Picard.BamToSam Documentation

Description:	Converts a BAM file to a SAM file.
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Summary

The SAM (Sequence Alignment/Map) file format is a generic nucleotide alignment format that describes the alignment of query sequences or sequencing reads to a reference sequence or assembly. BAM is the binary version of the SAM format. For more details on the SAM/BAM format, see the specification here: http://samtools.sourceforge.net/SAM-1.3.pdf.

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

Reference

Sequence Alignment/Map (SAM) Format, Version 0.1.2-draft (20090820). http://samtools.sourceforge.net/SAM1.pdf

Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R; 1000 Genome Project Data Processing Subgroup. The Sequence alignment/map (SAM) format and SAMtools. *Bioinformatics*. 2009;25:2078-2079. (http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2723002/?tool=pubmed)

Parameters

Name	Description
input.file (required)	A BAM file to be converted. For more details on the BAM format, see the specification here: http://samtools.sourceforge.net/SAM-1.3.pdf.
output.prefix (required)	A label used to name the output file.

Output File

1. <output.prefix>.sam
   The input BAM file converted to SAM format.

Platform Dependencies

Module type: Data Format Conversion

CPU type: any

OS: any

Language: Java

Module Version Update Notes

Date	Version	Description
05/07/13	2	Renamed from BamToSam to Picard.BamToSam