



Differential Functional Analysis and Change Motifs in Gene Networks to Explore the Role of Anti-sense Transcription

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Résumé en anglais	Several transcriptomic studies have shown the widespread existence of anti-sense transcription in cell. Anti-sense RNAs may be important actors in transcriptional control, especially in stress response processes. The aim of our work is to study gene networks, with the particularity to integrate in the process anti-sense transcripts. In this paper, we first present a method that highlights the importance of taking into account anti-sense data into functional enrichment analysis. Secondly, we propose the differential analysis of gene networks built with and without anti-sense actors in order to discover interesting change motifs that involve the anti-sense transcripts. For more reliability, our network comparison only studies the conservative causal part of a network, inferred by the C3NET method. Our work is realized on transcriptomic data from apple fruit.
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Liens

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