

Advanced Docker Course

Use Case: Comparing Aligners

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

- BWA
- Bowtie2

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

Use Case: Images for pipelines

Base

```
FROM ubuntu:18.04
```

```
LABEL author="Raoul Jean Pierre Bonnal"
```

```
LABEL maintainer="bonnal@ingm.org"
```

```
ENV TINI_VERSION="v0.18.0"
```

```
ENV MINICONDA_VERSION="3-4.5.4"
```

```
ENV LANG=C.UTF-8 LC_ALL=C.UTF-8
```

```
ENV PATH=/opt/conda/bin:$PATH
```

```
ENV DEBIAN_FRONTEND=noninteractive
```

```
RUN apt-get update --fix-missing && \  
    apt-get install -y \  
        apt-utils \  
        bzip2 \  
        build-essential \  
        ca-certificates \  
        curl \  
        git \  
        wget \  
        procps \  
        uid-runtime
```

```
WORKDIR /opt
```

```
RUN wget --quiet https://repo.anaconda.com/miniconda/Miniconda${MINICONDA_VERSION}-Linux-x86_64.sh -O miniconda.sh  
    chmod ugo+x miniconda.sh
```

Use Case: Images for pipelines

Base

```
FROM bionic-ingm-base:0.1

#
# How to build
# docker build -t ingm-elixir:0.1 .
# docker tag ingm-elixir:0.1 localhost:5000/ingm-elixir:0.1
# docker push localhost:5000/ingm-elixir:0.1
#
LABEL software.iread="https://www.biorxiv.org/content/early/2017/10/04/135624www.libpls.net/iread"

ENV DEBIAN_FRONTEND=noninteractive
#RUN apt-get update && install apt-get -y liblapack3 libboost1.62-dev gawk
RUN apt-get update && apt-get install -y pigz unzip libparallel-forkmanager-perl

# libparallel-forkmanager-perl required by iREAD 0.8.0
# argparse is required by iREAD 0.8.0

WORKDIR /opt

RUN conda create -n elixir python=2.7 &&\
    /bin/bash -c "source activate organoids && \
        conda install -c bioconda \
            samtools=1.8 \
            bedops=2.4.35 \
            argparse=1.4.0 \
            fastqc=0.11.7 \
```