



HAL
open science

A new method for modeling reactions and regulations to analyze high-throughput data

Pierre Blavy, Florence Gondret, Sven Thiele, Carito Guziolowski, Sandrine Lagarrigue, Jaap J. van Milgen, François Moreews, Anne Siegel

► **To cite this version:**

Pierre Blavy, Florence Gondret, Sven Thiele, Carito Guziolowski, Sandrine Lagarrigue, et al.. A new method for modeling reactions and regulations to analyze high-throughput data. 4. International Symposium on Animal Functional Genomics, Sorcha De Gras; Sorcha De Gras, Oct 2011, Dublin, Ireland. <hal-02748096>

HAL Id: hal-02748096

<https://hal.inrae.fr/hal-02748096v1>

Submitted on 3 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

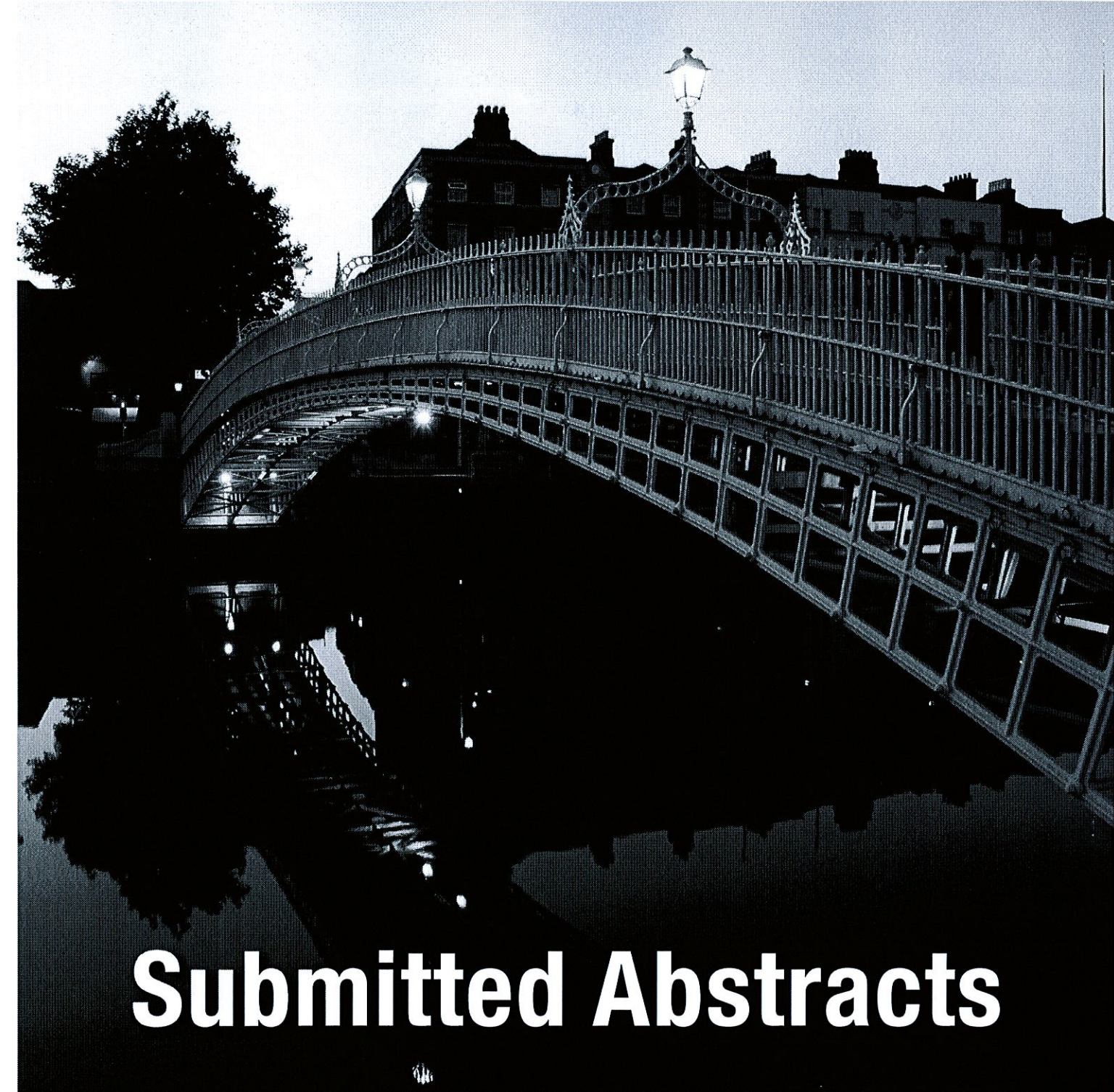


HAL Authorization

4th International Symposium on Animal Functional Genomics

Dublin, Ireland

Monday 10th October – Wednesday 12th October 2011



Submitted Abstracts

Note: this is a searchable document – please search by author name



A new method for modeling reactions and regulations to analyze high-throughout data

Pierre Blavy^{1,2,8}, 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'Élevage, 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 gene-set of interest or elucidating causative genes among candidates located in a specific portion of the genome.