Bowtie 2 Support Package for Bioinformatics Toolbox

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% Bowtie 2 is an ultrafast, memory-efficient short read aligner. It aligns
% short DNA sequences (reads) to the human genome at a rate of over 25
% million 35-bp reads per hour. Bowtie indexes the genome with a
% Burrows-Wheeler index to keep its memory footprint small: typically about
% 2.2 GB for the human genome (2.9 GB for paired-end).
%
% This support package installs the compiled binaries for Bowtie 2 so that
 they
% can be used with Bioinformatics Toolbox (TM) in MATLAB.
%
% Bowtie 2 [1] was originally developed by Ben Langmead and Cole Trapnell at
% Johns Hopkins University and the project is maintained at their website
% [2].
%
%  [1] - Langmead B, Salzberg S. Fast gapped-read alignment with Bowtie 2.
%        Nature Methods. 2012, 9:357-359.
%  [2] - http://bowtie-bio.sourceforge.net/bowtie2/index.shtml
%
%   See also BOWTIE2, BOWTIE2BUILD, BOWTIE2INSPECT, BOWTIE2ALIGNOPTIONS,
%   BOWTIE2BUILDOPTIONS, BOWTIE2INSPECTOPTIONS.
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