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Mapping ONT Reads to Reference Sequences with Minimap2 and Samtools

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Protocol status: Working

We use this protocol and it's working

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Abstract

This simple protocol maps ONT raw reads to Reference Sequences by Minimap2 and Samtools.



Install requirement software

- 1 `git clone https://github.com/lh3/minimap2`
`cd minimap2 && make`
- 2 `conda create -n samtools`
`conda activate samtools`
`conda config --add channels bioconda`
`conda config --add channels conda-forge`
`conda install -c bioconda samtools`

Align reads to reference sequences (two options as bellow)

- 3 `# Without index reference sequence`
`minimap2 -ax map-ont /path/to/list/references.fasta /path/to/raw/reads.fastq.gz >`
`/path/to/output/folder/alignment_reads.sam`
- 4 `# Index reference sequences first`
`minimap2 -d /path/to/index/references.mmi`
`/path/to/reference/sequences/references.fasta`
`# Align reads to reference sequences with ONT reads`
`minimap2 -ax map-ont /path/to/list/references.fasta /path/to/raw/reads.fastq.gz >`
`/path/to/output/folder/alignment_reads.sam`

Keep only mapped reads

- 5 `samtools view -bS -F 4 /path/to/output/folder/alignment_reads.sam >`
`/path/to/mapped/reads.bam`

Sort out the mapped reads

- 6 `samtools sort /path/to/mapped/reads.bam -o /path/to/mapped/reads_sort.bam`

Convert mapped reads to FASTQ or FASTA file for downstream analysis

- 7 `samtools fastq /path/to/mapped/reads_sort.bam > /path/to/mapped/reads_sort.fastq`