Differential Network Analysis of Anti-sense Regulation

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Résumé en anglais	A challenging task in systems biology is to decipher cell regulation mechanisms. By comparing networks observed in two different situations, the differential network analysis approach enables to highlight interaction differences that reveal specific cellular responses. The aim of our work is to study the role of natural anti-sense transcription on cellular regulation mechanisms. Our proposal is to build and compare networks obtained from two different sets of actors: the "usual" sense actors on one hand and the sense and anti-sense actors on the other hand. Our study only considers the most significant interactions, called an Extended Core Network; therefore our differential analysis identifies important interactions that are impacted by anti-sense transcription. This paper first introduces our inference method of an Extended Core Network; this method is inspired by C3NET, but whereas C3NET only computes one interaction per gene, we propose to consider the most significant interactions for each gene. Secondly, we define the differential network analysis of two extended core networks inferred with and without anti-sense actors. On a local view, this analysis relies on change motifs that describe which genes have their most important interactions modified when the anti-sense transcripts are considered; they are called AS-impacted genes. Then from a more global view, we consider how the relationships between these AS-impacted genes are rewired in the network with anti-sense actors. Our analysis is performed by computing Steiner trees that represent minimal subnetworks connecting the AS-impacted genes. We show that the visualisation of these results help the biologists to identify interesting parts of the networks.
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