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RÉUNION INTERDISCIPLINAIRE DE
CHIMIOTHÉRAPIE ANTI-INFECTIEUSE

LUNDI 13 & MARDI 14
DÉCEMBRE 2021

Palais des Congrès
Paris

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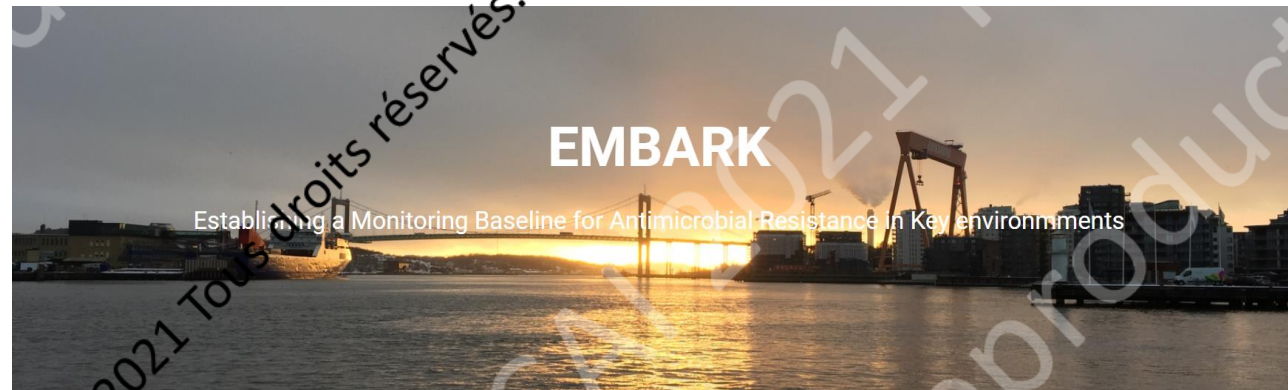


R I C A I

ResFinderFG 2.0:

a database of antibiotic resistance genes obtained by functional metagenomics.

Dr Rémi GSOUWIND
Prof. Etienne RUPPE
13th December 2021



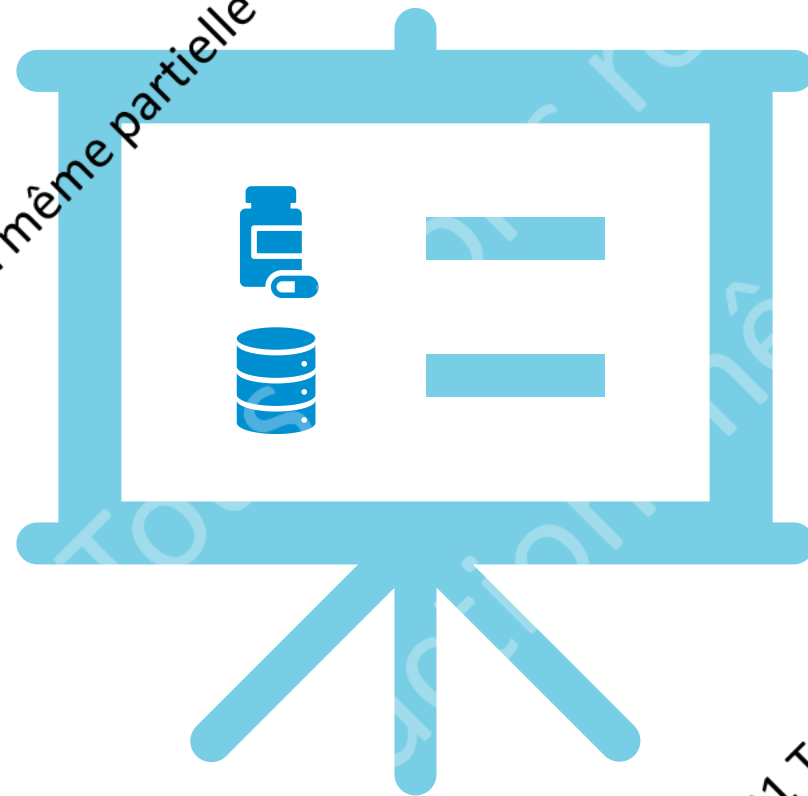
Infection • Antimicrobiols • Modelling • Evolution



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Outline

- Introduction
 - Antibiotic resistance
 - Functional metagenomics
- ResFinder FG 2.0
 - Construction methods
 - Results
- Conclusion



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Antibiotic resistance → Global threat, one health



New tools to combat antibiotic resistance → Metagenomics.



Sequence based → Unknown genes ?



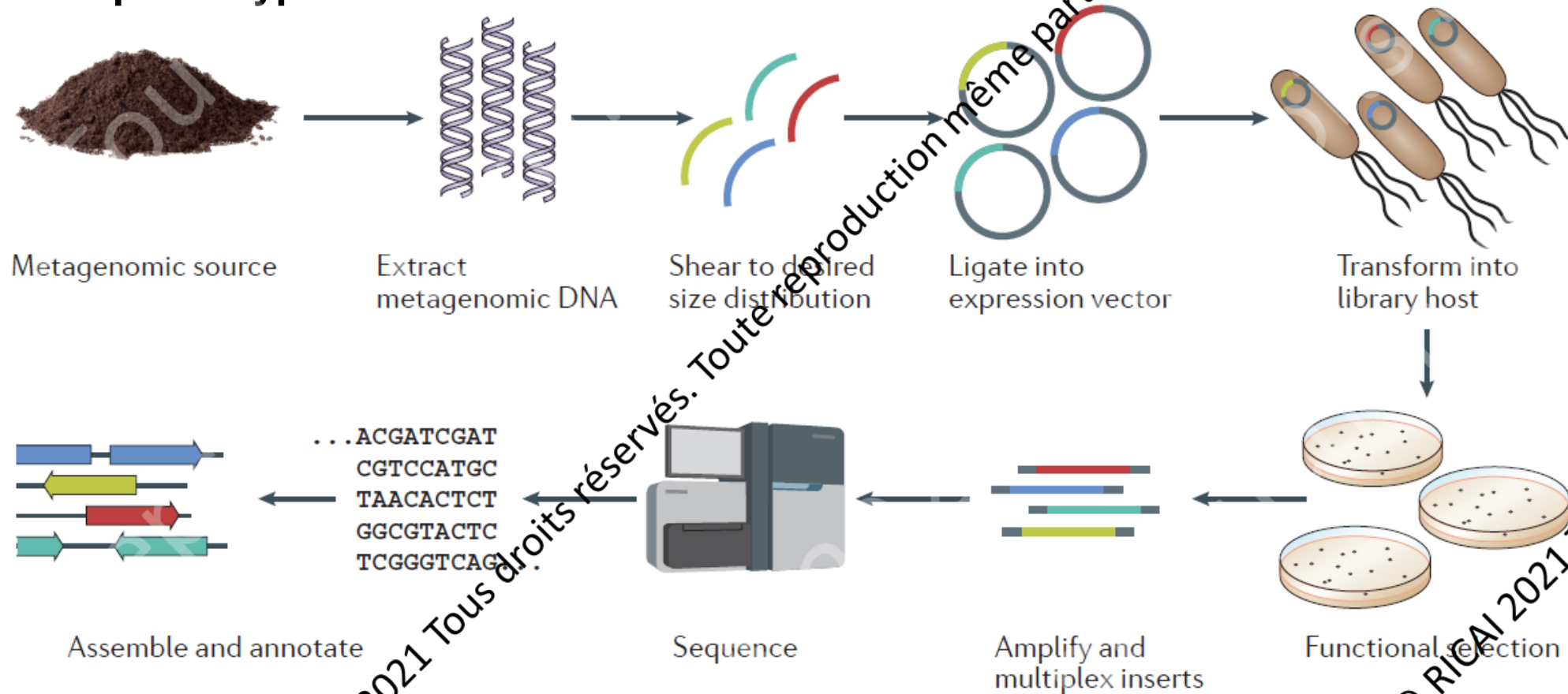
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→ **Functional metagenomics.**

Functional metagenomics

Culture and sequence unbiased technique that has been developed to mine metagenomes for various **phenotypes**.



➔ New ARGs, database ?

ResFinder FG

Database with antibiotic resistance genes **characterized functionally** using functional metagenomics.

ResFinder FG 1.0:

<https://cge.cbs.dtu.dk/services/ResFinderFG/>



2016

4 publications.

2282 genes.

25 ATB used for selection.

Pehrsson, E. C. *et al.* (2016)

Moore, A. M. *et al.* (2013)

Sommer, M. O. A. *et al.* (2009)

Forsberg, K. J. *et al.* (2014)

Goal:

Update ResFinder FG with all the functional metagenomics data available.

ResFinder FG 2.0:

« functional metagenomics » [Title/Abstract]
 Publications cited by the 4 publications
 Publications which cited 1 of the 4 publications

**ResFinder FG 1.0:****4 publications:**

Pehrsson, E. C. *et al.* (2016)
 Moore, A. M. *et al.* (2013)
 Sommer, M. O. A. *et al.* (2009)
 Forsberg, K. J. *et al.* (2014)

Review filtering.
 Functional metagenomics check.
 Sequences availability.

Accession numbers

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Accession numbers



```

>EU408346.1 Uncultured bacterium BLR1 genomic sequence
CTGCAGCAGATCTTCGAGAACCGCAACCTGCCGCTCAAGCCAGATGCGGCTGGCTGCCGCACG
ACTGGCTGTTTCGAGGACGGCATGCGCCG...
>KX126046.1 Uncultured bacterium clone AmoxDisc_TwinA_T10e1_TRSX_1208 genomic sequence
CATCCAGTCACGGAGATATAAATGCGGCTTCGGTGCAATGCTTGCGGGTAGTTGTGATAA
AGCCCGATACTGGCGCAAGAACGCGGACTGCGGC

```



CDHIT

Unique sequences



PROKKA

> 40k annotations ARGs ?



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ResFinder 4.0

PROKKA

228 unique annotations = ARGs

> 40k annotations

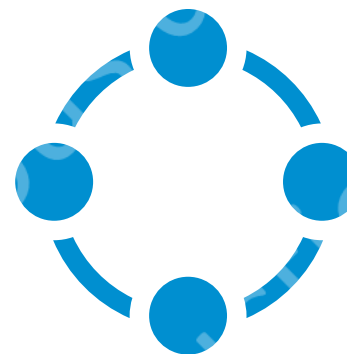


Only ARGs < 10k annotations

GB info

Sequence

Annotation



Source

Antibiotic used for selection



Antibiotic-annotation correspondance
Gene size
Unique annotation/accession number

Genes included in ResFinder FG 2.0

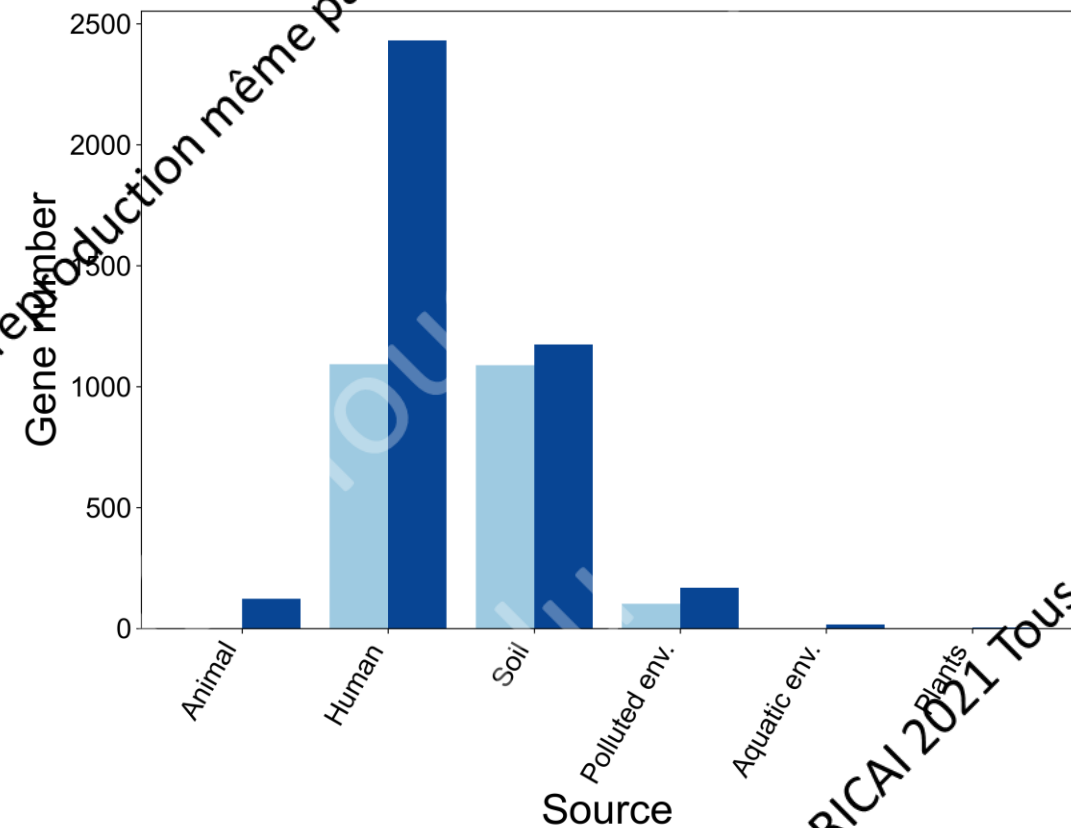
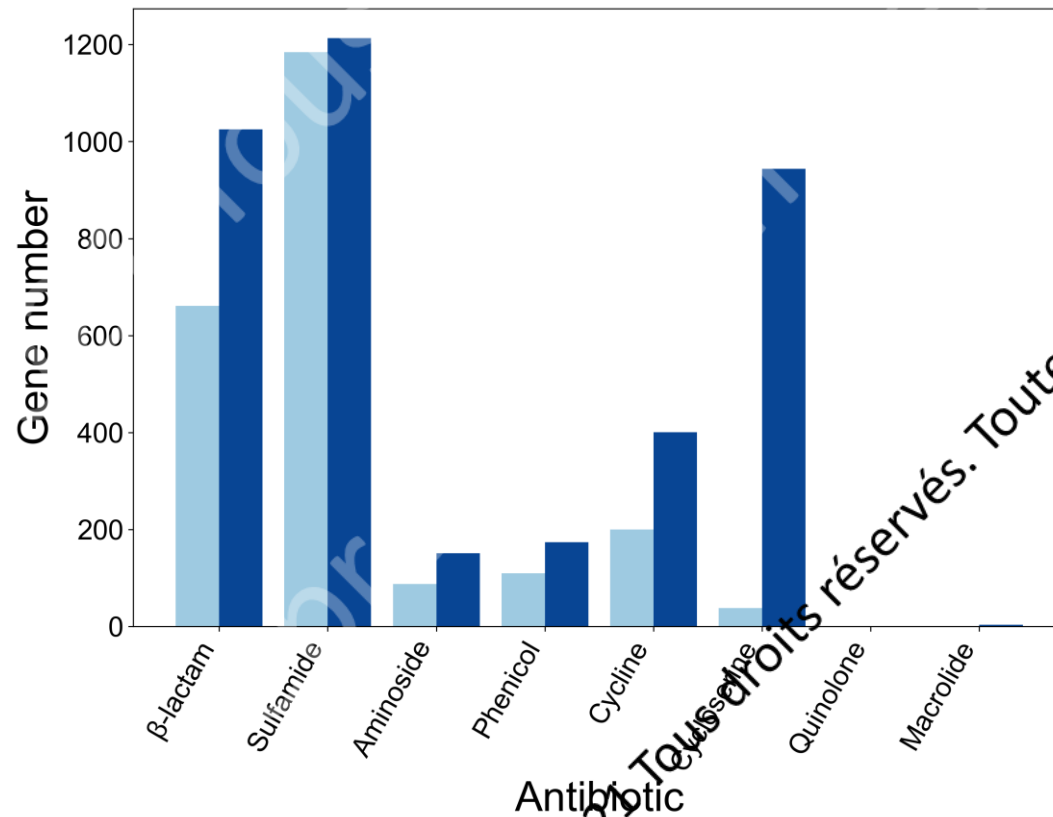


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ResFinder FG 2.0:

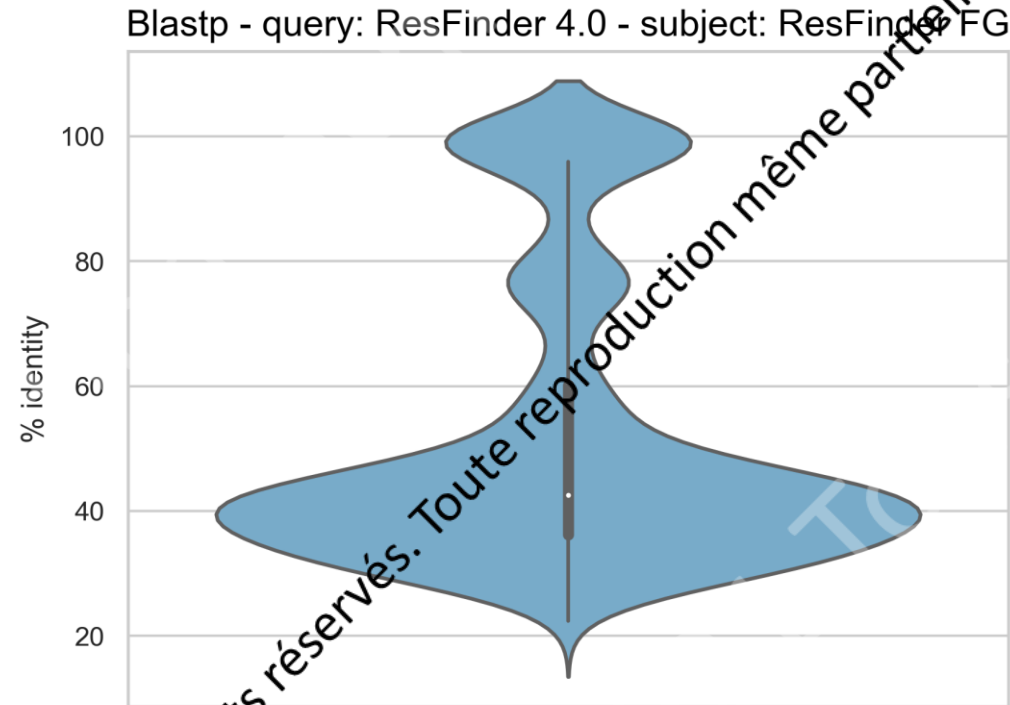
50 publications included (2004-2021)

→ 3'913 genes (+ 71% compared to ResFinder FG 1.0).



ResFinder FG 1.0
ResFinder FG 2.0

ResFinder FG 2.0 (3'913 genes) vs ResFinder 4.0 (3'181 genes):

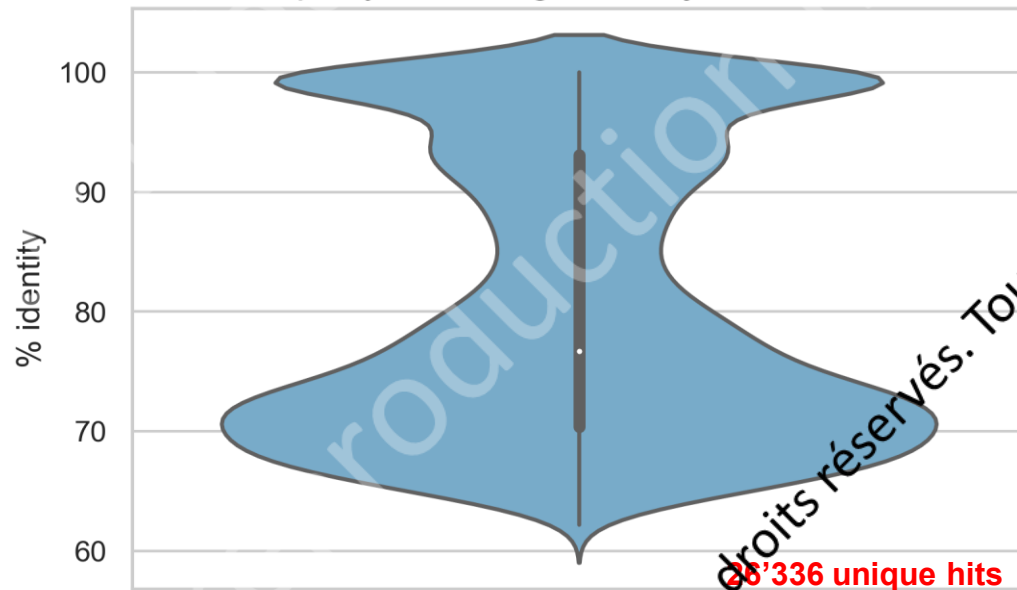


- 125 shared proteins (100% identical)
- 3'893 hits ; 3'245 proteins below 80% amino acid identity
- Mean pident = 52% ; Median pident = 43%

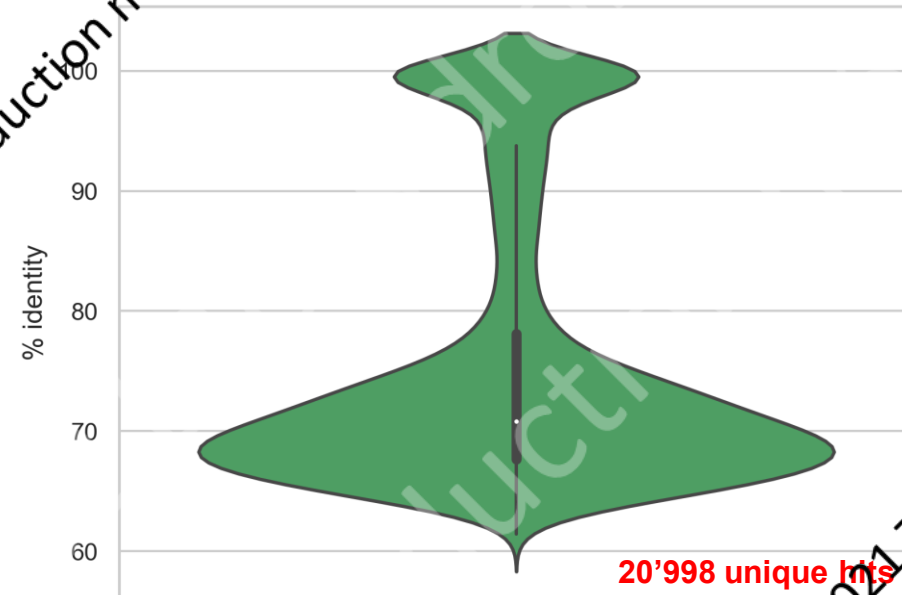
GMGCgut vs ResFinder FG 2.0/ResFinder 4.0:

→ **GMGCgut**: Catalog of **52'544'908 genes** from the intestinal microbiota.
<https://gmgc.embl.de/>

Blastn - query: GMGCgut - subject: ResFinder FG



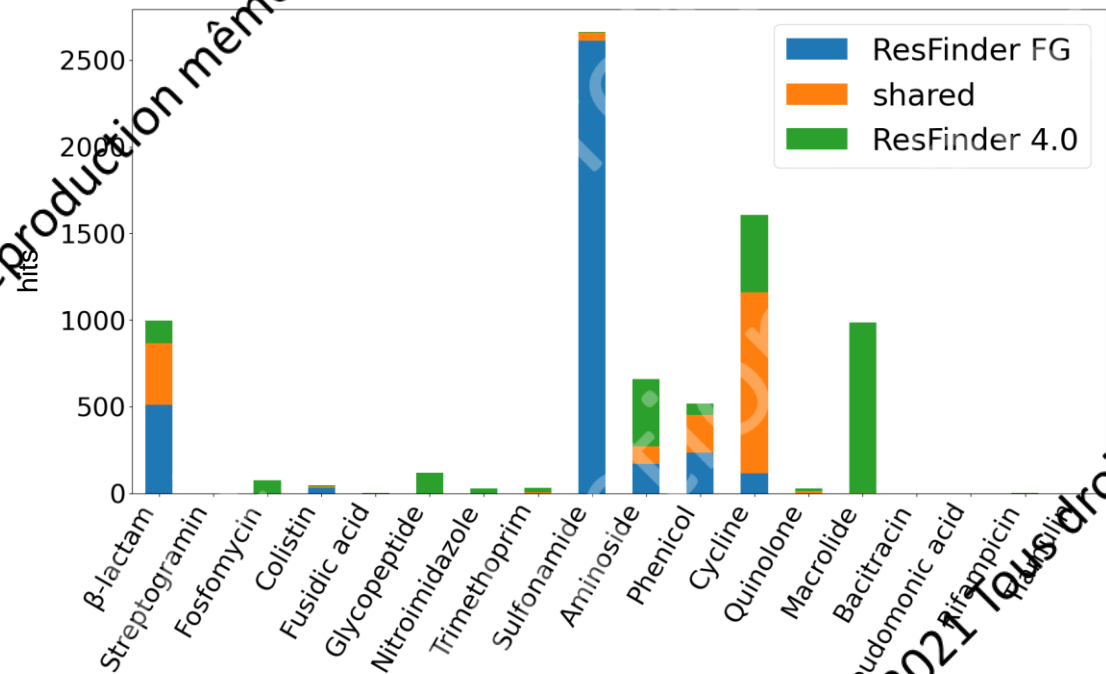
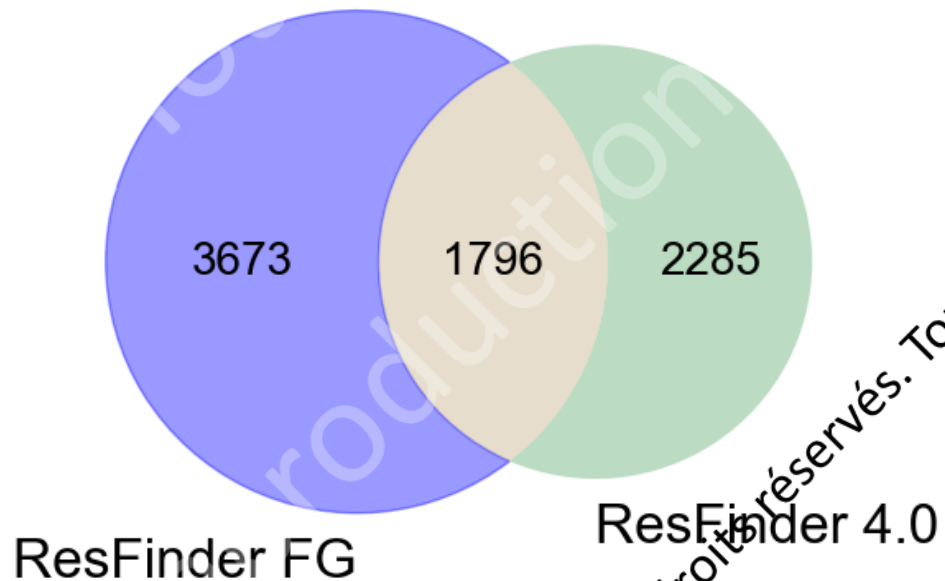
Blastn - query: GMGCgut - subject: ResFinder 4.0



→ **% identity**: similar distribution.

GMGCgut vs ResFinder FG 2.0/ResFinder 4.0:

- Genes with >80% identity.
- Cycloserine and disinfectant discarded.



- More **database specific hits** than shared hits.
- Antibiotic family is sometime **associated with one specific DB.**

- **ResFinder FG** allows to identify genes that were **functionally verified using functional metagenomics**.
- It comprises **specific genes** that are not present in ResFinder 4.0.
- Using ResFinder FG along with other databases should allow to have an **exhaustive description** of the ARGs content.
- **Guidelines for homogenization** in functional metagenomics data is needed to ease database update process.

Thank you for your attention !



Dr Luis Pedro Coelho
Dr Svetlana Ugarcina Perovic

Big Data Biology Lab
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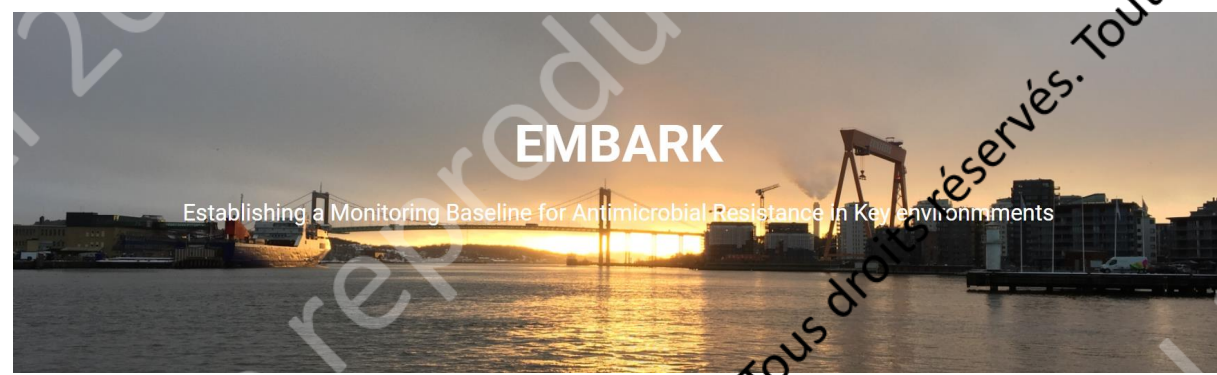
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