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#!/bin/bash
#SBATCH -J tophat2_cufflinks
#SBATCH -p dna
#SBATCH -N 4
#SBATCH --mem=20G
#SBATCH --cpus-per-task=4
#SBATCH -o slurm.%j.%x.out # STDOUT
#SBATCH -e slurm.%j.%x.err # STDERR
#SBATCH --mail-type=END # 发送哪一种 email 通知: BEGIN, END, FAIL,
                        ALL
#SBATCH --mail-user=jxsu22@m.fudan.edu.cn

echo "Usage:"
echo "  tophat2_cufflinks.sh {mode} {threads} {transcriptome-
                        index} {bowtie2-index} {SRR} {fq1} [{fq2}] "
echo ""

INDEX=$PWD/00_index
DATA=$PWD/01_rawdata
RESULT=$PWD/02_result

mode=$1
if test -z $mode # 检测字符是否为空
then
    echo "please input the mode(single or paired)"
    exit
fi
threads=$2
if test -z $threads
then
    echo "please input the number of threads"
    exit
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fi

Annotation=$3
if test -z $Annotation
then
    echo "please input transcriptome-index(/share/Genomes/
        Homo_sapiens/UCSC/hg19/Annotation/Genes/hg19_genes/
        genes.gff)"
    exit
fi

bowtie2Index=$4
if test -z $bowtie2Index
then
    echo "please input bowtie2-index(/share/Genomes/
        Homo_sapiens/UCSC/hg19/Sequence/Bowtie2Index/genome)"
    exit
fi

SRR=$5
if test -z $SRR
then
    echo "please input SRR id"
    exit
fi

fq1=$6
if test -z $fq1
then
    echo "please input fasta1"
    exit
fi
```

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if [ "$mode" == "paired" ];then

    fq2=$7
    if test -z $fq2
    then
        echo "please input fasta1"
        exit
    fi
fi

#=====

echo "Running info"
echo "Project:    "$PWD
echo "Read:       "$SRR
echo "Annotation: "$Annotation
echo "Genome:     "$bowtie2Index
echo " " "

#####RUN#####

mkdir -p ${RESULT}/tophat2/${SRR}
mkdir -p ${RESULT}/cufflinks/${SRR}

if [ "$mode" == "single" ];then
    # 如果是单端
    tophat2 -p ${threads} -o ${RESULT}/tophat2/${SRR} ${INDEX}
        ${bowtie2Index} ${DATA}/${fq1}
elif [ "$mode" == "paired" ];then
    # 如果是多端
    tophat2 -p ${threads} -o ${RESULT}/tophat2/${SRR} ${INDEX}
        ${bowtie2Index} ${DATA}/${fq1} ${DATA}/${fq2}
fi

```

```
cufflinks -p ${threads} -o ${RESULT}/cufflinks/${SRR} -G ${  
    INDEX}/${Annotation} ${RESULT}/tophat2/${SRR}/accepted_hits.  
bam  
  
echo " "  
echo " Running ${SRR} is completed."  
echo " "
```