NetworkCommons: bridging data, knowledge, and methods to build and evaluate context-specific biological networks

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Abstract

Summary

We present NetworkCommons, a platform for integrating prior knowledge, omics data, and network inference methods, facilitating their usage and evaluation. NetworkCommons aims to be an infrastructure for the network biology community that supports the development of better methods and benchmarks, by enhancing interoperability and integration.

Availability and implementation

NetworkCommons is implemented in Python and offers programmatic access to multiple omics datasets, network inference methods, and benchmarking setups. It is a free software, available at https://github.com/saezlab/networkcommons, and deposited in Zenodo at https://doi.org/10.5281/zenodo.14719118.