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OZAN KAHRAMANOGULLARI CURRICULUM VITAE

INFORMAZIONI PERSONALI (NON INSERIRE INDIRIZZO PRIVATO E TELEFONO FISSO O CELLULARE)

COGNOME	KAHRAMANOGULLARI
NOME	OZAN
DATA DI NASCITA	18/10/1977

Data

12/7/2021

Luogo

Trento

Ozan Kahramanoğlu, PhD

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ORCID: 0000-0001-5178-7470

May 19th, 2021

Current Position

2020 – **VP AI-Systems Biology**
ThinkNode Life Science Inc., San Diego, California, USA

Previous Positions

2019 – 2020 **Researcher**
Department of Cellular, Computational and Integrative Biology (CIBIO)
& Department of Mathematics, **University of Trento**, Italy

2014 – 2019 **Assistant Professor - RTDa**
Department of Mathematics, **University of Trento**, Italy

2009 – 2017 **Researcher**
The Microsoft Research - University of Trento
Centre for Computational and Systems Biology, Italy

2006 - 2009 **Research Associate**
Department of Computing, **Imperial College** &
Centre for Integrative Systems Biology at Imperial College

2005 – 2006 **Teaching Assistant, Dresden University of Technology**

2001 – 2002 *Institute for Artificial Intelligence*
Teaching: “Logik” course, taught in German language

2000 **Software Developer**, Hybris GmbH, Dresden, Germany

Qualifications

2002 – 2006 **PhD Computer Science, Dresden University of Technology**, Germany
Grant: “DFG Graduiertenkolleg 446” at the University of Leipzig

1999 – 2002 **MSc Computer Science, Dresden University of Technology**, Germany
Grade: 1.5 (excellent), thesis published at the KI’03 Conference, LNCS, Springer

1994 – 1999 **BSc Mathematics, Hacettepe University**, Ankara, Turkey

Grants

2020 *ASSEMBLE Plus* Transactional Access program, PI
Understanding Coral Colony Morphology via Stochastic Modelling (UNICOMS)
ca. 10000 € for access to Observatoire Océanologique de B. sur mer.

2017 – 2019 *European Union Horizon 2020 - Living Architecture*
Project leader: modelling of phosphate economy in *E. coli*, **University of Trento**
PI: Prof. Martin Hanczyc 217.218,75 € (3.216.555 € to 6 institutions).

2006 – 2009 *Biotechnology and Biological Sciences Research Council*
Post-doctoral research, CISBIC, **Imperial College**, UK
PI: Prof. L. Cardelli & Prof. P. Gardner, ca. 150.000 £

2002 – 2005 *German Research Foundation* PhD Studentship, “DFG Graduiertenkolleg 446”
University of Leipzig & Dresden University of Technology, Germany
PI: Prof. G. Brewka, ca. 60.000 €

2004 **Protheo Group, LORIA**, Nancy, France, November- December, 2004
German Academic Exchange Service, *Visiting researcher grant*

2001 **University of Amsterdam**
Institute for Logic, Language and Computation, January - July, 2001
German Academic Exchange Service, *Exchange student grant*

Supervision of Research Students

- 2019 – Elena Righetti - MSc Thesis, **University of Trento**, Dep. of Mathematics
Bacterial response mechanisms to changes in external phosphate levels.
- 2015 – 2018 Cansu Uluseker - PhD Thesis, grade: *cum laude* (with honors), 15.10.2018.
University of Trento, Dep. of Cellular, Comp. and Integrative Biology.
Thesis: A systems and synthetic biology framework for regulatory systems.
Researcher at the *University of Stavanger*.
- 2014 – 2017 Federico Reali - PhD Thesis, grade: *cum laude* (with honors), 24.3.2017.
University of Trento, Department of Mathematics. *Thesis*: Dynamical models for diabetes: insights into insulin resistance and type 1 diabetes.
Researcher at *The Microsoft Research - University of Trento COSBI*
- 2016 Andrea Giachino - BSc Thesis, grade: *cum laude* (with honors), 26.9.2016.
Centre for Integrative Biology, **University of Trento**. *Thesis*: Intrinsic Regulation of Actin Steady-State. PhD student at the Newcastle University.

Teaching Activities

- 2014 – *Assistant Professor*. Preparation and teaching of a course each semester.
Systems Biology (Italian), Modelling and Simulation of Biological Systems,
Biological Networks, Biostatistics, Advanced Topics in Biomathematics
University of Trento, Italy
- 2006 – 2009 *Teaching Assistant*. Assisting tutorials for two hours per week per semester.
Formal Software Verification, Robotics, Programming, Bioinformatics.
Imperial College, UK
- 2005 – 2006 *Teaching Assistant*. Four hours per week held in German language.
- 2001 – 2002 Logic, **Dresden University of Technology**

Miscellaneous

- 2020 Topical Board member of MDPI Journal /Biology/
Editor for the special issue *Computational Methods in Synthetic Biology*
- 2014 – 2019 Faculty member, Organiser of bi-weekly modelling seminars
Department of Mathematics, University of Trento, Italy
- 2006 – 2009 Organiser of the Internal Seminar
CISBIC, Imperial College, UK
- 2002 – 2005 Speaker of the Graduiertenkolleg 446 PhD Programme
University of Leipzig, Germany
- 2000 – 2002 Student representative of the Examination Commission
International Masters Programme in Computational Logic
Dresden University of Technology, Germany.

Reviewer for Journals Logical Methods in Computer Science, Adaptive Behaviour, Bioinformatics, Nucleic Acid Therapeutics, Journal Of Computational Physics, BMC Bioinformatics, Artificial Life Journal, Natural Computing, Journal of Artificial Intelligence Research, BMC Systems Biology, Transactions on Computational Systems Biology, Science of Computer Programming, Formal Aspects of Computing, Theoretical Computer Science, Genetic Programming and Evolvable Machines, Molecular BioSystems, Adaptive Behavior, PLoS Computational Biology.

Languages

English (*fluent*), German (*fluent*), Italian (*fluent*), Dutch (*beginner*), Turkish (*mother tongue*)

Research Statement of Ozan Kahramanoğulları

My research in biology is interdisciplinary and the computer science notion of interaction is its unifying theme: I am interested in explaining experimental observations in terms of behaviour that emerges from the interactions of system components. Synthetic biology accommodates this computer science point of view, also because it strives for establishing engineering principles. In my broader research in biology, I address real-world problems of practical relevance by using computer science methods along with those from applied mathematics, statistics and machine learning. I strive for considerations that cleanly connect neighbouring fields. In some cases, the problem in hand serves as a testbed for the methods I develop. In others, I use standard modelling and simulation techniques to provide answers to questions with an impact on society.

I extensively use off-the-shelf computational methods for investigations in biology. In some cases, where standard optimized methods are not applicable, I design and implement the tools that I need. Due to my formal training, I am equally at ease with theoretical concepts as well as practical aspects of software design and implementation. I routinely implement scripts and tools, for a variety of tasks, including data extraction and analysis, automated model construction, deterministic and stochastic simulation, and search.

I use simulation models to provide answers to quantitative questions in biology with implications on society. Examples to the questions that I have addressed in my published research include:

- “what are the conditions that provide efficacy to a cancer drug?”,
- “what are the biochemical mechanisms that result in insulin resistance?”,
- “what are the genetic interventions that increase the *E. coli* phosphate intake for recycling wastewater?”.

These investigations commonly use characterizations of the subject system’s dynamical properties in a formal language, for example, as differential equation systems or stochastic rule-based systems.

Computer science and representational A.I. My background in logic and computer science has been especially useful in my research: I use logic, in particular proof theory, as a formal tool to connect the representational aspects of practical problems with theoretical notions in computing. This use of logic is similar to its broader use in computing; logic is used to model computation, implicitly or explicitly, in type theory, operational semantics, denotational semantics, and axiomatic semantics as well as hardware and software verification. Logic plays a fundamental role in representational A.I. and in language design.

Computer science and biology. A recurring notion in my research is resource-sensitivity. Resource-sensitive interactions are studied in A.I. planning and concurrent information systems. Moreover, chemical reaction network representations in biological system models rely on resource-sensitivity. However, the concepts in these disciplines differ in their perspective and focus. In my work, by cleanly bridging these domains, I carry methods across disciplines as complementary instruments that highlight different properties of the subject system. My published research provides evidence for the efficacy of this approach in providing new perspectives: by bridging resource-sensitive A.I. planning and concurrency with a logic-based operational semantics, I could provide a concurrency theoretic interpretation for the former. In follow-up work, I used the observation that the state space of a chemical reaction network can be interpreted with a concurrency semantics by abstractions on the Markov chain representation. This way, I could implement an algorithm that displays the causal information flow in the stochastic models and apply it to real-world biological problems. To my surprise, I could also use the observations on biology models in my research on proof search to prune the search space. This way, I could couple heuristics with concurrency for efficiency.

The computational metaphor on biological systems expose other perspectives as well: I am currently exploring an application of the ideas above to analyse signal transduction in large biological networks from extracellular to genetic components in cells. Thanks to the availability of biological pathway data on many online databases, for example, KEGG and Reactome, large models can be automatically constructed. Moreover, by the integration of omics data, which is now broadly available, again from online databases, these models can be further parametrised. I am currently exploring the potential of such large models in identifying biomarkers by combining techniques from machine learning, graph theory, and representational A.I. My recent collaboration with a start-up in the U.S.A. is based on similar considerations.

Computer-aided design of synthetic biology applications. The immediate and ideal testbed for the ideas above is in synthetic biology, central to my research interests. This exciting field, at the crossroad of various

fields, is receiving increasing attention around the world, also at the industrial level. The collective effort in this field aims at bringing biology from a qualitative to a quantitative setting that uses systematic principles as in mature areas of engineering to design and develop living technologies. For the coming years, I aim at further developing a methodology for computer-aided design of new synthetic biology-applications. I have applied computerized design principles to successfully predict adequate genetic interventions performed by my collaborators at the Spanish National Research Council. I believe that bringing these considerations to a broader computer-aided design setting can accelerate the technological developments in domains varying from medicine to energy. It is thus one of the topics that I will pursue within the next years.

I am interested in the complementarity of numerical machine learning methods and representational A.I.. Life sciences will most-likely benefit from integration and processing of information from various sources by hybrid systems. These will accommodate an increasing amount of data coming from wearable and integrated sensors, as in IoT technologies, as well as online sources and exploit the complementarity of different techniques to process them. Clean integration of data to models poses challenges, which can, however, drastically impact life sciences. The related research questions, with an impact on society in scientific and technological terms, in particular, in the emerging field of personalised medicine, are central to my interests. I am currently collaborating with a start-up in the U.S.A. with this vision in an ecosystem of similar others.

Synthetic biology and machine learning. My research heavily relies on data. I use established methods from machine learning and statistics to fit the models to experimental data, and also to interpret the simulations with the models. Model optimization, clustering, principal component analysis, and regression are examples of the methods that I commonly use and, in certain cases, implement. My recent work in synthetic biology, part of the EU Horizon 2020 project Living Architecture mentioned above, is a prime example for this. In ongoing research, I aim at developing a systematic methodology to generalize our results for computer-aided design of synthetic biology applications in a broader context. A related question that I am exploring in my ongoing research is based on applying machine learning methods to predict nucleotide sequences that would optimize synthetic DNA promoters and mRNA sequences for certain tasks. Currently, I am exploring the industrial spin-off potential of this vision; in the U. S. and Japan industrial applications of synthetic biology are picking up rapidly and Europe is now following suit with accommodating legislations.

A.I with impact on society. My research explores connections between neighbouring fields to address real-world scientific questions. Much research in systems and computational biology is based on using established methods from applied mathematics and statistics. However, the recent developments in A.I. should result in new avenues for exploration with great potential for impact to accelerate the research in biology. My extensive hands-on experience in cross-disciplinary applications puts me in a unique position to lead and execute an integrative research agenda. I thus believe that my background and experience qualify me to explore this potential by bridging the expertise readily available at the Department of Computer Science at various research groups.

Outlook. Over the next years, I plan to develop my research to accommodate the vision above. At one end of the spectrum, this line of research will target applications as in my past research. At the other, I aim at developing technologies and computational tools for a broader audience. Obtaining external funding by grants is of great importance for this. As detailed in my CV, in the past, my research has benefitted from grants from various external funding agencies; I prioritize this highly also for the near future. On this note, my more recent proposal “Understanding Coral Colony Morphology via Stochastic Modelling”, was granted for the 7th call of the EU ASSEMBLE Plus program. This proposal is a part of a collaboration with researchers in France, whereby we study three coral species morphology via stochastic models and machine learning.

My track record demonstrates my scientific potential through international collaborations across disciplines. Throughout my career, I have supervised numerous projects and participated in larger teams. I believe that my scientific experience and my international profile make me a strong candidate for this position, an opportunity that will allow me to expand my scientific horizon. By doing so, I believe that I can contribute to the scientific and financial growth of the department and further my knowledge and experience to advance in my career. I am thus looking forward to having an opportunity to introduce myself in person.

Teaching Statement of Ozan Kahramanoğulları

Throughout my career, I have taught and tutored courses on various topics in computer science, theoretical and applied, as well as in applied mathematics, statistics and systems biology. I have collected broad international experience, first as a student at international courses, including my MSc and PhD, and then as a researcher. Besides English, which is the standard language at the graduate level, I have taught in German and Italian to students who are native speakers. I have supervised PhD, MSc, BSc theses, and numerous other projects to students from various backgrounds and walks of life.

Like my research, my teaching activities are based on interdisciplinary considerations. I try to encourage my students possibly to think out of the box, also by carrying over points of views and ideas across disciplines instead of attacking a problem in the "standard way". I put an effort in contextualising the methods and techniques that I teach as inspiring stories. At my courses and the projects that I supervise, I prioritize maintaining a friendly atmosphere, whereby students feel encouraged to freely express their thoughts. I believe that the role of the instructor should be guidance rather than delivering the facts and the rules to the students. I thus encourage my students to proactively apply the methods they have learned to real-world problems to develop original thinking. I aim at providing the means for this at my courses so that they can consolidate their knowledge by practice.

Within the last years, I have contributed to the joint Master's Programme in Quantitative and Computational Biology at the University of Trento. For this, I have taught a course per semester, twice my contractual duties, which involved the preparation and evaluation of these courses. The students have been from a variety of backgrounds, including biology, mathematics, computer science, and physics. The courses were also offered to the students at the computer science and mathematics departments besides the students of the master's program. I aimed at exploiting this diverse landscape to benefit the students by enhancing their interactions.

For this program, in the fall semester, I have taught a course on statistics that is based on applying state of the art methods in data science to addressing biological problems. I have designed this course in a hands-on manner, whereby students are required to prepare a small research project, where they independently apply the methods that they have learned. In the spring semester, I have given a course on modelling of biological systems based on similar considerations. This course uses methods from computer science, physics, and applied mathematics to address biological problems. Before my faculty appointment at the University of Trento, I have assisted numerous courses during my postdoc at Imperial College as well as my MSc and PhD studies. During my employment at Imperial College as a Research Associate, I have tutored a course per semester, which include topics such as Formal Software Verification, Robotics, Introduction to Object Oriented Programming, and Bioinformatics. During my studies in Germany, I have given tutorials twice a week on logic in German language in classes with as many as forty students. I have gained hands-on experience in the supervision of PhD and MSc projects as detailed in my CV. All my graduate students are now researchers at various research institutes, in Italy and abroad.

Due to my formal training, I am equally at ease with theoretical concepts as well as practical aspects of computer science. In my research and teaching, I routinely use digital platforms for research dissemination and outreach. I thus believe that, besides my scientific track record, my teaching experience makes me a strong candidate for the position. As my track record demonstrates, I can accommodate the teaching responsibilities of this position in accordance with the needs of the Department of Computer Science, also in the context of the social changes as in the case of Covid-19 pandemic that has moved academic activities to the digital platforms. As detailed in my research statement, my research aims at responding to real-world scientific problems that have an impact on the society. This aspect together with the diverse expertise readily available at the Department of Computer Science presents far reaching opportunities. I believe that as a member of this department, I can contribute to its scientific and financial growth and further my knowledge and experience to advance in my career. I am thus looking forward to having an opportunity to introduce myself in person.

The three most significant papers are (i.), (ii.), and (iii.) below. I am the P.I. of (i.), which introduces new directions for computational design of synthetic biology technologies. The results of this recent paper have already been used by two IGEN teams for designing applications. (ii.) reports on my first project on applying computer science methods to biological problems. It has raised interest in both computer science and biology communities. (iii.) constitutes a bridge that connects my earlier theoretical work with my more recent research in biology and provides a foundation for applications. It has received attention also from a theoretical point of view.

Journal Papers. *: corresponding author, †: alphabetical order

Righetti, E; Uluseker, C.; Kahramanoğulları, O.*

Stochastic Simulations as a Tool for Assessing Signal Fidelity in Gene Expression in Synthetic Promoter Design. **submitted**, 2021.

Righetti, E; Kahramanoğulları, O.*

The inverse correlation between robustness and sensitivity to autoregulation in two-component systems. **submitted**, 2021.

Sottile, S; Kahramanoğulları, O.*, Sensi, M

Epidemic outbreak probability and size in scale free networks depend on the starting node. arXiv preprint arXiv:2011.10595, **submitted**, 2021.

(i.) Uluseker, C.; Torres-Bacete, J; García, J.; Hanczyc, M.; Nogales, J.; Kahramanoğulları, O.*, Quantifying dynamic mechanisms of auto-regulation in *Escherichia coli* with synthetic promoter in response to varying external phosphate levels, **Scientific Reports**, 9, 2019.

Reali, F., Morine, M., Kahramanoğulları, O., Raichur, S, Schneider, H; Crowther, D.; Priami, C. Mechanistic interplay between ceramide and insulin resistance, **Scientific Reports**, 7, 2017.

Kahramanoğulları, O.*, Cardelli L.

Gener: A minimal programming module for chemical controllers based on DNA strand displacement, **Bioinformatics**, 31(17), 2015.

Kahramanoğulları, O.,

Interaction and Depth against Nondeterminism in Proof Search,

Logical Methods in Computer Science, 10 (2:5), 2014.

Kahramanoğulları, O.*, Lynch J.,

Stochastic Flux Analysis of Chemical Reaction Networks,

BMC Systems Biology, 7:133, 2013.

Kahramanoğulları, O.*, Fantaccini G., Lecca P., Morpurgo D., Priami C.,

Algorithmic modeling quantifies the complementary contribution of metabolic inhibitions to gemcitabine efficacy, **PLoS ONE**, 7(12), 2012.

Kahramanoğulları, O.*, Cardelli L.,

An Intuitive Modelling Interface for Systems Biology,

International Journal of Software and Informatics, 7:4, 2012.

Kahramanoğulları, O., Lynch J., Jordan F.,

CoSbiLab LIME: a language interface for stochastic dynamical modelling in ecology,

Environmental Modelling and Software, 26:685-687, 2011.

(ii.) Cardelli, L., Caron, E., Gardner, P., Kahramanoğulları, O.*†, Phillips A.,

A Process Model of Rho GTP-binding Proteins, **Theoretical Computer Science**, 410, 2009.

Gurry T. and Kahramanoğulları, O., Endres R.,

Biophysical Mechanism for Ras-Nanocluster Formation and Signaling in Plasma Membrane,

PLoS ONE, 4, 2009.

(iii.) Kahramanoğulları, O.,

On Linear Logic Planning and Concurrency, **Information and Computation**, 207 (11), 2009.

Kahramanoğulları, O.,

System BV is NP-complete, **Annals of Pure and Applied Logic**, 152 (1-3), 2008.

Books and Chapters

Kahramanoğulları, O., Vaggi F., Phillips A., 2012,
Process Modeling and Rendering of Biochemical Structures: Actin,
Biomechanics of cells and tissues: experiments, models and simulations,
Lecture Notes in Computational Vision and Biomechanics, Springer.

Kahramanoğulları, O., 2012,
Nondeterminism and Language Design in Deep Inference,
A Proof Theoretic Approach to Logic Programming,
Lambert Academic Publishing, ISBN 978-3-659-13475-3.

Kahramanoğulları, O., 2012,
Process algebra models in biology: the case of phagocytosis,
Bioinformatics & Computational Systems Biology:
Recent Advances and Applications, IGI Global.

Published Conference and Workshop Papers

Kahramanoğulları, O., Lorenzo Bramanti, Maria Carla Benedetti, 2019,
Stochastic Mechanisms of Growth and Branching in Mediterranean Coral Colonies.
Proc. of 8th International Conference on the Theory and Practice of Natural Computing,
TPNC 2019, Kingston, Canada, December 9-11, 2019, LNCS, Springer.

Kahramanoğulları, O., Cansu Uluşeker, Martin M. Hanczyc, 2019,
Stochastic Mechanisms of Information Flow in Phosphate Economy of *Escherichia Coli*.
Proc. of the 3rd International Conference on Numerical Computation: Theory and Applications,
NUMTA 2019, Le Castella, Italy, June 15-21, 2019, LNCS, Springer.

Kahramanoğulları, O., 2019,
On Quantitative Comparison of Chemical Reaction Network Models.
Proceedings of 3rd Workshop on Program Equivalence and Relational Reasoning.
PERR 2019, Prague, April 6, EPTCS.

Kahramanoğulları, O., 2019,
Enumerating Dominant Pathways in Biological Networks by Information Flow Analysis.
Proceedings of 4th International Conference on Algorithms for Computational Biology
AlCoB 2019, Berkley, USA, June 28-30, LNCS, Springer.

Cansu Uluşeker, Martin M. Hanczyc, Kahramanoğulları, O., 2018,
Mechanisms of Switching Response to External Phosphate Levels in *Escherichia coli*.
Artificial Life Conference Proceedings, 23-27 July, 2018, Tokyo.

Cansu Uluşeker, Jesús Torres-Bacete, José L. García, Martin M. Hanczyc,
Juan Nogales, Kahramanoğulları, O., 2017,
A Dynamic Model of the Phosphate Response System with Synthetic Promoters in *E. coli*.
Proc. of the International Conference on Artificial Life, 4-8 September, 2017, Lyon.

Kahramanoğulları, O., 2017,
Quantifying Information Flow in Chemical Reaction Networks.
Proceedings of 4th International Conference on Algorithms for Computational Biology
AlCoB 2017, Aveiro, Portugal, June 5-6, LNCS, Springer.

Kahramanoğulları, O., 2017,
Deep Proof Search in MELL.
Proceedings of Logic for Programming, Artificial Intelligence, and Reasoning,
21st International Conference, Proc. of LPAR'17, Maun Botswana, May 7-12.

Kahramanoğlu, O., 2016,
 Simulating Stochastic Dynamic Interactions with Spatial Information and Flux.
 Proc. of 5th International Conference on the Theory and Practice of Natural Computing,
 TPNC 2016, Sendai, Japan December 12-13, 2016, LNCS, Springer.

Kahramanoğlu, O., 2016,
 True Concurrency of Deep Inference Proofs.
 Proceedings of 23rd Workshop on Logic, Language, Information and Computation,
 WoLLIC 2016, August 16-19, 2016, Puebla, Mexico, LNCS 9803, Springer.

Zunino R., Nikolic D., Priami C., Kahramanoğlu, O., Priami C., Schiavinotto T., 2015,
 ℓ : An Imperative DSL to Stochastically Simulate Biological Systems.
 Proceedings of Programming Languages with Applications to Biology and Security 2015,
 LNCS 9465, Springer.

Kahramanoğlu, O., Lynch J., Priami C., 2014,
 Algorithmic Systems Ecology: Experiments on Multiple Interaction Types and Patches.
 Proceedings of InSuEdu 2012, LNCS 7991, Springer.

Kahramanoğlu, O., Jordan F., Priami C., 2011,
 Composability: Perspectives in Ecological Modeling.
 Proceedings of ANB 2011, LNCS 6479, Springer.

Lecca P. and Kahramanoğlu, O., Morpurgo D., Priami C., Soo R. A., 2011,
 Modelling and estimating dynamics of tumor shrinkage with BlenX and KInfer.
 13th International Conference on Modelling and Simulation,
 March 30 - April 1, Cambridge, UKSim 2011, IEEE.

Kahramanoğlu, O., 2010,
 Flux Analysis in Process Models via Causality.
 3rd Workshop "From Biology To Concurrency and back".
 Proceedings of FBTC'10, March 27, 2010, Paphos, Cyprus, EPTCS 19.

Kahramanoğlu, O., Cardelli L., Caron E., 2009,
 An Intuitive Automated Modelling Interface for Systems Biology.
 Fifth Workshop on Developments in Computational Models
 Computational Models From Nature., Rhodes, Greece, Proceedings of DCM'09, EPTCS 9.

Cardelli, L., Caron, E., Gardner, P., Kahramanoğlu, O., Phillips A., 2009,
 A Process Model of Actin Polymerisation,
 Proceedings of the workshop From Biology To Concurrency and back, FBTC'08,
 Reykjavik, Volume 229 of ENTCS, Elsevier.

Kahramanoğlu, O., 2008,
 On Linear Logic Planning and Concurrency,
 Proceedings of the 2nd International Conference on Language and Automata Theory
 and Applications, LATA'08, Tarragona, Spain, Volume 5196 of LNCS, Springer.

Kahramanoğlu, O., Cardelli, L., Gardner, P., 2008,
 A Process Model of Rho GTP-binding Proteins in the Context of Phagocytosis,
 Proceedings of the workshop From Biology To Concurrency and back, FBTC'07,
 Lisbon, Portugal, Volume 194 of ENTCS, Elsevier.

- Kahramanoğlu, O., 2008,
Maude as a Platform for Designing and Implementing Deep Inference Systems,
Proceedings of the Eighth International Workshop on Rule-Based Programming,
RULE'07, Paris, France, Volume 219 of ENTCS, Elsevier.
- Kahramanoğlu, O., 2006,
Reducing Nondeterminism in the Calculus of Structures,
Proceedings of the 13th International Conference on Logic for
Programming Artificial Intelligence and Reasoning, LPAR'06,
Phnom Penh, Cambodia, Volume 4246 of LNCS, Springer.
- Kahramanoğlu, O., 2006,
System BV is NP-complete,
Proceedings of the 12th Workshop on Logic, Language, Information and Computation,
WoLLIC'05, Florianapolis, Brazil, Volume 143 of ENTCS, Elsevier.
- Kahramanoğlu, O., Moreau P-E., Reilles A., 2005,
Implementing Deep Inference in TOM,
Proceedings of the Workshop on Structures and Deduction 2005, SD'05,
satellite workshop of ICALP 2005, July 11 - 15, Lisbon, Portugal.
- Kahramanoğlu, O., 2005,
Towards Planning as Concurrency,
Proceedings of the IASTED International Conference on
Artificial Intelligence and Applications, AIA'05, Innsbruck, Austria, Acta Press.
- Kahramanoğlu, O., 2004,
System BV without the Equalities for Unit,
Proceedings of the 19th Int. Symposium on Computer and Information Sciences,
Kemer, Turkey, Volume 3280 of LNCS, Springer.
- Kahramanoğlu, O., 2004,
Implementing system BV of the calculus of structures in Maude,
Proceedings of the ESSLLI-2004 Student Session, 117-127, Nancy, France.
Short-listed for best paper.
- Kahramanoğlu, O., Thielscher, M., 2003,
A Formal Assessment Result for Fluent Calculus Using the Action Description Language \mathcal{A}_k ,
Proceedings of the 26th Annual German Conference on Artificial Intelligence,
KI'03, Hamburg, Volume 2821 of LNAI, Springer.

Invited Talks

- Sep. 2020 *Modelling Life: from biomolecular signalling to coral morphology*
The Oceanological Observatory, National Scientific Research Center (CNRS)
Banyuls-sur-mer, France
- June 2019 *Stochastic Mechanisms of Information Flow in Phosphate Economy of E. Coli*
Numerical Computations: Theory and Algorithms. The 3rd International
Conference and Summer School, Crotone, Italy, June 15 – 21, 2014.
Special Session on Computational Methods for data analysis
- June 2014 *A theory of model equivalence based on stochastic simulation fluxes*
5th Workshop on Logic and Systems Biology, associated with CSL/LICS 2014,
Vienna, Austria, July 13, 2014,
- June 2011 *An algorithmic model of gemcitabine mechanisms of action*
PharmSciFair, Pharmaceutical Sciences for the Future of Medicines,
Prague, Czech Republic, June 13-17, 2011.
- Dec. 2009 *Processes of Biology*
University of Turin, Department of Computer Science, Turin, Italy.
- Nov. 2007 *A Deductive Language for Everything*
University of Bath, Department of Computer Science.
- Nov. 2007 *A Process Model of Rho GTP-binding Proteins*
Joint CISB Meeting, Newcastle, UK.
- May 2007 *Deep Inference in Theorem Proving*
University of Cambridge, Computer Laboratory.
- Dec. 2006 *Interaction and Depth against Nondeterminism in Proofs*
University of Birmingham, School of Computer Science.
- Nov. 2005 *Deep Inference and Nondeterminism*
Programming Systems Lab, Saarland University, Saarbrücken.
- Nov. 2004 *Implementing Deep Inference*
Protheo Group at LORIA, Nancy.

Other Papers and Talks at Conferences and Workshops

Kahramanoğulları, O., Maria Carla Benedetti, Lorenzo Bramanti
Stochastic mechanisms of growth and branching in mediterranean coral colonies
11th Conference on Dynamical Systems Applied to Biology and Natural Sciences DSABNS 2020
Trento, Italy, February 4-7, 2020.

Kahramanoğulları, O., Cansu Uluşeker, Martin M. Hanczyc.
Stochastic mechanisms of auto-regulation in *Escherichia coli* with synthetic promoter
in response to varying external phosphate levels.
Italian Regional Conference on Complex Systems CCS/Italy,
FBK, Trento, July 1-3, 2019.

Kahramanoğulları, O.
Deep inference for proof search.
5th International Workshop on Structures and Deduction. Affiliated with FSCD '19.
Dortmund, Germany, June 29-30, 2019.

Kahramanoğulları, O., Martin M. Hanczyc.
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