Inference and Differential Analysis of Extended Core Networks: a way to study Anti-Sense Regulation

Submitted by Marc Legeay on Tue, 12/06/2016 - 15:19

Titre	Inference and Differential Analysis of Extended Core Networks: a way to study Anti-Sense Regulation
Type de publication	Communication
Type	Communication avec actes dans un congrès
Année	2016
Langue	Anglais
Date du colloque	15-18/12/2016
Titre du colloque	IEEE International Conference on Bioinformatics and Biomedicine (BIBM)
Auteur	Legeay, Marc [1], Duval, Béatrice [2], Renou, Jean-Pierre [3]
Pays	Chine
Ville	Shenzhen
Résumé en anglais	A key issue in bioinformatics is to decipher cell regulation mechanisms. By comparing networks observed in two different situations, differential network analysis enables to highlight 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 on the influence of anti-sense transcription. Our inference method of an Extended Core Network is inspired by C3NET, but whereas C3NET only computes one interaction per gene, we propose to consider the most significant interactions for each gene. We define the differential network analysis of two extended core networks inferred with and without anti-sense actors. This relies on change motifs that describe which gene-gene interactions of the extended core network are modified when we integrate anti-sense actors in the data. As our method ocuses on the most significant interactions, these motifs highlight the impact of anti-sense transcription. The networks motifs obtained by our workflow are then compared with assessed biological knowledge. The study reported in this paper is realized on transcriptional data from apple fruit in a context of fruit ripening; the change motifs revealed by our analysis are matched on a protein-protein interaction network and give a small set of interesting actors that deserve further biological investigation.
URL de la notice	http://okina.univ-angers.fr/publications/ua15217 [4]
DOI	10.1109/BIBM.2016.7822532 [5]
Lien vers le document en ligne	https://cci.drexel.edu/ieeebibm/bibm2016/BIBM2016Program.pdf [6]

Liens

[1] http://okina.univ-angers.fr/marc.legeay/publications
[2] http://okina.univ-angers.fr/beatrice.duval/publications
[3] http://okina.univ-angers.fr/publications?f%5Bauthor%5D=11747
[4] http://okina.univ-angers.fr/publications/ua15217
[5] http://dx.doi.org/10.1109/BIBM.2016.7822532
[6] https://cci.drexel.edu/ieeebibm/bibm2016/BIBM2016Program.pdf

Publié sur *Okina* (http://okina.univ-angers.fr)