throughput scMetaG methods. To this end, we developed Bascet and Zorn, a bioinformatic toolkit for complete, end-to-end analysis of massive scMetaG data sets (>1 million cells). Enabled by recent advances in droplet microfluidics, we use Bascet and Zorn to develop and optimize a high-throughput scMetaG method on a ten-species mock community. To showcase their utility on a real-world sample, we use Bascet and Zorn to characterize a human saliva sample, generating single-amplified genomes (SAGs) from >10k prokaryotic cells. Overall, Bascet and Zorn enable reproducible scMetaG analysis, allowing users to query microbiomes at unprecedented resolution and scale.

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2. Towards large-scale proactive surveillance of AMR

Johan Bengtsson-Palme, Chalmers University of Technology, SciLifeLab, johan.bengtsson.palme@chalmers.se

Abstract: There is growing recognition of the crucial role of the environment as both a reservoir and dissemination route for AMR. Environmental monitoring and risk assessment of antibiotic resistance genes (ARGs) are essential for identifying high-risk ARGs and environments that may significantly impact human health. Yet, ARG abundance data are scattered across various databases, publications, and repositories, making comprehensive analyses challenging. This knowledge gap hinders evidence-based policy decisions and targeted interventions. We are developing a comprehensive understanding of AMR distribution in various environments through large-scale analysis of publicly available metagenomic data, enabling us to develop predictive models capable of estimating ARG content and abundance in unsampled environments, and identifying sampling gaps in current environmental AMR data. Identifying the future major AMR risks will allow us to use proactive surveillance to act on emerging resistance threats before they become prevalent in healthcare settings.

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3. Characterising insights in infection biology through the use of routine clinical datasets in healthcare

Damien Ming, Imperial College London, The Fleming Initiative, d.ming@imperial.ac.uk

Abstract: Pathogen biology and the subsequent host response are major determinants in clinical outcome during infection. There is growing interest in understanding individual susceptibility to infections and risks associated with treatment success or failure with antimicrobial resistance being a significant factor in healthcare worldwide. The talk will highlight approaches to make use of routinely collected clinical data through data-driven methods and machine learning, to provide insights to guide future clinical management and research.

4. Machine learning identifies genetic and ecological determinants of antibiotic resistance gene dissemination

Daniel Lund, Chalmers University of Technology, dlund@chalmers.se

Abstract: The dissemination of mobile antibiotic resistance genes (ARGs) among pathogens poses a major public health threat, yet the mechanisms determining this gene flow remain poorly understood. To address this, we aimed to identify genetic and environmental factors fundamental to successful horizontal ARG transfer. Using a phylogenetic framework, we identified instances of horizontal ARG transfer in ~1 million bacterial genomes and integrated this data with over 20,000 metagenomes representing five different environments. We then developed random forest models that could reliably predict ARG transfer between bacteria. Our results showed that genetic incompatibility, quantified by nucleotide composition dissimilarity, reduces the likelihood of gene transfer between evolutionarily distant bacteria, whereas environmental co-occurrence increases transfer probability, especially in human and wastewater microbiomes. Together, these findings provide a data-driven framework for predicting ARG dissemination and elucidate key mechanisms underlying this evolutionary process.

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5. Using EHR data and AI for improved infection surveillance and antimicrobial stewardship

Suzanne Ruhe-van der Werff, Karolinska Institutet, Department of Medicine Solna, suzanne.ruhe.van.der.werff@ki.se

Abstract: Healthcare-associated infections (HAI) and antimicrobial resistance (AMR) are interconnected health issues often tackled together in the field of infection prevention and control. In our research group we have access to a copy of the electronic health record data from the Karolinska University Hospital from 2010 onwards. This data we use to improve the automated surveillance of HAI and the antimicrobial treatment of patients to reduce the spread of infection and AMR. Artificial intelligence has been used in different ways and with different degrees of success for these efforts.

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6. Building the economic case for diagnostics to address AMR

Nina Zhu, Imperial College London, The Fleming Initiative, jiayue.zhu09@imperial.ac.uk

Abstract: Prudent use of diagnostics is a critical step towards optimising antimicrobial use. However, diagnostics are currently undervalued, and guidance and targets around diagnostics are absent from countries' national action plans. Existing evidence is insufficient to demonstrate cost-effectiveness of diagnostics in addressing AMR, due to limit in data and technical capacity to operationalise existing valuation frameworks of diagnostics. Utilising data linkage and machine learning enabled modelling strategies, we propose methods bridging macro and microeconomic approaches, expanding from the conventional health technology assessment, to guide robust cost-of-illness analysis of AMR and economic evaluation of diagnostic stewardship interventions.

7. Phenotypic Antibiotic Susceptibility Testing at the limit of one bacterial cell

David Fange, Uppsala University, david.fange@icm.uu.se

Abstract: The blood of a septic patient contains only a few bacteria per milliliter. Recently, various techniques have been developed for extracting these few bacteria from a blood sample. Independent of how these bacteria are separated from the blood cells, we want to learn from them how to treat the infection. Here, we describe how a phenotypic Antibiotic Susceptibility Test can be executed with a single bacterial cell by making averages over time instead of populations, if we account for the experimental noise and cell-to-cell variability. We use the method to make preliminary estimates for how long it takes to distinguish a single susceptible from a resistant cell with statistical confidence. We also exemplify how it is possible to sequentially test different antibiotics, or different concentrations of the same antibiotic, on one cell lineage until a susceptible phenotype is detected.

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8. Image analysis and machine learning for live single cell classification and phenotyping

Carolina Wählby, Uppsala University, Dept. IT, SciLifeLab, carolina.wahlby@it.uu.se

Abstract: For effective treatment of bacterial infections, it is essential to identify the species causing the infection as early as possible. Current methods typically require hours of overnight culturing of a bacterial sample and a larger quantity of cells to function effectively. We show that phase contrast time-lapse microscopy combined with AI in the form of deep learning is sufficient for classification of seven different species of bacteria relevant to human health. The classification is performed on living bacteria and does not require fixation or staining, meaning that the bacterial species can be determined as the bacteria reproduce in a microfluidic device, enabling parallel determination of susceptibility to antibiotics. The experiments suggest that spatiotemporal features can be learned from video data of bacterial cell divisions, with both texture and morphology contributing to classifier decision. Still, several challenges remain, but this proof of principle study brings us closer to real-time diagnostics that could transform the initial treatment of acute infections.

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9. Low-Cost Biosensors for Patient-Level Diagnostics in the Era of AI-Driven Antimicrobial Stewardship

Sanjiv Sharma, University of Liverpool, Fleming Initiative; CAMO-Net; David Price Evans Group for Global Health, sanjiv.sharma@liverpool.ac.uk

Abstract: Antimicrobial resistance (AMR) is not only a microbiological crisis but increasingly a data crisis—driven by delayed diagnostics, empirical prescribing, and unmonitored therapeutic drug exposure. I will present a new generation of low-cost, AI-integrated electrochemical biosensors designed to move infectious disease management from centralized laboratories to real-time, patient-level clinical decision systems. Our platforms combine redox-active molecularly imprinted polymers (MIPs) with highly porous gold nanostructures fabricated on scalable printed circuit boards costing less than £0.10 per unit. These reagent-free devices enable sensitive detection of clinically actionable biomarkers in undiluted biofluids and have been translated to therapeutic drug monitoring of rifampicin and vancomycin, demonstrating strong agreement with LC-MS/MS while operating at the

point of care. Artificial intelligence is embedded at the core of the system. Machine learning models perform automated signal classification, non-linear regression, and interference correction, transforming raw electrochemical outputs into clinically interpretable dosing guidance. Integrated with portable potentiostat and cloud-linked interfaces, these biosensors function as distributed data-generating nodes, enabling adaptive dosing, AUC/MIC optimisation, and real-time antimicrobial stewardship—supporting predictive, data-driven precision therapy to combat resistance globally.

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10. Machine-learning for prediction of antimicrobial resistance from genomics data

Christian Giske, Karolinska Institutet, christian.giske@ki.se

Abstract: The presentation will review recent publications using machine-learning for antimicrobial susceptibility prediction. A particular emphasis will be put on appropriate design for studies and good examples of initiatives that have advanced the field. The talk will cover limitations in some of the presently available studies and pitfalls when interpreting data.

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11. Pathways towards translation of AI research to impact. The Uganda experience.

Daudi Jjingo, Makerere University, Uganda, African Center of Excellence in Bioinformatics, djjingo@idi.co.ug

Abstract: In this short talk, I will explore the challenges and opportunities on the pathway to use of AI to enable research into AMR and it's eventual translation into real impact for population health. The talk covers the entire value chain, from problem conception, to study design, data collection, data storage and retrieval, data analysis, interpretation and translation. It covers areas such as training, infrastructure, systems and initial research strands being pursued.

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12. AI-driven diagnostic support for antibiotic-resistant infections.

Anna Johnning, Fraunhofer-Chalmers Centre, Chalmers University of Technology, anna.johnning@fcc.chalmers.se

Abstract: Efficient treatment of bacterial infections requires rapid and accurate diagnostics. Current cultivation-based methods can be slow, endangering patients, and contributing to the overprescription of broad-spectrum antibiotics. To address this, we have developed a deep learning framework based on transformers and conformal prediction to predict antibiotic susceptibility in clinical isolates using patient data and incomplete diagnostic information. We trained this framework with a unique dataset representing the full diagnostic results from three major Swedish hospitals over ten years, including more than 1.6M clinical isolates and more than 6.8M antibiotic susceptibility tests. Our model is able to predict susceptibility to 46 antibiotics across 49 bacterial species with overall high accuracy, demonstrating its potential for evidence-based guidance of antibiotic treatment. Ongoing work includes implementation in clinical settings, assessment of robustness and fairness across hospitals, and evaluation of the impact on the mortality of patients suffering

from antibiotic-resistant infections.

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13. PAI-powered decentralised diagnostic technologies

Nick Moser, Imperial College London, The Fleming Initiative, n.moser@imperial.ac.uk

Abstract: Dr. Moser is a Google DeepMind Academic Fellow associated with the Fleming Initiative and the Department of Computing
at Imperial College London. In this talk, he will explore the transformative potential of artificial intelligence in reshaping diagnostic frameworks, moving beyond the limitations of traditional centralized laboratories.
He will discuss how AI can complement and enhance current
methodologies across the full decentralized diagnostic workflow, from the computational discovery of novel biomarkers and their translation into clinical tools, to real-time detection and broader epidemiological surveillance. A major focus of the presentation will be a detailed case study on the rapid detection of infectious pathogens at the point of need, demonstrating how machine
learning algorithms can be leveraged alongside novel biosensor technology to ensure robustness, accuracy and speed. By enabling these next-generation translational approaches, AI will be the key to addressing the urgent global health challenge of antimicrobial resistance.

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14. Leveraging digital technologies to enhance multiplexing in real-time PCR

Jesus Rodriguez-Manzano, Imperial College London, UK, j.rodriguez-manzano@imperial.ac.uk

Abstract: Real-time amplification techniques, such as qPCR, are key methods for detecting and quantifying nucleic acids in biology and medicine. Multiplexing enables the simultaneous detection of multiple DNA or RNA targets within a single reaction, improving throughput and efficiency in molecular diagnostics. However, conventional multiplexing approaches are typically limited to three or four targets or require complex instrumentation. Recent advances in machine learning offer data-driven solutions that exploit information contained in amplification and melting curves to classify multiple targets within a single reaction. Combined with thermodynamic modelling and computational simulation, these approaches support improved assay design and enable more scalable and cost-effective multiplex diagnostics.

Poster abstracts

1. ?

Sophia Axillus, Chalmers University of Technology, SciLifeLab, Centre for Antibiotic Resistance Research (CARe), axillus@chalmers.se

Abstract: The global spread of antibiotic resistance is driven by horizontal gene transfer (HGT) of resistance genes, yet our understanding is limited because we typically observe only the endpoints of dissemination while the underlying transfer network remains hidden. This is challenging because HGT is unobservable in real time, continuously occurring, and only partially sampled. However, the same mechanisms govern both observed and unobserved events, suggesting that predictive modeling can help infer the missing structure. Here, we develop a graph neural network framework to infer the underlying HGT network itself. By integrating past transfer events with genetic and physiological features, the model learns dissemination patterns that generalize to unseen events. Our approach shows strong predictive performance across resistance gene classes and enables exploration of the hidden HGT network, including differences between gene classes and how hosts, environments, and taxa shape the spread of antibiotic resistance.

Keywords: **Antibiotic resistance , Horizontal gene transfer, Graph neural networks, Predictive modeling, AI, Statistical Modeling**

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2. Can AI help us detect antibiotic resistance from whole genome sequences?

Oskar Fraser-Krauss, Imperial College London, of123@ic.ac.uk

Abstract: Whole-genome sequencing captures rich information about bacterial samples, including determinants of resistance, but extracting meaningful representations for downstream analysis remains challenging. Recent transformer-based foundation models pretrained on bacterial genomes offer a promising approach for generating informative sequence embeddings that can improve prediction and characterization of AMR phenotypes.

Keywords: **Antibiotic resistance, whole genome sequencing, machine learning, artificial intelligence, bacterial infection**

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3. Bioinformatics software for single-cell metagenomics

Johan Henriksson, Umeå University, SciLifeLab, johan.henriksson@umu.se

Abstract: It is now possible to sequence up to a million individual bacteria genomes in a single experiment. This unprecedented amount of novel data calls for new software, and new approaches, to enable analysis. We have developed the first pipeline (Zorn/Bascet) and file formats for the purpose: http://zorn.henlab.org/. Our approaches especially leverage a new type of vector analysis to enable reference-free analysis. We are furthermore developing a dedicated single-cell metagenomic data viewer that enables deep visualization of genomic data. All our software is implemented in Rust, and we aim to build a bioinformatics community around this new language (http://tinyurl.com/rustnorth). We welcome community input to help prioritize our software development.

Keywords: **Single cell methods development; bioinformatics methods development; genetic screens; CAR T cells**

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4. AIDx – AI Diagnostics Excellence Cluster: A National Initiative for AI-Integrated Clinical Genomics in Sweden

Rene Kaden, Uppsala University Hospital, SciLifeLab, rene.kaden@akademiska.se

Abstract: AIDx is a Vinnova-funded national initiative (2025–2026) coordinating hospitals, medical faculties, and research groups across Sweden to prepare the ground for integrating artificial intelligence into clinical genomic diagnostics. Rooted in clinical practice, the initiative is driven by healthcare-defined needs and aims to establish the structures, data infrastructure, and collaborative frameworks required for future AI implementation. Spanning cancer, rare diseases, infectious diseases, and complex diseases, the work includes harmonizing access to large-scale genomic and clinical data through the National Genomics Platform, mapping real-world diagnostic requirements across multiple healthcare regions, and addressing regulatory compliance with GDPR, the EU AI Act, and the European Health Data Space. By connecting Genomic Medicine Sweden, SciLifeLab, and seven university hospitals, AIDx lays the foundation for reduced diagnostic turnaround times, improved pipeline reliability, and individualized patient care. The cluster actively seeks collaboration with AI research groups, health technology companies, and international precision medicine initiatives.

Keywords: **Antibiotic resistance, whole genome sequencing, machine learning, artificial intelligence, bacterial infection**

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5. Data-driven real-time surveillance of bacterial pathogens in Sweden

Gunnar Kahlmeter, EUCAST, The European Committee on Antimicrobial Susceptibility Testing, gunnar.kahlmeter@kronoberg.se

Abstract: Erik Kristiansson1, 2, Anna Johnning1,2,3, Hanna Billström4, Gunnar Kahlmeter5

1 Division of Applied Mathematics & Statistics, Department of Mathematical Sciences, Chalmers University of Technology & Gothenburg University, Gothenburg (Sweden).
2 Centre for Antibiotic Resistance Research in Gothenburg (CARe), Gothenburg (Sweden).
3 Department of Systems & Data Analysis, Fraunhofer-Chalmers Centre, Gothenburg (Sweden).
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5 EUCAST Development Laboratory, Växjö (Sweden).

Surveillance of bacterial pathogens is a fundamental pillar of public health and vital to detecting outbreaks, tracking antimicrobial resistance (AMR), and monitoring other disease trends. Here, we present a new data-driven method for analyzing Svebar data, a surveillance infrastructure that daily collects all isolates of bacteria and fungi and available antimicrobial susceptibility test (AST) results from Swedish microbiology laboratories. Our method is based on robust time-trend analysis of pathogen prevalences and AMR results. Machine learning, in combination with statistical modelling, is used to efficiently remove cyclic and seasonal effects and detect significant long-term trends and short-term deviations. We apply the methods to six full years of data (15 million isolates, 42 million cultures) and demonstrate high sensitivity in identifying both long- and short-term trends at the regional and national levels. We conclude that Svebar, in combination with dedicated data analysis methods, can enable autonomous surveillance of pathogens, with near-real-time detection of outbreaks.

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6. A statistical method for defining wild-type distributions and calculating epidemiological cut-off values

Erik Kristiansson, Chalmers University of Technology, DDLS, erik.kristiansson@chalmers.se

Abstract: Erik Kristiansson1, 2, Anna Johnning1,2,3, Gunnar Kahlmeter4

1 Division of Applied Mathematics & Statistics, Department of Mathematical Sciences, Chalmers University of Technology & Gothenburg University, Gothenburg (Sweden).
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3 Department of Systems & Data Analysis, Fraunhofer-Chalmers Centre, Gothenburg (Sweden).
4 EUCAST Development Laboratory, Växjö (Sweden).

Minimum inhibitory concentrations (MICs) and inhibition zone diameter (IZD) distributions of bacterial isolates are used to establish epidemiological cut-off values (ECOFFs), which guide antibiotic treatment in human and veterinary medicine. Deriving ECOFFs can, however, be challenging due to large biological and technical variability. Manual steps without formal statistical assessment are, therefore, often necessary. Here, we present a new method for analyzing MIC and IZD distributions to estimate ECOFFs. The method estimates wildtype distributions robustly, minimizing the influence of outliers and antibiotic-resistant isolates. ECOFFs are, then, derived as three standard deviations from the wildtype mean. The method was applied to 15,442 MIC distributions (9.3 million isolates) and 4,376 IZD distributions (2,9 million isolates) from EUCAST, and the results matched well with existing ECOFFs (correlation of 0.93) while also providing greater robustness, transparency, and statistical confidence. All derived ECOFFs are publicly available via EUCAST (https://

mic.eucast.org).

Keywords: **AI/ML, microbial genomics, transmission, evolution, diagnostics, surveillance**

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7. Title: Nanopore s5PSeq enables rapid phenotypic antimicrobial susceptibility testing

HonglianLiu, Karolinska Institutet, SciLifeLab, honglian.liu@scilifelab.se

Abstract: Rapid phenotypic antimicrobial susceptibility testing (AST) remains a major bottleneck in clinical microbiology, particularly for slow-growing or anaerobic pathogens such as Clostridioides difficile. Conventional AST requires overnight culture, while genotypic prediction alone cannot reliably capture phenotypic resistance. We developed a rapid nanopore-compatible 5′P degradome assay (s5PSeq) that measures antibiotic-induced ribosome-stalling signatures as a molecular proxy for growth inhibition, enabling rapid phenotypic AMR detection.

To assess its clinical utility, we applied s5PSeq to erythromycin-sensitive and -resistant C.difficile clinical isolates. Exponentially growing cultures were exposed to erythromycin for 10 minutes, total RNA was extracted, and s5PSeq libraries were generated using a streamlined 4-hour workflow. Libraries were sequenced on Illumina or nanopore platforms, and phenotypic susceptibility was assessed by quantifying antibiotic-induced ribosome-stalling signatures. To mimic complex clinical samples, s5PSeq was also applied to mixtures containing treated C. difficile RNA combined with RNAs from other bacterial species.

s5PSeq captured drug-specific ribosome-stalling signatures that correlated with growth inhibition across antibiotics and species. In C. difficile, erythromycin-sensitive isolates displayed characteristic stalling at proline-rich and R/K-x-R/K motifs, while resistant isolates lacked these signals. Nanopore sequencing enabled accurate phenotypic discrimination with as few as ~3,000 reads per sample, allowing >1,500 samples per PromethION flow cell or 24 samples per low-cost Flongle flow cell. In mixed-species backgrounds, s5PSeq robustly detected stalling only in sensitive C. difficile, and concurrent analysis of rRNA reads accurately reconstructed species composition, demonstrating feasibility for complex diagnostic samples.

Nanopore-enabled s5PSeq provides a rapid, information-rich phenotypic readout of antimicrobial susceptibility, detecting drug response within minutes of antibiotic exposure and requiring only thousands of reads. Its compatibility with inexpensive nanopore platforms, minimal workflow, and ability to function in mixed-species samples highlight its potential as a practical phenotypic-molecular AST for clinical microbiology laboratories."

Keywords: **Rapid AMR diagnostics**

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8. Title: Machine learning identifies genetic and ecological determinants of antibiotic resistance gene dissemination

David Lund, Chalmers University of Technology, dlund@chalmers.se

Abstract: The dissemination of mobile antibiotic resistance genes (ARGs) among pathogens

poses a major public health threat, yet the mechanisms determining this gene flow remain poorly understood. To address this, we aimed to identify genetic and environmental factors fundamental to successful horizontal ARG transfer. Using a phylogenetic framework, we identified instances of horizontal ARG transfer in ~1 million bacterial genomes and integrated this data with over 20,000 metagenomes representing five different environments. We then developed random forest models that could reliably predict ARG transfer between bacteria. Our results showed that genetic incompatibility, quantified by nucleotide composition dissimilarity, reduces the likelihood of gene transfer between evolutionarily distant bacteria, whereas environmental co-occurrence increases transfer probability, especially in human and wastewater microbiomes. Together, these findings provide a data-driven framework for predicting ARG dissemination and elucidate key mechanisms underlying this evolutionary process.

Keywords: **Bioinformatics, Genomics, Metagenomics, Machine learning, Antibiotic resisatance genes, Horizontal gene transfer**

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9. The JAMREYE dashboard – a joint tool to facilitate data driven implementation and development of AMR surveillance across Europe

Sofia Ny, Public Health Agency of Sweden, EU-JAMRAI 2, sofia.ny@folkhalsomyndigheten.se

Abstract: Currently, decentralized and complex AMR surveillance systems in Europe complicates joint data driven development, implementation and expansion of surveillance. To address this, we conducted a European wide cross-sectional survey on national AMR surveillance systems in spring 2025. The results are presented in the JAMREYE dashboard, which visualises national surveillance information from 28 countries, covering 5 culture materials, 8 bacterial priority pathogens, and 12 resistances, including WGS surveillance at national AMR expert and reference laboratories. The dashboard is a publicly accessible resource for exploring ongoing national AMR surveillance efforts in Europe. We intend to continuously update it to track progress over time and welcome feedback from the scientific community on how to improve its content.

Access the JAMREYE dashboard here (launched 2026-01-19): https://eu-jamrai.eu/surveillance/surveillance-dashboard/

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10. Global epidemiology of antimicrobial resistance in people living with chronic lung infection

Ollie Pitts, Imperial College London, Data Science Institute, National Heart & Lung Institute, op423@ic.ac.uk

Abstract: Antimicrobial resistance (AMR) is a major global threat for people with chronic lung infection, yet its epidemiology in bronchiectasis (Bx) and cystic fibrosis (CF) remains poorly characterised. We retrospectively analysed longitudinal AMR data from 110,323 respiratory samples in 19,143 individuals across 11 cities on three continents (2012–2024). Significant geographic variation in AMR was observed, particularly for Pseudomonas aeruginosa in Europe and Klebsiella pneumoniae in Hong Kong. High multi- and extensive drug resistance (MDR/XDR) burdens were identified in emerging pathogens, including

Escherichia coli (CF: MDR-32.6%;XDR-12.4%; Bx: MDR-39.2%;XDR-4.9%) and K. pneumoniae (CF: MDR-22.7%;XDR-15.6%; Bx: MDR-13.4%;XDR-1.5%). Longitudinal increases in AMR were seen for P. aeruginosa to aminoglycosides (p=<0.0001;OR/yr:1.36;(95%CI:1.24-1.49)), cephalosporins (p=0.03;OR/yr:1.08;(95%CI:1.007-1.153)) and fluoroquinolones (p=0.02;OR/yr:1.05;(95%CI:1.007-1.105)), and for K. pneumoniae to carbapenems (p=<0.0001;OR/yr:1.69;(95%CI:1.40-2.04)) and cephalosporins (p=0.001;OR/yr:1.12;(95%CI:1.04-1.19)). Patterns of concurrent and disjoint resistance were assessed to inform potential cyclical antimicrobial choices, with strong regional variation in disjoint resistance identified. These findings highlight a growing, geographically variable global AMR burden in bronchiectasis and CF.

Keywords: **AI, Chronic Respiratory Diseases, Bioinformatics, Microbial Resistance**

12. AI-driven innovation against antimicrobial resistance

Francisco Salvà Serra, RISE Research Institutes of Sweden, francisco.salva.serra@ri.se

Abstract: Antimicrobial resistance (AMR) is a major threat to modern medicine and already causes more than one million deaths annually. Innovative strategies to address this problem are urgently needed. RISE focusses on applied research to accelerate transformation and strengthen competitiveness for businesses, society, and Sweden. With strong expertise and infrastructure in artificial intelligence (AI) and AMR, RISE contributes to translating research into groundbreaking and implementable solutions. Here we present case studies, including: (i) how data on thousands of surgical procedures has the potential to help preventing nosocomial infections in operating rooms; (ii) how AI-driven omics could lead to better diagnostics and prevention of infectious diseases (the DOUBLE BARRIER concept); and (iii) how AI supports increased efficiency and effectivity in drug formulation.

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13. Best-practice bioinformatics workflow for extraction of clinical indicators from simulated E. coli metagenomes

Divya Shridar, Uppsala University, divya.shridar@it.uu.se

Abstract: Antibiotic resistance (AMR) is one of the greatest threats to public health globally. Multidrug resistance exhibited by extended-spectrum ß-lactamase (ESBL) producing Escherichia Coli (E. coli) has been associated with antibiotic therapy failure. For effective infection control, it is imperative that ESBL-producing E. coli is well-surveilled. A proposed methodology for non-invasive surveillance of ESBL-producing E. coli is wastewater metagenomics.

Wastewater epidemiology quantifies pathogens in communal wastewater samples to assess their prevalence in the population and predict imminent outbreaks. It has been successful for several viruses, but targeting bacterial pathogens has proved more difficult. Wastewater metagenomics is thus the analysis of the functional gene composition of the wastewater microbial community through DNA sequencing, annotation and bioinformatic analysis.

Bioinformatically, of interest is the identification of multi-locus sequence type (MLST), serotype, virulence factors (VF) and antibiotic resistance genes (ARGs) from wastewater

metagenomes. This begs the question, what is the best-practice workflow that allows for reliable identification of these clinical features from E. coli metagenomes?

Keywords: **Pipeline development, Metagenomics, Environmental Surveillance, AMR**

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14. Epidemiology and risk factors of nosocomial ESBL infections in elective surgery patients: a retrospective cohort analysis

Anisia Talianu, Imperial College London, anisia.talianu18@imperial.ac.uk

Abstract: Surgery-associated infections (SAIs) affect up to 11% of patients in the United Kingdom within seven days of surgery, despite standard prophylaxis. SAIs significantly increase the patient's risk of morbidity and mortality, and their management often requires further antibiotic prescribing. Excessive use of antibiotic agents accelerates the emergence of antimicrobial resistance (AMR), a global health emergency projected to cause 10 million deaths annually by 2050. Infections caused by extended-spectrum beta-lactamase (ESBL)-producing Enterobacterales pose additional challenges due to resistance to first-line antibiotics, often requiring escalation to broad-spectrum agents that further drive AMR. A clearer understanding of ESBL infection patterns in surgical patients is needed to support early risk assessment and antimicrobial stewardship.

We conducted a retrospective cohort study of adult elective surgery patients admitted to Imperial College Healthcare NHS Trust (ICHNT) between January 2015 and August 2025. Electronic health record and microbiology data were analysed to compare ESBL-positive and ESBL-negative infections and identify resistance risk factors. Univariate statistical analyses were used to assess associations between ESBL status and organism type, infection site, comorbidities, ethnicity, socioeconomic deprivation, and demographic factors.

Keywords: **AMR**

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15. Tracking antibiotic resistance genes between different bacteria: using large-scale metagenomic and genomic data

Laleh Varghaei, Chalmers University of Technology, varghaei@chalmers.se

Abstract: Despite growing concerns about antibiotic resistance genes (ARGs), their variation and dissemination across environments and bacterial hosts remain poorly understood. It is unclear which ARG variants are present in different environments and how they disseminate into pathogenic bacteria.

To address this, we analyzed genomic and metagenomic data to track the distribution, variation and spread of ARGs across bacteria and environments, including the human gut and wastewater. We examined mutation patterns in 2,671,924 genomic and 6,770 metagenomic samples and applied sequence clustering to characterize variation within and across ARG families.

Our results show that the pipeline can identify ARG variants and capture genetic variation across large-scale datasets. The genetic variation differs substantially between ARG families

and many gene variants observed in pathogenic bacteria are not commonly detected in wastewater or human gut. Future analyses will focus on identifying environments that may promote ARG variants associated with pathogenic bacteria.

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16. The Swedish Pathogens Portal

Nalina Hamsaiyni Venkatesh, Umeå University, SciLifeLab, hamsaiyni.v@gmail.com

Abstract: The Swedish Pathogens Portal, developed by SciLifeLab Data Centre aims to serve as a one-stop shop for sharing infectious disease and pandemic preparedness data from Sweden. It promotes Open and FAIR research outputs through direct and indirect support to the research community, including workflows for data sharing, guidance on metadata and GDPR compliance, and new data-type specific repositories. Key aims include facilitating easy sharing of diverse data types such as genomics, serology, environmental monitoring, imaging, and epidemiology. The portal seeks to gather community feedback to prioritise needs, such as clear repository guidance and ontology support.

Keywords: **Data Driven Life Sciences, Infectious Diseases**