Looking through **all** the genomic data ever published: the Logan project

Roland Faure[1], Anton Nekrutenko[2], Kelsey Beavers[3], Wei Shen[4], Rayan Chikhi[1]

[1]Institut Pasteur [2]Pennsylvania State University [3]Texas Advanced Computing Center [4]Chongqing Medical University

EAGS, February 2026

Slides available (CC-BY) at: `rolandfaure.github.io`

POV: you have a favorite sequence

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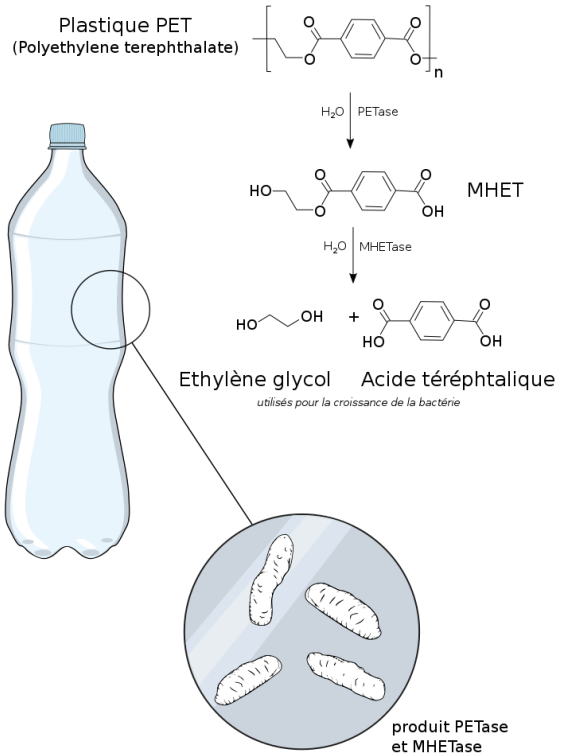

- Wow, a PETase!!

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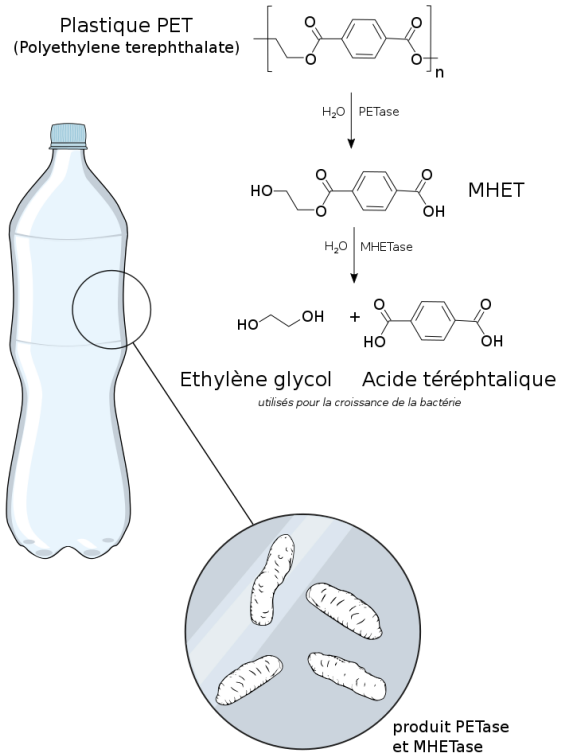
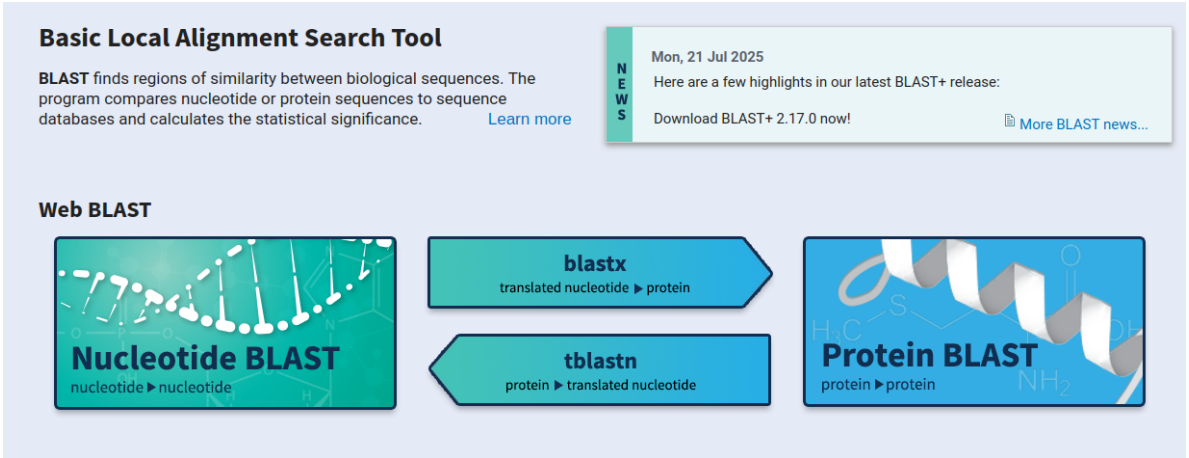


- Wow, a PETase!!
- Has this already been described?
- Is it found somewhere else? Where?
- I want to find other PETases!

Let's BLAST the PETase



select all 50 sequences selected — GenBank | Graphics | Distance tree of results | MSA Viewer

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Vibrio gazogenes strain ATCC 43942 chromosome 1, complete sequence	Vibrio gazogenes	1618	1618	100%	0.0	100.00%	3471064	CP018835.1
Vibrio gazogenes strain PB1 chromosome 1, complete sequence	Vibrio gazogenes	1416	1416	100%	0.0	94.98%	3516273	CP092587.1
Vibrio gazogenes strain DSM 21264 chromosome 1, complete sequence	Vibrio gazogenes	1416	1416	100%	0.0	94.98%	3516262	CP151640.1
Vibrio gazogenes ATCC 29988 DNA, chromosome 1, complete sequence	Vibrio gazogenes	1416	1416	100%	0.0	94.98%	3516247	AP024873.1
Vibrio spartinae CECT 9026 DNA, chromosome 1, complete sequence	Vibrio spartinae	1321	1321	100%	0.0	92.64%	4003627	AP024907.1
Vibrio spartinae strain 3.6 chromosome 1, complete sequence	Vibrio spartinae	1321	1321	100%	0.0	92.64%	3817659	CP046268.1

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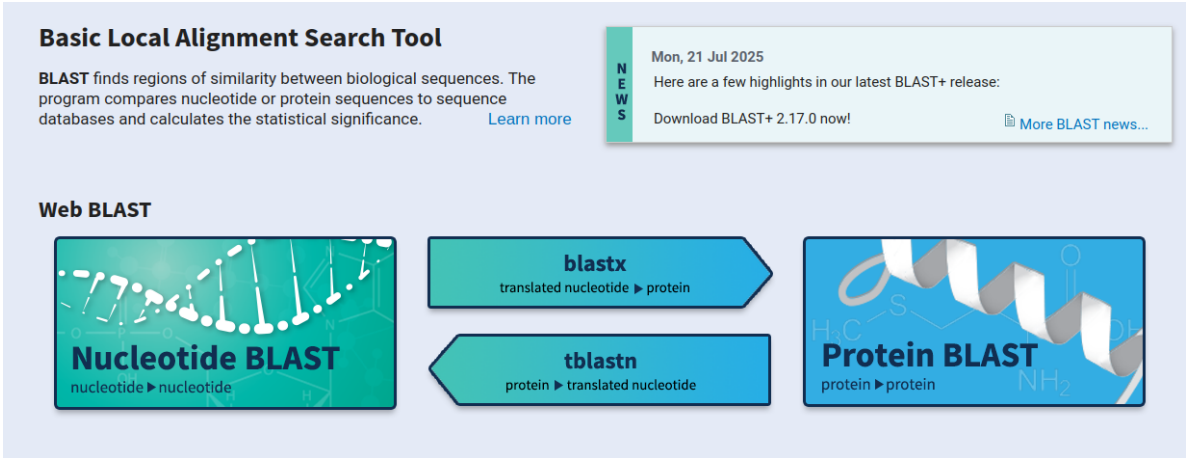

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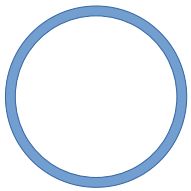
- Found 50 hits from a few different species

What is indexed in BLAST exactly?

In BLAST nr/nt



Well-assembled genomes

Non-redundant

NOT in BLAST nr/nt

Random pieces of sequenced genomes

Every version of every sequence

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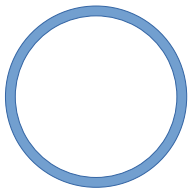
In BLAST nr/nt



Well-assembled genomes

Non-redundant

0.1%

NOT in BLAST nr/nt

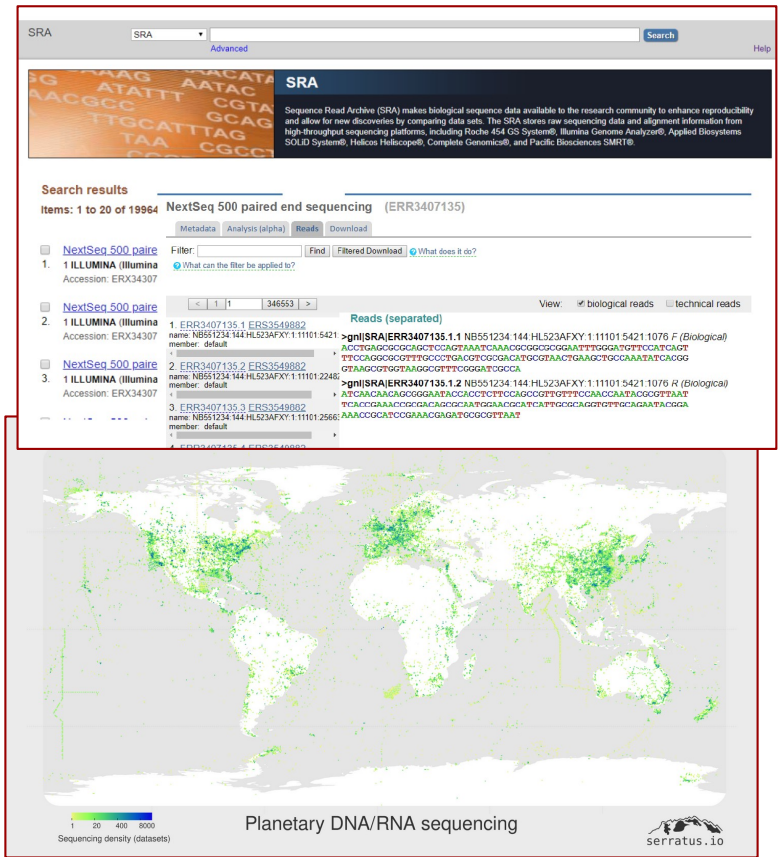
Random pieces of sequenced genomes

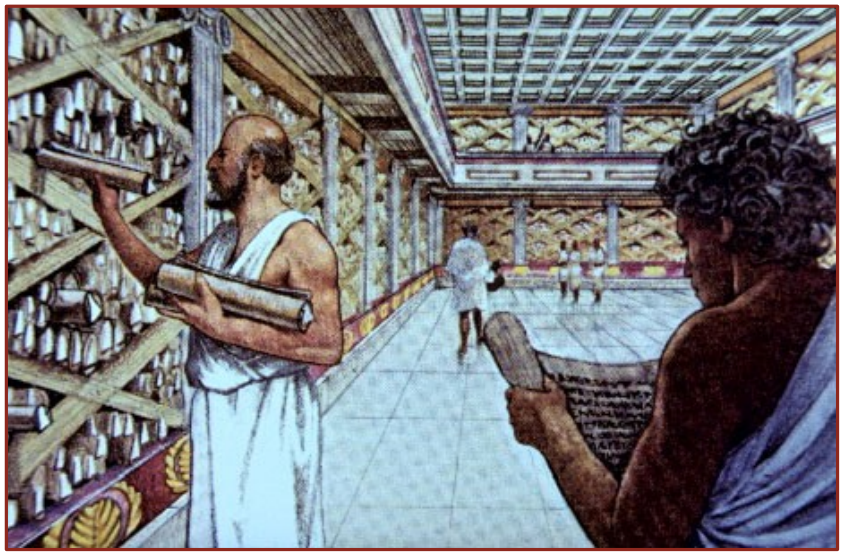
Every version of every sequence

99.9%

The biggest database: **the SRA**

SRA: All public sequencing reads, 80 PB of data





"Library of Alexandria" for genetics

Slide Credits: Rayan Chikhi

Let's BLAST against *everything*

- Let's align our sequence against all the reads of the SRA

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A thousand years later...

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A thousand years later...

- Doing this is the primary goal of the **Logan project**

The Logan project: step 1

27 millions accessions, **50PB**

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For all accessions

Raw reads → Contigs/Unitigs

```
ACAGCAGT
CAGTCGTA
CGTATAA
```

→

```
ACAGCAGT
   CAGTCGTA
      CGTATAA
```

→

```
ACAGCAGTCGTATAA
```

Logan

27 millions accessions, **~1PB**

https://github.com/IndexThePlanet/Logan

Let's BLAST against *everything* - second try

- Let's align our sequence against all the ~~reads of the SRA~~ contigs of Logan

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- Doable!

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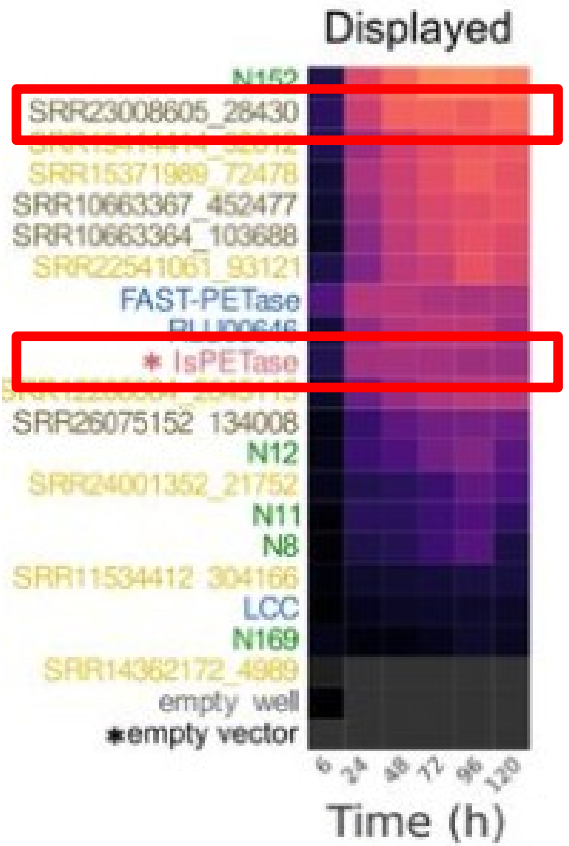
- Let's align our sequence against all the ~~reads of the SRA~~ contigs of Logan
- Doable! *If you have 10 000$*

Finding new PETase in the SRA



PETase from SRR23008605 degrades plastic faster than previously known PETase!!

Logan: Planetary-Scale Genome Assembly Surveys Life's Diversity, Chikhi et al., 2025

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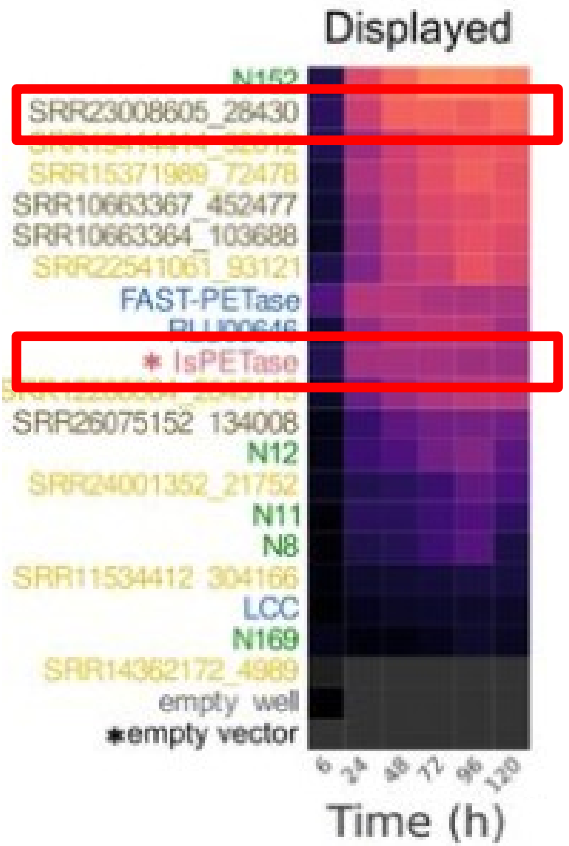

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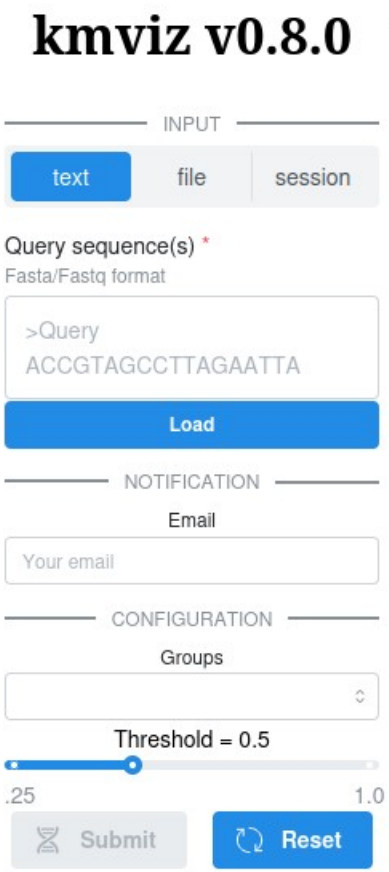
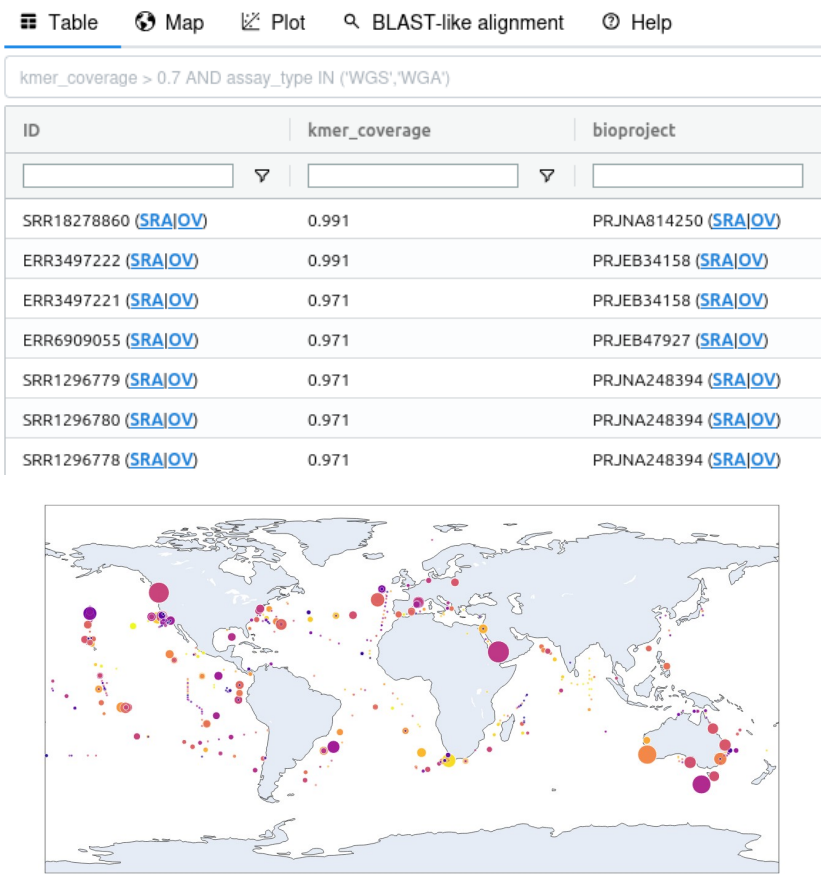
- Let's try to browse for cheaper, shall we?

Browsing Logan: strategy 1 - **Logan-search.org**



5 minutes later



Let's BLAST against *everything* - third try

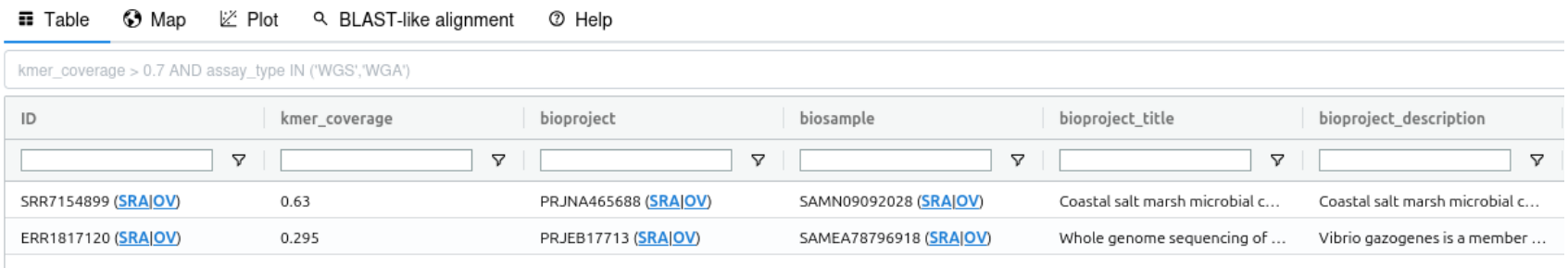


Table Map Plot BLAST-like alignment Help

kmer_coverage > 0.7 AND assay_type IN ('WGS','WGA')

ID	kmer_coverage	bioproject	biosample	bioproject_title	bioproject_description
SRR7154899 (SRA|OV)	0.63	PRJNA465688 (SRA|OV)	SAMN09092028 (SRA|OV)	Coastal salt marsh microbial c...	Coastal salt marsh microbial c...
ERR1817120 (SRA|OV)	0.295	PRJEB17713 (SRA|OV)	SAMEA78796918 (SRA|OV)	Whole genome sequencing of ...	Vibrio gazogenes is a member ...

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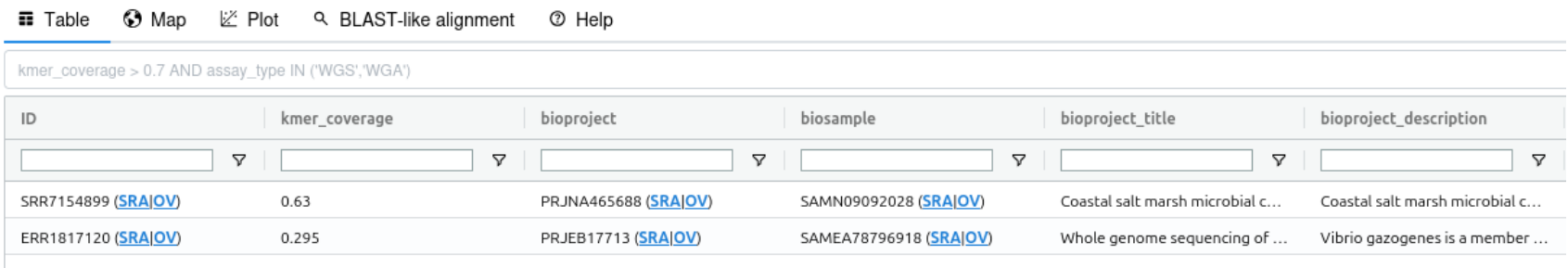
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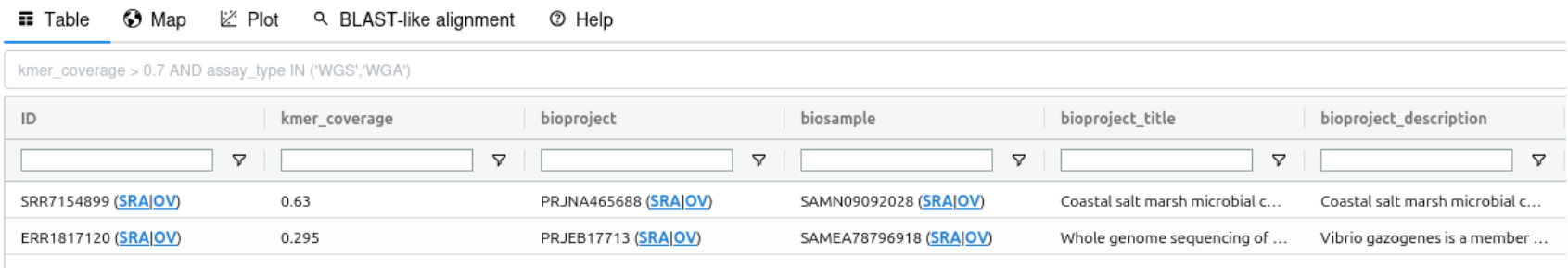
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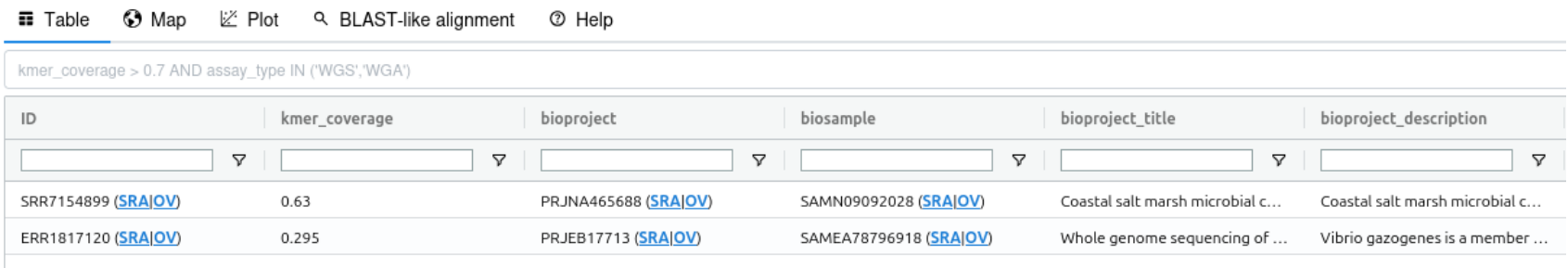
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- *Logan: Planetary-Scale Genome Assembly Surveys Life's Diversity* - biorXiv

Browsing Logan: strategy 2 - **LexicMap**

Article | Open access | Published: 10 September 2025

Efficient sequence alignment against millions of prokaryotic genomes with LexicMap

Wei Shen ✉, John A. Lees & Zamin Iqbal ✉

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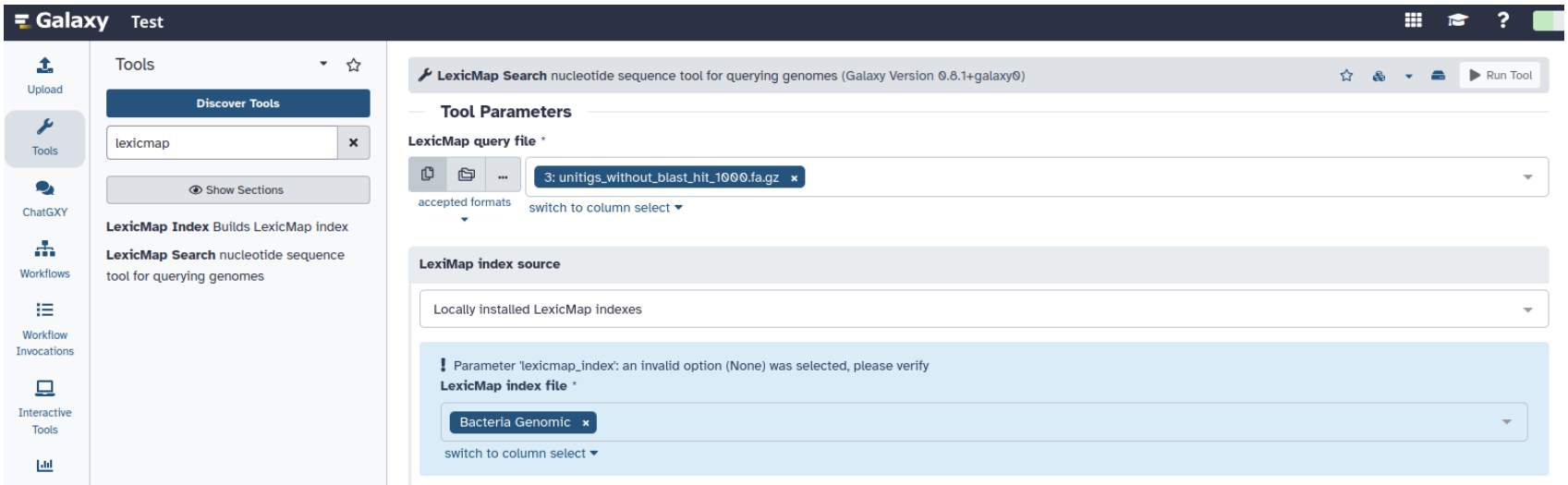

- Few hours of computation to return results
- Soon available on Galaxy (`usegalaxy.org`)

Let's BLAST against *everything* - fourth try

- 200 results
- Detects sequences with $\geq$ 70% similarity

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- 200 results
- Detects sequences with $\geq$ 70% similarity
- PETase found e.g. in "Fermented Xuecai"

Source: chillcrispbyxueci.substack.com

Limits of LexicMap

- Relatively slow
- Still less sensitive than BLAST or DIAMOND...

Browsing Logan: strategy 3 - **protein search**

- Let's focus only on the proteins (100x smaller)

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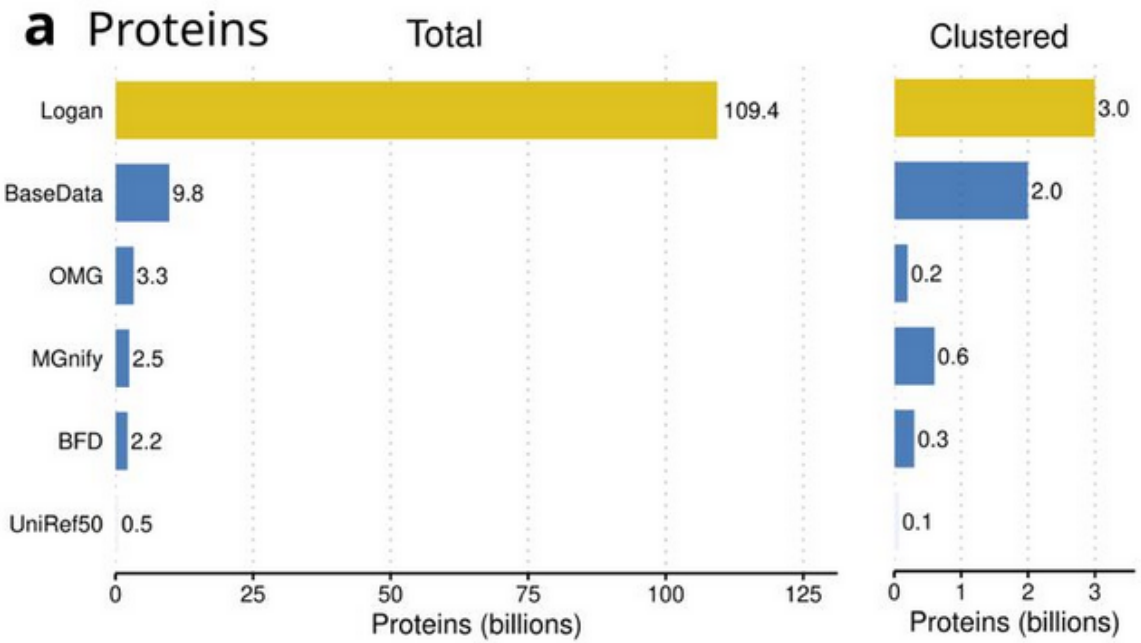
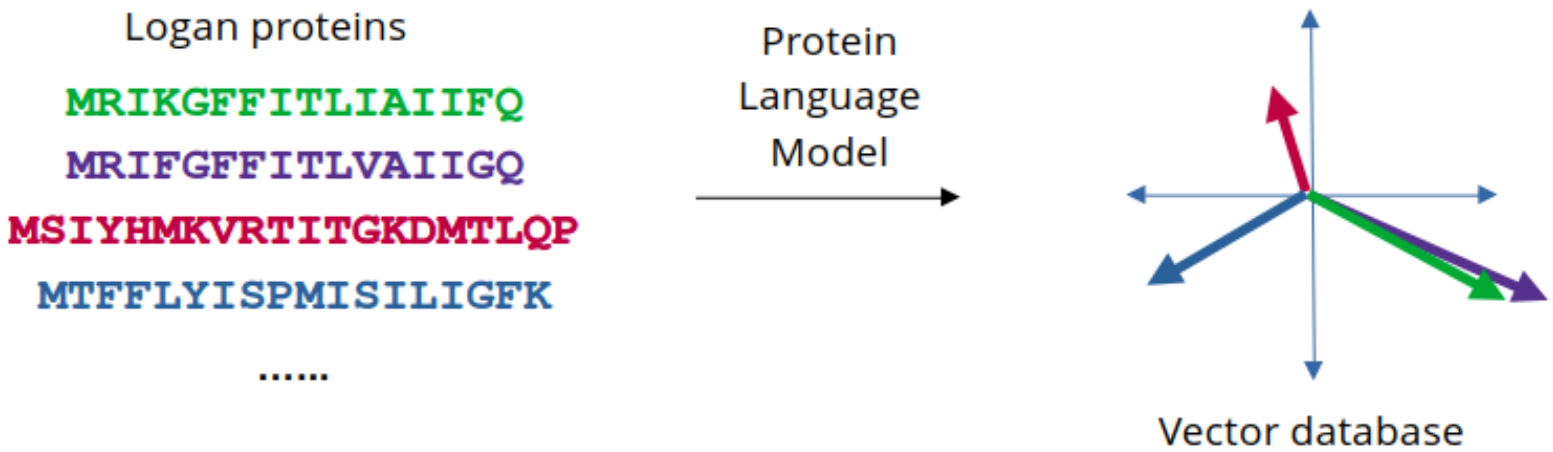
- Let's focus only on the proteins (100x smaller)
- Detect proteins of Logan with Prodigal
- 100 billion proteins clustered in 3 billion clusters (accessible online)



Browsing Logan: strategy 3 - **protein search**

- With Protein Language Models, proteins can be transformed in vectors
- We can build a search engine on vectors (just like Google)



Let's look for the PETase

- One hour computation
- 300k results!
- Down to 20% amino-acid identity!

```
Query_10001  150  YHQIDEKEIGIVGYSQGGAGAYNTLEGKDGDK---FKTM-VTVSG---    ------VTESIGEKLHLPVWIYDPSKVTI  213
Query_10002  98   QPEVDANRVALIGWALGGGVVVAEAADDQRVK--AVVTCNAIGDGERS[5]DEQswsRLQD-DMVRDRPERARSGRSRTV  176
Query_10003  95   EK-TGNPRVGVVGYCAGGGLALMLAAQRP-----------DAVKAVA   PYY---------GLIPWPGAQPDWAAIDA  149
Query_10004  130  SAFVDPERIGVIGFSHGGWTLLDFLGGPPAIHasATATDARDGLRSVV   AVYpycGADVQAGLGKWP--------ADV  198
Query_10005  151  YQKVDTEHIGISGHSQGGVGVFNAISEQPHSN---LYTCAVSLSP---    ------TQQDLAEALKIP---YDPTKTQI  212
Query_10006  99   DP-RCTGKVGIVGFCMGGGFTLLLAPRG-------------IFDAAA   PNY---------GVLP---RDLSALSSSC  148
Query_10007  99   LEFVDPDRIGVLGVCAGGGYSVNAAMTEHRIKavGTVVGANIG-----[4]ENNpiqTLEAIGKQRTAEANGAEPMIINW  174
Query_10008  136  GKFILSNKIAVIGHSMGGYTALALAGGIPWTQeaERVETSSDARVKAI    ----------VLMAPGAGWFMNSLSKVTI  202
```

Soon available on Galaxy

- Soon on Galaxy (usegalaxy.org)

- Maybe also distributed and installable?? (a few TB of data)

Limits of this index

- Only full proteins

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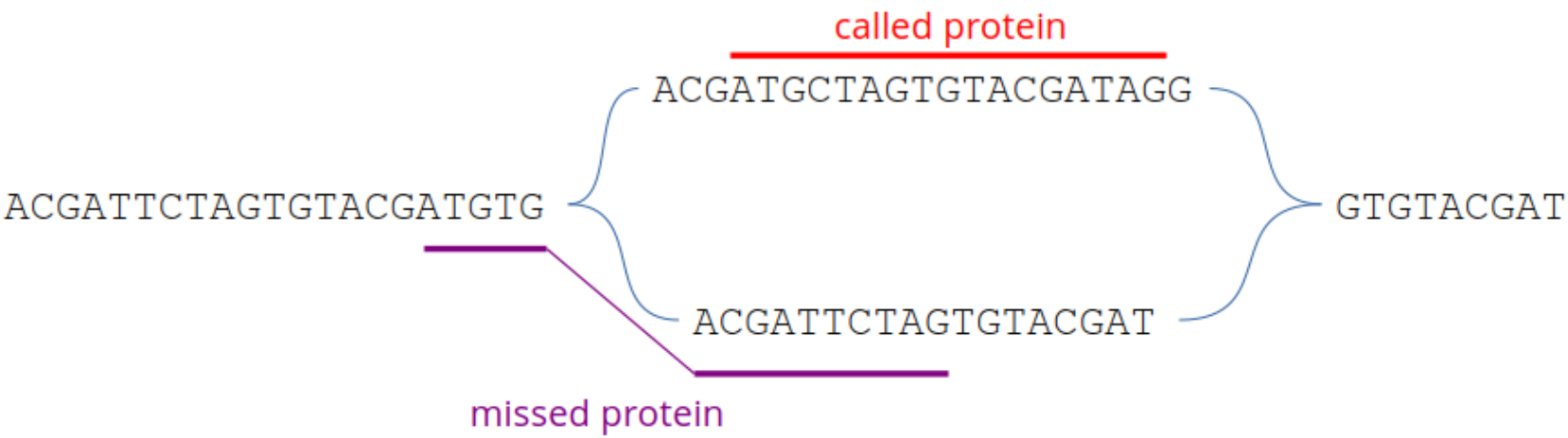
- 90% proteins missing in the database because of the protein calling



Take-home messages

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- Upcoming: more sensitive searches, online on Galaxy
- We are looking for applications, contact us!

Acknowledgments

- Rayan Chikhi
- Logan team: Téo Lemane, Pierre Peterlongo, Artem Babaian & others
- Galaxy team: Anton Nekrutenko, Björn Grüning, Patrik Smeds, Nate Coraor
- TACC team: Kelsey Beavers, Felix Zuo
- Wei Shen

Rayan Chikhi

Galaxy PROJECT

TACC
TEXAS ADVANCED COMPUTING CENTER

aws