Implementing a multilayer framework for pathway data integration, analysis and visualization

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Personalized medicine, i.e. a medicine focused on the individual and proactive in nature, promises an improved health care by customizing the treatment according to patient needs[3]. The methods to analyze data, model knowledge and store interpretable results vary widely. A common approach is to use networks for modelling and organizing this information.

Network theory has been used for many years in the modelling and analysis of complex systems, as epidemiology, biology and biomedicine [1]. As the data evolves and becomes more heterogeneous and complex, monoplex networks become an oversimplification of the corresponding systems [3]. This imposes a need to go beyond traditional networks into a richer framework capable of hosting objects and relations of different scales [4], called Multilayered Network.

These complex networks have contributed in many contexts and fields [1], and they are very applicable in the investigation of biological networks [2].

In order to enrich this investigation, we aim to implement a multilayer framework that can be applicable in various domains, especially in the field of pathway modelling.

Our idea is to integrate pathways and their related knowledge into a multilayer model, where each layer represents one of their elements. The model offers a feature we call "Selective Inclusion of Knowledge", as well as a collection of related knowledge into a single graph, like diseases and drugs. The main layers are mapped to the entities of the pathways and the additional knowledge, for instance, a convenient model would have 3 layers respectively representing proteins, drugs and diseases. The model imports knowledge from multiple sources like the Reactome database, PharmGKB, DrugBank, OMIM and other public sources.

The submitted poster will give an overview of the various models of multilayered networks, then it will describe the model we are building, and the workflow of implementing it into R as well as the future plan. The workflow consists of multiple R packages, of which we present the first implemented package, **mully** [5], that provides the multilayer layout. The data import and the integration will be done by another package to be implemented, **Multipath**.

Keywords: Multilayer Networks, Network Biology, Network Theory, Pathway Modelling

References

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5. **mully** *R Package is available on **Github**:* https://github.com/frankkramer-lab/mully