

A Supplemental materials

A.1 Details of Experimental Study

Benchmarking commands Lemur was run as:

```
python lemur.py -d path-to-db -tax-path path-to-taxonomy
               -t 8 -minimap2-AS -r species r
               -i path-to-input.fastq -nof -o outdir
```

Magnet was run as:

```
python magnet.py -c lemur_report_file -i input_fastq_file -o output_path
-m ont
```

Kraken 2 was run as:

```
kraken2 -db kraken2-db/k2_fungistd -threads 8
        -output path-to-out.txt -report path-to-out.report.txt
        path-to-input.fastq
```

Melon was run as:

```
melon -d path-to-db -t 8 -o outdir path-to-input.fastq
```

Centrifuger was run as:

```
centrifuger -u path-to-input.fastq
            -x centrifuger-db/cfr_hpv+gbsarscov2
            -t 8 -o outdir
```

pbsim3 settings The following command was used for generating reads with pbsim3:

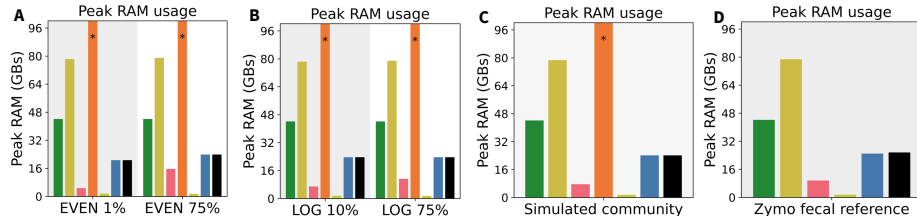
```
pbsim3 --seed 42 --strategy wgs --depth 50.0 --method qshmm
       --qshmm pbsim3/data/QSHMM-ONT.model --length-mean 4050
       --length-sd 1000 --difference-ratio 39:24:36 --accuracy-mean
0.95
       --id-prefix {accession}
       --prefix ../Data/Simulated/Base-reads-MAGs/{accession}/{accession}
       --genome ../Data/Genomes/ncbi_datasets-MAGs/data/{accession}/*.fna
```

NCBI Taxonomy To convert scientific names to NCBI taxonomy identifiers and backwards, the Environment for Tree Exploration (ETE) toolkit was used [14]. The corresponding `taxa.sqlite` NCBI taxdump was obtained on 01/18/2024 and has been fixed for all evaluations.

A.2 Details of Experimental Results

Table 4. 9 Genera predicted by Kraken2/Melon.

Genus	Isolation Source	Citation
<i>Anaeropeptidivorans</i>	Biogas fermenter	25
<i>Caloranaerobacter</i>	Marine thermal vents	53
<i>Caminicella</i>	Marine thermal vents	2
<i>Vallitalea</i>	Marine sediment	26
<i>Caproiciproducens</i>	WW treatment plant	18
<i>Lachnoanaerobaculum</i>	Human/Gut feces	12
<i>Monoglobus</i>	Human/Gut feces	19
<i>Solibaculum</i>	Human/Gut feces	43
<i>Vescimonas</i>	Human/Gut feces	24


Fig. 7. Peak RAM usage for the tools evaluated on Zymo EVEN (A), Zymo LOG (B), simulated metagenome (C), and Zymo fecal reference (D) datasets.