

## CircoNET: An Interactive Multi-Modal Network Visualization Platform for Complex Biomedical Data Integration

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### Abstract

The exponential growth of multi-omics datasets in systems medicine has created an urgent need for intuitive visualization tools that can effectively represent complex biological networks while remaining accessible to domain experts without extensive computational training. Current network visualization approaches often require specialized programming skills or fail to handle the scale and complexity of modern biomedical datasets, creating significant barriers for biological discovery. We present CircoNET, a web-based interactive visualization platform designed specifically for large-scale multi-modal biological networks. Our tool addresses critical limitations in existing approaches by combining computational efficiency with user-friendly design. CircoNET employs an R backend for robust network computation and coordinate optimization, generating JSON data structures that feed into a JavaScript frontend providing real-time interactive visualization capabilities. The platform enables comprehensive network exploration through dynamic layout adjustment, intelligent node and edge filtering, customizable color schemes for multi-modal data representation, and export functionality for publication-ready figures in scalable vector formats. Unlike existing tools, CircoNET seamlessly integrates heterogeneous data types while maintaining computational performance on networks containing massive nodes and interactions. We demonstrate CircoNET's capabilities using TCGA genome-wide omics data integrated into gene regulatory networks, showcasing its ability to reveal previously obscured biological relationships across multiple data modalities. CircoNET can significantly reduce the technical barrier for biologists and bioinformaticians to explore, analyze, and communicate complex network-based findings, thereby accelerating research in biomedicine.