

Advanced Docker Course

Use Case: Comparing Aligners

We want to compare some short-read aligners (all of them are available via conda):

- BWA
- Bowtie2
- Gmap
- STAR

We want to run those programs, and to store the results outside the container for a later analysis.

The data are stored [here](#)

Using the aligners

BWA

- `bwa index lambda_virus.fa.gz` to build the index
- `bwa aln lambda_virus.fa.gz reads_1.fq.gz -f reads_1.fq.gz.sai`
to build the *sai* file
- `bwa samse lambda_virus.fa.gz reads_1.fq.gz.sai reads_1.fq.gz -f result.sam`
to compute the alignments

Bowtie2

- the index is already built
- `bowtie2 -x index/lambda_virus -U reads_1.fq.gz` to compute the alignments

Using the aligners

Gmap

- `bwa index data/lambda_virus.fa.gz` to build the index
- `bwa mem data/lambda_virus.fa.gz data/reads_1.fq.gz` to compute the alignments

STAR

- the index is already built
- `bowtie2 -x data/index/lambda_virus -U data/reads_1.fq.gz` to compute the alignments