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- 9.1 Any notice authorised or required to be given to KULEUVEN under this Agreement shall be in writing and shall be deemed to be duly given if left at or sent by registered post.
- 9.2 The terms and conditions herein contained constitute the entire agreement between the Parties and supersede all previous agreements and understandings, whether oral or written, between the parties hereto with respect to the subject matter thereof.

Article 10 - Conflicts

In the event of conflicts in the interpretation and/or performance of this Agreement, the parties shall first undertake to settle their differences amicably. If no amicable settlement can be reached concerning the execution and/or interpretation of this Agreement, such conflict shall be brought before the courts of Leuven and Belgian Law shall be applicable.

Choose one of the options below:

By downloading and or installing the Software and associated files on your computing system you agree to use the Software under the terms and condition as specified in this Agreement.

Or

By crossing the I agree button below you acknowledge that you agree on terms of use specified above.

I agree to the terms of use specified above:	
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Annex A: DISTILLER

Contributors: KULeuven: Tijl De Bie, Karen Lemmens, Hong Sun, Qiang Fu, Riet De Smet, Kristof Engelen

Framework: itemset mining

Data sources: microarray data, interaction data

Result: module network

Description

DISTILLER (Data Integration System To Identify Links in Expression Regulation) is a data integration framework that searches for transcriptional modules by combining expression data with information on the direct interaction between a regulator and its corresponding target genes (Lemmens et al., 2009). The inferred modules contain a minimal number

of genes (i.e. gene content threshold) that must be co-expressed in a sufficiently large number of conditions and share motif instances for the same regulator(s).

The framework builds upon advanced itemset mining approaches that have been designed to have good scalability, efficient memory use, and a small number of user parameters. It includes a condition selection or bicluster strategy in which co-expression of genes is required in only a significant subset of the complete condition set. By including this condition selection we can apply the algorithm to large expression compendia where interesting genes are not necessarily co-expressed in all measured conditions. Our approach also makes it straightforward to include any number of data sources related to transcriptional interactions such as additional microarrays, ChIP-chip or motif data.

Reference

K. Lemmens, T. De Bie, T. Dhollander, S. De Keersmaecker, I. Thijs, G. Schoofs, A. De Weerdt, B. De Moor, J. Vanderleyden, J. Collado-Vides, K. Engelen, and K. Marchal. <u>DISTILLER: a data integration framework to reveal condition dependency of complex regulons in Escherichia coli.</u> 2009. Genome biology, 6;10:R27.