



## Workflow report

Toolbox for generic NGS analyses

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# 1 Samples

## 1.1 Parallel execution (step number < 1000)

Samples	Job ID	Status
toto	001	Normal
tata	007	Error

## 1.2 Global execution (step number >= 1000)

Samples	Job ID	Status
toto—tata	001	Normal

# 2 Workflow

## 2.1 Workflow description

## 2.2 Software version

```
TOGGLE :  
- /usr/local/TOGGLE-0.3.5 : Release 0.3.4, 27th of September, 2017  
- Latest version of TOGGLE is Release 0.3.5, 8th of November, 2017  
  
JAVA : /usr/bin/java -Xmx12g -jar (openjdk version "1.8.0_65")  
  
fastqc :  
- /usr/local/FastQC-0.10.1/fastqc  
- FastQC v0.10.1  
  
cutadapt : /usr/local/cutadapt-1.10/bin/cutadapt (cutadapt version 1.10)  
  
bwa : /usr/local/bwa-0.7.12/bwa (Version: 0.7.12-r1039)  
  
picard : /usr/bin/java -Xmx12g -jar /usr/local/picard-tools-2.5.0/picard.jar (↔  
Version: 2.5.0(2c370988aefe41f579920c8a6a678a201c5261c1_1466708365))  
  
samtools : /usr/local/samtools-1.3.1/bin/samtools ( Version: 1.3.1 (using htslib↔  
1.3.1))  
  
GATK : /usr/bin/java -Xmx12g -jar /usr/local/gatk-3.6/GenomeAnalysisTK.jar (↔  
Version: 3.6-0-g89b7209)
```

## 2.3 Line code

```
tata...
```

## 2.4 Software configuration

```
$order  
1=fastqc  
2=cutadapt  
3=bwaAln  
4=bwaSampe  
5=picardToolsSortSam  
6=samtoolsflagstat  
7=samtoolsview  
8=samToolsIndex  
9=gatkRealignerTargetCreator  
10=gatkIndelRealigner
```

```

11=picardToolsMarkDuplicates
1000=gatkHaplotypeCaller
1001=gatkVariantFiltration
1002=gatkSelectVariants

$cleaner
3
4
9

#PUT YOUR OWN SGE CONFIGURATION HERE
$sge
-q bioinfo.q
-b Y
-V

#Scp transfert
$scp
/scratch

$cutadapt
-O=10
-m=35
-q=20
--overlap=7
# Adaptator1 is removed in the forward (-b) and reverse (-B) reads (5' and 3' ←
  position)
-b ADAPTATOR1REVERSE -B ADAPTATOR1REVERSE
# Same traitement is done for the forward adaptator sequence
-b ADAPTATOR1FORWARD -B ADAPTATOR1FORWARD

$bwa aln
-n=5

$bwa sampe
-a 500

$picardToolsSortSam
SORT_ORDER=coordinate
VALIDATION_STRINGENCY=SILENT
CREATE_INDEX=TRUE

$samToolsView
-h
-b
-f=0x02

$gatkRealignerTargetCreator
-T=RealignerTargetCreator

$gatkIndelRealigner
-T=IndelRealigner

$picardToolsMarkDuplicates
VALIDATION_STRINGENCY=SILENT
CREATE_INDEX=TRUE
REMOVE_DUPLICATES=TRUE

$gatkHaplotypeCaller
-T=HaplotypeCaller
-rf BadCigar

$gatkVariantFiltration
-T=VariantFiltration
--filterName 'FILTER-DP' --filterExpression 'DP<10 || DP>600' --filterName '←
  LowQual' --filterExpression 'QUAL<30'

$gatkSelectVariants
-T=SelectVariants
--selectType=SNP

```

## 2.5 How to cite TOGGLE?

[?]