ESGEM-AMR

ESCMID

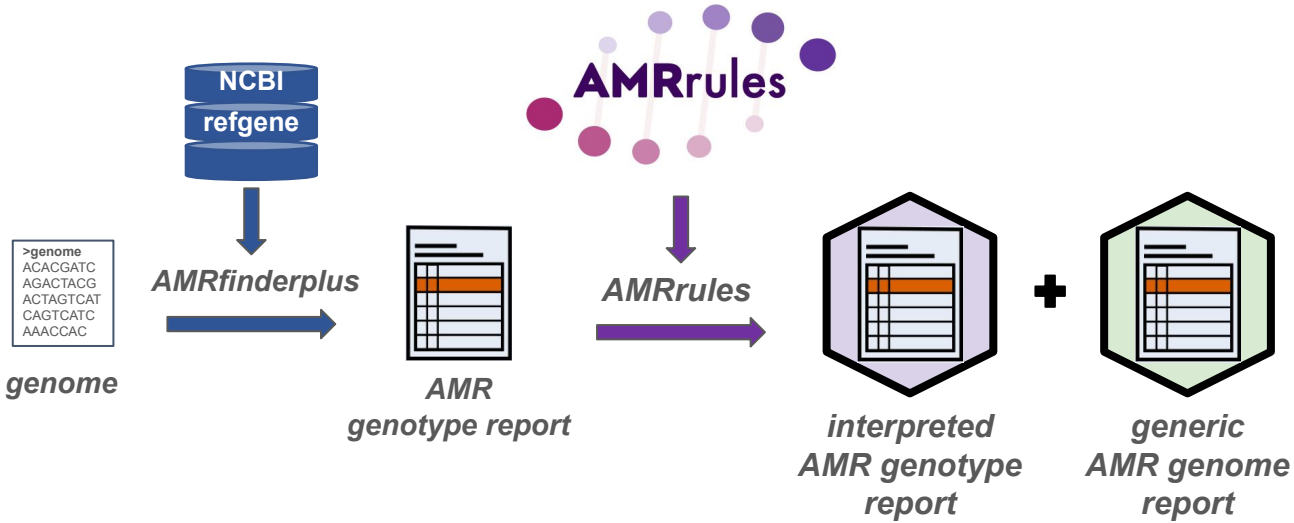
AMRrules

Agenda

1. AMRrules engine
2. Updates from subgroups
   - *Shewanella*
   - *Burkholderia*
   - *Bordetella*
3. Resources update
4. 2026 Planning

AMRrules Python package

https://github.com/AMRverse/AMRrules



Rules in first beta release:

- Acinetobacter baumannii
- Enterobacter
- Enterococcus faecalis
- Enterococcus faecium
- Escherichia coli
- Klebsiella pneumoniae
- Neisseria gonorrhoeae (acquired resistances,
- Pseudomonas aeruginosa
- Salmonella
- Staphylococcus aureus
- Yersinia

Installation:

```
conda create -n amrrules_beta -c bioconda
python=3.12 pip

conda activate amrrules_beta

git clone
https://github.com/interpretAMR/AMRrules
cd AMRrules

make dev
```

Download resources (only required on initial install or when wanting to update NCBI/CARD dbs):

```
amrrules --download-resources
```

Rules for v1 release **(v0.6 spec)**

- *Acinetobacter baumannii*
- *Enterobacter*
- *Enterococcus faecalis*
- *Enterococcus faecium*
- *Escherichia coli*
- *Klebsiella pneumoniae*
- *Pseudomonas aeruginosa*
- *Salmonella*
- *Staphylococcus aureus*
- *Yersinia*
- *Neisseria gonorrhoeae* (acquired)
- *Klebsiella oxytoca*
- *Bordetella*
- *Shewanella*
- *Burkholderia*
- *Legionella*
- *Achromobacter xylosoxidans*

Interpretation engine: running

bit.ly/AMRrules

amrrules --input tests/data/debug/WHO_alpha_2024_amrf.tsv --output_prefix test_gono_WHO_alpha
--output_dir tests/data/output --organism 's__Neisseria gonorrhoeae' --annot_opts full --no-rule-interpretation nwtR

16 hits matched a rule and 0 hits did not match a rule.
Output written to tests/data/output/test_gono_WHO_alpha_interpreted.tsv.
Summary output written to tests/data/output/test_gono_WHO_alpha_genome_summary.tsv.

amrrules --input tests/data/input/test_data_amrfp_multiSpp.tsv --output_prefix test_multiSpp
--output_dir tests/data/output --organism_file tests/data/input/test_data_sppCalls.tsv

UserWarning: The following sample IDs from the organism file are not present in the input file:
NOT_IN_INPUT_FILE
As there are no entries in the input file for these samples, they won't have interpretation results.
Please check your input file if this is not what you expect.
  warnings.warn(f"The following sample IDs from the organism file are not present in the input file:\n{'\n'.join(missing_from_input)}\r
samples, they won't have interpretation results. Please check your input file if this is not what you expect.")
71 hits matched a rule and 89 hits did not match a rule.
Output written to tests/data/output/test_multiSpp_interpreted.tsv.
Summary output written to tests/data/output/test_multiSpp_genome_summary.tsv.

Organism file example

SAMD00028844	s__Acinetobacter baumannii
SAMD00000649	s__Escherichia coli
SAMD00055728	s__Klebsiella pneumoniae
SAMD00002817	s__Staphylococcus aureus
SAMD00019033	s__Pseudomonas aeruginosa
SAMEA1572980	s__Neisseria gonorrhoeae
SAMD00499917	s__Yersinia enterocolitica

Matches "Name" in AMRFP input

Valid organism from --organism flag

Annotated AMRFP Report

bit.ly/AMRrules
(v1-in dev)

AMRfinderplus output

genotype interpretation

Name	Gene symbol	Class	Subclass	Hierarchy node	ruleID	context	drug	drug class	phenotype	clinical category	evidence grade	version	organism
SGH10	emrD	EFFLUX	EFFLUX	emrD	-	-	-	-	-	-	-	0.1.0	-
SGH10	oqxB19	PHENICOL/ QUINOLONE	PHENICOL/ QUINOLONE	oqxB19	KPN0003	core	ciprofloxacin	-	wildtype	S	moderate	0.1.0	s__Klebsiella pneumoniae
SGH10	oqxA	PHENICOL/ QUINOLONE	PHENICOL/ QUINOLONE	oqxA	KPN0002	core	ciprofloxacin	-	wildtype	S	moderate	0.1.0	s__Klebsiella pneumoniae
SGH10	blaSHV-11	BETA-LACTAM	BETA-LACTAM	blaSHV-11	KPN0001	core	-	penicillin beta-lactam	wildtype	R	strong	0.1.0	s__Klebsiella pneumoniae
SGH10	fosA	FOSFOMYCIN	FOSFOMYCIN	fosA5_fam	KPN0004	core	fosfomycin	-	wildtype	S	moderate	0.1.0	s__Klebsiella pneumoniae

- ‘minimal’ and ‘full’ annotation options (default is ‘minimal’)
- ‘full’ additionally contains:
  - breakpoint, breakpoint standard, evidence code, evidence limitations, PMID, rule curation note

Example genome summary report

(v1.0 - in development)

name	drug	drug class	clinical category	phenotype	evidence grade	markers (non-S)	markers (S)	markers (no rule)	ruleIDs	combo rules	organism
SAMD00028844	amikacin	aminoglycoside antibiotic	S	wildtype	high	-	ant(3")-IIa (core)	-	ACI0165	-	s__Acinetobacter baumannii
SAMD00028844	-	fluoroquinolone antibiotic	R	nonwildtype	high	gyrA_S81L	-	parC_S84L	ACI0162	-	s__Acinetobacter baumannii
SAMD00055728	-	penicillin beta-lactam	R	wildtype	high	blaSHV-1 (core)	-	-	KPN0001	-	s__Klebsiella pneumoniae
SAMD00055728	chloramphenicol	phenicol antibiotic	R	nonwildtype	very low	-	-	catB2;catA1	-	-	s__Klebsiella pneumoniae

Example genome summary report (v1.0 - in development)

name	drug	drug class	clinical category	phenotype	evidence grade	markers (non-S)	markers (S)	markers (no rule)	ruleIDs	combo rules	organism
SAMD00028844	amikacin	aminoglycoside antibiotic	S	wildtype	high	-	ant(3")-Ia (core)	-	ACI0165	-	s__Acinetobacter baumannii
SAMD00028844	-	fluoroquinolone antibiotic	R	nonwildtype	high	gyrA_S81L	-	parC_S84L	ACI0162	-	s__Acinetobacter baumannii
SAMD00055728	-	penicillin beta-lactam	R	wildtype	high	blaSHV-1 (core)	-	-	KPN0001	-	s__Klebsiella pneumoniae
SAMD00055728	chloramphenicol	phenicol antibiotic	R	nonwildtype	very low	-	-	catB2;catA1	-	-	s__Klebsiella pneumoniae

--no-rule-interpretation: ‘nwtR’ or ‘nwtS’

- How to interpret a marker if it has no rule in the genome summary report
- Sets clinical category to R or S, phenotype to nonwildtype
- Evidence grade defaults to ‘very low’ regardless of choice

AMRrules package - steps to v1.0 release

1. Incorporate additional core gene rules submitted
    - *Bordetella, Shewanella, Burkholderia pseudomallei, Legionella, Proteus mirabilis, Achromobacter xylosoxidans.*
2. Accept hAMRonized AMRfinderplus input
3. Flesh out documentation
4. Call on working group to beta-test on supported organisms

- Test genomes and output files will be distributed for review
- WG members will be asked to test software on own genomes

AIM: Release by early March (ahead of Wellcome AMR Conference)

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   - *Burkholderia*
   - *Bordetella*
   - *Achromobacter xylosoxidans*
3. Resources update
4. 2026 Planning

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1. AMRrules engine

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   - *Bordetella*

3. Resources update

4. 2026 Planning

bioRxiv
THE PREPRINT SERVER FOR BIOLOGY

New Results

A comprehensive AMR genotype-phenotype database (CABBAGE)

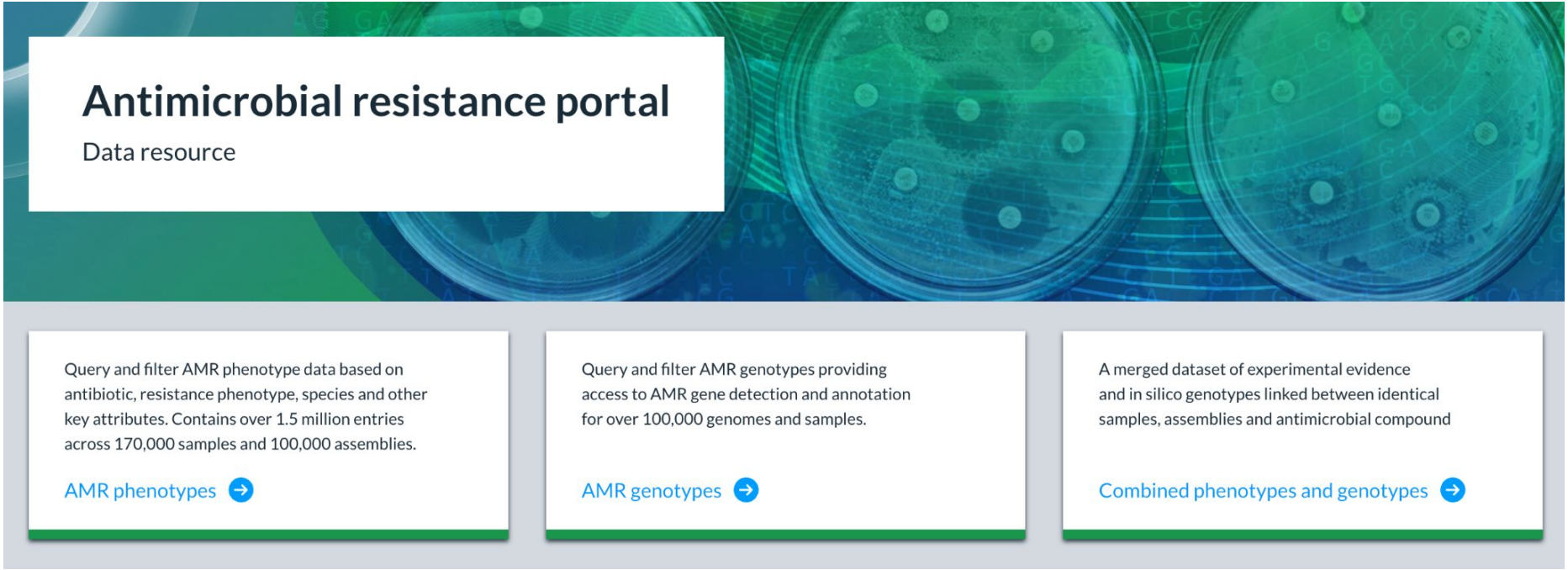
Emily Dickens, Romain Derelle, Robert Beardmore, Anita Suresh, Swapna Uplekar, Andrey G Azov, Tatiana A Gurbich, Bilal El Houdaigui, Jon Keatley, Sofiia Ochkalova, Orges Koci, Nadim M Rahman, Anu Shivalikanjli, Andrea Winterbottom, Galabina Yordanova, Helen Parkinson, Andrew D Yates, Robert D Finn, John A Lees, Leonid Chindelevitch

doi: https://doi.org/10.1101/2025.11.12.688105

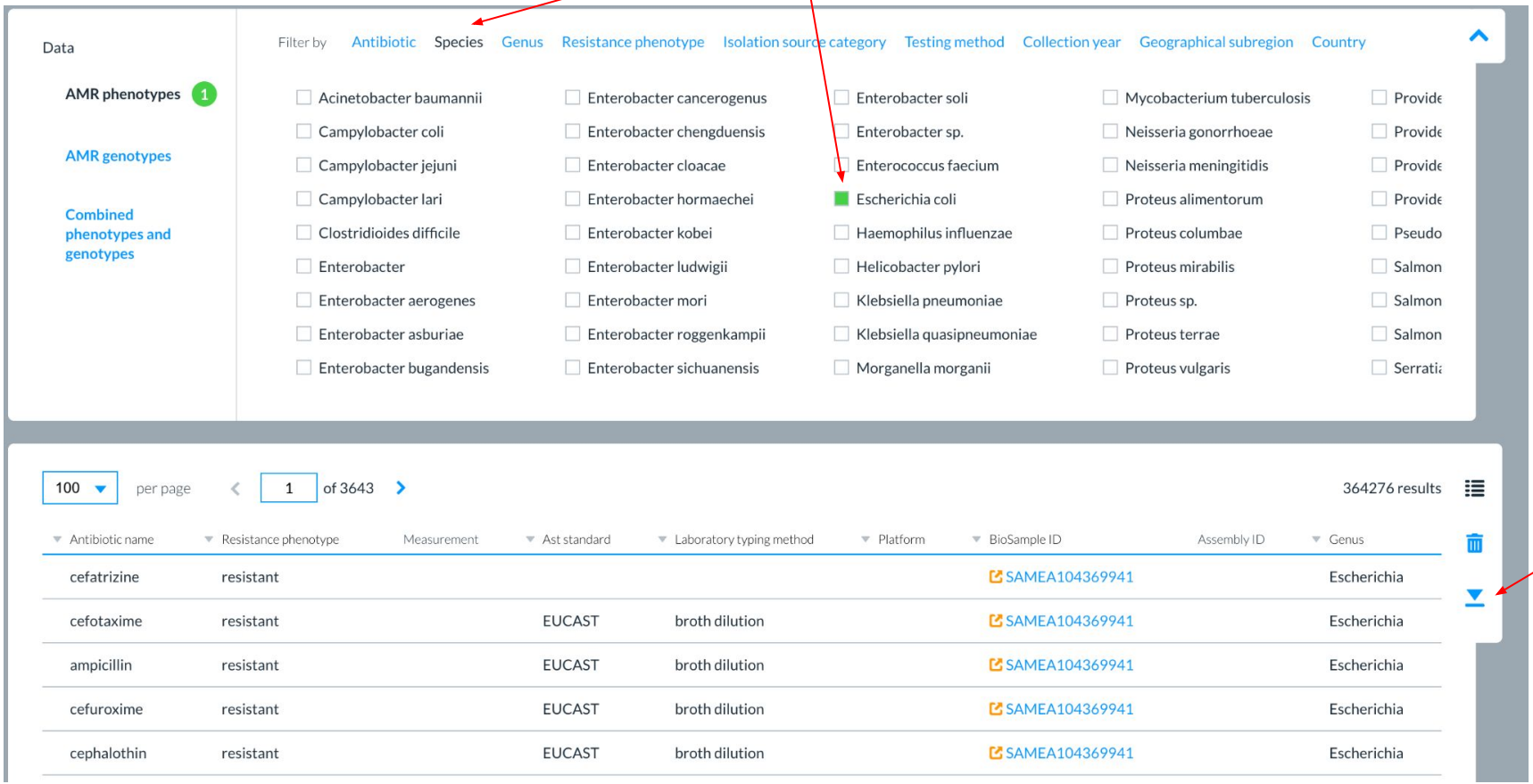
https://www.biorxiv.org/content/10.1101/2025.11.12.688105v2

EBI AMR Portal

https://www.ebi.ac.uk/amr/



https://ftp.ebi.ac.uk/pub/databases/amr_portal/releases/


Choose species
Data
AMR phenotypes 1
AMR genotypes
Combined phenotypes and genotypes
Filter by Antibiotic Species Genus Resistance phenotype Isolation source category Testing method Collection year Geographical subregion Country
Acinetobacter baumannii
Campylobacter coli
Campylobacter jejuni
Campylobacter lari
Clostridioides difficile
Enterobacter
Enterobacter aerogenes
Enterobacter asburiae
Enterobacter bugandensis
Enterobacter cancerogenus
Enterobacter chengduensis
Enterobacter cloacae
Enterobacter hormaechei
Enterobacter kobei
Enterobacter ludwigii
Enterobacter mori
Enterobacter roggenkampii
Enterobacter sichuanensis
Enterobacter soli
Enterobacter sp.
Enterococcus faecium
Escherichia coli
Haemophilus influenzae
Helicobacter pylori
Klebsiella pneumoniae
Klebsiella quasipneumoniae
Morganella morganii
Mycobacterium tuberculosis
Neisseria gonorrhoeae
Neisseria meningitidis
Proteus alimentorum
Proteus columbae
Proteus mirabilis
Proteus sp.
Proteus terrae
Proteus vulgaris
100 per page
1 of 3643
364276 results
Antibiotic name
Resistance phenotype
Measurement
Ast standard
Laboratory typing method
Platform
BioSample ID
Assembly ID
Genus
cefatrizine resistant SAMEA104369941 Escherichia
cefotaxime resistant EUCAST broth dilution SAMEA104369941 Escherichia
ampicillin resistant EUCAST broth dilution SAMEA104369941 Escherichia
cefuroxime resistant EUCAST broth dilution SAMEA104369941 Escherichia
cephalothin resistant EUCAST broth dilution SAMEA104369941 Escherichia
Download

EBI AMR Portal - Genotypes

https://www.ebi.ac.uk/amr/methods/

AllTheBacteria

Assemblies used for genotyping were generated by the AllTheBacteria collaboration. The assembly pipeline, uses Shovill (v1.1.0), and are processed with a simple pipeline to download reads, run Shovill, and remove contigs matching the human genome (using MUMmer v4.0.0rc1). Full methods are in the preprint Hunt M *et al.* 2025.

Annotation using mettannotator

mettannotator is a bioinformatics pipeline that generates an exhaustive annotation of prokaryotic genomes using existing tools. The output is a GFF file that integrates the results of all pipeline components. Results of each individual tool are also provided. Version `4.0.23` of AMRFinderPlus was used alongside database version `4.0 2025-07-16.1`. In future versions UniFIRE will be used to generate additional *in silico* predictions. v1.5.0 of mettannotator was used by this portal.

NOTE: not all biosamples with phenotype data appear in the genotype DB

For now we suggest using the AMRFinderPlus results direct from AllTheBacteria as this is more complete

Agenda

1. AMRrules engine updates

- Improved support for mutation types
- Genome summary report

2. CABBAGE AST database and EBI AMR data portal

3. AMRgen & AMRrulemakeR

- Discussion of quantitative fields to include in spec

4. QualiBact recap

AMRgen R package

https://github.com/AMRverse/AMRgen

Import AST results to standard format using AMR classes

```
import_ast("~/Downloads/Ecoli_AST_EBI.csv", format="ebi", interpret_eucast = T, interpret_ecoff = T)
import_ast("~/Downloads/Ecoli_AST_NCBI.csv", format="ncbi", interpret_eucast = T, interpret_ecoff = T)
```

	id	drug_agent	mic	disk	pheno_eucast	pheno_clsi	ecoff	guideline	method	source	pheno_provided	spp_pheno
	<chr>	<ab>	<mic>	<dsk>	<sir>	<sir>	<sir>	<chr>	<chr>	<chr>	<sir>	<mo>
1	SAMN02437318	CAZ	>16	NA	R	R	R	CLSI	Microscan	33659219	R	B_ACNTB_BMNN
2	SAMN02437318	CTX	>32	NA	R	R	S	CLSI	Microscan	33659219	R	B_ACNTB_BMNN
3	SAMN02437318	LVX	>4	NA	R	R	R	CLSI	Microscan	33659219	R	B_ACNTB_BMNN
4	SAMN02437318	MEM	>=16	NA	R	R	R	CLSI	Vitek	33659219	R	B_ACNTB_BMNN
5	SAMN02437318	TCY	>8	NA	NA	R	NA	CLSI	Microscan	33659219	R	B_ACNTB_BMNN
6	SAMN02437318	TGC	1	NA	R	NA	NA	CLSI	Vitek	33659219	S	B_ACNTB_BMNN
7	SAMN02437332	CAZ	>16	NA	R	R	R	CLSI	Microscan	33659219	R	B_ACNTB_BMNN
8	SAMN02437332	CTX	>32	NA	R	R	S	CLSI	Microscan	33659219	R	B_ACNTB_BMNN
9	SAMN02437332	LVX	4	NA	R	I	R	CLSI	Microscan	33659219	I	B_ACNTB_BMNN
10	SAMN02437332	MEM	>=16	NA	R	R	R	CLSI	Vitek	33659219	R	B_ACNTB_BMNN

AMR package classes

source to track unique datasets

AMRgen R package

https://github.com/AMRverse/AMRgen

```
geno <- import_amrfp("amrfinderplus.tsv", sample_col = "Name")
```

Input

	Name	`Gene symbol`	`Element type`	`Element subtype`	Class	Subclass	Method
	<chr>	<chr>	<chr>	<chr>	<chr>	<chr>	<chr>
1	002_S03	aac(3)-IIe	AMR	AMR	AMINOGLYCOSIDE	GENTAMICIN	EXACTX
2	002_S03	aph(3'')-Ib	AMR	AMR	AMINOGLYCOSIDE	STREPTOMYCIN	EXACTX
3	002_S03	aph(6)-Id	AMR	AMR	AMINOGLYCOSIDE	STREPTOMYCIN	EXACTX
4	002_S03	aadA2	AMR	AMR	AMINOGLYCOSIDE	STREPTOMYCIN	EXACTX
5	002_S03	aadA1	AMR	AMR	AMINOGLYCOSIDE	STREPTOMYCIN	PARTI…
6	002_S03	oqxB	AMR	AMR	PHENICOL/QUINOLONE	PHENICOL/QU…	BLASTX
7	002_S03	oqxA	AMR	AMR	PHENICOL/QUINOLONE	PHENICOL/QU…	EXACTX
8	003_S08	rmtB1	AMR	AMR	AMINOGLYCOSIDE	AMINOGLYCOS…	ALLEL…
9	003_S08	aac(3)-IId	AMR	AMR	AMINOGLYCOSIDE	GENTAMICIN	EXACTX
10	003_S08	aph(3')-Ia	AMR	AMR	AMINOGLYCOSIDE	KANAMYCIN	EXACTX

Import AMRfinderplus results and parse mutations and drugs/classes

Output

	Name	gene	mutation	node	`variation type`	marker	marker.label	drug_agent	drug_class	`Gene symbol`
	<chr>	<chr>	<chr>	<chr>	<chr>	<chr>	<chr>	<ab>	<chr>	<chr>
1	002_S03	ompK36	Asp135AspGlyAsp	ompK36	Protein variant detected	ompK36_D135DGD	ompK36:Asp135AspGlyAsp	NA	Carbapenems	ompK36_D135D…
2	002_S03	gyrA	Ser83Ile	gyrA	Protein variant detected	gyrA_S83I	gyrA:Ser83Ile	NA	Quinolones	gyrA_S83I
3	002_S03	parC	Ser80Ile	parC	Protein variant detected	parC_S80I	parC:Ser80Ile	NA	Quinolones	parC_S80I
4	002_S03	aac(3)-IIe	NA	aac(3)-IIe	Gene presence detected	aac(3)-IIe	aac(3)-IIe	GEN	Aminoglycosi…	aac(3)-IIe
5	002_S03	aph(3'')-Ib	NA	aph(3'')-Ib	Gene presence detected	aph(3'')-Ib	aph(3'')-Ib	STR1	Aminoglycosi…	aph(3'')-Ib
6	002_S03	aph(6)-Id	NA	aph(6)-Id	Gene presence detected	aph(6)-Id	aph(6)-Id	STR1	Aminoglycosi…	aph(6)-Id
7	002_S03	aadA2	NA	aadA2	Gene presence detected	aadA2	aadA2	STR1	Aminoglycosi…	aadA2
8	002_S03	aadA1	NA	aadA1	Inactivating mutation detected	aadA1	aadA1:-	STR1	Aminoglycosi…	aadA1
9	002_S03	oqxB	NA	oqxB	Gene presence detected	oqxB	oqxB	NA	Amphenicols	oqxB
10	002_S03	oqxA	NA	oqxA	Gene presence detected	oqxA	oqxA	NA	Amphenicols	oqxA
11	002_S03	oqxB	NA	oqxB	Gene presence detected	oqxB	oqxB	NA	Quinolones	oqxB
12	002_S03	oqxA	NA	oqxA	Gene presence detected	oqxA	oqxA	NA	Quinolones	oqxA

copy for each class

AMRrules syntax for specifying variants

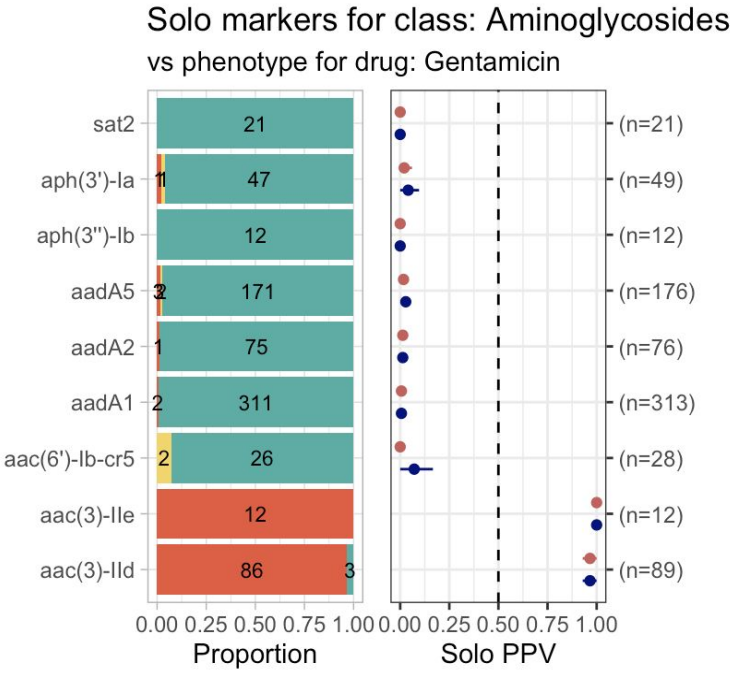
marker.label for analysis (node:mutation)

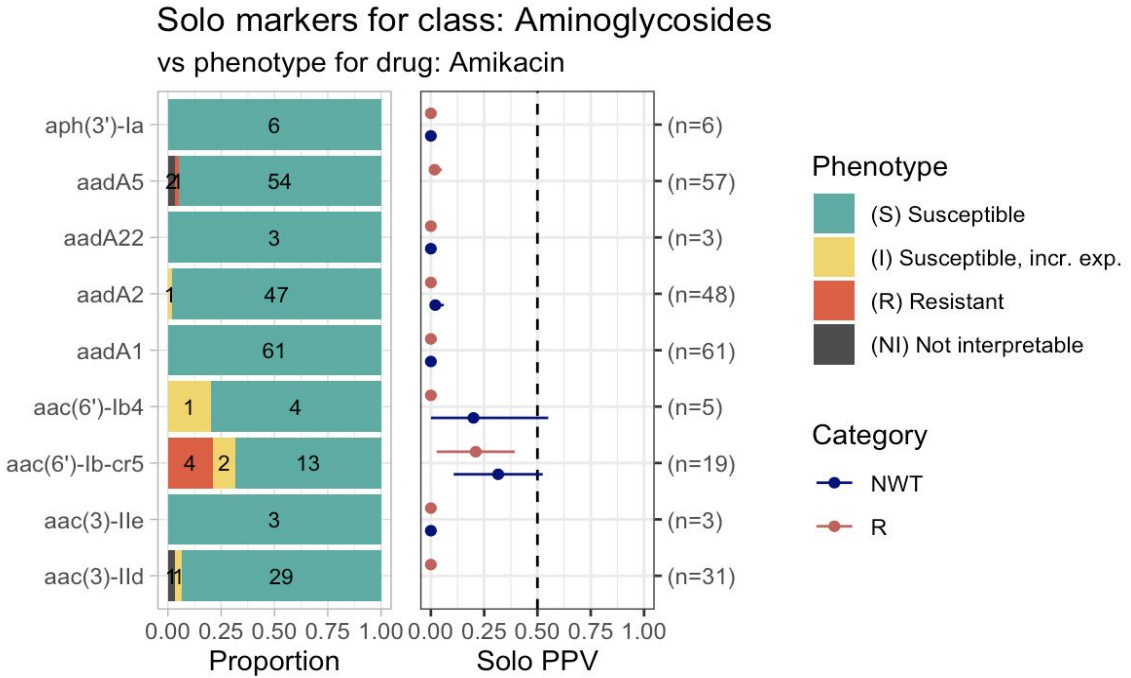
AMRgen R package

https://github.com/AMRverse/AMRgen

Calculate positive predictive value (PPV) of markers found 'solo'

```
solo_ppv_analysis(geno, ast, drug_class_list=c("Aminoglycosides"), antibiotic="Gentamicin")
solo_ppv_analysis(geno, ast, drug_class_list=c("Aminoglycosides"), antibiotic="Amikacin")
```



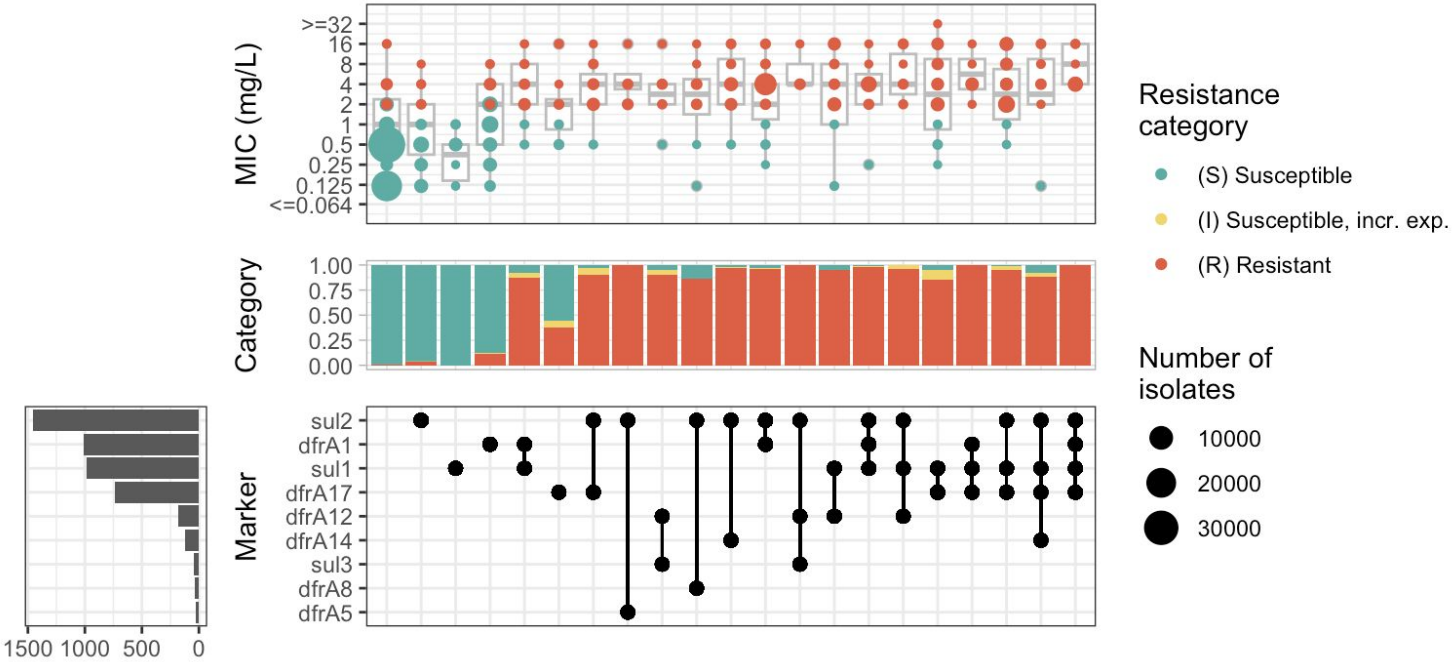


AMRgen R package

https://github.com/AMRverse/AMRgen

Upset plot, to explore MIC distribution associated with marker combinations

```
amr_upset(get_binary_matrix(geno, ast, antibiotic="Trimethoprim-sulfamethoxazole",
          drug_class_list=c("Trimethoprims", "Sulfonamides"), min_set_size=20, assay="mic")
```



AMRgen R package

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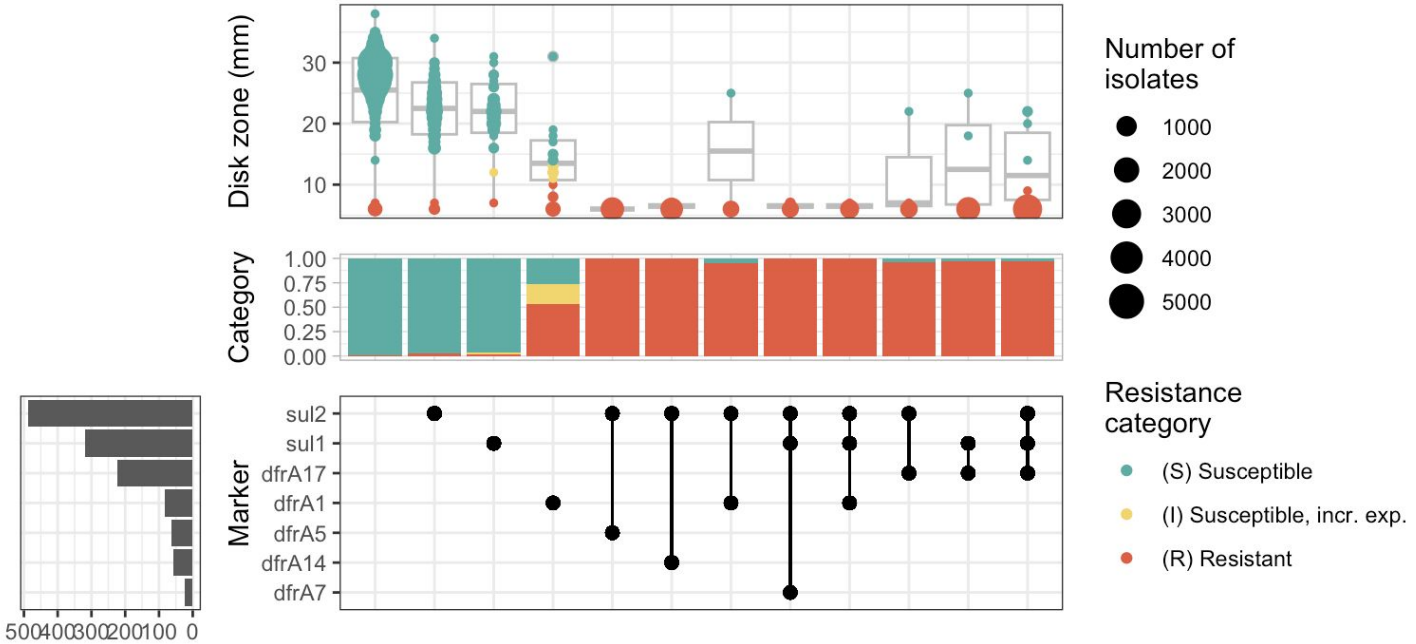
Upset plot, to explore MIC distribution associated with marker combinations

```
amr_upset(get_binary_matrix(geno, ast, antibiotic="Trimethoprim-sulfamethoxazole",
          drug_class_list=c("Trimethoprims", "Sulfonamides"), min_set_size=20, assay="disk")
```



AMRrulemakeR package

https://github.com/AMRverse/AMRrulemakeR

```
analysis <- amrrules_analysis(afp, ast, antibiotic="Ciprofloxacin", drug_class_list=c("Quinolones"), species="E. coli")
```

```
amrrules_analysis(
  geno_table,
  pheno_table,
  antibiotic,
  drug_class_list,
  species,
  sir_col = "pheno_eucast",
  ecoff_col = "ecoff",
  sir_provided_col = "pheno_provided",
  geno_sample_col = "Name",
  pheno_sample_col = "id",
  marker_col = "marker.label",
  minPPV = 1,
  mafLogReg = 5,
  mafUpset = 1,
  info = NULL
)
```

Value

A list containing:

`reference_mic_plot`	EUCAST reference MIC distribution plot
`reference_disk_plot`	EUCAST reference disk zone distribution plot
`summary`	Output of `summarise_data` showing sample and breakpoint summaries
`solo_stats`	PPV statistics for individual markers
`solo_binary`	Binary matrix of individual marker presence by sample
`amr_binary`	Binary matrix of AMR marker presence by sample
`ppv_plot`	Bar plot summarizing PPV results
`logistic_mat`	Binary matrix used in logistic regression
`logistic_plot`	Plot of logistic regression estimates
`ppv_logistic_plot`	Combined PPV/logistic plot
`modelR`	Logistic model for predicting resistance
`modelNWT`	Logistic model for predicting NWT (non-wild-type)
`allstatsR`	Merged statistics for R category
`allstatsNWT`	Merged statistics for NWT category
`upset_mic_plot`	Upset plot for MIC data
`upset_disk_plot`	Upset plot for disk data
`upset_mic_summary`	MIC data summarised per marker or combination
`upset_disk_summary`	Disk diffusion data summarised per marker or combination
`combination_summary_values`	Summary of genotype combinations from both MIC and disk
`afp_hits`	List of AMR markers detected
`species`	The species used in the analysis
`antibiotic`	The antibiotic used in the analysis

AMRrulemakeR package

https://github.com/AMRverse/AMRrulemakeR

```
analysis <- amrrules_analysis(afp, ast, antibiotic="Ciprofloxacin", drug_class_list=c("Quinolones"), species="E. coli")

rules <- makerules(analysis)
```

amrrules_analysis() result

```
makerules(
  amrrules,
  minObs = 3,
  low_threshold = 20,
  core_threshold = 0.9,
  use_mic = TRUE,
  mic_S = NULL,
  mic_R = NULL,
  mic_ecoff = NULL,
  use_disk = TRUE,
  disk_S = NULL,
  disk_R = NULL,
  disk_ecoff = NULL,
  guide = "EUCAST 2025",
  bp_site = NULL,
  rule_prefix = NULL,
  ruleID_start = 1000,
  note_prefix = "Quantitative geno-pheno analysis by ESGEM-AMR WG",
  regression = TRUE
)
```

Propose rulesets based on outputs of `amrrules_analysis()`

For single markers and combinations

AMRrulemakeR package

https://github.com/AMRverse/AMRrulemakeR

PPV for S/I/R and WT/NWT EUCAST calls for individual markers and combinations, interpreted from:

- combined MIC or disk measures
- MIC data only
- Disk data only

Solo PPV for S/I/R and WT/NWT calls from any source (EUCAST calls from MIC or disk measures, plus S/I/R calls from public data without assay measures)

Call category & WT/NWT from all 4 sources, check for agreement

- MIC+disk > MIC or disk (largest sample) > extended data
- If marker not found solo, check if logistic regression with all markers included supports no effect (95% CI 1 and p>0.05) => call WT S

AMRrulemakeR package

https://github.com/AMRverse/AMRrulemakeR

```
rules <- makerules(analysis, guide="EUCAST 2025", bp_site=NULL, weak_threshold=20, core_threshold=0.9)
```

ruleID	organism	gene	nodeID	mutation	variation type	drug	phenotype	clinical	breakpoint	breakpoint star	breakpoint condition	evidence code	evidence	marker
ECO1029	s_Escherichia coli	aac(6')-Ib-cr5	aac(6')-Ib-cr5	-	Gene presence detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	aac(6')-Ib-cr5
ECO1030	s_Escherichia coli	acrR	acrR	Arg45Cys	Protein variant detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	acrR:Arg45Cys
ECO1031	s_Escherichia coli	gyrA	gyrA	Asp87Asn	Protein variant detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	gyrA:Asp87Asn
ECO1032	s_Escherichia coli	gyrA	gyrA	Asp87Gly	Protein variant detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	gyrA:Asp87Gly
ECO1033	s_Escherichia coli	gyrA	gyrA	Asp87Tyr	Protein variant detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	gyrA:Asp87Tyr
ECO1034	s_Escherichia coli	gyrA	gyrA	Ser83Ala	Protein variant detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	gyrA:Ser83Ala
ECO1035	s_Escherichia coli	gyrA	gyrA	Ser83Leu	Protein variant detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	gyrA:Ser83Leu
ECO1036	s_Escherichia coli	gyrA	gyrA	Ser83Val	Protein variant detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	gyrA:Ser83Val
ECO1037	s_Escherichia coli	marR	marR	Ser3Asn	Protein variant detecte	Ciprofloxacin	nonwildtype	S	MIC <= 0.25 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	marR:Ser3Asn
ECO1038	s_Escherichia coli	parC	parC	Ala56Thr	Protein variant detecte	Ciprofloxacin	wildtype	S	MIC <= 0.25 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	parC:Ala56Thr
ECO1039	s_Escherichia coli	parC	parC	Ser57Thr	Protein variant detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	parC:Ser57Thr
ECO1040	s_Escherichia coli	parC	parC	Ser80Ile	Protein variant detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	parC:Ser80Ile
ECO1041	s_Escherichia coli	parE	parE	Asp475Glu	Protein variant detecte	Ciprofloxacin	nonwildtype	S	MIC <= 0.25 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	parE:Asp475Glu
ECO1042	s_Escherichia coli	parE	parE	Ile355Thr	Protein variant detecte	Ciprofloxacin	nonwildtype	S	MIC <= 0.25 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	parE:Ile355Thr
ECO1043	s_Escherichia coli	parE	parE	Ile529Leu	Protein variant detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	parE:Ile529Leu
ECO1044	s_Escherichia coli	qnrB19	qnrB19	-	Gene presence detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	qnrB19
ECO1045	s_Escherichia coli	qnrB4	qnrB4	-	Gene presence detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	qnrB4
ECO1046	s_Escherichia coli	qnrS1	qnrS1	-	Gene presence detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	qnrS1
ECO1047	s_Escherichia coli	qnrS13	qnrS13	-	Gene presence detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	qnrS13
ECO1048	s_Escherichia coli	qnrS2	qnrS2	-	Gene presence detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	qnrS2
ECO1049	s_Escherichia coli	soxR	soxR	Gly121Asp	Protein variant detecte	Ciprofloxacin	wildtype	S	MIC <= 0.25 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	soxR:Gly121Asp
ECO1050	s_Escherichia coli	soxS	soxS	Ala12Ser	Protein variant detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	soxS:Ala12Ser
ECO1051	s_Escherichia coli	gyrA	gyrA	Gly81Asp	Protein variant detecte	Ciprofloxacin	wildtype	S	MIC <= 0.25 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	-	gyrA:Gly81Asp
ECO1052	s_Escherichia coli	qnrA1	qnrA1	-	Gene presence detecte	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	-	qnrA1
ECO1053	s_Escherichia coli	qnrB	qnrB	-	Gene presence detecte	Ciprofloxacin	wildtype	S	MIC <= 0.25 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	-	qnrB
ECO1054	s_Escherichia coli	qnrB7	qnrB7	-	Gene presence detecte	Ciprofloxacin	wildtype	S	MIC <= 0.25 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	-	qnrB7
ECO1055	s_Escherichia coli	ECO1037 & ECO1041	-	-	-	Ciprofloxacin	nonwildtype	I	MIC > 0.25 & <= 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	marR:Ser3Asn, parE:Asp475Glu
ECO1056	s_Escherichia coli	ECO1035	-	-	-	Ciprofloxacin	nonwildtype	R	MIC > 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	gyrA:Ser83Leu, parC:Ser80Arg
ECO1057	s_Escherichia coli	ECO1035 & ECO1045	-	-	-	Ciprofloxacin	nonwildtype	R	MIC > 0.5 mg/L	EUCAST 2025	Non-meningitis	ECO:0001103	low	gyrA:Ser83Leu, qnrB4

rule curation note

Quantitative geno-pheno analysis by ESGEM-AMR WG. gyrA:Ser83Val. Category call 'I' based on Solo PPV. MIC. Disk. Phenotype call 'nonwildtype' based on MIC. Disk. R PPV=33% (3/9). NWT PPV=91% (10/11). 5 solo datasets: 1 S, 3 I, 2 R. MIC: median 0.5 [IQR 0.5-0.5]; n=5. 5 MIC datasets: 1 S, 2 I, 2 R. Disk: median 22 [IQR 21-22]; n=5. 2 disk datasets: 1 S, 1 I, 2 R.

https://happykhan.github.io/qualibact/

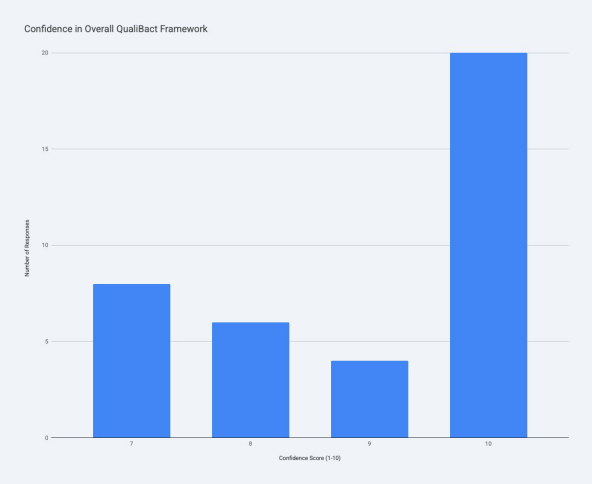
Qualibact update

39 responses across multiple genera

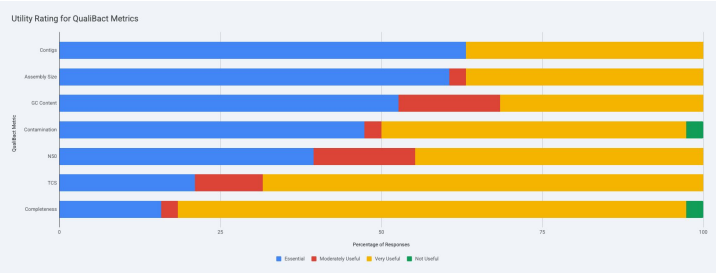
- **High Consensus: 86.8%** of the responses for all individual thresholds (N50, Contigs, GC, Completeness, Contamination, TCS, and Assembly Size) indicated *Yes* to agreement.
- **Targeted Disagreement:** Disagreement (*No*) accounted for only **6.4%** of the responses. The specific comments provided for the 'No' were concerns about the Assembly Size being "too strict" for certain well-assembled genomes or suggestions to "loosen" thresholds to accommodate species diversity.
- **Need for Refinement:** A small number of responses (**1.6%** total) noted that thresholds were "Not defined" for their specific species, but this is due to the minimum number of genomes to be included (≥100).
- Collectively, scores of **8, 9, or 10** account for **78.9%** of all responses, with the lowest score observed being 7, which still indicates a high level of confidence.
- Through the introduction of new genomes, we have updated the metrics for *Achromobacter xylosoxidans*.

Reminder:
Qualibact currently works for SPAdes assemblies.
Thresholds will not be changed manually.

Overall confidence



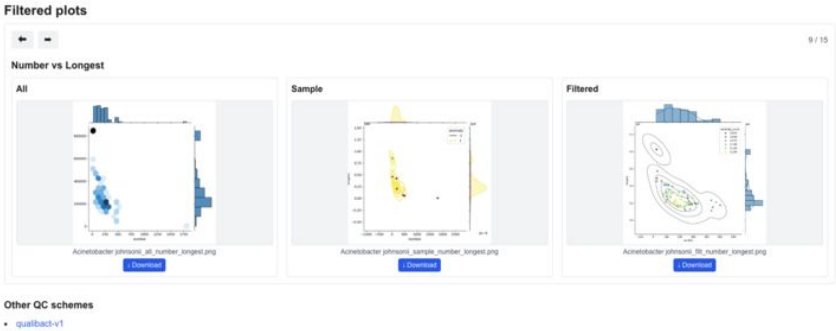
Utility of QualiBact metrics



Qualibact update

Work under development:

- Versioned rules.
- Scored rules depending on the number of genomes included.
- New dynamic visualisations will be introduced on the website.
- Comparing MLST and AMR calls between high quality and rejected genome lists.
- Manuscript intended for early next year, ahead of Wellcome AMR.



Reminder:
Contributions can be made through
https://happykhan.github.io/qualibact/contributing/

Agenda

1. AMRrules engine

2. Updates from subgroups

- *Shewanella*
- *Burkholderia*
- *Bordetella*

3. Resources update

4. 2026 Planning

2026 Planning - Manuscripts

1. **AMRgen R package** (Q1)
2. **AMRrules** (Q2)
   - *Concept* - aims, principles, working group model
   - *Specification* (v1.0) - format for how rules are specified, use of standard ontologies, new/modified ontologies/syntax
   - *Implementation* - how rules are applied to interpret AMRfp output (Python package v1.0)
3. **Core gene rules** (Q2)
   - Why interpreting core gene rules is important but challenging
   - Approach to defining rules
   - Summary of rules - comparison across pathogens, gaps in knowledge
4. **Quantitative approach and acquired gene rules** (Q4)

Subgroup specific papers?

Approach & authorship policy (ESGEM-AMR TORs)

Group authors

- All papers developed as a Working Group activity are to include the group "**ESCMID Study Group for Epidemiological Markers - Antimicrobial Resistance Working Group (ESGEM-AMR)**" in the author list, and a list of all individual group members are to be included in the manuscript text. This ensures that all group members are tracked as authors via PubMed.

- Journal guidelines require that all group authors must meet the usual criteria for authorship including reading and approving the paper, and if the journal requires conflict-of-interest statements to be completed they must be completed individually by all group authors.

Approach & authorship policy (ESGEM-AMR TORs)

Individual authors

1) In addition to the group authorship, publications are to include as **individual authors** those people meeting the following criteria:
   a) members of the analysis group established for that paper or working group, including the agreed lead author/s; AND/OR
   b) individuals contributing unpublished data for use in the paper; AND/OR
   c) others making significant contributions to data interpretation, manuscript writing or editing.
2) The list of individual authors, and author order, should be discussed early in the process of developing a publication plan.

Approach & authorship policy (ESGEM-AMR TORs)

Preparation and circulation of manuscript drafts

- An analysis group should be established by the lead author/s for each planned and approved Working Group manuscript, and Members given the opportunity to self-nominate for inclusion.

- Draft manuscripts must be circulated to Working Group Members with sufficient lead time to allow them to read and approve the manuscript, and a clear date by which a response is required to ensure their inclusion as an author (minimum of two weeks).

AMRgen R package (Q1)

Analysis group leads: Matthijs Berends (Data & Tools group) & Kat Holt

Contributors – code development:

- all those who contributed (including via the Jan 2025 hackathon)
- please volunteer if you want to help add or refine functions

Contributors – testing and examples:

- please volunteer if you want to help develop example use cases to include in the paper (and in package documentation and vignettes)

AMRrules paper (Q2)

Leads: Natacha Couto, Kat Holt, Jane Hawkey

- *Concept* - aims, principles, working group model
- *Specification* (v1.0) - format for how rules are specified, use of standard ontologies, new/modified ontologies/syntax
- *Implementation* - how rules are applied to interpret AMRfp output (Python package v1.0)

Propose: Single author = ESGEM-AMR (no individual authors)

All ESGEM-AMR members invited to join as group authors, listed in paper and indexed in PubMed.

Criteria to be included in group list:

- Read and edit draft manuscript
- Complete form confirming agreement to publish and inclusion as co-author

AMRrules paper

“AMRrules: Interpretive Standards for Antimicrobial Resistance Genotypes”.

ESCMID Study Group for Epidemiological Markers - Antimicrobial Resistance Working Group (ESGEM-AMR).

Journal, Year

(Criteria to be included in group authorship list: ESGEM-AMR members who edit and review manuscript)

Review > BMJ Glob Health. 2020 Nov;5(11):e002244. doi: 10.1136/bmjgh-2019-002244.

Whole-genome sequencing as part of national and international surveillance programmes for antimicrobial resistance: a roadmap

NIHR Global Health Research Unit on Genomic Surveillance of AMR

Collaborators – collapse

Collaborators

NIHR Global Health Research Unit on Genomic Surveillance of AMR: Celia Carlos, Marietta Lagrada, Polle K Macaranas, Agnettah M Olorosa, June Gayeta, Melissa Ana Masim, Elmer M Herrera, David M Aanensen, Khalil Abudahab, Monica Abrudan, Silvia Argimon, Harry Harste, Mihir Kekre, Ali Molloy, Dawn Muddyman, Anneke Schmider, Ben Taylor, Anthony Underwood, Nicole Wheeler, María Del Pilar Donado Godoy, Johan Fabian Bernal Morales, Alejandra Arevalo, Maria Fernanda Valencia Guerrero, Erik Cristopher Dustin Osma Castro, Iruka N Okeke, Anderson O Oaikhena, Ayorinde Oluwatobiloba Afolayan, Jolaade J Ajiboye, Ravikumar K L, Geetha Nagaraj, Varun Shammana, Vandana Govindan, Akshata Prabhu, Darmavaram Sravani, Shincy M R, Rajitha G V, Carolin Vegvari, John Stelling

PMID: 33239336 PMCID: PMC7689591 DOI: 10.1136/bmjgh-2019-002244

AMRrules paper

Review > BMJ Glob Health. 2020 Nov;5(11):e002244. doi: 10.1136/bmjgh-2019-002244.

Whole-genome sequencing as part of national and international surveillance programmes for antimicrobial resistance: a roadmap

NIHR Global Health Research Unit on Genomic Surveillance of AMR

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Collaborators

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PMID: 33239336 PMCID: PMC7689591 DOI: 10.1136/bmjgh-2019-002244

⇦ **Single author = working group**

⇦ **List of group authors:**
(Criteria to be included: all ESGEM-AMR members who edit and review manuscript)

Core gene rules (Q2)

Leads: Natacha Couto, Kat Holt

- *Why interpreting core gene rules is important but challenging*
- *Approach to defining rules*
- *Summary of rules, comparison across pathogens, gaps in knowledge*

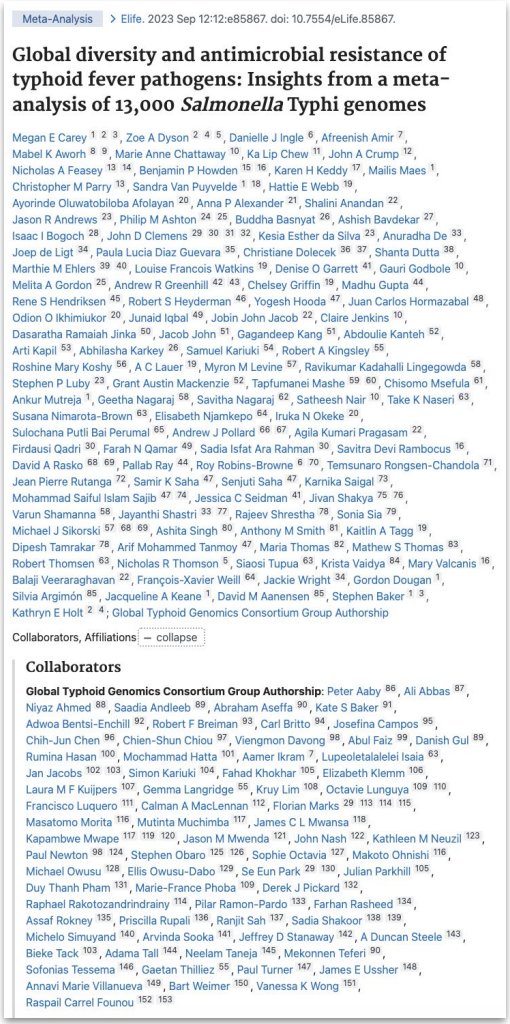
Propose: *Individual authors:* Members of subgroups contributing core gene rules to v1.0

Criteria to be included as individual author:

- Subgroup leads
- Individuals whom subgroup lead confirms engaged meaningfully in rule curation, and/or who shared data
- Individuals who contribute to comparing and summarising core gene rules for paper

***Group authors:* All ESGEM-AMR members invited to join as group authors.**

All authors (individual or group) must read and edit draft manuscript, complete form confirming agreement to publish and inclusion as co-author



Meta-Analysis › Elife. 2023 Sep 12:12:e85867. doi: 10.7554/eLife.85867.

Global diversity and antimicrobial resistance of typhoid fever pathogens: Insights from a meta-analysis of 13,000 *Salmonella* Typhi genomes

Megan E Carey [1 2 3], Zoe A Dyson [2 4 5], Danielle J Ingle [6], Afreenish Amir [7], Mabel K Aworh [8 9], Marie Anne Chattaway [10], Ka Lip Chew [11], John A Crump [12], Nicholas A Feasey [13 14], Benjamin P Howden [15 16], Karen H Keddy [17], Mailis Maes [1], Christopher M Parry [13], Sandra Van Puyvelde [1 18], Hattie E Webb [19], Ayorinde Oluwatobiloba Afolayan [20], Anna P Alexander [21], Shalini Anandan [22], Jason R Andrews [23], Philip M Ashton [24 25], Buddha Basnyat [26], Ashish Bavdekar [27], Isaac I Bogoch [28], John D Clemens [29 30 31 32], Kesia Esther da Silva [23], Anuradha De [33], Joep de Ligt [34], Paula Lucia Diaz Guevara [35], Christiane Dolecek [36 37], Shanta Dutta [38], Marthie M Ehlers [39 40], Louise Francois Watkins [19], Denise O Garrett [41], Gauri Godbole [10], Melita A Gordon [25], Andrew R Greenhill [42 43], Chelsey Griffin [19], Madhu Gupta [44], Rene S Hendriksen [45], Robert S Heyderman [46], Yogesh Hooda [47], Juan Carlos Hormazabal [48], Odion O Ikhimiukor [20], Junaid Iqbal [49], Jobin John Jacob [22], Claire Jenkins [10], Dasaratha Ramaiah Jinka [50], Jacob John [51], Gagandeep Kang [51], Abdoulie Kanteh [52], Arti Kapil [53], Abhilasha Karkey [26], Samuel Kariuki [54], Robert A Kingsley [55], Roshine Mary Koshy [56], A C Lauer [19], Myron M Levine [57], Ravikumar Kadahalli Lingegowda [58], Stephen P Luby [23], Grant Austin Mackenzie [52], Tapfumanei Mashe [59 60], Chisomo Msefula [61], Ankur Mutreja [1], Geetha Nagaraj [58], Savitha Nagaraj [62], Satheesh Nair [10], Take K Naseri [63], Susana Nimarota-Brown [63], Elisabeth Njamkepo [64], Iruka N Okeke [20], Sulochana Putli Bai Perumal [65], Andrew J Pollard [66 67], Agila Kumari Pragasam [22], Firdausi Qadri [30], Farah N Qamar [49], Sadia Isfat Ara Rahman [30], Savitra Devi Rambocus [16], David A Rasko [68 69], Pallab Ray [44], Roy Robins-Browne [6 70], Temsunaro Rongsen-Chandola [71], Jean Pierre Rutanga [72], Samir K Saha [47], Senjuti Saha [47], Karnika Saigal [73], Mohammad Saiful Islam Sajib [47 74], Jessica C Seidman [41], Jivan Shakya [75 76], Varun Shamanna [58], Jayanthi Shastri [33 77], Rajeev Shrestha [78], Sonia Sia [79], Michael J Sikorski [57 68 69], Ashita Singh [80], Anthony M Smith [81], Kaitlin A Tagg [19], Dipesh Tamrakar [78], Arif Mohammed Tanmoy [47], Maria Thomas [82], Mathew S Thomas [83], Robert Thomsen [63], Nicholas R Thomson [5], Siaosi Tupua [63], Krista Vaidya [84], Mary Valcanis [16], Balaji Veeraraghavan [22], François-Xavier Weill [64], Jackie Wright [34], Gordon Dougan [1], Silvia Argimón [85], Jacqueline A Keane [1], David M Aanensen [85], Stephen Baker [1 3], Kathryn E Holt [2 4]; Global Typhoid Genomics Consortium Group Authorship

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Core gene rules paper

⇦ **Individual authors:**
individuals contributing directly
(members of subgroups contributing core genes)

⇦ **Group authors:**
All other ESGEM-AMR working group members
(who read and approve manuscript)

> Genome Med. 2025 May 9;17(1):51. doi: 10.1186/s13073-025-01470-4.

The TyphiNET data visualisation dashboard: unlocking Salmonella Typhi genomics data to support public health

Zoe A Dyson [# 1 2 3], Louise Cerdeira [# 4], Vandana Sharma [4], Megan E Carey [4], Kathryn E Holt [5 6]; Global Typhoid Genomics Consortium

Collaborators, Affiliations — collapse

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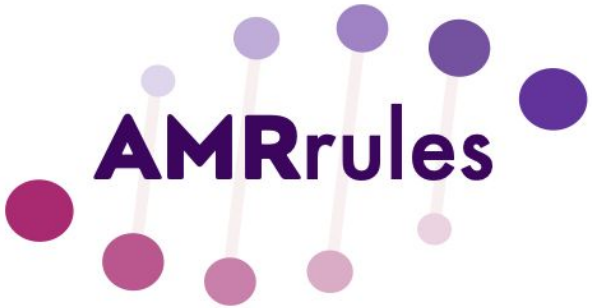
2026 Planning

1. **Fix monthly meeting dates?**
2. **Who is attending Wellcome AMR?** (23-25 March, Hinxton, UK)
3. **ESCMID global meetup?** (17-21 April, München, Germany)
4. **Collaboration with WHO AMR team on AMR Gene Catalog**

Questions? / Any other business?

ESGEM-AMR

ESCMID



https://github.com/interpretAMR/AMRrulesCuration