The RCX Extension Hub: A Resource for Implementations Extending the R Adaption of the Cytoscape Exchange Format

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Abstract. Public repositories provide access to biological networks for investigations, and subsequently serve to distribute the network encoded biomedical and even clinically relevant results. However, inclusion of complementary information requires data structures and implementations customized to the integrated data for network representation, usage in supporting application, and extending analysis functionality. Partitioning of this information into individual aspects of a network facilitates compatibility and reusability of the network-based results, but also requires support and accessibility of the extensions and their implementations. The RCX extension hub offers overview and access to extensions of the Cytoscape exchange format implemented in R. The hub supports the realization of self-customized extension through guides, example implementations, and a template for the creation of R extension packages.

Keywords. Bioinformatics, biological networks, R, data models, extensibility.

1. Introduction

Biological networks capture complex association between biological entities, mechanism associated with their function and their involvement in biological processes. Within analyses the networks are enriched with diverse information, including their visualization, provenance history, and usage in additional applications. The NDEx platform [1] is an online commons for biological networks that uses the Cytoscape exchange (CX) format for transmission: It separates a network into its different aspects to modularize its contents. Within the statistical programming language R the *ndexr* package [2] allows querying the NDEx platform, retrieve and upload networks, manage their properties, and share them with specific people and groups. Thereby, the *RCX* package [3] adapts the CX data structure to standard R data types and implements methods for conversion, validation, summarization, visualization, and extension.

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2. Methods

The RCX extension hub organizes the information around the development of custom aspects and their implementation. The hub therefore is structured in three sections: an overview over existing extensions, guiding the adaptation process through tutorials, and supporting the implementation with a package creation template. The RCX extension template can be used to create all required files, generic functions, and setup to build a functional package. Newly created extension packages can be registered raising GitHub issues through the hub.

3. Results

The RCX extension hub supports developers with their implementation by providing detailed guides and highlighting the requirements. Furthermore, the officially provided extensions serve as exemplary implementations illustrating representative use cases.

4. Discussion

In contrary to object-oriented programming languages, R approaches data in a vector and table-oriented manner and therefore requires an adaptation of the JSON encoded data objects contained in the CX networks. Nevertheless, this additional work required for the data transformation is paid off by the afforded accessibility to standard bioinformatics analysis tools and workflows provided by the R language. With this approach implementation of the different versions of the same aspect can also be easily managed.

5. Conclusion

The RCX extension hub forms a resource for the management of R implementations of custom CX aspects. It provides available extensions together with their intended applications, along with guides, examples, and templates for the development of own extension packages, and makes the hub a valuable resource and contact point for R-based network biology. All necessary source code of the official extensions is publicly available through the provided links and the RCX extension hub itself is hosted at https://frankkramer-lab.github.io/RCX-Extension-Hub.

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