

# QuACN: Analysis of Complex Biological Networks using R

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Classical analysis of biological data is mainly based on investigating single, isolated features. As it is now understood that most diseases are driven by sets of interacting genes or proteins this has shifted towards a more complex and holistic perception of this problem [Strohman \(2002\)](#). The first step in network-based analysis of complex biological data is inferring valid and robust network representations of the data. A plethora of packages for this task are available in R, e.g. [Langfelder and Horvath \(2008\)](#); [Meyer et al. \(2008\)](#); [Altay and Emmert-Streib \(2010\)](#). A topological analysis of the network provides new insights, as the structure of a network represents the biological function. A quantitative approach is to use so called topological network descriptors, which represent a network structure by a numeric value. Note, that different descriptors capture different structural patterns of the network topology. A small selection of topological network descriptors is available in the **igraph** package [Csardi and Nepusz \(2006\)](#). Recently we published the package **QuACN** on CRAN [Mueller et al. \(2011\)](#). **QuACN** provides a multitude of different topological network descriptors. We want to draw ones attention to the group of parametric graph entropy measures [Dehmer and Emmert-streib \(2008\)](#); [Dehmer and Mowshowitz \(2011\)](#), which are exclusively available in **QuACN**. These measures assign a probability value to each vertex of a graph by using information functionals to calculate the graph's information-content. Topological network descriptors can be used for a multitude of applications in the structural analysis of (biological) networks, e.g. supervised and unsupervised machine learning, or the integrative analysis of networks. Here, we present selected examples of descriptor-based approaches.

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