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Web Server issue

WashU Epigenome Browser update 2025

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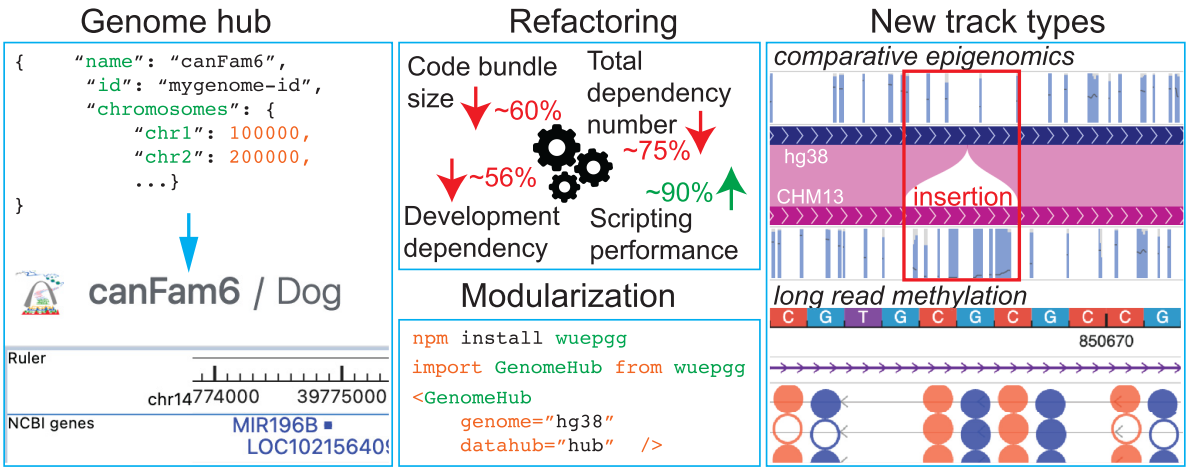
Abstract

The WashU Epigenome Browser (https://epigenomegateway.wustl.edu/) is a web-based tool for exploring genomic data and providing visualization, investigation, and analysis of epigenomic datasets. Since its 2018 update, the redesigned user interface and newly developed features have enhanced how investigators interact with both the Browser and the extensive genomic data it hosts. The rapid evolution of the JavaScript ecosystem has presented new challenges and opportunities in maintaining and developing the WashU Epigenome Browser. In this update, we present a completely rewritten codebase. This new codebase minimizes the use of external libraries whenever possible, resulting in a significantly smaller code bundle size after production compilation. The reduced code size improves loading efficiency and boosts the Browser's performance, with improved scripting, graphics rendering, and painting performance. Lowering external dependencies also allows for faster and more straightforward installation. Additionally, the update includes a redesign of the user interface to further enhance user experience and features a new modular design in the codebase that enables the Browser to be exported as stand-alone modules for use in other web applications. Several novel track types for long-read methylation data and single-cell methylation data visualization have been added, and we continue to update and expand the data hubs we host for major consortia. We constructed the first data hub to systematically compare genomic data mapped to different genome assemblies, focusing on comparisons between hg38 and the first human T2T genome, chm13, using our new comparative genomics track function. The WashU Epigenome Browser also serves as a foundation for other genomics platforms, such as the WashU Virus Genome Browser, developed for SARS-COV-2 research, the WashU Comparative Epigenome Browser, and the WashU Repeat Browser.

Graphical abstract



Introduction

Since its creation in 2001 [1, 2], the human genome assembly has served as a fundamental reference for human genetics and genomics research, providing a standardized coordinate system for organizing and analyzing genomic data. This milestone enabled the development of essential computational tools to visualize, interpret, and compare genomic datasets efficiently. One of the most significant breakthroughs in genomic data visualization was the introduction of the UCSC Genome Browser in 2002 [3], which allowed researchers to

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explore any region of the genome at various scales with annotation tracks in a web-based interface. As genomics research progressed, the rise of high-throughput sequencing technologies led to an explosion of large-scale datasets, necessitating more advanced genome browsers capable of handling and presenting massive amounts of information. Large research consortia, including ENCODE [4], Roadmap Epigenomics [5], 4D Nucleome [6], IHEC [7], IGVF [8], BICCN [9], and TaRGET [10], have contributed extensive genomic and epigenomic datasets to the scientific community. To maximize their impact, genome browsers have evolved to support interactive visualization, seamless data integration, and user-friendly exploration. By providing an accessible platform to navigate these complex datasets, genome browsers empower researchers to uncover novel insights into gene regulation, chromatin interactions, epigenetic modifications, and disease mechanisms.

Nowadays, a variety of genome browsers cater to different research needs: UCSC Genome Browser [11] and Ensembl [12] support a wide range of organisms, offering extensive genomic annotation and analysis tools. HiGlass [13] specializes in the smooth, interactive visualization of genome interaction maps, making it ideal for studying chromatin architecture. JBrowse 2 [14] and igv.js [15] are lightweight, flexible, and easily embeddable in web applications, allowing users to create customized genome browser instances tailored to specific research needs.

The WashU Epigenome Browser, first introduced in 2011 [16], has become a widely used tool for genomic data visualization and has undergone continuous development to meet the evolving demands of genomics research. The Browser provides specialized visualization tools for epigenomic datasets, enabling researchers to explore regulatory elements, chromatin states, and sequencing-based functional genomics data. Over 14 years, the Browser has advanced significantly, both conceptually and technologically, and has built a substantial user base among researchers and educators in genomics and related fields. Initially designed with a JavaScript frontend and C backend [16], the Browser has since evolved into an entirely frontend-based application as of 2019 [17] and later updated in 2022 [18], utilizing the Node.js engine and React framework. This transition has enabled efficient and scalable usage by shifting computation to client devices, removing backend dependencies, and reducing package size.

The continuous evolution of web technology, including the emergence of powerful JavaScript engines like Node.js and innovative frameworks such as Vite.js, presents an opportunity for a comprehensive refactoring of the Browser's codebase. In this update, we aim to optimize the Browser for modern standards of performance, modularity, and usability, to enhance the accessibility and functionality of genomic data visualization for an even broader audience. The overarching objective of this update is to create a versatile, pioneering tool for general-purpose genomic data visualization, and to provide a robust, efficient, and user-friendly experience while supporting the latest advances in biological data visualization.

New features

Genome hub

A best practice in genomics data visualization is to separate data storage from the visualization software, as genomic datasets are often massive. To address this challenge, we previously introduced the Data Hub Cluster concept [19], which serves as a scalable framework for hosting, organizing, and displaying large datasets. This approach has been successfully implemented to manage over 200 000 datasets generated by consortia such as Roadmap Epigenomics, ENCODE, and others, enabling efficient data visualization while maintaining system performance. Beyond organizing and displaying datasets, the Data Hub Cluster concept has also facilitated genetic variant annotation for complex traits [20], making integrating and interpreting diverse genomic information easier. However, an initial limitation was that each data hub remained tied to a specific genome assembly, which had to be pre-hosted by the Browser. This restriction made it challenging to visualize data for genome assemblies that were not already integrated into the system.

To overcome this limitation, we have expanded the concept to incorporate genome information directly within the data hubs, allowing datasets from custom genomes to be displayed seamlessly without requiring prior genome assembly integration in the Browser. This enhancement significantly improves flexibility for researchers working with newly sequenced or less commonly studied genomes. This new Genome Hub feature functions similarly to the UCSC Genome Browser's Assembly Hub [11, 21] but with a more streamlined and user-friendly configuration process. We used the dog assembly *canFam6* as an example to illustrate how the Genome Hub enables users to easily visualize custom genome datasets within the Browser, eliminating the need for preloaded genome assembly information (Fig. 1). This advancement ensures that researchers can efficiently explore and analyze genomic data across a broader range of organisms and genome versions.

Enhancement of performance

We redesigned the Browser's caching mechanism to enhance data retrieval efficiency and improve user experience. By implementing an optimized caching strategy, we ensure that data are fetched and stored more efficiently, reducing redundant operations and improving performance during visualization (Fig. 2A). A key improvement is the adoption of a LIFO (last-in, first-out) queue, which prioritizes the most recently fetched data. This approach minimizes memory overhead while ensuring that frequently accessed data remain readily available, leading to smoother interactions within the Browser.

The JavaScript ecosystem evolves rapidly, and some of the packages we previously used have become deprecated, creating compatibility issues when users attempt to install the Browser with the latest Node.js engine. To address this challenge, we undertook a complete codebase rewrite, aiming to minimize dependencies and enhance performance. By leveraging more native JavaScript and reducing reliance on third-party libraries, we successfully decreased the development dependency packages from 143 to 57, and the total number of dependencies from over 3000 to 791, a significant reduction compared to the previous version. This optimization has resulted in a substantial decrease in the compiled bundle size, shrinking from 44.3 to 19.4 MB, including all JavaScript files (Fig. 2B). Smaller JavaScript files contribute to faster loading times in the web browser, while fewer dependencies reduce overhead and improve efficiency. As a result, the rendering and painting speeds have been improved substantially (34% and 47%, respectively), whereas the scripting of the Browser has

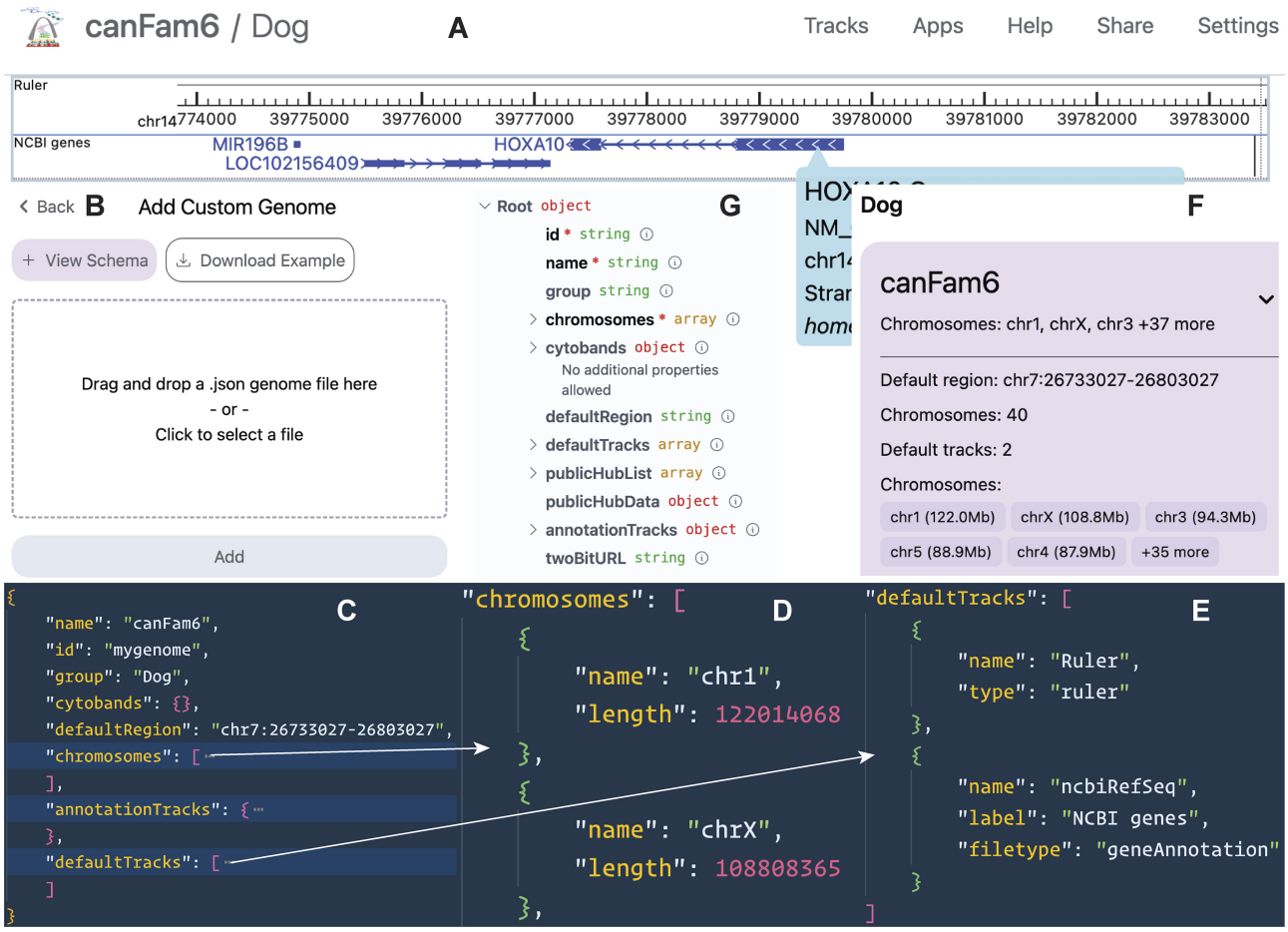

Figure 1. How to load the dog genome (canFam6) using the genome hub feature in the WashU Epigenome Browser. This feature allows users to seamlessly upload and visualize custom genomes without the need for preloading genome assembly information into the Browser system. (**A**) A screenshot of the Browser interface after successfully loading the canFam6 custom genome. (**B**) The user interface (UI) that enables users to upload a custom genome encoded in JSON format. (**C**) A quick preview of the JSON file structure, which includes required attributes such as a unique genome ID, genome name, and chromosome list. (**D**) The structure of the chromosome array, defining the individual chromosome information within the genome. (**E**) The structure of the default track object, which specifies which default tracks are displayed for the genome. (**F**) After the initial upload of the JSON file, the summary information that the Browser will display for the custom genome. (**G**) The complete schema of the custom genome JSON file, detailing optional attributes such as cytobands and public data hubs. Required attributes are marked with a star for clarity. The example JSON file schema is provided in Supplementary Note 1. The files for examples with minimal (canFam6) and extensive (hg38) genome information in JSON format are available in Supplementary Files S1 and S2, respectively.

improved drastically by 7.5-fold, enhancing the overall user experience (Fig. 2C).

Modularization

The recent updates have made it much simpler to embed the current Browser into other web applications. The Browser is modularized and published as a package (https://www.npmjs.com/package/wuepgg), enabling users to import it as a reusable and customizable component for genomic data visualization. This modular approach enables researchers and developers to add genomic visualization tools to their own platforms with minimal adjustments. Thus, the Browser can operate as an independent visualization module within larger applications, providing versatility and compatibility for various research and analysis workflows (Fig. 3).

New user interface

We have redesigned the UI to enhance usability and provide a more streamlined experience for Browser users (Fig. 4). Instant search function is available on the genome selection page for picking the genome of interest quickly. Previously, the menus covered the entire screen, obstructing access to the browser content. Since full-screen menus were unnecessary, we updated the menu system to slide in from the right side. Users can now open menus by clicking on a tab in the top-right corner, such as the “Tracks” tab. This change enables users to browse public data hubs in a compact view while maintaining access to their genome browser workspace. For menus requiring more space, such as the text tracks menu, the UI now expands the menu to half of the screen width instead of taking up the entire display. In cases where users view the browser on a narrow screen, the menu pulls up from the bottom, covering the full screen instead of opening from the side. Navigation within menus has also been improved. Users can now seamlessly switch between menu screens without losing their place. For example, within the Tracks tab, users can navigate to the annotation tracks screen and back. Additionally, menu tabs preserve their navigation position; so, if a user switches to the Apps tab and then returns to the Tracks tab, they will resume where they left off instead of being reset to the main menu.

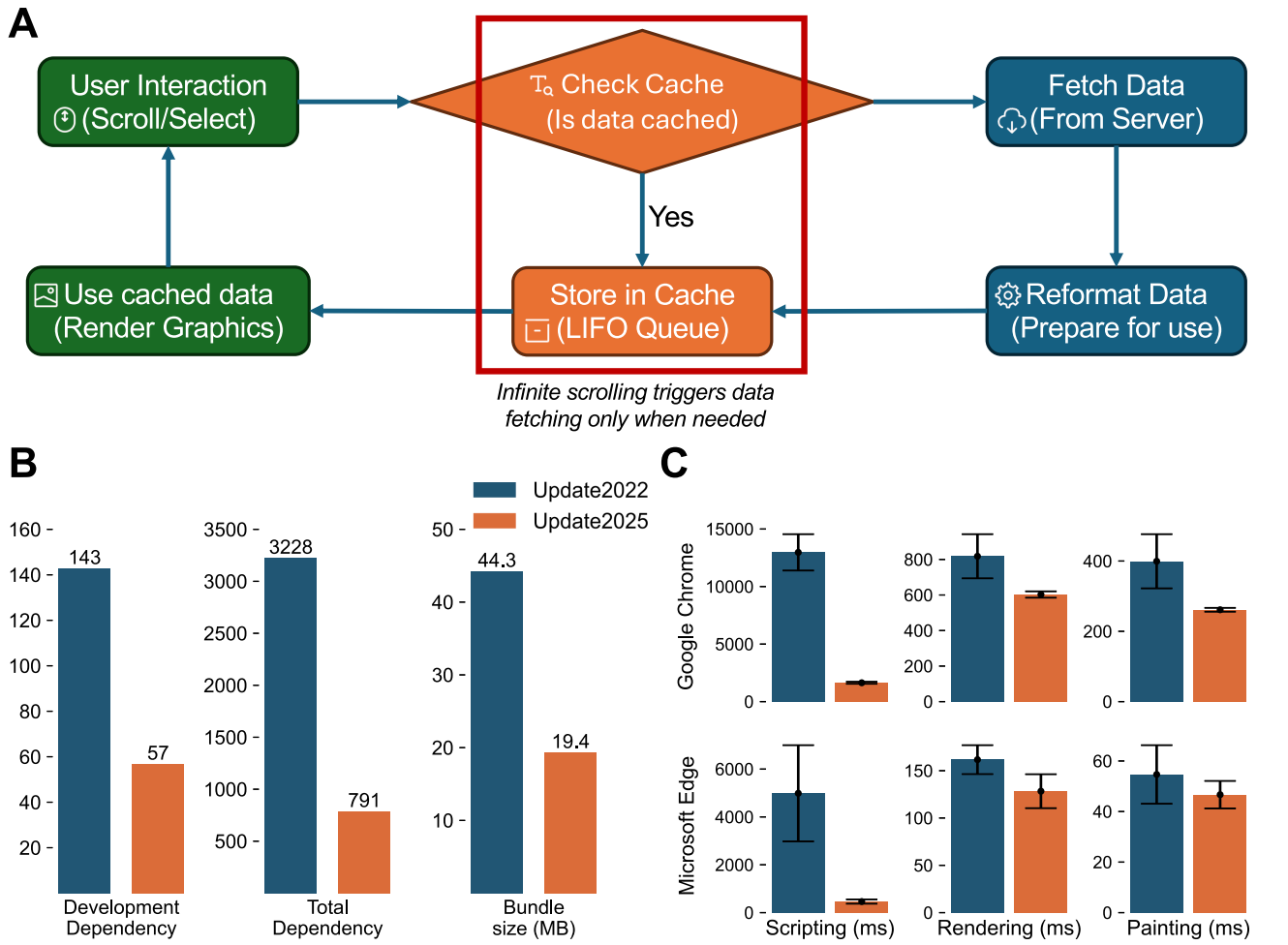

Figure 2. New caching strategy, dependency reduction, and performance enhancements. (**A**) The impact of the newly implemented caching strategy, which optimizes data handling by prioritizing recently fetched data using a LIFO queue. (**B**) The reduction in both the number of dependent packages and the total code bundle size. The Development Dependency panel lists the number of packages required for local development, while the Total Dependency panel reflects the overall number of packages these developmental dependencies rely on. The Bundle Size panel represents the total file size of the compiled JavaScript files. (**C**) Improvements in scripting, rendering, and painting performance as measured using web browsers' performance testing tools (Google Chrome/Microsoft Edge). Three replicates provide consistent validation of these enhancements. Scripting refers to the time spent executing JavaScript code, rendering is the process of visually displaying the web page, and painting represents the conversion of webpage layout into actual pixels on the screen. *Y*-axis represents the time in milliseconds. The data hub for the test is included in Supplementary Note 2. The screenshots for the test are included in Supplementary File S3.

Another major enhancement is the new session manager. Previously, switching between sessions required users to manually download and manage session files. Now, by clicking on the browser logo in the top-left corner, users can access the session manager, where sessions are stored locally in the browser and can be switched between freely. This update significantly simplifies session management, making it easier for users to save, switch, and restore their workspace configurations efficiently.

Comparative epigenomics visualization, hub helper, and comparison to UCSC Genome Browser

One of the novel track types we introduced is the GenomeAlign track [22], designed to facilitate comparative epigenomics visualization. This track leverages pairwise genome alignment, using synteny information to link corresponding genomic segments across different assemblies. By aligning and comparing sequences, it enables researchers to explore genomic variations and structural differences; more importantly, researchers can directly visualize and compare functional genomics data in the context of genetic variations. We applied the GenomeAlign track to visualize data between the widely used human genome reference hg38 and the recently completed chm13 [23] human genome sequence (Fig. 5A). This comparison highlights previously unresolved genomic regions and provides new insights into structural variations that were missing in earlier assemblies. Beyond comparing different genome builds, this track type is also valuable for visualizing personalized genomes against a reference genome, helping to uncover biological information that may be missed due to reference bias. Recent advances in pan-genomics methods, such as methylGrapher [24], avoided linear reference bias by mapping whole-genome bisulfite (WGBS) sequencing reads to the pangenome graph [25, 26], helped identify structural variation (Fig. 5B) and transposable element polymorphism (Fig. 5C) signatures in personalized genome. The GenomeAlign track enhances comparative genomics and personalized medicine by providing an interactive, alignment-based visualization that improves

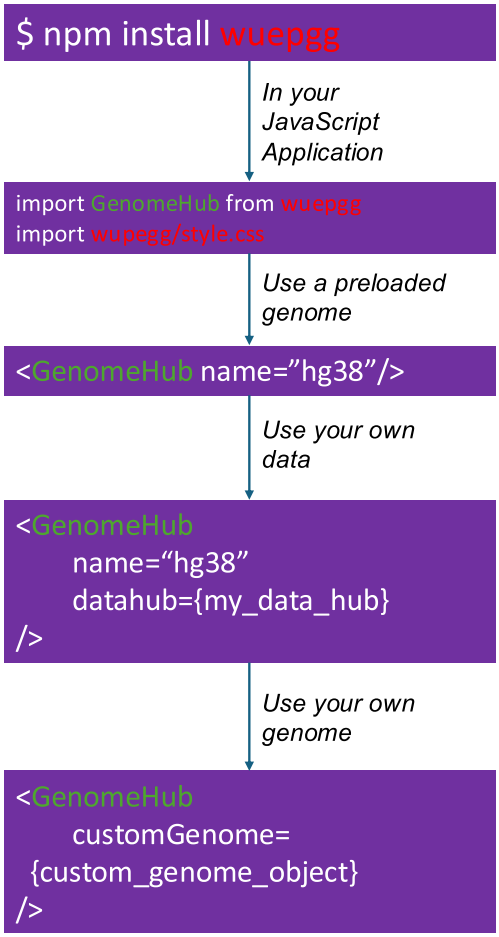

Figure 3. Using the Browser as a module in your web application. By installing the package, users can easily import and render the Browser within their own software. There are multiple ways to use the package: (i) Loading a preloaded genome—By simply specifying the name of a preloaded genome, users can render the same genome as the one available in the Browser without additional configuration. (ii) Providing custom data—Users can include their own datasets by using the dataHub property, allowing the integration of specific genomic tracks for analysis. (iii) Using a custom genome—For users who wish to visualize custom genome assemblies, the customGenome property can be used. The syntax for defining a custom genome follows the same structure as described in Fig. 1. Supplementary Note 3 provides a step-by-step tutorial of how to run the Browser in a local computer and use the Browser as a module in another web application.

our ability to interpret genomic data across individuals and populations.

To create custom visualizations in the Browser, users must first set up a data hub to organize their desired tracks. This process typically requires manually entering data hub configurations in JSON syntax or writing scripts for automation. To streamline this process, we developed a companion web application called Hub Helper, which provides a one-stop solution for generating data hubs. Instead of manually coding JSON files or handling format conversions, users simply specify the files they want to visualize, and Hub Helper automatically takes care of data hub generation. Figure 5D illustrates the workflow of the Hub Helper app, demonstrating how it simplifies data hub creation and facilitates seamless visualization setup. This tool significantly reduces the technical barrier for researchers, making it easier to configure and manage large-scale genomic data visualizations in the Browser. The Hub Helper App is available at https://hub-helper.epigenomegateway.org.

We obtained essential data, including genome and gene annotations, from the UCSC Genome Browser, which is a standard source of genome annotation for many research projects. Our goal has been to develop a lightweight genome browser that allows users to set up a local copy with minimal effort. With this update, installing a local version of the Browser has become even easier, and users can now import it as a module into their own applications. We have placed a strong emphasis on enhancing visualization functionality, supporting new data types, and improving modularization. The updated architecture allows users to modify the code more easily, adapting it to their specific research needs. The smaller and more efficient codebase further simplifies customization and integration, making the Browser more accessible and adaptable for various genomics applications.

Other miscellaneous and data hub updates

Several miscellaneous updates have been introduced to enhance the Browser's functionality and user experience. One notable improvement is the support for multiple customizable highlighting areas. This allows users to specify and annotate as many highlighted regions as needed, with options to label and color each region individually. Session management has also been improved. Users can now sort sessions by name or date and download them for later use, making it easier to restore previous visualizations.

Additionally, Dropbox-hosted track files can now be visualized, provided the files are set to be publicly accessible, offering greater flexibility in managing and sharing genomic datasets. A dark theme option has also been introduced for users who prefer a darker background, improving accessibility and reducing eye strain during extended analysis sessions.

Two new track types have been developed to support emerging sequencing technologies. The ModBed track [27] visualizes long-read methylation data generated from PacBio and Oxford Nanopore sequencing platforms, offering new insights into base-resolution modifications. Similarly, the BallC track [28] displays single-cell methylation data, such as those produced by snm3C-seq [29] technology, enabling in-depth analysis of epigenomic variations at the single-cell level. These updates further enhance the Browser's versatility, making it an even more powerful tool for genomic data exploration. A brief comparison of long-read and single-cell data visualization on genome browsers is provided in Supplementary Table S1.

We have also updated our gene annotation tracks to the latest version of GENCODE [30] and MANE [31], and track collections by incorporating new datasets from major data portals such as ENCODE [4], 4DN [6], IHEC [7], and IGVF [8]. These updates ensure that the WashU Epigenome Browser remains up to date with the latest publicly available epigenomic datasets, providing users with a more comprehensive resource for data exploration. The number of newly added tracks is detailed in Table 1.

Outlook

As the field of genomics continues to grow, the demand for more sophisticated, scalable, and integrative visualization tools increases. Future genome browsers will likely leverage

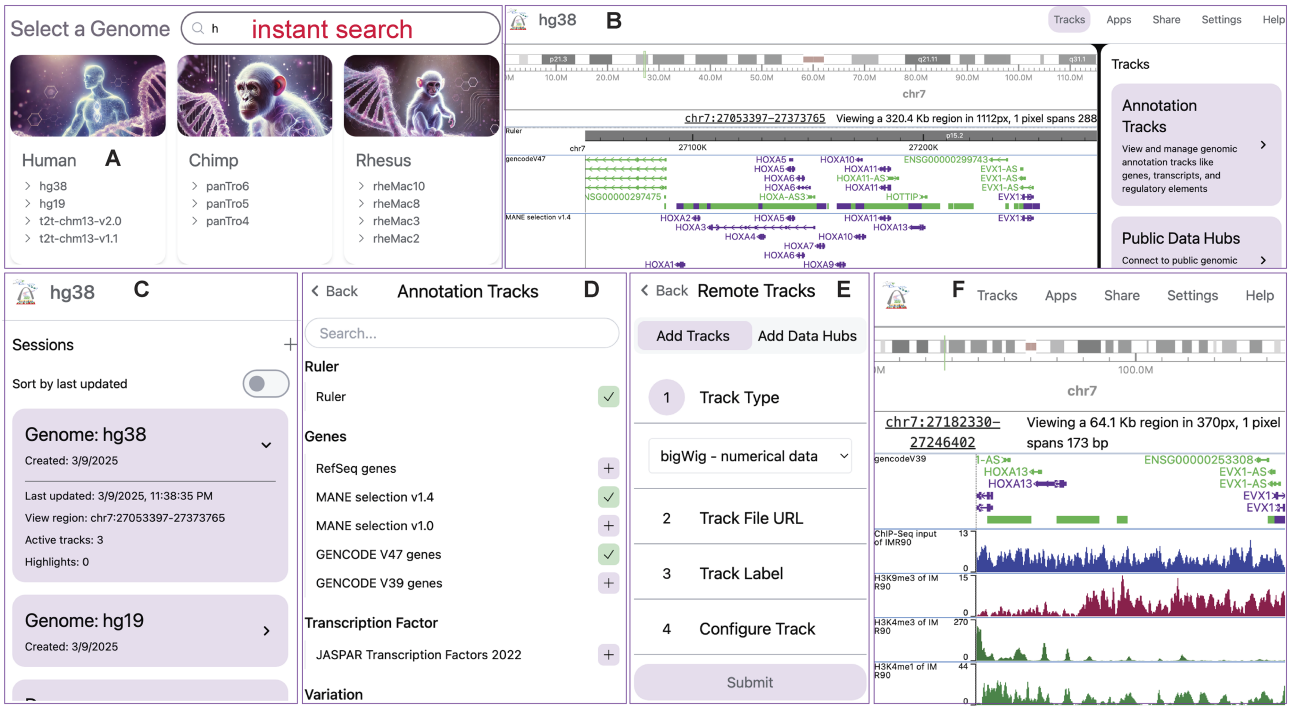

Figure 4. New UI improvements. (**A**) The updated genome selection page now includes an instant search function, allowing users to quickly find genome assemblies by typing letters. The screenshot illustrates a search for the letter "h", displaying matching genome assemblies. (**B**) The slide-in Apps menu is shown in the hg38 genome view, displaying several tracks from top to bottom: the ruler track, GENCODE version 47 gene annotation track, and the latest MANE (v1.4) gene selection track. This menu design allows users to manage their tracks while maintaining visibility of the genome browser. (**C**) The new session manager enables users to seamlessly switch between sessions from different genome assemblies without the need for manual file downloads. Sessions are stored locally in the browser for easier management. (**D**) The annotation tracks interface provides an improved layout for selecting and managing annotation tracks, making track configuration more intuitive. (**E**) The remote track addition interface now features a step-by-step guide, simplifying the process of loading external datasets into the Browser. (**F**) The mobile-friendly interface displays how the Browser adapts to mobile devices, with the hg19 genome loaded alongside the default Roadmap data hub. The responsive design ensures smooth interaction and visualization on smaller screens.

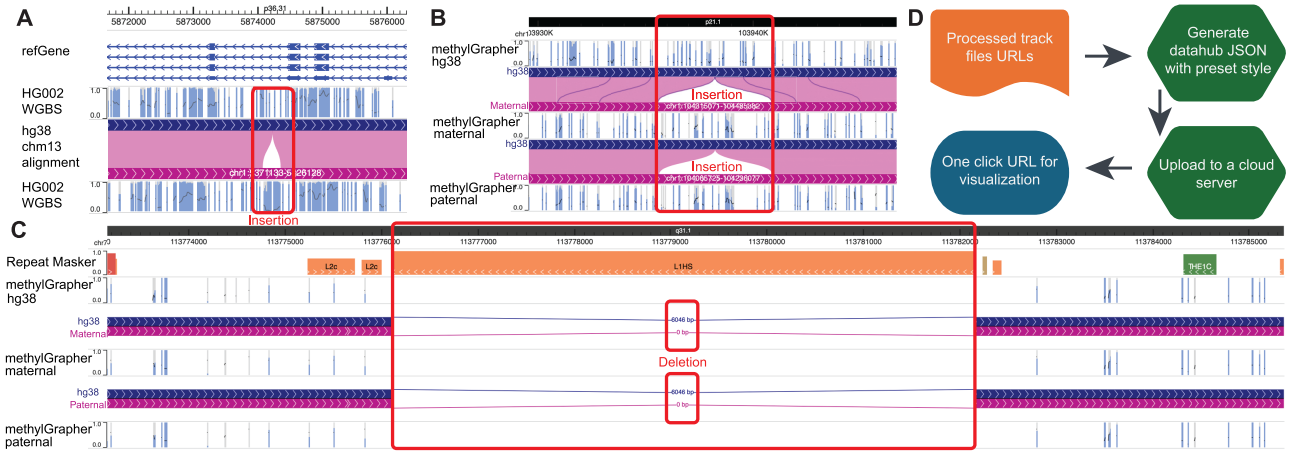

Figure 5. Comparative epigenomics visualization and hub helper. (**A**) The GenomeAlign track, showcasing the genome alignment between hg38 and chm13 for comparative epigenomics analysis. WGBS data were aligned to both hg38 and chm13; alignment track was generated by pairwise alignment between hg38 and chm13. The rectangle box indicates an insertion in chm13. (**B**, **C**) methylGraph was applied to align WGBS data to the human pangenome graph, and then the alignment was subjected to the linear individual haplotype resolved genomes (maternal and paternal). The rectangle box in panel (B) indicates an insertion, and the big rectangle box in panel (C) indicates a missing L1HS element in the individual genomes. WGBS and methylGrapher tracks are displayed as methylC track [32]; the height of the blue bar represents the methylation percentage, while the black line indicates the coverage. refGene: reference gene annotation. Repeat Masker: repeats annotation from the RepeatMasker program. L1HS: human-specific subfamily of LINE-1 retrotransposons. (**D**) Workflow of the Hub Helper App. The Hub Helper App simplifies the process of creating and managing data hubs for the WashU Epigenome Browser. Users can provide URLs to their track files, and with a single click, the app generates a hub URL and uploads it to a cloud server that we host. Once the hub URL is created, an instant one-click link is provided, allowing users to immediately visualize their data in the Browser. Importantly, users' data remain on their own servers—the Hub Helper App does not store private data. The generated hub URL is not public unless the user chooses to share it.

Table 1. Newly added tracks from major genomics consortia in this update

Project	Genome assembly	Collection	Tracks' count
ENCODE	hg38	Epigenomes from four individuals (ENTEx)	2102
		Rush Alzheimer's Disease Study	1180
		Stem cell differentiation	124
		Deeply profiled cell lines	346
		Human donor matrix	7213
		Immune cells	3358
		Human reference epigenomes	6177
		Protein knockdown using the auxin-inducible degron	374
	hg19	Epigenomes from four individuals (ENTEx)	2
		Human donor matrix	16
		Immune cells	4
		Human reference epigenomes	40
	mm10	Mouse reference epigenomes	2193
		Mouse development matrix	2780
4DN	hg38		4233
	mm10		1348
	galGal5		103
	dm6		6
	danRer11		35
IHEC	hg38		16 248
	hg19		13 310
	mm10		2854
IGVF	hg38		7
	mm39		7

The table includes the data portal name hosting the track files, the genome assembly associated with the tracks, the data collection name (if applicable), and the number of tracks added.

advancements in cloud computing, artificial intelligence, and real-time data processing to enhance usability and analytical capabilities. These innovations will further enable researchers to interpret vast amounts of genomic information, driving discoveries in human health, disease, and evolutionary biology.

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Supplementary data

Supplementary data is available at NAR online.

Conflict of interest

None declared.

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Data availability

The WashU Epigenome Browser is an open-source project, with its source code available on GitHub at https://github.com/twlab/eg3 (https://doi.org/10.5281/zenodo.15269109). The Browser can be accessed online at https://epigenomegateway.wustl.edu/ and https://epigenomegateway.org/, which is hosted on Amazon Cloud Services. Both sites support HTTP and HTTPS protocols, ensuring secure and seamless access for users worldwide. The Hub Helper App is hosted at https://hub-helper.epigenomegateway.org.

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