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Author	<b>Kristoffer Forslund</b>	
Title (English)	<b>Reconstruction of dynamic mRNA networks</b>	
Title (Swedish)		
Abstract	<p>This work uses computer simulations to evaluate algorithms that analyze gene regulatory networks by systematically perturbed gene expression measurements. To investigate the accuracy of a family of such algorithms, they are applied repeatedly to a variety of simulated gene regulatory networks over a range of conditions. Thereby, statistical comparisons may be made between different methods. Specifically, an algorithm called Mode of action by Network Identification (MNI) is shown to be at least comparable to its parent method, and is shown to be able to distinguish between direct and indirect target genes for a given treatment under noise-free circumstances. To further evaluate the performance of MNI, further research might apply it to a wider range of existing expression data collections.</p>	
Keywords	Gene regulation, MNI, system recovery, simulation, mRNA, perturbation method	
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