

GRN2SBML: automated encoding and annotation of inferred gene regulatory networks complying with SBML.

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Abstract

GRN2SBML automatically encodes gene regulatory networks derived from several inference tools in systems biology markup language. Providing a graphical user interface, the networks can be annotated via the simple object access protocol (SOAP)-based application programming interface of BioMart Central Portal and minimum information required in the annotation of models registry. Additionally, we provide an R-package, which processes the output of supported inference algorithms and automatically passes all required parameters to GRN2SBML. Therefore, GRN2SBML closes a gap in the processing pipeline between the inference of gene regulatory networks and their subsequent analysis, visualization and storage.

Involved units

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