



Workshop Title	Pitfalls and Directions: Interpreting the Output of Current Antibiotic Resistance Gene Annotation Tools
Facilitators and contributors Details of the individuals leading and contributing to the workshop, including: • Workshop facilitators • Guest speakers or contributors • Their roles in the session	Juan S. Inda-Díaz – Queensland University of Technology, Australia (Lead Facilitator) Luis Pedro Coelho – Queensland University of Technology, Australia (Facilitator) Johan Bengtsson-Palme – Chalmers University of Technology, Sweden (Facilitator) Willem van Schaik – University of Birmingham, UK (Facilitator) Furthermore, the following individuals have expressed interest in being speakers and/or active participants: Víctor Hugo Jarquín Díaz - Max Delbrück Center for Molecular Medicine (Active participant) Nicolas Godron - Université Paris Cité, France (Active participant) Faith Adegoke - Queensland University of Technology (Active participant)
Background An overview of the context and rationale for the workshop, outlining the key issue, challenge, or opportunity it addresses, and why this topic is timely and relevant.	Sequencing-based detection of ARGs is foundational to global antimicrobial resistance surveillance. However, current computational pipelines produce strikingly inconsistent results. These discrepancies severely distort our understanding of the resistome and the evolutionary and ecological interpretations of bacterial adaptation as well as sway public health risk assessments and policy decisions. Metagenomic detection of ARGs is particularly challenging in environmental microbiomes, due to the large diversity of ARGs that can be present, composed by well-characterized and latent genes, those that are not currently represented in databases. This workshop addresses the urgent need to understand the strengths and limitations of each annotation pipeline as well as critically evaluate and clearly communicate their output and inferences of the resistome.
Workshop Aims A description of the purpose of the workshop and its intended focus. This section highlights what participants can expect to explore, learn, or develop during the session.	Facilitate Hands-On Learning: Provide participants with an interactive, hands-on exploration of ARG annotation outputs and resistome characterisation. Evaluate Pipeline Influence: Build deep awareness of how the choice of antibiotic resistance gene (ARG) annotation pipeline influences resistome characterisation. Explore Sources of Variation: Highlighting critical methodological and database-driven sources of variation among commonly used pipelines and identify pitfalls in interpreting tool outputs. Assess High-Stakes Consequences: Bridge the gap between bioinformatics and real-world impact by analysing how pipeline discrepancies distort ecological interpretations and sway public health or policy decisions. Shape Best Practices & Consensus: Promote broader community dialogue on best practices for data communication, culminating in the co-development of a concise consensus framework for ARG reporting.
Participant Takeaways A summary of what participants will gain from attending the workshop. This may include new knowledge, practical skills,	An exploration of parameters that influence ARG predictions, identity thresholds, database choice and gene classes, and ontology mapping.

tools, frameworks, or shared resources, as well as any tangible outputs (e.g. ideas, draft materials, or collaborative outcomes).	A shared understanding for interpreting resistome profiles, emphasising a clear communication of resistome inference. Example datasets (Zenodo) and apps (Shiny) for comparing ARG tools. Development of guidelines that can balance the detection of well-characterised ARGs and the identification of latent ARGs. These resources will support participants in designing robust resistome studies and communicating results to multidisciplinary audiences, from microbiologists to bioinformaticians and policymakers. The insights from the workshop will be captured in a publicly available document to be shared within the community. Interested participants will have the opportunity to join a writing group to further this into a white paper or a peer-reviewed opinion article.
Expected Impact An outline of the broader value of the workshop, including how it may: • Influence research, policy, or practice • Support collaboration and knowledge exchange • Contribute to future work or ongoing initiatives	By addressing inconsistencies in ARG annotation pipelines, this workshop will help strengthen the reliability and comparability of resistome studies across multiple fields. Participants will gain an understanding of the technical strengths and drawbacks of current pipelines and learn frameworks for evaluating and communicating the results of different pipelines. The workshop will promote methodological transparency in sequence-based AMR detection and encourage harmonisation among researchers and institutions that develop and/or use ARG detection software. Ultimately, this workshop aims to promote critical data knowledge among participants, with the hope of reducing misinterpretations that could affect risk assessment, public health decisions, and intervention strategies.
Who should attend? Information on the intended audience for the workshop, including: • Relevant backgrounds, sectors, or expertise • The level of participation expected (e.g. discussion, group work, problem-solving)	Ideal participants: Researchers and professionals with experience in metagenomics, bioinformatics, or AMR surveillance. We welcome academics, public-health scientists, and data analysts from research institutes and government agencies. No prior experience with ARG pipelines is required, though basic familiarity with sequencing data and functional annotation is recommended. The workshop encourages active participation through small-group discussions and hands-on problem-solving.
Workshop Schedule and Duration A summary of the structure and flow of the workshop, including: • Key session components • Interactive or breakout activities	Duration: 1.5 hours. 0:00–0:10 – Introduction: Why ARG annotation matters (presentation) 0:10–0:25 – Demonstration: Comparing outputs from major ARG pipelines 0:25–0:55 – Breakout: Identify pitfalls in tool output interpretation 0:55–1:15 – Group synthesis: Building a checklist for transparent reporting 1:15–1:30 – Discussion and drafting of a joint direction / white paper