

Antimicrobial Resistance Tools

Several **bioinformatics tools** are used to detect **antimicrobial resistance (AMR)** from genomic data. These tools analyze whole genome sequences (WGS) or metagenomic data to identify resistance genes, mutations, and mobile genetic elements linked to AMR. Here are some commonly used tools:

1. AMR Gene Detection Tools

These tools compare genomic sequences to known AMR gene databases.

- **CARD (Resistance Gene Identifier - RGI)**
 - Uses the **Comprehensive Antibiotic Resistance Database (CARD)**.
 - Identifies resistance genes, mutations, and efflux pumps.
 - Website: <https://card.mcmaster.ca>
- **ResFinder**
 - Developed by the **Center for Genomic Epidemiology (CGE)**.
 - Identifies acquired AMR genes from bacterial genomes.
 - Website: <https://cge.cbs.dtu.dk/services/ResFinder/>
- **ARG-ANNOT**
 - Focuses on **antibiotic resistance genes (ARGs)** in bacterial genomes.
 - Uses BLAST-based searches against a curated AMR database.
- **AMRFinderPlus**
 - Developed by the **NCBI**.
 - Identifies AMR genes, mutations, and mobile elements.
 - [GitHub: https://github.com/ncbi/amr](https://github.com/ncbi/amr)

2. Mutation-Based AMR Prediction

Some antibiotics confer resistance through **mutations** in key genes (e.g., gyrA for fluoroquinolone resistance).

- **PointFinder**
 - Detects **point mutations** in genes associated with AMR.
 - Works alongside **ResFinder**.
- **Mykrobe**
 - Detects AMR genes and mutations, optimized for **tuberculosis and Staphylococcus aureus**.
 - Uses Bayesian models to infer resistance.
 - [GitHub: https://github.com/iqbal-lab/Mykrobe](https://github.com/iqbal-lab/Mykrobe)

3. Mobile Genetic Element & Plasmid Detection

AMR genes often spread via **plasmids, integrons, and transposons**.

- **PlasmidFinder**
 - Identifies plasmid replicons in bacterial genomes.
 - Works with **ResFinder**.

- Website: <https://cge.cbs.dtu.dk/services/PlasmidFinder/>
- **ISfinder**
 - Identifies **insertion sequences (IS elements)** that can carry AMR genes.
 - Website: <https://www-is.biotoul.fr>

4. Metagenomic AMR Analysis

For complex samples (e.g., environmental or clinical microbiomes).

- **MEGARes**
 - Database and pipeline for **AMR detection in metagenomic data**.
- **DeepARG**
 - Uses **deep learning** to classify AMR genes in metagenomes.
 - Website: <https://bench.cs.vt.edu/deeparg>
- **ShortBRED**
 - Uses **protein-level markers** to detect AMR genes in metagenomic reads.

5. Workflow & Pipeline Tools

For high-throughput AMR detection in WGS data.

- **ARIBA**
 - Automates AMR gene detection from raw sequencing reads.
 - Works with multiple AMR databases.
 - [GitHub: https://github.com/sanger-pathogens/ariba](https://github.com/sanger-pathogens/ariba)
- **Pathogenwatch**
 - Web-based tool integrating AMR detection and genomic epidemiology.
 - [Website: https://pathogen.watch](https://pathogen.watch)

References

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