The Microsoft Research - University of Trento
Centre for Computational and Systems Biology

# CoSBi 2007 Annual Scientific Report

**We opened CoSBi in December 2005 with both a goal and an ideal organisational structure in mind.**

The goal is twofold. First, we want to enhance our understanding of fundamental biological processes at system level by using programming language theory to design new conceptual tools. We create computational abstractions that can be executed to visualise the time-course dynamics of biological systems. We re-design many verification and analysis computer science techniques and adapt them to the life science applicative domain in order to answer new kinds of questions.

Secondly, computer science is looking more and more to parallelism even in PC processors. Biological systems are the most parallel systems ever studied and we hope to use our better understanding of how living systems handle information to design new computational paradigms, programming languages and software development environments. The net result would be the design and implementation of better applications firmly grounded on new computational, massively parallel paradigms in many different areas.

The ideal CoSBi organisational structure is a research centre in which many different disciplines cohabit on a peer-to-peer basis to have a major impact on computer science and biology. Researchers contribute with their different backgrounds to accomplish our hope of working as a single team. This is a first step in creating a common language between our researchers that is necessary in order to become the new kind of scientists of tomorrow. We have the ambitious goal of making CoSBi a place where research activities are carried out differently from any other place in the world.

Two years from the opening, I'm proud of the results we have obtained thanks to the marvelous CoSBi team that makes realising our goal closer and closer each day. I'm proud that our ideal organisational structure is now concrete. It is a pleasure to see scientists from different backgrounds, cultures and personal histories share the same views, exchange ideas and cooperate through understanding each other. Our researchers understand that CoSBi's goal can be attained only by playing at system level, as a team, and they are doing a great job. Finally, I'm even prouder that we invest and focus on ideas, our main asset along with our human capital, because as long as people continue to look first at applications rather than at their enabling ideas, we can only say that we live in the technology society, a step behind the knowledge society we all are aiming for.

President and CEO of CoSBi

## Our motto

"Quegli che pigliavano per altore altro che la natura maestra de' maestri s'affaticavano invano".

*Those who took other inspiration than from nature, master of masters, were labouring in vain.*

## CoSBi at a glance

Inaugurated on 7 December 2005, the CoSBi Centre is a multidisciplinary joint venture between Microsoft Research and the University of Trento. The Centre is located in Povo, a suburb of Trento, Italy. Here at CoSBi (acronym of Computational and Systems Biology), we hope to bridge the gap between computer science and biology with the goal of developing new conceptual and software tools to help unravel the logic of life.

### WHERE TO FIND US

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38100 Povo (Trento) - Italy
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# Our team

**CORRADO PRIAMI (I)**

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CoSBi President and CEO

Education and positions: Master's degree and PhD in Computer Science from the University of Pisa, Italy. Postdoctoral researcher at École Normale Supérieure Paris, France. Assistant and Associate Professor of Computer Science at the University of Verona, Italy. Current Professor of Computer Science at the University of Trento, Italy.

Research interests: computational methods for systems biology, semantics and design of programming languages, quantitative analysis of complex (biological) systems, multi-level, multi-scale biological interactions, Horizontal Gene Transfer.

"Research is a splendid game of curiosity, optimism and persistence" (Corrado)

**IVAN MURA (I)**

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senior researcher

Education and positions: Master's degree in Computer Science and PhD in Computer Science Engineering from the University of Pisa, Italy. Junior researcher at the Italian National Research Council in Pisa, Italy. Project Manager at Motorola, Torino, Italy.

Research interests: Markov chains based modeling techniques, operations research, theoretical biology, statistical analysis of simulation results, pathways modeling, bio-inspired computational formalisms, modeling frameworks for systems biology.

"No, no, you're not thinking, you're just being logical" (Niels Bohr)

**ATTILA CSIKASZ-NAGY (H)**

csikasz@cosbi.eu

researcher

Education and positions: Master's degree in Bioengineering and PhD in Chemistry from the Budapest University of Technology and Economics, Hungary. Postdoctoral researcher at Virginia Tech, Usa.

Research interests: cell cycle regulation: DNA replication and mitosis in space and time, spatial and temporal pattern of cell growth and morphology, molecular network dynamics, coupled ODE systems, reaction-diffusion equations.

"I think it was this curiosity about the natural world which awoke my early interest in science" (Paul Nurse)

**ORKUN SOYER (TR)**

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researcher

Education and positions: Master's degree in Chemistry from the Bogazici University, Turkey. PhD in Chemistry from the University of Michigan, USA. Postdoctoral researcher at the Swiss Federal Institute of Technology (ETH) in Zürich, Switzerland.

Research interests: evolution of biological systems such as signaling pathways, topology-dynamics relation, bacterial chemotaxis, host-parasite interactions, robustness and modularity.

"My research recipe is: a touch of can-do attitude, chunk of smartness, just enough of simplicity, and a full spoon of novelty. Stir well and present furiously" (Orkun)

**PAOLO BALLARINI (I)**

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junior researcher

Education and positions: Master's degree and PhD in Computer Science from the University of Torino, Italy. Postdoctoral researcher at the University of Liverpool, UK, and at the University of Glasgow, UK.

Research interests: formal methods for systems biology, qualitative and quantitative analysis, application of model-checking techniques, temporal logic reasoning, formal modeling to the verification of large biological systems.

"The advantage of the emotions is that they lead us astray, and the advantage of science is that it is not emotional" (Oscar Wilde)

**MATTEO CAVALIERE (I)**

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junior researcher

Education and positions: Master's degree in Computer Science from the University of Salerno, Italy. PhD in Computer Science, Logic and Artificial Intelligence from the University of Seville, Spain.

Research interests: bio-inspired computing (DNA computing, membrane computing), theoretical biology, theory of computation, automata and formal languages, Horizontal Gene Transfer, cancer development.

"The real voyage of discovery consists not in seeking new landscapes but in having new eyes" (Marcel Proust)

**ADAOHA IHEKWABA (UK)**

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junior researcher

Education and positions: Bachelor's degree in Pharmaceutical Sciences from the University of Greenwich, London, UK. PhD in Computational Biology from the University of Manchester, UK. Postdoctoral researcher at the University of Manchester, UK. Visiting scholar at the Virginia Bioinformatics Institute, Virginia Tech, USA.

Research interests: oscillatory systems, biochemistry of living cells, fluorescent imaging, computer based mathematical modeling, reverse engineering modeling.

"The heart has its reasons of which reason knows nothing" (Blaise Pascal)

**CELINE KUTTLER (D)**

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junior researcher

Education and positions: Master's degree in Computer Science from Saarland University in Saarbruecken, Germany. PhD in Computer Science from the University of Lille I, France.

Research interests: computational modeling of genetic regulatory networks, languages for systems biology.

"Science does not progress from hypothesis via experiment to conclusion; instead, the progress of science is tremendously disorderly" (Max Delbruck)

**HIROYUKI KUWAHARA (J)**

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junior researcher

Education and positions: Master's degree and PhD in Computer Science from the University of Utah, USA.

Research interests: efficient computational quantitative analysis of biological systems, computational analysis of systems-level biological properties, computational analysis to control and design biological systems.

"I am still learning" (Michelangelo Buonarroti)

### PAOLA LECCA (I)

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junior researcher

Education and positions: Master's degree in Theoretical Physics and PhD in Computer Science from the University of Trento, Italy.

Research interests: stochastic chemical reaction kinetics, biological networks predictive modeling and simulation, experimental techniques to monitor the quantitative aspects of chemical kinetics.

"Measure what is measurable, and make measurable what is not so" (Galileo Galilei)

### RADU MARDARE (RO)

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junior researcher

Education and positions: Master's degree of Science in Logic from Bucharest University, Romania. PhD in Computer Science from the University of Trento, Italy. Post-doctoral researcher at the University of Trento, Italy.

Research interests: computational models and model verification techniques for systems biology, logics for transition systems, logics for process-algebraical semantics, dynamic-epistemic logics, model checking, probabilistic model checking.

"If logic is a mirror-image of the world, as Wittgenstein believed, then the image of a mirror into a mirror is logically consistent" (Radu)

### TOMMASO MAZZA (I)

mazza@cosbi.eu

junior researcher

Education and positions: Master's degree in Computer Science Engineering from the University of Calabria, Italy. PhD in Computer Science and Biomedical Engineering from the 'Magna Graecia' University of Catanzaro, Italy.

Research interests: topological characterisation and analysis of Bio-networks, parallel and distributed computing and simulation of bio-networks, bio-data handling, storing and compression, standard languages for biology.

"Each of us is in truth an idea of the Great Gull, an unlimited idea of freedom" (Richard Bach, in *Jonathan Livingston Seagull*)

### LORENZO DEMATTÉ (I)

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PhD student

Education and positions: Master's degree in Computer Science from the University of Trento, Italy. Post-graduate researcher at IASMA, San Michele all'Adige, Italy.

Research interests: languages for concurrent and distributed systems, concurrency theory, security, process algebras, computational models for systems biology, prediction of protein functions, evolutionary biology.

"What I cannot create, I do not understand" (Richard Feynman)

### MICHELE FORLIN (I)

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PhD student

Education and positions: Master's degree in Statistics from the University Ca' Foscari of Venice, Italy. Second level International Master's in Computational and Systems Biology at CoSBi. Research collaboration with the University of Venice, Italy.

Research interests: data mining for biological systems, evolutionary computation, computational intelligence, high dimensional design of experiments, computational models for systems biology.

"After climbing a great hill, one only finds that there are many more hills to climb" (Nelson Mandela)

### ROBERTO LARCHER (I)

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PhD student

Education and positions: Master's degree in Computer Science from the University of Trento, Italy. Second level International Master's in Computational and Systems Biology at CoSBi.

Research interests: computational models for systems biology, process algebras, semantics, dynamics of biological networks.

"Everything should be made as simple as possible, but not simpler" (Albert Einstein)

### ALIDA PALMISANO (I)

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PhD student

Education and positions: Master's degree in Computer Science from the University of Trento, Italy.

Research interests: computational models for systems biology, process algebras, semantics, inference of rate parameters and biological networks, cell cycle.

"There are 10 kinds of people in the world: those who understand binary and those who don't" (Anonymous)

### ALESSANDRO ROMANEL (I)

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PhD student

Education and positions: Master's degree in Computer Science from the University of Trento, Italy. Post-graduate researcher at CREATE-NET, Trento, Italy.

Research interests: semantics of programming languages, concurrency theory, process algebras, computational models for systems biology, immune system modeling.

"An answer is always the stretch of road that's behind you. Only a question can point the way forward" (Jostein Gaarder)

### SEAN SEDWARDS (UK)

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PhD student

Education and positions: B. Eng. in Electronic Engineering from the University College London, UK. B.Sc. Computing Science from Oxford Brookes University, UK. Freelance software engineer. Owner and designer of an audio amplifier company.

Research interests: dissipative structures and robust behaviour in stochastic dynamical systems, immune systems, coupled non-linear oscillators, amorphous and quantum computing.

"What you need is that your brain is open" (Paul Erdős)

### JUDIT ZÁMBORSZKY (H)

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PhD student

Education and positions: Master's degree in Bioengineering from the Budapest University of Technology and Economics, Hungary.

Research interests: computational models for systems biology, cell cycle regulation in mammals and yeasts, circadian rhythm, molecular network dynamics, studying and analysing biological systems.

"Motivation is what gets you started. Habit is what keeps you going" (Jim Ryun)

## Our scientific advisory board

JUDY ARMITAGE - University of Oxford, UK
GIANFRANCO BALBO - University of Torino, Italy
MARVIN CASSMAN - Former Director, National Institute of General Medical Sciences, NIH, USA

DAVID HAREL - Weizmann Institute of Science, Israel
LEROY HOOD - Institute for Systems Biology, USA
MANUEL PEITSCH - Novartis, Switzerland

# Shaping the future

Systems biology aims at understanding the organising principles and emergent properties of a system arising from the interaction of biological entities that coordinates multi-level behaviour. The success of the discipline can only be achieved through the integration of many different disciplines glued together by computational approaches.

Computer science is becoming a recognised driver, underpinning the progress of science and hence also of systems biology. The scientific challenge that drives our activities is:

*complete understanding of biological systems that are multi-components interacting at multiple levels internally with each other and externally with the environment at population level.*

Since our research of fundamental understanding is inspired by the need of putting it into practice, we also tackle technological challenges in order to build the needed machinery to address our scientific challenge. We want to provide the scientific community with the following tools freely available for non-commercial purposes:

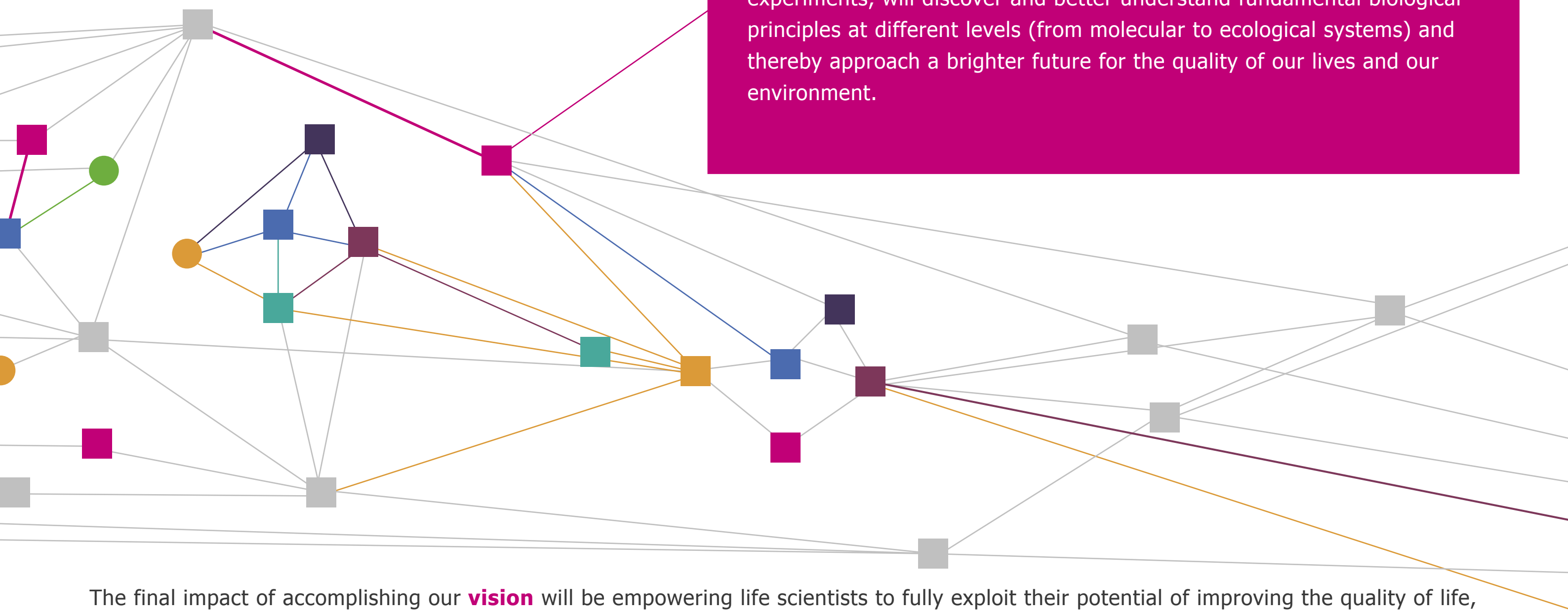
*new predictive conceptual and computational frameworks that are plug-in based for abstraction, perturbation, verification and artificial design of biological systems that are equipped with a full set of new analysis techniques to address problems which cannot be solved with today's technology.*

At the present, there is a lack of multidisciplinary scientists that are able to manage different domains, and this limits the possibility of accomplishing the above. Therefore, we need a:

*new generation of highly computationally literate scientists that bridge the gap between life sciences and artificial systems sciences by sharing concepts, ideas, tools and knowledge expressed in a common scientific language.*

## OUR VISION

We help grow a new kind of scientist that, empowered with novel conceptual and computational tools smoothly connecting models and experiments, will discover and better understand fundamental biological principles at different levels (from molecular to ecological systems) and thereby approach a brighter future for the quality of our lives and our environment.



The final impact of accomplishing our **vision** will be empowering life scientists to fully exploit their potential of improving the quality of life, health care and environmental protection. We will also have the additional benefit of providing computer scientists with a new generation of computational abstractions and languages to address complexity, interaction and emergent behaviour in many different applicative domains.

In order to enable our **vision**, we define our strategic objectives as follows:

**1** The design and development of an integrated artificial plug-in based biological laboratory connecting computational modeling with experiments and built on top of a biology programming language to experiment on the spatial and temporal dynamics of biological systems as well as on their evolution with new conceptual and computational tools that can answer new relevant questions.

**2** Predictive models of multi-level, multi-component biological systems at population level interacting internally and externally with the environment and other systems.

**3** Large dissemination of our new conceptual/computational tools in the life sciences community.

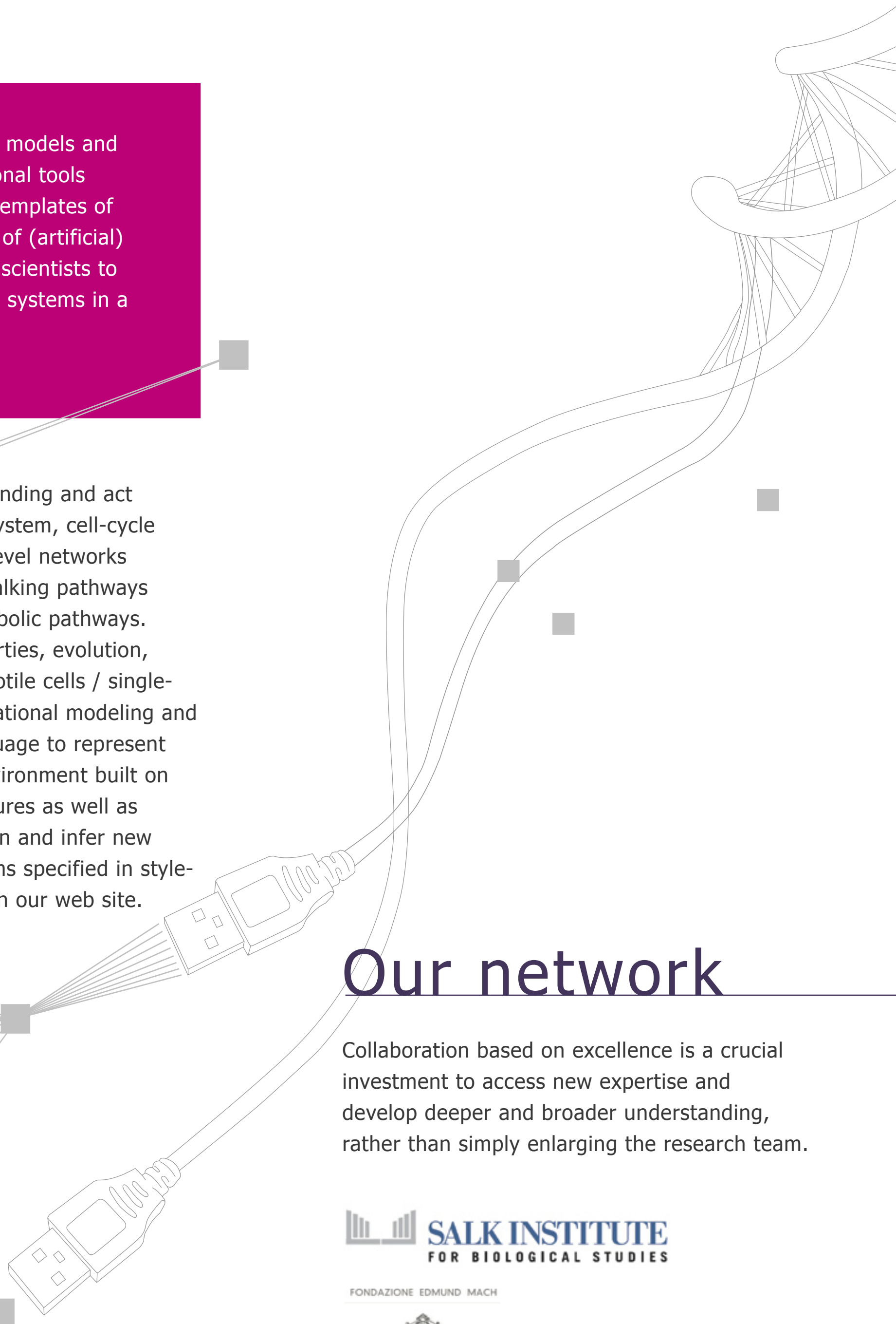
**4** Definition and implementation of new languages and bio-inspired paradigms that enhance programming and software development techniques in computer science applications characterised by complexity and interactions between components.

The steps we consider necessary to achieve our strategic objectives constitute our **mission**. Our winning idea is creating a modeling and analysis framework based on programming language theory rather than on classic mathematical approaches. Our models are different in that they are executable rather than simply solvable. Executable means that we can predict/describe the flow of control between species and reactions (e.g. not only the time, but also the causality relation among the events that constitute the history of the dynamics of the model). In other words, computational modelling is similar to programming a system rather than only describing the outcome of the system. Our conceptual framework is built to satisfy properties of modularity, compositionality and scalability that allow the user, along with the knowledge acquired, to build models incrementally. Our criteria for success are the realisation of computational tools based on the conceptual framework mentioned above to obtain predictive, integrated and user-friendly environments largely utilized by life scientists all over the world.

## OUR MISSION

To contribute to the future of science through connecting models and experiments by means of new conceptual and computational tools integrated in a user-friendly environment equipped with templates of major biological components for drag-and-drop modeling of (artificial) organisms or populations and used by a large part of life scientists to predict the behaviour of multi-level, multi-scale biological systems in a modular, compositional, scalable and executable manner.

The three main areas of biology that inspire our understanding and act as drivers for our scientific challenges are: the immune system, cell-cycle regulation at different levels of abstraction, and system level networks that sense their environment and are made up of cross-talking pathways interacting both with gene regulatory networks and metabolic pathways. For instance, we address the analysis of the global properties, evolution, and dynamics of signaling pathways in a population of motile cells / single-celled organisms. Since we base our research on computational modeling and analysis, we have developed both a new executable language to represent multi-level biological systems and a hybrid simulation environment built on top of it equipped with graphical model visualisation features as well as analysis tools to investigate the results of model execution and infer new hypotheses. We also created an applet to simulate systems specified in style-based chemical reactions. Both tools are available through our web site.



## Our network

Collaboration based on excellence is a crucial investment to access new expertise and develop deeper and broader understanding, rather than simply enlarging the research team.

SALK INSTITUTE FOR BIOLOGICAL STUDIES

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UNIVERSITÀ DEGLI STUDI DI TRENTO
CENTRE FOR INTEGRATIVE BIOLOGY
CIBIO

# Our main publications

Robert Brijder, **Matteo Cavaliere**, Agustín Riscos Núñez, Grzegorz Rozenberg, Dragos Sburlan. Membrane systems with proteins embedded in membranes. Theoretical Computer Science. In press.

**Matteo Cavaliere**, Rudi Freund, Marion Oswald, Dragos Sburlan. Multiset random context grammars, checkers, and transducers. Theoretical Computer Science, issue 372, 136 – 151, 2007

**Matteo Cavaliere**, **Radu Mardare**, **Sean Sedwards**. A multiset-based model of synchronizing agents: computability and robustness. Theoretical Computer Science. In press.

Federica Ciocchetta, **Corrado Priami**, Paola Quaglia. An automatic translation of SBML into Beta-Binders. IEEE/ACM Transactions of Computational Biology and Bioinformatics. In press.

**Attila Csikasz-Nagy**, Bela Gyorffy, Alt Wolfgang, John J. Tyson, Bela Novák. Spatial controls for growth zone formation during the fission yeast cell cycle. Yeast, issue 25: 59-69, 2008.

**Attila Csikasz-Nagy**, O. Kapuy, Bela Gyorffy, Bela Novák, John J. Tyson. Modeling the Septation Initiation Network (SIN) in Fission Yeast Cells. Current Genetics, issue 51: 245 - 255, 2007

**Attila Csikasz-Nagy**, Bela Novák, John J. Tyson. Reverse engineering models of cell cycle regulation, in Cellular Oscillatory Mechanisms, eds. Maroto, M. & Monk, Landes Bioscience, 2008

**Lorenzo Dematté**, Davide Prandi, **Corrado Priami**, **Alessandro Romanel**. Effective index: a formal measure of drug effects. Proceedings of the second Conference Foundations of Systems Biology in Engineering, 485 - 490, 2007

**Lorenzo Dematté**, **Corrado Priami**, **Alessandro Romanel**, **Orkun Soyer**. A formal and integrated framework to simulate evolution of biological pathways. Proceedings of the fifth International Conference on Computational Methods in Systems Biology, LNBI 4695, Springer-Verlag, 106 - 120, 2007

Maria Luisa Guerriero, John Heath, **Corrado Priami**. An automated translation from a narrative language for biological modelling into process algebra. Proceedings of the fifth International Conference on Computational Methods in Systems Biology, LNBI 4695, Springer-Verlag, 136 – 151, 2007

Richard A. Goldstein, **Orkun Soyer**. Evolution of taxis responses in bacteria: non-adaptive dynamics, PLoS Computational Biology, 2008. In press.

**Adaoha Ihekwaba**, Stephen J. Wilkinson, Dominic S. Waithe, David S. Broomhead, Peter Li, Rachel Grimley, Neil Benson. Bridging the gap between in silico and cell based analysis of the NF-KB signaling pathway by in vitro studies of IKK2. FEBS Journal, issue 27: 1678 - 1690, 2007

**Hiroyuki Kuwahara**, Chris Myers. Production-passage-time approximation: a new approximation method to accelerate the simulation process of enzymatic reactions. Proceedings of the eleventh Annual International Conference Research in Computational Molecular Biology, 176 – 180, 2007

**Paola Lecca**, Simulating the cellular passive transport of glucose using a time-dependent extension of Gillespie algorithm for stochastic pi-calculus. Journal of Data Mining and Bioinformatics, issue 4(1): 315 - 336, 2007

Bela Novák, John J. Tyson, Bela Gyorffy, **Attila Csikasz-Nagy**. Irreversible cell cycle transitions due to systems-level feedback. Nature Cell Biology, issue 9: 724 - 728, 2007

Davide Prandi, **Corrado Priami**, Paola Quaglia. Communicating by compatibility. Journal of Logic and Algebraic Programming. In press.

**Sean Sedwards**, **Tommaso Mazza**. Cyto-Sim: a formal language model and stochastic simulator of membrane-enclosed biochemical processes. Bioinformatics, issue 23, 2800 – 2802, 2007

**Orkun Soyer**. Emergence and maintenance of functional modules in signaling pathways, BMC Evolutionary Biology, issue 7, 205, 2007

**Judit Zámborszky**, Christian I. Hong, **Attila Csikasz-Nagy**. Connection between the cell cycle and the circadian rhythm in mammalian cells. FEBS Journal, issue 274, 248, 2007

**Judit Zámborszky**, Christian I. Hong, **Attila Csikasz-Nagy**. Computational analysis of mammalian cell division gated by a circadian clock: quantized cell cycles and cell size control. Journal of Biological Rythms, issue 07, 45, 2007

# Our 2007 events

2 - 5 October 2007 - International Conference “**Biology without Borders”** BwB07: a unique scientific meeting that brought together leading scientists from diverse fields and topics covered in systems biology.

# Our seminars and visitors program

Rich interactions with the scientific community to exchange ideas and foster potential collaborations are an extremely valuable resource for us.

A Judy Armitage, Modelling the E.coli chemosensory pathway: strengths and weaknesses; Systems Biology in Oxford: Microbial Sensory Networks and Cautionary Tales, University of Oxford, UK

B Gianfranco Balbo, Stochastic Petri nets in practice, University of Torino, Italy

Andrea Becchetti, Modulation of the cerebral cortex by the ascending cholinergic system: physiology, pathology and theoretical problems, University of Milano Bicocca, Italy

Dennis Bray, Computer-based analysis of bacterial chemotaxis, University of Cambridge, UK

C Luca Cardelli, Artificial biochemistry, Microsoft Research Cambridge, UK

Jorge Carneiro, Regulation robustness in the immune system, Instituto Gulbenkian de Ciência, Portugal

Marvin Cassman, Modularity and robustness in mechanistic modeling, National Institute of General Medical Sciences, USA

Sailesh Chutani, Rethinking the role of ICT in healthcare, Microsoft Research, USA

Andrea Ciliberto, An autocatalytic circuit is required for an efficient sequestration of Cdc20 by Mad2, IFOM - Firc Institute for Molecular Oncology-Milano, Italy

Melvin Cohn, Default model of the decision process of the immune system, Salk Institute for Biological Studies, USA

G Yuri Gurevich, The abstract state machine approach, Microsoft Research, USA

H Leroy Hood, Systems biology and systems medicine, Institute for Systems Biology, USA

K Ehud Keinan, Bio-molecular computing devices, Technion Israel Institute of Technology, Israel

Marek Kwiatkowski, A process algebraic approach to robustness and evolvability of biochemical pathways, University of Edinburgh, UK

L David Liberles, Gene duplication and functional evolution, University of Wyoming, USA

M Pedro Mendes, Adventures in reverse engineering of biochemical networks, University of Manchester, UK

Vanna Micheli, Purine metabolism of human erythrocyte as a model of study, University of Siena, Italy

Hisao Moriya, Upper limit dosage of genes involved in cell division cycle in S. pombe, Japanese Foundation For Cancer Research, Japan

Andrea Musacchio, Protein networks that control the process of microtubule-kinetochore attachment during cell division, IEO Milano, Italy

N Richard R. Neubig, Simplicity and complexity in G protein signaling, University of Michigan, USA

P Csaba Pal, Evolution of metabolic networks, University of Oxford, UK

Manuel Peitsch, How can systems biology impact pharmaceutical research?, Novartis, Switzerland

Alberto Policriti, Stochastic biological modeling and differential equations, University of Udine, Italy

S Marcel Salathé, Sex - the queen of puzzles in evolutionary biology, ETH Zürich, Switzerland

Guido Sanguinetti, Bayesian inference in systems biology and bioinformatics: some examples, University of Sheffield, UK

Vladimiro Sassone, Semantic barbs: what's in an observation?, University of Southampton, UK

T John J. Tyson, Regulation of the eukaryotic cell cycle: From Molecular Networks to Cell Physiology, Virginia Polytechnic Institute, USA

W Rich Williams, Structure and dynamics of complex food webs, Microsoft Research Cambridge, UK

Z Jason Zwolak, PET: A tool for estimating rate constants in models of molecular networks, Virginia Tech, USA

# Our upcoming events

## PhD Course on Computational and Systems Biology 2008

The "**CoSBi PhD course 2008**" brings together young researchers from different disciplines to learn the basic methods and recent results of computational and systems biology from some of the leading scientists of the field.

## Conference on Converging Sciences 2008

**"ConSci 08"** aims at connecting computer and life scientists to explore the potential of computational conceptual tools as enabling technology for future avenues in unravelling the logic of life.

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## Our shareholders

CoSBi is a limited liability consortium shared 50% by Microsoft Research Cambridge and 50% by the University of Trento

Microsoft Research
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# Our computational tools

We develop, maintain and support the Beta Workbench (BWB) framework built on top of our newly defined BlenX programming language based on the process calculus Beta-binders. The main features that the framework supports are: typed and dynamically varying interfaces of biological components; quantitatively determined sensitivity-based interaction; one-to-one correspondence between biological components and objects specified in the model independently of the number of states in which the component can be; description and dynamic generation of complexes based on the quantitative notion of binding affinities; spatial information; hybrid parameter specification; global conditions on the amount of components or complexes in the system at a given time, on the simulation time or simulation steps that enable specified events; de-coupling the qualitative description of the model from the quantities needed to drive execution; Markov chain generation. BWB is equipped with graphical input and output interfaces.

We also implemented Cyto-Sim, a simulator of chemical-based specification of the dynamics of biological systems that can be accessed via web applets and is based on P-systems.

For more details and downloads: **http://www.cosbi.eu/Rpty_Soft.php**

# Our open positions

Working at CoSBi means developing ideas in a challenging and interdisciplinary environment where researchers from different disciplines interact on a day-to-day basis. English is CoSBi’s official language.
CoSBi is an environment where people are encouraged to think big. We promote this process by reducing the bureaucracy almost to zero.
CoSBi has openings in the following areas:

- senior researchers
- researchers
- post-doc/junior researchers
- PhD programmes
- developers
- visiting scientists (for 6 months and longer)

Information on how to apply is available on our website:

**http://www.cosbi.eu/Careers_Home.php**

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AD Sonia Lunardelli <**mu**grafik> **mu**group®