



UNIVERSIDAD ADOLFO IBÁÑEZ  
FACULTAD DE INGENIERÍA Y CIENCIAS  
DOCTORATE IN COMPLEX SYSTEMS ENGINEERING

**“MODELING OF PLANT RESPONSES TO THE ENVIRONMENT  
THROUGH GENE REGULATORY NETWORKS INFERENCE”**

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Submitted as a requirement for the degree of Doctor of Complex Systems  
Engineering of the Universidad Adolfo Ibáñez, February 2018

## ACKNOWLEDGMENTS

First, I would like to express my sincere gratitude to my advisors Prof. Bernardo González and Prof. Gonzalo A. Ruz for their continuous support of my PhD work and related research, especially for their patience, motivation, knowledge and experience and also for the great opportunity to do science with them. Their guidance helped me all the time during the research and writing of this thesis. Bernardo and Gonzalo, you know how immensely grateful I am of you for all these years working together.

Bernardo and Cedric Little, thanks for allowing me to study while working for the UAI-Bioengineering Laboratory, I appreciate this very much.

Besides my PhD advisors, I would like to thank Prof. Sergio Rica, Prof. Marco Montalva, and especially Prof. Eric Goles, for being present in all these years as a PhD student. Eric, thank you for all the opportunities you gave me, starting from meeting both national and international recognized scientists, as well as working together and giving rise to coauthored publications. Your passion for science is admirable and undoubtedly leaves a mark on every student of the program, including myself for sure.

My deeply thanks also to Prof. Josefina Poupin for helping me with the structure of this writing and more importantly for giving me support beyond the scientific grounds. Jose, you know well how important you are in my life.

A special greeting to Daniella Pooley for her work and support to the students of this program, thanks Dani for always being so close to us.

Also, I thank my PhD classmates for the stimulating discussions mostly in the first year of courses, for the sleepless nights we were working together before deadlines and for the shared joys of overcoming every academic challenge in this PhD program that was completely new in Chile: Gustavo Rodríguez, Pablo Leiva, Esteban Román, Felipe Urbina, Raimundo Sánchez, Vasco Cortés, Javier Vera and Axel Araneda. I will also thank my friends and colleagues in the UAI-Bioengineering Laboratory for giving me courage and strength in this process, especially Prof. Thomas Ledger, Raúl Donoso and Daniela Ruiz.

A special mention to Gonzalo Fuenzalida, my new boss, for giving me enough time to write this thesis. Thanks Gonzalo for your generosity and constant support.

Last but not the least, I would like to thank my family: my husband, Diego; my parents, Pedro and Macarena; and my siblings, Karla, Diego, Heidi and Pablo for supporting me spiritually throughout my PhD training.

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## ABSTRACT

The huge data sets in biology, mainly due to the exponential development of high-throughput technologies and the growing computational power, represent a big challenge, usually not related with the acquisition of the data, but with the subsequent activities such as data processing, analysis, knowledge generation and getting insights for the research questions of interest. In such a sense, the approach of inferring gene regulatory networks (GRNs) has contributed importantly to understand functioning of living organisms.

Because of the global population increment and climate change pose a challenge to worldwide crop production, there is a need to intensify agricultural production in a sustainable manner and to find solutions to combat abiotic stress, pathogens and pests. How plants respond to environmental changes, and how such knowledge could engender new technologies, for example, to increase crop yields, are issues that could be addressed using GRNs. Additionally, beneficial plant-microbe interactions represent a promising sustainable solution to improve agricultural production, therefore the study of such interactions becomes relevant. The research described in this thesis attempts to model plant responses to environmental changes, specifically salinity and pathogens, through GRNs inference. For the GRNs inference different evolutionary algorithms were utilized and the mathematical model used to represents the GRNs were threshold Boolean networks.

The first chapter of this thesis addresses the theoretical framework, the study model and the objectives.

The second chapter of this thesis described and characterized for the first time the mechanism used by the well-known beneficial bacterium *Paraburkholderia*

*phytofirmans* PsJN to protect *Arabidopsis thaliana* plants against a common pathogenic bacterium (*Pseudomonas syringae* DC3000). Results at the phenotypic, biochemical and transcriptional level were published and constitutes a contribution to the development and application of biopesticides based on beneficial bacteria.

The third chapter further explores the regulatory mechanism of the defense response and induced systemic resistance (ISR), triggered by strain PsJN in *Arabidopsis*. To achieve this, a GRN underlying ISR response was inferred using empirical time-series data of certain defense-related genes, differential evolution algorithm and threshold Boolean networks.

The fourth chapter tackles the study of ISR response from a genome-wide point of view. A transcriptomic analysis was performed to understand global changes in gene expression of plants primed by strain PsJN and infected with *P. syringae* DC3000, in contrast with non-primed plants.

The fifth and final chapter aimed at inferring a GRN involved in the underlying salt stress response in *Arabidopsis* plants using transcriptomic time-series data, genetic algorithms and threshold Boolean networks to better understand the regulatory process under saline growth conditions with the final goal of developing crops with enhanced tolerance to this important environmental threat.