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RingNet: An Interactive Platform for Multi-Modal Data Visualization in Networks

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Abstract

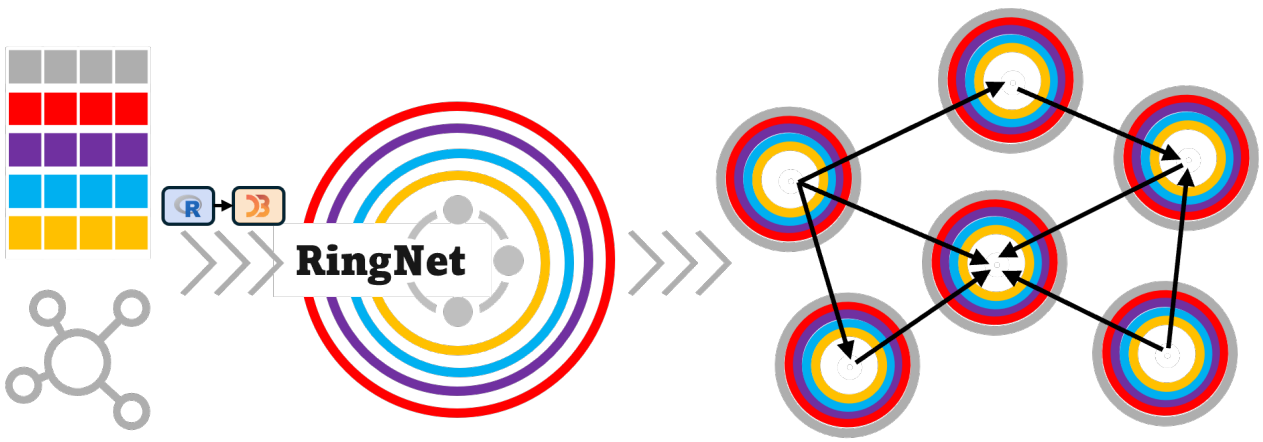
The exponential growth of multi-omics datasets in systems medicine has created an urgent need for intuitive visualization tools. These tools must be able to effectively represent complex biological networks and remain accessible to domain experts without extensive computational training. Current network visualization approaches often require specialized programming skills and/or cannot handle the scale and complexity of modern biomedical datasets, which creates significant barriers to biological discovery. We develop RingNet, a web-based interactive visualization tool that integrates computational efficiency with flexible, user-driven exploration. The tool meets the community's need to visualize multi-modal datasets within a single, compact network representation. RingNet uses an R backend for network computation and coordinate optimization. This generates JSON data structures that feed into a JavaScript and HTML frontend, which provides real-time, interactive visualization functions. It offers dynamic layout adjustments, node and edge filtering, and customizable color schemes for representing data. It can export reproducible, publication-ready figures in SVG and PDF formats. In our case studies, we visualize a gene regulatory network in breast cancer and a cell-to-cell communication network in atopic dermatitis. This demonstrates RingNet's ability to reveal biological relationships across multiple data modalities. RingNet lowers the barrier to exploring, analyzing, and communicating network medicine findings, thereby accelerating research.

Keywords network visualization, multi-omics data visualization, interactive web-based tool, network medicine, network biology

Abbreviations copy number variation (CNV), comma-separated value (CSV), http strict transport security (HSTS), hypertext markup language (HTML), hypertext transfer protocol secure (HTTPS), portable document format (PDF), scalable vector graphic (SVG), the cancer genome atlas (TCGA), transport layer security (TLS)

Graphical Abstract

RingNet is a tool for visualizing multi-modal data in networks.



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Key Messages

- RingNet enables intuitive, interactive visualization of multi-omics networks without requiring advanced computational or programming expertise.
- RingNet integrates efficient backend computation with real-time, flexible frontend exploration in a single, web-based framework.
- RingNet reveals cross-modal biological relationships and produces reproducible, publication-ready figures that accelerate research.

Introduction

Network visualization provides an intuitive abstraction for complex data by encoding relationships between entities as edges connecting nodes. By emphasizing connectivity, dependency and topology, networks allow complex systems to be studied as structured, interacting units rather than isolated variables. In computational biology, network-based representations have therefore become central to modeling molecular interactions, regulatory dependencies and functional associations, supporting both exploratory visualization and integrative analysis (Barabási et al., 2011; Zitnik et al., 2024). Human biology operates across multiple hierarchical scales. Molecular components, including genes, transcripts, proteins, and metabolites, form pathways and regulatory networks that interact at the cellular, tissue, and organismal levels. High-throughput technologies now generate multi-omics datasets (e.g., genomics, epigenomics, transcriptomics, proteomics, and metabolomics) that capture this layered organization (Pinu et al., 2019). Interpreting such data requires analytical and visualization approaches that can preserve biological hierarchy while enabling navigation across molecular layers and contextual relationships (Schaffer and Ideker, 2021; Kumar et al., 2025).

Encoding biomedical data in network-based representations enables the incorporation of these relationships into a wide range of big data tasks, including data integration (Valous et al., 2024; Baião et al., 2025), module detection(Lazareva et al., 2021; Gézsi and Antal, 2024), and mechanistic interpretation (Schulte-Sasse et al., 2021; Lai et al., 2022) that are naturally fused with graph machine learning methods. Network visualization tools allow quantitative omics measurements to be overlaid onto interaction graphs, facilitating the identification of coordinated subnetworks and key regulatory elements. General-purpose platforms such as Cytoscape serves as foundational infrastructure for biological network visualization, offering an extensible environment for integrating diverse omics data with molecular interaction networks (Shannon et al., 2003). Building on this paradigm, web-based platforms such as OmicsNet emphasize interactive and scalable visualization, including three-dimensional network layouts that facilitate the integration of heterogeneous molecular interactions and multi-omics data (Zhou et al., 2022). Several tools are developed to address specific challenges in multi-omics network visualization. NaviCom focuses on pathway-centric visualization by projecting multi-omics measurements onto curated signaling and metabolic maps, enabling intuitive "network portraits" of molecular perturbations (Dorel et al., 2017). MiBiOmics targets interactive exploration and multilayer network inference through a user-friendly Shiny-based interface, lowering the barrier for integrative multi-omics analysis (Zoppi et al., 2021). Omics Visualizer in Cytoscape allows network nodes to display different data sets, but only one value per set (Legeay et al., 2020). More recently, Arena3D supports hierarchical visualization of graphs using super nodes to connect different networks (Kokoli et al., 2023). SmCCNet 2.0 extends its network inference function by integrating phenotype information with multi-omics network construction and interactive visualization, facilitating the discovery of disease-associated subnetworks (Liu et al., 2024). Complementary efforts focus on enhancing the visualization of complex, heterogeneous outputs rather than network inference itself. Transomics2cytoscape enables layered, trans-omics network visualization within Cytoscape, explicitly representing relationships between molecular layers in stacked network layouts (Nishida et al., 2024). Visualization-centric frameworks, such as MINGLE (Coletti et al., 2025) and aplot (Xu et al., 2025), emphasize coordinated, compositional views that integrate network-derived summaries with heatmaps, genomic tracks or other plot types, supporting comparative and contextual interpretation of multi-omics data.

Despite substantial progress, existing tools usually optimize for specific data modalities, visualization metaphors, or analytical workflows. As an alternative, they visualize cross-omics as separate networks and then combine them using prior knowledge, such as information about molecular interactions. Therefore, a tool capable of visualizing diverse multi-omics datasets within a single, compact network representation is needed. To address this gap, we develop the web-based tool RingNet. The tool combines an R-based backend that transforms networks and multi-modal data into JSON-formatted graph objects and a JavaScript-powered web frontend that uses the JSON file to create interactive visualizations that users can customize. The tool's functions include network decomposition for scalability, sample-based alignment for different types of data, and an interchange format that enables direct, attribute-driven visual mapping. Our goal in developing RingNet is to bridge molecular layers, preserve biological context, and support scalable, interactive exploration. This complements the visualization tools currently available for network biology and network medicine research.

Methods

RingNet's design and architecture

RingNet is a three-tier architecture (Supplementary Figure S1). **(I) The layer for managing users' sessions.** Users upload CSV files via a web page. The server then validates the inputs, creates a unique session identifier, stores the uploaded assets in a session directory, and sends back a JSON payload that describes the file paths and session metadata. **(II) The backend for data processing and export.** The core function of RingNet reads the interaction graph (edges and nodes), group membership, and one or more data types, such as omics data. The program harmonizes samples and features across inputs, constructs group-induced subgraphs, computes network statistics and two-dimensional layouts using the R package ggplot2, attaches omics vectors and standardized variants, and exports a JSON file. **(III) The frontend for interactive visualization.** The frontend uses JavaScript to load the JSON file from the backend and renders group networks with interactive controls. Node and edge attributes, including size, color, directionality, curvature, and ring encodings, are mapped to visual channels. The viewer has export functions and

supports SVG, PDF, and JSON output.

Frontend configuration. The RingNet frontend viewer is a browser-based visualization client implemented with D3.js (v6) (`https://d3js.org`). Its primary responsibility is to consume the RingNet JSON artifact produced by the backend and support interactive exploration, visual encoding configuration, and export (Supplementary Figure S2). The viewer is designed to minimize the browser workload, so intensive processing (such as subgraph extraction, data normalization, and JSON artifact preparation) is handled by the backend while users focus on rendering and interaction. Specifically, the viewer first loads a JSON artifact from a session-scoped path. Then, it renders a selected network as an SVG scene. Finally, it provides interactive controls for filtering, recoloring, rescaling, and exporting, depending on the user's needs.

Deployment and security configuration. RingNet uses Apache as a web server and reverse proxy to securely and uniformly provide access to the application (Supplementary Figure S3). Apache handles Transport Layer Security (TLS) termination, Hypertext Transfer Protocol Secure (HTTPS) enforcement, security headers, and access control. It also routes both static viewer assets and API requests under a single domain. Backend services remain bound to internal ports, which improves security isolation. JSON artifacts are served through authorized API endpoints to prevent unauthorized access and directory traversal. HTTPS is enforced via port 443, with redirects from port 80, as well as with optional HTTP Strict Transport Security (HSTS). This architecture simplifies user configuration, improves performance through user-side rendering, and supports reproducibility via session-scoped artifacts and exportable session state.

The implementation of network visualization in RingNet

RingNet requires three mandatory input tables provided in comma-separated values (CSV) format (Figure 1). **(I) Graph edges.** The edge table provides interactions within networks. It must contain two columns that specify the source and target of each interaction. An optional weight column is supported to include qualitative or quantitative information, such as the correlation coefficient of the interacting nodes. If the weight column is absent, the weights are initialized to the default value of 1. Optional annotation fields, such as interaction type or interaction identifier, are preserved and propagated to the output when present. **(II) Graph nodes.** The node table defines network nodes and must contain a unique identifier or symbol for each one. **(III) Node group.** The group table assigns each node to a single group. The table must contain a group column and an identifier column for network nodes. Duplicate identifiers are removed to enforce a one-to-one mapping between nodes and group assignments. Additionally, RingNet supports up to five data matrices with continuous, integer, or categorical values in CSV format. Each matrix should have rows that correspond to the sector elements of a ring diagram (e.g., patient samples) and columns that correspond to the nodes of a network (e.g., genes). Row names are treated as identifiers for sector elements and are used for cross-modal alignment. RingNet harmonizes heterogeneous inputs through intersection-based alignment rules defined at the level of sample and node identifiers. These rules guarantee consistency of indices across multiple modalities without imposing assumptions of numerical comparability between heterogeneous data types.

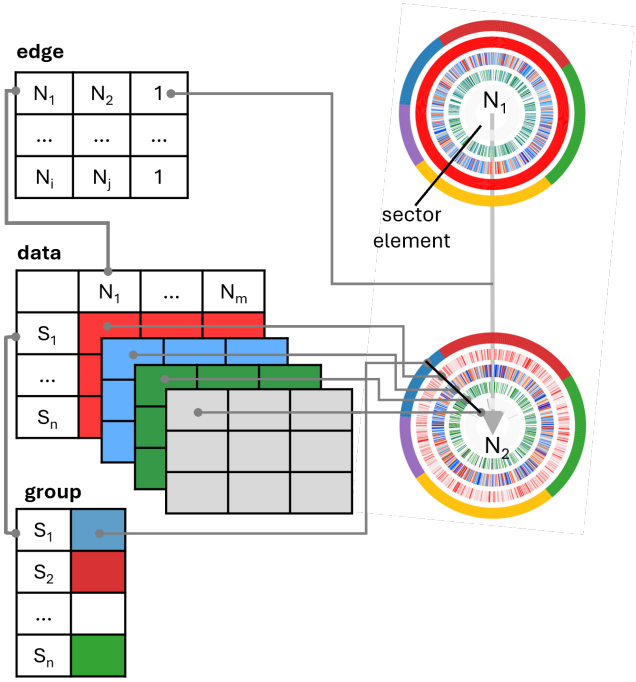

Figure 1 RingNet's visualization protocol. RingNet can integrate up to four numerical data sets and one categorical data set into a node. Each data matrix has a structure in which the rows represent sector elements (e.g., samples) and the columns represent network nodes (e.g., genes). In a node, each ring represents one data matrix, with the categorical matrix on the outside and the numeric matrices inside. Each ring contains the same number of sector elements and data from the same sample are shown on the aligned segment sectors on all five rings, enabling the joint visualization of multi-modal data within a single node. The edge table shows the interactions between nodes (e.g., gene-gene interactions), which can be assigned arbitrary (e.g., 0 or 1) or numerical weights (e.g., correlation coefficients). Grey lines indicate the source of data that RingNet uses to visualize a network. Grey lines represent shared identifiers of different data that enable cross-modal alignment.

Network construction and layout at the backend. The network is constructed using the R package igraph. By default, the network is regarded as directed, but it can also be set as undirected. When treating the network as directed, node connectivity summaries may include total degree, in-degree, and out-degree. For undirected graphs, only total degree is used. RingNet computes two-dimensional node coordinates for each network using stress-based layout (graphlayouts::layout_with_stress). The algorithm treats edges as elastic constraints between nodes. Nodes that are directly or strongly connected are placed closer together. In contrast, nodes that are connected only indirectly or separated by intermediate nodes are positioned further apart. Consequently, the layout expands the overall graph structure so that densely connected nodes become compact and sparsely connected or weakly interacting nodes are pushed further apart. The coordinates are scaled by a constant factor to improve visual separation. If the stress-based layout optimization fails, as in the case of very small or fragmented networks, RingNet uses a generic force-directed layout (graphlayouts::layout_nicely). The resulting coordinates are exported as fixed node attributes, which enables deterministic frontend rendering without requiring users to

compute the layout.

Network visualization at the frontend. RingNet exports visualization-ready JSON groups containing nodes and edges with precomputed layouts, identifiers, multi-modal data to support efficient interactive network rendering. In the frontend visualization, each node in the network can have up to five rings, each representing a data set. For numeric data, RingNet provides raw, min-max, and z-score normalization options to enable flexible frontend visualization. RingNet also provides raw, min-max, and z-scored weights for visualizing edges in the network. Node labels are identifiers (e.g., gene symbol, patient sample id, and cell type). Users can filter nodes and edges by their containing values and topology-derived properties such as node degree, and customize their aesthetic properties, such as node and edge colors.

Multiple network visualizations. RingNet also supports multiple network visualization. Specifically, RingNet uses a process-based cluster with a configurable number of CPU cores (parallel::makeCluster), exports the necessary objects to the workers, and applies parLapply over the network identifiers. This design leads to near-linear speedups when network sizes are balanced, and memory overhead is manageable. The main trade-off is the replication of data matrix and edge table memory across multiple CPUs. Under the current configuration, RingNet can simultaneously compute and visualize up to 25 moderately sized networks, (ranging from 52 to 1,872 nodes and from 20 to 6,100 edges) within several minutes (Supplementary Table S1). Processing the largest network requires approximately 21 seconds and reaches a peak memory consumption of about 400 MB, with memory usage increasing steadily during execution.

Results

RingNet is a powerful tool that integrates multi-modal data into networks, enhancing the data visualization demanded by the biomedical community (Figure 2). The community generates complex data to characterize and understand human diseases such as cancer. For example, the TCGA project is the first to generate large-scale, multi-omics profiles for patients across 33 cancer types that enables systematic cross-cancer analyses (Cancer Genome Atlas Network, 2012). Additionally, an increasing number of single-cell projects generate RNA-seq data for millions of cells to characterize tumor microenvironments (Yuan et al., 2019; Han et al., 2023), immunology (Yin et al., 2026), and autoimmune diseases such as atopic dermatitis (He et al., 2020). These complex data require a sophisticated tool for network-based visualization and integrative exploration to reveal relationships across molecular layers.

The primary function of RingNet is to integrate different data sets into a network node. These data sets can contain numerical and categorical values, allowing for the combination of different types of information. Aligned data for a node's sector elements (representing a patient or cell) makes interpreting results more convenient. Matching the profile of one object allows information to be associated, thereby enriching the information hierarchy and ensuring better explanations and interpretations. RingNet's comprehensive collection of functionalities establishes it as a robust tool for creating composite networks, empowering researchers to produce sophisticated and intuitive data visualizations. RingNet enables effective communication and in-depth interpretation of network science through precise control and annotation of elements. RingNet also provides a function for the parallel visualization of multiple networks, which facilitates the creation of a series of networks for comprehensive analysis, such as gene set enrichment analysis (Subramanian et al., 2005). Specifically, users can visualize multiple networks of identified enriched pathways in a single run. This function enables users to efficiently generate visualization results from large-scale analyses. Furthermore, since RingNet supports uploading JSON files for computed networks, users do not need to rerun the tool to reproduce the results. Instead, they can use the JSON file for their network. RingNet can then directly visualize the results. Both functions can save users significant time when visualizing massive networks or repeatedly refining the final network output. Finally, the web-based and developer versions make RingNet a suitable tool for researchers with different programming skill levels.

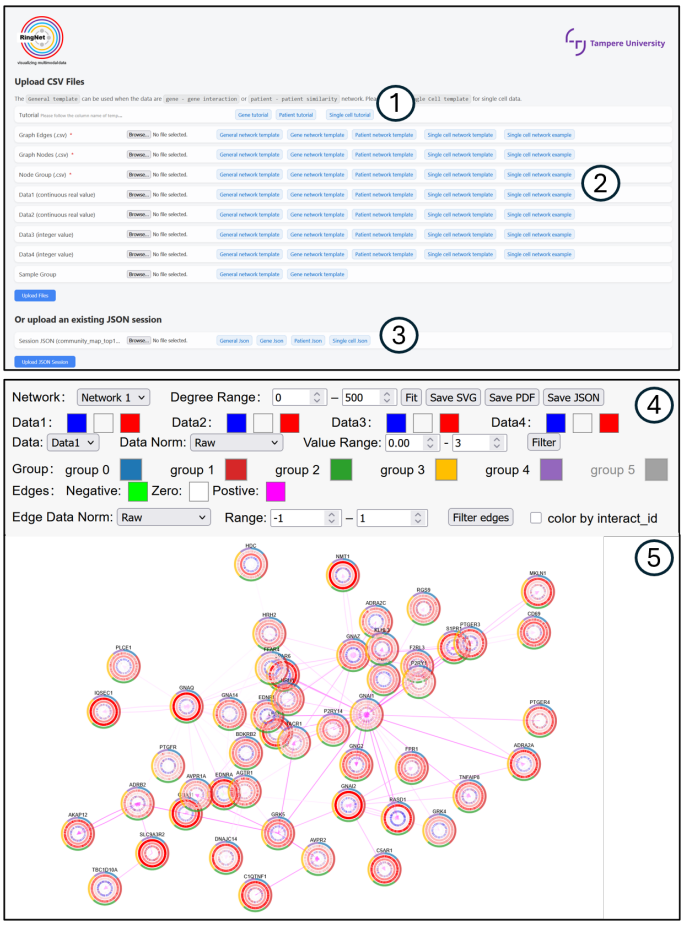

Figure 2 RingNet's web interface. The top panel is the interface where users can upload their files, including the tutorial (1), options for uploading CSV files (2), and options for uploading JSON files (3). In the backend, R will use the CSV files to generate a JSON file. In the frontend, the generated JSON file is visualized as a network. The bottom panel shows the interactive user interface for adjusting the network's aesthetics (4) and the network drawing area (5).

Visualizing multi-omics data for the TCGA breast cancer cohort

Integrating and visualizing patients' profiles is essential for understanding the complex relationships between multi-omics data and for unravelling patterns hidden in a large cohort (Figure 3). Here, we demonstrate how RingNet can effectively combine and display TCGA data for breast cancer patients, including genomic mutations, copy number variations, DNA methylation, transcriptomics, and clinical annotations (Cancer Genome Atlas Network 2012). We begin with a gene regulatory network for breast cancer that contains 8,185 genes and 48,534 molecular interactions derived from Omnipath (Türei et al., 2021). Next, we identify a subnetwork of 16 genes related to the GPCR pathway that modulate proliferation, survival, angiogenesis, invasion, and immune evasion in breast cancer (Arang and Gutkind, 2020). Then, we use RingNet to map the omics data of 651 patients from TCGA and genes' expression correlation coefficients onto the network's nodes and edges, respectively.

As a result, we obtain a network comprising multiple layers of information (Figure 4 top). From the network, we can see whether patterns exist between the omics profiles of genes and the tumor stages of patients. Some genes consistently exhibit high expression levels (e.g., GNAQ, GNA11, and GNAI2), some exhibit low expression levels (e.g., TACR1 and HRH2), and some exhibit mixed high and low expression levels (e.g., AGTR1 and GNB5). It can show correlation between specific molecular profiles, such as the correlation pattern between a gene's expression and DNA methylation levels in the cohort. For example, TACR1 exhibits high methylation and low expression levels, while GNA11 exhibits high methylation and high expression levels. It can reveal whether patients have amplified or deleted copy number variations or mutations in certain genes. For example, most genes in the cohort exhibit copy number variation. AGTR1 and GNAZ show deleted and amplified copy number variation in most patients, respectively, and few gene mutations are observed in the cohort. It can also show whether genes that interact with a specific type of interaction, such as stimulation or inhibition, and quantify them using expression correlation coefficients. Taken together, RingNet allows for the effective integration of genomics data into a molecular network to uncover data pattern and variation in the cohort.

Visualizing cell-cell communication network in patients with atopic dermatitis

Single-cell analysis emerges as a crucial tool in functional genomics with widespread applications in disease research. Key steps in single-cell transcriptomic analysis include cell clustering, identifying marker genes, and annotating cell types. These components are typically visualized collectively, often relying on existing tools that limit the integration of additional information. We demonstrate RingNet's capabilities by applying it to scRNA-seq data from lesional human skin cells of patients with atopic dermatitis (He et al., 2020). This dataset contains information on 39,042 cells that comprise the microenvironment of this autoimmune disease. We use CellChat to infer the intercellular communication network between the identified cells. This tool models the probability of cell-to-cell communication by integrating gene expression with prior knowledge of interactions between signaling ligands, receptors, and cofactors, based on the law of mass action (Jin et al., 2021). Afterwards, we use RingNet to visualize the disease's cell-cell communications (Figure 4 bottom). The network shows how different types of cells communicate in the microenvironment and the cells' gene expression profiles. Specifically, inflammatory dendritic cells (Inflam. DC), conventional DCs (cDC1, cDC2), T cells (TC, Inflam. TC, CD40LG^{+} TC), Natural killer T cells (NKT), and Langerhans cells (LC) form dense communication hubs with fibroblast populations (Inflam. FIB, COL11A1^{+} FIB, FBN1^{+} FIB, APOE^{+} FIB). Mechanistically, these interactions are mediated by ligand-receptor signaling, including cytokines, chemokines, and costimulatory molecules (e.g., CD40-CD40LG). Activated immune cells stimulate fibroblasts to produce extracellular matrix components, inflammatory mediators, and growth factors, while fibroblasts feedback to immune cells, sustaining immune cell recruitment, polarization, and tissue remodeling. This bidirectional signaling underlies epidermal thickening, fibrosis, and chronic inflammation typical of atopic dermatitis (He et al. 2020). Together, the results demonstrate the potential of RingNet to enhance visualization in single-cell data and advance our understanding of the underlying cell and molecular biology of atopic dermatitis.

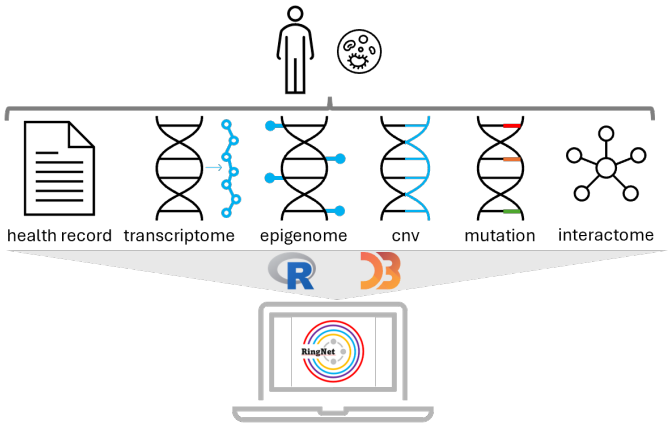

Figure 3 Multi-omics data integration in network visualization using RingNet. Multi-omics data, including DNA methylation, gene expression, somatic mutation, and copy number variation (CNV), as well as clinical records and molecular interactome data from a cohort study, are processed in R to build a network. This network is then exported as a JSON file that contains the omics profiles embedded within the nodes, as well as the network's topology. The web interface uses HTML and D3.js to render the network, in which each node has a multi-ring layout displaying different types of data. Users can explore and refine the network through interactive operation.

Conclusion

RingNet provides an interactive framework for visualizing multi-modal data within networks, enabling intuitive user-driven exploration. Its core strength lies in the compact, ring-based representation of multiple data layers at the sector element level (e.g., genes, samples, or cell groups), ensuring consistent alignment across modalities within each network node. This design allows users to directly assess correlations among diverse data types while simultaneously comparing distributional patterns across nodes or predefined groups. Such alignment supports clear interpretation of intra-sample relationships and reveals group-level heterogeneity, stratification effects, and coordinated shifts across data layers. Case

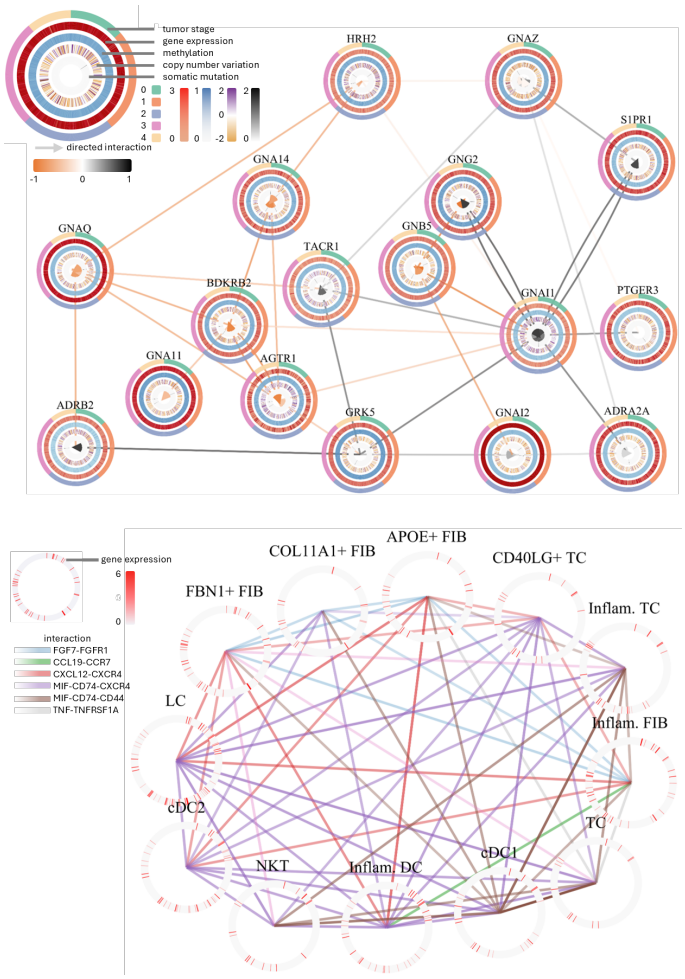

Figure 4 Case studies. The top panel shows a gene regulatory network for breast cancer. Each node (i.e., gene) contains five rings that show omics data from the TCGA breast cancer cohort. From the outside in, the rings show the following: patients' tumor stages, gene expression profile, DNA methylation profile, copy number variation, and somatic mutation profile. There are 468 sector elements in each ring, representing the corresponding profiles of 651 patients. The edges represent directed gene-gene interactions, and their colors indicate positive or negative expression correlation coefficients, respectively. The bottom panel shows a cell-to-cell communication network in a single-cell study of atopic dermatitis. Each node represents a cell type and contains a ring whose sector elements represent the cell's expression profiles of 555 genes. Edges represent inferred cell-to-cell communications by CellChat. Edge color represents different ligand-receptor interactions for intercellular communication, while edge intensity represents the strength of communication between cells. The genes' descriptions can be found in Supplementary Table S2.

studies in breast cancer genome-wide omics and atopic dermatitis single-cell communication networks demonstrate RingNet's ability to uncover meaningful biological patterns and relationships. Beyond these examples, the framework can integrate computational analysis outputs, such as model-derived feature importance scores, alongside experimental measurements to support transparent interpretation and hypothesis generation. Overall, RingNet lowers barriers to exploring and communicating complex network-based biological insights.

Conflicts of interest

The authors declare that they have no competing interests.

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Data availability

The RingNet is available at https://ringnet.rd.tuni.fi, which also hosts all datasets used in this study. The source code for RingNet is accessible at https://github.com/laixn/ringnet.

Author contributions statement

LZ: methodology; software; data curation; writing – original draft; writing – review and editing. **XL**: conceptualization; methodology; software; data curation; investigation; validation; formal analysis; supervision; funding acquisition; visualization; project administration; resources; writing – original draft; writing – review and editing.

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