

Modernization of the Cytoscape ecosystem

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Project Website: <http://www.cytoscape.org/>

Source Code: <https://github.com/cytoscape/>

License: LGPL/MIT License

Abstract

Cytoscape is the de-facto standard biological network analysis and visualization platform – its first version was released in 2002. Compared to other systems biology tools, it is one of the oldest applications and it has one of the largest user and developer communities. Maintaining sustainability of such platform is a challenge due to its desktop-only deployment, evolving user needs and changing funding scenarios. Cytoscape's extensibility mechanism is a plugin architecture, called Apps, and has been a great way to satisfy diverse community needs. However, it is insufficient for modern bioinformatics workflows requiring massive memory and parallelization, such as is available on emerging web- and cloud-based application platforms.

Today, data analysis/visualization tools are in transition from desktop applications to loosely coupled, large-scale distributed systems with support for different types of clients, including web browsers and command line applications. The desktop version of Cytoscape is not designed to support such use cases. To provision for these modern bioinformatics workflows, we are modernizing Cytoscape ecosystem using mainstream technologies and design techniques including a service-oriented architecture with microservices, containers, browser-based visualization components, and web/native hybrid applications. The new Cytoscape ecosystem, called Cytoscape Cyberinfrastructure (CI) is the main project for modernizing the Cytoscape platform.

In this presentation, we will discuss the technical challenges of modernizing long-lived, widely-used bioinformatics applications and will introduce the new Cytoscape CI architecture and technologies we used for the process.

