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Evolution of Gene Regulatory Networks

Guest Editors:

Dr. Marek Mutwil

School of Biological Sciences, Nanyang Technological University, 60 Nanyang Drive, Singapore, 637551, Singapore

Dr. Federico Manuel Giorgi

Department of Pharmacy and Biotechnology, University of Bologna, 40126 Bologna, Italy

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Message from the Guest Editors

Dear Colleagues,

Prediction of gene regulatory networks and gene function is currently among the most active topics in computational biology. The overwhelming accumulation of highthroughput sequencing data, capturing genomes and gene expression data for thousands of organisms species, requires us to invent novel bioinformatical approaches to efficiently process this data. Furthermore, it is becoming clear that the evolution of novel traits, such as organs, tissues, and metabolites, cannot be fully explained by genomic approaches since genomics might not reveal which genes work together to express a given trait. Consequently, current approaches use transcriptomics, proteomics, metabolomics and novel data processing and machine learning algorithms to try to infer the gene function and regulation.

This Special Issue invites research articles, reviews, and short communications including but not limited to: methods to construct functional and gene regulatory networks, novel approaches to process high-throughput data to produce these networks, and comparative approaches that study the evolution of these networks.

Dr. Marek Mutwil Dr. Federico Manuel Giorgi *Guest Editors*







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Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan

Department of Pathology, The University of Alabama at Birmingham, 1825 University Blvd, SHEL 814, Birmingham, AL 35294-2182, USA

Message from the Editor-in-Chief

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Genes Editorial Office MDPI, Grosspeteranlage 5 4052 Basel, Switzerland Tel: +41 61 683 77 34 www.mdpi.com mdpi.com/journal/genes genes@mdpi.com X@Genes_MDPI