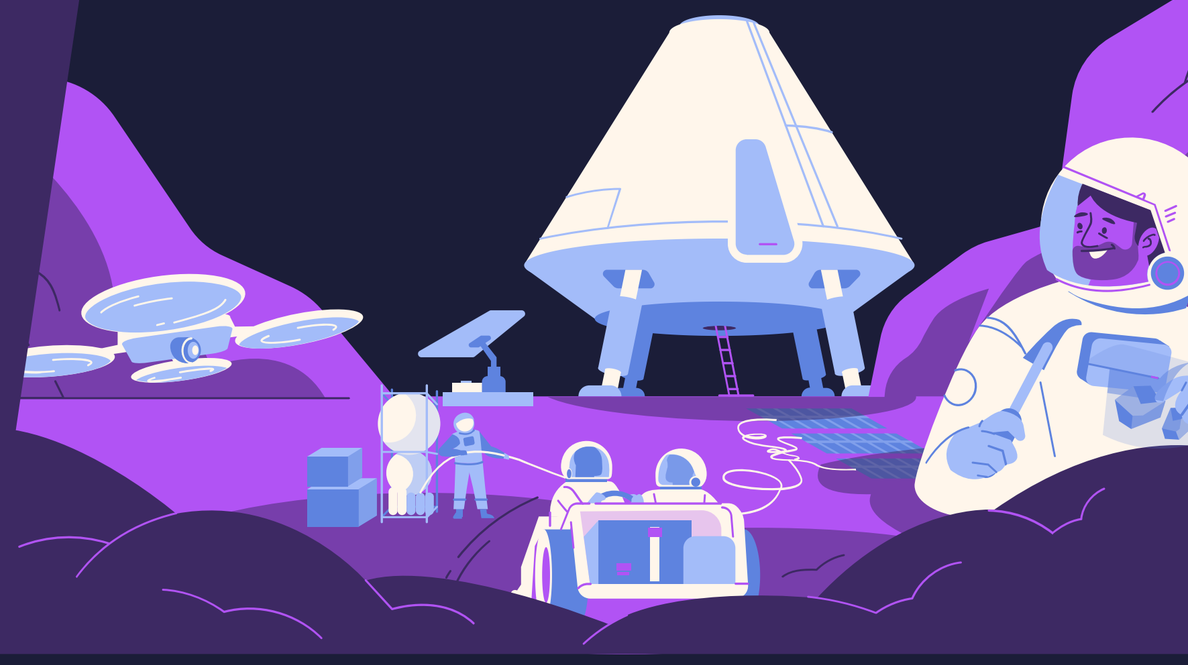
PLAGIARISM DETECTOR AND DNA MATCHER



INTRODUCTION

PLAGIARISM DETECTION

With the rise of digital content, plagiarism has become a significant issue. The aim of this project is to detect similarities between texts and ensure the originality of content.

DNA MATCHING

DNA sequencing comparison is essential in genetic research and forensics. This system helps match DNA sequences to identify common ancestry or genetic traits.

APPLICATIONS

Plagiarism Detection: Academics, publishing, content verification.
DNA Matching: Forensics, genealogy, genetic research.

LCS ALGORITHM

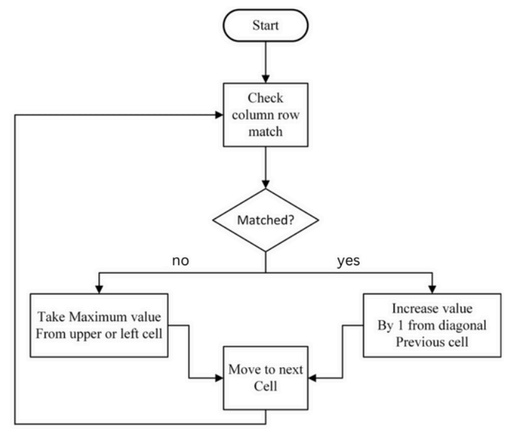
LONGEST COMMON SUBSEQUENCE

Finds the longest subsequence common to two sequences, ignoring minor differences.

HOW IT WORKS

Input: Two sequences (text or DNA).
Process: LCS algorithm identifies common subsequences.
Output:

Plagiarism: Similarity score, highlighting matching sections.
DNA: Similarity index for genetic analysis.



ADVANTAGES & CONCLUSION

ADVANTAGES OF USING LCS

1. Identifies exact subsequences, making it ideal for detecting complex similarities.
2. Applicable to both text-based and biological data.
3. Relatively simple and quick to implement in most programming environments.

CONCLUSIONS

This project demonstrates the utility of the LCS algorithm in two distinct domains—text comparison for plagiarism detection and biological sequence matching for DNA analysis. By harnessing the power of LCS, both problems can be tackled with efficient and reliable solutions.

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