Resistance Gene Identifier (RGI)

Prediction of antimicrobial resistance (AMR) genes in metagenomic sequencing data

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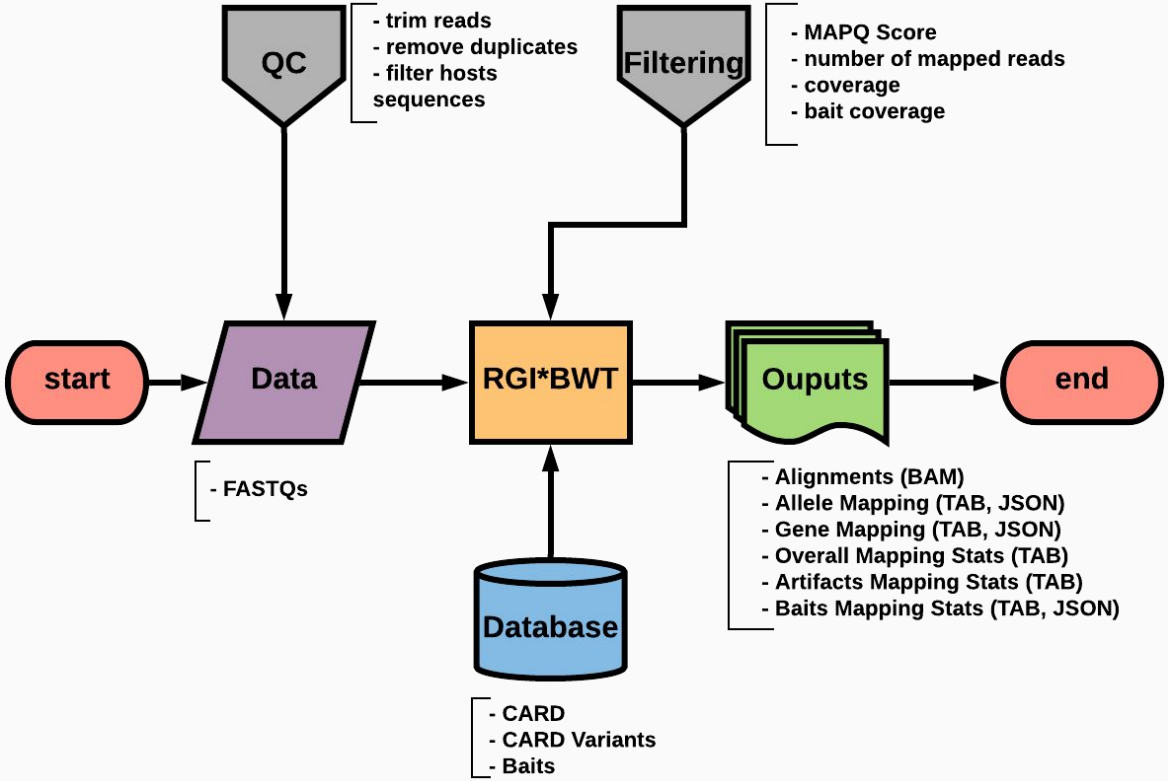
01 Objective

Identify AMR genes from metagenomic samples without the need for assembly

02 Methods

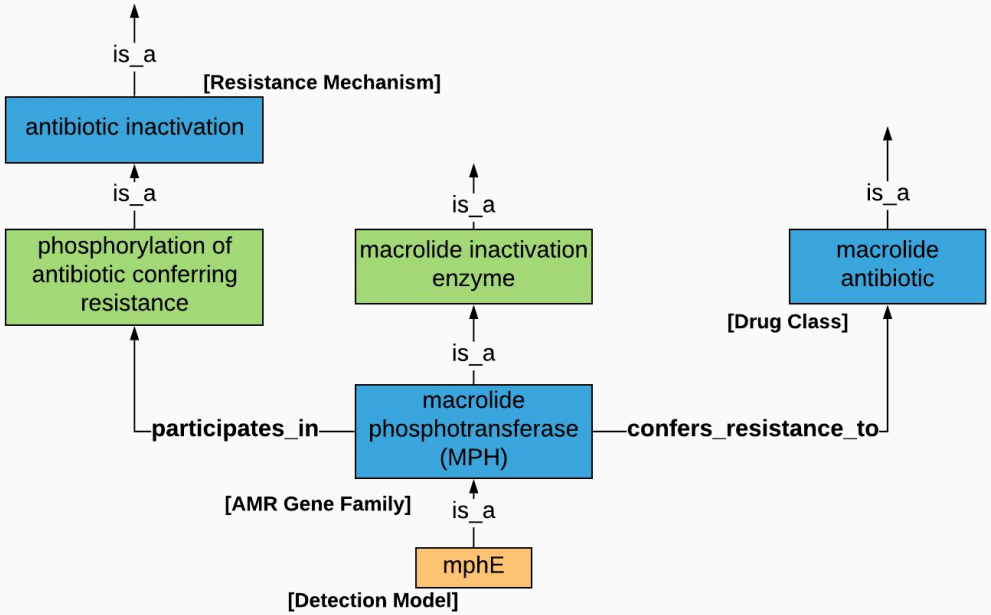
Use RGI*BWT and CARD datasets

Pipeline: RGI*BWT

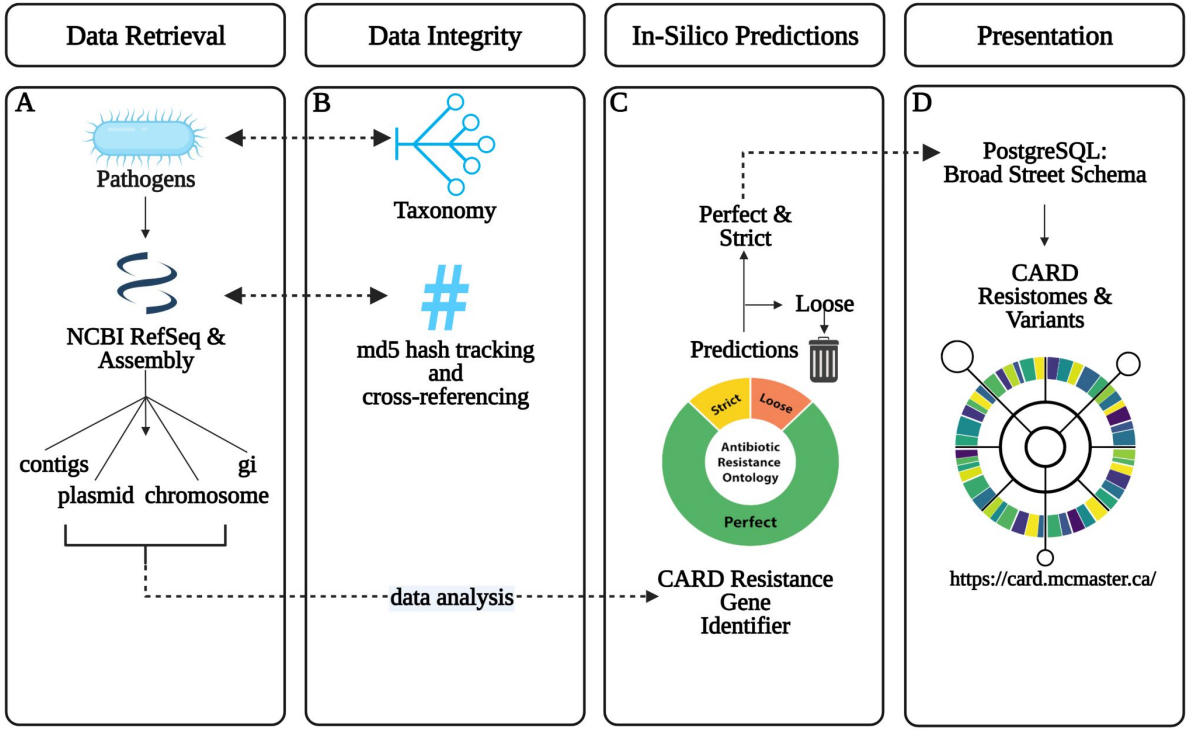


https://github.com/arpcard/rgi

Data: CARD-Canonical



DATA: CARD-Variants



doi:10.1093/nar/gkac920

03 Results

Predicting AMR genes from clinical and wastewater samples

Clinical Samples

14 samples

Type of data
- Clinical isolates

Motives
- Evaluate CARD AMR baits Version 1 to pull AMR genes

Data collection
- Sampled from Hamilton, Ontario, Canada

Sequencing
- Target bait capture (CARD baits V1) and shotgun

Wastewater Samples

2 samples

Type of data

- Metagenomic wastewater samples

Motives

- Evaluate new CARD AMR baits to pull AMR genes

Data collection

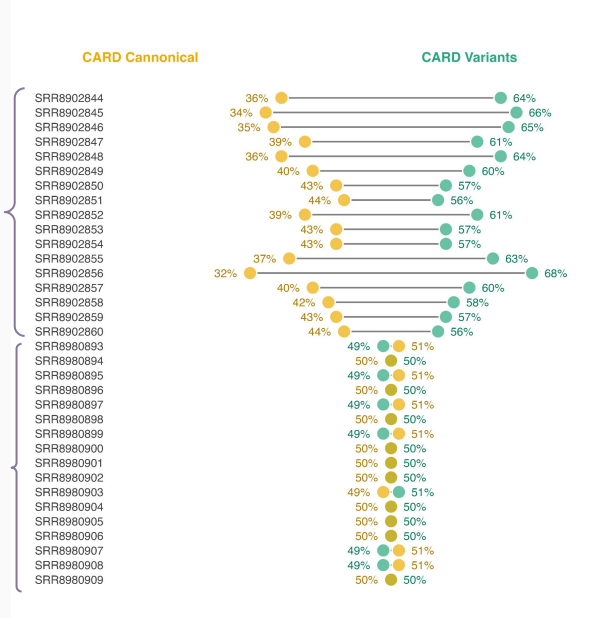
- Sampled from Hamilton wastewater treatment plant in November 2022 and March 2023

Sequencing

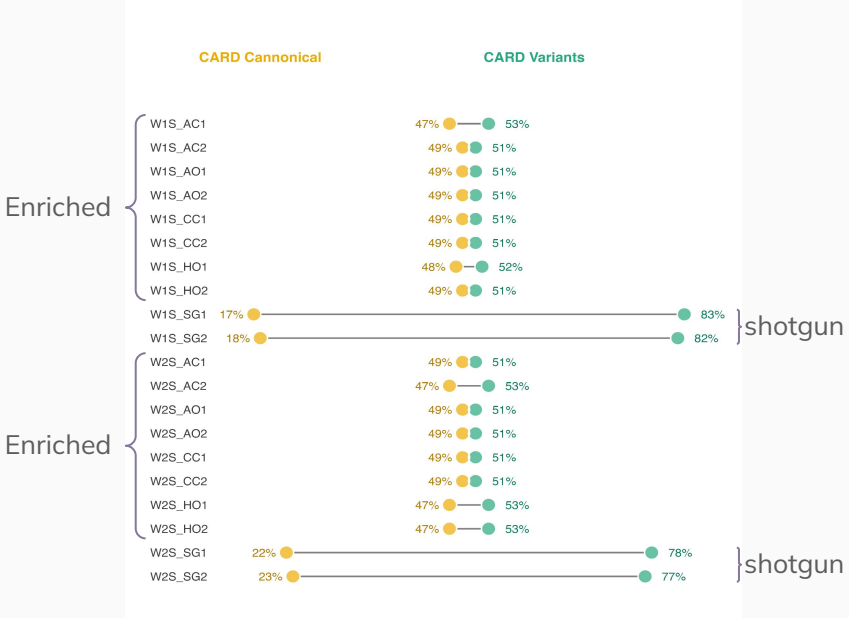
- Enriched with allCARD(AC), clinicalCARD (CC), Arbor-synthesized (AO), In-house-synthesized (HO) baits, and Shotgun (SG)

Results

Clinical



Wastewater



04 Conclusion

Bait capture methods and CARD *in silico* variants helps recover more AMR-related reads

Thanks!

Do you have any questions?

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My poster is #151 - Poster Session B

05 Supplementary

Data: CARD-Canonical