SortSam Documentation

Description: Sorts a SAM or BAM file in a specified order.

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Summary

This module sorts and indexes a SAM or BAM file. This module will **only** generate an index file when the **output format** is "BAM", and the **sort order** is "coordinate". The module does not generate index files for SAM output files.

Also note that SortSam can convert an input SAM file to an output BAM file, or an input BAM file to an output SAM file. To convert between formats, change the output format to SAM or BAM accordingly.

The BAM format is the binary equivalent of the SAM format. For more information on this format, see the specification: http://samtools.sourceforge.net/SAM-1.3.pdf.

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

Parameters

Name	Description
input file (required)	Input file in SAM or BAM format. For more information on this format, see the specification: http://samtools.sourceforge.net/SAM-1.3.pdf.
sort order (required)	Specifies the sort order. Options include: • coordinate: the file sorts by chromosome and start position • queryname: the file sorts by the read IDs • unsorted: this option is only supported when the Group Order in the SAM/BAM header is "none" Default: coordinate
output format (required)	The format of the output file. Either SAM or BAM. Default: BAM
output prefix (required)	The prefix to use for the output file name.

Output Files

1. <output.prefix>.sorted.<output.format>

   This is the sorted SAM or BAM file.
   For more information on the SAM/BAM format, see the specification:
   http://samtools.sourceforge.net/SAM-1.3.pdf. BAM is the binary equivalent of SAM.

2. <output.filename>.bai

   This file contains the index for the coordinate sorted BAM output file.

Platform Dependencies

Module type:	Preprocess & Utilities
CPU type:	any
OS:	any
Language:	Java (minimum version 1.6)