

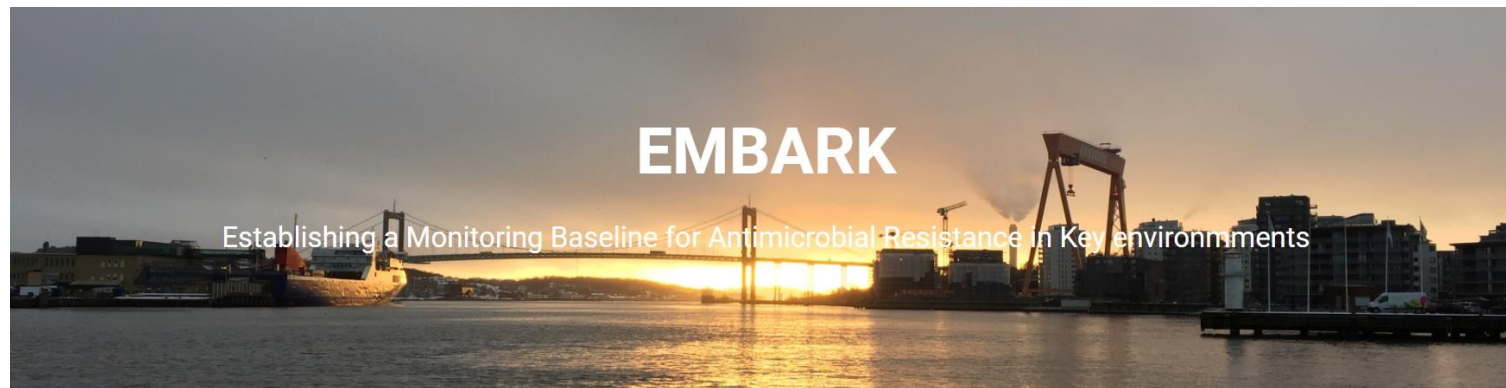


International Conference on Clinical Metagenomics

ResFinderFG 2.0:

a database of antibiotic resistance genes obtained by functional metagenomics.

Rémi GSCHWIND, Marie PETITJEAN, Svetlana UGARCINA PEROVIC, Luis Pedro COELHO, Etienne RUPPE
21st-22nd October 2021

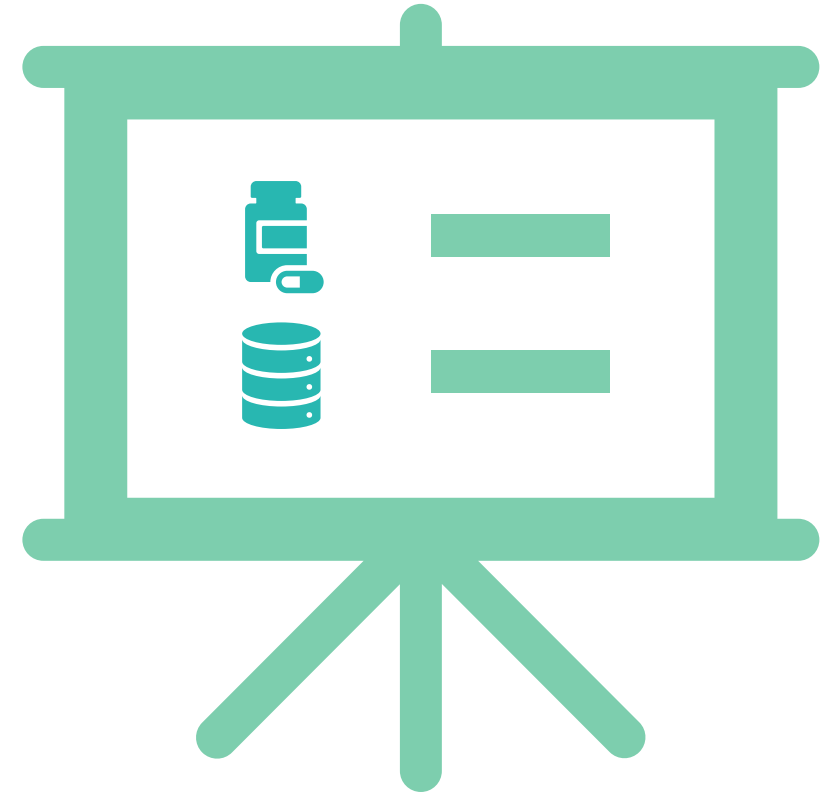


Infection • Antimicrobials • Modelling • Evolution

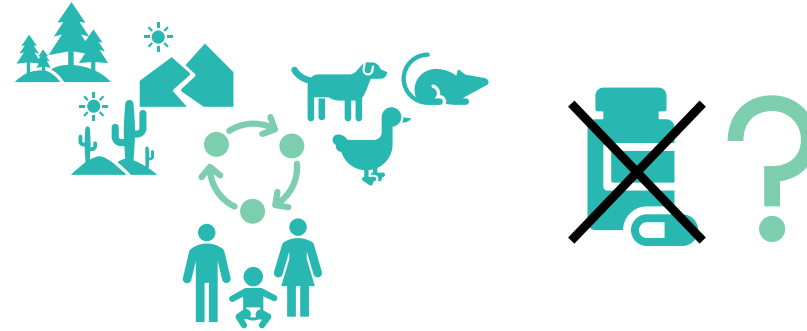


Outline

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



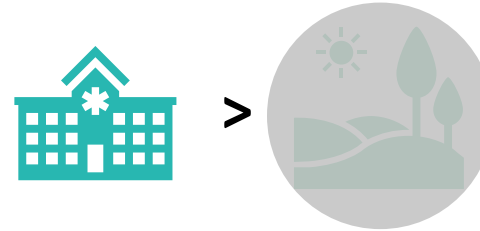
Antibiotic resistance → global threat



New tools to better understand antibiotic resistance → Metagenomics



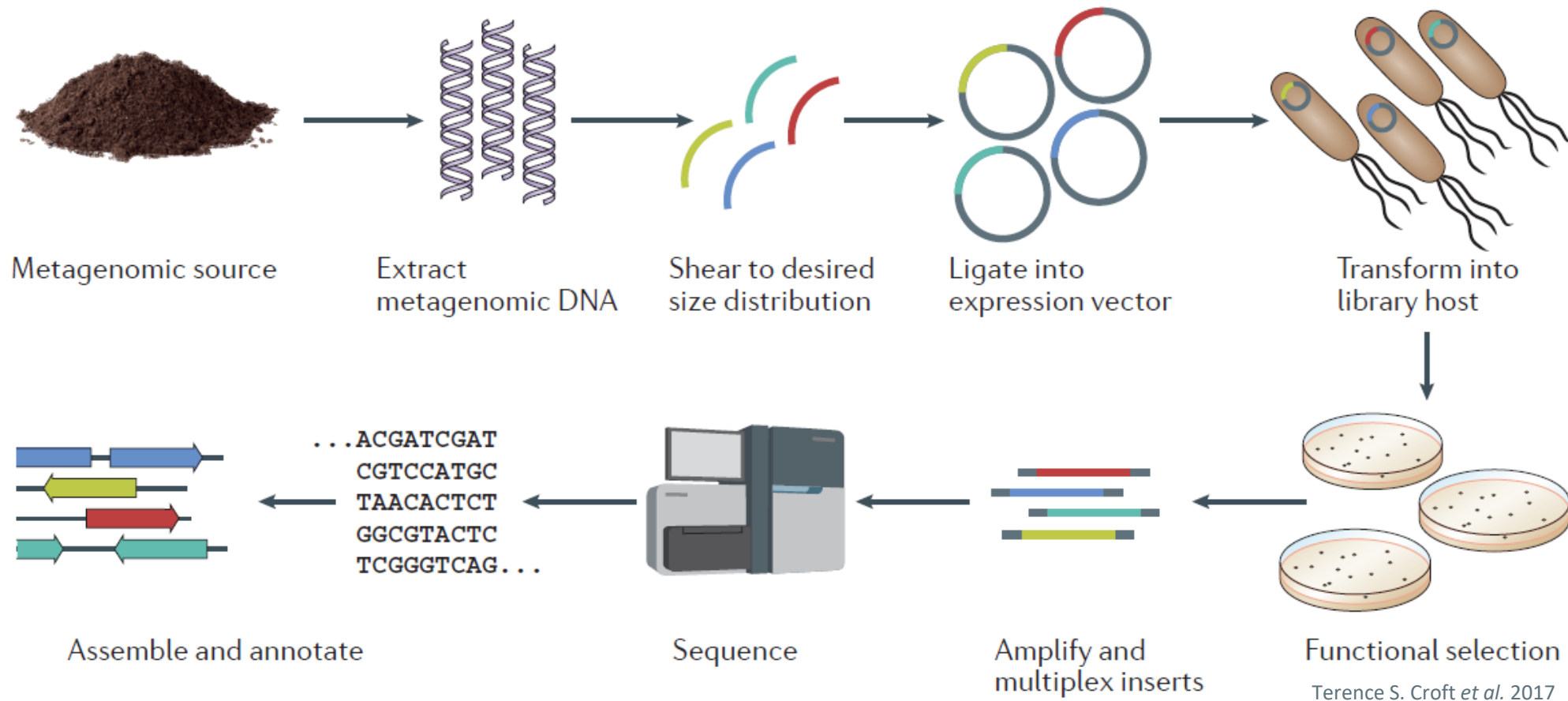
Sequence based → Unknown genes ?



→ **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:



4 publications.
2282 genes.
25 ATB used for selection.

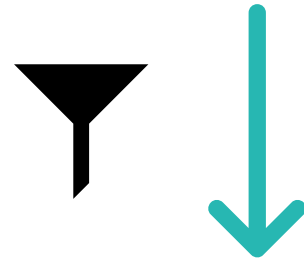
Goal: update ResFinder FG with all the functional metagenomics data available.

ResFinder FG 2.0:

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

**ResFinder FG 1.0:**

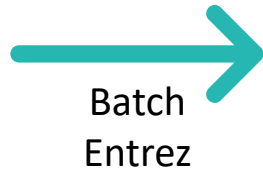
4 publications: Pehrsson, E. C. *et al.* (2016)
Moore, A. M. *et al.* (2013)
Sommer, M. O. A. *et al.* (2009)
Forsberg, K. J. *et al.* (2014)



Reviews.
Functional metagenomics.
Sequences availability.

Accession numbers

Accession numbers



>EU408346.1 Uncultured bacterium BLR1 genomic sequence
 CTGCAGCAGATCTTCGAGAACCGCAACCTGCCGCTCAAGCCAGGATGCGGCTGGCTGC
 CGCACGACTGGCTGTTTCGAGGACGGCATGCGCCG...
 >KX126046.1 Uncultured bacterium clone AmoxDisc_TwinA_Time1_TRSX_1208 genomic sequence
 CATCCAGTCACGGAGATATAAATGCGGCTTCGGTGCAATGCTTGCGGGTAGTTGTGATAA
 AGCCCGATACTGGCGCAAGAACGCGGACTGCGGC...

23'764 inserts



Unique Sequences

21'135 inserts



> 40k Annotations
 → x ORFs/inserts

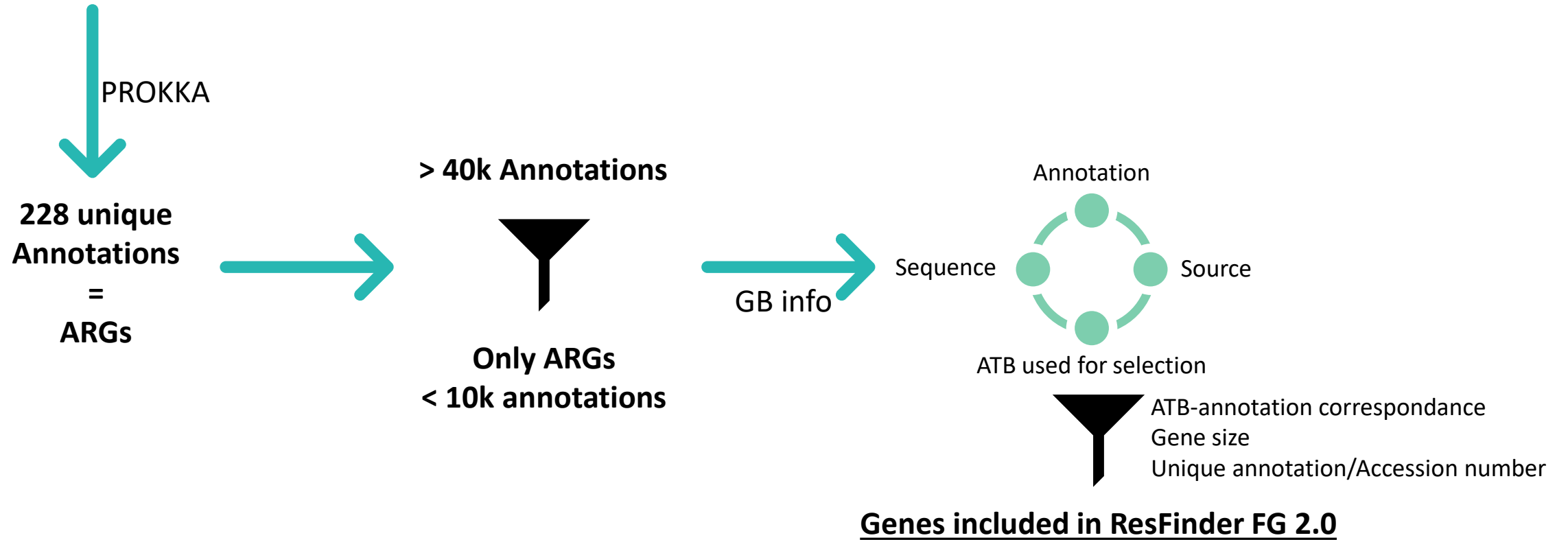
ARGs ?



ARG

CATCCAGATGCGGAGATATAAATGCGGCTTCGGTGCAATGCTTGCGGATGGTTGTGATAAAGCCCGATACTGGCGCAAGAACGCGGACTGCGGCTGCAGCAGATCTTCATGAACCGCAACCTGCCGCTCAAGCCAGGATGCGGCTGGCTGCCGCACGACTGGCTGTTTCGAGGACGGCATGCGCCG

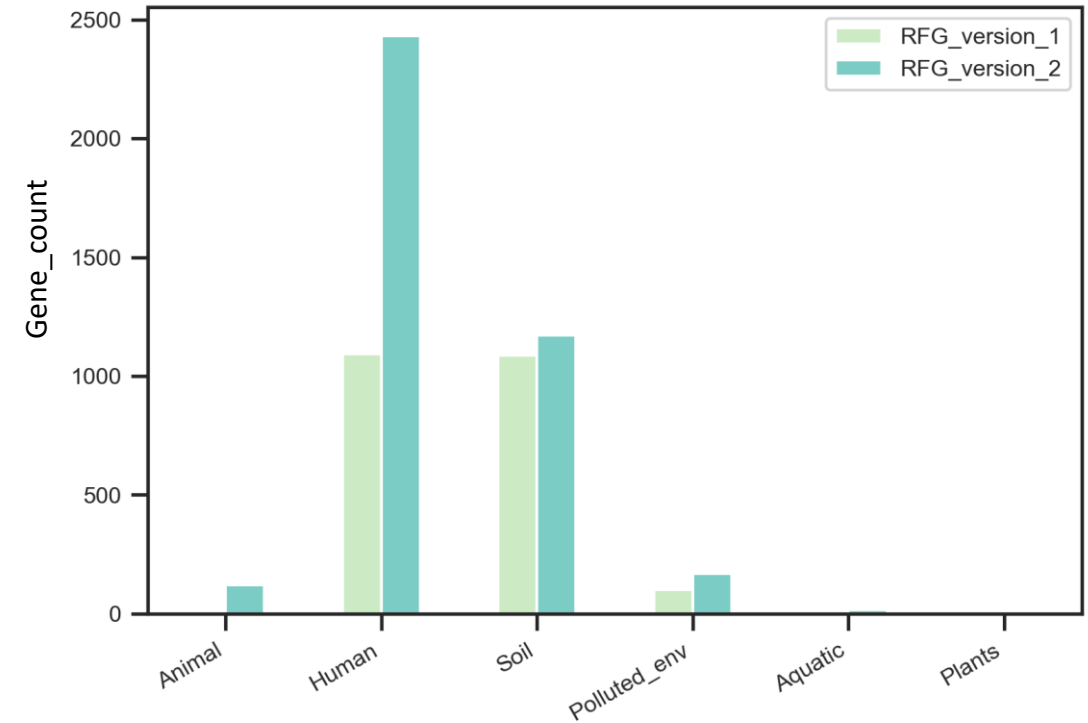
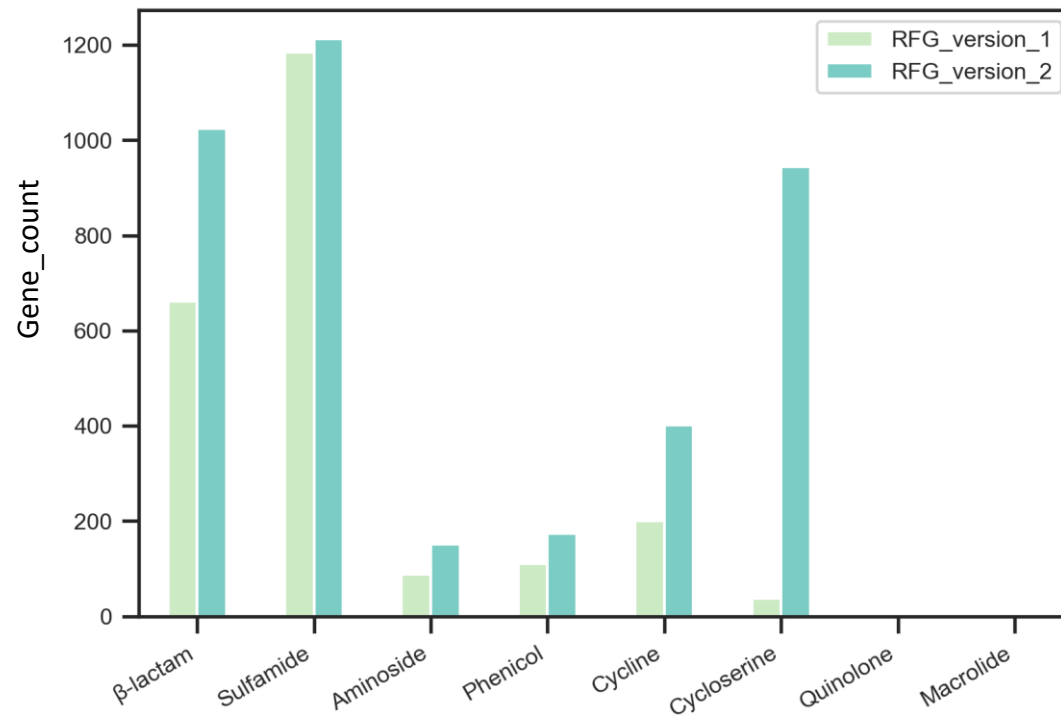
ResFinder 4



ResFinder FG 2.0:

50 publications included (2004-2021)

→ 3913 genes (+ 71% compared to ResFinder FG 1.0)



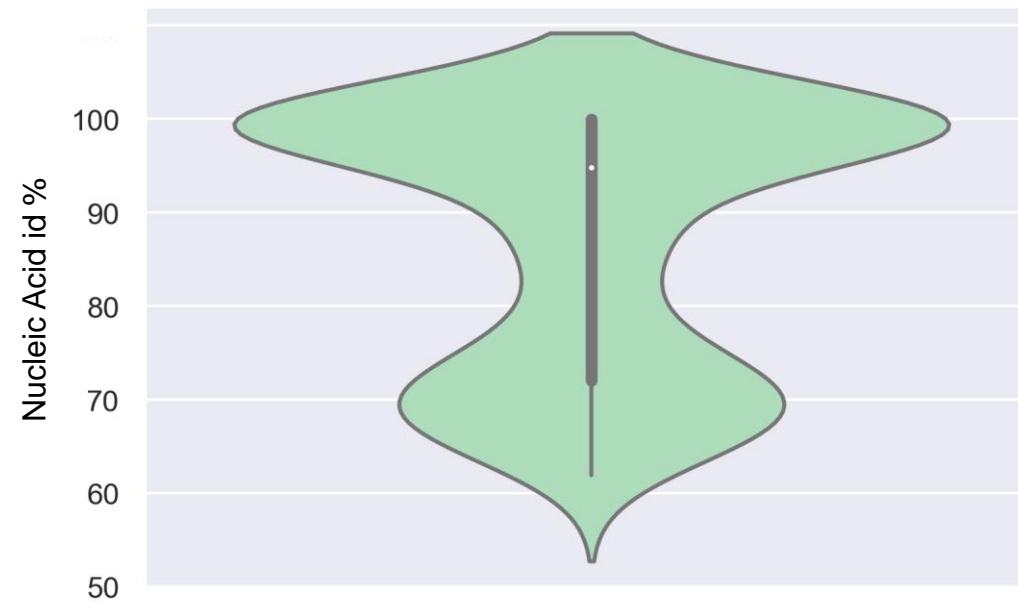
ResFinder FG 2.0 vs ResFinder 4:

blastn (min cov = 50%)

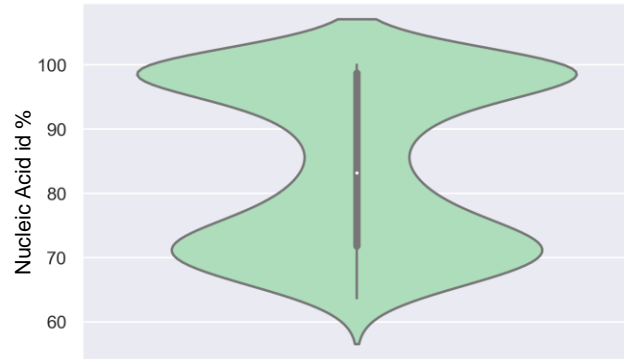
→ **61 shared genes** (nucleic acid % identity = 100%; cov = 100%)

→ **195 genes with cov > 50%**

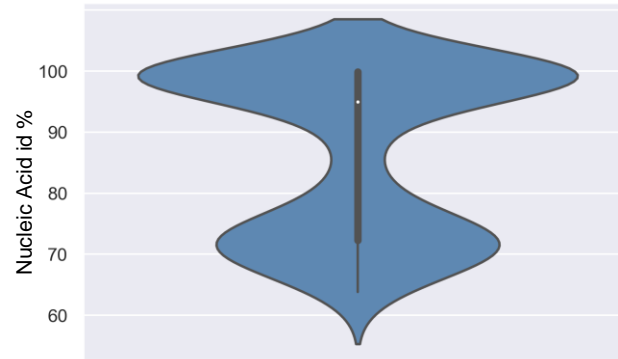
→ **Mean nucleic acid % identity = 87%**



Waste water gene catalog

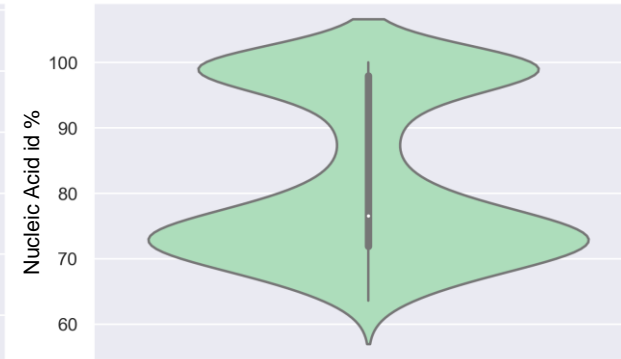


ResFinder FG

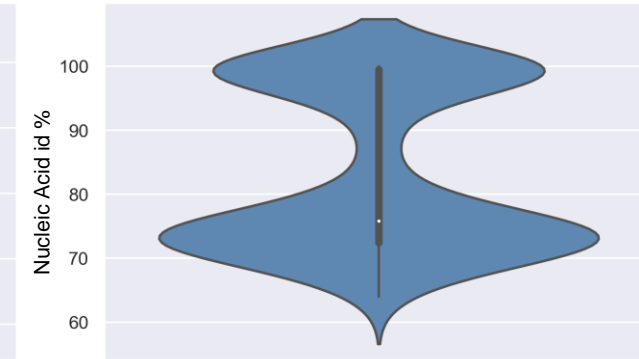


ResFinder 4

Oral gene catalog

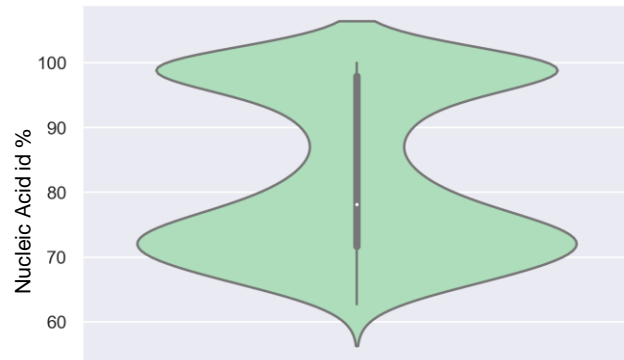


ResFinder FG

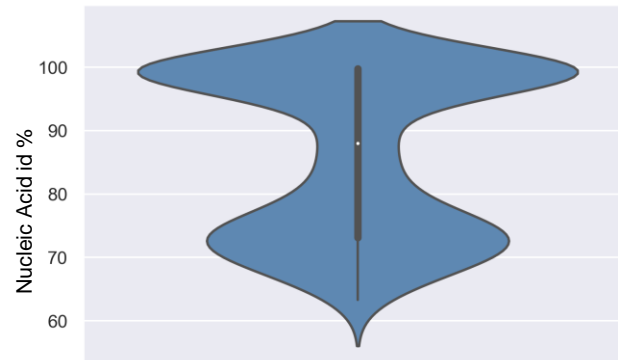


ResFinder 4

Skin gene catalog

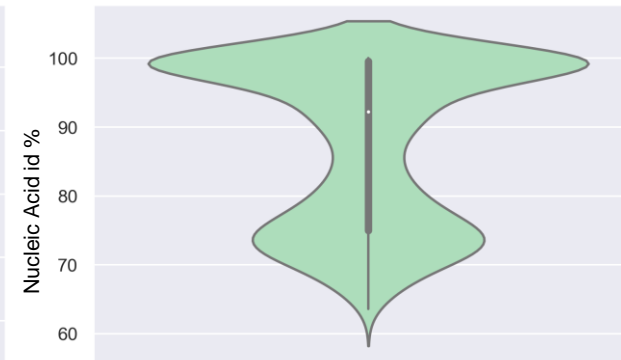


ResFinder FG

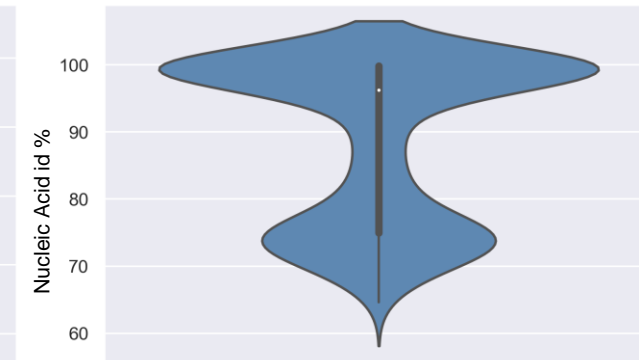


ResFinder 4

Gut gene catalog



ResFinder FG



ResFinder 4

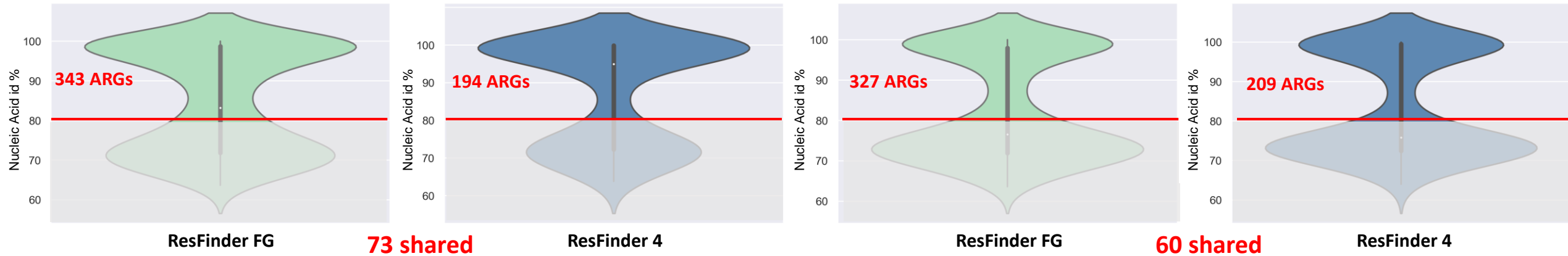
Global Microbial Gene Catalog (GMGC)

```
blastn -query GMGC10.human-gut.95nr.fna -task blastn -out GMGCgut_vs_resF4.out -subject resfinder4.fasta -qcov_hsp_perc 50 -outfmt "6 qseqid sseqid pident qlen slen qcovhsp length mismatch gapopen qstart qend sstart send evalue bitscore"
```

Waste water gene catalog

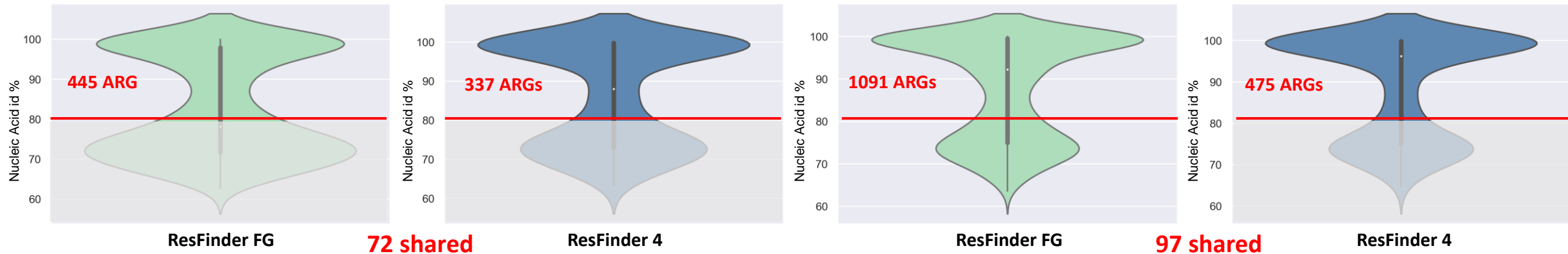
Oral gene catalog

>80%



Skin gene catalog

Gut gene catalog



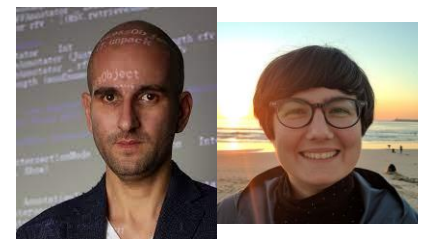
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```

- **ResFinder FG** allows to identify genes that were **functionally verified using functional metagenomics**.
- It comprises **specific genes** that are not present in ResFinder 4.
- 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.



International Conference on Clinical Metagenomics



Dr Luis Pedro Coelho

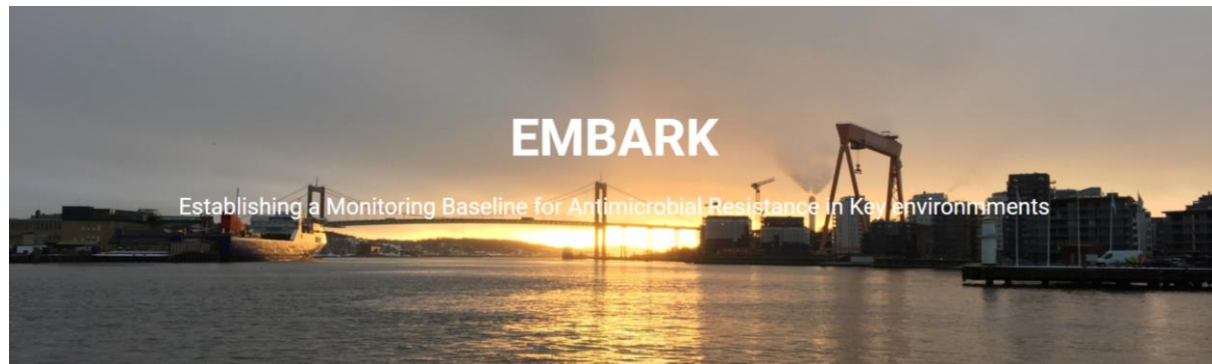
Dr Svetlana Ugarcina Perovic

Big Data Biology Lab
Fudan University

ResFinderFG 2.0:

a database of antibiotic resistance genes obtained by functional metagenomics.

Dr Rémi GSCHWIND
Pr Etienne RUPPE
21-22 October 2021



Infection • Antimicrobials • Modelling • Evolution



Thanks for your attention !

