



Modelling environmental antibiotic-resistance gene abundance: A meta-analysis

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	INTRODUCTION		QUESTION
ſ	 Human and veterinary antibiotics are crucial against disease and infection 	ſ	Does antibiotic selective pressure correlate with ARG
	• Worldwide antimicrobial resistance crisis is rapidly unfolding		

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- Environmental emissions due to high consumption and limited treatment
- Unknown effect of antibiotic pollution on antibiotic-resistance genes (ARG)

• Necessary risk assessment of resistance selection due to antibiotic pressure

abundance?

Does the environmental matrix influence ARG abundance?



RESULTS & DISCUSSION



Figure 1. TASP and TARG in sediments, surface water and wastewater. Unique cases are expressed as dots and the model predictions using unconditional (population-level) values are expressed as solid lines. TASP equal to 1 (risk threshold) is indicated by the dashed vertical lines.

6 Linear mixed-effects model architecture

 $TARG = TASP + Matrix + (1|Country) + (1|Year) + (Matrix|Class) + (1|Study/Sample) + \varepsilon$

7 Model selection and evaluation



CONCLUSION

- Antibiotic selective pressure positively correlates with antibiotic-resistance gene abundance
- Interaction effects significantly affect resistance gene abundance



Figure 2. TASP and TARG stratified by therapeutic class and matrix. Sample data is expressed in isocontours after two dimensional Gaussian kernel density estimation. TASP equal to 1 (risk threshold) is indicated by the dashed vertical lines.



- In sediment, most antibiotic classes exert selective pressure above the risk threshold
- In surface water and wastewater, class-specific gene estimation is less reliable
- Antibiotic pressure and matrix should be considered in resistance risk assessment

