Walter Fontana

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PERSONAL DATA

Citizenship	USA
Languages	German, Italian, English: fluent French: good

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

PROFESSIONAL APPOINTMENTS

2004 — present	**Professor of Systems Biology** Department of Systems Biology Harvard Medical School, Boston, MA
2019 — 2020	**INRIA Chair in Informatics and Computational Sciences** Collège de France, Paris
2004 — 2019 1994 — 1998	**External Faculty** Santa Fe Institute, Santa Fe, NM
2001	**Visitor,** Program in Statistical Physics and Biological Information, Institute for Theoretical Physics, UCSB, Santa Barbara, CA
1999 — 2000	**Program in Theoretical Biology** Institute for Advanced Study, Princeton, NJ
1998 — 2004	**Professor** Santa Fe Institute, Santa Fe, NM
1997 — 2000	**Associate Professor** Institute for Theoretical Chemistry University of Vienna, Vienna, Austria

- *venia legendi* 04/16/1997
- resigned tenure 12/31/2000 when relocating to the USA on a non-tenured 6-year position at the Santa Fe Institute

1995 — 1997	**Research Scholar** IIASA – Intl. Institute for Applied Systems Analysis Laxenburg, Austria
1994 — 1997	**Assistant Professor** Institute for Theoretical Chemistry University of Vienna, Vienna, 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

2013 — present	*Philanthropic gift*
2015 — 2017	*Active Context (DARPA-BAA-15-18 "Communicating with Computers")* W911NF-15-1-0544 (original PI, co-PI since 2016)
2015 — 2017	Glenn Award, Glenn Foundation for Medical Research
2014 — 2018	*Executable Knowledge (DARPA-BAA-14-14 "BigMechanism")* W911NF-14-1-0367 (PI)
2009 — 2015	*The Variability of the lifespan phenotype in C. elegans* NIH R01 AG034994
2012 — 2013	*Identifying genes affecting sarcopenia with the C. elegans lifespan machine (II).* Sanofi-Aventis Innovation Award Program (continuation)
2011 — 2012	*Identifying genes affecting sarcopenia with the C. elegans lifespan machine (I).* Sanofi-Aventis Innovation Award Program
2010 — 2012	*Rule-based modeling of the Wnt pathway.* Novartis Research Collaboration, Novartis A13141
2009 — 2010	*Automated Acquisition of C. elegans Survival Curves with a Flatbed Scanner.* ARRA Competitive Revision Supplement NIH 1 R03 AG032481-S1
2008 — 2010	*Automated Acquisition of C. elegans Survival Curves with a Flatbed Scanner.* NIH 1 R03 AG032481
2008 — 2009	*A systems approach to the dynamics of aging in C. elegans* Paul F. Glenn Labs Pilot Project grant
2002 — 2003	*Models of Signaling Networks* (with D. Krakauer) The Proteus Foundation
2001 — 2003	*A Founding Program in the Study of Robustness*

	The David and Lucile Packard Foundation Co-PI with J.P. Crutchfield, S. Forrest, and S.A. Levin PI: E. Jen
2002 — 2004	*Innovation in Natural, Experimental and Applied Evolution* The David and Lucile Packard Foundation Co-PI with F. Arnold, D. Erwin and R. Lewontin. PI: T. Kepler
1999 — 2001	*Biology of Information* The Rose-Legett Foundation
1999 — 2001	*Functional Organization in Molecular Systems* Austrian Science Foundation, P13565-MAT
1997 — 1999	*Adaptive Dynamics and Self-Organization* Austrian Ministry of Science and Transport GZ 308.951/4-IV/B/3/96 Co-PI with U. Dieckmann and K. Sigmund

PROFESSIONAL ACTIVITIES

2022 — present	**Advisory Board**, Albert Einstein Institute for Advanced Study in the Life Sciences, Albert Einstein College of Medicine
2021 — present	**Scientific Board of Advisors**, Program on Agency, Directionality, and Function. (John Templeton Foundation program grant to the University of Minnesota, PI Alan Love)
2010 — 2019	**Science Steering Committee**, Santa Fe Institute
2006 — 2012	**Science Board**, Santa Fe Institute, Santa Fe, NM
1997 — present	**External Faculty**, Konrad Lorenz Institute for Research in Evolution and Cognition, Altenberg, Austria
2005 — 2010	**Board of Directors,** Plectix BioSystems Inc., Cambridge, MA
2005	**Founder**, Plectix BioSystems Inc., Cambridge, MA Instrumental in raising 2 rounds of venture capital from premium investors.

Editorial Boards

2023 - present	*Foundations for Interdisciplinarity in the Life Sciences: Concise Monographs, Springer*
2004 — 2012	*LNCS Transactions on Computational Systems Biology*
1998 — 2016	*Complexity*
1993 — 2005	*Artificial Life*
1998 — 2003	*Journal of Theoretical Biology*

Academic Committees

2006	*Search Committee Brigham and Women's Hospital (Professor of Medicine in Quantitative Systems Biology), Harvard Medical School*
2004—2010	*Search Committee Senior Faculty Systems Biology, Harvard Medical School*
2004—10, 2016, 2019	*Search Committee Junior Faculty Systems Biology, Harvard Medical School*

2006—2009	*Promotions, Reappointments, and Appointments Committee, Harvard Medical School*
2004—present	*Standing Committee on Higher Degrees in Systems Biology, Harvard University*
2004—2010	*Appointments and Review Committee, Santa Fe Institute*
2004—2014, 2018	*Omidyar Fellows Review Committee, Santa Fe Institute*
2011—2015	*Subcommittee of Professors, Harvard Medical School*
2013—2014	*Chair, Presidential Search Committee, Santa Fe Institute*
2012—2013, 2020—present	*Admissions Committee, Systems Biology Graduate Program, Harvard Medical School*
2009—11, 2013—14, 2020—21	*Admissions Committee, Frontières du Vivant, Graduate Program, Centre de Recherche Interdisciplinaire, Paris*
2022—present	*Harvard Medical School Distinguished Prizes and Awards Advisory Committee*

Program Committees

2010	*CS2Bio 2010 (Computer Science and Biology)*
2011	*SASB 2011 (Static Analysis and Systems Biology)*
2013	*CMSB 2013 (Computational Methods in Systems Biology)*

NIH Study Sections

2005	*National Centers for Biomedical Computing*
2007	*Modeling and Analysis of Biological Systems*
2009	*ARRA*
2010	*F05 Fellowships*
2010	*RISE program evaluator*

TEACHING

Fall 2019	Biology of Information, Collège de France (Paris)

A newly assembled course presenting, in a somewhat idiosyncratic fashion, aspects of how information is represented, transmitted, processed, and acquired in biological systems at the molecular level. Far from being polished, my goal is to evolve this first attempt into a reasonable survey for students at the advanced undergraduate and graduate level.

Spring 2005, Spring 2006	SB101 – Systems Biology (with J. Gunawardena, L. Cantley, and M. Kirschner)
Fall 2006—Fall 2009	SB200 – Systems Biology (with J. Gunawardena and J. Paulsson)
Fall 2013, Fall 2014	Medical Sciences 300qc (Conduct of Science)

SB101 (later SB200) was a new course aimed at seniors / first year graduate students from engineering and the natural sciences with the goal of conveying a working knowledge of mathematical and computational techniques that are applied in simple biological situations to produce models and explore their behavior. Mathematical thinking is used to appreciate the shape of ideas and to agree with others about the meaning of concepts. The course was developed and co-taught with Professors Gunawardena, Cantley, Kirschner and Paulsson.

PEER–REVIEWED PUBLICATIONS

An open bullet ○ indicates computer science literature with alphabetical (traditional) author order

- A. Ershova, D. Minev, F. E. Corea-Dilbert, D. Yu, J. Deng, W. Fontana and W. M. Shih. Enzyme-Free Exponential Amplification via Growth and Scission of Crisscross Ribbons from Single-Stranded DNA Components. *J. Am. Chem. Soc.*, 146, 1, 218-227 (2024)
- W. Fontana. Informatique et sciences numériques, Résumé des cours et travaux. *Annuaire du Collège de France*, **120**, 41-51 (2023)
- ○ J. L. Andersen, R. Fagerberg, C. Flamm, W. Fontana, J. Kolčák, C. V. F. P. Laurent, D. Merkle and N. Nøjgaard. Representing Catalytic Mechanisms with Rule Composition. *J. Chem. Inf. Model*, **62**, 5513-5524 (2022)
- Y. Katz and W. Fontana. Probabilistic Inference with Polymerizing Biochemical Circuits. *Entropy* **2022**, 24, 629 (2022)
- ○ J. L. Andersen, R. Fagerberg, C. Flamm, W. Fontana, J. Kolčák, C. V. F. P. Laurent, D. Merkle and N. Nøjgaard. Graph Transformation for Enzymatic Mechanisms. *Bioinformatics*, **37**, i392-i400 (2021)
- R. J. H. Ross and W. Fontana. Balancing conservative and disruptive growth in the voter model. *J. Stat. Phys.* **183**:15 (2021)
- N. Nøjgaard, W. Fontana, M. Hellmuth and D. Merkle. Cayley Graphs of Semigroups Applied to Atom Tracking in Chemistry. *Journal of Computational Biology*, **28** (7), 701-715 (2021)
- W. Fontana. Du calcul au vivant : le défi d'une science de l'organisation. *Leçons inaugurales du Collège de France*. nº 291. Collège de France | Fayard. ISBN: 978-2-213-71683-1. (2020) [From computation to life: The challenge of a science of organization. English version online.]
- A. Ortiz-Muñoz, H. F. Medina-Abarca and W. Fontana. Combinatorial protein-protein interactions on a polymerizing scaffold. *Proc. Natl. Acad. Sci. USA*, **117** (6), 2930–2937 (2020)
- R. Ross and W. Fontana. Modeling random walkers on growing random networks. *Physica A*, **526,** 121117 (2019)
- R. Ross, C. Strandkvist and W. Fontana. A random walker's view of networks whose growth it shapes. *Phys. Rev. E*, **99**, 062306 (2019)
- R. Ross, C. Strandkvist and W. Fontana. Compressibility of random walker trajectories on growing networks. *Physics Letters A*, **383**, 2028-2032 (2019)
- D. Abramov, J. Otto, M. Dubey, C. Artanegara, P. Boutillier, W. Fontana and A. G. Forbes. RuleVis: Constructing Patterns and Rules for Rule-Based Models. *IEEE VIS* (Short Papers), 191-195 (2019)
- J. Laurent, H. F. Medina-Abarca, P. Boutillier, J. Yang and W. Fontana. A Trace Query Language for Rule-based Models. In: Computational Methods in Systems Biology (CMSB 2018), M. Češka and D. Šafránek (Eds.), *Lecture Notes in Bioinformatics*, **11095**, 220-237 (2018)
- J. Laurent, J. Yang and W. Fontana. Counterfactual Resimulation for Causal Analysis of Rule-Based Models. Intl. Joint Conference on Artificial Intelligence (IJCAI-18), 1882-1890 (2018)
- ○ Cristescu, W. Fontana and J. Krivine. Interactions between causal structures in graph rewriting systems. In: Third International Workshop on Formal Reasoning about

Causation, Responsibility, and Explanations in Science and Technology (CREST 2018), B. Finkbeiner and S. Kleinberg (Eds.), *Electronic Proceedings in Theoretical Computer Science*, **286**, 65-78 (2018)

- P. Boutillier, M. Maasha, X. Li, H. F. Medina-Abarca, J. Krivine, J. Feret, I. Cristescu, A. G. Forbes and W. Fontana. The Kappa platform for rule-based modeling. *Bioinformatics*, **34**/13, i583-i592 (2018)
- J. Apfeld and W. Fontana. Age-Dependence and Aging-Dependence: Neuronal Loss and Lifespan in a *C. elegans* Model of Parkinson's Disease. *Biology*, **7**/1 (2018)
- A. G. Forbes, A. Burks, K. Lee, X. Li, P. Boutillier, J. Krivine and W. Fontana. Dynamic Influence Networks for Rule-Based Models. *IEEE Transactions on Visualization and Computer Graphics*, **24**(1), 184-194 (2018)
- N. Stroustrup, W. E. Anthony, Z. M. Nash, V. Gowda, A. Gomez, I. F. López-Moyado, J Apfeld* and W Fontana*. The temporal scaling of *C. elegans* ageing. *Nature,* **530**, 103-107 (2016)
- A. Basso-Blandin, W. Fontana, and R. Harmer. A knowledge representation meta-model for rule-based modelling of signalling networks. In: Developments in Computational Models (DCM 2015), C. A. Munoz and J. A. Perez (Eds.), *Electronic Proceedings in Theoretical Computer Science* **204**, 47-59 (2015)
- C. Romero, D. S. Marks, W. Fontana*, and J. Apfeld*. Regulated spatial organization and sensitivity of cytosolic protein oxidation in *C. elegans*. *Nature Communications*. **5**.5020 (2014)
- D. A. Fernandes de Abreu, A. Caballero, P. Fardel, N. Stroustrup, Z. Chen, K.-H. Lee, W. D. Keyes, Z. M. Nash, I. F. López-Moyado, F. Vaggi, A. Cornils, M. Regenass, A. Neagu, I. Ostojic, C. Liu, Y. Cho, D. Sifoglu, Y. Shen, W. Fontana, H. Lu, A. Csikasz-Nagy, C. Murphy, A. Antebi, E. Blanc, J. Apfeld, Y. Zhang, J. Alcedo, and Q.-L. Ch'ng. An Insulin-to-Insulin Regulatory Network Orchestrates Phenotypic Specificity in Development and Physiology. *PLOS Genetics*, **10** (3), e1004225 (2014)
- N. Stroustrup, B. E. Ulmschneider, Z. M. Nash, I.F. López Moyado, J. Apfeld, and W. Fontana. The *Caenorhabditis elegans* Lifespan Machine. *Nature Methods*, **10**, 665–670 (2013)
- M. Rowland, W. Fontana, and E. J. Deeds. Crosstalk and competition in signaling networks. *Biophys. J.* **103**(11), 2389–2398 (2012)
- V. Danos, J. Feret, W. Fontana, R. Harmer, J. Hayman, J. Krivine, C. Thompson-Walsh, and G. Winskel. Graphs, Rewriting and Pathway Reconstruction for Rule-Based Models. In: Foundations of Software Technology and Theoretical Computer Science (FSTTCS 2012). D. D'Souza, T. Kavitha and J. Radhakrishnan (Eds.), *Leibniz International Proceedings in Informatics*, **18**, 276-288 (2012)
- E. J. Deeds, J. Krivine, J. Feret, V. Danos, and W. Fontana. Combinatorial complexity and compositional drift in protein interaction networks. *PLoS ONE* **7**(3): e32032 (2012)
- E. J. Deeds, J. A. Bachman, and W. Fontana. Optimizing ring assembly reveals the strength of weak interactions. *Proc. Natl. Acad. Sci. USA,* **109**(7), 2348-2353 (2012)
- E. Smith, S. Krishnamurthy, W. Fontana, and D. C. Krakauer. Non-equilibrium phase transitions in biomolecular signal transduction. *Phys. Rev. E*, **84**:051917 (2011)
- D. C. Krakauer, J. P. Collins, D. Erwin, J. C. Flack, W. Fontana, M. D. Laubichler, S. J. Prohaska, G. B. West and P. F. Stadler. The Challenges and Scope of Theoretical Biology. *J. Theor. Biol.*, **276**, 269-276 (2011)
- R. Harmer, V. Danos, J. Feret, J. Krivine, and W. Fontana. Intrinsic Information Carriers in Combinatorial Dynamical Systems. *Chaos*, **20**, 037108 (2010)

- V. Danos, J. Feret, W. Fontana, R. Harmer, and J. Krivine. Abstracting the differential semantics of rule-based models: exact and automated model reduction. In: Proceedings of the 25th Annual IEEE Symposium on Logic in Computer Science (LICS), J-P Jouannaud (Ed.), pp. 362--381 (2010). IEEE Computer Society Press.
- T. Kolokotrones, V. Savage, E. Deeds, and W. Fontana. Curvature in metabolic scaling. *Nature*, **464**, 753-756 (2010)
  - E. J. Deeds, V. M. Savage and W. Fontana. Reply to MacKay [*J. Theor. Biol.* **280**, 194-196 (2011)] *J. Theor. Biol.*, **280**, 197–198 (2011)
- S. E. Hulme, S. S. Shevkoplyas, A. P. McGuigan, J. Apfeld, W. Fontana, and G. M. Whitesides. Lifespan-on-a-Chip: microfluidic chambers for performing lifelong observation of *C. elegans*. *Lab on a Chip,* **10**, 589-597 (2010)
- V. Danos, J. Feret, W. Fontana, R. Harmer, and J. Krivine. Rule-based Modelling and Model Perturbation. In: Priami C., Back R. J., Petre I. (Eds.) Transactions on Computational Systems Biology XI. *Lecture Notes in Computer Science*, **5750**:116-137 (2009)
- J. Feret, V. Danos, J. Krivine, R. Harmer and W. Fontana. Internal coarse-graining of molecular systems. *Proc. Natl. Acad. Sci. USA,* **106**, 6453-6458 (2009)
- V. Danos, J. Feret, W. Fontana, R. Harmer, and J. Krivine. Investigation of a biological repair scheme. In: Workshop on Membrane Computing 9, D. Corne et al. (Eds.), *Lecture Notes in Computer Science (WMC 2008)*, **5391**:1-12 (2009)
- V. Danos, J. Feret, W. Fontana, R. Harmer, and J. Krivine. Rule-based modeling, symmetries, refinements. In: Formal Methods in Systems Biology (FMSB 2008), J. Fisher (Ed.), *Lecture Notes in Bioinformatics*, **5054**:103-122 (2008)
- V. Savage, E. Deeds, and W. Fontana. Sizing up allometric scaling theory. *PLoS Computational Biology*. **4**(9): e1000171 (2008)
- V. Danos, J. Feret, W. Fontana, and J. Krivine. Abstract interpretation of cellular signalling networks. In: VMCAI 2008, F. Logozzo et al. (Eds.), *Lecture Notes in Computer Science*, **4905**:83–97 (2008)
- W. Fontana. Systems biology, models, and concurrency. In: Proceedings of the 35th annual ACM SIGPLAN-SIGACT symposium on Principles of Programming Languages (POPL), 2008
- S. E. Hulme, S. S. Shevkoplyas, J. Apfeld, W. Fontana, and G. M. Whitesides. A Microfabricated Array of Clamps for Immobilizing and Imaging *C. elegans*. *Lab on a Chip,* **7**, 1515-1523 (2007)
- V. Danos, J. Feret, W. Fontana, R. Harmer, and J. Krivine. Rule-based Modelling of Cellular Signalling. In: CONCUR 2007, L. Caires and V. T. Vasconcelos (Eds.), *Lecture Notes in Computer Science*, **4703**:17-41 (2007)
- V. Danos, J. Feret, W. Fontana, and J. Krivine. Scalable simulation of cellular signaling networks. In: APLAS 2007, Z. Shao (Ed.), *Lecture Notes in Computer Science,* **4807**:139–157 (2007)
- S. Krishnamurthy, E. Smith, D. Krakauer, and W. Fontana. The stochastic behavior of a molecular switching circuit with feedback. *Biology Direct*, 2007, **2**:13 (31 May 2007)
- W. Fontana. Pulling Strings [Perspective]. *Science,* **314**. 1552-1553 (2006)
- W.S. Hlavacek, J.R. Faeder, M.L. Blinov, R.G. Posner, M. Hucka, and W. Fontana. Rules for Modeling Signal Transduction Systems. *Science STKE,* Vol. 2006, Issue **344**, pp. re6, 18 July 2006
- W. Fontana. The Topology of the Possible. In: Understanding Change - Models, Methodologies and Metaphors. A. Wimmer and R. Kössler (Eds.), Palgrave Macmillan, (2006)

- L.W. Ancel-Myers and W. Fontana. Evolutionary Lock-in and the Origin of Modularity in RNA Structure. In *Modularity –Understanding the Development and Evolution of Natural Complex Systems*, W. Callebaut and D. Rasskin-Gutman (Eds.), pp.129-141, MIT Press, Cambridge, MA (2005)
- 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)
- W. Fontana. Modelling 'Evo-Devo' with RNA. *BioEssays*, **24**, 1164–1177 (2002)
- N.V. Fedoroff and W. Fontana. Small numbers of big molecules. *Science*, **297**, 1129–1131 (2002)
- 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)
- L.W. Ancel and W. Fontana. Plasticity, Evolvability and Modularity in RNA. *J. Exp. Zool. (Mol. Dev. Evol.),* **288**, 242–283 (2000)
- C. Flamm, W. Fontana, I. Hofacker and P. Schuster. RNA Folding at Elementary Step Resolution. *RNA*, **6**, 325-338 (2000)
- P. Schuster and W. Fontana. Chance and Necessity in Evolution: Lessons from RNA. *Physica D: Nonlinear Phenomena*, **133**, 427-452 (1999)
- 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)
- W. Fontana and P. Schuster. Shaping Space: The Possible and the Attainable in RNA Genotype-Phenotype Mapping. *J. Theor. Biol.*, **194**, 491–515 (1998)
- W. Fontana and P. Schuster. Continuity in Evolution: On the Nature of Transitions. *Science*, **280**, 1451–1455 (1998)
- 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

  Tutorial appendices on λ-calculus (Appendix A), type theory (Appendix B) and proof-theory (Appendix C) can be obtained with the main text at https://walterfontana.science. Excerpts have 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)
  - 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)
- 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)
- 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)
  - 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)
- 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)
- W. Fontana and P. Schuster. A Computer Model of Evolutionary Optimization. *Biophysical Chemistry*, **26**, 123–147 (1987)

Manuals

- P. Boutillier, J. Feret, J. Krivine and W. Fontana. The Kappa Language and Kappa Tools. kappalanguage.org (2018—present)

Essays and Commentary

- W. Fontana and P. Honegger. The Wheels of Chemistry. (Book chapter) *arXiv:2209.04731* (2022)
- M. D. Laubichler, G. B. Muller, W. Fontana and G. P. Wagner. Sacrificing Dialogue for Politics? *Science*, **309**, 1324 (2005)
- W. Fontana, J. Karkanias, L.G. Meredith, and M. Radestock. Lab-to-lab connectivity and semantics in the life sciences. Position Paper for the W3C workshop on "Semantic Web for Life Sciences". 27-28 October 2004, Cambridge, MA. Published online (2004)
- 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)
- W. Fontana. Book Review: "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

- Involved in funding and coordinating the development of the Kappa platform, a graph-rewrite language with simulation and analysis tools for modeling complex interaction systems of abstract protein agents. (Developers and coordinators include Pierre Boutillier, Jean Krivine, Jérôme Feret, Russ Harmer, and Vincent Danos.)

  www.kappalanguage.org
- The first generation of the *Vienna RNA Package* (www.tbi.univie.ac.at/RNA) with I.L. Hofacker, P.F. Stadler, L.S. Bonhoeffer, M. Tacker and P. Schuster.

EXTRACURRICULAR ACTIVITIES

1996 — 2010	Paraglider pilot (USA P4, Austria P4)
2001 — 2005	Private pilot (airplane single-engine land, VFR)