

# Biodegradation and bioremediation in wastewater treatment systems

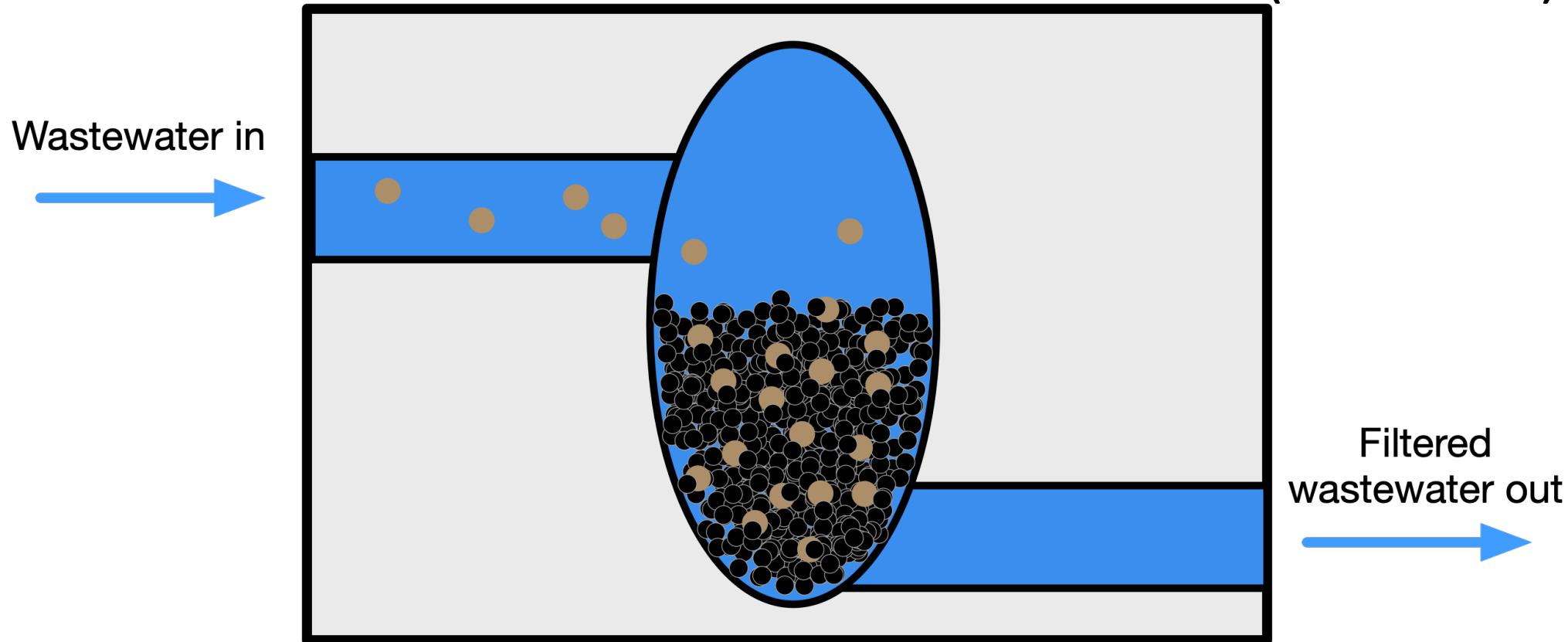
Greg Gloor

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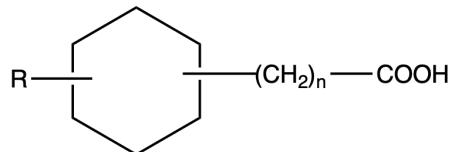
[github.com/gglloor/compositions/presentations](https://github.com/gglloor/compositions/presentations)

# Problem: Activated charcoal filters (Suncor)

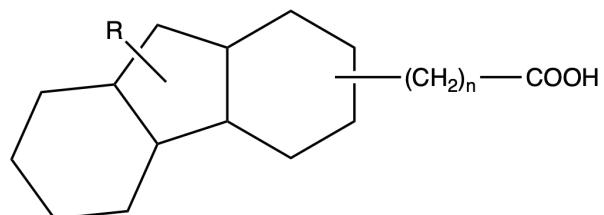
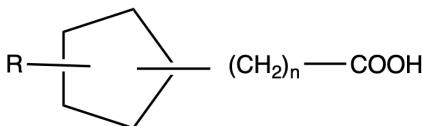


- Napthenic acids
- Activated charcoal granules

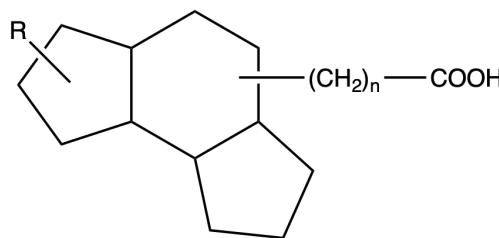
# Naphthenic acids



$Z = -2$



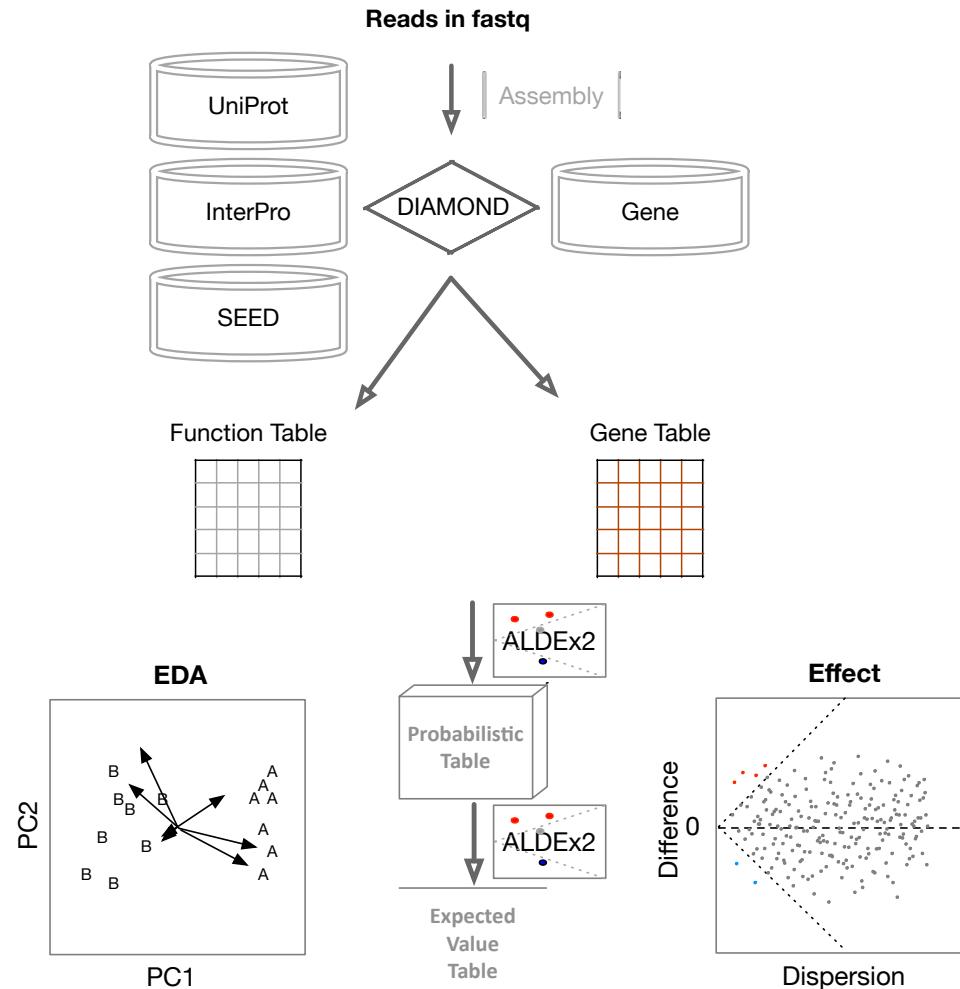
$Z = -6$



Naphthenic acids

- Significant environmental toxin
- 1 billion m<sup>3</sup> naphthenic acid-containing wastewater annually
- Known that bacteria biodegrade naphthenic acids over time when concentrated

# Functionalizing meta-seq 'omes

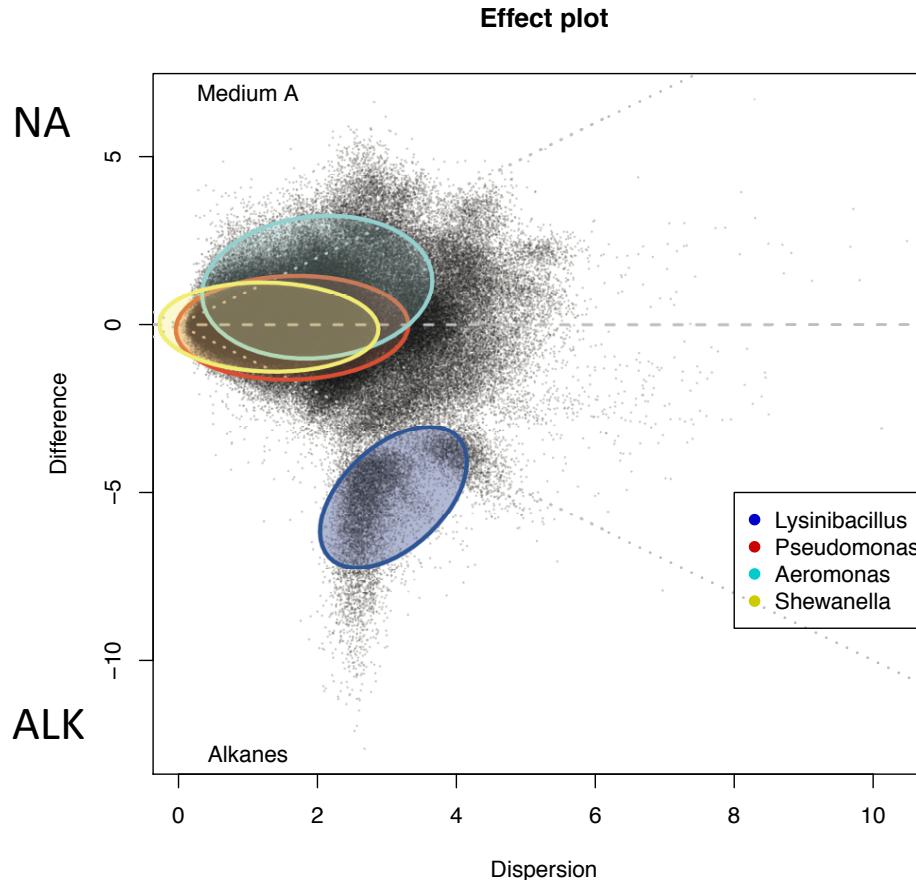


A sequence is a sequence  
is a sequence until it is  
annotated

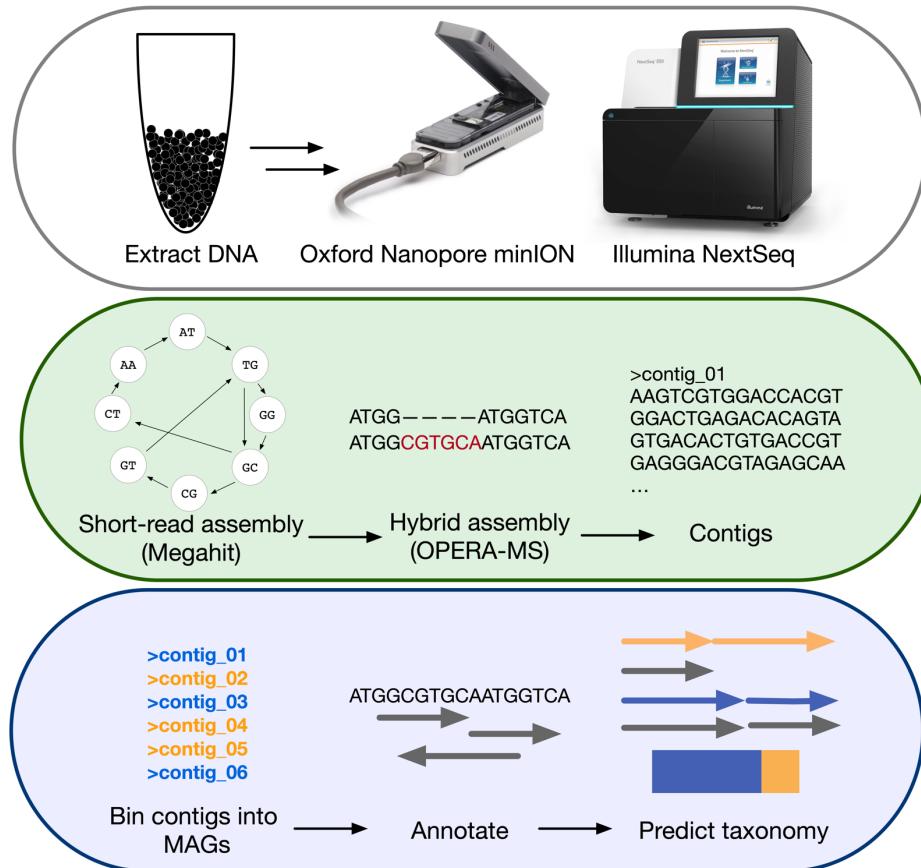
**Fernandes et al. 2014.** Unifying the analysis of high-throughput sequencing datasets: characterizing {RNA}-seq, 16{S} r{RNA} gene sequencing and selective growth experiments by compositional data analysis. **Microbiome**  
**Gloor et al. 2017.** Microbiome Datasets Are Compositional: And This Is Not Optional. **Frontiers in Microbiology**  
**Macklaim & Gloor 2018.** From RNA-seq to Biological Inference: Using Compositional Data Analysis in Meta-Transcriptomics. **Meth. Mol. Bio.**  
**Gloor, Macklaim, Fernandes, 2016.** Displaying Variation in Large Datasets: Plotting a Visual Summary of Effect Sizes. **J. of Comp. and Graph. Statistics**

# Meta-transcriptome of refinery aeration basin

- grown in two carbon sources
- Each point is a gene (>250k)
- Y-axis is difference between groups
- X-axis is dispersion within group
- *Lysinibacillus* prefers alkanes



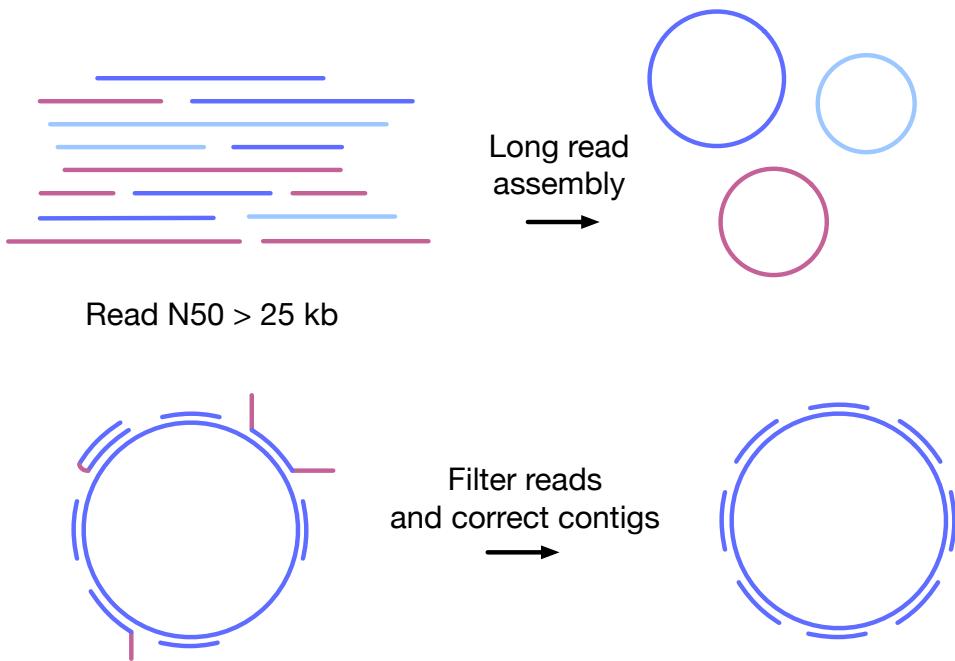
# What are we missing?



- Less than 10% of the reads map to known bacterial species
- Need to identify who is there before asking what they are doing
- MAGs are best way to do this
- MAGs from short reads only are incomplete and artificial

# Protocol: MAGs that rival single isolate QC!

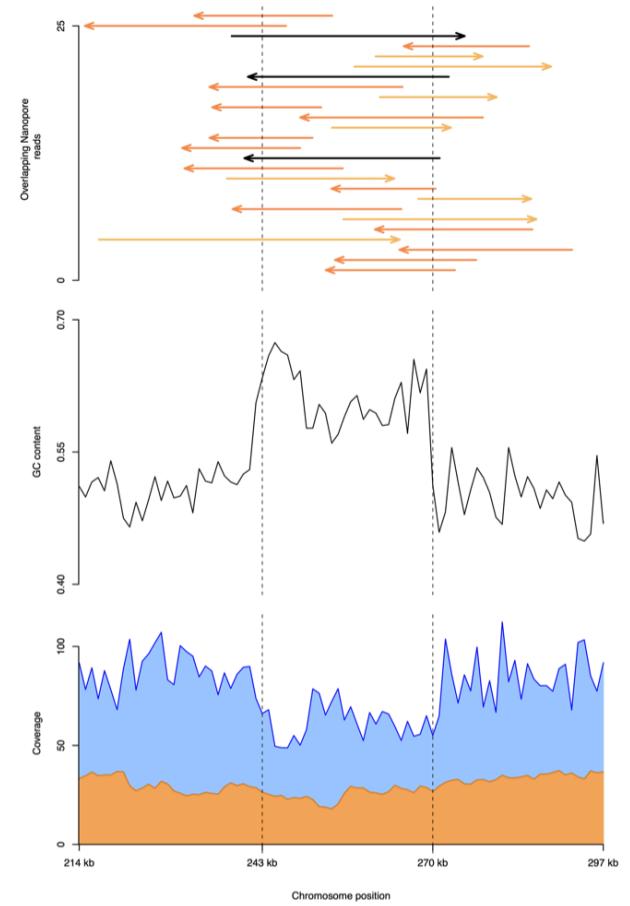
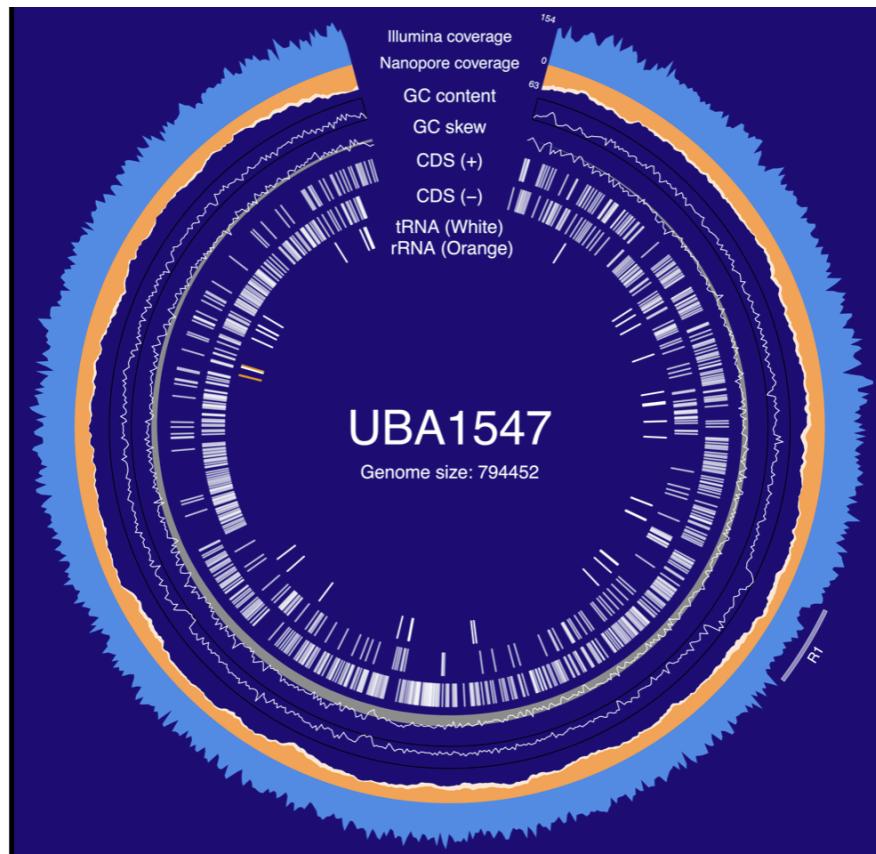
1. High molecular weight DNA extraction
2. Oxford Nanopore minION and Illumina NextSeq



- 13 MAGs representing more than 60% of total DNA sequenced<sup>2</sup>

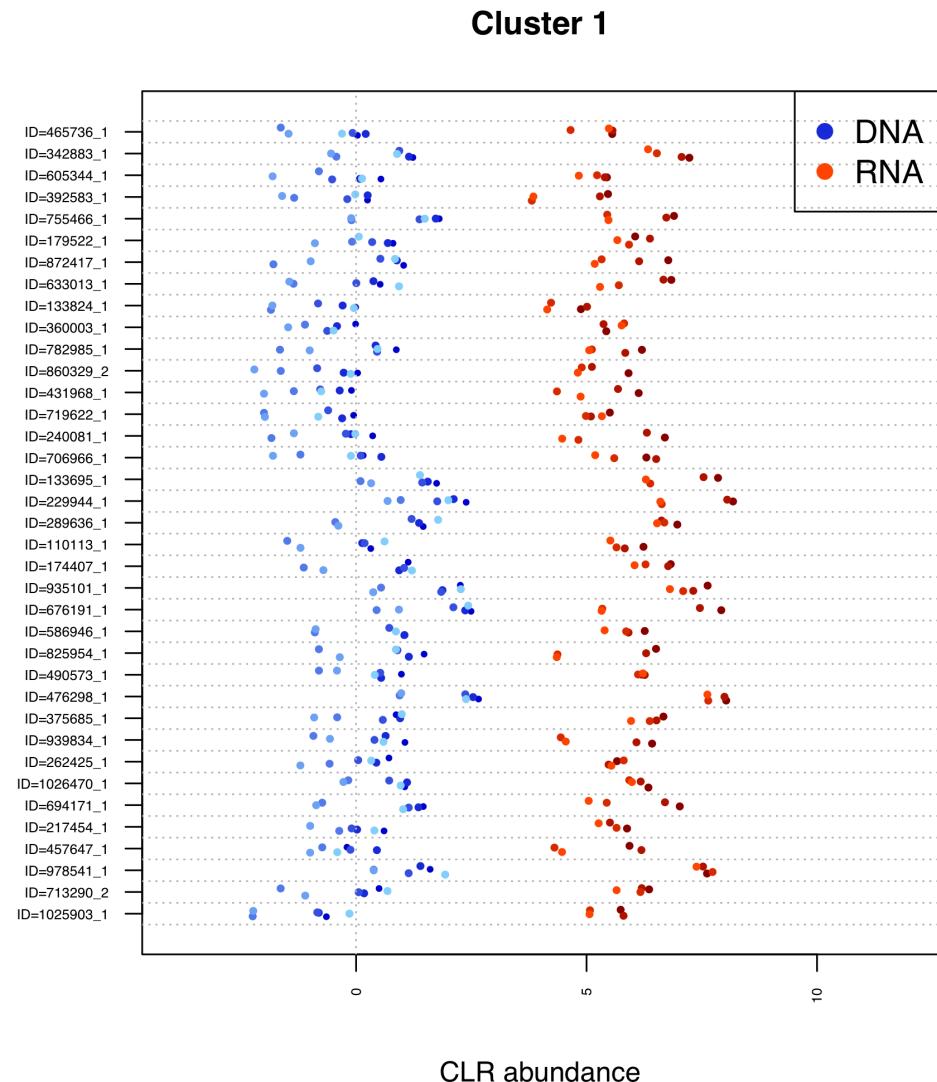
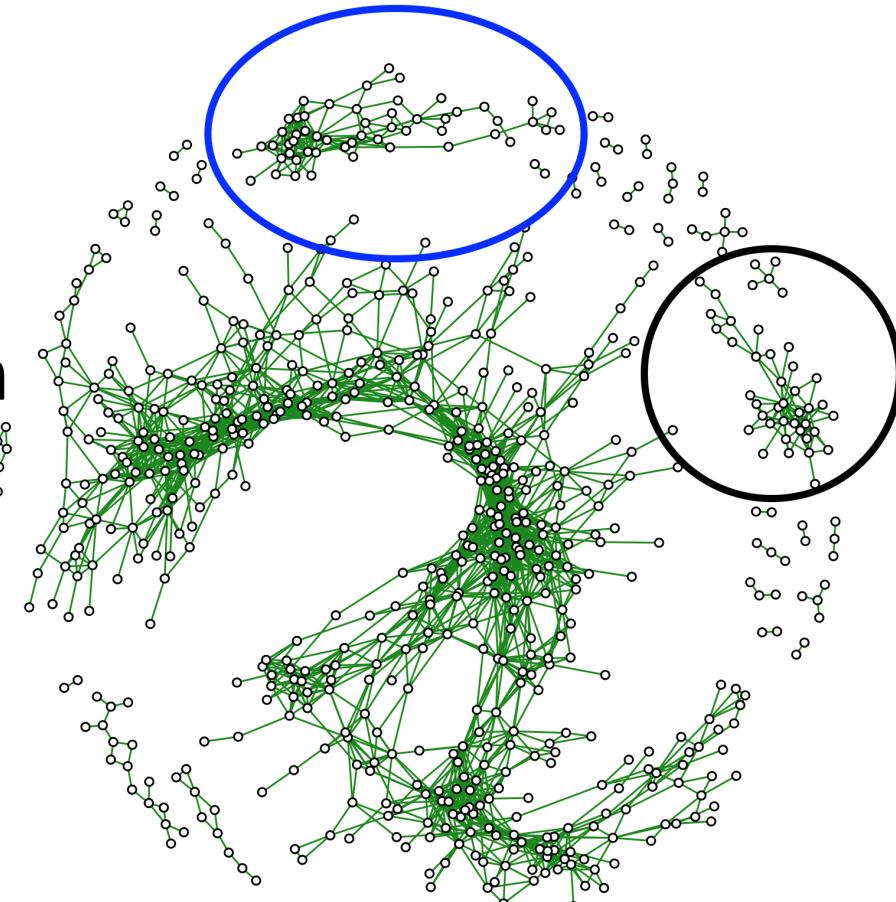
Length	%GC	%C	%R	Illumina coverage	Nanopore coverage	rRNA genes	tRNA genes	Predicted taxonomy
3.14	62.8	98.59	0.00	392	193	2	48	Parvibaculum
4.47	64.4	100.00	2.82	402	94	2	49	Rhizobiaceae
3.73	63.9	100.00	0.00	68	32	2	46	Unknown
3.84	63.5	98.59	1.41	184	67	4	45	Blastomonas
3.74	72.4	100.00	0.00	121	39	4	63	UBA2363
5.16	42.6	98.59	0.00	180	97	6	40	Algoriphagus
3.98	66.9	100.00	1.41	41	16	4	51	Tabrizicola
3.96	71.9	98.59	2.82	125	57	2	53	UBA4742
4.68	66.1	100.00	2.82	57	17	4	52	Rhodobacteraceae
5.79	66.3	100.00	2.82	35	14	4	55	Aquimonas
0.79	51.0	85.92	4.23	88	36	2	40	UBA1547
3.06	65.9	100.00	0.00	1107	355	2	48	Brevundimonas
2.88	64.4	100.00	0.00	94	35	2	44	Oceanicaulis

# UBA1547 – genome plasticity



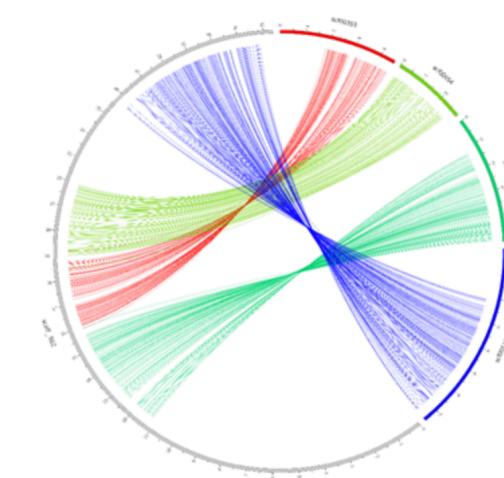
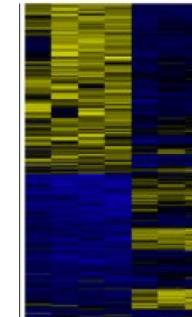
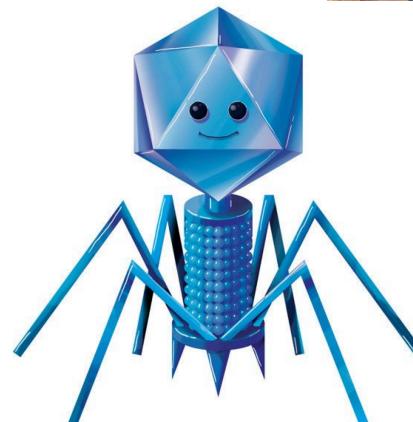
# How does this help?

ORFs associated  
with hydrocarbon  
degrading genes  
circled in blue  
and black



# Next steps?

- Full catalogue of genes/genomes
- Syntenic regions / operons
- Plasmids and phage
- Meta-transcriptome of NA enriched cultures
- Synthetic communities for remediation



# Acknowledgements

<https://github.com/dgiguere/complete-and-validated-genomes-from-a-metagenome>

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Github: dgiguere

