FastqToSam Documentation

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

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Summary

This module converts a file in FASTQ format to a SAM or BAM file. For more information on the FASTQ format, see the specification: http://maq.sourceforge.net/fastq.shtml. SAM is a standard short read alignment that allows aligners to attach custom tags to individual alignments. The BAM format is the binary equivalent of SAM. For more information on the SAM format, see the specification: http://samtools.sourceforge.net/SAM-1.3.pdf.

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

Parameters

Name	Description
fastq file (required)	Input FASTQ file (optionally gzipped) either for single-end reads or for the first read in paired-end reads.
fastq file 2 (optional; required if paired-end data)	Input FASTQ file (optionally gzipped) for the second read in paired-end read data.
quality format (required)	A value describing how the quality values are encoded in the FASTQ file. Options are Solexa, Illumina, and Standard. Default: Standard
read group name (optional)	The read group name.
sample name (required)	The sample name to insert into the read group header.

library name (optional)	The library name to insert into the LB attribute in the read group header.
platform unit (optional)	The platform unit (often run_barcode.lane) to insert into the read group header.
platform (optional)	The platform type (e.g., Illumina, SOLiD) to insert into the read group header.
sort order (required)	The sort order for the output SAM or BAM file. Default: coordinate
output format (required)	The format of the output file. Either SAM or BAM. Default: BAM
output file (required)	The prefix to use for the output file name.

Output Files

1. SAM or BAM file

   The module creates either a SAM or BAM file from a single FASTQ file or it takes two FASTQ files and builds pairing information in the SAM or BAM file. For more information on the SAM format (and BAM, the binary equivalent of SAM), see the specification: http://samtools.sourceforge.net/SAM-1.3.pdf.

Platform Dependencies

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