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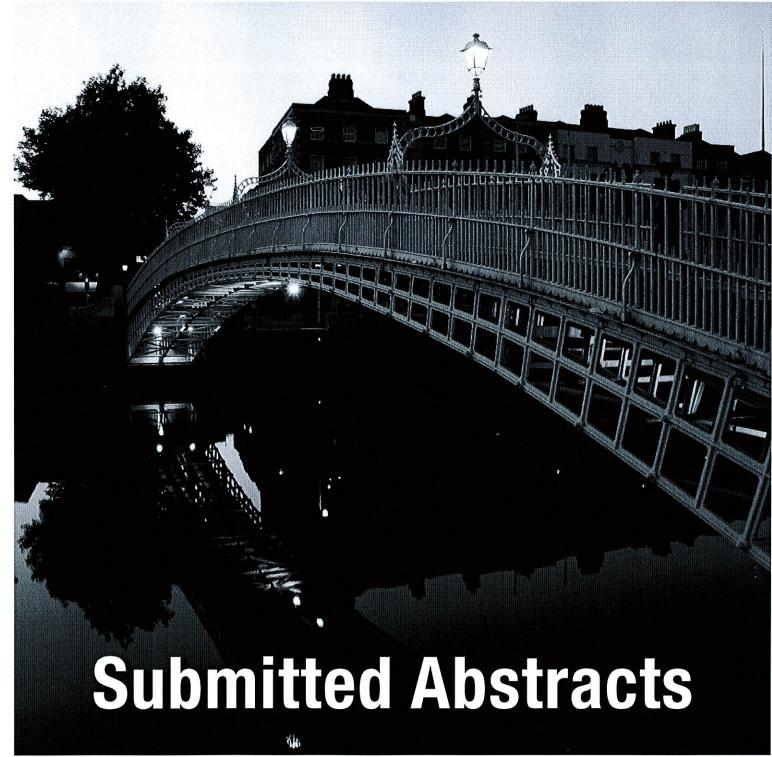
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A new method for modeling reactions and regulations to analyze highthroughout data

<u>Pierre Blavy^{1,2,8}</u>, Florence Gondret^{1,2}, Sven Thiele³, Carito Guziolowski⁴, Sandrine Lagarrigue^{5,6}, Jaap van Milgen^{1,2}, François Moreews^{1,8}, Anne Siegel^{7,8}

¹INRA, SENAH-UMR1079 Systèmes d'Elevage, Nutrition Animale et Humaine, F-35590 Saint Gilles, France

²AgroCampus-Ouest, SENAH-UMR1079, F-35000 Rennes, France

³Universität Potsdam, Institut für Informatik August-Bebel-Straße 89, D-14482 Potsdam, Germany

⁴Bioquant, University of Heidelberg, Im Neuenheimer Feld 267 - BQ24, D-69120, Germany

⁵AgroCampus-Ouest, UMR 598 Génétique Animale, F-35000 Rennes, France

⁶INRA, UMR 598 Génétique Animale, F-35000 Rennes, France

⁷CNRS, UMR 6074 IRISA, Campus de Beaulieu, F-35042 Rennes, France

⁸INRIA Rennes Bretagne Atlantique, Projet Symbiose, Campus de Beaulieu, F-35042 Rennes, France Corresponding author: pierre.blavy@irisa.fr

Recent experimental animal biology techniques produce large datasets that describe the variation of thousands of molecules according to various conditions like environment or breed. Bioinformatics tools allow the clustering of these data and their annotation based on ontologies or produce functional networks of specific pathways. However, pointing out key regulators of pathways and integrating datasets as a whole remains difficult. This study proposes a new method for modeling both reactions and their regulations at transcriptional and metabolic levels in a single formalism based on influence network (i.e., a directed graph). This network was analyzed to identify key regulators, make prediction on phenotypes or find a set of candidates that explain the variations of a set of targets. For that, information from the Transpath literature database was merged in a common formalism integrating both flux and molecular quantities in an influence network. Such a network was then analyzed with computational constrained-based approaches (answer set programming). To test the method, lists of differentially-expressed genes according to breed-related differences in pig adiposity or fasting effects on chicken liver were used. The produced networks were analyzed to check consistencies between knowledge and experimental data, to make predictions on unobserved molecules or fluxes, and to find the minimal set of variables among a set of candidates that explain variation in lipid metabolism. This method could help biologists to solve problems like finding the main regulators of a geneset of interest or elucidating causative genes among candidates located in a specific portion of the genome.