

Outbreaks, typing and AMR/Day 7

Antimicrobial resistance genes and point mutations detection in *Salmonella*

Section of Foodborne infections, Dep. of bacteria, parasites and fungi, Statens Serum Institute

March 2024

Specific objectives of the AMR session

Lecture:

1. Explain what is AMR, how it develops and how it spreads
2. Explain the difference between antimicrobial resistance phenotype and genotype

Practical exercise:

1. Utilise command-line tools to identify AMR genes and point mutations (PMs).
2. Explain why different bioinformatic tools may give different results.
3. Discuss the difference between a tool, a database, and a method.
4. Explain the difference between genotype and phenotype.

Outline

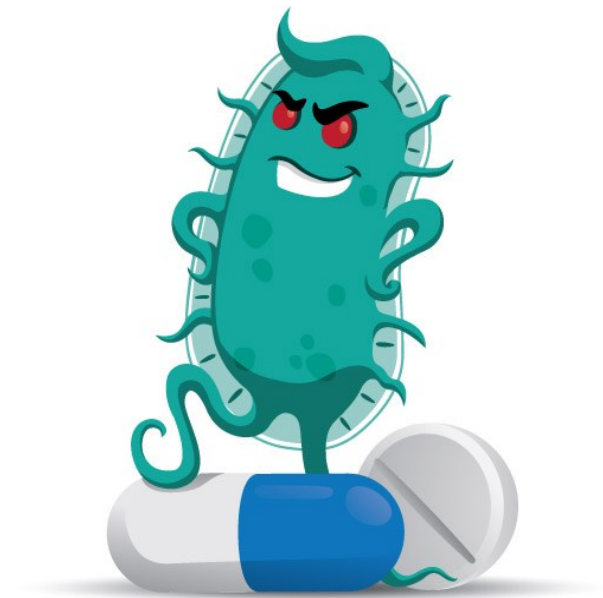
This session consists of the following elements:

<i>14.30-14.50</i>	Introduction to AMR
<i>14.50-15.50</i>	Practical exercise
<i>15.50-16.00</i>	Discussion

Introduction to AMR

What is AMR

Antimicrobial resistance (AMR) is the ability of microorganisms to **persist or grow in the presence of drugs** designed to inhibit or kill them



ID 160274360

© [Luciano Cosmo Barbosa Gomes](#)

| Dreamstime.com

How bacteria become resistant?

Acquired resistance

Microorganisms have a **natural ability to evolve genetically** to counter/resist the drugs

- The changes occur inside their genomes **when they are exposed to antimicrobial** drugs

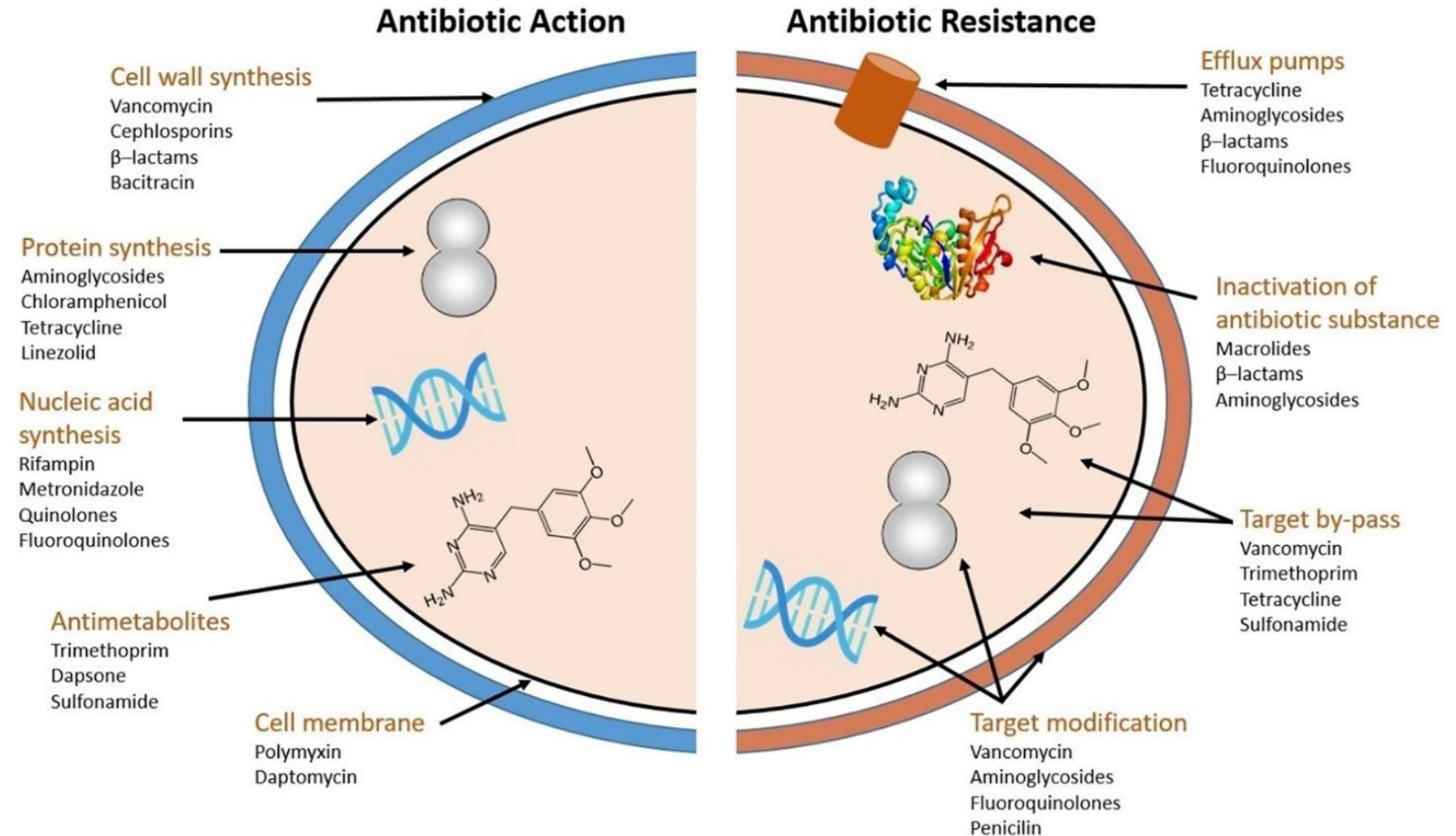
Intrinsic resistance

Some bacteria have an innate ability to resist antibiotics without being exposed to a drug

Antimicrobial action and resistance mechanisms

Genetic resistance determinants:

- Genes
- Chromosomal point mutations



[Antibiotic action and resistance mechanisms](#) by [Uluseker et al. \(2021\)](#) CC BY 4.0 DEED

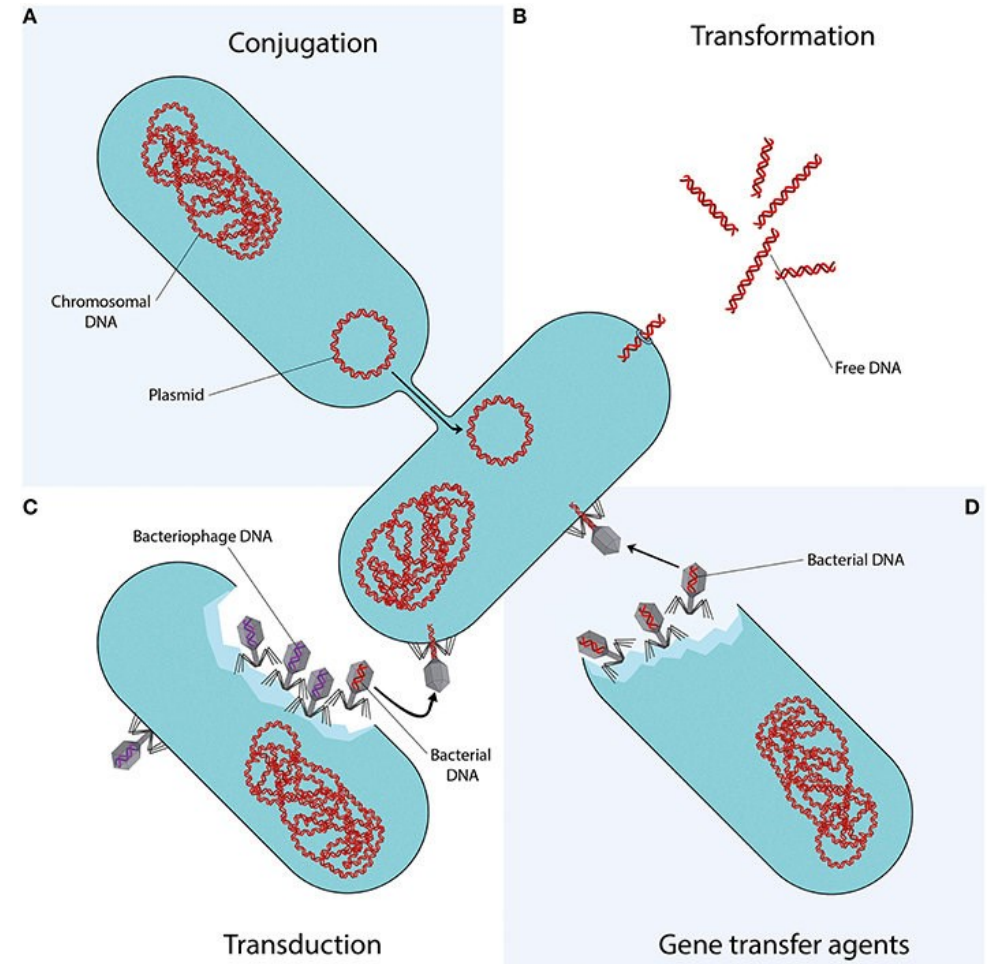
How resistance spread between the bacteria

Vertical transmission:

- genes and point mutations
- reproductive

Horizontal transmission: →

- genes
- non-reproductive
- intra- and inter- species spread
- most concerning



[Mechanisms of horizontal gene transfer](#) by [Wintersdorff et al. \(2016\)](#) CC BY 4.0 DEED

Question

How do we detect resistance to antimicrobials?

How do we detect AMR?

Phenotypic antimicrobial susceptibility testing:

- Bacteria growth at higher antibiotic concentrations compare to the wild type (non-resistant) populations

Genotypic detection of AMR:

- Presence of genes/chromosomal mutations mediating AMR

Phenotypic vs. Genotypic resistance

Discordance between the results:

- Phenotypic +/genotypic -
- Phenotypic -/genotypic +

What are the possible causes of discordance?

Phenotypic vs. Genotypic resistance

Possible causes of discordance:

- Errors in the phenotypic/genotypic testing (skills, options, reporting, different strains, etc.)
- Loss of plasmid during cultivation/DNA extraction
- Phenotypic resistance is not expressed or is close to the breakpoint (weakly expressed)
- Gene/point mutation is absent from the sequence (poor quality, assembly issues, etc.)
- Gene/point mutation absent from the database(s) in use

Recommended article: [Yee et al. 2021](#)

Why we look at AMR?

To inform PH actions:

- National level surveillance (DanMap)
- EU level surveillance (ECDC)
- Global surveillance (GLASS)

Benchmarking of bioinformatic tools for AMR

No standard approach of testing and reporting genetic resistance

- Ring-Trial (FWD AMR-refLabCap)
 - various combinations tools, databases, thresholds reporting strategies are in use: difficult to compare the results

In general good agreement in the results, except for some specific AMR determinants

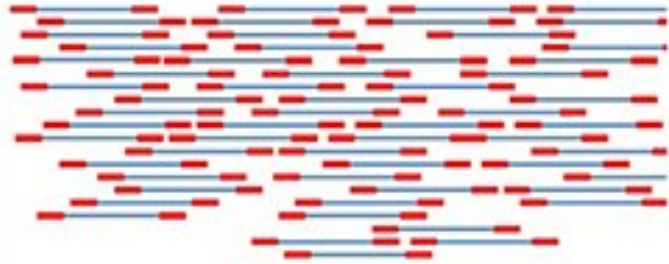
Take home

- Bacteria evolve to survive antibiotics
- Resistance can be acquired or intrinsic
- Resistance is determined by genes and point mutations found in bacterial genomes:
 - account for certain resistance mechanisms to various types of antimicrobials
 - can be transmitted between bacteria either vertically or horizontally
- Resistance can be detected with phenotypic and genotypic methods
 - discordance between the results is possible and often can be explained
- Standardised testing and reporting of AMR is necessary to follow the trends and to inform PH actions for its reduction

Interactive lecture #1: ResFinder + PointFinder

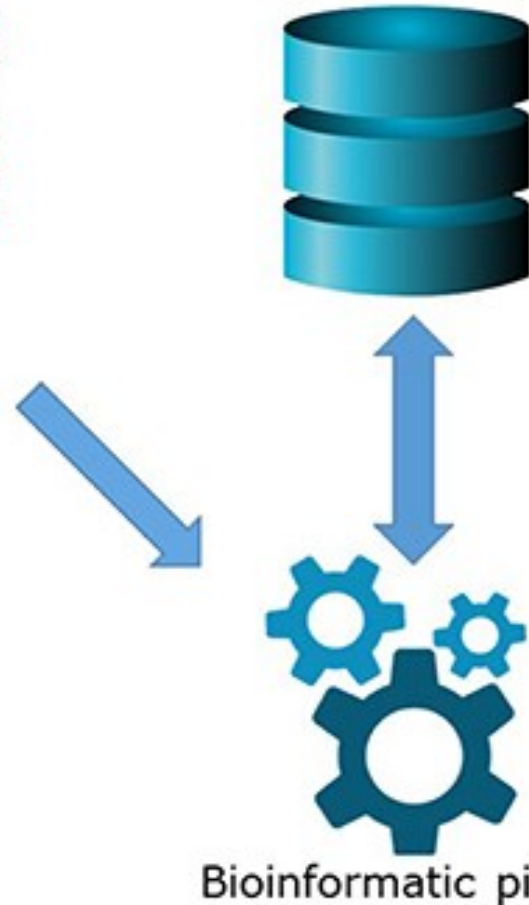
AMR detection *in silico*

AMR gene/mutations database



Input sequence data as
raw reads or assemblies

```
>SRR1146436.1.length.4074.cov.498.472351
GTCAATACGGTCTCCGTTGACGCTTACGCTTATTTAAAGTGATATTGTTGTCGAGGAT
CTGGGGGCTAGTCTATCTTCAGCTTACGGGCTATCTGACGATGTGACCCAGCATATGGT
GCCAAAGCCATATCAGTCTCTCTCTTTGAGTTCACCTAGCATTGTTATCTCCCTTAAAAA
TTGAGGGGACAACTATGCTGACACAGAGGGTTATTACCGGATCTCGATGGACGTTATTGA
GTGATCTCTTCCATGAACTCGCCACGGGAAATATCTGCGCCAGCGGGCCAGTAATGGGT
TAAAGTATAGAGTTAAGTTTGGTGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
CGAAAAAGAGATTATAAAAATTAATAATATCAGAAATACATTAGTACACTTTATTATATACA
TCTAATTGTACAAATGGATGTATAAAGAAAGAGAGAGTAAATATCATTAGAAATGAACT
CATATTTCTTGGAGAGATGTTAATATATCAGTAAAGTCCAAATATTCAGGAAAGGAG
TATATCGCAATCAGATTAAACAGGGCTAAAAAACACTATCAATATCTATATGATAGTGT
TTTTAGCACATTATATTCATCAGGATTTTATTTAAAAAGCTAATAAAAGCTATTTTATAT
CGCTATGACATAACTTCTATGTAGCCATACTAATGATAAACTTCTTTTCAGAGAGTTTT
AAGCCCTTGGTAAATTTGCCAGTCCAGCAATCATATTCACCCAGATATTTGGGTTATTGT
TCAAGGGCAATATTTATTTTATTTTCTAAAAATCCCGCTATACATTAGTTAATATAAT
AGCAGTCCCGCATTTTCACTGAAAAATTAGCGCATTACTCATATCTGTGTAAATAAAAAG
GGCGGGTTTTGAGCGGTTAAATAAGTCCGATCAAAATTCGAAATGTTGTGTGTATAGAA
CTGTCCGCAATATTTGAAATTAATAAGAGGGGTTATCGCCGAAACAGGAAATTTGG
ACAAATGCTTCCATTAAATAAGGGGTTGTGATATTTGTGATGTCACCAACCATGAA
AATCGGATTAACCAATGGAGATATCTTTCTTCCGAGATTCAAGCTCAGGAAATAATCCCT
CATAACATATATGAACTCATTTTAAATGTTGTTGAAATCCAGGATGTCCTCTCATAT
ATTTCTTTTTATAATAGAAAAAGTGTATGCGATGGTTCTGGTGAATATAAAACTTT
```



Bioinformatic pipeline

Plain language report
of identified AMR genes

The principle of *in silico* AMR determinant detection using a search algorithm to query input DNA by [Hendriksen et al. \(2019\) CC BY 4.0 DEED](#)

ResFinder

Databases

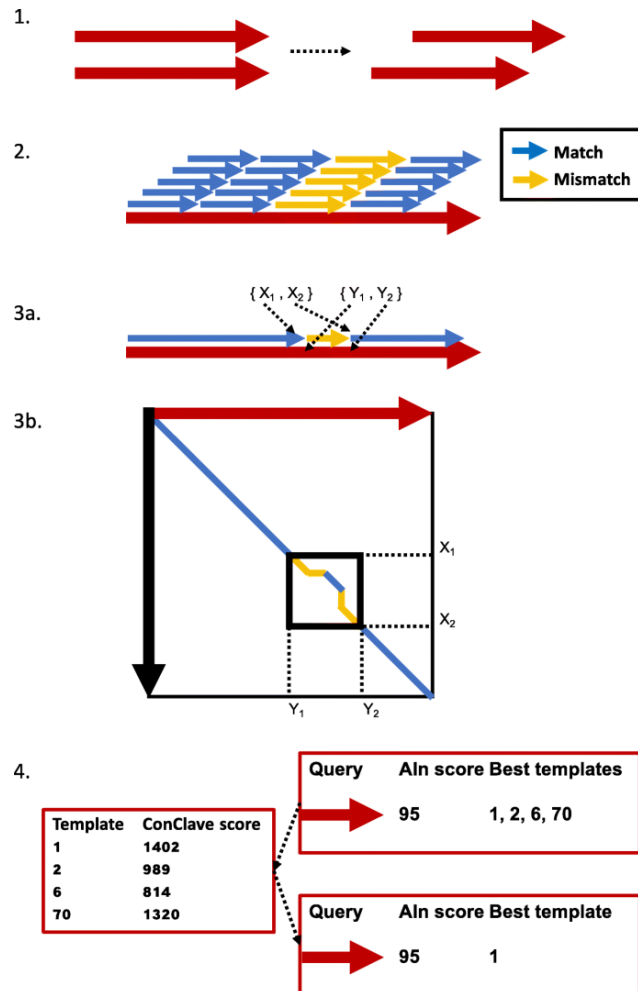
- ResFinderdb
 - Nucleotide
 - AMR ECOFF (epidemiological cut-off) predictions
- PointFinderdb

Softwares

- ResFinder
- PointFinder

ResFinder					
genes			point mutations		
input	method	db	input	method	db
DNA fastq	KMA	nucleotide	DNA fastq	KMA	nucleotide
DNA fasta	BLASTN		DNA fasta	BLASTN	
Protein fasta	-	-	Protein fasta	-	-

Method: KMA



KMA (k-mer alignment) is able to map raw reads directly against redundant databases, it also scales well for large redundant databases.

KMA uses k-mer seeding to speed up mapping and the Needleman-Wunsch algorithm to accurately align extensions from k-mer seeds.

Multi-mapping reads are resolved using a novel sorting scheme (ConClave scheme), ensuring an accurate selection of templates.

[Overview of step 1–4 of the KMA algorithm](#) by [Clausen et al. \(2018\)](#) CC BY 4.0 DEED

Web tool




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Services

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ResFinder

Version

4.4.1 

ResFinder identifies acquired genes and/or finds chromosomal mutations mediating antimicrobial resistance in total or partial DNA sequence of bacteria.

ResFinder software: (2023-08-22)

ResFinder database: (2023-04-12)

PointFinder database: (2023-05-03)

DisinFinder database: (2023-04-12)

Chromosomal point mutations:

Acquired antimicrobial resistance genes:

Command line tool

Pull requests Repositories Projects ?

</> ResFinder

</> Source

- Commits
- Branches
- Pull requests
- Pipelines
- Deployments
- Issues
- Jira issues
- Security
- Downloads

Genomic Epidemiology / CGE

ResFinder Clone

master Filter files

Name	Size	Last commit	Message
scripts		2022-05-25	Add json class script
src/resfinder		2023-11-27	Fix issue with promoter sub mutations
tests		2023-10-27	Fix issues #112 #114 and promoter m...
.gitattributes	491 B	2022-04-08	Add .gitattributes
.gitignore	247 B	2023-02-09	Ignore files in tmp_out
.gitmodules	116 B	2018-01-03	Added blaster submodule

Documentation

 Pull requests Repositories Projects



 ResFinder

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README.md

ResFinder documentation

ResFinder identifies acquired antimicrobial resistance genes in total or partial sequenced isolates of bacteria.

Important if you are updating from a previous ResFinder version

It is no longer recommended to clone the ResFinder bitbucket repository unless you plan to do development work on ResFinder.

Instead we recommend installing ResFinder using pip as described below.

There are several good reasons why the recommended installation procedure has changed, among those are the increasing size of the repository that has risen to several hundreds of megabytes, due to the long history of ResFinder. Its easier for users. And it makes sure your installation will be a tested release of the application.

Installation

ResFinder consists of an application and 1-3 databases. The databases can be used without the

Main script

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ResFinder

Source

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Genomic Epidemiology / CGE / ResFinder

run_resfinder.py

Pull requests Check out

Source master 7be7614 Full commit

resfinder / src / resfinder / run_resfinder.py Edit

```
1 #!/usr/bin/env python3
2 import io
3 import sys
4 import os
5 import subprocess
6 from argparse import ArgumentParser
7 import pickle
8 import json
9 import hashlib
10
11 from cgelib.output.result import Result
12 from cgelib.utils.loaders_mixin import LoadersMixin
13 from cgelib.utils.pliers_mixin import PliersMixin
14
15 from resfinder.cge.config import Config
```


History



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Genomic Epidemiology / CGE / ResFinder

Commits

Compare

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Search commits

All branches

Author	Commit	Message	Date	Builds
Nils Hofmann	ead8537	cgecore_impleme	2024-01-08	
Nils Hofmann	20e912f	cgecore_impleme	2024-01-08	
Nils Hofmann	300d2a5	cgecore_impleme	2024-01-05	
Nils Hofmann	413b7bc	cgecore_impleme	2024-01-03	
Nils Hofmann	778227c	cgecore_impleme	2024-01-03	
RolfSK	7be7614	Fix issu... 4.4.2	2023-11-27	
RolfSK	3a15d89	Change ... 4.4.1	2023-11-02	

Issues/Questions

 Pull requests  Repositories  Projects

 ResFinder

 Source

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 Issues

 Jira issues

 Genomic Epidemiology / CGE / ResFinder




Issues

Filter by: All

Open

[Advanced search](#)

Issues (1–1 of 1)

Title	T	P	Status	Votes	Assignee	Created	Updated
#104: Can pointfinder results contain the location of the mutation in the assembly?			NEW		 Edison Alain von	2023-02-07	2023-04-21

Database



Pull requests Repositories Projects



resfinder_db

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Genomic Epidemiology / Databases

resfinder_db

Clone

master

Files



Name

Size

Last commit

Message

.gitignore	11 B	2022-06-16	Update gitignore file
CHECK-entries.sh	2.33 KB	2019-01-23	CHECK-entries: make sure to escape r...
INSTALL.py	5.38 KB	2023-04-12	Fix version check incompatibilities, that...
README.md	5.37 KB	2021-04-20	Added history file to content overview
VERSION	7 B	2023-10-27	Bump version number

Database documentation


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README.md

ResFinder Database documentation

The ResFinder database is a curated database of acquired resistance genes.

Content of the repository

1. <AMR class>.fsa - DNA sequence of the genes from a specified AMR class
2. phenotypes.txt - Translation table for genotype to phenotype prediction
3. phenotype_panels.txt - For selected species, lists the relevant phenotypes
4. INSTALL.py - Script for indexing the database with KMA
5. CHECK-entries.sh - Script examining whether there is consistency between the databases and the phenotypes.txt
6. antibiotic_classes.txt - Lists the relevant antibiotic classes
7. config - Configuration file that describes the content of the databases
8. notes.txt - Lists additional notes of the entries in the databases
9. history.txt - history file of ResFinderDB commits dating back to 2018/01/01

Database history


 Pull requests  Repositories  Projects



 resfinder_db

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 Genomic Epidemiology / Databases / resfinder_db










Commits

Compare



Clone



 All branches 

	Author	Commit	Message	Date
	 Andrea Laguna	97d1fe0	Added new genes	2024-01-28
	 Andrea Laguna	5c183e1	Fixed records in ...	2024-01-22
	 geopyr	04e8210	Updates on hist...	2023-12-04
	 RolfSK	208efbd	MERGED  4 tags	2023-10-27
	 RolfSK	1cdccf0	Bump version nu...	2023-10-27
	 geopyr	7558fb0	Correction of ty...	2023-10-26
	 geopyr	8117fca	Updated all.fsa ...	2023-09-21

Database issues/questions


 Pull requests  Repositories  Projects



 resfinder_db

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 Genomic Epidemiology /  Databases /  resfinder_db









Issues

Filter by: All

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Advanced search

Issues (1–4 of 4)

Title	T	P	Status	Votes	Assignee	Created	Updated
#15: No klebsiella in phenotype_panels.txt			NEW			2023-01-04	2023-01-09
#12: qacL missing for disinfectant resistance			NEW			2022-04-19	2022-04-19
#11: OXA-244 not associated with carbapenem resistance?			NEW			2022-01-14	2022-02-01
#6: Does all the resistance genes in the database are functional?			NEW			2021-04-12	2021-09-01

Practice #1: ResFinder + PointFinder

Introduction to the exercise

practicals/manuals: AMR_practicals.docx

See: [How to use this document](#)

Conda environment with required software: CGEfinders and NCBItypers

Path to working folder: ~/BTG_2024

Path to assemblies: ~/BTG_2024/precomputed_data/day7/amr

Path to databases: ~/BTG_2024/data/databases

Path to output: ~/BTG_2024/amr/output

Path to precomputed output: ~/BTG_2024/precomputed_data/day7/amr

Introduction to the exercise (example)

Conda environment with required software: CGEfinders

Path to working folder: ~/BTG_2024/amr

Path to assemblies: ~/BTG_2024/precomputed_data/day7/amr/SRR27241771/SRR27241771.fasta

Path to databases:

~/BTG_2024/data/databases/resfinder_db

~/BTG_2024/data/databases/pointfinder_db

Path to output:

~/BTG_2024/amr/output/SRR27241771/ResFinder_results_tab.txt

~/BTG_2024/amr/output/SRR27241771/ PointFinder_results.txt

Path to precomputed output:

~/BTG_2024/precomputed_data/day7/amr/SRR27241771/resfinder/ResFinder_results_tab.txt

~/BTG_2024/precomputed_data/day7/amr/SRR27241771/resfinder/PointFinder_esults.txt

Recap #1

SRR27241771 (Genes)

Resistance gene	Identity	Alignment Length/Gene Length	Coverage	Position in reference	Contig	Position in contig	Phenotype	Accession no.
aac(6')-Iaa	99.54	438/438	100	1..438	SRR27241771_12/1	52440..52877	Amikacin, Tobramycin	NC_003197
aadA16	99.65	846/846	100	1..846	SRR27241771_27/1	78..923	Spectinomycin, Streptomycin	EU675686
blaTEM-1B	100	861/861	100	1..861	SRR27241771_37/1	534..1394	Amoxicillin, Ampicillin, Cephalothin, Piperacillin, Ticarcillin	AY458016
mph(A)	100	906/906	100	1..906	SRR27241771_47/1	4965..5870	Erythromycin, Azithromycin, Spiramycin, Telithromycin	D16251
floR	98.19	1214/1215	99.9177	1..1214	SRR27241771_105/1	3191..4404	Chloramphenicol, Florfenicol	AF118107
qnrB6	100	645/645	100	1..645	SRR27241771_117/1	192..836	Ciprofloxacin	EF523819
ARR-3	100	453/453	100	1..453	SRR27241771_27/1	3636..4088	Rifampicin	JF806499
sul1	100	840/840	100	1..840	SRR27241771_53/1	4..843	Sulfamethoxazole	U12338
tet(B)	100	1206/1206	100	1..1206	SRR27241771_72/1	1421..2626	Doxycycline, Tetracycline, Minocycline	AP000342
dfrA27	100	474/474	100	1..474	SRR27241771_27/1	1104..1577	Trimethoprim	FJ459817

SRR27241771 (Point mutations)

Mutation	Nucleotide change	Amino acid change	Resistance	PMID

SRR27241772 (Genes)

Resistance gene	Identity	Alignment Length/Gene Length	Coverage	Position in reference	Contig	Position in contig	Phenotype	Accession no.
aph(6)-Id	99.88	837/837	100	1..837	SRR27241772_44/1	7618..8454	Streptomycin	M28829
aph(3'')-Ib	100	804/804	100	1..804	SRR27241772_44/1	8454..9257	Streptomycin	AF321551
aac(6')-Iaa	98.63	438/438	100	1..438	SRR27241772_51/1	48278..48715	Amikacin, Tobramycin	NC_003197
aph(3')-Ia	100	816/816	100	1..816	SRR27241772_68/1	115..930	Unknown Aminoglycoside, Kanamycin, Kanamycin, Neomycin, Neomycin, Kanamycin, Lividomycin, Paromomycin, Ribostamycin	V00359
aadA2	100	564/792	71.212121	229..792	SRR27241772_100/1	1..564	Spectinomycin, Streptomycin	JQ364967
aadA2	100	564/819	68.864469	256..819	SRR27241772_100/1	1..564	Spectinomycin, Streptomycin	NC_010870
aadA1	100	792/792	100	1..792	SRR27241772_113/1	1556..2347	Spectinomycin, Streptomycin	JQ414041
blaCTX-M-15	100	876/876	100	1..876	SRR27241772_63/1	254..1129	Amoxicillin, Ampicillin, Aztreonam, Cefepime, Cefotaxime, Ceftazidime, Ceftriaxone, Piperacillin, Ticarcillin	AY044436
mph(A)	99.5	604/921	65.472313	319..921	SRR27241772_100/1	7203..7806	Erythromycin, Azithromycin, Spiramycin, Telithromycin	U36578
floR	98.19	1214/1215	99.917695	1..1214	SRR27241772_44/1	3269..4482	Chloramphenicol, Florfenicol	AF118107
cmIA1	99.92	1260/1260	100	1..1260	SRR27241772_113/1	204..1463	Chloramphenicol	M64556
sul2	99.88	816/816	100	1..816	SRR27241772_44/1	9318..10133	Sulfamethoxazole	AY034138
sul1	100	840/840	100	1..840	SRR27241772_100/1	1069..1908	Sulfamethoxazole	U12338
sul3	100	792/792	100	1..792	SRR27241772_113/1	4029..4820	Sulfamethoxazole	AJ459418
tet(A)	99.92	1275/1275	100	1..1275	SRR27241772_44/1	5083..6357	Doxycycline, Tetracycline	AF534183
dfrA12	100	498/498	100	1..498	SRR27241772_7/1	614..1111	Trimethoprim	AM040708

SRR27241772 (Point mutations)

Mutation	Nucleotide change	Amino acid change	Resistance	PMID
gyrA p.S83F	TCC -> TTC	S -> F	Nalidixic Acid, Ciprofloxacin	10471553
gyrA p.D87G	GAC -> GGC	D -> G	Nalidixic Acid, Ciprofloxacin	11283069
parC p.T57S	ACC -> AGC	T -> S	Nalidixic Acid, Ciprofloxacin	15388468
parC p.S80I	AGC -> ATC	S -> I	Nalidixic Acid, Ciprofloxacin	15388468

Interactive lecture #2: AMR FinderPlus

AMRFinderPlus

Database

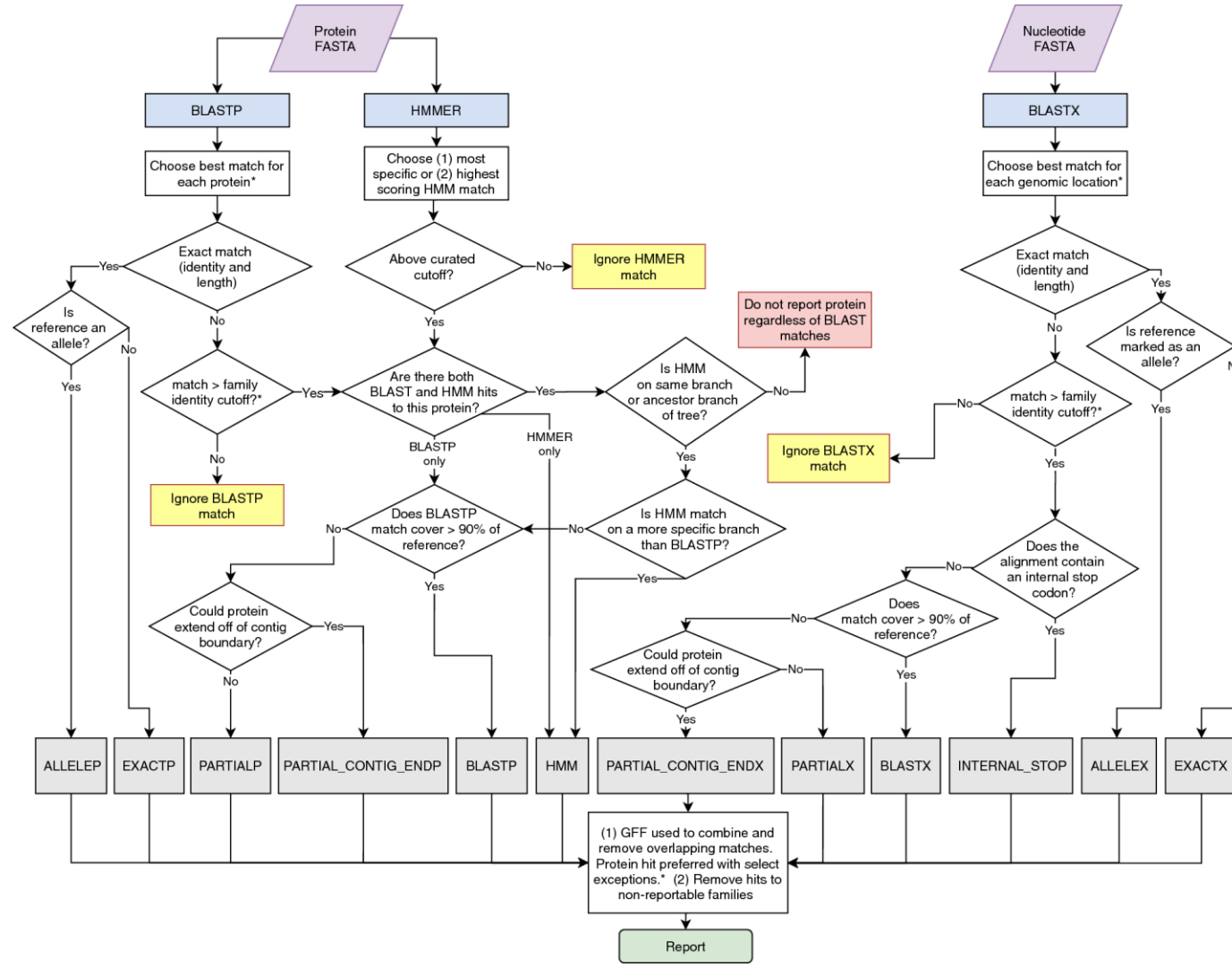
- Genes
 - Protein
 - Highly curated database
 - Hierarchical structure for AMR proteins
 - Manually curated cutoffs
 - Associated hierarchical names
- Point mutations
 - Literature, CARD and ResFinder.

Software

- BlastRules
- Protein fasta
 - BLASTP
 - HMMER
- Nucleotide fasta
 - BLASTX (translated nucleotide)

AMRFinderPlus					
genes			point mutations		
input	method	db	input	method	db
DNA fastq	-	-	DNA fastq		-
DNA fasta	BLASTX	protein	DNA fasta	BLASTN	nucleotide
Protein fasta	BLASTP		Protein fasta	-	-

AMRFinderPlus



Method: HMMER

Start with a multiple sequence alignment

↓

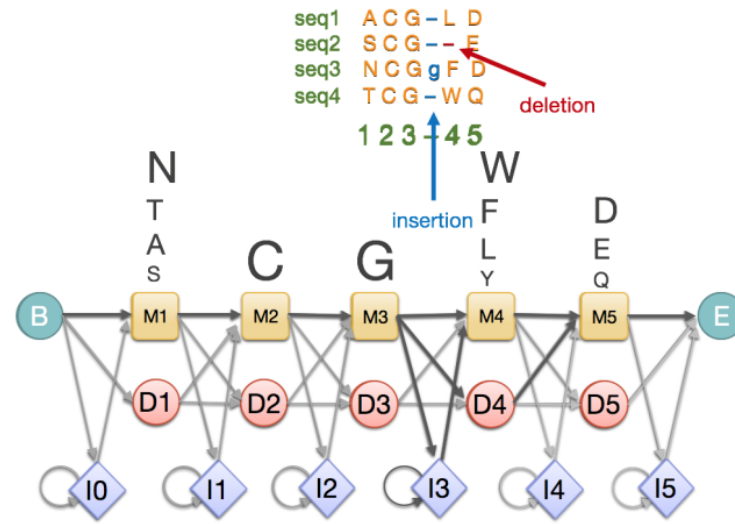
Insertions / deletions can be modelled

↓

Occupancy and amino acid frequency at each position in the alignment are encoded

↓

Profile created



HMMER is used for searching sequence databases for sequence homologs, and for making sequence alignments. It implements methods using probabilistic models called profile hidden Markov models (profile HMMs).

Sensitive homology searches. You're working on a specific sequence family, and you've carefully constructed a representative multiple sequence alignment. The HMMER hmmbuild program lets you build a profile from your alignment, and the hmmsearch program lets you search your profile against a sequence database looking systematically for more homologs.

<http://eddylab.org/software/hmmer/Userguide.pdf>

Copyright (C) 2023 Howard Hughes Medical Institute. HMMER and its documentation are freely distributed under [the 3-Clause BSD open source license](#)

AMRFinderPlus database

Core

- AMR elements (genes and proteins)
- Point mutations

Plus

- Stress and virulence
 - Biocide resistance
 - Heat resistance
 - Acid resistance
 - Metal resistance
- Other "AMR" genes

AMRFinderPlus

... GTGCATCTGACTCCTGAGGAGAAG ...

DNA

... CACGTAGACTGAGGACTCCTCTTC ...

↓ Transcription

... GUGCAUCUGACUCCUGAGGAGAAG ... RNA

↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓

Translation

... V H L T P E E K ... Protein

No web tool

AMR genes

Resistance-associated point mutations

Other genes (stress, virulence)



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National Center for Biotechnology Information

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[Antimicrobial Resistance](#) > AMRFinderPlus

Search page ^ v

AMRFinderPlus

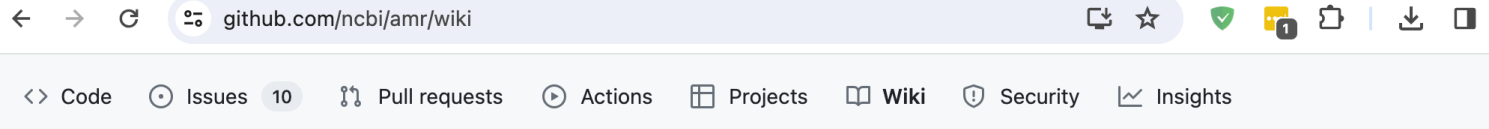
NCBI has developed AMRFinderPlus, a tool that identifies AMR genes, resistance-associated point mutations, and select other classes of genes using protein annotations and/or assembled nucleotide sequence. AMRFinderPlus is used in the [Pathogen Detection pipeline](#), and these data are displayed in [NCBI's Isolate Browser](#). AMRFinderPlus relies on NCBI's curated [Reference Gene Database](#) and curated collection of [Hidden Markov Models](#). For more information on how AMRFinderPlus operates, please see the [Methods section](#) of the [AMRFinderPlus documentation](#). See our [documentation](#) for a description of all our [NCBI antimicrobial resistance resources](#).

NCBI has made AMRFinderPlus software and databases open source and freely available

<https://www.ncbi.nlm.nih.gov/pathogens/antimicrobial-resistance/AMRFinder/>



Documentation



Home

Arjun Prasad edited this page on Jul 11, 2023 · 76 revisions

NCBI Antimicrobial Resistance Gene Finder Plus (AMRFinderPlus)

release [amrfinder_v3.12.8](#) [bioconda v3.12.8](#) [docker hub 3.12.8-2024-01-31.1](#)

Overview for AMRFinderPlus 3.11

This software and the accompanying database identify acquired antimicrobial resistance genes in bacterial protein and/or assembled nucleotide sequences as well as known resistance-associated point mutations for several taxa. With AMRFinderPlus we added select members of additional classes of genes such as virulence factors, biocide, heat, acid, and metal resistance genes.

Note that AMRFinderPlus reports gene and point mutation presence/absence; it does not infer phenotypic resistance. Many of the resistance genes detected by AMRFinderPlus may not be relevant for clinical management or antimicrobial surveillance. See the [Note regarding Genotype vs. Phenotype](#) for more information.

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Installing AMRFinderPlus

- [Overview](#)
- [Install with bioconda](#) (recommended)
- [Docker Image](#)
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- [Test your installation](#)

Running AMRFinderPlus

- [Usage \(syntax/options\)](#)
- [--organism option](#)
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Issues/Questions

ncbi / amr

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10 Open ✓ 96 Closed	Author	Label	Projects	Milestones	Assignee	Sort
AMRProt bug can't reproduce 2						
#138 opened 5 days ago by Nanderson246						
Makefile bug bug 8						
#130 opened on Oct 6, 2023 by cjw85						
amrfinder running with options --ident_min and --coverage_min bug can't reproduce 1						
#126 opened on Jun 20, 2023 by stalact						
intermittent 1;31m*** ERROR *** bug can't reproduce 10						
#123 opened on May 16, 2023 by taffners						
amrfinder_update cannot connect to FTP and thus download #bug #help bug can't reproduce 11						
#120 opened on May 4, 2023 by geboro						
[Feature request] Option to use Diamond instead of Blast enhancement 8						
#111 opened on Feb 26, 2023 by jolespin						

History

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AMRFinderPlus v3.12.8 Latest

AMRFinderPlus v3.12.8 includes a new database format version. Because this version is incompatible with AMRFinderPlus databases from previous versions, `amrfinder -u` must be run once the software update is installed to get the latest version of the database.

This update includes the changes:

- Reference proteins now have stop codons. Input proteins that are not terminated with a " *character* are assumed to have a " at the end.
- Extended proteins are no longer "EXACT" hits, so the protein names will be that of the parent node for alleles.
- If a protein is hit by blast and the Blast Rule is violated, the Blast Rule of the parent family is checked, etc.

Database

Index of /pathogen/Antimicrobial_resistance/AMRFinderPlus/database/latest

Name	Last modified	Size
Parent Directory		-
allele_counts_by_year/	2024-02-05 11:11	-
AMR.LTB	2024-02-05 11:11	95M
AMRProt	2024-02-05 11:11	3.8M
AMRProt-mutation.tab	2024-02-05 11:11	139K
AMRProt-suppress	2024-02-05 11:11	608
AMRProt-susceptible.tab	2024-02-05 11:11	3.7K
AMR_CDS	2024-02-05 11:11	8.9M
AMR_DNA-Acinetobacter baumannii	2024-02-05 11:11	303
AMR_DNA-Acinetobacter baumannii.tab	2024-02-05 11:11	452
AMR_DNA-Campylobacter	2024-02-05 11:11	6.8K
AMR_DNA-Campylobacter.tab	2024-02-05 11:11	1.5K
AMR_DNA-Clostridioides difficile	2024-02-05 11:11	2.9K
AMR_DNA-Clostridioides difficile.tab	2024-02-05 11:11	295
AMR_DNA-Enterococcus faecalis	2024-02-05 11:11	2.9K
AMR_DNA-Enterococcus faecalis.tab	2024-02-05 11:11	390
AMR_DNA-Enterococcus faecium	2024-02-05 11:11	2.9K
AMR_DNA-Enterococcus faecium.tab	2024-02-05 11:11	388
AMR_DNA-Escherichia	2024-02-05 11:11	7.6K
AMR_DNA-Escherichia.tab	2024-02-05 11:11	7.5K
AMR_DNA-Klebsiella oxytoca	2024-02-05 11:11	166
AMR_DNA-Klebsiella oxytoca.tab	2024-02-05 11:11	726
AMR_DNA-Neisseria gonorrhoeae	2024-02-05 11:11	5.9K
AMR_DNA-Neisseria gonorrhoeae.tab	2024-02-05 11:11	2.2K
AMR_DNA-Salmonella	2024-02-05 11:11	1.6K
AMR_DNA-Salmonella.tab	2024-02-05 11:11	406
AMR_DNA-Staphylococcus aureus	2024-02-05 11:11	3.3K
AMR_DNA-Staphylococcus aureus.tab	2024-02-05 11:11	1.7K
AMR_DNA-Streptococcus pneumoniae	2024-02-05 11:11	2.9K
AMR_DNA-Streptococcus pneumoniae.tab	2024-02-05 11:11	825
ReferenceGeneCatalog.txt	2024-02-05 11:11	1.8M
ReferenceGeneHierarchy.txt	2024-02-05 11:11	1.0M
amr_targets.fa	2024-02-05 11:11	1.5M
changelog.txt	2024-02-05 11:11	1.4M
changes.txt	2024-02-05 11:11	1.4M
database_format_version.txt	2024-02-05 11:11	7
fam.tab	2024-02-05 11:11	302K
taxgroup.tab	2024-02-05 11:11	1.2K
version.txt	2024-02-05 11:11	13

Practice #2: AMR FinderPlus

Introduction to the exercise

practicals/manuals: AMR_practicals.docx

See: [How to use this document](#)

Conda environment with required software: CGEfinders and NCBItypers

Path to working folder: ~/BTG_2024

Path to assemblies: ~/BTG_2024/precomputed_data/day7/amr

Path to databases: ~/BTG_2024/data/databases

Path to output: ~/BTG_2024/amr/output

Path to precomputed output: ~/BTG_2024/precomputed_data/day7/amr

Introduction to the exercise (example)

Conda environment with required software: NCBItypers

Path to working folder: ~/BTG_2024/amr

Path to assemblies:

~/BTG_2024/precomputed_data/day7/amr/SRR27241771/SRR27241771.fasta

Path to databases: ~/BTG_2024/data/databases/amrfinderplus

Path to output: ~/BTG_2024/amr/output/SRR27241771/amrfinderplus_output.tsv

Path to precomputed output:

~/BTG_2024/precomputed_data/day7/amr/SRR27241771/amrfinderplus/output.tsv

Recap #2

SRR27241771 (Genes and point mutations)

Contig id	Start	Stop	Strand	Gene symbol	Scope	Element type	Class	Method	% Coverage of reference sequence	% Identity to reference sequence
SRR27241771_101/1	3911	4144	-	merE	plus	STRESS	MERCURY	BLASTX	100	96.15
SRR27241771_101/1	4144	4506	-	merD	plus	STRESS	MERCURY	BLASTX	100	90.08
SRR27241771_101/1	4527	6209	-	merA	plus	STRESS	MERCURY	BLASTX	100	93.23
SRR27241771_101/1	6995	7339	-	merT	plus	STRESS	MERCURY	BLASTX	99.14	99.13
SRR27241771_101/1	7429	7854	+	merR	plus	STRESS	MERCURY	BLASTX	98.61	92.96
SRR27241771_105/1	3191	4402	+	floR	core	AMR	PHENICOL	EXACTX	100	100
SRR27241771_113/1	47515	49704	+	sinH	plus	VIRULENCE	NA	EXACTX	100	100
SRR27241771_117/1	192	833	+	qnrB6	core	AMR	QUINOLONE	ALLELEX	100	100
SRR27241771_15/1	19613	20143	-	sodC1	plus	VIRULENCE	NA	BLASTX	100	99.44
SRR27241771_27/1	81	923	-	aadA16	core	AMR	AMINOGLYCOSIDE	EXACTX	100	100
SRR27241771_27/1	1107	1577	-	dfrA27	core	AMR	TRIMETHOPRIM	EXACTX	100	100
SRR27241771_27/1	3639	4088	-	arr-3	core	AMR	RIFAMYCIN	EXACTX	100	100
SRR27241771_37/1	537	1394	-	blaTEM-1	core	AMR	BETA-LACTAM	ALLELEX	100	100
SRR27241771_42/1	18124	18699	-	terD	plus	STRESS	TELLURIUM	BLASTX	100	95.31
SRR27241771_42/1	18751	19788	-	terC	plus	STRESS	TELLURIUM	BLASTX	100	90.46
SRR27241771_42/1	19814	20266	-	terB	plus	STRESS	TELLURIUM	BLASTX	100	90.73
SRR27241771_42/1	21449	22027	-	terZ	plus	STRESS	TELLURIUM	EXACTX	100	100
SRR27241771_42/1	28598	29062	+	terW	plus	STRESS	TELLURIUM	EXACTX	100	100
SRR27241771_47/1	4968	5870	-	mph(A)	core	AMR	MACROLIDE	EXACTX	100	100
SRR27241771_53/1	7	843	-	sul1	core	AMR	SULFONAMIDE	EXACTX	100	100
SRR27241771_53/1	840	1184	-	qacEdelta1	core	STRESS	QUATERNARY AMMONIUM	ALLELEX	100	100
SRR27241771_63/1	23575	24036	-	golS	plus	STRESS	GOLD	EXACTX	100	100
SRR27241771_63/1	24051	26336	-	golT	plus	STRESS	COPPER/GOLD	BLASTX	100	99.74
SRR27241771_63/1	26613	27836	+	mdsA	plus	AMR	EFFLUX	BLASTX	100	98.04
SRR27241771_63/1	27836	31000	+	mdsB	plus	AMR	EFFLUX	EXACTX	100	100
SRR27241771_69/1	11799	12980	-	emrD	plus	AMR	EFFLUX	BLASTX	100	92.64
SRR27241771_72/1	1424	2626	-	tet(B)	core	AMR	TETRACYCLINE	EXACTX	100	100

SRR27241772 (Genes and point mutations)

Contig id	Start	Stop	Strand	Gene symbol	Scope	Element type	Class	Method	% Coverage of reference sequence	% Identity to reference sequence
SRR27241772_100/1	1	561	+	aadA2	core	AMR	AMINOGLYCOSIDE	PARTIAL_CONTIG_ENDX	71.1	100
SRR27241772_100/1	728	1072	+	qacEdelta1	core	STRESS	QUATERNARY AMMONIUM	ALLELEX	100	100
SRR27241772_100/1	1069	1905	+	sul1	core	AMR	SULFONAMIDE	EXACTX	100	100
SRR27241772_100/1	7222	7806	-	mph(A)	core	AMR	MACROLIDE	PARTIAL_CONTIG_ENDX	64.78	100
SRR27241772_101/1	85573	87762	+	sinH	plus	VIRULENCE	NA	BLASTX	100	98.77
SRR27241772_106/1	12719	13900	-	emrD	plus	AMR	EFFLUX	BLASTX	100	92.89
SRR27241772_107/1	5690	5803	+	astA	plus	VIRULENCE	NA	BLASTX	100	97.37
SRR27241772_109/1	9063	11108	+	ireA	plus	VIRULENCE	NA	BLASTX	100	99.85
SRR27241772_113/1	204	1460	+	cmIA1	core	AMR	PHENICOL	EXACTX	100	100
SRR27241772_113/1	1556	2344	+	aadA1	core	AMR	AMINOGLYCOSIDE	EXACTX	100	100
SRR27241772_113/1	2517	2846	+	qacL	core	STRESS	QUATERNARY AMMONIUM	EXACTX	100	100
SRR27241772_113/1	4032	4820	-	sul3	core	AMR	SULFONAMIDE	EXACTX	100	100
SRR27241772_21/1	6553	7014	-	golS	plus	STRESS	GOLD	BLASTX	100	99.35
SRR27241772_21/1	7029	9314	-	golT	plus	STRESS	COPPER/GOLD	BLASTX	100	99.48
SRR27241772_21/1	9591	10814	+	mdsA	plus	AMR	EFFLUX	BLASTX	100	98.28
SRR27241772_21/1	10814	13978	+	mdsB	plus	AMR	EFFLUX	BLASTX	100	99.53
SRR27241772_44/1	3269	4480	+	floR	core	AMR	PHENICOL	BLASTX	100	99.75
SRR27241772_44/1	5086	6282	-	tet(A)	core	AMR	TETRACYCLINE	BLASTX	100	99.75
SRR27241772_44/1	7624	8454	-	aph(6)-Id	core	AMR	AMINOGLYCOSIDE	BLASTX	99.64	100
SRR27241772_44/1	8457	9257	-	aph(3'')-Ib	core	AMR	AMINOGLYCOSIDE	EXACTX	100	100
SRR27241772_44/1	9321	10133	-	sul2	core	AMR	SULFONAMIDE	EXACTX	100	100
SRR27241772_47/1	171835	174468	+	gyrA_D87G	core	AMR	QUINOLONE/TRICLOSAN	POINTX	100	99.77
SRR27241772_47/1	171835	174468	+	gyrA_S83F	core	AMR	QUINOLONE/TRICLOSAN	POINTX	100	99.77
SRR27241772_53/1	45066	47321	-	parC_S80I	core	AMR	QUINOLONE	POINTX	100	99.6
SRR27241772_63/1	254	1126	+	blaCTX-M-15	core	AMR	BETA-LACTAM	ALLELEX	100	100
SRR27241772_68/1	118	930	-	aph(3')-Ia	core	AMR	AMINOGLYCOSIDE	EXACTX	100	100
SRR27241772_7/1	617	1111	-	dfrA12	core	AMR	TRIMETHOPRIM	EXACTX	100	100

Resources

Tool	Item	Links
ResFinder	Online server	http://genepi.food.dtu.dk/resfinder
	Original paper	https://pubmed.ncbi.nlm.nih.gov/22782487/
	Database repository	https://bitbucket.org/genomicepidemiology/resfinder_db/src/master/
	Tool repository	https://bitbucket.org/genomicepidemiology/resfinder/src/master/
	Tool documentation	https://cge.food.dtu.dk/services/ResFinder/instructions.php

Tool	Item	Links
PointFinder	Online server	N/A
	Original paper	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5890747/
	Database repository	https://bitbucket.org/genomicepidemiology/pointfinder_db/src/master/
	Tool repository	https://bitbucket.org/genomicepidemiology/pointfinder/src/master/
	Tool documentation	N/A

Tool	Item	Links
AMRFinderPlus	Online server	N/A
	Original paper	https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6811410/
	Database repository	https://ftp.ncbi.nlm.nih.gov/pathogen/Antimicrobial_resistance/AMRFinderPlus/database/3.11/2023-11-15.1/
	Tool repository	https://github.com/ncbi/amr
	Tool documentation	https://github.com/ncbi/amr/wiki

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