

# Generating a gene sequence

## 1. Problem Overview

In bioinformatics and AI, generating a gene sequence that closely matches a desired target sequence (representing the optimal or healthy gene) is a key problem.

In this task, two AI agents take turns selecting nucleotides (gene elements) from a shared pool. Goal of this game is to build a gene sequence that matches a target gene sequence as closely as possible.

## 2. Game Setup

- Pool: A list of gene elements (e.g, nucleotides like A, T, C, G)
- Target gene: A given target sequence (e.g, "ATCG")
- SID: Student ID, which determines position weight ranges.

## 3. Turns

- Two agents take turns selecting nucleotides to build the gene sequence. Agent 1 takes the first turn.
- Agent 1 tries to maximize similarity to the target gene.
- Agent 2 tries to minimize that similarity.
- After an agent selects a nucleotide, that nucleotide is removed from the pool, and the next agent must choose from the **remaining nucleotides** in the pool.
- This process continues until the pool is empty.

## 4. Utility Function

$$\text{Utility} = -\sum_{i=0}^{N-1} (w_i \cdot |ASCII(gene[i]) - ASCII(target[i])|)$$

- $N$  = Max length of the gene sequence or target;  $\text{Max}(\text{len}(\text{gene}), \text{len}(\text{target}))$
- $W_i$  = Weight at position  $i$  if available, otherwise 1
- $ASCII(\text{gene}[i])$  = ASCII of gene sequence character at  $i$  (or 0 if out of bounds)
- $ASCII(\text{target}[i])$  = ASCII of target sequence character at  $i$  (or 0 if out of bounds)

## 5. Weights

- Weights for each position correspond to the **last  $n$  digits of your student ID**, where  **$n$  is the length of the target**.

## Task I

Implement **minimax search with alpha-beta pruning** to generate the best possible gene sequence, given:

- A pool of nucleotides
- A target gene sequence
- Student ID

### Input

- The first line contains comma-separated uppercase letters — the initial **nucleotides pool**.
- The second line contains a string — the **target** gene sequence. A target can contain only the elements from the pool. The length of the target should not be greater than your student id.
- The third line contains a space-separated integer— **Your student ID**.

### Output

- The first line contains a string — the gene sequence built by the minimax algorithm that gives the best utility score.
- The second line contains a number — the final utility value.

### Sample Input and Output

Sample Input	Output
A,T,C,G ATGC 1 8 1 0 4 0 5 2	Best gene sequence generated: AGCT Utility score: -54
A,T,C,G GCAT 2 3 1 8 8 8 1 1	Best gene sequence generated: TGAC Utility score: -153
A,T,C,G CGAT 1 5 0 7 2 2 7 1	Best gene sequence generated: GTAC Utility score: -51

# Utility Calculation Breakdown For Task I

## Case 1 for sample input 1:

Gene sequence = "ATGC", Target = "ATGC", Weights = [4, 0, 5, 2];

ASCII Values: A=65, T=84, C=67, G=71.

$$\begin{aligned}\text{Score} &= -(4 \times |A - A| + 0 \times |T - T| + 5 \times |G - G| + 2 \times |G - G|) \\ &= -(4 \times |65 - 65| + 0 \times |84 - 84| + 5 \times |71 - 71| + 2 \times |67 - 67|) \\ &= -(4 \times 0 + 0 \times 0 + 5 \times 0 + 2 \times 0) \\ &= -(0 + 0 + 0 + 0) \\ &= 0\end{aligned}$$

## Case 2 for sample input 1:

Gene sequence = ATCG, Target = ATGC, Weights = [4, 0, 5, 2];

ASCII Values: A=65, T=84, C=67, G=71.

$$\begin{aligned}\text{Score} &= -(4 \times |A - A| + 0 \times |T - T| + 5 \times |C - G| + 2 \times |G - C|) \\ &= -(4 \times |65 - 65| + 0 \times |84 - 84| + 5 \times |67 - 71| + 2 \times |71 - 67|) \\ &= -(4 \times 0 + 0 \times 0 + 5 \times 4 + 2 \times 4) \\ &= -(0 + 0 + 20 + 8) \\ &= -28\end{aligned}$$

## Case 3 for sample input 1:

Gene sequence = AGCT, Target = ATGC, Weights = [4, 0, 5, 2]

ASCII Values: A = 65, G = 71, C = 67, T = 84

$$\begin{aligned}\text{Score} &= -(4 \times |A - A| + 0 \times |G - T| + 5 \times |C - G| + 2 \times |T - C|) \\ &= -(4 \times |65 - 65| + 0 \times |71 - 84| + 5 \times |67 - 71| + 2 \times |84 - 67|) \\ &= -(4 \times 0 + 0 \times 13 + 5 \times 4 + 2 \times 17) \\ &= -(0 + 0 + 20 + 34) \\ &= -54\end{aligned}$$

## **Case 4:**

Gene sequence = AGCTS, Target = ATGC, Weights = [4, 0, 5, 2]

ASCII Values: A = 65, G = 71, C = 67, T = 84, S = 83

$$\begin{aligned}\text{Score} &= -(4 \times |A - A| + 0 \times |G - T| + 5 \times |C - G| + 2 \times |T - C| + \text{default\_weight} \times |S - 0|) \\ &= -(4 \times |65 - 65| + 0 \times |71 - 84| + 5 \times |67 - 71| + 2 \times |84 - 67| + 1 \times |83 - 0|) \\ &= -(4 \times 0 + 0 \times 13 + 5 \times 4 + 2 \times 17 + 83) \\ &= -(0 + 0 + 20 + 34 + 83) \\ &= -137\end{aligned}$$

\*Target[4] = 0 as the gene sequence contains more nucleotides than the target.

## Task II

In this part of the game, the pool may include a special nucleotide 'S' at the rightmost position—representing a rare, powerful gene found in golden blood.

### Rules:

- If **Agent 1 (Maximizer)** picks 'S', it activates a **genetic booster**:
  - **Genetic Booster:** All **remaining weights** in the evaluation function starting from 'S' position will be multiplied by this equation => **(first 2 digits of your student id / 100)**
- Agent 2 plays normally. Meaning, even if agent 2 encounters nucleotide 'S', it will play normally as it was playing in the previous task (minimize that similarity).

Your goal is to help Agent 1 to decide whether using 'S' leads to a better utility score.

### Sample Input and Output

Sample Input	Output
A,T,C,G ATGC 1 8 1 0 4 0 5 2	No With special nucleotide Best gene sequence generated: SCTAG, Utility score: -96.38
A,T,C,G GCAT 2 3 1 8 8 8 1 1	YES With special nucleotide Best gene sequence generated: STGAC, Utility score: -126.11
A,T,C,G CGAT 1 5 0 7 2 2 7 1	NO With special nucleotide Best gene sequence generated: SACGT, Utility score: -94.65

Explanation:

1. NO, because without special nucleotide Score: -54 but With special nucleotide Score: -96.38
2. YES, because without special nucleotide Score: -153 but With special nucleotide Score: -126.11

## Utility Calculation Breakdown For Task II

Gene sequence = SCTAG, Target = ATGC, Weights = [4, 0, 5, 2]

Here, S is at position 0. So new weights = [0.72, 0, 0.9, 0.36] [All weights starting from position 0 are multiplied by the first 2 digits of SID / 100]

ASCII Values: A = 65, G = 71, C = 67, T = 84, S = 83

$$\begin{aligned}\text{Score} &= - (0.72 \times |S - A| + 0 \times |C - T| + 0.9 \times |T - G| + 0.36 \times |A - C| + \text{default\_weight} \times |G - 0|) \\ &= - (0.72 \times |83 - 65| + 0 \times |67 - 84| + 0.9 \times |84 - 71| + 0.36 \times |65 - 67| + 1 \times |71 - 0|) \\ &= - (0.72 \times 18 + 0 \times 17 + 0.9 \times 13 + 0.36 \times 2 + 1 \times 71) \\ &= - (12.96 + 0 + 11.7 + 0.72 + 71) \\ &= -96.38\end{aligned}$$

\*\*If gene sequence is CTSAG, weights will be [4, 0, 0.9, 0.36]. (All weights starting from position 2 are multiplied by [first 2 digits of SID / 100])