cdBEST: chromatin domain Boundary Element Search Tool

cdBEST is a tool/software developed in Perl to search the chromatin domain boundary element sequences in 12 *Drosophila* species. cdBEST uses recognition sequences of boundary interacting proteins and looks for 'motif clusters' under a set of constrains to predict boundary element sequences. Apart from *Drosophila*, cdBEST can be used in several other insect genomes, where the boundary interacting proteins are conserved.

Authors: Arumugam Srinivasan & Rakesh K Mishra

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Contact: asrini@ccmb.res.in , mishra@ccmb.res.in
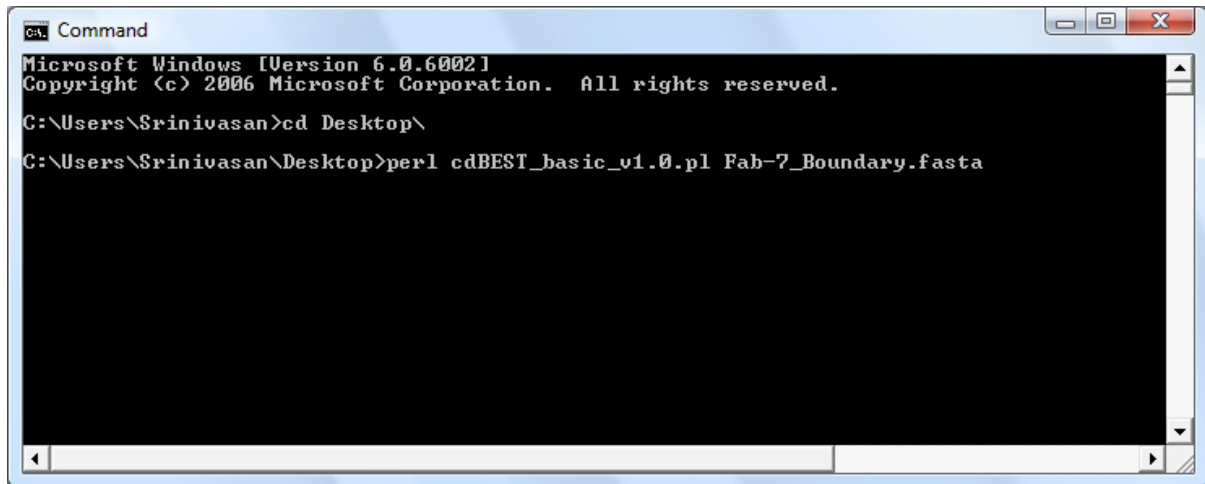
cdBEST_basic_v1.0

This version is a command line Perl script requires Perl alone, can be used in Linux and Mac computers directly without any additional requirements (as Perl is inbuilt). However, a Microsoft Windows computer requires Perl installation. cdBEST_basic uses FASTA formatted sequence file and produces 4 different text output files.

Installation instructions for cdBEST_basic_v1.0:

1.   Perl is installed by default in Linux and Mac OS, so you can run cdBEST_basic directly using the terminal (command-line).
2.   In Microsoft Windows you to have download and install Perl from Perl Installer file such as ActivePerl Windows Installer (MSI) file or Strawberry Perl Installer (MSI) file.

Running a boundary search with cdBEST_basic_v1.0:

To run cdBEST_basic_v1.0, you should start command prompt in windows or terminal in Mac OS & Linux OS. Then go to the folder/directory where the cdBEST script is located and type perl cdBEST_basic_v1.0.pl fasta_file