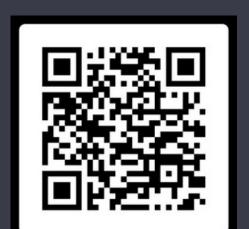
Is dillution the solution to pollution?

Bacteriological assessment of a wastewater treatment plant



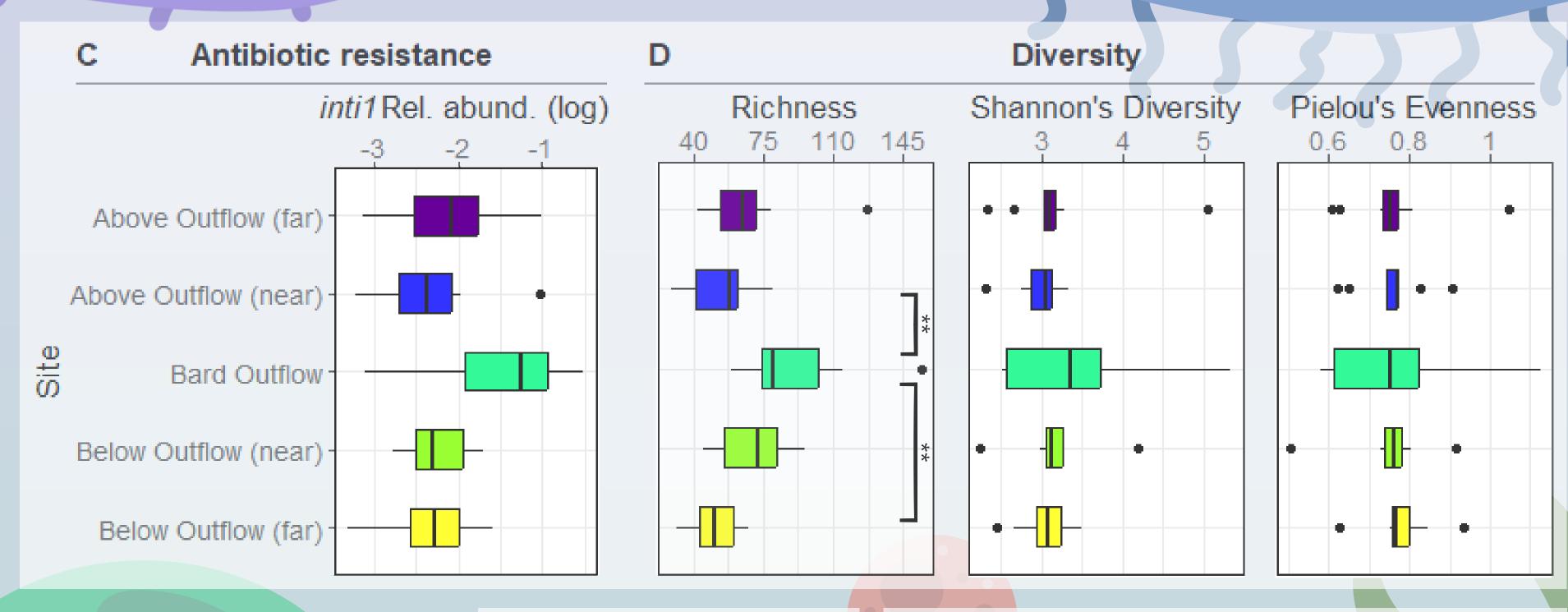
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The impact of a wastewater treatment plant along the Saw Kill River was assessed using 16S and an antibiotic resistance marker. The outflow displayed higher richness and a distinct bacterial community, including potential pathogens, possibly lost in the river due to dilution.

To investigate the impact of Wastewater treatment plants (WWTP) on a river's bacterial community through two molecular indicators.

Sequenced 16S rRNA and *intl1* amplicon reads, a marker for antibiotic resistance, were gathered from five sites along Saw Kill River. This data was extracted from Santana et al. (2022).

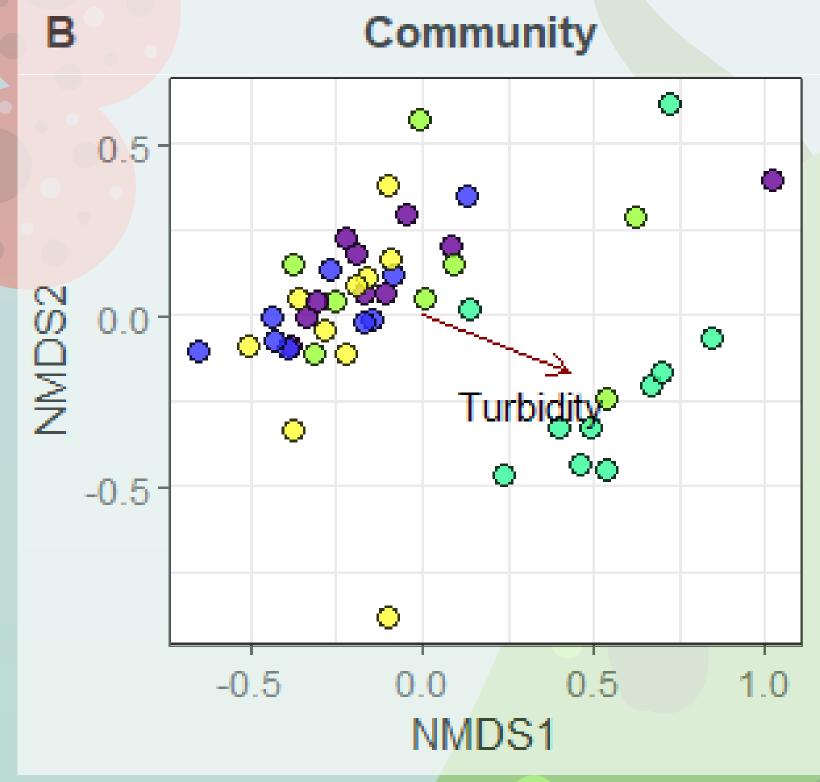


C No differences in intl1 relative abundance, nor in other alpha diversity indexes along the sample sites.

D Higher species richness in Bard Outflow compared to Above Outflow (near) and Below Outflow (far).

Sites

- Above Outflow (far)
- Above Outflow (near)
- Bard Outflow
- Below Outflow (near)
- Below Outflow (far)



B Bard Outflow bacterial community composition differed from the river, potentially affected by turbidity.

Betaproteobacteriales dominated all samples, and Campylobacterales were more abundant in the outflow.



The outflow may not affect the river water, and although potentially harmful pathogens were found, dilution might be masking the effects in the river water. Further research is needed, e.g. sediments.