BProm

BProm Prediction of bacterial promoters.

As a part of bacterial genome analysis suite of programs, and to enforce operon and gene prediction by FGENESB program, we introduce BProm, bacterial promoter prediction program. **Method description:**

Algorithm predicts potential transcription start positions of bacterial genes regulated by sigma 70 promoters (major E.coli promoter class). Linear discriminant function (LDF) combines characteristics describing functional motifs and oligonucleotide composition of these sites. BProm has accuracy of E.coli promoter recognition about 80%. Its specificity is also about 80% when tested on sets containing promoter and non-promoter sequences in equal numbers. It is not advisable to run BProm on whole genomes: To increase specificity, run BProm on a region between two neighboring ORFs located on the same strand, or on a sequence upstream from an ORF, keeping in mind that most promoters are located within 150 bp region from protein coding sequence.

BProm output:

First line - name of your sequence;

Second and Third lines - LDF threshold and the length of presented sequence

4th line - The number of predicted promoters

Next lines - positions of predicted promoters, and their scores with 'weights' of two conserved promoter boxes. Promoter position assign to the first nucleotide of the transcript (Transcription Start Site position).

After that we present elements of Transcriptional factor binding sites for each predicted promoter (if they found).

For example:

```
BProm Sat Jan 18 21:11:25 EST 2003
>Region of
                    E.coli genome between
                                                             protein id="AAC76687.1"
                                                                                                  and
protein id="AAC7668
 Length of sequence-
 Threshold for promoters - 0.20
 Number of predicted promoters -
 Promoter Pos: 145 LDF- 6.02
 -10 box at pos. 130 ctttatgat Score
-35 box at pos. 109 tttaat Score
 Oligonucleotides from known TF binding sites:
 For promoter at
                          145:
      fis: TCTTTAAT at position 107 Score - rpoD17: TTATGATA at position 132 Score - lexA: ATAAATAA at position 137 Score - rpoD17: ATAATAAT at position 141 Score -
                                                                     7
                                                                    14
```