BedToGtf Documentation

Description: Converts a BED file to GTF or GFF format.

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Summary

This module converts a BED file to GTF or GFF format. BED format is used to define genome annotations and genomic regions. It contains 3 required fields: the name of the chromosome, the starting position of the feature on the chromosome, and the end position of the feature. It can also contain 9 other fields, including the name of the BED line, a score, strand definition, several display-related specifications, and information about the exons in the BED line. For more information on the BED format, see the UCSC file format FAQ: http://genome.ucsc.edu/FAQ/FAQformat.html

GTF (Gene Transfer Format) and GFF (General Feature Format) each contain descriptions of features/sequences, including start, end, and frame. For more information on the GTF format, see the specification: http://mblab.wustl.edu/GTF22.html. For more information on the GFF format, see the specification: http://www.sanger.ac.uk/resources/software/gff/.

The BED to GFF conversion is an implementation of the BED to GFF converter from Galaxy Tools.

Parameters

Name	Description
bed.file (required)	The input BED file. The BED file should have at least 12 columns of data for the module to create a GTF file.
output.format (required)	Specifies whether the output file will be in GTF or GFF format.
output.prefix (required)	The prefix for the output file name. Default: <bed.file_basename>

Output Files

1. GTF/GFF file

The output file contains all the information from the BED file in the specified format. For more information on the GTF format, see the specification: http://mblab.wustl.edu/GTF22.html. For more information on the GFF format, see the specification: http://www.sanger.ac.uk/resources/software/gff/.

Platform Dependencies

Module type:	Preprocess & Utilities
CPU type:	any
OS:	any
Language:	Java (minimum version 1.5)