

AuraGenome: An LLM-Powered Framework for On-the-Fly Reusable and Scalable Circular Genome Visualizations

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Circular genome visualizations are essential for exploring structural variants and gene regulation. However, existing tools often require complex scripting and manual configuration, making the process time-consuming, error-prone, and difficult to learn. To address these challenges, we introduce AuraGenome, a large language model (LLM)-powered framework for rapid, reusable, and scalable generation of multilayered circular genome visualizations. AuraGenome combines a semantic-driven multiagent workflow with an interactive visual analytics system. The workflow employs seven specialized LLM-driven agents, each assigned distinct roles, such as intent recognition, layout planning, and code generation, to transform raw genomic data into tailored visualizations. The system supports multiple coordinated views tailored for genomic data, offering ring, radial, and chord-based layouts to represent multilayered circular genome visualizations. In addition to enabling interactions and configuration reuse, the system supports real-time refinement and high-quality report export. We validate its effectiveness through two case studies and a comprehensive user study. AuraGenome is available at <https://github.com/Darius18/AuraGenome>.

The proliferation of high-throughput sequencing technologies has transformed genomics into a data-intensive field. Modern experiments

generate massive volumes of sequence-based data—such as structural variations, gene expression profiles, and chromosomal rearrangements—that are both large scale and heterogeneous. These characteristics make data interpretation challenging using traditional visualization methods. Visualization thus plays a crucial role, helping researchers explore complex relationships, uncover patterns, and effectively communicate findings.

Circular genome visualizations offer aesthetic appeal and spatial efficiency for representing long genomic sequences and their interconnections.¹ Tools, such as Circos,² have become standard for

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visualizing genomic alterations and chromosome structures in circular layout. However, they rely heavily on manual configuration and scripting, imposing steep learning curves and time-consuming workflows. Researchers often need to iteratively adjust parameters to fit data-specific requirements, which can impede productivity and limit the clarity or expressiveness of the final output. These limitations highlight the demand for intelligent, automated visualization solutions tailored to the unique characteristics of circular genomic data.

Recent advances in large language models (LLMs) offer new possibilities for generating genome visualizations via natural language. While LLMs can automate complex workflows, applying them in genomics remains challenging due to the need for precise intent parsing, domain data integration, and generation of meaningful, publication-ready visualizations.

To address these challenges, we present AuraGenome, an LLM-powered framework that enables genomics experts to rapidly generate, flexibly customize, and efficiently reuse multilayered circular genome visualizations. AuraGenome is grounded in task-specific requirements, identified through close collaboration with genomics experts to reflect real-world workflow needs. Based on the requirements, we conducted feasibility studies using LLMs for D3-based genome visualizations and selected GPT-4o and DeepSeek-R1 as the foundation of a semantics-driven multiagent workflow. This workflow decomposes complex visualization tasks into modular steps—such as intent recognition, layout recommendation, code generation, validation, explanation, and refinement.

Built atop this workflow, the interactive visual analytics system supports generation and editing of circular genome visualizations in three distinct layouts—ring, radial, and chord—with multilayer composition and domain-specific operations. A layer-aware reuse mechanism further enables tracing, adapting, and repurposing visualization steps to support efficient iteration and narrative report construction. We validate AuraGenome through two real-world case studies and both quantitative and qualitative user evaluations. In sum, the main contributions are summarized as follows.

- 1) A semantics-driven multiagent workflow that orchestrates seven LLM-based agents to transform data input into visualization-ready code output tailored for circular genome representation.
- 2) A visual analytics system that enables iterative refinement, direct manipulation, and layer-aware reuse to support the construction of complex, multilayered genome visualizations.

- 3) A comprehensive evaluation through two case studies and mixed-method user studies, demonstrating the framework's effectiveness in enhancing usability and efficiency.

RELATED WORK

Circular Genomic Visualization Applications

Circular layouts, with their compactness and multidimensional representation capabilities, are more suitable than linear visualizations for displaying the global features of genomes. Circular layouts map data onto channels, such as angles, radius, and layers, effectively illustrating hierarchical relationships and the distribution of significance across multiple data dimensions, such as gene functional regions, mutation distributions, and expression levels.

In bioinformatics, circular layouts have proven to be a highly effective visualization approach. In a study on the collinearity of the bZIP gene family in poplar, Zhao et al.³ employed a circular layout analysis method to explore gene functions and regulatory mechanisms by visualizing gene density, homologous blocks, and the distribution of segmental duplicated gene pairs. Peng et al.⁴ utilized circular layouts to depict plasmid structures carrying various genes, alongside sequence alignment results of other Enterobacteriaceae bacteria sharing similar plasmid backbones, thereby illustrating plasmid gene structures, multidrug resistance regions, and homology. Garcia et al.⁵ in their study of the Lima bean genome, used circular layouts to display multiple features to understand genome organization and evolution. Similarly, Zhang et al.⁶ adopted circular layouts to present genome characteristics in tea tree research, visualizing genetic diversity and evolutionary history. Despite their widespread use, these circular layouts largely rely on manual design, limiting their efficiency and general applicability.

Conventional Methods and Challenges in Genome Visualizations

Circos is one of the most widely used tools, generating circular visualizations through modular configurations to display genomic variations, expression levels, and chromosome structures. BioCircos⁷ reimplements Circos using a JavaScript library, enhancing interactivity. IntelliCircos⁸ leverages LLMs and a curated example-based dataset to support the intelligent generation of Circos-based visualizations through natural language input.

Several tools have been presented to support genome visualizations in different contexts. For

example, CGView⁹ and GView¹⁰ focus on browsing microbial genome annotations. BLAST Ring Image Generator¹¹ is designed specifically for comparing multiple prokaryotic genomes, utilizing BLAST results to produce circular images with an emphasis on comparative genomics. The PanVa visual analysis tool, developed by Brandt et al.¹² introduces novel aggregated graphical encoding techniques to assist researchers in exploring gene variations within complex genotype–phenotype relationships. Gosling¹³ provides a syntactic framework supporting circular layouts, with its follow-up work, AutoGosling,¹⁴ leveraging deep learning to optimize genomic visualization parameters. GlyphCreator¹⁵ is developed to parse existing circular visualization and enable secondary creation.

These tools depend on parameterized designs, making them poorly adaptable to diverse data types and lacking support for automation. This results in low generation efficiency and a reliance on user expertise, highlighting the need for automation and intelligence, which serves as the entry point for this study.

Visualization Generation by LLMs

The emergence of LLMs has enabled promising advances in the automatic generation of data visualizations, greatly reducing the technical threshold for manual design. For instance, CHAT2VIS¹⁶ translates natural language queries and tabular data into executable Python code, ChartGPT¹⁷ decomposes chart generation into multistep reasoning through fine-tuned FLAN-T5-XL, and LIDA¹⁸ employs a modular pipeline to support exploratory visual analysis and narrative construction. These approaches effectively address basic visualization needs and mitigate limitations in semantic understanding and long-context reasoning.

However, the generation of complex, customized, and interactive visualizations remains a significant challenge, particularly in scientific domains, such as genomics.⁸ Existing models often struggle to capture the intricate data relationships, layout dependencies, and intertrack interactions that characterize these specialized charts. As noted by Cui et al.¹⁹ LLMs frequently fail to retain contextual detail or integrate intermediate-level signals when processing long input sequences. In genomic visualization scenarios, these limitations lead to the omission of key features, incomplete logic, and the generation of erroneous code, especially when dealing with multitrack genome layouts or multiomics data integration.

REQUIREMENT ANALYSIS

Over the past two years, we worked closely with genomics experts in ongoing research projects to identify challenges in current workflows. These collaborations revealed pressing pain points in genome visualizations and highlighted the need for more intelligent and user-friendly tools, which motivated the formulation of our research objectives.

We began by analyzing 42 genomics papers published in top-tier journals (e.g., *Nature* and *Cell*), focusing specifically on the use of circular visualizations to represent complex genomic information, such as chromosomal rearrangements, gene interactions, and differential expression patterns. Rather than analyzing full texts, we systematically reviewed key figures in papers to identify common visualization types, usage contexts, and design goals. Through this process, we derived a taxonomy of three major layout styles: ring-based, radial, and chord-based circular genome visualizations. We also examined the tools used to generate these figures, finding that most relied on static platforms, such as Circos, which offer limited customization and interactivity. These findings informed our visual design and motivated our choice of a D3-based code to support extensibility and dynamic control.

To complement these figure-derived insights with domain-specific needs, we conducted semistructured interviews and design discussions with eight genomics experts (average experience: 8.6 years) from areas, such as cancer genomics, comparative genomics, transcriptomics, and bioinformatics tool development. These experts were selected from ongoing collaborations and research networks. During sessions, experts reviewed representative circular visualizations extracted from the 42 papers, provided feedback through scenario walkthroughs, and engaged in feature prioritization and mockup evaluations. Their feedback validated the proposed layout taxonomy and further shaped our understanding of critical challenges. Based on these findings, we distilled six key requirements that a genome visual analytics framework should fulfill to enhance analytical efficiency, expressiveness, and usability.

R1—Structured Data Ingestion and Profiling: It efficiently ingests tabular genomic data and performs automatic feature recognition and statistical profiling to support data familiarization and downstream tasks.

R2—Task-Aware Recommendation: It recommends suitable circular layouts based on semantics and analytic intent, such as detecting structural variations, comparing gene expression, or analyzing

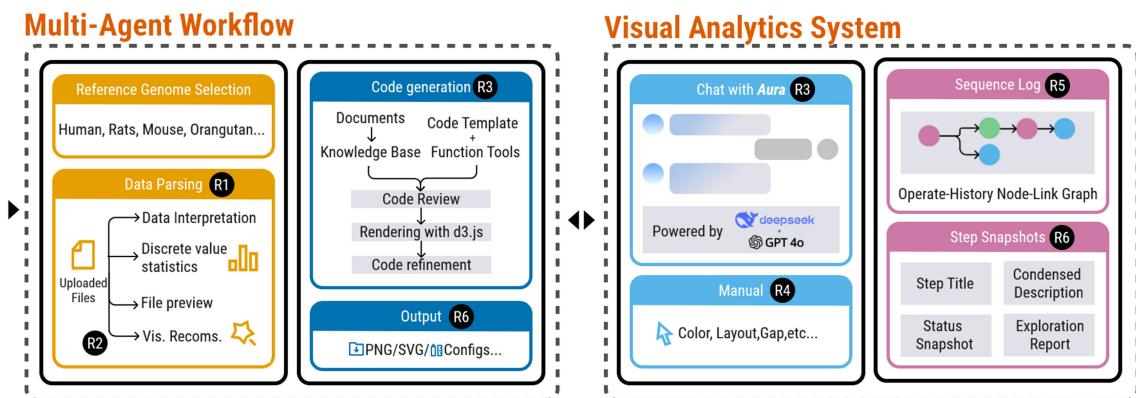


FIGURE 1. Overview of the AuraGenome framework, which integrates a modular multiagent workflow with an interactive visual analytics system to enable end-to-end generation, refinement, and exploration of genome-scale circular visualizations. Together, these two components fulfill six core requirements (R1–R6) to ensure scalability, interpretability, and reproducibility in genomic data visualizations.

methylation patterns, thereby reducing manual trial-and-error.

R3—Natural Language-Driven Control: It allows users to configure visualizations using natural language commands, supporting domain-specific actions, such as interval binning, differential gene labeling, and feature toggling, for supporting semantically aligned user interactions.

R4—Code-Free Incremental Refinement: It enables direct interaction with visualization styles—such as track ordering, radial spacing, and color encoding—without coding, allowing real-time, iterative refinement.

R5—High-Flexibility Interaction: It provides intuitive rules for code reuse, facilitating rapid adaptation to diverse visualization tasks with minimal effort.

R6—Narrative Exploration and Summarization: It supports annotation of specific tracks or elements and generates structured summaries to facilitate reporting, interpretation, and presentation.

FROM REQUIREMENTS TO AURAGENOME

To address the six task requirements identified through expert interviews and literature analysis, we presented AuraGenome, a framework that supports the intelligent generation and interactive refinement of circular genome visualizations. AuraGenome integrates a semantic-driven multiagent workflow with a user-facing visual analytics system, enabling a seamless transition from raw genomic data to publication-

ready visualizations. As shown in Figure 1, AuraGenome framework consists of two core components: a semantic multiagent workflow and a visual analytics system.

The workflow introduces specialized LLM-based agents responsible for key subtasks, including intent recognition, data parsing (R1), visualization recommendation (R2), and code generation and refinement (R3–R5). These agents are configured based on pre-evaluation of model capabilities and are enhanced through structured prompts, modular code abstraction, and retrieval-augmented grounding.

The system enables users to refine, adjust, and manage visualizations through both direct manipulation and natural language input (R3). It supports visual parameter editing (R4), trackwise customization (R5), and summarization of analytical steps (R6). In particular, we formalize three representative layout strategies for circular genome visualizations: ring (concentric stacking of feature tracks), radial (center-out projection), and chord (arc-based linking of genomic loci). These layouts can be selected, composed, and refined interactively through novel interface elements, such as the parameter panel and sequence log, which together enable visual code reuse, stepwise branching, and traceable generation history.

AURAGENOME MULTIAGENT WORKFLOW

Prestudy for Agent Assignment

To construct an effective multiagent workflow for genomic visualizations, we first conducted a

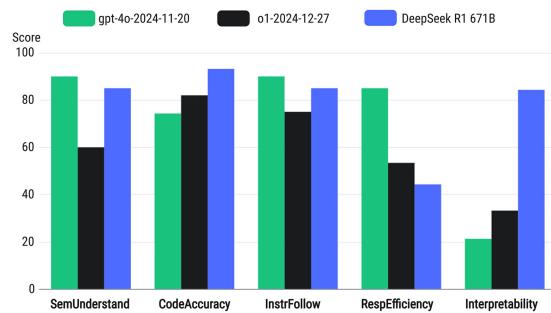


FIGURE 2. Comparison of LLM output assessments across five evaluation dimensions in GenoVis-300 dataset.

prestudy evaluating the capabilities of LLMs on domain-specific tasks. We created a benchmark dataset, *GenoVis-300*, containing 300 natural language prompts derived from real genomics use cases. These prompts spanned six key task types: data parsing, chart recommendation, D3.js code generation, code modification, explanation, and style adjustment. We listed three LLMs—GPT-4o-2024-11-20, GPT-o1-2024-12-27, and DeepSeek-R1-671B as candidates—to evaluate across five criteria relevant to the *AuraGenome* workflow: semantic understanding, code accuracy, instruction following, response efficiency, and output interpretability.

Each model was rated on a normalized 0–100 scale, where scores above 90 reflected accurate and complete results, 70–89 indicated mostly correct outputs with minor issues, 50–69 reflected partial success with notable omissions, and scores below 50 indicated critical errors. Evaluations were independently conducted by three genomics experts using anonymized outputs and a standardized rubric to ensure fairness and consistency.

As shown in Figure 2, GPT-4o performed best in semantic parsing and explanation tasks and DeepSeek-R1 excelled in structured code generation. GPT-o1 showed moderate performance but struggled with layout consistency. These results guided our agent-model assignment strategy: GPT-4o was assigned to language-oriented agents, while DeepSeek-R1 was chosen for code-focused agents. This division supports a modular workflow where each agent operates on tasks aligned with the LLM’s strengths.

Multiagent Workflow Construction

Given the diverse and complex nature of genomic visualization tasks—ranging from semantic interpretation to code synthesis and validation—monolithic

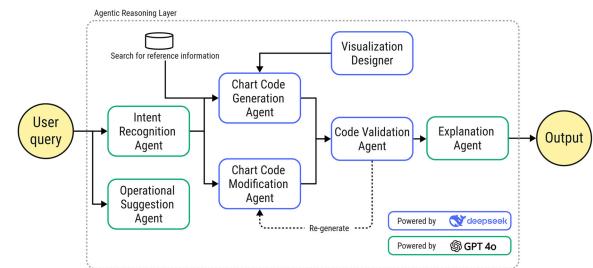


FIGURE 3. Overview of the multiagent workflow for generating visualization-ready chart code from user queries. Each agent is responsible for a distinct function—ranging from intent recognition and operational suggestion to code generation, validation, and semantic explanation—while communicating through structured message passing.

prompting strategies often suffer from instability and lack of control. Based on iterative experiments on multiagent workflow, we designed a modular, multiagent workflow where each LLM-based agent is responsible for a specific subtask aligned with its model capabilities. This design enables finer grained orchestration, greater controllability, and better task transparency.

Figure 3 provides an overview of the multiagent workflow. Each agent is positioned along a data-to-visualization pipeline, handling a specific functional scope and interfacing with others through clearly defined message-passing mechanisms. The operational details of each agent are as follows.

1. *Intent Recognition Agent*: The intent recognition agent serves as the entry point of the multiagent workflow, responsible for interpreting the user’s natural language input and routing it to the appropriate downstream process. Specifically, it distinguishes between two core categories of requests: visualization generation (e.g., “draw a circular layout plot for SNP distribution”) and code modification (e.g., “change the color of the mutation track”).

Rather than relying on keyword triggers or hand-crafted rules, this agent leverages the LLM’s semantic parsing capability to identify user intent at a functional level. This classification enables the system to activate only the relevant agents, reducing unnecessary computation and maintaining contextual focus. By modularizing intent routing, the system supports extensibility to new task types and ensures robustness under ambiguous user input.

2. *Visualization Designer Agent*: The visualization designer agent streamlines chart selection by analyzing the structural and semantic input—such as mutation types, zygosity profiles, and chromosomal locations—and recommending an appropriate layout.

This agent relies on embedded domain heuristics and data-profile templates to map data features to visualization strategies (e.g., heatmaps for expression data or links for structural variation). It also generates textual rationales that accompany each recommendation, improving transparency and helping users understand the rationale behind the system’s suggestions. This agent bridges the gap between raw genomic data and visualization design, enabling prelayout planning.

3. *Chart Code Generation Agent*: The chart code generation agent transforms user-specified visualization designs into executable chart code. Given the complexity of genome-scale circular visualization and the flexibility of D3.js, direct code generation by LMs can be error-prone and hard to control. To address this, the agent employs a hybrid approach that integrates LLM generation with structured code templates and high-level utility functions.

This abstraction reduces the granularity of code-level decisions, allowing the agent to focus on content selection and parameter instantiation rather than low-level implementation details. It ensures that generated charts conform to best practices in layout structure and semantic consistency. The modularity also improves maintainability and supports downstream code reuse and refinement.

4. *Chart Code Modification Agent*: Instead of generating code from scratch, many operations involve incremental changes to existing visualizations—such as adjusting colors, track spacing, or label formats. The chart code modification agent is designed to handle such requests through in-place parameter tuning within previously generated codes.

This agent preserves the integrity of the chart structure while applying precise updates aligned with the user’s intent. It parses the code context, identifies relevant parameters, and rewrites only the affected components. This design promotes continuity in the visualization process, avoids unintended side effects, and supports real-time iteration and visual feedback.

5. *Code Validation Agent*: The code validation agent serves as a safeguard that inspects generated code for syntax errors, data mismatches, or domain-inconsistent configurations before execution. Rather than relying solely on runtime error detection, this agent performs static checks based on domain-specific rules, such as track overlap avoidance, supported parameter values, and consistent color mapping. It uses a validation prompt schema to guide the LLM in diagnosing potential issues and suggesting fixes. While performance validation was addressed in the earlier model pre-study, this agent’s role in the pipeline is to provide real-time, explainable verification and reduce user debugging burden.

6. *Explanation Agent*: The explanation agent provides semantic annotations for generated code, helping users understand what each block of code does, why it was generated, and how it relates to the genomic dataset. This agent compares new and previous code versions, highlights the differences, and outputs human-readable commentary for each modification.

7. *Operational Suggestion Agent*: To support user exploration and reduce cognitive load, the operational suggestion agent generates actionable prompts based on the current chart state and user goals. These suggestions include next-step operations (e.g., “add a gene density track” and “switch to cytoband view”).

Optimization for LLM-Based Agents

While the multiagent architecture in AuraGenome enables modular task delegation, the reliability and quality of LLM-generated outputs—especially for complex genomic visualization tasks—critically depend on how each agent is instructed, grounded, and controlled. To address this, we introduce three complementary strategies to enhance agent execution quality: a structured prompt design for role alignment, a retrieval-augmented generation (RAG) mechanism for grounded code synthesis, and a modular abstraction layer to reduce code-level complexity.

RAG for Code Generation

To further stabilize generation and align outputs with domain-specific conventions, we integrate a RAG mechanism into the chart generation and validation agents. Prior to code synthesis, the agent retrieves relevant templates from a curated knowledge base of validated chart examples, each

annotated with metadata, such as chart type, data modality, and genomic scale.

Retrieval is performed using a hybrid strategy that combines semantic vector matching (weight 0.7) and keyword-based exact search (weight 0.3). Retrieved examples are injected into the prompt as in-context references, grounding the model’s generation process. This approach improves fidelity to biological conventions, reduces hallucinated code patterns, and enhances output stability—especially in multturn interactions or layout-specific tasks.

Modular Code Interfaces for Reusability and Stability

Although D3.js is a flexible and expressive library for interactive visualizations, its fine-grained syntax and tightly coupled configuration logic pose significant challenges for LLMs, especially in producing robust and maintainable code. To alleviate these issues, we abstract commonly used visualization patterns into reusable utility functions and decompose the codebase into modular, semantically coherent components. This restructuring reduces the generation complexity and enables LLMs to focus on higher level content specification rather than low-level implementation details.

The modular architecture separates core responsibilities into logically distinct layers. Data processing routines—such as genomic binning, mutation filtering, and data downsampling—are isolated from interaction behaviors, which handle operations, such as region highlighting, track reordering, and feature selection. The rendering logic is kept lightweight, invoking these modular components to assemble multilayered circular layouts, including ring, radial, and chord layouts. This modular architecture offers several benefits: it shortens the prompt length, reduces cognitive load for agents, and improves output generalizability across diverse tasks. Moreover, it supports structured prompt construction, allowing the system to reference and invoke specific functionality through scoped instructions.

Algorithm 1. Structured Prompt Construction in Blocks for Agent Execution.

Require: User input U (e.g., data file, textual instruction); Agent role R ; Model type M
Ensure: Final prompt P to be executed by LLM agent
Initialize empty prompt P
Embed role definition into P :
 “You are an expert in R, assisting the user with a genomic visualization task.”

```

Insert user context  $U$  as task description
Add <search_and_reading> block:
  Retrieve top- $k$  relevant templates from knowledge base
   $\mathcal{K}$  using hybrid search
  Append results to  $P$  as in-context references
Add <tool_calling> block:
  Instruct the model to use predefined utility functions
  from code library  $\mathcal{L}$ 
Add <layout_constraints> block:
  Enforce chart layout logic and prevent track overlap
if agent  $R$  is a validation agent then
  Add <error_detection> block:
    Check for syntax, logic, and parameter errors
  Add <final_review> block:
    Ensure modifications preserve prior valid outputs
end if
Add <suggested_adjustments> block:
  Ask model to suggest up to 3 improvements (e.g., style,
  color, spacing)
Append <output_format> block:
  Specify required output format (e.g., JSON,
  JavaScript, Markdown) for system integration
return Final structured prompt  $P$ 

```

Prompt Construction Architecture for Agent Execution To ensure consistency, reliability, and domain alignment, we design a structured prompt construction architecture supporting all LLM-based agents. Rather than relying on ad-hoc inputs, each agent dynamically assembles its prompt using a modular schema tailored to its role, input context, and output format.

This architecture significantly reduces hallucinations, improves reasoning traceability, and facilitates integration with RAG and utility libraries. The prompt template includes a role definition, task context, optionally retrieved templates, tool function references, layout constraints, and validation or output formatting blocks. This structured prompt ensures that each LLM invocation is aware of its role, operates within domain-safe constraints, and delivers well-structured, machine-consumable output. The complete construction process is summarized in Prompt Strategy 1.

AURAGENOME VISUAL ANALYTICS SYSTEM

System Overview

The visual analytics system of AuraGenome is designed to interactively generate, refine, and manage multilayered circular genome visualizations through a combination of natural language interaction and direct manipulation. As illustrated in Figure 4, the

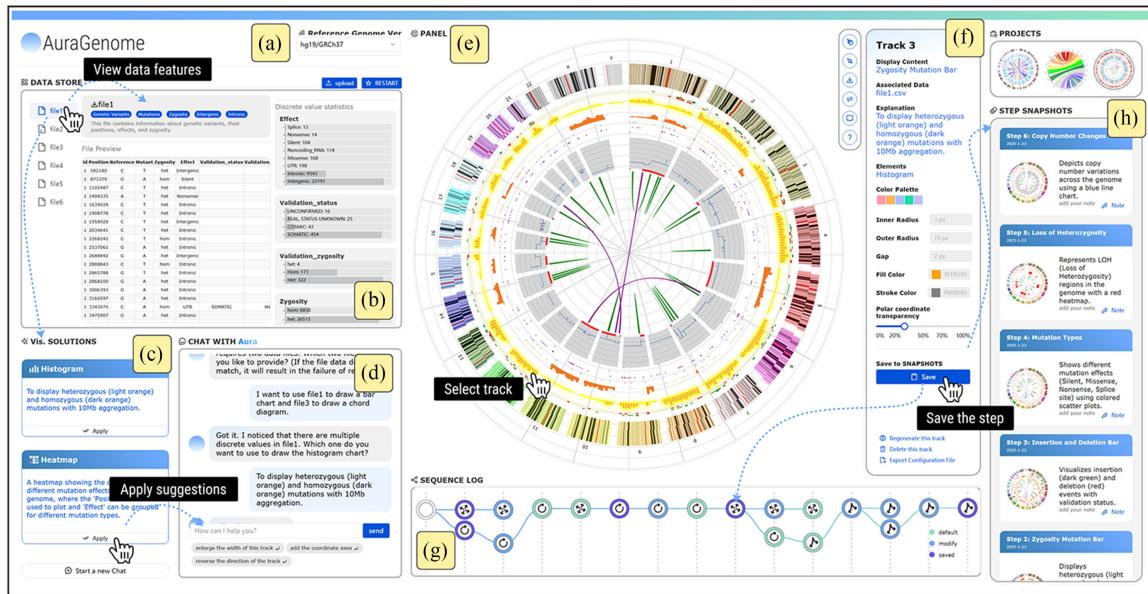


FIGURE 4. Visual analytics system interface of AuraGenome. Users begin by selecting reference data and exploring genomic features and statistics in (a) Reference Genome Selection and (b) Data Store View. (c) Visualization Solution Panel provides recommendations that applied and refined through (d) Chat with Aura Panel. (e) Central Visualization Panel and (f) Parameter Panel enable visual exploration and layerwise interaction. (g) Sequence Log View captures each generation step for reuse, while (h) Project History and Step Snapshots View supports project management and report output.

interface comprises multiple coordinated panels that together support the entire analytical workflow—from genome selection and data inspection to visualization generation and narrative reporting.

- (a) *Reference Genome Selection:* It enables selecting from standard genome assemblies (e.g., hg19/GRCh37), which serve as the foundational coordinate system for layout construction and alignment.
- (b) *Data Store View:* It presents uploaded genomic datasets alongside extracted features (e.g., mutation categories, zygosity types, and validation status). This view facilitates initial familiarization with data and informs downstream visualization recommendations.
- (c) *Visualization Solution Panel:* It suggests agent-driven visualization templates based on inferred data characteristics and conventional visual mappings. Users can directly apply these suggestions to expedite layout design and reduce manual configuration.
- (d) *Chat with Aura Panel:* It is a conversational interface that bridges users with the backend multiagent workflow. Natural language commands—such as “increase spacing of Track 3”

or “highlight LOH (Loss of Heterozygosity) regions”—are semantically parsed and dispatched to the appropriate agents for contextual chart modification.

- (e) *Central Visualization Panel:* It displays the multitrack circular genome chart, supporting layered rendering of structural variants, mutations, and genomic annotations with rich encoding strategies.
- (f) *Track Parameter Panel:* It offers fine-grained, layer-specific customization options, including radius, color, spacing, and angular transparency. All adjustments are reflected in real time within each visualization, promoting iterative refinement.
- (g) *Sequence Log View:* It visualizes the generation process through a node-link graph, where each node represents a distinct code-level output (e.g., a complete track or layout modification). In contrast to traditional action-level timelines, this abstraction emphasizes reusable configurations and logical checkpoints, allowing users to branch from prior states and efficiently explore design alternatives.
- (h) *Project History and Step Snapshots View:* It maintains comprehensive project records and allows users to bookmark intermediate visual

states. Snapshots can be annotated and serve as references for reporting, side-by-side comparison, or iterative editing.

The subsequent sections focus on the Central Visualization and Track Parameter Panels, along with the Sequence Log View, detailing their visual encodings and interaction design principles.

Central Visualization and Parameter View

The Central Visualization and Parameter View serves as the core canvas of the AuraGenome system, supporting dynamic construction and real-time refinement of multilayered circular genome visualizations. As shown in Figure 4(e), the visualizations are anchored to a user-specified reference genome (e.g., hg19), which defines the genomic coordinate system. New tracks are added from the outermost ring inward, following a sequential layout mechanism that enables a layered representation of heterogeneous genomic features.

The system supports three distinct track layouts—ring, radial, and chord—directly aligned with the three layout categories defined in our earlier design analysis. These styles enable users to map genomic data onto concentric rings for layered features, radial axes for attribute-specific distributions, and curved links for intersegment relationships, respectively. A polar coordinate grid in the background provides visual scaffolding to facilitate alignment, comparison, and scale estimation. For each uploaded dataset, users can select relevant attributes (e.g., mutation zygosity, variant type, and expression values) as the basis for visualizations. Through the parameter panel [see Figure 4(e)], users configure track-specific properties, including encoding types, color schemes, inner/outer radii, spacing, and border styles. Each track may include an annotation to describe the underlying data and rationale for the chosen visual encoding.

This view supports two primary interaction pathways for visualization specification: (1) recommendation-based initialization, where users adopt suggested layouts generated by the visualization designer agent, and (2) dialogue-based customization, where users issue natural language commands (e.g., “make the inner track blue” or “reduce the outer radius of track 3”), which are interpreted and executed by the multiagent workflow.

After each step, each visualization remains fully interactive. Users can refine elements directly via panel interactions, enabling real-time updates to styling,

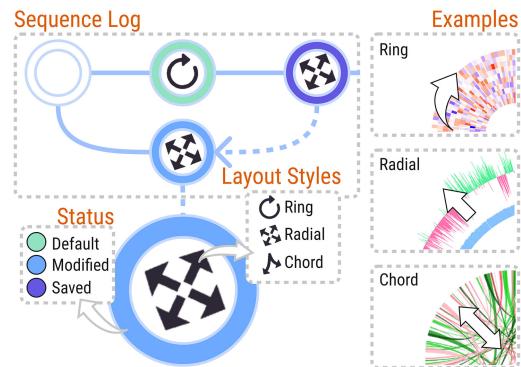


FIGURE 5. Visual design of Sequence Log View. Each node represents a generation step, with the inner icon indicating the layout type (ring, radial, or chord) and the outer ring encoding the generation status (default, modified, or saved).

geometry, and track ordering. The interface supports reordering, in-place editing, and annotation overlays, allowing iterative refinement of the layout. Final visualizations can be exported to the Step Snapshots View, preserving the current configuration along with all parameter settings and user notes. This whole process facilitates downstream reporting and publication.

Sequence Log View

The Sequence Log View [see Figure 4(f)] is a node-link-based visualization designed to encode and navigate the LLM-driven process of genomic visualization generation. It explicitly represents the stepwise evolution of a user’s analytical path, capturing both the structural diversity of generated charts and the decision logic behind each step.

The visual design is illustrated in Figure 5, which details the encoding of layout types and generation statuses. Each node in the sequence is visually encoded using an inner and outer region. The inner region denotes the layout type used in that step—ring, radial, or chord—while the outer region encodes the generation status, distinguishing default, modified, and saved checkpoints through color. The sequence is arranged from left to right, with each column representing a distinct generation step. Nodes are horizontally aligned to reflect chronological order, while their vertical positions can be freely adjusted to improve visual clarity.

Connections between nodes are rendered using quadratic Bézier curves, with vertical dashed separators delineating generative stages. Each node is coupled with detailed metadata—including layout configuration, applied parameters, and associated

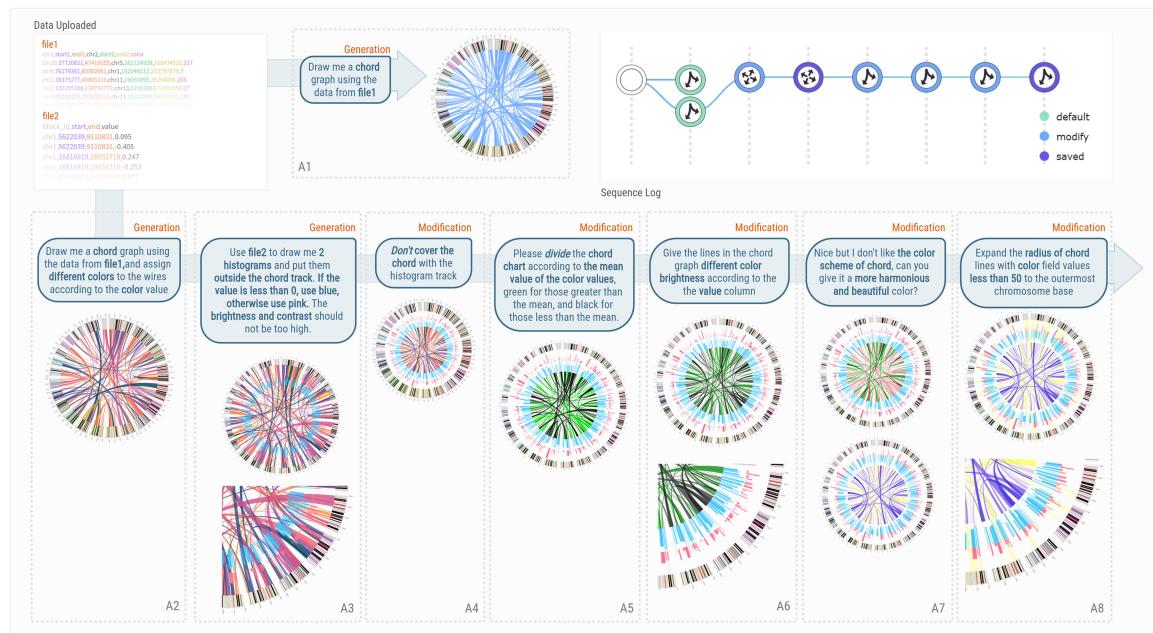


FIGURE 6. Visualization workflow for AML case study. (A1) and (A2) Data upload and autoparsing of chromosomal translocation and gene expression profiles. (A3) Visualization recommendation and selection of chord + ring layout. (A5) First-generation result with default color scheme. (A6) and (A7) Interaction-based customization of color styles for enhanced visual contrast.

model responses—ensuring high interpretability and workflow traceability. In cases of generation failure or suboptimal results, users can rebranch from any previous node to resume iteration with full context. The view also supports efficient reuse: users may double-click a node to draw a dashed link to subsequent steps and collaborate with agents to selectively inherit code and parameters. This helps avoid repeating past errors while maintaining focus on the current branch context.

Overall, the Sequence Log View provides a structured, interpretable, and interactive mechanism that enables users to trace generation history, modify intermediate states, and strategically reuse successful configurations, enhancing control, reliability, and efficiency in the genomic visualization process.

CASE STUDIES

To evaluate the practical effectiveness and generalizability of the AuraGenome framework, we conducted two real-world case studies involving distinct genomic analysis tasks. These studies serve to validate both the multiagent workflow and the visual analytics system in supporting domain-specific generation, exploration, and reuse of circular genome visualizations.

The system requirements were originally derived through iterative co-design sessions with eight genomics experts. To ensure objective evaluation, the following case studies were carried out by a separate group of two extra experts—denoted as E_A and E_B (mean experience: 10.3 years)—who were not involved in previous sections. These experts applied AuraGenome to authentic genomic analysis scenarios, enabling us to assess its usability and effectiveness in real-world contexts while minimizing evaluative bias.

Case 1: Chromosomal Translocation and Gene Expression Profiling in Acute Myeloid Leukemia (AML)

In this case, E_A aimed to investigate chromosomal translocation patterns in AML, a hematologic malignancy often driven by specific structural variants. The overall workflow is illustrated in Figure 6.

To examine the positional distribution of breakpoints and their potential correlation with functional genomic regions, E_A uploaded a curated dataset of chromosomal translocations. Leveraging AuraGenome's automated parsing and feature extraction, the system computed translocation frequencies and mapped them to brightness levels within a circular layout [see Figure 6(A5)]. To visualize interchromosomal associations, E_A selected a chord layout, which

highlighted recurrent co-occurrences of breakpoints across different chromosomes.

To complement the structural data, E_A incorporated a second dataset containing gene expression profiles, which was rendered as a dual-colored annular bar chart encircling the chord layout. Red bars indicated regions of upregulated expression, while blue bars represented downregulated zones. This integration enabled visual alignment of structural variants with transcriptional activity, supporting exploratory hypotheses on regulatory disruptions and disease mechanisms in AML.

When the default color scheme failed to clearly distinguish between structural and expression-related patterns, E_A engaged the system's natural language interface with the prompt: "Can you give it a more harmonious and beautiful color?" Aura responded with several palette suggestions, from which E_A selected a violet and lemon-yellow combination to improve visual contrast [see Figure 6(A6) and (A7)]. The adjustment was immediately applied via the parameter panel and reinforced through backend code modifications guided by the LLM agent.

The entire process—from data upload to visualization refinement—was completed within 20 min. Notably, E_A identified that the genomic region chr1:16816819–18551718 exhibited both a high frequency of translocation breakpoints and significant gene upregulation. This integrated insight led E_A to annotate the region as a potential biomarker for AML, suggesting it as a candidate for future experimental validation.

Case 2: Somatic Mutation Landscape of the COLO-829 Genome

To evaluate the reusability and task adaptability of AuraGenome, we conducted a second case study involving expert E_B , who aimed to replicate and extend insights from a widely cited study in Nature²⁰ that mapped the somatic mutation landscape of the COLO-829 melanoma genome. Building on the workflow established by E_A , this case demonstrates that how the Sequence Log View facilitates the inheritance and contextual reuse of prior visualization logic.

Instead of initiating a new pipeline from scratch, E_B accessed the sequence log from Case 1 and created a new root node branching from an earlier step [see Figure 7(a)]. Although the visual outputs were independent, the new workflow retained structural and contextual linkage to its source, allowing E_B to reuse layout strategies and code components. Upon uploading a new mutation dataset for the COLO-829 genome,

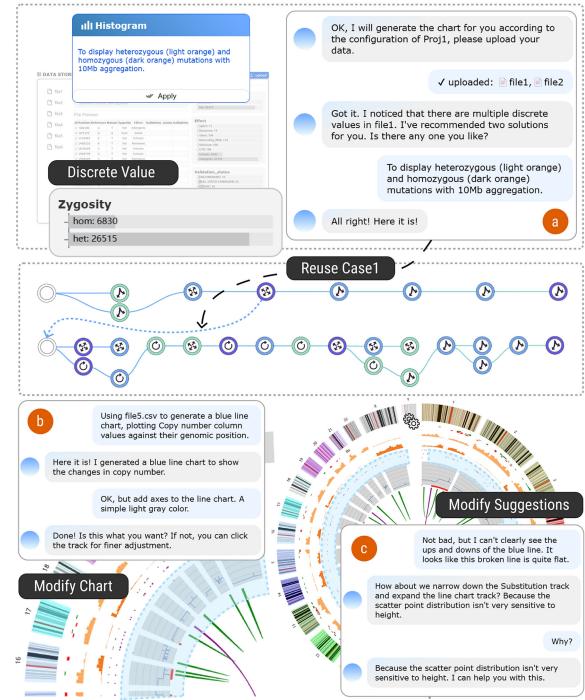


FIGURE 7. Visualization workflow excerpt from the COLO-829 case study. (a) Reuse the configuration from Case 1 and automatically parse the new dataset. (b) Generate and modify the copy number variation track. (c) Receive suggestions and explanations from Aura, followed by interactive and iterative modifications.

AuraGenome initialized a fresh workflow using layout configurations derived from the inherited context.

Following E_B uploaded the mutation dataset, AuraGenome automatically rendered two tracks: an orange bar chart encoding zygosity information and a chord layout representing chromosomal rearrangements. E_B subsequently uploaded an additional dataset with insertion and deletion events and issued a natural language instruction to display validated entries using a dual-color scheme. The system accurately filtered and visualized these mutations according to the user's intent.

Additional customization involved creating a substitution mutation track, with categorical encoding for mutation types using distinct color assignments, alongside a copy number variation track rendered as a blue line chart. When overlapping between adjacent tracks reduced visual clarity, E_B invoked the system's recommendation module to refine the layout. Adjustments to track spacing and height were made to enhance overall readability [see Figure 7(c)].

The resulting chart included seven fully customized genomic tracks and reproduced the structure of the original Nature visualizations with high fidelity. More importantly, AuraGenome's interface preserved full interactivity throughout the process, enabling incremental edits and layout reconfigurations. The system also recorded each generation step and its associated metadata within the Step Snapshots View, producing a transparent and reproducible workflow that facilitates downstream analysis, sharing, and collaborative validation.

USER STUDY

To evaluate the effectiveness and usability of the AuraGenome, we conducted an in-lab user study focusing on system learnability, user experience across disciplines, and its utility in real analysis tasks.

Study Design and Implementation

Participants and Tasks

In total, 12 participants with a background in biology (average experience: 4 ± 1.5 years) were recruited for the experiment, including 10 bioinformatics researchers (P_1-P_{10}) and two wet-lab researchers (P_{11} and P_{12}). Each participant was instructed to complete the same visualization task: constructing a multilayered circular chart using the provided genomic variation data (e.g., chromosome location, mutation type, and zygosity). The task was performed using both Circos and AuraGenome. Performance was evaluated through quantitative analysis of task completion time, accuracy, and a posttask questionnaire. Additional qualitative feedback was collected via follow-up interviews.

Procedure

The study adopted a within-subject crossover design. Participants were randomly assigned to two groups: Group A ($n = 6$) used Circos first, followed by AuraGenome after a 48-h interval, and Group B ($n = 6$) followed the reverse order. Each session consisted of the following steps.

1. *Training (15 min)*: A standardized introduction to both tools was provided through documentation and guided walkthroughs.
2. *Task Execution (maximum 150 min)*: We recorded the task completion time and logged all parameter modifications for later analysis.
3. *Questionnaire (10 min)*: Participants completed a six-item Likert scale survey evaluating confidence, usability, and overall satisfaction.

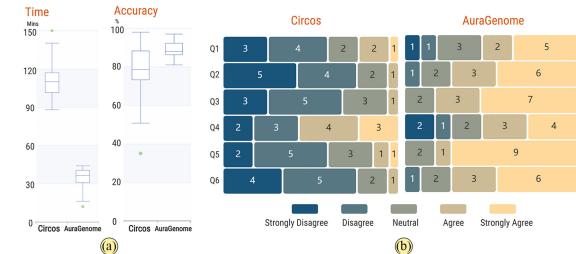


FIGURE 8. Quantitative analysis results. (a) Task completion time and accuracy comparison and (b) user ratings across six evaluation questions.

4. *Interview (15 min)*: Participants provided open-ended feedback regarding system usability, task experience, and suggestions for improvement.

Quantitative Results

AuraGenome significantly outperformed Circos in both task efficiency and output accuracy. On average, participants completed the assigned visualization task in 34 min (Standard Deviation (SD) = 9.16) using AuraGenome, compared to 112 min (SD = 16.5) with Circos—a 69% reduction in time. Notably, one participant was unable to complete the task within the allotted time when using Circos. As shown in Figure 8(a), accuracy scores, evaluated by two independent genomics experts, averaged 89% (SD = 4.61) with AuraGenome versus 76% (SD = 18.31) with Circos. AuraGenome also exhibited lower performance variance across participants, suggesting improved consistency.

To assess user experience, we administered a six-item Likert-scale questionnaire adapted from the NASA Task Load Index (NASA-TLX) framework, covering the following dimensions [see Figure 8(b)].

- Q1: Confidence in the accuracy of generated results.
- Q2: Perceived ease of learning and use.
- Q3: Efficiency in achieving intended outcomes.
- Q4: Satisfaction with overall system functionality.
- Q5: Ease of fine-tuning and customization.
- Q6: Overall satisfaction and enjoyment.

AuraGenome achieved significantly higher ratings than Circos on five of six questions (Q1–Q3, Q5, and Q6; $p < 0.05$, Mann–Whitney U test), with Q4 (functionality) also trending positively ($p = 0.0588$). In addition, 11 out of 12 participants reported that AuraGenome was easier to use and customize, and eight expressed greater confidence in the correctness.

These findings demonstrate that AuraGenome provides notable improvements in usability, efficiency,

and accuracy over traditional tools, particularly benefiting users with limited programming expertise.

Qualitative User Reflections

To complement the quantitative results, we collected open-ended feedback from 12 participants through posttask interviews and questionnaires. We summarized them for further thematic analysis. The result revealed four recurring reflections about AuraGenome's usability, functionality, and areas for growth.

Natural Language as a Shift in Interaction Paradigm

All participants embraced the natural language interface as a major improvement over traditional config-file editing. Chat with Aura lowered the barrier to entry and allowed users to express visualization intent more directly (P_2 , P_3 , P_8 , and P_{10}). The real-time visualization generation further reduced trial-and-error, streamlining the configuration process (P_1 , P_2 , P_4 , and P_9).

Integration of Domain Knowledge

Participants highlighted that AuraGenome reduced the burden of preselecting visualization strategies by automatically recommending composite charts tailored to the input data type. In contrast to traditional workflows requiring prior layout selection before track configuration, P_6 noted, “*The ‘variant + heatmap’ combo matched my study better than my own plan.*” By surfacing context-aware suggestions, the system not only accelerated chart creation but also introduced users to more informative visual encodings than they might have initially decided.

Cross-Disciplinary Usability

The system was seen as accessible to both computational and wet-lab users. While experienced users valued the ability to issue fine-grained commands, including suggestions for direct SVG editing (P_4 and P_{10}), wet-lab participants noted that they could independently produce publication-ready charts—an empowering capability for nonprogrammers (P_{11} and P_{12}). This cross-disciplinary flexibility was highlighted as a key advantage over traditional tools.

Areas for Growth

Few participants also identified opportunities for refinement, particularly in balancing automation with control. Some expressed a desire for richer data previews (P_1), editable annotation history (P_4), and better visibility into the sequence of steps taken. Others (P_5) noted that automated defaults occasionally misaligned with their intent, suggesting that

optional confirmation or stepwise override could improve usability.

DISCUSSION AND LIMITATIONS

Capability of AuraGenome in Supporting Complex Visualization Tasks

AuraGenome's multiagent workflow is deliberately designed to decompose complex visualization requests into manageable subtasks—such as intent recognition, layout planning, and code generation—handled by role-specific LLM agents. This structured collaboration enables the system to reliably interpret domain-specific goals and produce customized, multi-track genome visualizations. Unlike prior approaches that generate Circos-based configuration or rely on predefined templates, AuraGenome produces flexible D3-based script, supporting rich interactivity, dynamic interaction, and reuse. Together, these design elements make AuraGenome well suited for handling the complex tasks of circular genome visualizations.

End-User Expertise and Interaction Fluency

User experience varied with domain expertise, yet AuraGenome proved adaptable across the spectrum—from bioinformatics specialists to experimental researchers with limited visualization backgrounds. The natural language interface, paired with real-time visual feedback and well-aligned agent behavior, enabled users to express high-level goals without needing technical vocabulary or implementation knowledge. Participants consistently highlighted the system's predefined interactive mechanisms—such as dynamic track reordering, attribute refinement, and visual reuse—as unexpectedly intuitive and powerful. These features not only facilitated iterative correction and fine-tuning, but also encouraged exploratory behavior, allowing users to experiment with alternative layout patterns, highlight strategies, or comparative track compositions. AuraGenome's layered feedback, affordance-rich UI, and modular agent structure collectively support both directed editing and open-ended exploration, reinforcing its value as a user-centric tool.

Limitations and Boundary Conditions

While AuraGenome demonstrates strong adaptability, several functional boundaries remain. The current workflow and system are tailored for circular genome visualizations and do not yet support linear or hybrid visualization generation, which are equally significant

in genomic analysis. In addition, performance would be modestly affected by the agents when handling ambiguous, conflicting, or poorly structured prompts, occasionally leading to redundant tracks or minor layout inconsistencies. However, these issues do not interrupt task execution. Thanks to the multiagent workflow, such errors are mitigated through agent-level coordination and fallback strategies, ensuring smooth task progression. These observations point to directions for further refinement while confirming that AuraGenome remains robust and reliable in handling complex genomic visualization tasks.

CONCLUSION AND FUTURE WORK

In this article, we presented AuraGenome, an LLM-powered framework for generating rapid, reusable, and scalable circular genome visualizations. By integrating multiagent collaboration with interactive visual analytics, AuraGenome enables natural language-driven visualization generation, significantly improving both efficiency and output quality. Two real-world case studies and a comprehensive user study demonstrate its effectiveness in enhancing task performance and reducing cognitive load in genomic research workflows.

In future work, we plan to refine the multiagent workflow to capture more fine-grained user intents and support richer interactions with visualization outcomes. We also aim to extend support beyond circular layouts, enabling multiview genomic representations that accommodate diverse analytical needs. In addition, we will enhance the robustness of LLM-driven generation through improved retrieval grounding and validation strategies, thereby increasing reliability and reducing the risk of hallucinated outputs.

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