**BEAR AND STEADY GENE**

This Node.js program solves the “Steady Gene” problem by finding the smallest substring that can be replaced to make the gene steady. It first reads input from the standard input, storing the gene sequence and its length. The steadyGene function counts occurrences of each nucleotide and uses a sliding window technique to efficiently identify the minimum-length substring that balances all nucleotides.

The algorithm decreases the count of nucleotides as the window expands and increases it when shrinking the window from the left, updating the minimum length whenever a valid window is found. Finally, the main function writes the result to the output. This approach ensures the solution is both clear and optimized for large gene sequences.