

Solutions and Practical Problems in Gene Regulatory Network Inference

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The inference of gene regulatory networks from mRNA expression data is characterized by the development of many different approaches with their specific performances, data requirements, and inherent biases. The recent community-wide DREAM challenge conducted a large assessment of inference approaches. The accuracy of predictions was evaluated against experimentally supported interactions in the procaryote model organism *E. coli*, the eucaryote model organism *S. cerevisiae* and in silico target systems. Further analysis revealed not only which inference strategies are particularly successful but also which kind of specific information was utilized from the different types of experimental measurements. The challenge evaluation also revealed several weaknesses and limitations of current methods for the generation of artificial datasets as well as the state of the art inference methods. For instance, none of the examined approaches was able to achieve robust predictions from *S. cerevisiae* data.