

Life portal - Demo

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About the Lifeportal

Lifeportal gives you easy access to the High Performance Computing cluster Abel at the University of Oslo. The Galaxy based Lifeportal has a continuously growing list of services, and among them the most widely used tools from the former Biportal.

[More about Lifeportal](#)

[Lifeportal news](#)

Partners



History

Unnamed history
538.6 KB

13: SAM-to-BAM (1.0) on data
12: converted BAM

12: Map with BWA for Illumina (0.7.8) on data 11: mapped reads

11: FASTQ Groomer on data
10

10: sample.fastq

4: Abel handshake

3: Add column on data 2

2: Convert on data 1

Basic example - File manipulation

- Create new history
- Upload a text file with one column of data
- Convert spaces in to tabs (Text Manipulation -> Convert delimiters to TAB)
- Add column
- Compute an expression on every row
- Create a workflow
- Run the workflow on another file

Example job script

```
#!/bin/bash
```

```
#SBATCH --job-name=RCS1115_hello
```

```
#SBATCH --account=xxx
```

```
#SBATCH --time=00:01:05
```

```
#SBATCH --ntasks=1
```

```
#SBATCH --mem-per-cpu=512M
```

Resources

```
source /cluster/bin/jobsetup
```

```
set -o errexit
```

Setup

```
sleep 1m
```

```
python hello.py
```

Job

Example 2- Sequence mapping

- Get Data
 - `ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/phase3/data/HG00096/sequence_read/SRR062641.filt.fastq.gz`
 - Uncompress
 - Trimm it - to make the processing faster
- Upload to Lifeportal

Example 2- Sequence mapping

- Look at the data in lifeportal
- Groom
 - NGS: QC and manipulation -> FASTQ Groomer
- Map to HG18
 - Map with BWA for Illumina (0.7.8)
- Convert to BAM
 - NGS: SAM Tools -> SAM-to-BAM (1.0)
- Create workflow, share URL
 - <https://lifeportal.uio.no/u/sabryr%40uio.no/w/mapping1flow>

Lifeportal

Tools

bwa

NGS: Mapping

- Map with BWA for Illumina (0.7.8)
- Map with BWA for SOLID (0.7.8)
- Map with BWA (Version 0.7.8) This new version BWA (0.7.5) use 'mem' algorithm for mapping, dosen't need 'aln', 'samse', 'sampe' and picard AddOrReplace anymore.

Workflows

- All workflows

QNAME	FLAGNAME	POS	MAPQCIGAR	MRNMMPOSISIZESEQ
@SQ SN:chr10 LN:135374737				
@SQ SN:chr10_random LN:113275				
@SQ SN:chr11 LN:134452384				
@SQ SN:chr11_random LN:215294				
@SQ SN:chr12 LN:132349534				
@SQ SN:chr13 LN:114142980				
@SQ SN:chr13_random LN:186858				
@SQ SN:chr14 LN:106368585				
@SQ SN:chr15 LN:100338915				
@SQ SN:chr15_random LN:784346				
@SQ SN:chr16 LN:88827254				
@SQ SN:chr16_random LN:105485				
@SQ SN:chr17 LN:78774742				
@SQ SN:chr17_random LN:2617613				
@SQ SN:chr18 LN:76117153				
@SQ SN:chr18_random LN:4262				
@SQ SN:chr19 LN:63811651				
@SQ SN:chr19_random LN:301858				
@SQ SN:chr1 LN:247249719				
@SQ SN:chr1_random LN:1663265				
@SQ SN:chr20 LN:62435964				
@SQ SN:chr21 LN:46944323				
@SO SN:chr21 random LN:1679693				

History

Mapping_1
251.9 KB

6: Map with BWA for Illumina (0.7.8) on data 4: mapped reads

4: FASTQ Groomer on data 3

3: sample.fastq

**Tool: SAM-to-BAM (1.0)**

Version: 1.0

Choose the source for the referen list:

Locally cached ▾

SAM File to Convert

Data input 'input1' (sam)

Edit Step Actions

Rename Dataset ▾

output1 ▾

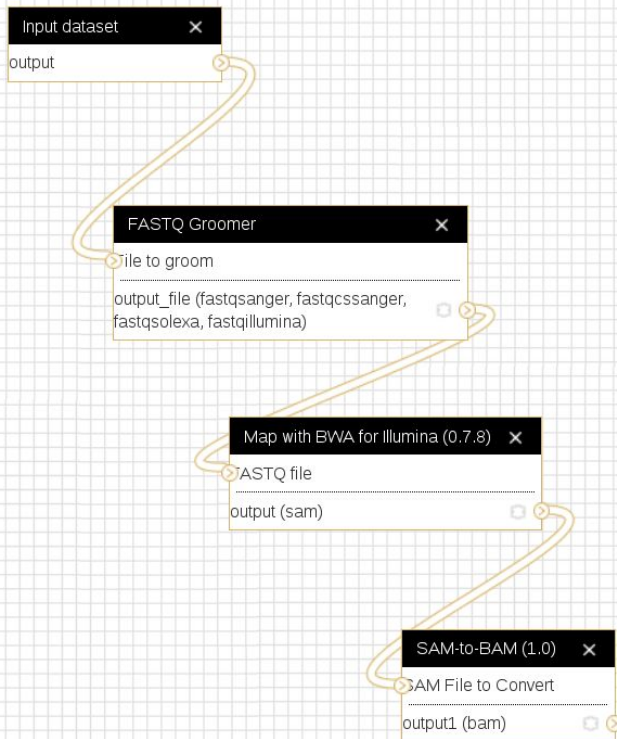
Add actions to this step; actions are applied when this workflow step completes.

Edit Step Attributes**Annotation / Notes:**

Add an annotation or notes to this step annotations are available when a workflow is viewed.

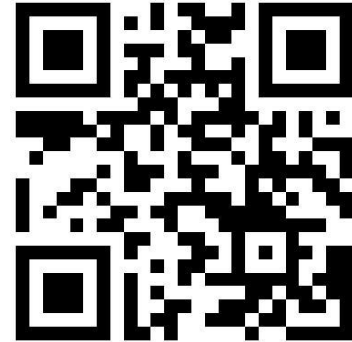
What it does

This tool uses the [SAMTools](#) toolkit to produce an indexed BAM file based on sorted input SAM file.



Thank you.

<http://www.uio.no/english/services/it/research/hpc/abel/>



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