NextFlow Introduction

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Introduction

The goal of this exercise is to recreate the pipeline showned in Figure 1 represented by its DAG

Channel factory

You may want to use the have a look at the `fromFilePairs` methods to create the channel when working with paired end data

Mapping

The mapping command to use is the following:

```
insert mapping command here
```

Samtools view

The goal is to convert the `sam` file into a compressed binary `bam` file using `samtools view`

The samtools command to use is the following:

```
samtools view -S -b input.sam > output.bam
```

Samtools sort

The goal is to sort the reads mapped on the reference genome by position

The samtools command to use us the following:

```
samtools sort input.bam > output.sorted.bam
```

Bedtools

The goal is to compute the coverage of the reference genome provided with the aligned reads

The bedtools command to use is the following:

```
insert bedtools command here
```
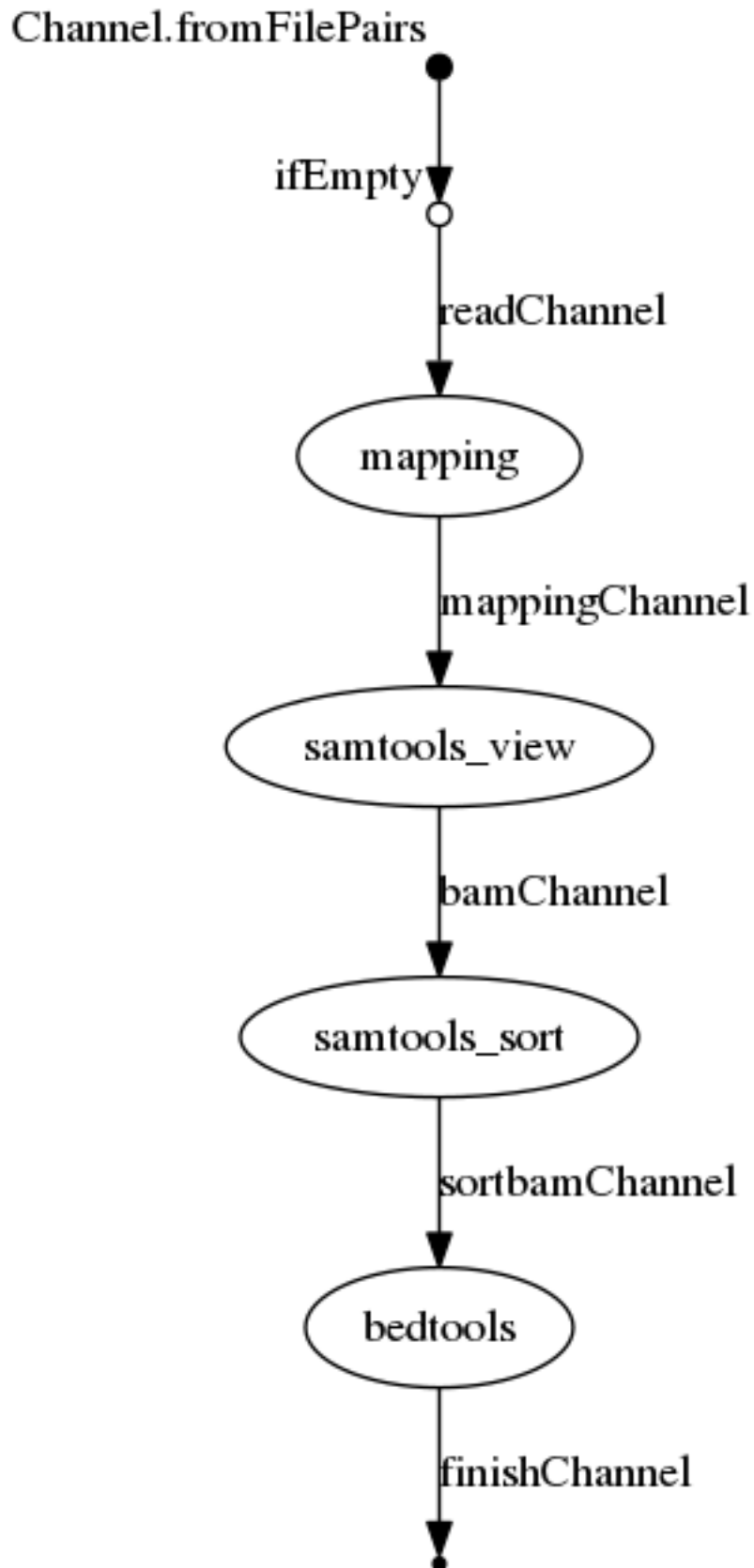
Figure 1: Directed Acyclic Graph (DAG) of the desired pipeline. Ellipses represent processes, arrows represents channels