AQUIFER COMMUNITIES – CAN THEY PREDICT CHANGES IN AOTEAROA'S SOURCE (GROUND)WATER

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water NEW ZEALAND
The New Zealand Water & Wastes Association Waiora Aotearoa

water NEW ZEALAND CONFERENCE & EXPO
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Tākina, Te Whanganui-a-Tara Wellington

INTRODUCTION – 'THE WATER PLANET'

- 71 % of the earth's surface is covered with water
- 3 % of the earth's water is freshwater
- 2.5 % of the earth's freshwater is unavailable: locked up in glaciers, polar ice caps, atmosphere, soil, and deep inaccessible aquifers
- 0.5 % is available freshwater: includes groundwater

Table1. Percentages of water on earth

	%
Oceans	97.2
Ice Caps/Glaciers	2.0
Groundwater	0.62
Freshwater Lakes	0.009
Inland seas/salt lakes	0.008
Atmosphere	0.001
Rivers	0.0001
TOTAL	**99.8381**

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- Global popn. increasing: 1950 (2.5 billion) ⟶ 2023 (< 8 billion)
- Land use practices: industrial applications, urban development and farming
- Release pollutants that infiltrate groundwater aquifers, threatening drinking water supplies
  - Metals (arsenic, manganese)
  - Petroleum products
  - Plastics
  - Pathogenic bacteria
  - Nutrients (nitrogen and phosphorus)

https://wrytin.com/kashish4/global-population-jxniqgzz

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Q. How are pollutants removed from groundwater?

- Aquifers naturally filter groundwater by forcing it to pass through small pores and between sediment particles
- Predatory organisms i.e., stygofauna, protozoa, bacteriophages feed on pathogenic bacteria and biofilms
- Biological (bacterial) communities utilise contaminants as energy (carbon) sources

BIOLOGICAL – BACTERIAL COMMUNITIES

- Bacterial communities can adapt to subtle changes in the chemical composition of a groundwater system
- Changes in bacterial communities could potentially be used as an early warning of a change in water quality i.e., nitrate contamination and changes in ecosystem functioning

INTERNATIONAL RESEARCH

Links found between bacterial communities and water quality

- Overseas research has found that increased organic contamination has a negative effect on bacterial diversity
- Bacterial community compositions in polluted environments shift towards less diverse but more specialised communities
- Bacterial populations affiliated with Proteobacteria, Actinobacteria and Acidobacteria are dominant in environments polluted with organic compounds and pesticides

BALABAN, N., YANKELZON, I., ADAR, E., GELMAN, F., RONEN, Z. & BERNSTEIN, A. 2019. The spatial distribution of the microbial community in a contaminated aquitard below an industrial zone. Water, 11, 2128.
HOLMSGAARD, P. N., DEALTRY, S., DUNON, V., HEUER, H., HANSEN, L. H., SPRINGAEL, D., SMALLA, K., RIBER, L. & SØRENSEN, S. J. 2017. Response of the bacte
on-farm biopurification system, to which diverse pesticides are introduced over an agricultural season. Environmental Pollution, 229, 854-862.

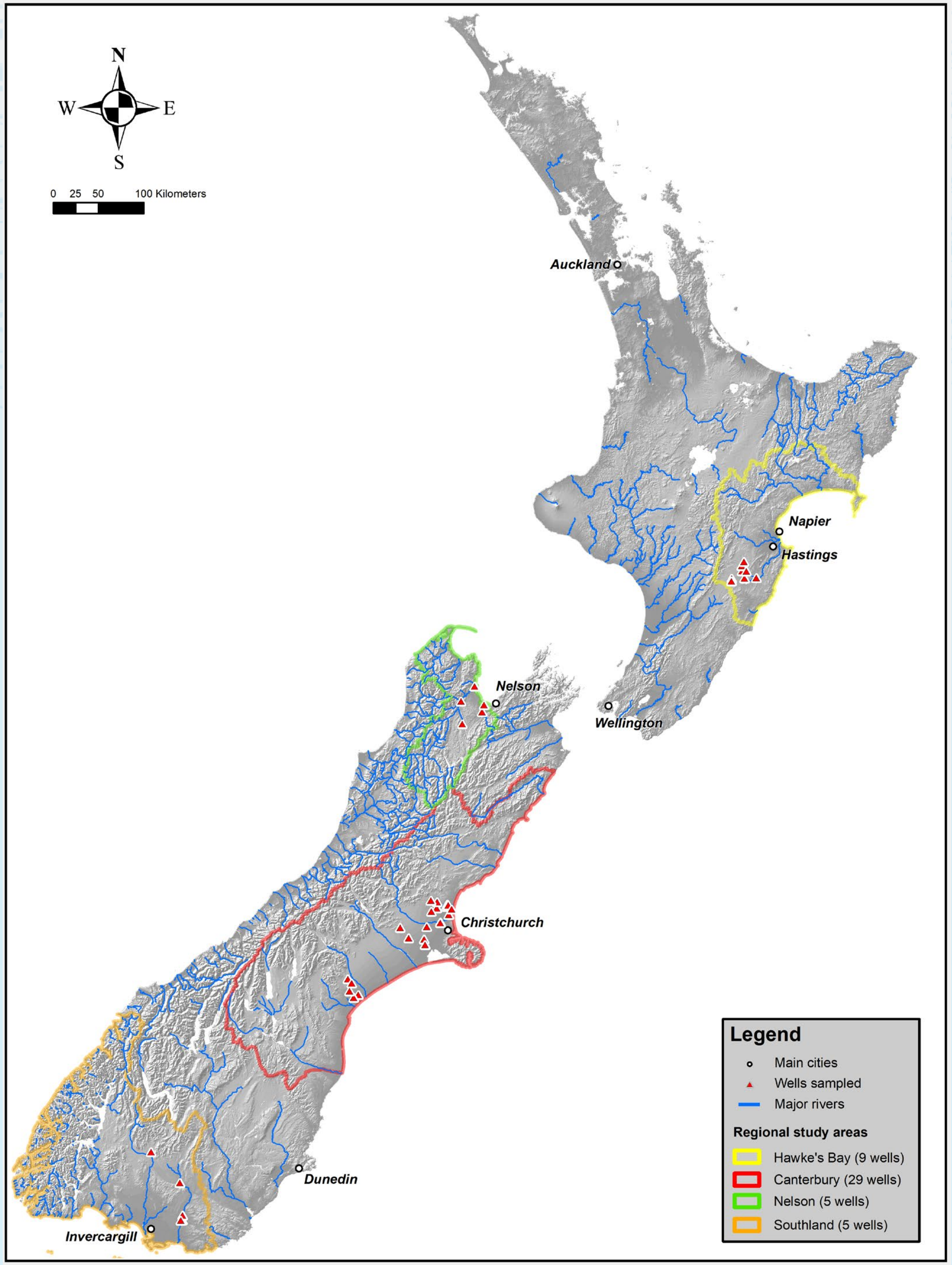
STUDY QUESTIONS

- Can differences in bacterial communities be used to help predict changes in water quality
- Does the composition of a bacterial community change depending on aquifer geology (location)

WHAT WE DID

Sampled:

- 49 wells (shallow aquifers) in four regions
- Well parameters: pH, temp, dissolved oxygen, nitrate, total nitrogen etc.
- Extracted DNA: sequenced bacteria

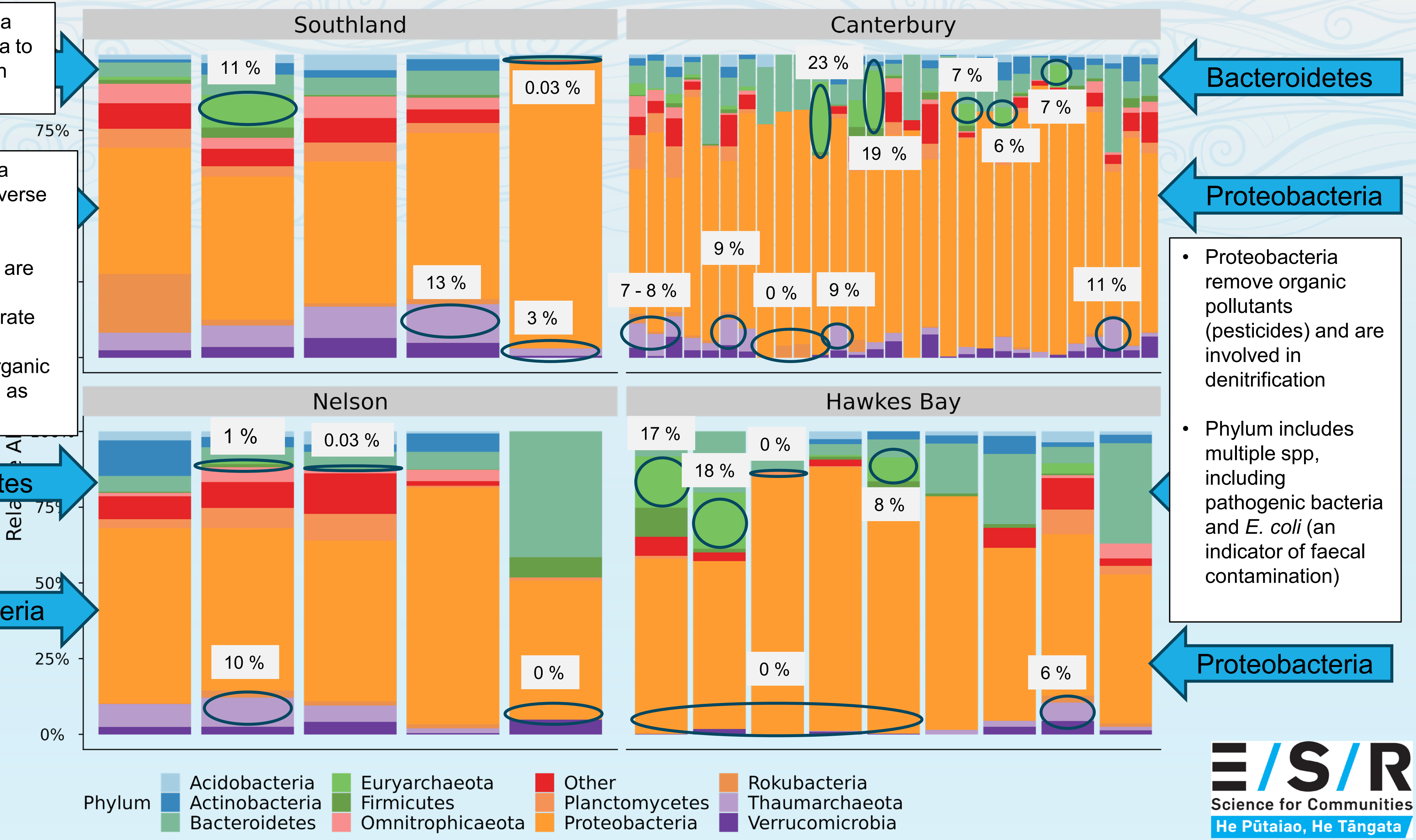


ANALYSIS

- Calc. bacterial abund. (different species within a community)
- Calc. diversity
  - Alpha - How many different bacterial species are detected within each sample
  - Beta - The difference in bacterial composition between samples (regions)
- Evaluated correlations: between bacterial abund. and well parameters
- Machine learning to assess bacterial abund. and nitrate classification

- Thaumarchaeota oxidise ammonia to nitrite (1st step in nitrification)

- Bacteroidetes is a phenotypically diverse group
- Within this group are spp. capable of denitrification, nitrate reduction and degradation of organic compounds such as diesel



- Proteobacteria remove organic pollutants (pesticides) and are involved in denitrification
- Phylum includes multiple spp, including pathogenic bacteria and *E. coli* (an indicator of faecal contamination)

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SOUTHLAND WELLS (EXAMPLE)

Pristine

- Located in upper catchment
- 10 km upgradient is a pristine source water

Contaminated

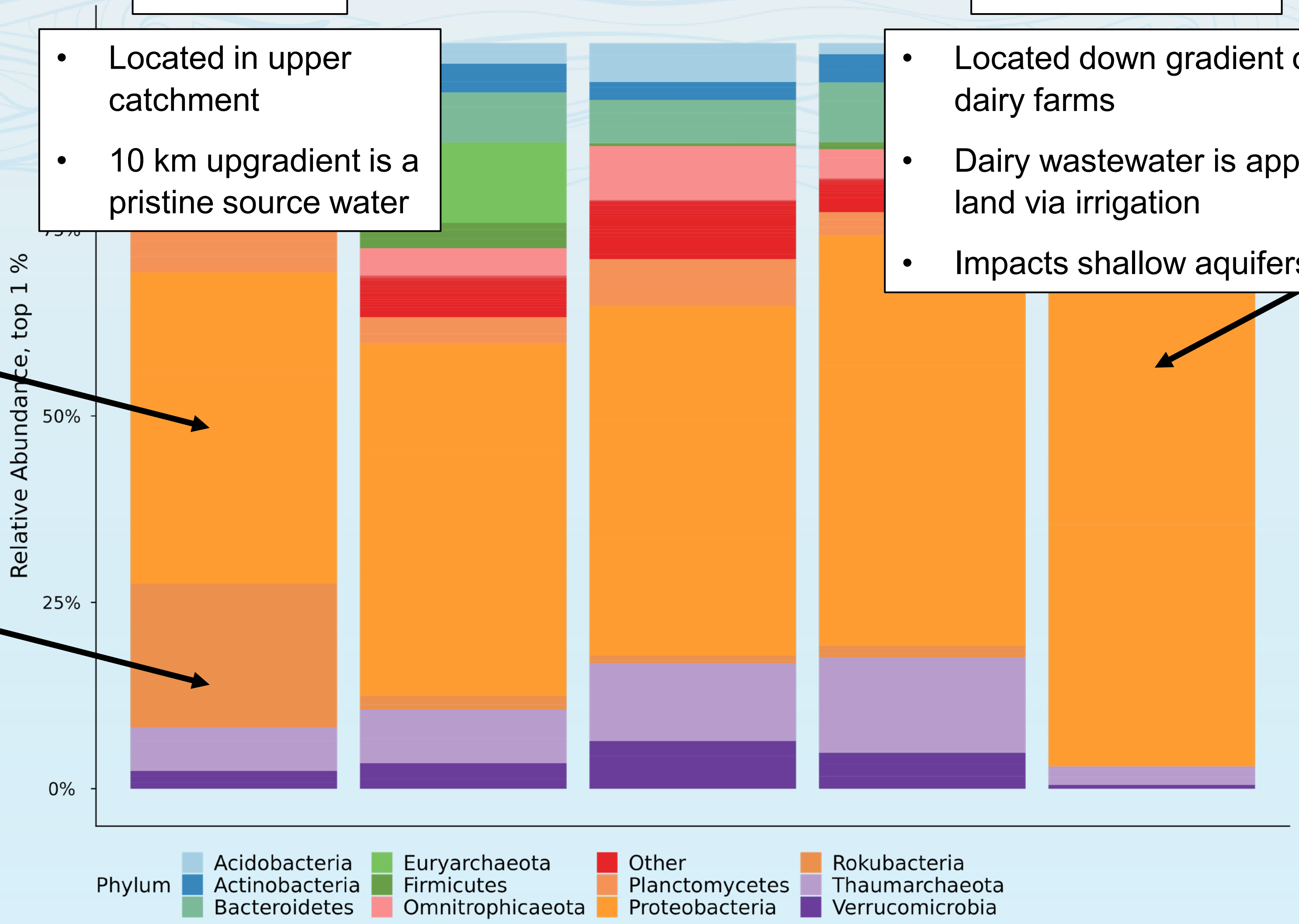
- Located down gradient of three dairy farms
- Dairy wastewater is applied to land via irrigation
- Impacts shallow aquifers

Proteobacteria 95 %

Proteobacteria 42 %

Rokubacteria 19 %

- Large genomes, adapted to survive in low nutrient envts



SOUTHLAND WELLS (EXAMPLE)

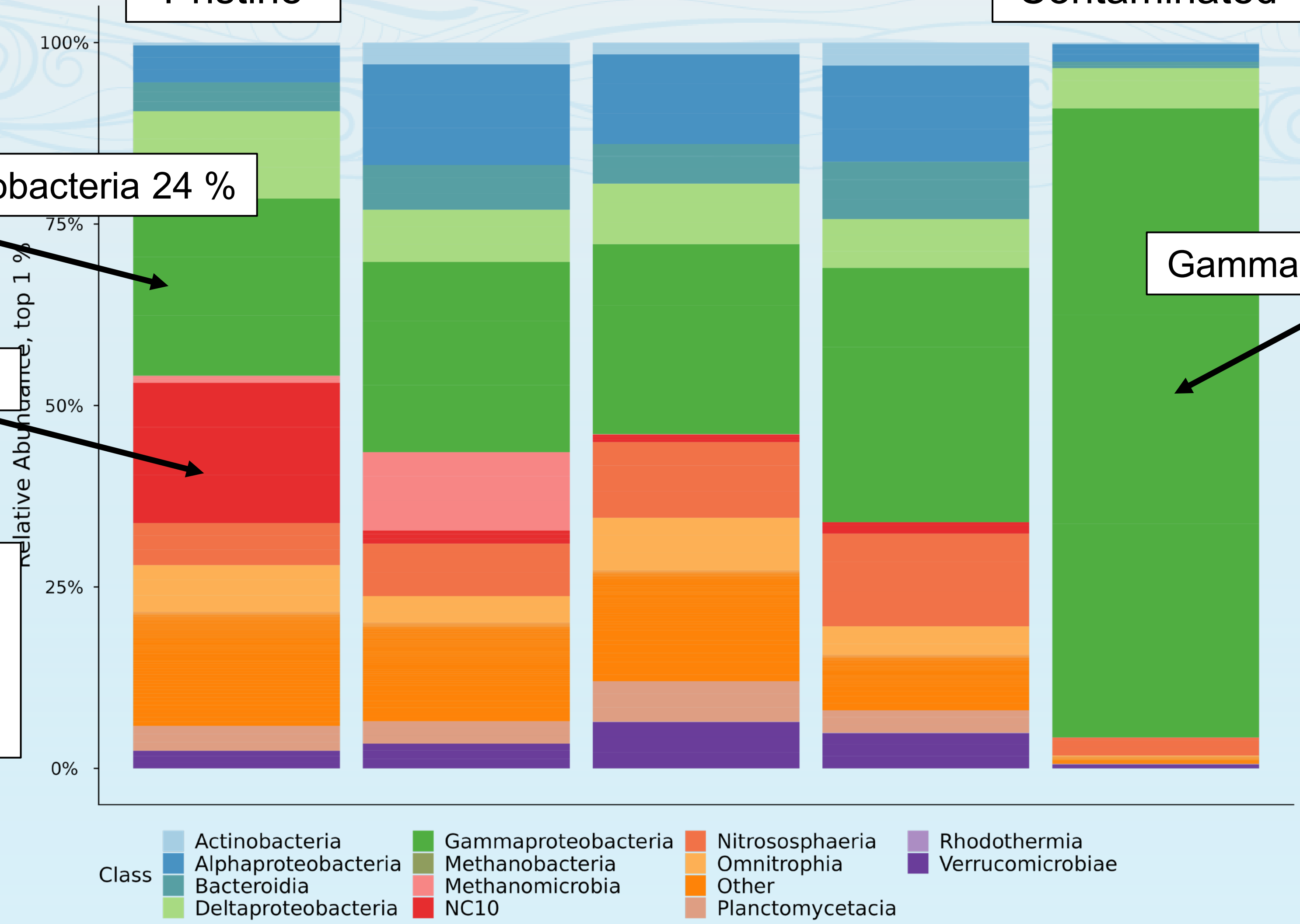
Pristine

Contaminated

Gammaproteobacteria 24 %

NC10 19 %

- Anaerobic oxidation of methane (nitrite dependant)



Gammaproteobacteria 87 %

- ~250 genera
- Involved in organic carbon turnover and nitrogen and sulphur cycling processes

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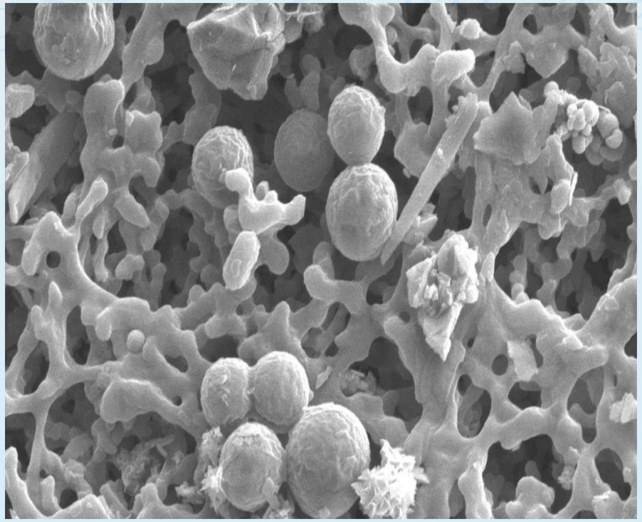
AQUIFER BACTERIA

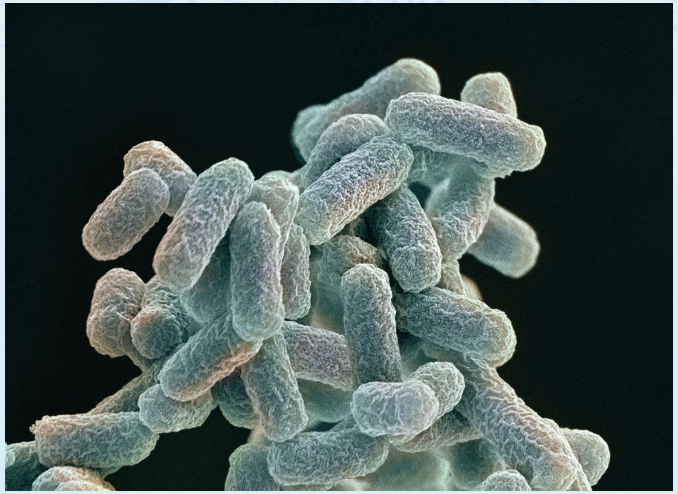
Pseudomonas denitrificans

Aquifer biofilm



https://www.auckland.ac.nz/en/news/2020/04/21/secret-life-of-our-aquifers.html

E. coli (Proteobacteria)



https://pixels.com/ (Steve Gschmeissner)

~2.0 x 0.5 microns

Indicator of faecal contamination

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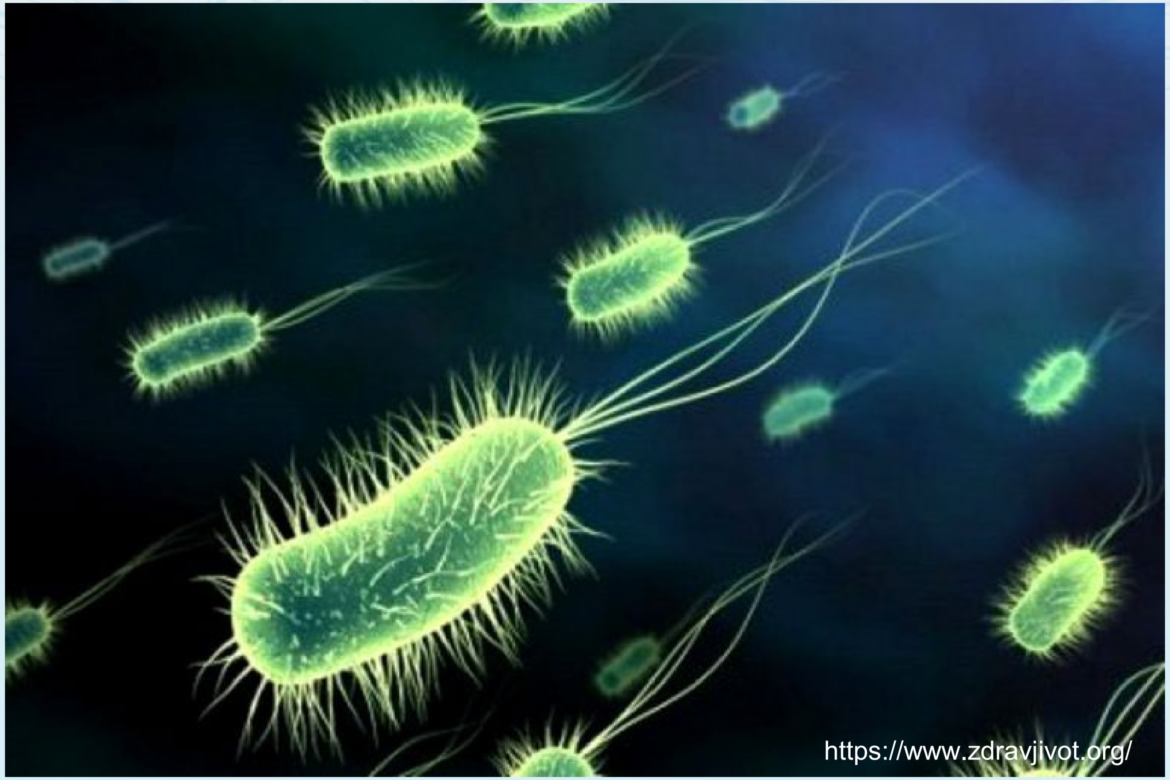
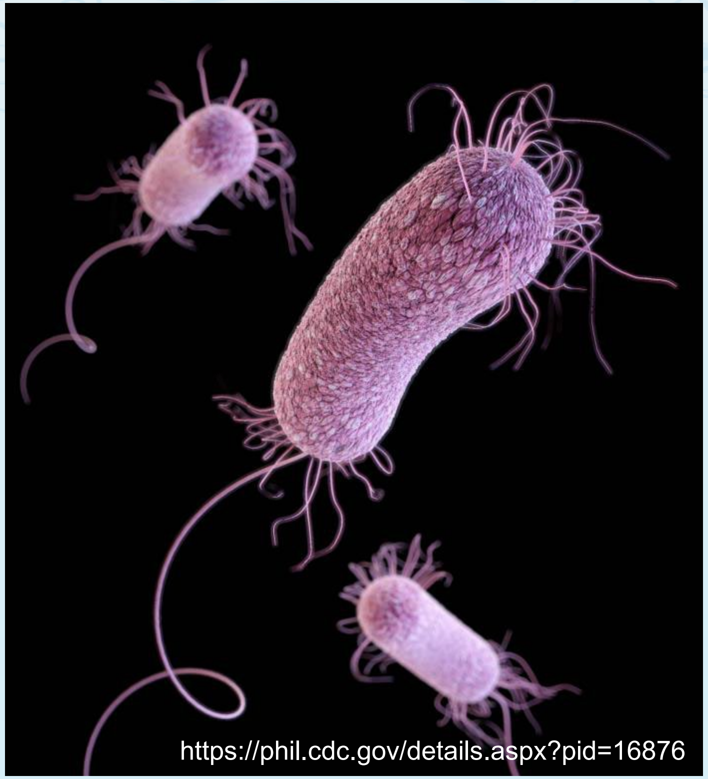
PROTEOBACTERIA

Pseudomonas denitrificans



~ 1.05 x 0.8 microns

Pseudomonas aeruginosa



1.5-3 × 0.5-0.8 microns

Denitrification

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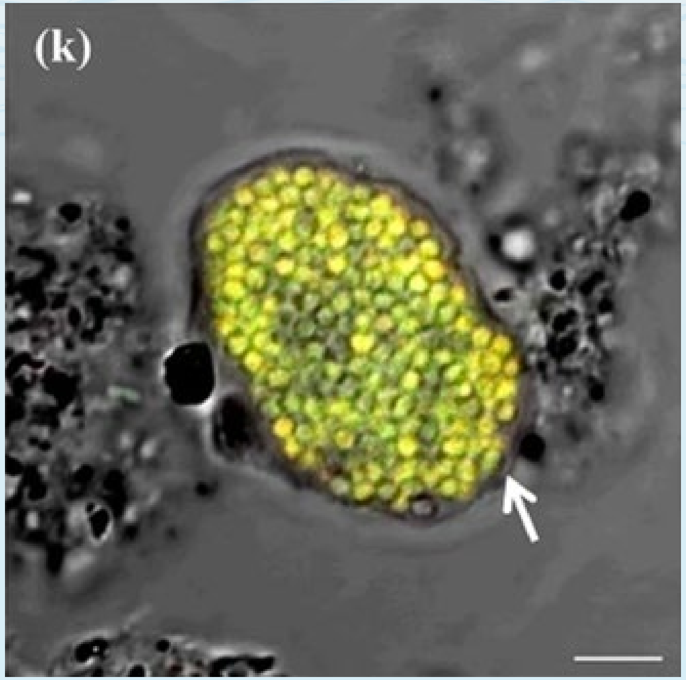
ROKUBACTERIA

NC10



10 - 30 microns, round or oval, honeycomb-shaped microcolonies

Denitrifying methanotroph

HE, Z., CAI, C., WANG, J., XU, X., ZHENG, P., JETTEN, M. S. & HU, B. 2016. A novel denitrifying methanotroph of the NC10 phylum and its microcolony. Scientific reports, 6, 32241.

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ALPHA DIVERSITY - *SOUTHLAND*

Less contamination = more bacterial diversity

Higher contamination = less bacterial diversity

	Shannon Index (spp. diversity)
Pristine	5.6
Contaminated	1.8

	Observed Index (# of spp.)
Pristine	530
Contaminated	55

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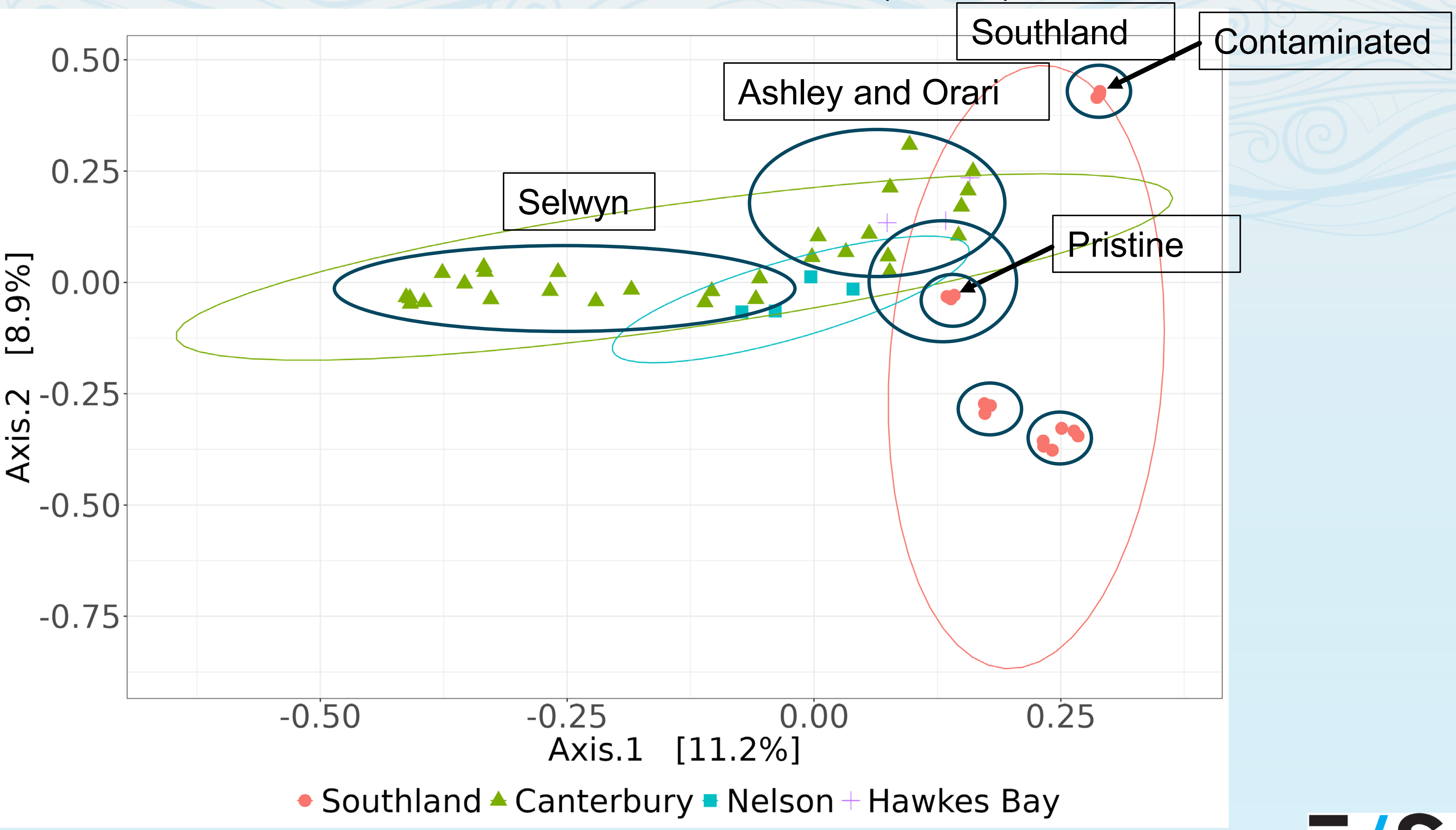
BETA DIVERSITY - PRINCIPAL COORDINATE ANALYSIS (PCOA)



- Axes – show the percent of total variation explained by each axis
- The closer the two sample points are, the more similar their bacterial composition

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DIFFERENCES - *Southland*

- Cooler climate
- Aquifers have a unique geology, being thin, long and shallow with alluvial deposits
- The alluvial deposits - underlain with Gore lignite sedimentary rock
  - Formed from naturally acidic compressed peat
- Average thickness of alluvial deposit ~10 – 15 m
- In contrast: Canterbury Plains
  - Thickness of alluvial gravel commonly exceeds 100 m

DIFFERENCES - *Southland*

Parameter	Unit	Southland	Other regions (range)
*pH		5.8	6.6 - 7.0
*Temperature	^{o}C	10.4	13.1 - 13.9
DOC	mg/L	0.6	1.7 - 2.2
DO	mg/L	6.3	1.4 - 5.7
Specific conductance	uS/cm	340	149 - 175
Nitrate	mg/L	5.5	1.1 - 2.5
Total nitrogen	mg/L	5.7	1.1 - 2.6

* p-value < 0.002

Median

Lower

Higher

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CORRELATIONS

- Significant positive correlations were found between several bacterial spp. and pH
- Moderate correlations were found between bacterial spp. and total nitrogen, organic reactive phosphorus and nitrate

MACHINE LEARNING – RANDOM FOREST

- Used a small subset of groundwater data
- Assessed bacterial abund. and nitrate classification using Random Forest

NZ Drinking Water Std	Nitrate-N (mg/L)	Category
WHO MAV	0 – 1	Pristine
	1 – 11.3	Below MAV
	< 11.3	Above MAV

Correctly predicted: **90 %** of nitrate classifications using Rel. Abund. of Thaumarecaeota and Prote

CONCLUSIONS

Q. Can differences in bacterial communities be used to help predict changes in water quality

- Contaminated wells had more Proteobacteria than pristine wells and less bacterial diversity
- Correlations were identified between bacteria and pH, total nitrogen, organic reactive phosphorus and nitrate
- Random Forest: correctly predicted 90 % of nitrate classifications using abundances of Thaumarecaeota and Proteobacteria

CONCLUSIONS

Q. Does the composition of a bacterial community change depending on the well geology (location)

- The Southland region had a different geology and a different bacterial composition (community) compared to the other regions

OVERALL CONCLUSION:

- While differences in the bacterial community were not apparent from abundance data (at level of phyla or genera)
  - Diversity data indicated differences in bacterial composition based on geology
  - Correlation and machine learning pipelines showed links between bacterial taxa and groundwater parameters, including nitrate

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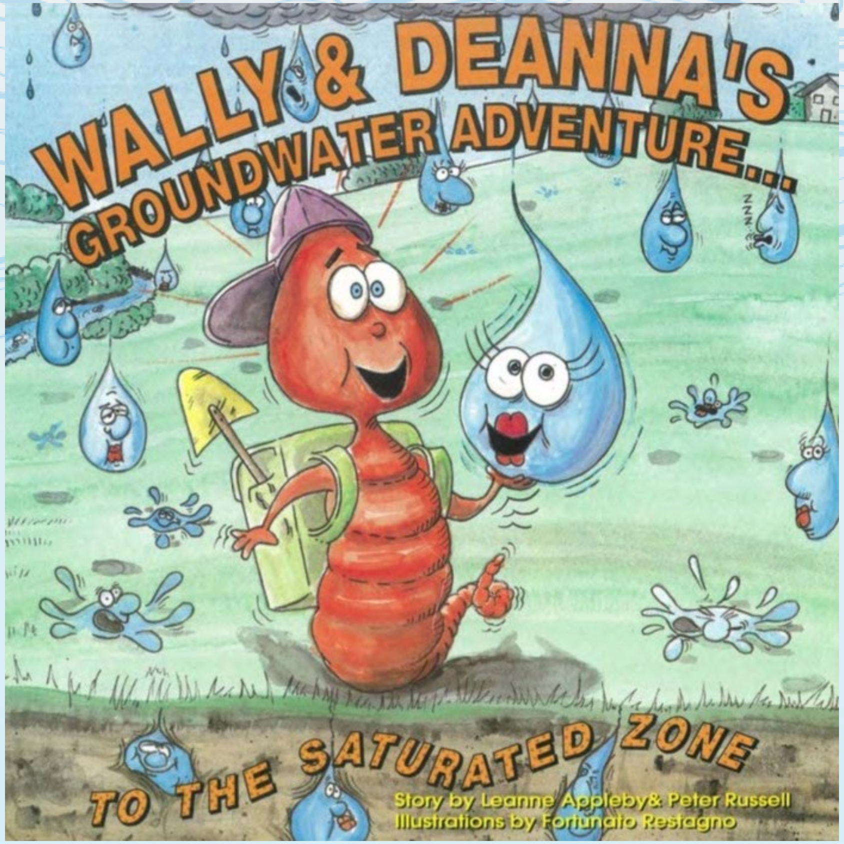
ACKNOWLEDGEMENTS

- Funding: ESR SSIF funding

- Thanks for listening!



https://gw-project.org/groundwater-education-for-children/