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Visualization and Implementation of a Bioinformatics Analysis Workflow Management System Using ComfyUI

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The advancement of next-generation sequencing technologies has led to an unprecedented explosion of data in biological fields such as genomics and transcriptomics. While this big data is a critical resource for elucidating complex biological phenomena, its effective utilization requires advanced computational skills. However, a significant entry barrier persists for many biologists who are unfamiliar with programming or the Command Line Interface (CLI), hindering their ability to conduct data-driven research.

Although Workflow Management Systems (WFMS) have emerged to address these issues, they often introduce another technical hurdle for non-experts due to complex installation processes and the steep learning curve required to master platform-specific conventions.

In this study, we propose a new paradigm to overcome these limitations by leveraging ComfyUI, a node-based generative AI platform originally developed for image creation, to build an intuitive bioinformatics analysis environment. ComfyUI encapsulates individual analytical steps into 'nodes,' allowing users to visually construct an entire pipeline by connecting them. This approach enables the clear and transparent design of complex processes—such as data loading, quality control (QC), and sequence alignment—much like a flowchart.

This node-based paradigm eliminates the need to memorize CLI commands and systematically Consequently, researchers can shift their focus from the technical complexities of the analysis to the biological interpretation of their data.

The ultimate goal of this research is to actively utilize ComfyUI's custom node functionality to modularize core bioinformatics tools, thereby establishing a GUI-based analysis workflow that is easily accessible to non-experts. Furthermore, we aim to provide experts with a flexible framework for rapidly modifying and managing complex pipelines. We anticipate that this open-source initiative will foster community-driven development, contributing to the creation of a sustainable and collaborative ecosystem that maximizes the efficiency and accessibility of bioinformatics analysis.