RSeQC.infer_experiment Documentation

Description: Detect library type of an RNA-seq BAM file for downstream quantification.

Author: Liguo Wang, Mayo Clinic. Wrapped as a module by Anthony S. Castanza, Mesirov Lab, UCSD School of Medicine.

Contact: Module specific issues: genepattern.org/help

Summary: This module is used to "guess" how RNA-seq read were oriented in the original experiment. This is done by comparing the strand orientation of reads in a BAM file with the standedness of transcripts in a matching BED file.

Source documentation: http://rseqc.sourceforge.net/#infer-experiment-py

Basic Parameters:

Name	Description
BAM file	A BAM file containing the mapped RNA-seq reads that you want to reconstruct the library type of.
BED file	A reference in BED12 format to compare the read mappings in the BAM against.
	This need not match the reference used in producing the BAM file exactly, but the closer the match, the more accurate the library type inference.
	Reference BED files are available from: https://sourceforge.net/projects/rseqc/files/BED/

Output Files:

Name	Description
<infer_result>.txt	A text file containing the result of the RSeQC library type inference.

Guide to interpreting results: First row gives the RSeQC result, subsequent rows give the read orientation parameters that should be selected for the given quantification tool.

RSeQC Result (Majority of Reads)	No clear majority	++,-- (Single End)	+-,-+ (Single End)	1++,1--,2+-,2-+ (Paired End)	1+-,1-+,2++,2-- (Paired End)
Parameter to use for Salmon / Sailfish	-l U (SE) / -l IU (PE)	-l SF	-l SR	-l ISF	-l ISR
Parameter to use for TopHat / Cufflinks	library-type fr-unstranded	library-type fr-secondstrand	library-type fr-firststrand	library-type fr-secondstrand	library-type fr-firststrand
Parameter to use for HISAT2	default	--rna-strandedness F	--rna-strandedness R	--rna-strandedness FR	-rna-strandedness RF
Parameter to use for HTSeq	stranded --no	stranded --forward	stranded --reverse	stranded --forward	stranded --reverse

Module Language: Python
Source Repository: https://github.com/genepattern/RSeQC.infer_experiment/releases/tag/v1
Docker image: genepattern/docker-python37:0.1

Version	Comment
1	Initial release.