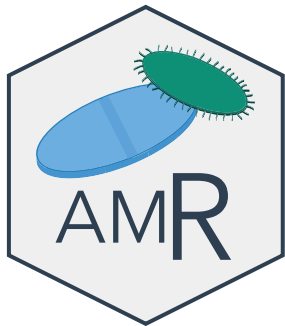# Antimicrobial Resistance (AMR) Data Analysis in R

Works on Windows, macOS and Linux with **all versions of R** since R-3.0

Provides the **full microbiological taxonomy** and data on **all antimicrobial drugs**

Applies all recent **CLSI and EUCAST clinical breakpoints** for MICs and disk zones

Corrects for duplicate isolates, **calculates and predicts AMR** per antibiotic class

Integrates with **WHONET**, ATC, **EARS-Net**, PubChem, **LOINC** and **SNOMED CT**

Completely **dependency-free**, highly suitable for places with **limited resources**