Highly sensitive and ultrafast read mapping for RNA-seq analysis

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Supplementary Data

Default command line parameters for the programs:

python mapsplice.py -c ~/GENOMES/MAP_SPLICE/ -x ~/GENOMES/MAP_SPLICE/hs.73 -1 <fastq-input-file> -p 12 -o <output-dir>

STAR --genomeDir ~/GENOMES/STAR/ --readFilesIn <fastq-input-file> --runThreadN 12 --outFileNamePrefix <output-dir>

tophat2 -p 12 --no-sort-bam -o <output-dir> ~/GENOMES/BOWTIE2/hs.73 <fastq-input-file>

~/HISAT/hisat-0.1.6-beta/hisat --novel-splicesite-outfile Junction.bed -p 12 -x ~/GENOMES/HISAT_INDEX/hs.73 reads.fq -S results.sam

hpg-aligner rna -i ~/$GENOME /HPG-ALIGNER -f <fastq-input-file> -o <output-dir>