

Inference of differential gene regulatory networks from gene expression data using boosted differential trees

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Summary

Diseases can be caused by molecular perturbations that induce specific changes in regulatory interactions and their coordinated expression, also referred to as network rewiring. The detection of such complex changes in regulatory connections remains a challenging task. We have developed a non-parametric ensemble method called BoostDiff (boosted differential regression trees) to infer a differential network discriminating between two conditions. To build the differential trees, we propose differential variance improvement as a novel splitting criterion. Variable importance measures derived from the resulting models are used to reflect changes in gene expression predictability and to build the output differential networks. In several examples, BoostDiff identifies context-specific networks that are enriched with genes of known disease-relevant pathways and complements standard differential expression analyses.