Walter Fontana

Santa Fe Institute
1399 Hyde Park Road
Santa Fe, NM 87501 USA

www.santafe.edu/~walter

Office: +1 505.946.2731
Fax: +1 505.982.0565
Mobile: +1 505.690.3829
Email: walter@santafe.edu

PERSONAL DATA

Born	November 3rd 1960
Citizenship	Italian
Visa status	Permanent resident of the USA
Languages	German, Italian, English, French; fluent

EDUCATION

1987	**PhD**, *Theoretical Chemistry* University of Vienna, Vienna, Austria Thesis supervisor: Prof. Peter Schuster graduated with highest honors
1984	**MSc**, *Biochemistry* University of Vienna, Vienna, Austria Thesis supervisor: Prof.Peter Schuster
1978 – 1983	*Studies in Biochemistry* University of Vienna, Vienna, Austria

RESEARCH AND PROFESSIONAL EXPERIENCE

1998 – present	**Research Professor** Santa Fe Institute, Santa Fe, NM
2001	**Visitor,** Program in Stat.Physics and Biological Information Institute for Theoretical Physics UCSB, Santa Barbara, CA
1999 – 2000	**Member,** Program in Theoretical Biology Institute for Advanced Study Princeton, NJ
1997 – 2000	**Associate Professor** Institute for Theoretical Chemistry University of Vienna, Vienna, Austria • *venia legendi* (theoretical chemistry) 04/16/1997 • resigned tenure on 12/31/ 2000

1994 – 1997	**Assistant Professor** Institute for Theoretical Chemistry University of Vienna, Vienna, Austria
1995 – 1997	**Research Scholar** IIASA – Intl. Institute for Applied Systems Analysis Laxenburg, Austria
1994	**Visiting Scientist** Interval Research Corporation Palo Alto, CA
1991 – 1993	**Postdoctoral Fellow** Santa Fe Institute, Santa Fe, NM
1989 – 1991	**Postdoctoral Fellow** (Director's Fund) Theoretical Division and Center for Nonlinear Studies Los Alamos National Laboratory Los Alamos, NM
1987 – 1989	**Research Assistant** Institute for Theoretical Chemistry University of Vienna, Vienna, Austria

RESEARCH GRANTS

2002 – 2003	*Models of Signaling Networks* 2002: US$ 149,170 2003: US$ 150,000 (with D.Krakauer) The Proteus Foundation
2001 – 2003	*A Founding Program in the Study of Robustness* US$ 995,000 The David and Lucile Packard Foundation Principal scientist with J.P.Crutchfield, S.Forrest, E.Jen and S.A.Levin. PI: Erica Jen
2002 – 2004	*Innovation in Natural, Experimental and Applied Evolution* US$ 150,000 The David and Lucile Packard Foundation Co-PI with F.Arnold, D.Erwin and R.Lewontin. PI: Tom Kepler
1999 – 2001	*Biology of Information* US$ 400,000 The Rose-Legett Foundation
1999 – 2001	*Functional Organization in Molecular Systems* AS 1,777,120 (approx US$ 100,000) Austrian Science Foundation Project P13565-MAT Principal Investigator

1997 – 1999	*Adaptive Dynamics and Self-Organization* AS 1,284,000 (approx US$ 100,000) Austrian Ministry of Science and Transport Contract No. GZ 308.951/4-IV/B/3/96 Co-PI with U.Dieckmann and K.Sigmund

PROFESSIONAL ACTIVITIES

1998 – 2003	Editorial Board, *Journal of Theoretical Biology*
1998 – present	Editorial Board, *Complexity*
1993 – present	Editorial Board, *Artificial Life*
1997 – present	Counseling Scientist, Konrad Lorenz Institute for Research in Evolution and Cognition Altenberg, Austria
1994 – 1998	External Faculty, Santa Fe Institute, Santa Fe, NM
past 3 years	Referee for: *Journal of Theoretical Biology, Proceedings of the Royal Society, Science, Nature, Physical Review Letters, The American Naturalist, Proceedings of the National Acdemy of Science USA, Bioinformatics, Journal of Molecular Evolution, RNA, Nucleic Acids Research, Gene, Advances in Complex Systems, Artificial Life*

EXTRACURRICULAR ACTIVITIES

1996 – present	Paraglider pilot (USA P4, Austria P4)
2001 – present	Private pilot (airplane single-engine land, VFR)

MANUSCRIPTS IN PREPARATION

- Stochastic Molecular Switches
  (with E.Smith, S.Krishnamurty and D.Krakauer)

- Generalized Signaling Cascades
  (with D.Krakauer)

- Neutrality in Technology Landscapes: Beyond Exploration versus Exploitation
  (with Jose Lobo and John Miller)

PUBLICATIONS

- S.Krishnamurthy, E.Smith, D.Krakauer and W.Fontana
  Non-equilibrium phase transitions in a cellular signaling chain
  submitted (2003) [pdf]

- J.Arjan, G.M.de Visser, J.Hermisson, G.P.Wagner, L.W.Ancel, H.Bagheri, J.L.Blanchard, L.Chao, J.M.Cheverud, S.F.Elena, W.Fontana, G.Gibson, T.F.Hansen, D.Krakauer, R.C.Lewontin, C.Ofria, S.H.Rice, G.von Dassow, A.Wagner, and M.C.Whitlock
  Perspective: Evolution and Detection of Genetic Robustness
  Evolution, **57**(9), 1959-1972 (2003) [pdf]

- W.Fontana
  Modelling 'Evo-Devo' with RNA
  BioEssays, **24**, 1164-1177 (2002) [pdf]

- N.V.Fedoroff and W.Fontana
  Small numbers of big molecules
  Science, **297**, 1129-1131 (2002) [pdf]

- W.Fontana
  The Topology of the Possible
  to appear in *Market Emergence and Transformation*,
  J.Padgett and W.Powell (eds.) [pdf]

- B.M.R.Stadler, P.F.Stadler, G.Wagner and W.Fontana
  The topology of the possible: Formal spaces underlying patterns of evolutionary change
  J. theor. Biol., **213**(2), 241-274 (2001) [pdf]

- L.W.Ancel and W.Fontana
  Evolutionary Lock-in and the Origin of Modularity in RNA Structure,

in *Modularity -Understanding the Development and Evolution of Complex Natural Systems*, W.Callebaut and D.Rasskin-Gutman, editors, MIT Press, in press (2002) [pdf]

- L.W.Ancel and W.Fontana
  Plasticity, Evolvability and Modularity in RNA,
  J. Exp. Zool. (Mol. Dev. Evol.), **288**, 242-283 (2000) [pdf]

- C.Flamm, W.Fontana, I.Hofacker and P.Schuster
  RNA Folding at Elementary Step Resolution,
  RNA, **6**, 325-338 (2000) [pdf]

- P.Schuster and W.Fontana
  Chance and Necessity in Evolution: Lessons from RNA,
  Physica D: Nonlinear Phenomena, **133**, 427-452 (1999) [pdf]

- S.Wuchty, W.Fontana, I.Hofacker and P.Schuster
  Complete Suboptimal Folding of RNA and the Stability of Secondary Structures,
  Biopolymers, **49**, 145–165 (1999) [pdf]

- W.Fontana and P.Schuster
  Shaping Space: The Possible and the Attainable in RNA Genotype-Phenotype Mapping,
  J. Theor. Biol., **194**, 491-515 (1998) [pdf]

- W.Fontana and P.Schuster
  Continuity in Evolution: On the Nature of Transitions,
  Science, **280**, 1451-1455 (1998) [pdf]

- W.Fontana and L.W.Buss
  The Barrier of Objects: From Dynamical Systems to Bounded Organizations,
  in: *Boundaries and Barriers*, J.Casti and A.Karlqvist (eds.), pp.56–116, Addison-Wesley, 1996

  The tutorial appendices on λ-calculus (Appendix A), type theory (Appendix B) and proof-theory (Appendix C) can be obtained with the main text as [pdf]. A brief summary has appeared as:
  - Walter Fontana, "On organization" in *The future of science has begun: Approaches to Artificial Life and Artificial Intelligence*, Fondazione Carlo Erba, volume 4, 23-40 (1996) [pdf]
  - Reprinted in the report on the workshop *Emergence, Entropy, and the Creative Universe*, T. Bernold (editor), pages 207-222 (1998), Swiss Science Council, Advance Detection in Research Policy (FER) publication 182/1998.

- M.Huynen, P.F.Stadler and W.Fontana
  Smoothness within Ruggedness: The role of neutrality in adaptation,
  Proc. Natl. Acad. Sci. USA, **93**, 397-401 (1996) [pdf]

- W.Fontana
  Molekulare Semantik: Evolution zwischen Variation und Konstruktion,
  in: *Evolution: Entwicklung und Organisation in der Natur*,
  V.Braitenberg and I.Hosp (eds.), rororo -science 1 9706 5, 69–106 (1994)
  - Reprinted in: *Origenes de la vida. En el centenario de Aleksandr Ivanovich Oparin*,
    F.Moran, J. Pereto and A. Moreno (eds.), pp. 269–302, Editorial Complutense, 1995

- W.Fontana, G.Wagner and L.W.Buss
  Beyond Digital Naturalism,
  Artificial Life, **1/2**, 211–227 (1994)
  - Reprinted in: *Artificial Life: an Overview*, Chris Langton (editor),
    pp. 211–227, MIT Press, Cambridge, MA, 1995

- I.L.Hofacker, W.Fontana, P.F.Stadler, L.S.Bonhoeffer, M.Tacker and P.Schuster
  Fast Folding and Comparison of RNA Secondary Structures,
  Chemical Monthly, **125**, 167–188 (1994)

- W.Fontana and L.W.Buss
  'The Arrival of the Fittest': Toward a Theory of Biological Organization
  Bull. Math. Biol., **56**, 1–64 (1994)

- P.Schuster, W.Fontana, P.F.Stadler and I.Hofacker
  From Sequences to Shapes and Back: A Case Study in RNA Secondary Structures
  Proc. Roy. Soc. (London) B, **255**, 279–284 (1994) [pdf]

- M.Tacker, W.Fontana, P.F.Stadler and P.Schuster
  Statistics of RNA Melting Kinetics
  European Journal of Biophysics, **23**, 29–38, (1994)

- W.Fontana and L.W.Buss
  What would be conserved if 'the tape were played twice'?
  Proc. Natl. Acad. Sci. USA, **91**, 757–761 (1994) [pdf]
  - Reprinted in: *Complexity: Metaphors, Models, and Reality*,
    George A. Cowan, David Pines, and David Meltzer (eds.),
    pp. 223–244, Addison-Wesley, Reading, MA, 1994

- W.Fontana, D.A.M.Konings, P.F.Stadler, and P.Schuster
  Statistics of RNA Secondary Structures
  Biopolymers, **33**, 1389–1404 (1993)

- W.Fontana, P.F.Stadler, E.Bauer, T.Griesmacher, I.L.Hofacker, M.Tacker, P.Tarazona, E.D.Weinberger and P.Schuster
  RNA Folding and Combinatory Landscapes

Phys.Rev.E, **47**, 2083-2099 (1993) [pdf]

- P.F.Stadler, W.Fontana and J.H.Miller
  Random Catalytic Reaction Networks
  Physica D, **63**, 378-392 (1993)

- W.Fontana
  Algorithmic Chemistry
  in: *Artificial Life II*, C.G.Langton et al. (eds.),
  pp. 159-209, Addison-Wesley, 1991

- R.J.Bagley, J.D.Farmer and W.Fontana
  Evolution of a Metabolism
  in: *Artificial Life II*, C.G.Langton et al. (eds.),
  pp. 141-158, Addison-Wesley, 1991

- W.Fontana
  Functional Self-Organization in Complex Systems
  in: *1990 Lectures in Complex Systems*, SFI Studies in the Sciences of Complexity, Lecture Notes Vol. III, L.Nadel and D.Stein (eds.),
  pp. 407-426, Addison-Wesley, 1991

  - Reprinted in: *Pattern Formation in the Physical and Biological Sciences*,
    H. F. Nijhout, L. Nadel, and D. Stein (eds.),
    pp. 43-63, Addison-Wesley, Reading, MA, 1997

- W.Fontana, T.Griesmacher, W.Schnabl, P.F.Stadler and P.Schuster
  Statistics of Landscapes based on Free Energy, Replication and Degradation Rate Constants of RNA Secondary Structures
  Chemical Monthly, **122**, 795-819 (1991)

- W.Fontana, W.Schnabl and P.Schuster
  Physical Aspects of Evolutionary Optimization and Adaptation
  Phys.Rev.A, **40**, 3301-3321 (1989) [pdf] [erratum]

- W.Fontana and P.Schuster
  A Computer Model of Evolutionary Optimization
  Biophysical Chemistry, **26**, 123-147 (1987)

Perspectives and Commentary

- W.Fontana and S.Ballati
  Complexity: An Essay
  Complexity, **4**, 14-16 (1999)

- W.Fontana
  Keine Information ohne Evolution

Ethik-und Sozialwissenschaften, **9**, 198-200 (1998)

Book Reviews

W.Fontana
The Theory of Evolution and Dynamical Systems
by J.Hofbauer and K.Sigmund
Mathematical Biosciences, **96**, 135-137 (1989)

Theses

W.Fontana
A Computer Model of Evolutionary Optimization
PhD Thesis (in German), University of Vienna, Austria (1987)

W.Fontana
Molecular Replication and Random Selection: On a Simple Stochastic Model of Non-Darwinian Behavior
Master Thesis (in German), University of Vienna, Austria (1984)

Public Domain Software Packages

I.L.Hofacker, W.Fontana, P.F.Stadler, L.S.Bonhoeffer, M.Tacker and P.Schuster
Vienna RNA Package
http://www.santafe.edu/~walter/RNA/rna.html

Walter Fontana – Invited Lectures and Seminars since 1998

1998

- 18th annual CNLS conference, Los Alamos, NM
- Astrobiology Roadmapping Workshop, NASA Ames, Moffett Field, CA

1999

- Public Lecture, Institute for Advanced Study, Princeton, NJ
- Seminar, Penn State University, State College, PA

2000

- Public Lecture, The Rockefeller University, New York, NY
- Plenary lecture, American Physical Society Meeting, Minneapolis, MN
- Conference on Modularity, Hanse Institute for Advanced Study, Delmenhorst, Germany

2001

- Seminar, ITP, Santa Barbara, CA
- Lecture, 4th International Conference on Biological Physics, Kyoto, Japan
- Seminar, University of Arizona, Tucson, AZ
- Seminar, University of Michigan, Ann-Arbor, MI

2002

- Workshop on Collective Intelligence, SFI, Santa Fe, NM
- Santa Fe Institute Science Board Symposium, Santa Fe, NM
- Lecture, Center for Development Research, Bonn, Germany

2003

- Lecture, Gordon Research Conference Quant. Genetics and Genomics, Ventura, CA
- Seminar, Scripps Institute, La Jolla, CA
- Lecture, BioCONCUR 2003 (Biology and Concurrency), Marseille, France
- Lecture, ONR (Mini-Symposium, Progress Review Northwest Region), Seattle, WA
- Lecture, OOPSLA 2003, Anaheim, CA
- Lecture, Rocky Mountain Regional Bioinformatics Meeting, Aspen, CO

Walter Fontana - Research

---

1 – formalization and emergence of functional organization

The formal structure of evolutionary theory is based upon the dynamics of (populations of) "individuals." It therefore assumes the entities whose existence it is supposed to explain. At the heart of the existence problem is determining how biological organizations arise in ontogeny and in phylogeny. The research theme we called *Algorithmic Chemistry* (AlChemy) was an attempt at constructing a formal framework for thinking about molecular organization through an abstraction of chemistry. Our stance was to view molecules as rules of transformation and to exploit a mathematical theory of functions (λ-calculus) to represent abstract "molecules" that act upon one another generating new molecules or rules of transformation. Under suitable boundary conditions this model generates self-maintaining collectives of rules whose mutual transformations permit the continuous regeneration of these same rules. The "organization" of such a system is specified by the relationships of transformation that enable self-maintenance, i.e. the algebraic structure of the system. This framework permits to address the robustness of organizations with respect to the elimination of components (self-repair), the addition of components not belonging to the organization (constrained extension) and the merger of autonomous organizations into higher-order structures (integration).

$$A \equiv A_i^n \equiv \lambda^{i-1}.A_1^{n-i+1}$$

$$A_1^{n-i+1} \circ Y \Rightarrow \lambda^{n-i}.Y$$

$$\lambda^k.X \circ Y \Rightarrow \lambda^{k-1}.X \quad (k>0)$$

$$\mathrm{A} = \{A\}$$

$$\mathrm{A}^* = \{\lambda^k.A_1^1 \mid 0 \le k \le n-1\} \quad (i=n)$$

$$\mathrm{A}^* = \{\lambda^k.A_1^{n-i+1} \mid k \ge 0\} \quad (i<n)$$

The algebraic structure of a simple self-maintaining set of λ-expressions

Although this thread has slipped into the background of my portfolio, its basic vision remains intact. I'm gravitating back to it from a wider and updated perspective in the pursuit of a research center on "biology and computation."

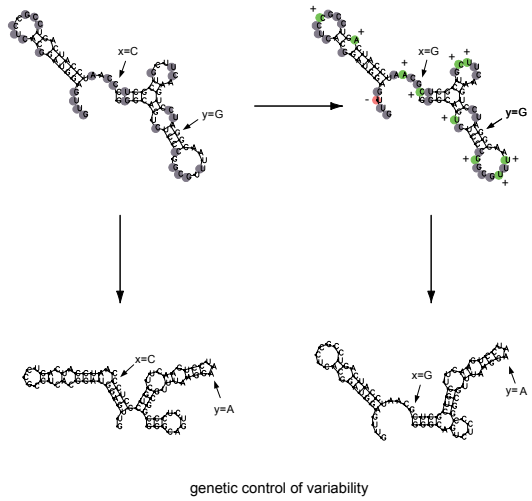
Key collaborator: **Leo Buss** (Yale)

Selected papers:

- W.Fontana and L.W.Buss, The Barrier of Objects: From Dynamical Systems to Bounded Organizations, in: *Boundaries and Barriers*, J.Casti and A.Karlqvist (eds.), pp.56–116, Addison-Wesley, 1996 [pdf]
- W.Fontana and L.W.Buss, 'The Arrival of the Fittest': Toward a Theory of Biological Organization *Bull. Math. Biol.*, **56**, 1-64 (1994)
- W.Fontana and L.W.Buss , What would be conserved if 'the tape were played twice'?, *Proc. Natl. Acad. Sci. USA*, **91**, 757–761 (1994) [pdf]

2 – genotype-phenotype mappings

The heritable modification of biological phenotypes occurs by mutation of the genotype. Accessing one phenotype from another is therefore an indirect process mediated by the mapping from genotype to phenotype (development). Evolutionary dynamics and innovation therefore depend on the statistical features of this mapping. I studied this mapping at the level of a single type of molecule: RNA. An RNA molecule is a sequence (genotype) that folds into a shape (phenotype). The statistical analysis of RNA folding has produced insights that may generalize to more complex systems. The most consequential feature is the notion of a *neutral network*: a mutationally connected set of sequences folding into the same shape and spanning a web through sequence space. Neutral networks allow populations to drift across genotype space without losing their current phenotype. In this way, populations can access many more novel phenotypes than if they were confined to a small region of genetic space. Neutral networks dispel the dichotomy of robustness versus evolvability by demonstrating that robustness enables change. Prompted by this line of work, researchers at MIT's Whitehead Institute discovered neutral networks in RNA test tube experiments (Schultes and Bartel, *Science*, 289, 448-452, 2000).



The context dependent effects of mutations on RNA structure.

The adjacency of neutral networks can be used to define a notion of *phenotype space* based on the *accessibility* of phenotypes through genetic mutation rather than phenotypic similarity. Other concepts that emerged from this line of research are *shape space covering* (that all frequent shapes occur within a relatively small neighborhood of any random sequence) and *plasto-genetic congruence* (that the genetic variability of a shape on a given sequence correlates with the alternative structures accessible by thermal fluctuations). Plasto-genetic congruence suggests a trade-off between genetic robustness and phenotypic plasticity.

Key collaborators: **Peter Schuster** (Vienna), **Peter Stadler** (Vienna), **Lauren Ancel-Meyers** (Austin)

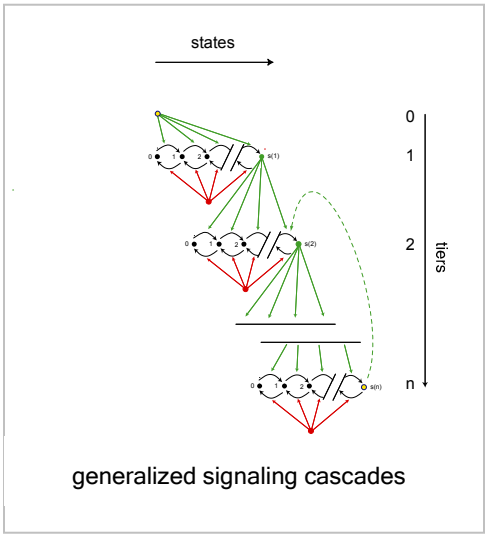
Selected papers:

- W.Fontana, Modelling 'Evo-Devo' with RNA, *BioEssays*, **24**, 1164–1177 (2002) [pdf]
- L.W.Ancel and W.Fontana , Plasticity, Evolvability and Modularity in RNA, *J.Exp.Zool. (Mol.Dev.Evol.),* **288**, 242–283 (2000) [pdf]
- W.Fontana and P.Schuster, Continuity in Evolution: On the Nature of Transitions, *Science*, **280**, 1451–1455 (1998) [pdf]
- P.Schuster, W.Fontana, P.F.Stadler and I.Hofacker, From Sequences to Shapes and Back: A Case Study in RNA Secondary Structures, *Proc. Roy. Soc. (London) B*, **255**, 279–284 (1994) [pdf]

3 – distributed molecular control

Organization is deeply shaped by mechanisms and processes of regulation and control. In collaboration with David Krakauer, I'm developing and analyzing models of molecular signal transduction networks. These networks generate cellular behavior in response to signals intercepted at the cell surface. We study simple molecular communication mechanisms that underlie functional behavior and how networks might reconfigure themselves dynamically to "learn," "memorize," "represent," "parse" and "integrate" biological information. Specific projects include:

Switching and stochasticity in phosphorylation chains. Molecular signaling often involves the concurrent phosphorylation and dephosphorylation of a target molecule at multiple sites. A bistable switch can result when the fully phosphorylated target molecule feeds back positively on the phosphorylation of its precursors. In molecular systems, unlike in electronic circuits, the shape of a "potential surface" is often maintained by the same processes whose dynamics that potential governs. This is the province of statistical many-body theory. We use analytical and numerical techniques to study the existence of switches as a function of particle number.



generalized signaling cascades

Generalized signaling cascades. Signaling pathways contain cascades comprising several tiers of sequentially activated kinases. Within each tier, kinases may be phosphorylated at multiple sites. This project is about understanding the (deterministic and stochastic) dynamics of multiple phosphorylation in the context of cascade depth.

Dynamically reconfigurable networks. Signaling networks can modulate the expression of genes. Some of these genes may code for components of the signaling network that controls their expression. Such a feed-back loop enables a signaling network to reconfigure itself in response to signals. This project is about the dynamical characterization of such networks and their potential for simple forms of learning.

Key collaborators: **David Krakauer** (Santa Fe), **Supriya Krishnamurty** (Stockholm), **Eric Smith** (Santa Fe)

Selected papers:

- S.Krishnamurthy, E.Smith, D.Krakauer and W.Fontana, Non-equilibrium phase transitions in a cellular signaling chain, submitted (2003) [pdf]

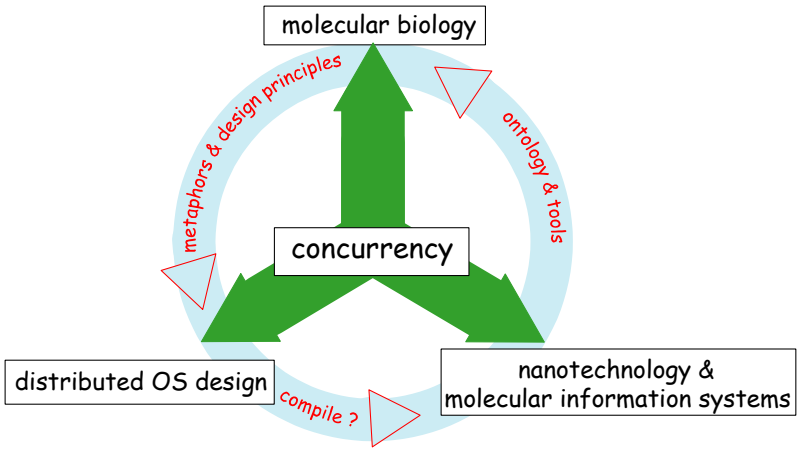
Papers in preparation:

- Generalized Signaling Cascades (with D.Krakauer)

The computational (or informational) perspective has become commonplace in thinking about biological systems. It is far from obvious, however, what kind of computational system would make such a metaphor meaningful. That system is not a Turing machine. But if the notion of computation that Turing, Church and Hilbert developed in the 1930s is inadequate for molecular systems, what *are* we talking about?

The interaction between computation and biology is not limited to the implementation of traditional parallel algorithms with novel materials (as in today's notion of "DNA computing") or the clever coding of biological algorithms (such as "genetic algorithms" or "neural networks") in traditional programming languages. The mind-bending aspects arise when we try to understand what kind of "evolvable language" has evolved within a medium of macromolecules that control, destroy and manufacture one another. Has this chemical language a distillable abstract content or is it inextricably buried in its material substrate? What programming discipline does it entail? To ask such questions, language designers need biologists. To answer such questions, biologists need language designers.

In the traditional notion of computation, a "function" is an algorithm to which an input is supplied and from which an output is retrieved. Other than that, a function does not interact with the outside world. Dropping this restriction leads to the notion of "process." The output of a process is not specified by its internal structure alone, but depends on its interactions with other processes. A process implements behavior, not an input/output relation. The distinction between process and function is similar in kind and consequences to the distinction between open and closed systems in thermodynamics. Since the 70s, computer scientists have been developing theories of computation based on interaction, creating a field known as "concurrency." Its main thrust is the construction of formal languages for reasoning about systems of non-deterministically communicating processes. Such a framework is of concern to systems biologists and designers of distributed operating systems alike. Indeed, concurrency is now being applied in both domains.



Concurrency as a lingua franca

I believe this development to be significant in a more radical sense. Consider a typical agent-based simulation of a biomolecular system. The behavior of a molecule is represented with a piece of program written in some traditional language, such as C or Java. We know that a simulation is not a theory. But the question is not: Why should it? The question is rather: Why couldn't it? What would it take for it to actually be a theory?

A computer language is a formal system. Yet, the relation between syntax and semantics in traditional programming languages does not conform with the structure-behavior relation of biomolecules. The syntax of a program does not represent a molecule in such a way as to induce a correspondence between behaviors resulting from the syntactical modification of program and molecule. The answer to this mismatch must be a programming language that constitutes a theory of the desired domain of chemistry. We don't know whether or for which domains such a language exists, but concurrency frameworks like π-calculus are a starting point. Aviv Regev, Ehud Shapiro, Corrado Priami and others have shown that such a calculus can be used "as is" for simulating signal transduction pathways. The issue now is whether these calculi can be developed into a *mathematical method* adequate for producing theory that could not be achieved by other means. If this was the case, a program for simulating a biomolecular system would be at the same time a formula for reasoning about it abstractly.

A language of this kind might well become a *lingua franca*. A lingua franca permits "idioms" developed or discovered in one domain to be immediately available to other domains. (The theory of dynamical systems may serve as an example of a lingua franca.) The lingua franca envisioned here enables a conceptual, mathematical and technological trading zone between systems biology, concurrency theory and the design of operating systems and programmable (or evolvable) synthetic molecular information systems. My hope is to help bring about a research center dedicated to the development of such a lingua franca. Its primary motivation is the search for the foundations of a theoretical molecular biology, the notion(s) of computation it implies and the technologies it enables.

This way of thinking is a joint effort with **Greg Meredith** (Microsoft Redmond), **Luca Cardelli** (Microsoft Cambridge), **Cosimo Laneve** (Bologna), **Corrado Priami** (Trento), **Vincent Danos** (Paris), **David Krakauer** (Santa Fe), **Leo Buss** (Yale) and many others.

Walter Fontana – Background

The landscape of science is changing. The core of this change, long in the making, is the interaction between biology and computer science. Through this interaction, computer science – initially an engineering science – is being transformed into a basic science of nature, that is, a science with a mindset and the tools for explaining nature by means of theories and models, like physics, chemistry or biology. Through this same interaction, biology – initially a basic science – is acquiring the character of an engineering science, that is, a discipline of synthesis that shapes materials and configures systems in specific ways to generate specific behaviors. The convergence of biology and computer science is creating a conceptual trading zone reshaping the focal points of many disciplines. Perhaps this zone will connect with the social sciences through a view of the physical world of organized complexity that is more in keeping with the causal feedbacks, context-dependency, endogeneity and generativity of social phenomena.

I am a child of this transformation. Trained as a chemist, mentored as a theoretical molecular biologist by Peter Schuster (Vienna), educated in evolutionary biology by Leo Buss (Yale), self-taught in computer science and charmed by the social sciences through John Padgett (Chicago), I have straddled many divides (including the Atlantic) that are now coming together naturally (with the exception of the Atlantic). I have taken risks in pursuing a professional trajectory shaped by the desire for a broadly engaging cross-disciplinary environment more than by career safety. This, together with the desire to live in the USA, led to my decision of resigning tenure at the University of Vienna.

I have worked at non-degree granting institutions for three quarters of my 16 years in professional science. Consequently, I did not accumulate an extensive course teaching experience. In Vienna, however, I taught graduate seminars on select topics in the mathematical modeling of molecular evolutionary systems and supervised PhD theses. The tools I bring to research range from good mathematical practice (aspects of stochastic processes, dynamical systems, discrete mathematics and logic), excellent modelling skills and a richly diverse experience in programming and the use of computers.

Coming up with a good question is as exciting to me as trying to answer it. My work style is collaborative during many phases of a project and I stay involved at all levels of detail, from the conception to the implementation and analysis of a model. I have consciously avoided the formation of a research group, as I felt that such groups often require, and generate, directional inertia. Yet, I always had a keen interest in being a catalyst and contributing to the making and functioning of scientific institutions. At the Santa Fe Institute, I participated in writing large collaborative grants and core grants. I served on several postdoctoral selection committees and enjoyed cultivating relations with Trustees and the Business Network.