Picard.SamToFastq Documentation

Description:	Converts a SAM or BAM file to FASTQ format.
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Summary

This module converts a file in SAM format (or its binary equivalent, BAM format) to FASTQ format. SAM is a standard short read alignment that allows aligners to attach custom tags to individual alignments. For more information on the SAM format, see the specification at http://samtools.sourceforge.net. For more information on the FASTQ format, see the FASTQ specification (http://maq.sourceforge.net/fastq.shtml).

This module implements the SamToFastq function from Picard. For more information, see the Picard Web site: http://picard.sourceforge.net/.

Parameters

Name	Description
input.file (required)	The SAM or BAM file.
per.read.group (required)	Whether to output one FASTQ file per read group. Default: no
re-reverse. bases (required)	Whether to re-reverse bases and qualities of reads with negative strand flag set. Default: no
include.non.pf. reads (required)	Whether to include non-purity-filtered reads. Default: no
clipping.attribute (optional)	The attribute that stores the position at which the SAM record should be clipped. That is, if an attribute-value pair specifying the clipping position for each record is present in the SAM/BAM file, *clipping.attribute* can be set to the two-letter name of the attribute.

clipping.action (optional)	Action to take with clipped reads when a clipping attribute is specified. Options include: • trim reads and qualities • change bases to Ns • change base quality values Default: trim reads and qualities
clipping.action. quality.value (optional)	Value to which base quality values will be set when the *clipping action* is "change base quality values."
fastq.output.file.1 (optional)	The FASTQ output file name for a single-end FASTQ or the first end of a paired-end FASTQ. For more information on the FASTQ format, see the specification: http://maq.sourceforge.net/fastq.shtml. NOTE: This parameter is required if *per read group* is no and must not be set if *per read group* is yes.
fastq.output.file.2 (optional)	The FASTQ output file name for the second end of a paired-end FASTQ. NOTE: This parameter must not be set if *per read group* is yes.

Output Files

1. FASTQ file(s)

   The number of FASTQ files depends on the options specified: if the SAM file is for paired-end reads and if the *per read group* parameter is set to *yes*. For more information on the FASTQ format, see the specification: http://maq.sourceforge.net/fastq.shtml.

Platform Dependencies

Module type:	Data Format Conversion
CPU type:	any
OS:	any
Language:	Java, minimum version 1.6