Complete and validated genomes from metagenomes

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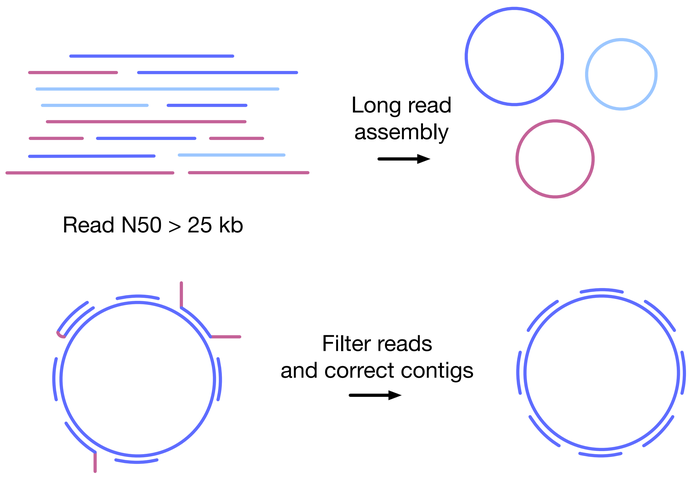
Introduction

- Investigating how an algal-bacterial community **degrades 1-adamantanecarboxylic acid**[1]
- Metagenome assembly typically results in fragmented, **incomplete assemblies**
- **Long read technology** enables resolving repetitive regions
- Complete genome quality is not achieved for most metagenomic-assembled genomes (MAGs)

Methods

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

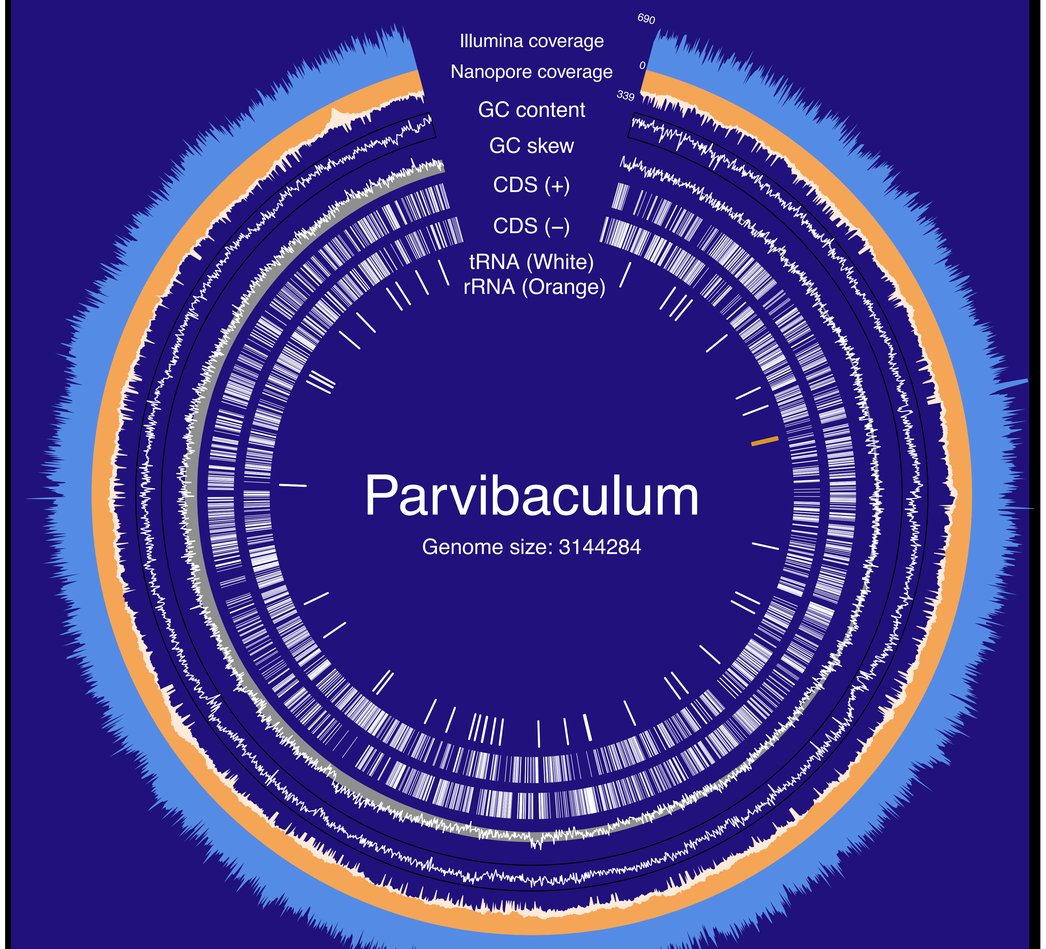


Results

- **13 MAGs** representing more than 60% of total DNA sequenced[2]

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

We **generated complete genomes** directly from **bacterial communities**



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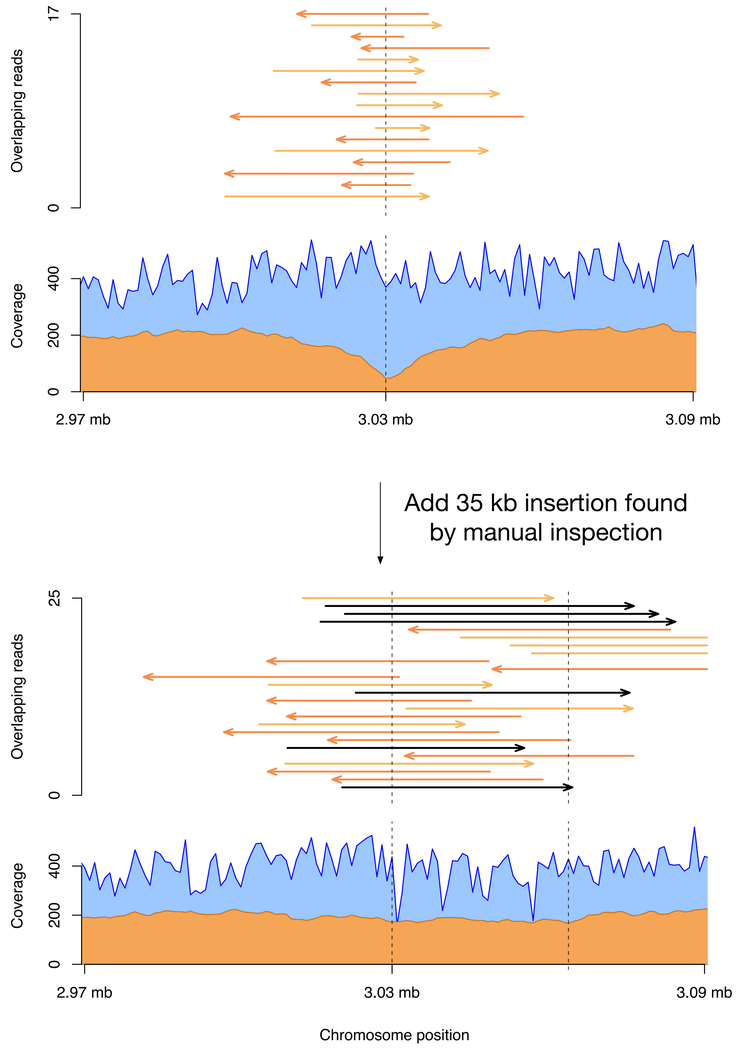
Discussion

- **Species level variants** with possible mobile genetic elements within a single species can be detected



- Genomes from **majority of population** recovered
- **10 of 13 MAGs** appear to be complete genomes
- Illumina-only assembly would result in fragmented assembly due to duplicated regions, variable GC content and coverage. **Ultra-long reads can help resolve genomes from metagenomes.**

Future work

- What pathways are present that contribute to 1-adamantanecarboxylic acid degradation?
- Can we identify functional mobile genetic elements?
- Can we apply this method to more diverse communities?

References

[1]Paulssen JM, Gieg LM. Biodegradation of 1-adamantanecarboxylic acid by algal-bacterial microbial communities derived from oil sands tailings ponds. Algal Research, 2019.
[2]Giguere DJ, et al. Complete and validated genomes from a metagenome. bioRxiv, 2020.

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