

## ANA TERESA FREITAS

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### PRESENT POSITIONS

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Associate Professor (with Habilitation) at the Departamento de Informática of Instituto Superior Técnico (IST), Lisbon Technical University ( <a href="http://www.ist.utl.pt">http://www.ist.utl.pt</a> )	<b>Presently</b>
Head of the Knowledge Discovery and Bioinformatics (KDBIO) research group, ( <a href="http://kdbio.inesc-id.pt">http://kdbio.inesc-id.pt</a> )	<b>2009 until now</b>
Assistant Professor (with tenure) at Universidade da Madeira (UMA), Madeira University ( <a href="http://www.uma.pt/">http://www.uma.pt/</a> )	<b>2009 - 2010</b>
Invited researcher (sabbatical leave) with the BAOBAB Team/Inria Rhône-Alpes UMR 5558 Biométrie et Biologie Évolutive, Université Claude Bernard, Lyon I, France.	<b>2008 - 2009</b>

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### EDUCATION

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BSc from Instituto Superior Técnico in Electrical Engineering and Computer Science	<b>1990</b>
MSc from Instituto Superior Técnico in Electrical Engineering and Computer Science (with honors)	<b>1994</b>
PhD from Instituto Superior Técnico in Electrical Engineering and Computer Science (with honors)	<b>2002</b>

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### RESEARCH INTERESTS

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My current research interests are centered in the areas of Computational Biology, Human genetics, Algorithms and Data Mining. The Knowledge Discovery and Bioinformatics group (KDBIO) where this research is developed is the most active and dynamic research group in his area, in Portugal, and integrates 10 PhDs, and approximately 25 grants, postdoctoral fellows and PhD students. Research in these areas has lead to several National projects and three European projects. I have co-authored about 88 papers in international journals and conferences in the areas of computational biology, bioinformatics and computer aided. I have participated in a number of programs and scientific committees of international conferences and I am a permanent reviewer of the main journals in the Computational Biology field, like Nucleic Acid Research, Bioinformatics Oxford journal, PlosOne, BMC Bioinformatics,

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Transactions in Computational Biology and Bioinformatics, etc ... During the last five years I have been Principal Investigator of seven national projects and participant of two research projects funded by the European Commission such as BIOHYPO and PNEUMOPATH (PI of the bioinformatics component).

In the context of the research area of petroleum microbiology I have a collaboration with the Laboratório Nacional de Computação Científica (LNCC) and Universidade Federal do Rio Grande do Norte (UFRN) from Brazil for more than four years now. This collaboration gave place to two International Journal papers, three publications in International Conferences and the participation of LNCC team in two Portuguese National project. Several software tools developed by the KDBIO group have been installed at the sequencing platform at LNCC to perform genome re-sequencing. Presently, I am developing computational tools to deal with metagenomics NGS data with the goal to identify important metabolic pathways, and later bacterial strains, that should be optimized for biodegradation.

My present research interests are focused on the areas of applications in genetics and medical diagnosis and metagenomics.

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## **BRIEF SUMMARY OF CAREER**

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From 1994 to 2002 I worked in the areas of computer aided design and integrated circuits manufacture. I was part of the team that built the first cleaning room in Portugal and the first Portuguese integrated circuit. In 2002, I got my PhD degree from the Technical University of Lisbon, under the supervision of Prof. Arlindo Oliveira, with a thesis entitled “Estimação da Potência em Circuitos Digitais Utilizando Técnicas de Enumeração Implícita”, that used concepts from the fields of low power circuits design, algorithms and logic synthesis. At the end of my PhD I decided to focus my research in what I believed would be a very important area in the coming decades, algorithms for computational biology. This initiative resulted in the Knowledge Discovery and Bioinformatics group of INESC-ID that, since then, became the best-known group in computational biology in the country, and a well-known group worldwide.

I have advised 4 PhD students and current advise 3 PhD students, in areas related with my major focus of research. I have also advised 14 MSc students and 14 Graduation students, in the Computational Biology field. I have participated at the organization of the PhD program on Computational Biology (FCT/IGC/Siemens) as a teacher and member of the scientific committee.

In the last five years I have decided to go from science into the market and try to overcome the numerous barriers of the highly complex "technology transfer landscape". The result is the new born company HEARTGENETICS GENETICS AND BIOTECHNOLOGY SA. Supported by Venture Capitals this new biotech company main goal is to create a new vision for medicine using genomic technologies and computational methods. Our main products in the area of cardiovascular diseases

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are the result of 10 years research in Portugal of the three founders, Alexandra Fernandes (PhD in Biotechnology from IST), Susana Santos (PhD in Molecular Biology from FCUL) and Ana Teresa Freitas (PhD in Electronics and Computer Engineer from IST). We have developed a DNA microchip to efficiently perform cardiovascular genetic tests and a clinical decision support system to improve diagnosis and prognosis. Presently I am the CEO of this company.

Prizes:

1- Prize Sartorius for Innovation in Biotechnology, at Micro-Biotec 2007, for the work that lead to the Yeabstract information system and the article YEABSTRACT-DISCOVERER: new tools to improve the analysis of transcriptional regulatory associations in *Saccharomyces cerevisiae* published in NAR. in 2008 (with a number of co-authors, see publication list).

2- Best paper award for the 2001 ICECS article “Circuit partitioning techniques for power estimation using the full set of input correlations” (with Arlindo Oliveira).

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## MAIN PUBLICATIONS

### Book chapters

- Susana R. Santos, Ana T. Freitas, Alexandra Fernandes, Overview of HCM genomics and transcriptomics: molecular tools in HCM assessment for application in clinical medicine. iConcept Press 2013. Accepted.

- Hélio C. Pais and Kenneth L. McMillan and Ellen M. Sentovich and Ana T. Freitas and Arlindo L. Oliveira, Improved Model Checking Techniques for State Space Analysis of Gene Regulatory Networks, included in the book Handbook of Research on Computational Methodologies in Gene Regulatory Networks, ISBN: 978-1-60566-685-3; 719 pp; October 2009, Published under Medical Information Science Reference, an imprint of IGI Global. Edited by: Sanjoy Das, Kansas State University, USA; Doina Caragea, Kansas State University, USA; Stephen Welch, Kansas State University, USA; William H. Hsu, Kansas State University, USA.

### International journals

- Miguel Teixeira and Pedro T. Monteiro and Joana Guerreiro and Joana Gonçalves and Nuno Mira and Sandra dos Santos and Tânia Cabrito and Margarida Palma and Catarina Costa and A. P. Francisco and Sara C. Madeira and Arlindo L. Oliveira and Ana T. Freitas and Isabel Sá-Correia, The YEABSTRACT database: an upgraded information system for the analysis of gene and genomic transcription regulation in *Saccharomyces cerevisiae*, Nucleic Acids Research , 42 (D1): D1-D6, Jan. 2014.

- Francisco Fernandes and Ana T. Freitas, slaMEM: Efficient retrieval of Maximal

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Exact Matches using a Sampled LCP Array, *Bioinformatics*, (), pp. , Nov. 2013.

- Cátia M. Machado and Dietrich Rebholz-Schuhmann and Ana T. Freitas and Francisco M. Couto, The semantic web in translational medicine: current applications and future directions, *Briefings in Bioinformatics*, (), pp. , Nov. 2013.

- Cátia M. Machado and Ana T. Freitas and Francisco M. Couto, Enrichment analysis applied to disease prognosis, *Journal of Biomedical Semantics*, 4(21), pp. , Oct. 2013,

- L. Furi and M.L. Ciusa and D. Knight and V. Di Lorenzo and N. Tocci and D. Cirasola and L. Aragonés and Joana Coelho and Ana T. Freitas and E. Marchi and L. Moce and P. Visa and J. B. Northwood and C. Viti and G. Orefici and the BIOHYPO Consortium and I. Morrissey and M. R. Oggioni, Evaluation of Reduced Susceptibility to Quaternary Ammonium Compounds and Bisbiguanides in Clinical Isolates and Laboratory-Generated Mutants of *Staphylococcus aureus*, *Antimicrobial agents and chemotherapy*, 57(8), pp. , Aug. 2013.

- Jorge dos Santos Oliveira and Nuno Mendes and Vitor Carocha and Clara Graça and Jorge A. P. Paiva and Ana T. Freitas, A computational approach for microRNA identification in plants: combining genome-based predictions with RNA-Seq data, , (), pp. , May. 2013.

- Joana Coelho and João Carriço and Daniel Knight and Jose Luis Martinez and Ian Morrissey and Marco R. Oggioni and Ana T. Freitas, The use of Machine Learning methodologies to analyse Antibiotic and Biocide susceptibility in *Staphylococcus aureus*, *PLOS ONE*, (), pp. , Feb. 2013.

- Paulo G. S. da Fonseca and Jorge A. P. Paiva and Luiz G. P. Almeida and Ana Tereza Vasconcelos and Ana T. Freitas, Empirical assessment of sequencing errors for high through-put pyrosequencing data, *BMC Research Notes*, 6(25), pp. , Jan. 2013.

- M.L. Ciusa and L. Furi and Daniel Knight and F. Decorosi and Marco Fondi and Carla Raggi and Joana Coelho and Luis Aragonés and Laura Moce and Pilar Visa and Ana T. Freitas and L. Baldassarri and Renato Fani and Carlo Viti and G. Orefici and Jose Luis Martinez and the BIOHYPO Consortium and Ian Morrissey and Marco R. Oggioni, A novel resistance mechanism to triclosan that suggests horizontal gene transfer and demonstrates a potential selective pressure for reduced biocide susceptibility in clinical strains of *Staphylococcus aureus*, *International Journal of Antimicrobial Agents*, 40(3), pp. 210-220, Sep. 2012, .

- Nuno Mendes and Ana T. Freitas and Steffen Heyne and Marie-France Sagot and Rolf Backofen, Navigating the unexplored seascape of pre-miRNA candidates in single-genome approaches, , 28(23), pp. 3034-3041, Sep. 2012, .

- Dulce Calçada and Susana Vinga and Ana T. Freitas and Arlindo L. Oliveira, Quantitative modeling of the *Saccharomyces cerevisiae* FLR1 Regulatory Network using an S-System Formalism, *Journal of Bioinformatics and Computational Biology*,

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9(5), pp. , Oct. 2011, World Scientific.

- Pedro T. Monteiro and Paulo J. Dias and Delphine Ropers and Arlindo L. Oliveira and Isabel Sá-Correia and Miguel C. Teixeira and Ana T. Freitas, Qualitative modelling and formal verification of the FLR1 gene mancozeb response in *Saccharomyces cerevisiae*, *IET Systems Biology*, 5(5), pp. 308-316, Sep. 2011, IET.

- Francisco Fernandes and Paulo G. S. da Fonseca and Luís M. S. Russo and Arlindo L. Oliveira and Ana T. Freitas, Efficient alignment of pyrosequencing reads for resequencing applications, *BMC Bioinformatics*, 12(163), pp. , Jun. 2011, BioMed Central.

- Jorge A P Paiva and Elisa Prat and Sonia Vautrin and Mauro D Santos and Hélène San-Clement and Sérgio Brommonschenkel and Paulo G. S. da Fonseca and Dário Grattapaglia and Xiang Song and Jetty S S Ammiraju and David Kudrna and Rod A Wing and Ana T. Freitas and Hélène Bèrges and Jacqueline Grima-Pettenati, Advancing Eucalyptus genomics: identification and sequencing of lignin biosynthesis genes from deep-coverage BAC libraries, *BMC Genomics*, 12(137), pp. , Mar. 2011, .

- Dário Abdulrehman and Pedro T. Monteiro and Miguel C. Teixeira and Nuno P. Mira and Artur B. Lourenço and Sónia C. dos Santos and Tânia R. Cabrito and A. P. Francisco and Sara C. Madeira and Ricardo Rubén dos Santos Aires and Arlindo L. Oliveira and Isabel Sá-Correia and Ana T. Freitas, YEASTRACT: Providing a programmatic access to curated transcriptional regulatory associations in *Saccharomyces cerevisiae* through a web services interface, *Nucleic Acids Research*, 39(1), pp. D136-D140 , Jan. 2011, .

- Miguel C. Teixeira and Paulo J. Dias and Pedro T. Monteiro and Arlindo L. Oliveira and Ana T. Freitas and Isabel Sá-Correia, Refining current knowledge on the yeast FLR1 regulatory network by combined experimental and computational approaches, *Molecular BioSystems*, 6(12), pp. 2471-2481, Nov. 2010, RCS Publishing.

- Nuno Mendes and Ana T. Freitas and Ana T. Vasconcelos and Marie-France Sagot, Combination of measures distinguishes pre-miRNAs from other stem-loops in the genome of the newly sequenced *Anopheles darlingi*, *BMC Genomics*, (), pp. 11:529, Oct. 2010, .

- Cátia M. Machado and Francisco Couto and Alexandra R. Fernandes and Susana Santos and Nuno Cardim and Ana T. Freitas, Unraveling Hypertrophic Cardiomyopathy Variability, *ERCIM NEWS*, 82(), pp. 48-49, Jun. 2010, ERCIM.

- Pedro T. Monteiro and Estelle Dumas and Bruno Besson and Radu Mateescu and Michel Page and Ana T. Freitas and Hidde de Jong, A service-oriented architecture for integrating the modeling and verification of genetic regulatory networks, *BMC Bioinformatics*, 10(450), pp. , Dec. 2009, BioMed Central.

- Francisco Fernandes and Luisa Pereira and Ana T. Freitas, CSA: An efficient

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algorithm to improve circular DNA multiple alignment, *BMC Bioinformatics*, 10(), pp. 230, Jul. 2009, BioMed Central.

- Nuno Mendes and Ana T. Freitas and Marie-France Sagot, Current tools for the identification of miRNA genes and their targets, *Nucleic Acids Research*, 8(37), pp. 2419-2433, May. 2009, .

- Francisco Fernandes and Ana T. Freitas and Jonas S. Almeida and Susana Vinga, Entropic Profiler - Detection of conservation in genomes using Information Theory, *BMC Research Notes*, 2(72), pp. , May. 2009, .

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- Alexandra M. Carvalho and Ana T. Freitas and Arlindo L. Oliveira and Marie-France Sagot, An Efficient Algorithm for the Identification of Structured Motifs in DNA Promoter Sequences, *IEEE Transactions on Computational Biology and Bioinformatics*, 3(2), pp. 126-140, Apr. 2006, IEEE. ]

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