BuildFastaIndex Documentation

Description: Indexes a FASTA file.

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Summary

This module indexes a reference sequence in FASTA format. The index file is given the extension FAI.

For more information on FASTA format, see a description of it here:
http://www.ncbi.nlm.nih.gov/BLAST/blastcgihelp.shtml

and also here:

http://zhanglab.ccmb.med.umich.edu/FASTA/

Parameters

Name	Description
fasta.file	A sequence in FASTA format. (gz compressed files are supported)
output.prefix	The prefix to use for the output file name.

Output Files

1. FAI file

    An index of a FASTA sequence file.

Platform Dependencies

        Module type: Preprocess & Utilities

        CPU type: any

        OS: any

        Language: C++; Perl