EDITORIAL

The Cytoscape Automation app article collection [version 1; referees: not peer reviewed]

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Abstract

Cytoscape is the premiere platform for interactive analysis, integration and visualization of network data. While Cytoscape itself delivers much basic functionality, it relies on community-written apps to deliver specialized functions and analyses. To date, Cytoscape's CyREST feature has allowed researchers to write workflows that call basic Cytoscape functions, but provides no access to its high value app-based functions. With Cytoscape Automation, workflows can now call apps that have been upgraded to expose their functionality. This article collection is a resource to assist readers in quickly and economically leveraging such apps in reproducible workflows that scale independently to large data sets and production runs.

Keywords

Cytoscape, Automation, App, Network Biology, Network Analysis, Network Visualization

This article is included in the Cytoscape Apps gateway.

Not Peer Reviewed

This article is an Editorial and has not been subject to external peer review.

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Editorial

Cytoscape is an open source software platform for interactive analysis, integration and visualization of networks and network data[1]. At heart, Cytoscape provides basic network analysis functionality (e.g., network import/export, network data analysis, visualization and layout) in a menu-driven desktop format. Most importantly, it also enables and encourages users to add extensions (called apps) that deliver custom features important for specific workflows (e.g., ClueGO[2] for enrichment analysis relative to various ontologies). To date, Cytoscape users can choose among over 330 apps written by over 550 authors.

In 2014, the CyREST app[3] was created to allow external programs to exercise core Cytoscape functionality as part of custom workflows. By authoring such workflows in common languages (such as R and Python), users can combine the best features of Cytoscape with those available in language-specific libraries, thus creating new value much more quickly and cheaply than writing conventional Cytoscape apps. Furthermore, such workflows can more easily integrate external applications (e.g., GenePattern and iGraph) and multiple large datasets. Finally, external workflows enable reproducibility not available using Cytoscape's standard mouse/keyboard/display interaction mode.

In 2018, Cytoscape Automation was created to enable external workflows to also call functionality in apps. For an app to be callable, it must be upgraded to support automation via either a Commands or Functions interface. As of March, 2018, app authors upgraded and released 22 apps.

This collection of Cytoscape app articles at *F1000Research* is intended to serve as a resource to researchers (as workflow authors) and app developers to understand the features and interfaces exposed by automation-enabled apps. They are written by the app authors themselves according to a template that calls for explaining newly available functions, how they can be called, and with real world examples. We intend that readers be able to quickly and economically incorporate Cytoscape app functionality as reproducible workflows that scale independently to large data sets and production runs.

Data availability

No data are associated with this article.

Competing interests

No competing interests were disclosed.

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References

1. Pico AR, Bader GD, Demchak B, *et al.*: **The Cytoscape app article collection [version 1; referees: not peer reviewed].** *F1000Res.* 2014; **3**: 138.
PubMed Abstract | Publisher Full Text | Free Full Text

2. Bindea G, Mlecnik B, Hackl H, *et al.*: **ClueGO: a Cytoscape plug-in to decipher functionally grouped gene ontology and pathway annotation networks.** *Bioinformatics.* 2009; **25**(8): 1091–1093.
PubMed Abstract | Publisher Full Text | Free Full Text

3. Ono K, Muetze T, Kolishovski G, *et al.*: **CyREST: Turbocharging Cytoscape Access for External Tools via a RESTful API [version 1; referees: 2 approved].** *F1000Res.* 2015; **4**: 478.
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