Picard.ReorderSam Documentation

Description:	Reorders reads in a SAM/BAM file to match the contig ordering in a provided reference file.
Author:	Picard team, gp-help@broadinstitute.org

Summary

This module reorders reads in a SAM/BAM file to match the contig ordering in a provided reference file, as determined by exact name matching of contigs. Reads mapped to contigs absent in the new reference are dropped. For more details on the SAM/BAM format, see the specification here: http://samtools.sourceforge.net/

ReorderSam runs substantially faster if the input is an indexed BAM file.

This module wraps the ReorderSam function in Picard.

Parameters

Name	Description
input.file (required)	Input file (BAM or SAM). If the BAM is indexed, the module will look for the index in the same folder as the input file. (Note: The index will not be valid with the output BAM file.)
reference.file (required)	Reference sequence to which to reorder reads. This is a FASTA file.
reference. sequence. dictionary (required)	The sequence dictionary for the reference sequence file.
allow.partial. overlap (required)	If yes, then the module allows only a partial overlap of the BAM contigs with the new reference sequence contigs. By default, this tool requires a corresponding contig in the new reference for each read contig Default: no.
allow.contig. length. discordance (required)	If yes, then the module permits mapping from a read contig to a new reference contig with the same name but a different length. Use with extreme caution and a full knowledge of the possible consequences. Default: no.
output.prefix (required)	The prefix of the output SAM or BAM file.

Output Files

1. SAM/BAM file

   A SAM or BAM file (depending on the input format) with the reordered reads. For more details on the SAM/BAM format, see the specification here: http://samtools.sourceforge.net/.

Platform Dependencies

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