Abstract

The analysis of biological networks plays an essential role in the post-genomic era. For the standard systems biology analysis software, Cytoscape, only few apps are available for simulating network dynamics. Hence, we introduce PetriScape, a Cytoscape plugin for modeling and simulating biological networks as Petri nets. In the second part of the thesis, we deal with epigenetic DNA methylation modifications, that are inheritable and of major impact in transcriptional gene regulation and, thus, in human health. We introduce the software DiMmeR (Discovery of Multiple Differentially Methylated Regions). It offers a set of highly parallelized statistical methods for efficiently identifying de-methylated regions in Illumina 450K and 850K EPIC chip data. In particular, DiMmeR is capable of computing empirical p-values through randomization tests, even for big data sets of hundreds of patients and thousands of permutations within a few minutes on a standard desktop PC. It is the first standalone platform that, independent of any third-party software libraries, computes regression coefficients, p-values and empirical p-values. It corrects for multiple testing using fixed family-wise error rates or false discovery rates, or by applying the step-down-min-P procedure. From raw data, via confounder detection, multiple testing correction and robustness analysis, down to region finding and mapping to the genome browser, it takes only some minutes – with all steps being guided by an interactive user interface. In summary, with DiMmeR we offer clinicians and biomedical researchers the first one-stop shop for sophisticated identification of statistically robust de-methylated regions in modern Illumina chip data.