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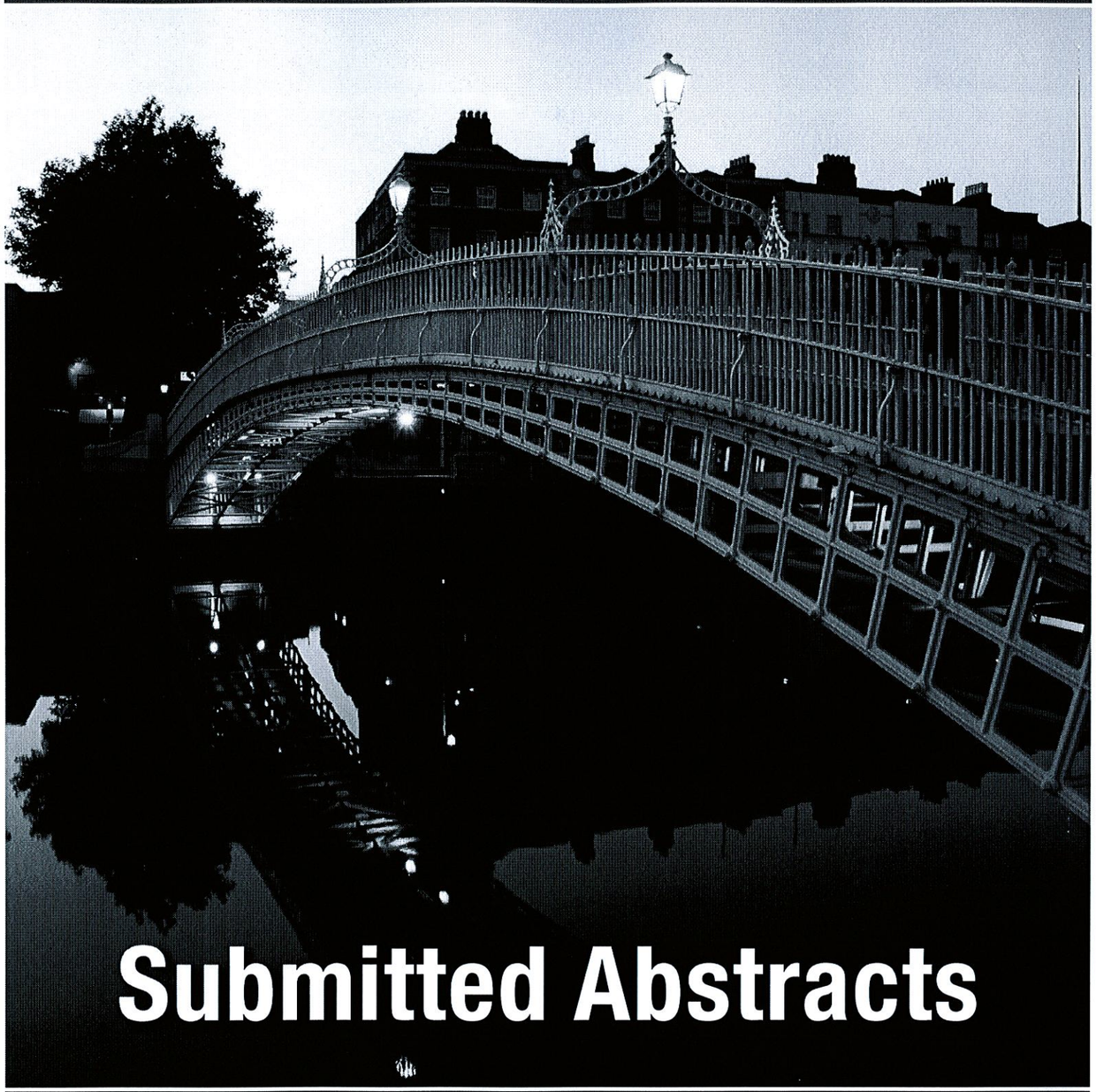
4th International Symposium on Animal Functional Genomics

Dublin, Ireland

Monday 10th October – Wednesday 12th October 2011



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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.