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#####  
####
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Description:

=====

Pipelines for data analysis

Running @triploid@uvigo.es

```
#####  
####  
#!/bin/bash -l  
#####  
####
```

Folder paths

```
#####  
####  
source $HOME/src/vc-benchmark-cesga/src/vcs.variables.sh
```

```
#####
####
simphyReplicateID=2
pipelinesName="ssp"
replicatesNumDigits=5
replicateID="$(printf "%0${replicatesNumDigits}g" $simphyReplicateID)"
ngsphyReplicatePath="$HOME/data/NGSphy_${pipelinesName}.${replicateID}"
simphyReplicatePath="$HOME/data/${pipelinesName}.${replicateID}"
referencesReplicatePath="$HOME/data/references/references.${pipelinesName}.${replicateID}"
#####
####
```

1. REFERENCE INDEXING WITH BWA

```
#####
####
for refereceFolder in $referencesReplicatePath; do
for fastaFile in $(find $refereceFolder -name "*.fasta"); do
qsub $HOME/src/vc-benchmark-cesga/jobs/2.analysis/ssp.analysis.1.sh $fastaFile
done
done
#####
####
```

2. GENERATION OF BWA COMMAND LINESs

```
#####
####
qsub -t $simphyReplicateID $HOME/src/vc-benchmark-cesga/jobs/2.analysis/ssp.analysis.2.sh
PE150DFLT HiSeq2500
qsub -t $simphyReplicateID $HOME/src/vc-benchmark-cesga/jobs/2.analysis/ssp.analysis.2.sh
SE150DFLT HiSeq2500
qsub -t $simphyReplicateID $HOME/src/vc-benchmark-cesga/jobs/2.analysis/ssp.analysis.2.sh
PE250DFLT MiSeqV3
qsub -t $simphyReplicateID $HOME/src/vc-benchmark-cesga/jobs/2.analysis/ssp.analysis.2.sh
SE250DFLT MiSeqV3
#####
```

####

3. MAPPINGS

```
#####  
####  
profiles=("SE150DFLT" "PE150DFLT" "SE250DFLT" "PE250DFLT" ) # ("PE150OWN") #  
for profileFOLDER in ${profiles[]};do numJobs=$(find  
"$HOME/data/mappings/${pipelinesName}.${replicateID}/scripts/" -name  
"${pipelinesName}.${replicateID}.${profileFOLDER}.bwa.commands." -type f | wc -l );  
echo $numJobs  
qsub -t 1-$numJobs $HOME/src/vc-benchmark-cesga/jobs/2.analysis/ssp.analysis.3.sh  
"$HOME/data/mappings/${pipelinesName}.${replicateID}/scripts/${pipelinesName}.${replicateID}  
.${profileFOLDER}.bwa.commands"  
done  
#####  
####
```

4. Generating BAMMING SORTING commands

```
#####  
####  
qsub -t $simphyReplicateID $HOME/src/vc-benchmark-cesga/jobs/2.analysis/ssp.analysis.4.sh  
PE150DFLT  
qsub -t $simphyReplicateID $HOME/src/vc-benchmark-cesga/jobs/2.analysis/ssp.analysis.4.sh  
SE150DFLT  
qsub -t $simphyReplicateID $HOME/src/vc-benchmark-cesga/jobs/2.analysis/ssp.analysis.4.sh  
PE250DFLT  
qsub -t $simphyReplicateID $HOME/src/vc-benchmark-cesga/jobs/2.analysis/ssp.analysis.4.sh  
SE250DFLT  
  
#####  
####
```

5. BAMMING SORTING # 12 threads

```
#####
####
profiles=("PE150DFLT" "PE150OWN" "SE150DFLT") #("PE250DFLT" "SE250DFLT") #
("SE150DFLT") #
bammingFile=$HOME/src/vc-benchmark-cesga/files/${pipelineName}.${replicateID}.p1.sh
for profileFOLDER in ${profiles[]};do find
"$HOME/data/mappings/${pipelineName}.${replicateID}/scripts/" -name
"${pipelineName}.${replicateID}.${profileFOLDER}.samtools.commands." -type f | sort >>
$bammingFile
done
numJobs=$(cat $bammingFile | wc -l )
qsub -pe threaded 12 -t 1-$numJobs -hold_jid 645985-645987 $HOME/src/vc-benchmark-
cesga/jobs/2.analysis/ssp.analysis.5.sh $bammingFile

#####
####
```

6. INFORMATION ON THE MAPPING

```
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####
```

To ask the view command to report solely “proper pairs” we use the -f option and ask for alignments where the second bit is true (proper pair is true).

```
samtools view -f 0x2 sample.sorted.bam
```

How many properly paired alignments are there?

```
samtools view -f 0x2 sample.sorted.bam | wc -l
```

Now, let’s ask for alignments that are NOT properly paired. To do this, we use the -F option (note the capitalization to denote “opposite”).

```
samtools view -F 0x2 sample.sorted.bam
```

How many improperly paired alignments are there?

```
samtools view -F 0x2 sample.sorted.bam | wc -l
```