



Simulating real data topologies with R

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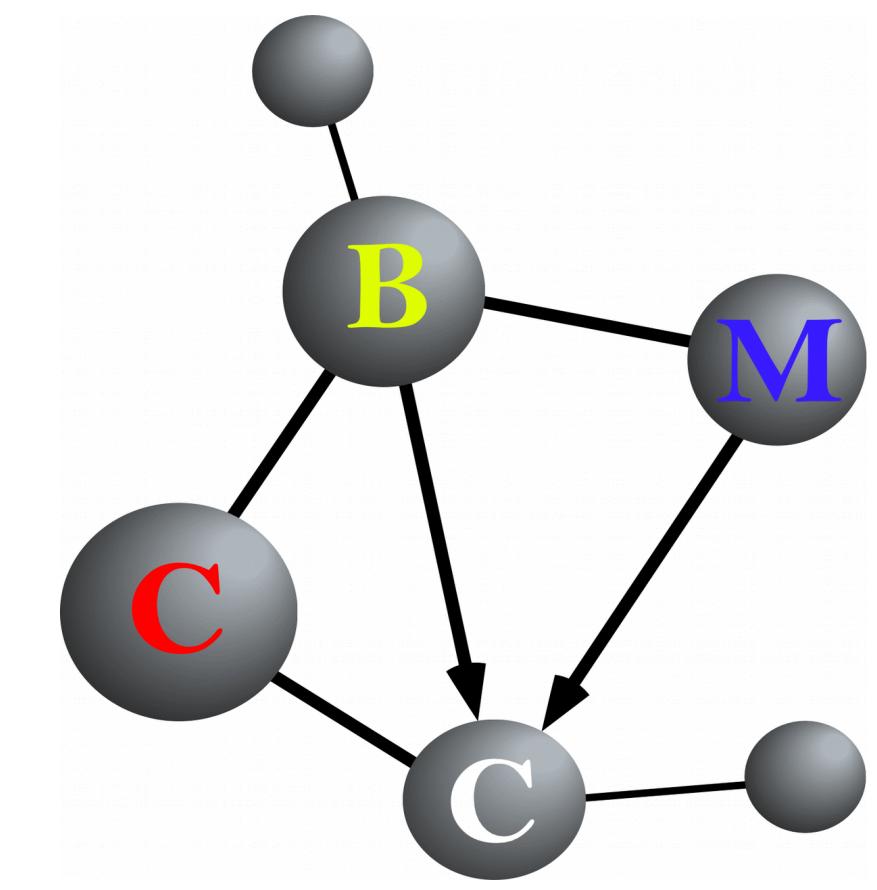
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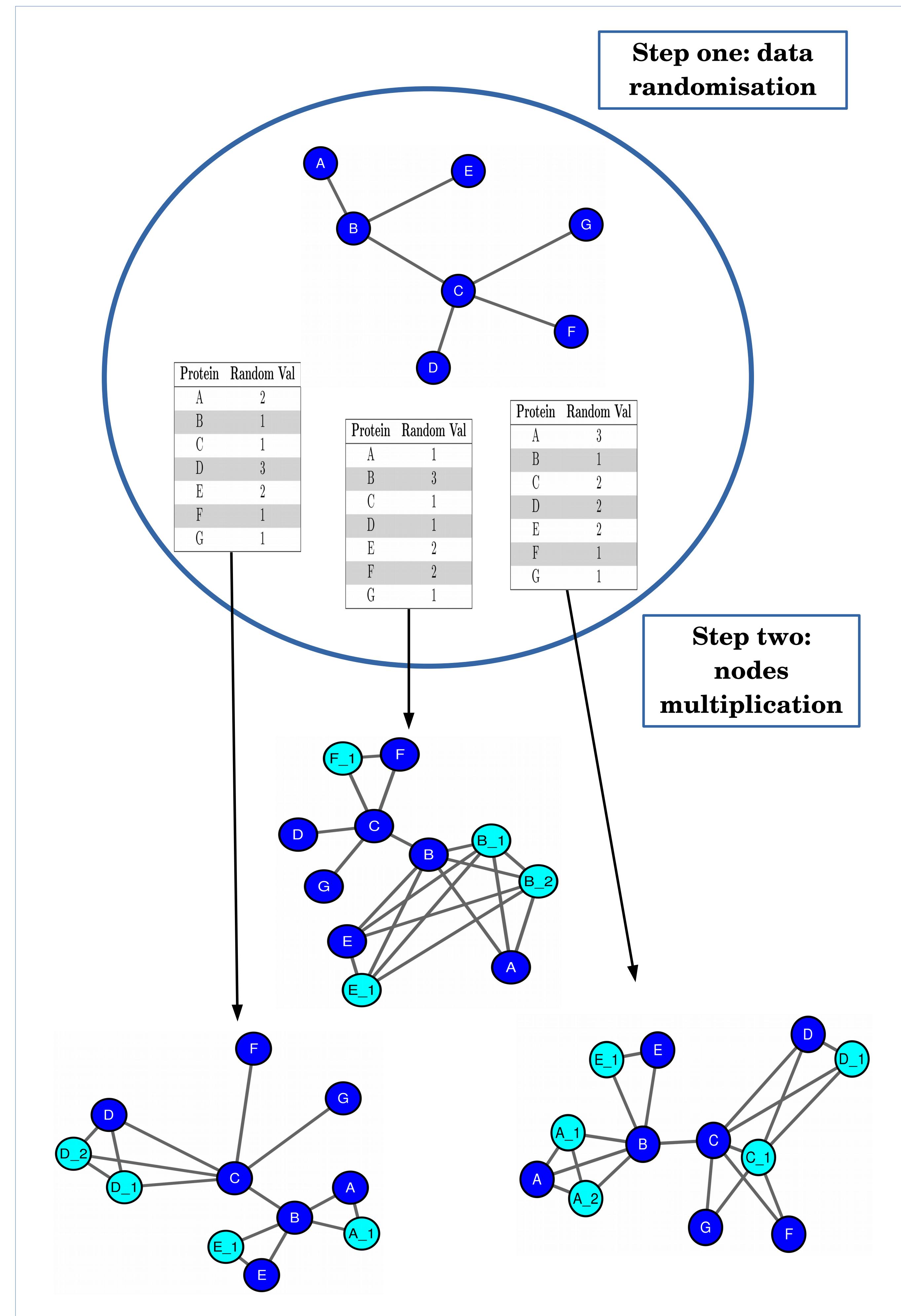
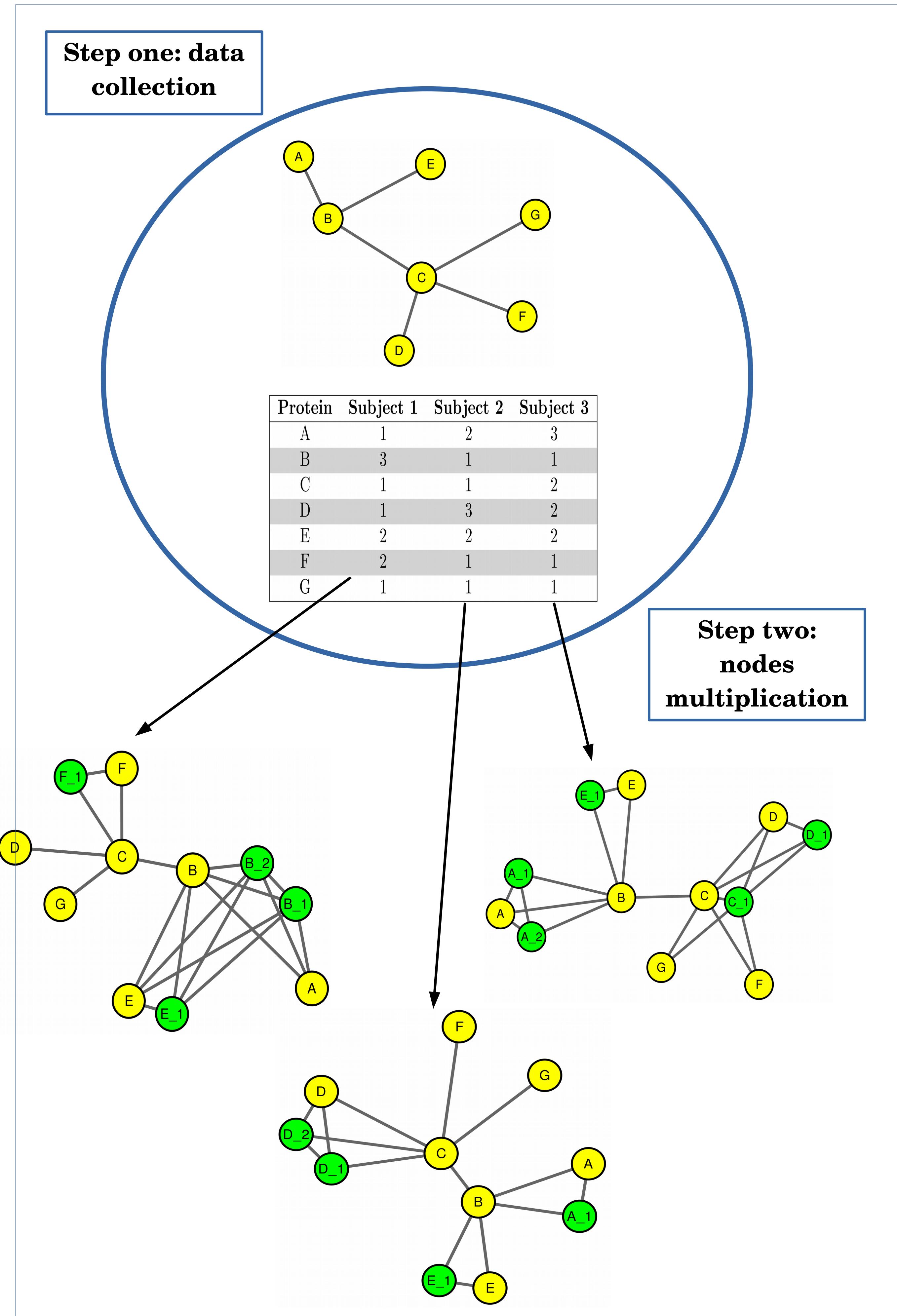
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Overview

Protein-protein interactions networks have, currently, limited applications due to their static nature and are not intended for representing specific experimental conditions. Today, a wealth of high throughput data are produced but the integration with biological networks is not always straightforward. Here, a novel methodology that permits to integrate quantitative data into complex networks, is presented, aiming at enhancing the predictive and modelling ability in the field of Personalized Medicine. The multiplication of the static topology allows to i) model specific experimental conditions and ii) simulate random experiments.



The function **addEdges()** allows the integration of experimental, quantitative data into an IGraph's graph, by the multiplication step thus personalising the original network in several, multiplied graphs.

Step three: network analysis
Degree Distribution
Topological Indexes
Clustering
Motifs and Patterns
Biological Enrichment
...

The function **rgSim()** allows generating a set of weighting arrays which are used for the random multiplication of the original network for generating a set of random networks.

Conclusions

The two functions, **addEdges()** and **rgSim()**, are developed for working in conjunction with the IGraph library, in the R environment. They permit the creation of personalised networks which aims at modelling quantitative datasets that have potential applications, for instance, in clinical studies which involve different experimental conditions. Moreover, the functions permit to multiply and analyse every kind of network and, also, permit to randomly generate sets of networks that could be useful as validation benchmark.

The R code is available at <http://www.cbmc.it/~scardonig/>