



TÉCNICO
LISBOA

D-DEI 2017

@ Caparide

Pedro Tiago Monteiro

IST - Universidade de Lisboa

MTP - Metodologia e Tecnologia da Programação

Pedro T. Monteiro

- **Assistant Professor** at IST - Universidade de Lisboa
Scientific area: MTP
- **Researcher** at INESC-ID Lisboa
Research group: SAT

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Short CV

- **BSc/MSc** – Information Systems and Computer Engineering from IST
- **Software developer** – iKnow - Consultoria em Tecnologias de Informação, SA
- **Dual PhD** – IBIS group at INRIA Grenoble Rhône-Alpes, FR
 - IST - Universidade de Lisboa, PT
 - Université Claude Bernard Lyon 1, FR
- **Postdoc** – Network Modelling group at Instituto Gulbenkian de Ciência
- **Lab. Associado + Investigador FCT** – INESC-ID
- **Invited Assistant Professor** – IST - Universidade de Lisboa

Object Oriented Programming - 2rd year LEIC-T

- 2012/2013 & 2013/2014 (Fall semester)

Compilers - 3rd year LEIC-A

- 2014/2015 & 2015/2016 (Spring semester)

Microbial Cell Factories - MSc MicroBiology

- 2013/2014, 2014/2015, 2015/2016 & 2016/2017 (Spring semester)

Teaching

Object Oriented Programming - 2rd year LEIC-T

- 2012/2013 & 2013/2014 (Fall semester)

Compilers - 3rd year LEIC-A

- 2014/2015 & 2015/2016 (Spring semester)

Microbial Cell Factories - MSc MicroBiology

- 2013/2014, 2014/2015, 2015/2016 & 2016/2017 (Spring semester)
-

Foundations of Programming - 1st year LEIC-T

- 2016/2017 (Fall semester)

Compilers - 3rd year LEIC-T

- 2016/2017 (Spring semester) – **Course responsible**

Research keywords:

- Biological regulatory networks
- Qualitative modeling
- (Boolean) Logical formalism
- Discrete event systems
- Discrete structures
- Graph algorithms
- Formal verification
- Temporal logic
- Model composition

Publication venues:

- Nucleic Acids Research, Frontiers in Genetics, Frontiers in Bioengineering and Biotechnology
- Bioinformatics, BMC Bioinformatics, BMC Systems Biology
- Theoretical Computer Science, Electronic Notes in Theoretical Computer Science, Chaos, PLOS One
- Computational Methods in Systems Biology, Static Analysis and Systems Biology

Research - MSc thesis

<http://yeastract.com> - Repository of regulatory associations in *S. cerevisiae*



YeastRACT



TÉCNICO LISBOA

bSrg IBB
Institute for Bioengineering and Biosciences



Home > Rank genes by TF > Result > Image

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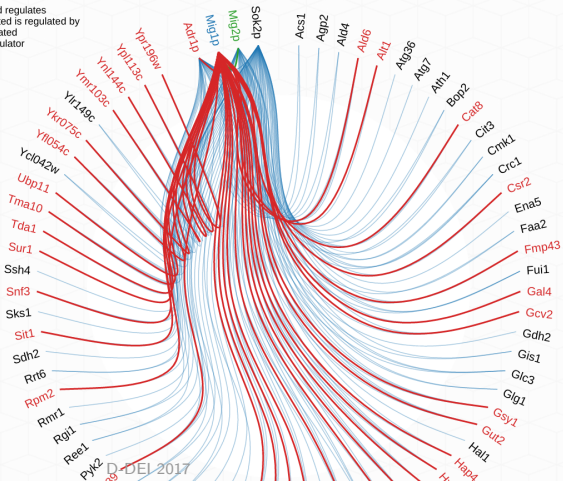
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Transcriptional Regulatory Network

Legend:

- Red arc - Selected regulates
- Green arc - Selected is regulated by
- Red node - Regulated
- Green node - Regulator



Research

Networks to models

No global view of functioning of the network available, despite abundant knowledge on network components

- Understanding of dynamics requires mathematical modeling and computer analysis and simulation
- Discipline often referred to as **Systems biology**

Use of models to analyse networks

- Understanding of the way in which particular molecular mechanisms control a cellular process
- Predicting novel phenomena that can be confronted with experimental data

Problem: Lack of integration between existing modelling and formal verification tools

- Models of biological regulatory networks have become increasingly larger
- Qualitative behaviours are represented using a state transition graph
- Qualitative behaviours cannot be manually verified (**combinatorial explosion!**)

PhD thesis – proposed three-part solution:

- High-level query templates of FAQ in the Systems Biology domain
(Monteiro et al, Bioinformatics 2008)
- Service oriented architecture between modeling and formal verification tools
(Monteiro et al, BMC Bioinformatics 2009)
- Definition and implementation of Computation Tree Regular Logic
(Mateescu et al, Theor. Comput. Sci. 2011)

PhD thesis – proposed three-part solution:

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Postdoc:

- Integration with NuSMV model checking tool
(Monteiro and Chaouiya, PACBB 2012)
(Monteiro et al, WODES 2014)
- Model and state space reduction
(Naldi et al, CMSB 2012)

ERGODiC (PTDC/EEI-CTP/2914/2014)

Formal methods for the analysis of modular gEnetic ReGulatOry network DynamiCs

Team:

- Pedro T. Monteiro (**PI**) INESC-ID/IST - U.Lisboa
- Inês Lynce INESC-ID/IST - U.Lisboa
- Claudine Chaouiya Instituto Gulbenkian de Ciência

Objectives:

- Characterization of model attractors (Boolean satisfiability)
- Characterization of basins of attraction
- Reachability properties (Model checking)

Research projects

FCT

CANTROL (PTDC/BBB-BIO/4004/2014)

Deciphering the mechanisms of transcriptional regulation that control antifungal drug resistance in the pathogenic yeast *Candida glabrata*: aiming the development of improved diagnosis and therapeutic approaches

Team:

- Miguel C. Teixeira (**PI**) IBB/IST - U.Lisboa
- A.G. Rodrigues FM - U.Porto
- Nuno P. Mira IBB/IST - U.Lisboa
- Pedro T. Monteiro INESC-ID/IST - U.Lisboa
- Claudine Chaouiya Instituto Gulbenkian de Ciência

Objectives:

- Build a repository of regulatory associations for *C.glabrata*
- Comprehensive transcriptional regulatory map
- Build model for multiple drug resistance in *C.glabrata*
- Screen for inhibitors of antifungal drug resistance

Research projects

FCT

CoMEDy (PTDC/BEX-BCB/0772/2014)

A Computational Modelling platform for Epithelial DYNamics to explore the role of epithelialmesenchymal transition and stemness acquisition in cancer recurrence

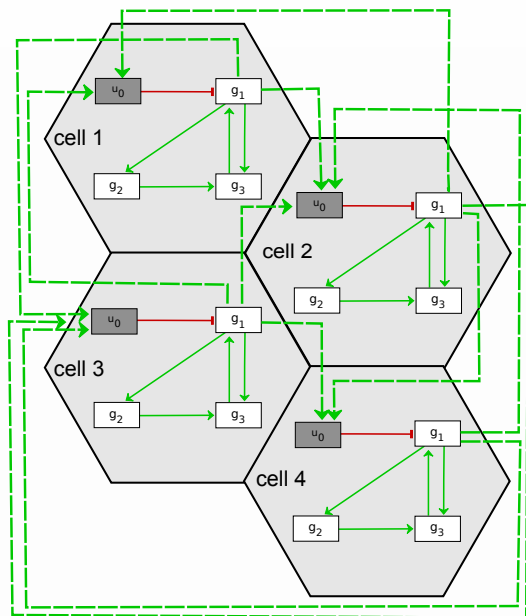
Team:

- Claudine Chaouiya (**PI**) Instituto Gulbenkian de Ciência
- Florence Janody Instituto Gulbenkian de Ciência
- Pedro T. Monteiro INESC-ID/IST - U.Lisboa

Objectives:

- Study Epithelial-Mesenchymal Transition (EMT) in metastasis
- Build multi-scale models for EMT in epithelial cells
- Study in silico and in vitro cell-cell and cell-microenvironment interactions

Research projects



Current CS-related interests:

- Classes of Boolean functions: (non-)monotone, (non-)degenerated, ...
- Partial order relation of Boolean functions
- Stochasticity in classes of Boolean models
- Semi-automatic model revision

Thank you!

<http://pedromonteiro.org>