Visualization of DNA sequences according to Chaos Game Representation (CGR)

24AIM144 Introduction to Data Compression

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1. Abstract

The rapid expansion of DNA sequence data necessitates the effective visualization and analysis of data. Chaos Game Representation (CGR) is a new way of graphically representing nucleotide sequences in a compact format. In this work, a Python script is introduced for translating DNA sequences to CGR images such that researchers and bioinformaticians can uncover concealed patterns and pathologies in genomic information. The script tries to provide an interactive interface and sequence upload capability for the generation of CGR plots.

2. Introduction:

DNA sequences are four-base long sequences of Adenine (A), Thymine (T), Cytosine (C), and Guanine (G). Sequence analysis may provide important information about genetic characteristics, mutations, and illnesses. Conventional analysis is text-based and requires much time. Chaos Game Representation

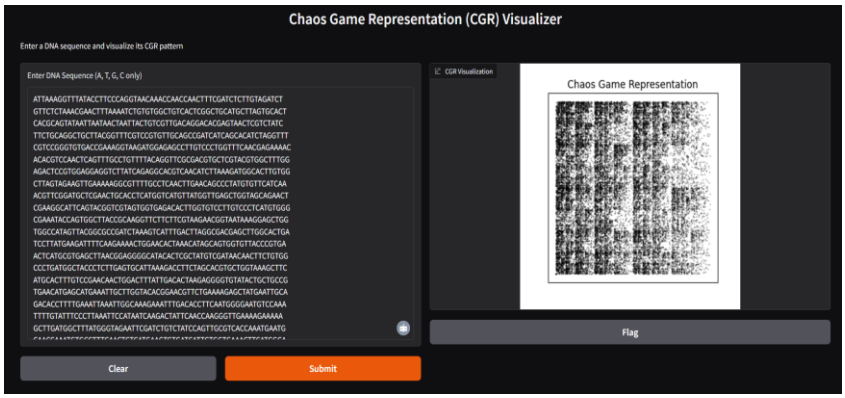
(CGR), found by Jeffrey in 1990, projects sequences on 2D space, and it forms pictures illustrating frequency and distribution of k-mers in a sequence. The graphical method is effective in recognizing patterns, repetition, or randomness in sequences in a matter of a few minutes.

3. Problem Statement

It is hard by text alone to comprehend and decipher long DNA sequences. There are insufficient graphical and intuitive tools to examine the pattern and distribution of the nucleotides of genomic sequences.

4. Objective

Create a basic, user-friendly web-based application or Gradio app for the visualization of CGR.



Accept raw DNA sequences as input.

TGTCTGGTAAAGGCCAACAACAACAAG

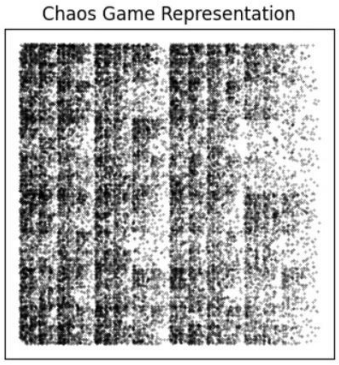
GCCAAACTGTCACTAAGAAATCTGCTGCTGAGGCTTCTAAGAAGCCTCGGCAAAAACGTA

CTGCCACTAAAGCATACAATGTAACACAAGCTTTCGGCAGACGTGGTCCAGAACAAACCC

AAGGAAATTTTGGGGACCAGGAACTAATCAGACAAGGAACTGATTACAAACATTGGCCGC

AAATTGCACAATTTGCCCCCAGCGCTTCAGCGTTCTTCGGAATGTCGCGCATTGGCATGG

Produce high-definition CGR shots of the given sequences.



Facilitate visualization of k-mer frequencies in genomic data.

5. Methodology

Input Handling: Accept DNA sequences as input in FASTA or string format.

CGR Algorithm:

1. Every vertex of a unit square is labeled with a nucleotide (A, T, C, G).
2. Start in the middle and half-step through the series, half-stepping to the appropriate corner based on the current nucleotide.
3. Plot all the points to construct the CGR image.
4. Visualization: Plot and color the points using matplotlib and seaborn in Python.
5. Web App: Frontend using Gradio for simplicity.

6. Tools and Technologies

- Python
- Matplotlib / Seaborn
- Gradio
- NumPy

7. Results

1. Successful CGR plots generated for different DNA sequences.
2. Visualizations establish unmistakable trends by sequence length and makeup.
3. Tool allows researchers to explore sequence structure intuitively.

8. Applications

- Bioinformatics research
- Genomic pattern recognition
- Mutation and anomaly detection
- Educational presentations of DNA structure

9. Conclusion

Chaos Game Representation is a powerful method for representing DNA sequences. The computer-generated representation bridges the gap between sequence information and intuitive sense through images. It gives scientists a new way of understanding genetic information.

10. Future Work

- Permit color-coding of higher-order k-mers.
- Embark on sequence alignment and clustering.
- Provide protein sequence and codon mapping assistance.
- Add saving and exporting of CGR images.

11. References

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Source Code:

```
import gradio as gr
import matplotlib.pyplot as plt


def generate_cgr(sequence):
    # Ensure uppercase and filter only A, T, G, C
    sequence = ''.join([base for base in sequence.upper() if base in "ATGC"])
    if len(sequence) < 2:
        return "Sequence too short!"


    # Assign corners to each base
```

```
    corners = {'A': (0, 0), 'T': (0, 1), 'G': (1, 1), 'C': (1, 0)}

    # Start from center
    x, y = 0.5, 0.5
    x_vals, y_vals = [x], [y]

    for base in sequence:
        cx, cy = corners[base]
        x = (x + cx) / 2
        y = (y + cy) / 2
        x_vals.append(x)
        y_vals.append(y)

    # Plot CGR
    fig, ax = plt.subplots(figsize=(4, 4))
    ax.plot(x_vals, y_vals, 'k.', markersize=0.5)
    ax.set_xticks([])
    ax.set_yticks([])
    ax.set_title("Chaos Game Representation")
    ax.set_aspect('equal')
    return fig

# Gradio interface
iface = gr.Interface(
    fn=generate_cgr,
    inputs=gr.Textbox(label="Enter DNA Sequence (A, T, G, C only)"),
```

```
    outputs=gr.Plot(label="CGR Visualization"),
    title="Chaos Game Representation (CGR) Visualizer",
    description="Enter a DNA sequence and visualize its CGR pattern"
)

iface.launch()
```