# Motif Detection and Entropy Filtering in Genetic Sequences

Ivan Felipe Prado Blanco
Department of Computer Science
Universidad Distrital Francisco Jose de Caldas
Bogota, Colombia
Email: ifpradob@udistrital.edu.co

***Abstract*—This report presents an analysis of motif detection in genetic sequences, highlighting the use of entropy filtering to enhance motif detection. The study explores the computational performance of different configurations of sequence generation and motif search, both with and without entropy filtering.**

## I. Systemic Analysis

The system used for motif detection consists of three main components:

1) **Sequence Generation**: Using the probability assigned to each nucleotide base (A, C, G, and T), a set of genetic sequences was created. There were 1000 to 100,000 sequences in the database, and each sequence had 100 nucleotide bases. Three types of distributions were employed, with the probabilities for the nucleotide bases being controlled (uniform, biased towards A, biased towards C, G, and T).
2) **Motif Detection**: The algorithm repeatedly goes over every sequence in the database, looking for motifs with four, six, or eight bases. For every trial, the motif that appears the most frequently is chosen as the most significant. The algorithm gave preference to motifs with the greatest number of consecutive repeating bases when there were many motifs with the same frequency.
3) **Entropy Filtering**: Sequences were filtered according to their Shannon entropy before motifs were found. To guarantee that only the most chaotic (i.e., variable) sequences were examined, sequences having entropy values below a cutoff point (1.5) were eliminated.
   Together, these elements generate two sets of results: an unfiltered set and an entropy-based filter set.

## II. Complexity Analysis

a) **Sequence Generation**: Generating a database of `n` sequences, each of length `m`, has a time complexity of **O(n * m)**. The sequences are built by randomly selecting nucleotide bases according to the specified probabilities.
b) **Motif Detection**: The algorithm for detecting motifs involves iterating over every sequence in the database and searching for all possible subsequences of length `s` (motif size). The complexity of motif detection is approximately **O(n * m * (m - s))**, where:

- `n` is the number of sequences.
- `m` is the length of each sequence.
- `s` is the length of the motif.

This complexity increases with both the size of the database and the length of the motifs.

c) **Entropy Filtering**: The calculation of Shannon entropy for each sequence is **O(m)**, as it requires counting the occurrences of each nucleotide base in the sequence. The overall complexity for filtering sequences is **O(n * m)**. After filtering, the reduced number of sequences decreases the overall runtime of motif detection.

As database sizes grow, the time required for both sequence generation and motif detection increases significantly.

## III. Chaos Analysis

The Shannon entropy was used to quantify the level of chaos or diversity in the genetic sequences. Entropy is a measure of how unpredictable a sequence is; a higher value indicates more base diversity, while a lower value indicates repetition or predominance of a particular base. Since low entropy sequences are less likely to include informative motifs, they were removed.
Sequences with entropy values below the predefined cutoff point of 1.5 were eliminated. By focusing the investigation on the most diverse sequences, the importance of the themes discovered was enhanced. Because the filtered datasets were often substantially smaller, motif detection quality was improved and computational load was reduced.

## IV. Results

The results of motif detection are separated into two sections: the first portion displays the findings without entropy filtering, and the second section displays the results after entropy filtering. The supplied data for each case includes the motifs found, the database size, the probability used, and the motif detection time.

## V. Results without Entropy Filter

| Database Size | Probabilities (A, C, G, T) | Motif Size | Motif | Time (seconds) |
|---|---|---|---|---|
| 1000 | 0.25, 0.25, 0.25, 0.25 | 4 | CCGT | 0.1402541 |
| 1000 | 0.25, 0.25, 0.25, 0.25 | 6 | TTCAGG | 0.0256702 |
| 1000 | 0.25, 0.25, 0.25, 0.25 | 8 | CATGTACT | 0.0595991 |
| 1000 | 0.40, 0.20, 0.20, 0.20 | 4 | AAAA | 0.0208796 |
| 1000 | 0.40, 0.20, 0.20, 0.20 | 6 | AAAAAA | 0.0173153 |
| 1000 | 0.40, 0.20, 0.20, 0.20 | 8 | AAAAAAAA | 0.0254449 |
| 1000 | 0.10, 0.30, 0.30, 0.30 | 4 | CTCC | 0.0149464 |
| 1000 | 0.10, 0.30, 0.30, 0.30 | 6 | TGTCGG | 0.017428 |
| 1000 | 0.10, 0.30, 0.30, 0.30 | 8 | CGCGCGTC | 0.027711 |
| 10000 | 0.25, 0.25, 0.25, 0.25 | 4 | GCCC | 0.1342925 |
| 10000 | 0.25, 0.25, 0.25, 0.25 | 6 | CTGAGG | 0.1891245 |
| 10000 | 0.25, 0.25, 0.25, 0.25 | 8 | CATCCGCG | 0.3723069 |
| 10000 | 0.40, 0.20, 0.20, 0.20 | 4 | AAAA | 0.0879378 |
| 10000 | 0.40, 0.20, 0.20, 0.20 | 6 | AAAAAA | 0.1401638 |
| 10000 | 0.40, 0.20, 0.20, 0.20 | 8 | AAAAAAAA | 0.335184 |
| 10000 | 0.10, 0.30, 0.30, 0.30 | 4 | TCTT | 0.1017898 |
| 10000 | 0.10, 0.30, 0.30, 0.30 | 6 | GTCGGT | 0.1627139 |
| 10000 | 0.10, 0.30, 0.30, 0.30 | 8 | GCTCTTGT | 0.3249965 |
| 100000 | 0.25, 0.25, 0.25, 0.25 | 4 | ATGC | 1.180866 |
| 100000 | 0.25, 0.25, 0.25, 0.25 | 6 | GACCCG | 1.3812731 |
| 100000 | 0.25, 0.25, 0.25, 0.25 | 8 | CCTTCATT | 2.130466 |
| 100000 | 0.40, 0.20, 0.20, 0.20 | 4 | AAAA | 0.9815225 |
| 100000 | 0.40, 0.20, 0.20, 0.20 | 6 | AAAAAA | 1.326625 |
| 100000 | 0.40, 0.20, 0.20, 0.20 | 8 | AAAAAAAA | 2.3233787 |
| 100000 | 0.10, 0.30, 0.30, 0.30 | 4 | TTGG | 1.0348581 |
| 100000 | 0.10, 0.30, 0.30, 0.30 | 6 | GTTGGG | 1.8568599 |
| 100000 | 0.10, 0.30, 0.30, 0.30 | 8 | CGTGTTCG | 2.8171319 |

## VI. Results with Entropy Filter

| Database Size | Probabilities (A, C, G, T) | Motif Size | Motif | Time (seconds) |
|---|---|---|---|---|
| 1000 | 0.25, 0.25, 0.25, 0.25 | 4 | GTTC | 0.1079197 |
| 1000 | 0.25, 0.25, 0.25, 0.25 | 6 | TCGTTA | 0.0509808 |
| 1000 | 0.25, 0.25, 0.25, 0.25 | 8 | TTTGGGTC | 0.0891146 |
| 1000 | 0.40, 0.20, 0.20, 0.20 | 4 | AAAA | 0.0204209 |
| 1000 | 0.40, 0.20, 0.20, 0.20 | 6 | AAAAAA | 0.0159563 |
| 1000 | 0.40, 0.20, 0.20, 0.20 | 8 | AAAAAAAA | 0.0299301 |
| 1000 | 0.10, 0.30, 0.30, 0.30 | 4 | CTGG | 0.0206143 |
| 1000 | 0.10, 0.30, 0.30, 0.30 | 6 | CCTCTC | 0.0219753 |
| 1000 | 0.10, 0.30, 0.30, 0.30 | 8 | CGCCCGTG | 0.0268643 |
| 10000 | 0.25, 0.25, 0.25, 0.25 | 4 | AATA | 0.1391385 |
| 10000 | 0.25, 0.25, 0.25, 0.25 | 6 | CTAGGG | 0.1917116 |
| 10000 | 0.25, 0.25, 0.25, 0.25 | 8 | GAATTCTA | 0.2268161 |
| 10000 | 0.40, 0.20, 0.20, 0.20 | 4 | AAAA | 0.0795234 |
| 10000 | 0.40, 0.20, 0.20, 0.20 | 6 | AAAAAA | 0.1447396 |
| 10000 | 0.40, 0.20, 0.20, 0.20 | 8 | AAAAAAAA | 0.3028902 |
| 10000 | 0.10, 0.30, 0.30, 0.30 | 4 | CCGC | 0.1141528 |
| 10000 | 0.10, 0.30, 0.30, 0.30 | 6 | CCCTTC | 0.128236 |
| 10000 | 0.10, 0.30, 0.30, 0.30 | 8 | GCGGGTTC | 0.238902 |
| 100000 | 0.25, 0.25, 0.25, 0.25 | 4 | AGCG | 1.0054838 |
| 100000 | 0.25, 0.25, 0.25, 0.25 | 6 | AGTGGG | 1.451668 |
| 100000 | 0.25, 0.25, 0.25, 0.25 | 8 | CTGGCAAT | 2.5702341 |
| 100000 | 0.40, 0.20, 0.20, 0.20 | 4 | AAAA | 0.951846 |
| 100000 | 0.40, 0.20, 0.20, 0.20 | 6 | AAAAAA | 1.3469202 |
| 100000 | 0.40, 0.20, 0.20, 0.20 | 8 | AAAAAAAA | 2.3153352 |
| 100000 | 0.10, 0.30, 0.30, 0.30 | 4 | GGGC | 1.0166267 |
| 100000 | 0.10, 0.30, 0.30, 0.30 | 6 | CCCTGG | 1.3368695 |
| 100000 | 0.10, 0.30, 0.30, 0.30 | 8 | TCCCTGGC | 2.5355223 |

## VII. Discussion of Results

The findings demonstrate a discernible difference between the theme detection tests carried out with and without entropy filtering:

a) **Impact of Database Size**: It makes sense that as the database grows, so does the amount of time needed to find motifs. Nonetheless, entropy-based sequence filtering minimizes the quantity of sequences that need to be processed, contributing to a reduction in computing time in larger databases.

b) **Impact of Probabilities**: The variety of motifs found increases when the probabilities are more balanced (e.g., 0.25 for all bases). Conversely, repeating bases like "AAAA" dominate the motifs when the probabilities are biased (e.g., 0.40 for A).

c) **Effectiveness of Entropy Filtering**: The sequences become less repetitive and the themes found are typically more diversified after entropy filtering. Entropy filtering was able to cut calculation time in the studies with larger databases (100,000 sequences) by about 10–20% without sacrificing the quality of the motifs found.

## VIII. Conclusion

This work showed that optimizing motif recognition in genetic sequences can be achieved by applying entropy filtering. The method was able to focus on more chaotic and diverse patterns by eliminating low-entropy sequences, which improved motif discovery while lowering computational complexity. The findings emphasize the trade-off between processing speed and sequence variability, particularly in the context of big datasets.

To further increase performance, future study could investigate more complex filtering methods or test various entropy thresholds. Further insights into scalability may also be obtained by expanding the technique to handle even larger databases (millions of sequences).

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