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Spectral classification of short numerical exon and intron sequences

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Abstract

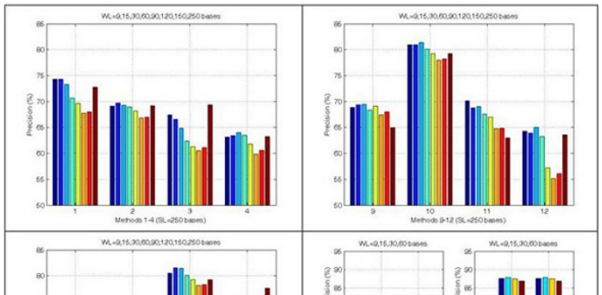
This research presents three new numerical representations for classifying short exon and intron sequences using discrete Fourier transform period-3 value. Based on the human genome, results indicate that the Complex Twin-Pair representation is attractive compared with other numerical representations and the approach has potential applications in genome annotation and read mapping.

Background

Current methods for genome annotation focus on sequence similarity or motif matching to known genes and there is a need for a complementary or more effective approach. It is known that protein coding (exonic or C-G rich) regions exhibit a period-3 property which is less prominent in noncoding (intronic or A-T rich) regions. The boundary between these 2 regions becomes less apparent as sequence length becomes shorter. The period-3 property is likely due to the 3-base-length of codons. C-G rich content in coding regions is due to nonuniform codon usage. For spectral analysis of period-3 value, a nucleotide sequence has to be converted to a numerical sequence. The choice of numerical representation affects how well its biological properties can be preserved and reflected.

Methodology

Based on exon and intron sequences downloaded from UCSC Genome Browser on Human (GRCh37/hg19) (http://genome.ucsc.edu/cgi-bin/hgText) using [1-3], the classification performance in precisions (%) were computed by applying the spectral analysis and thresholding of [4] to the following twelve numerical representation methods: 1. Integer Number; 2. Single Galois Indicator; 3. Paired Nucleotide Atomic Number; 4. Atomic Number; 5. Molecular Mass; 6. EIIP; 7. Paired Numeric; 8. Real Number; 9. Complex Number; 10. Complex Twin-Pair (C, G = -1; A, T = j); 11. Complex Bipolar-Pair Code I (C = -1; G = 1; A = j; T = -j); 12. Complex Bipolar-Pair Code II (C = -1; G = 1; A = -j; T = j). Methods 1-9 are specified in [4] and Methods 10-12 are new



Method	1 to 12		7, 10							
SL	250		150		300		450		600	
Type	Exon	Intron	Exon	Intron	Exon	Intron	Exon	Intron	Exon	Intron
SNTrain	1-2500	1-3000	1-2500	1-3000	1-3000	1-3000	1-1000	1-1000	1-2500	1-3500
SNTest	2501-3344	3001-3937	2501-3440	3001-3874	3001-3849	3001-3927	1001-1513	1001-1776	2501-3189	3501-4460

Figure 1 Precisions of methods obtained by different WL set and SL (SL: Sequence length in bases; WL: Window length in bases; SNTrain: Sequence numbers for training; SNTest: Sequence numbers for testing).

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numerical representations. In simulations, two adjacent windows are overlapped by 3 bases.

Results and conclusions

The results summarized in Figure 1 indicate that the approach is capable for effective classification of untrained short exon and intron sequences. Among the 3 new numerical representations, the Complex Twin-Pair (Method 10) achieves a precision of about 79% to 92% for a sequence length of 150 bases to 600 bases and a window length of 9 bases which is comparable with those of the Paired Numeric (Method 7).

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