**GenScan을 이용한 진핵생물의 서열 패턴 분석**

*Anlaysis of Eukaryotic Sequence Pattern using GenScan*

Yong-Gyu Jung, I-Suel Lim, Byung-Heun Cha

요약: 서열 상동성 분석은 생명현상에 관여하는 물질을 정렬, 색인하여 데이터베이스 하는 것으로, 생명정보학의 유용성을 입증하는 분야이다. 본 논문에서는 구조가 복잡한 진핵생물의 서열 패턴을 단백질 서열로 변환하기 위해 은닉마르코프모델을 이용하는 GenScan 프로그램을 이용한다. 진핵생물 서열 분석 중 최소거리 탐색 문제는 문제의 크기가 커지면 계산량이 기하급수적으로 증가하여 정확한 계산이 불가능해진다. 따라서 유사한 아미노산간의 치환과 상이한 아미노산간의 치환 점수를 차등화한 점수표를 적용하고, 은닉마르코프모델 등을 적용해 정교한 전이 확률모델을 작용한다. 변환된 서열을 서열 상동성 분석을 위해 사용하는 blast p를 이용하여, 은닉마르코프 모델을 도입함으로 인해 단백질 구조 서열로 변환하는 데에 있어서 우수한 기능을 제공할 수 있다.

Abstract: Sequence homology analysis in the substances in the phenomenon of life is to create database by sorting and indexing and to demonstrate the usefulness of informatics. In this paper, Markov models are used in GenScan program to convert the pattern of complex eukaryotic protein sequences. It becomes impossible to navigate the minimum distance, complexity increases exponentially as the exact calculation. It is used scorecard in amino acid substitutions between similar amino acid substitutions to have a differential effect score, and is applied the Markov models sophisticated concealment of the transition probability model. As providing superior method to translate sequences homologous sequences in analysis using blast p, Markov models. is secreted protein structure of sequence translations.

Key Words: eukaryotic, Hidden Markov Model, GenScan, blast p

Ⅰ. Introduction

Biological phenomena involved in the sorting and indexing all the materials in the database, the field of bioinformatics, the sequence phase demonstrated that sequence homology are analyzed usefulness.[1] - [2]

Protein key ingredient of life as a plain text string of one-dimensional structure of ownership that the first hypothesis was proposed in 1883 by Curtius. Since then many scientists further mutations and evolutionary process, both historical and more sequence information is encoded. Discovery of life mysteries is the remarkable development of modern molecular biology, biological phenomena are surprisingly 'chemical information', that it was.[3]

In the minimum distance problem, the searching space is increased exponentially by increasing complexity, the exact calculation becomes impossible. Bi-phase sequence analysis Thus, some hermeneutical methods applied to find efficiently an approximation is
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Between similar amino acid substitutions and different substitution score between amino acids have differential effect scorecard, or Markov models, and apply the sophisticated concealment or transfer (insertion, deletion, substitution) probability models are applied to more advanced algorithms. [4]

Hidden Markov models with complex relationships, such as intron and exon ongoing life issues in the case of more complex modeling is working properly.

II. Related research

1. prokaryotes and eukaryotes

Depending on the internal structure of cells can be divided into prokaryotes and eukaryotes. Prokaryotes are simple in structure. Which is found only in prokaryotic single-celled or colonial. Three stations of the way biological classification system (archaea, bacteria and eukaryotes classification) approach is the high taxes that bacteria and germs.

The cell membrane of eukaryotic organelles have their own will. Some fungi and unicellular forms, such as Ahmedabad, from bars, plants and animals, such as brown colonies and multicellular forms is still present.

The structure of prokaryotic and eukaryotic cells are shown in Fig. 1. All prokaryotic cells, eukaryotic cells have membrane. The cell membrane separates the internal and external support, and internal and external mass flow control, and also maintains the cell potential. Inner membrane of a salt, accounting for almost all of the cytoplasm. DNA in all cells with the gene and enzyme gene expression and protein and RNA with the information necessary to have. Chain of prokaryotic life in general, compared with its own eukaryotic cells typically are found in multicellular organisms.

Prokaryotic and eukaryotic cells in general larger than 10 times, 1000 times larger sense, by volume. The biggest difference between prokaryotic and eukaryotic cell lines specific to the case of eukaryotic cells are part of the cell membrane is surrounded by [6].

2. Hidden Markov Model

Secreted by each state Markov model with transition probability is a finite state machine, each state can also not be observed directly, but instead, each state has a chance to produce their state can be observed. Hidden Markov Model is shown in Table 1 below sets and two state model has a set of three is likely. [5]

<table>
<thead>
<tr>
<th>observabl e state</th>
<th>The visible state of the process</th>
</tr>
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<tbody>
<tr>
<td>hidden state</td>
<td>Hidden Markov process is represented by the state of the system</td>
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</table>

Ⅲ. GenScan

After the first genetic material was separated to determine the sequence of the gene function was seeking to identify the classical paradigm of molecular biology, as opposed genome sequence to decide first
place overall in the mechanical, chemical analysis of the sequence structure information through the genes, regulatory region of genes, RNA, and bioinformatics finding was transformed into a paradigm.

In case of gene finding, the first 6 to decrypt the frame long enough to read the so-called translation initiation frame (Open Reading Frame, ORF). Finding the most popular towing gene begins with a simple algorithm to find. Of course, the case of eukaryotes, complex relationships, such as introns, and exon the problem is more complex modeling.

The important thing to find genes of major issues such as the genomic sequence of the pattern analysis of the structure problem, namely, the problem is that the traditional informatics. Actually GenScan using the Hidden Markov Model is a pattern analysis algorithm [5]. Common local pattern analysis and mathematical analysis of global patterns (Ab Initio) are performed in sequence informatics through virtual sex search sites deduced sequence of the gene may be an inference is probabilistic. In other words, GenScan is a program to turn from the DNA sequence into an amino acid sequence. that turns. Splicing introns are removed, and the promoter alone. Exon poly (A)-signal and can be found to predict the ORF. Fig. 2 above provided by the MIT GenScan is a web server [7].

**IV. Experiments and experimental results**

1. Experiments

The algorithm used in this paper GenScan Eukaryotes or Eucaryote Gene Prediction program for the Exxon By Gene are given Intron structure and the predicted location.

NCBI (National Center for Biotechnology Information) is provided by GenBank search of the nucleotide sequence in progress in the state were randomly selected sequences. [8] In this paper, we use a randomly selected sequences CU326341. Fig. 4 as part of this sequence information, sequences, are registered as non-aligned status, and having the sequence of 1 to 178,302 indicates species of Sus scrofa pig. 1-9301 of the randomly selected sequences from sequence to sequence and copy 9412-25141 GenScan to convert the amino acid sequence respectively. Each two sets of experiments, using the blast p program of NCBI will detect whether homology. [8]

그림 2. The GenScan Web Server at MIT

**Fig. 2. The GenScan Web Server at MIT**

![GenScan Web Server](image)

**그림 3. CU216341 정보의 일부**

**Fig. 3. CU216341 Some of the information**

2. Experimental results

Randomly dividing Set 1 of a sequence from 1-9301 and Set 2 of sequence from 9412 to 25,141 in protein sequences using the GenScan blast p after switching to the next one on the diagramed put the results shown in Fig. 4.
A set of two blast p search results list of the top 10 dogs are part of the query list is shown as Fig. 5. Among these were the highest homology score XP_001787786.1 the "PREDICTED: similar to endonuclease reverse transcriptase [Bos taurus]" is defined. Converting it into protein sequences before the original DNA sequence data, part of CU216341 XP001787786.1 XP001787786.1 the most similar protein sequence data show the inference.

Using blast p experimental data and with the most similar protein sequences, protein sequences and XP001787786.1 to that used in the experiment of the protein sequence data for the validation of experimental results by comparing the lists look like the following shown in Fig. 6. Query sequence and a subject sequence, Compositional matrix adjust sequencing way, the above will appear similar arrangement referring to Fig. 6, Query sequence 34-419 and the subject of a 886-1272 check point will be similar.

Based on these results, numerical statistics, export data, 387 of the Identities of the 278 matches the import value has a value of approximately 71.8%, Positives value + value of the match, including the import value of 324 has 83.7%. - Gaps around because there are a value of 1 has a value of 0.2%.
E value expectation of the same size and configuration to match a randomly generated string from the database to measure the potential to occur. E value closer to 0 it becomes less and are more likely to occur by chance. The lower the value that matches E yirwojin is that the better.

E value of less than 1 can be a definite hit. Fig. 6 as a result of this paper, we present the case for the E value $3e^{-165}$ ($e \approx 2.71828$), so a kind of paper is less than the data used in judging the value of E (Sus crofa: pig) and similar proteins inferred data (Bos taurus: cattle) between the cross can be seen that a high homology.

VI. Conclusion

CU216341 used in this paper is data in the NCBI GenBank nucleotide sequence data provided by the vast progress of the eukaryotes within the discretion of the vertebrates, is one of the chosen pig process. The complex structures in order to analyze the structure of eukaryotic sequences that are based on concealment Markov model using the MIT GenScan converted to protein sequences was trying to express the probability of NCBI using blast p homology and similar kinds of tests came up with. In this experiment, the structure in complex eukaryotic sequences in the structural analysis of the program algorithm GenScan secreted protein structure due to the introduction of Markov models in sequence translations to provide a superior could see that.

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