Experiment

Experiment running example:

*(Picky)* theLAST/bin/lastdb -v -P 1 hg19.lastdb hg19.fa

samtools dict -H hg19.fa > hg19.seq.dict

picky/Picky-0.2.a/src/picky.pl script --fastq LongRead.fastq --thread 1 > run.sh

Let “theLAST/bin/lastal”, “picky/Picky-0.2.a/src/picky.pl”, “/refGenome/hg19.lastdb” and “/refGenome/hg19.fa” in “export LASTAL=”，“export PICKY=”，“export LASTALDB=” and “export LASTALDBFASTA=”.

(NanoSV) bedtools bamtobed -i sor.bam > sor.bed

/svim\_env/bin/NanoSV -t 1 -s /theSAMBAMBA/bin/sambamba -b sor.bed -o sor.vcf sor.bam

(pbsv) /thePBMM2/bin/pbmm2 align /refGenome/hg19.fa movie1.Q20.fastq ref.movie1.bam --sort --sample sample1 --rg '@RG\tID:movie1' or

/thePBMM2/bin/pbmm2 align /refGenome/hg19.fa movie1.Q20.fastq ref.movie1.bam --sort --preset CCS --sample sample1 --rg '@RG\tID:movie1'

/thePBSV/bin/pbsv discover ref.movie1.bam ref.sample1.svsig.gz

/thePBSV/bin/pbsv call /refGenome/hg19.fa ref.sample1.svsig.gz ref.var.vcf

（sniffles）

/theNGMLR/bin/ngmlr -t 1 -r /refGenome/hg19.fa -q sor.fastq -o sor.sam or

bwa mem -M -t 1 /refGenome/hg19.fa sor.fastq > sor.sam

samtools view -bS sor.sam > sor.bam

samtools sort sor.bam > sort\_sor.bam

samtools index sort\_sor.bam

/theSNIFFLES/bin/sniffles -m sort\_sor.bam -v output.vcf

(cutesv) /theCUTESV/bin/cuteSV sort\_sor.bam /refGenome/hg19.fa sor.vcf /theCUTESV/testData/

Recommendation

Installation-free mode, copy the code directly and run the following command.

Recommendation running example:

## python newSampleRecommend.py -f sample.fq

Then, the recommendation results will be printed in the console.