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#!/bin/bash
#$ -wd /home/merly/data
#$ -o /home/merly/output/ssp.analysis.4.o
#$ -e /home/merly/error/ssp.analysis.4.e
#$ -N doBAMsScript
module purge
#####
####
simphyReplicateID=$SGE_TASK_ID
profileFOLDER=$1 #"PE150OWN"
#####
####
pipelinesName="ssp"
replicatesNumDigits=5
replicateID="$(printf "%0${replicatesNumDigits}g" $simphyReplicateID)"
ngsphyReplicatePath="$HOME/data/NGSphy_${pipelinesName}.${replicateID}"
#####
####
distanceReference=("outgroup" "rndingroup")
sizes=("300" "500")
replicates=($(ls $ngsphyReplicatePath/${profileFOLDER}))
script="$HOME/data/mappings/${pipelinesName}.${replicateID}/scripts"
for distRefID in ${distanceReference[*]}; do
if [[ $profileFOLDER == *"150"* ]]; then
sizeID="300"
fi
if [[ $profileFOLDER == "250" ]]; then
sizeID="500"
fi
for replicateST in ${replicates[*]}; do nInds=$(ls
$ngsphyReplicatePath/$profileFOLDER/$replicateST/R1.fq.gz | wc -l) let nInds=nInds-1 for indID
in $(seq 0 $nInds); do echo "$distRefID - $sizeID |
${profileFOLDER}/${replicateST}/${pipelinesName}.${indID}"
outfile="$HOME/data/mappings/${pipelinesName}.${replicateID}/${profileFOLDER}/${replicateST}/${
pipelinesName}.${replicateID}.${replicateST}.${indID}.${distRefID}.${sizeID}.sam"
outputFILE="$(basename $outfile .sam).sorted.bam"
outputDIR="$(dirname $outfile)"
echo "samtools view -bSh $outfile | samtools sort - -o $outputDIR/$outputFILE -@ 12" >>
"${script}/${pipelinesName}.${replicateID}.${profileFOLDER}.samtools.sh"
echo "samtools index $outputDIR/$outputFILE" >>
"${script}/${pipelinesName}.${replicateID}.${profileFOLDER}.samtools.sh"
echo "rm $outfile" >> "${script}/${pipelinesName}.${replicateID}.${profileFOLDER}.samtools.sh"

```

done

done

done

split -l 120 -d -a 5

"\$HOME/data/mappings/\${pipelinesName}.\${replicateID}/scripts/\${pipelinesName}.\${replicateID}  
.\${profileFOLDER}.samtools.sh"

"\$HOME/data/mappings/\${pipelinesName}.\${replicateID}/scripts/\${pipelinesName}.\${replicateID}  
.\${profileFOLDER}.samtools.commands."

for file in \$(find "\$HOME/data/mappings/\${pipelinesName}.\${replicateID}/scripts/" -name  
"\${pipelinesName}.\${replicateID}.\${profileFOLDER}.samtools.commands.\*" -type f); do  
mv \$file "\$file.sh";

done