Computación natural con redes de procesadores evolutivos, y sus relaciones con las redes de neuronas y con los autómatas biomoleculares de Watson-Crick TIC2003-09319-C03

Carlos Martín Vide * Universidad Rovira i Virgili

José María Sempere Luna Universidad Politécnica de Valencia

Luis Fernando Mingo López Universidad Politécnica de Madrid

Abstract

The project aims at exploiting networks of evolutionary processors as a new bioinspired computational architecture and at exploring their connection with neural networks and Watson-Crick biomolecular automata. Issues of computational power, universality, complexity and applicability are addressed. The project is basically theoretical and mostly of a mathematical character, and intends to develop the field in close contact with other biomolecular unconventional models of computing.

Keywords: network of evolutionary processors, finite automaton, neural network, biomolecular computing, unconventional computing, theoretical computer science, formal language theory

1 Aims

1.1 Intended aims (URV = Rovira i Virgili University)

- 1. Consider systematically the string operations suggested by biological processes, devise computing (language generating) mechanisms based on them, and investigate their power and properties.
- 2. Simplify the networks of evolutionary processors (NEPs) defined so far and improve the existing results.
- 3. Examine the optimality of universality results in terms of the number of processors. Which are the size and the properties of sub-universal families of sets of vectors of natural numbers and of languages?

^{*}Email: cmv@astor.urv.es

- 4. What is the descriptional complexity of these networks with respect to different criteria similar to those investigated for many generative devices in formal language theory? Such criteria might be statical ones like the number of evolution rules, the size of the initial population, or dynamical ones like the number of evolutionary events.
- 5. Examine systematically the possibilities of solving NP-complete problems in polynomial/linear time and with polynomially bounded resources. Consider sets of NP-complete problems which can be uniformly treated in this framework.
- 6. It seems natural to investigate the effect of processing different objects, not only strings: trees, graphs, circular strings, pictural words. Consider networks with an enriched structure, maybe without good computability properties, but (hopefully) modeling the functioning of a biological system in a way relevant for biochemistry.
- 7. Examine the linguistic interpretation and relevance of the many operations with strings suggested by genome processes, and examine the relevance of NEPs for modelling the brain linguistic behaviour.

1.2 Intended aims (UPV = Technical University of Valencia)

- 1. Propose models of biomolecular finite automata as an alternative to present-day models. Refine and consider variants for present-day models.
- 2. Characterize computationally and from the viewpoint of complexity the models in 1, with a special emphasis on descriptional complexity aspects.
- 3. Study inductive inference aspects of biomolecular finite automata and of some languages based on operations with DNA (duplication, cross-over, splicing, etc.).
- 4. Develop synthetic and real test banks for the inductive inference of the models.
- 5. Elaborate biomolecular sequence processing tools based on finite automata: simulation of models and processing of DNA and proteomic sequences (search of genes, search of contexts, 'in silico' simulation of DNA micro-arrays, etc.).
- 6. Integrate biomolecular finite automata models into NEPs: dynamic extension of NEPs, by means of varying filters and evolutionary rules according to an inductive criterion.

1.3 Intended aims (UPM = Technical University of Madrid)

- 1. Simulate distributively a neural network.
- 2. Describe the similarities between neural networks and NEPs.
- 3. Formally define NEPs which involve learning.
- 4. Distributively implement NEPs.

2 Level of achieved success

2.1 Achieved aims (URV)

- 1. This goal was achieved by the results described in the third item of the next section. The operations considered in [1, 2, 12, 13, 24, 35, 52, 53] were splicing, translocation, duplication and Watson-Crick superposition. Furthermore, we considered two biological phenomena like cell-differentiation and gene shuffling. [12] is continued in [88], where duplication codes are investigated.
- 2. The papers [22, 47] are contributions to this objective. Some results are quite important, but there are still some problems which require a deeper investigation. A new direction was opened in [47], where so-called homogeneous and free NEPs were introduced. This direction seems very attractive offering a lot of possibilities and posing hard problems.
- 3. The paper [33] establishes the first result in this area. A more detailed discussion was started in [77] and [81]. The same program is to be applied to networks of splicing processors in [84].
- 4. Contributions [11, 10, 21, 41, 45] contribute to accomplish this objective. Some other papers like [77, 84] are in progress.
- 5. New solutions to NP-complete problems are presented in [22, 27]. Furthermore, in [22] one discusses the mathematical basis for a systematic study of NEPs as solving problem mechanisms. By the new characterizations in [77, 81, 84], we hope to shed more light on this topic.
- 6. We identified serious difficulties in our attempt to extend some of the results presented above to structures other than strings, especially tree-like structures. However, some work in progress seems to represent a promising starting point towards this direction.
- 7. The paper [23] represents a first step in this direction. Actually, a possible implementation is being undergone. Other computer scientists are working on different implementations. Several researchers and students from Spain, France, Germany, Hungary, India, Romania, etc. are working on different aspects offered by this new biologically inspired computational model.

2.2 Scientific-technical results (URV)

The results obtained so far by the members of the team can be divided into four main directions of research, all of them appearing as objectives and goals in the planned work programme:

1. Computational aspects of NEPs: power, computational complexity, descriptional complexity. Several computational aspects of NEPs were studied in [10, 21, 27, 33, 41], and it was shown that these mechanisms are able to solve hard problems which are intractable on usual computers. These mechanisms can either generate languages, accept languages or solve mathematical problems.

In [10], one shows that these devices viewed as language generators are computationally complete, that is they have the same computational power as a Turing machine, which

is the classical computing model widely investigated in theoretical computer science.

The same result holds for accepting NEPs ([21]). The proof presented there allowed us to obtain deeper results. First, a new characterization of the famous class NP: namely, this class is exactly the class of languages accepted by NEPs in polynomial time. It is worth mentioning that such results are quite rare in the literature.

Second, we propose in [33] a construction of an accepting NEP which behaves as a universal device in the class of all these devices. The construction is mainly based on the simulation of a Turing machine, as reported in [21], which can, in its turn, simulate any accepting NEP, and then an accepting NEP which simulates this Turing machine. It is clear that this approach can be applied to other bio-inspired computing models which are computationally complete.

On the other hand, we continue the research line started in some previous papers proposing solutions, having a linear number of computational steps, to other NP-complete problems based on NEPs as solving problem devices: 3-CNF-SAT and the Hamiltonian Path Problem in [27]. [41] is a survey discussing the most recent results and proposing some directions for further research.

The descriptional complexity of NEPs was studied in [11, 45, 47]. The measures investigated in these papers were the size, number of rules, and number of symbols. The results are rather unexpected, since NEPs with limited (polynomially bounded) resources are able to solve hard problems. Thus, [11] gives a rather complete picture of the size (number of nodes) of the NEPs generating or accepting some well-known classes of languages. One proves ([11]) that in all cases the underlying structure does not depend on a given language (this is the common case for many other bio-inspired computational models). [47] is a first step in an investigation regarding homogeneous and free NEPs. This is an extremely simple variant of generating NEP shown to be a computationally complete model in [10]. Two simplifications are considered: all filters are completely removed such that words can freely navigate in the networks, and all evolutionary operations are applied uniformly. In our view, this variant seems most suitable for a biological implementation. A survey presenting the most important results concerning the descriptional complexity of NEPs is given in [45].

The NEP model has drawn the attention of other researchers so that it was considered one of the main topics of a special workshop of the European Conference on Artificial Intelligence in 2004. As well, it was the subject of a special session of the International Work-Conference on the Interplay between Natural and Artificial Computation in 2005.

2. Possible applications and implementations of NEPs. Networks with other type of bioinspired processors. In [22], we replace the evolutionary processors placed in the nodes of NEPs with splicing processors. Actually, we replace the point mutations associated with each node in the original NEPs with another operation widely mentioned in the Darwinian evolution: that of splicing. We present linear time solutions to two NP-complete problems, namely SAT and the Directed Hamiltonian Path Problem, based on accepting networks of splicing processors having all resources (size, number of rules and symbols) linearly bounded by the size of the given instance.

The paper [23] proposes a very simple implementation of NEPs for accepting and analysing linguistic structures with the shape NP V NP. The formalization takes advantage of

NEPs' features -modularity, specialization and parallelism- to develop a syntactic recognizer able to distinguish correct sentences working with lineal strings as input and lineal labeled structures as output.

3. Combinatorial and algorithmic properties of some formal operations inspired by the genome evolution. In [1], we propose a computational model for cell differentiation and answer several decidability questions. The work was published in a journal with a wide visibility in the biological community, being previously presented in a very selective conference dedicated to bioinformatics.

Another approach to the main topic is [52], where we define a new operation inspired by Watson-Crick complementarity and annealing of DNA sequences. This operation turned out to be very useful in a formal description of some DNA experiments previously reported in the literature.

One of the chromosome rearrangements which appears very often in the genome evolution is duplication. Viewed as a formal operation on strings, it is investigated in [12]. Despite that several problems remained unsolved, the case of uniformly bounded duplication was solved completely.

A new type of shuffle inspired from genetics is introduced in [53]. We extend the basic shuffle on words and languages, a well-known operation in theoretical computer science, by introducing three synchronized shuffles. These synchronized shuffles have some relevance to molecular biology, since they may be viewed as the formal representations of various kinds of gene linkage during genome shuffling. More precisely, each synchronized shuffle preserves the genetic backbone of the organisms, as well as the linked genes, by requiring the synchronization of some predefined genes while all other genes are arbitrarily shuffled.

Several formal language based approaches in biology are discussed in [2], which was published in a high standard biological journal.

The problem of computing distances between genomes, in spite of huge advances, is still far from being solved. We contributed to this area with the paper [13], where we proposed a new translocation distance and gave two algorithms for computing it: a polynomial one and an approximate one.

The classical definition of splicing (a formal model of recombination of DNA molecules induced by restriction enzymes) is reconsidered in [35], where we started from the premise that the results reported so far spurred research aimed at finding finite H systems, with a definition that is both conceptually simple and as biochemically realistic as possible, which are able to perform universal computations. In a certain way, the systems we proposed in this paper represent just what the theory of splicing has been looking for, namely finite splicing systems that are computationally complete. Moreover, we consider that the new definitions are quite natural and well-motivated extensions of the classical splicing operation.

4. Interrelationships with other parallel or distributed computing systems like grammar and automata systems. We have considered also the applicability of a rather mature theory, that of automata and grammar systems, to attack some proposed problems in our work

plan. This aspect was studied in several papers: [24, 30, 42, 50]. The paper [24] is a good example of how a contextual system could help in modelling a real biological phenomenon. It turned out that automata systems were more appropriate for such purposes than grammar systems.

2.3 Scientific-technical results (UPV)

- 1. We have obtained a representation theorem for Watson-Crick finite automata.
- 2. We have formalized classes of languages accepted by Watson-Crick finite automata.
- 3. We have studied the descriptional complexity of minimal Watson-Crick finite automata.
- 4. We have obtained inference algorithms for subclasses of regular and context-free languages.
- 5. We have introduced learning and covering techniques for cellular models with membranes.

2.4 Scientific-technical results (UPM)

- 1. We have formally defined neural networks with axo-axonic connections. Among the biological neural connections, one has to distinguish: axo-synaptic, axo-somatic and axo-axonic connections. Artificial neural networks are usually based on axo-synaptic connections. A neural network with axo-axonic connections has been modelled. Such networks are a superset of the set of synaptic connections and show universality properties.
- 2. We have proved the universality of neural networks with axo-axonic connections, on the basis of Funahashi and Sprecher theorems, which show the universality of multi-level perceptrons.
- 3. We have applied axo-axonic networks to market prediction and temporal series analysis.
- 4. We have started to formalize NEPs with filters at the connections in order to incorporate learning, in a way similar to self-organizing maps.
- 5. We have compared neural models and NEPs to conclude that the best architecture for the latter ones is similar to self-organizing maps in neural networks.

3 Indicators of results

3.1 Staff being trained

3.1.1 (URV)

The dissertations of the following students of our International PhD School in Formal Languages and Applications (having been awarded the 2003, 2004 and 2005 MEC Mención de Calidad) have some connection with NEPs:

Artiom Alhazov: URV fellow, dissertation expected in 2006

Madalina Barbaiani: GENCAT fellow, dissertation expected in 2008

Leonor Becerra Bonache: MEC fellow, dissertation expected in 2006 Cristina Bibire: MEC fellow, dissertation expected in 2008 Liliana Cojocaru: MAEC-AECI fellow, dissertation expected in 2006 Carlos Cruz Reyes: GENCAT fellow, dissertation expected in 2008 Adrian Horia Dediu: URV fellow, dissertation expected in 2006 Szilárd Zsolt Fazekas: MEC fellow, dissertation expected in 2008 Adela Grando: MEC fellow, dissertation expected in 2007 Mihai Ionescu: MEC fellow, dissertation expected in 2008 Peter Leupold: MEC fellow, dissertation expected in 2006 Guangwu Liu: GENCAT fellow, dissertation expected in 2008 Remco Loos: MEC fellow, dissertation expected in 2007 Gabriela Martín: URV fellow, dissertation expected in 2007 Tsetsegkhand Namsrai: GENCAT fellow, dissertation expected in 2007 Anthonath Roslin Sagaya Mary: MAEC-AECI fellow, dissertation expected in 2008

3.1.2 (UPV)

Gloria Álvarez: UPV fellow, near DEA defense Marcelino Campos: UPV fellow, 1st year PhD student Piedad Peris: UPV fellow, 1st year PhD student

3.1.3 (UPM)

A new research group on natural computing has been created where three lecturers at the Technical School of Computer Science are starting to work for their dissertation on NEPs and their hardware implementation.

3.2 Publications (URV + UPV + UPM)

Note: The authors who are members of the research teams are written in bold.

3.2.1 Papers in refereed journals

- I. Ardelean, M. Gheorghe, C. Martín-Vide & V. Mitrana (2004), A Computational Model for Cell Differentiation, BioSystems, 76(1-3): 169-176.
- M. Gheorghe, V. Mitrana (2004), A Formal Language Based Approach in Biology, Comparative and Functional Genomics, 5: 91-94.
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- 11. J. Castellanos, P. Leupold, V. Mitrana (2005), On the Size Complexity of Hybrid Networks of Evolutionary Processors, Theoretical Computer Science, 330(2): 205-220.
- P. Leupold, C. Martín-Vide & V. Mitrana (2005), Uniformly Bounded Duplication Languages, Discrete Applied Mathematics, 146: 301-310.

3.2.2 Papers in LNCS volumes

- C. Martín-Vide & V. Mitrana (2004), A New Uniform Translocation Distance, in A. Fred, T. Caelli, R.P.W. Duin, A. Campilho & D. de Ridder, eds., Structural, Syntactic, and Statistical Pattern Recognition, Lecture Notes in Computer Science 3138: 279-286. Springer, Berlin.
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- A. Alhazov & M. Cavaliere (2004), Computing by Observing Bio-systems: The Case of Sticker Systems, in C. Ferretti, G. Mauri & C. Zandron, eds., DNA Computing, Lecture Notes in Computer Science 3384: 1-13. Springer, Berlin.
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- 17. P. Leupold, V. Mitrana & J.M. Sempere (2004), Formal Languages Arising from Gene Repeated Duplication, in N. Jonoska, G. Paun & G. Rozenberg, eds., Aspects of Molecular Computing: Essays Dedicated to Tom Head on the Occasion of His 70th Birthday, Lecture Notes in Computer Science 2950: 297-308. Springer, Berlin.

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- 19. L. Kari, C. Martín-Vide & A. Paun (2004), On the Universality of P Systems with Minimal Symport/Antiport Rules, in N. Jonoska, G. Paun & G. Rozenberg, eds., Aspects of Molecular Computing: Essays Dedicated to Tom Head on the Occasion of His 70th Birthday, Lecture Notes in Computer Science 2950: 254-265. Springer, Berlin.
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3.2.3 Papers in international conference proceedings

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- L.F. Mingo, J. Castellanos & F. Arroyo (2005), Time Series Analysis with Axo-Axonic Connections in Neural Networks, in Proceedings of the 2nd International Conference on Information Technology: 246-254.

3.2.4 Book chapters

- 37. C. Martín-Vide & G. Paun (2004), Language Generating by means of Membrane Systems, in G. Paun, G. Rozenberg & A. Salomaa, eds., Current Trends in Theoretical Computer Science: The Challenge of the New Century, vol. II: Formal Models and Semantics: 599-611. World Scientific, Singapore.
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- C. Martín-Vide & V. Mitrana (2005), Networks of Evolutionary Processors: Results and Perspectives, in M. Gheorghe, ed., Molecular Computational Models: Unconventional Approaches: 78-114. Idea Group, Hershey, PA.

3.2.5 Accepted papers in press

- 42. M.A. Grando & V. Mitrana, A Possible Connection between Two Theories: Grammar Systems and Concurrent Programming, Fundamenta Informaticae.
- 43. F. Manea, C. Martín-Vide & V. Mitrana, A Universal Accepting Hybrid Network of Evolutionary Processors, Electronic Notes in Theoretical Computer Science.
- 44. G. Bel-Enguix & M.D. Jiménez-López, Computing Dialogues with Membranes, Electronic Notes in Theoretical Computer Science.
- 45. C. Martín-Vide & V. Mitrana, Descriptional and Computational Aspects of Generating and Accepting Hybrid Networks of Evolutionary Processors, Grammars.
- 46. G. Bel-Enguix & M.D. Jiménez-López, Dynamic Meaning Membrane Systems: An Application to the Description of Semantic Change, Fundamenta Informaticae.
- J. Dassow, C. Martín-Vide & V. Mitrana, Free Generating Hybrid Networks of Evolutionary Processors, in Essays in Honour of Prof. Rani Siromoney. World Scientific, Singapore.
- 48. K.S. Dersanambika, K. Krithivasan, C. Martín-Vide & K.G. Subramanian, Local and Recognizable Hexagonal Picture Languages, International Journal of Pattern Recognition and Artificial Intelligence.
- 49. P. Dömösi, C. Martín-Vide & A. Mateescu, On Polyslender Context-Free Languages, Publicationes Mathematicae Debrecen.
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- 51. R. Gramatovici & C. Martín-Vide, Sorted Dependency Insertion Grammars, Theoretical Computer Science.
- P. Bottoni, A. Labella, V. Manca & V. Mitrana, Superposition Based on Watson-Cricklike Complementarity, Theory of Computing Systems.
- 53. M.H. ter Beek, C. Martín-Vide & V. Mitrana, Synchronized Shuffles, Theoretical Computer Science.

3.2.6 Other publications less directly related to the subject of the research project: refereed journals

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- 65. P. Dömösi, C. Martín-Vide & V. Mitrana (2004), Remarks on Sublanguages Consisting of Primitive Words of Slender Regular and Context-Free Languages, in J. Karhumäki, H. Maurer, G. Paun & G. Rozenberg, eds., Theory is Forever: Essays Dedicated to Arto Salomaa on the Occasion of His 70th Birthday, Lecture Notes in Computer Science 3113: 60-67. Springer, Berlin.

- 66. A. Cano, J. Ruiz & P. García (2004), Running FCRPNI in Efficient Time for Piecewise and Right Piecewise Testable Languages, in G. Paliouras & Y. Sakakibara, eds., Grammatical Inference: Algorithms and Applications, Lecture Notes in Computer Science 3264: 275-276. Springer, Berlin.
- 67. I. Perea & D. López (2004), Syntactic Modeling and Recognition of Document Images, in A. Fred, T. Caelli, R.P.W. Duin, A. Campilho & D. de Ridder, eds., Structural, Syntactic, and Statistical Pattern Recognition, Lecture Notes in Computer Science 3138: 416-424. Springer, Berlin.

3.2.8 Other publications less directly related to the subject of the research project: international conference proceedings

- L. Cojocaru & C. Martín-Vide (2004), Parallel Communicating Pushdown Transducer Systems, in J.M. Sempere & D. López, eds., Proceedings of the ECAI 2004 Workshop on Symbolic Networks: 41-56. Universidad Politécnica de Valencia, Valencia.
- C. Martín-Vide & V. Mitrana (2005), Further Properties of Path-Controlled Grammars, in Proceedings of Formal Grammar/Mathematics of Language, FG-MOL10: 139-150. CSLI, Stanford, CA.
- C. Martín-Vide & V. Mitrana (2005), Remarks on Arbitrary Multiple Pattern Interpretations, in Z. Ésik & Z. Fülöp, eds., Automata and Formal Languages: 200-212. University of Szeged, Szeged.

3.2.9 Other publications less directly related to the subject of the research project: book chapters

- 71. C. Martín-Vide & A. Mateescu (2004), GSMs and Contexts, in G. Paun, G. Rozenberg & A. Salomaa, eds., Current Trends in Theoretical Computer Science: The Challenge of the New Century, vol. II: Formal Models and Semantics: 581-587. World Scientific, Singapore.
- 72. P.H. Chandra, K.G. Subramanian, C. Martín-Vide, D.L. Van & P.S.P. Wang (2005), Parallel Contextual Array Grammars with Trajectories, in C.H. Chen & P.S.P. Wang, eds., Handbook of Pattern Recognition and Computer Vision: 55-70. World Scientific, Singapore.

3.2.10 Other publications less directly related to the subject of the research project: books

- 73. C. Martín-Vide, V. Mitrana & G. Paun, eds. (2004), Formal Languages and Applications. Springer, Berlin.
- 74. C. Martín-Vide, G. Mauri, G. Paun, G. Rozenberg & A. Salomaa, eds. (2004), Membrane Computing, Lecture Notes in Computer Science 2933. Springer, Berlin.

3.2.11 Papers in progress

- 75. L.B. Goncharova, Y. Jacques, C. Martín-Vide, A.O. Tarakanov & J.I. Timmis, Biomolecular Immune-Computer: Theoretical Basis and Experimental Simulator.
- P.H. Chandra, C. Martín-Vide, K.G. Subramanian, D.L. Van & P.S.P. Wang, Contextual Grammars for Pictorial Pattern Generation.
- 77. F. Manea, C. Martín-Vide & V. Mitrana, Descriptional Complexity of Some Universal Accepting Networks of Evolutionary Processors.
- 78. L. Pan & C. Martín-Vide, Further Remark on P Systems with Active Membranes and Two Polarizations.
- 79. E. Csuhaj-Varjú & V. Mitrana, Further Remarks on CD Pushdown Automata Systems.
- 80. J.D. Emerald, C. Martín-Vide, K.G. Subramanian & D.G. Thomas, Grammatical Inference of Some Subclasses of Contextual Grammars.
- 81. F. Manea, M. Margenstern & V. Mitrana, M.J. Pérez-Jiménez: New Characterizations of NP and PSPACE.
- H. Bordihn, H. Fernau, M. Holzer, V. Manca & C. Martín-Vide, On Iterated Sequential Transducers.
- 83. A. Atanasiu, C. Martín-Vide & K.G. Subramanian, On Regular Array Grammars.
- 84. F. Manea, C. Martín-Vide & V. Mitrana, On the Complexity of Accepting Networks of Splicing Processors.
- 85. A. Alhazov, C. Martín-Vide & Y. Rogozhin, On the Number of Nodes in Universal Networks of Evolutionary Processors.
- 86. L. Pan & C. Martín-Vide, P Systems with Active Membranes, Two Polarizations, and Restrictions of Rules.
- 87. R. Gramatovici, C. Martín-Vide & V. Mitrana, Some Remarks on Partially Blind One-Way Multicounter Machines.
- 88. P. Leupold & V. Mitrana, Uniformly Bounded Duplication Codes.

3.3 Technology transfer (UPM)

In the field of neural networks, joint implementation work is being done with the Russian Academy of Sciences under the INTAS scheme. The software will be available in Spanish, English and Russian. A distributed implementation of that software is being considered as well. Its commercialization or free circulation among public institutions and private companies can come after its applications have been exhibited in international conferences.

In the field of NEPs, a software implementation will be made available with the same purpose. The hardware implementation can be considered too, but likely will have to wait until a future research project will be carried out.

3.4 Collaboration with national and international groups (URV)

Intensive teaching (through lecturing participation in the International PhD School in Formal Languages and Applications) and research collaborations (in all the projects of the research group, including NEPs) exist with the following institutes:

- Austria: Department of Discrete Mathematics and Geometry, **Technical University of Vienna** (W. Kuich)
- Canada: Department of Computer Science, **Carleton University** (J. Oommen); Department of Mathematics and Statistics, **University of Ottawa** (D. Sankoff); School of Computing, **Queen's University** (K. Salomaa); Department of Computer Science, University of Waterloo (J. Brzozowski) Department of Computer Science, **University of Western Ontario** (L. Ilie, S. Yu)
- Czech Republic: Department of Computer Science, Masaryk University Brno (J. Gruska); Department of Computer Science, Silesian University (J. Kelemen)
- Finland: Research Center, Nokia (V. Niemi); Department of Mathematics, University of Turku (T. Harju, J. Karhumäki, J. Kari, M. Steinby)
- France: Laboratory of Algorithmic Informatics: Foundations and Applications, University Paris 7 (C. Choffrut, J.-É. Pin); Department of Computer Science, University of Marne-la-Vallée (M. Crochemore); Department of Computer Science, University of Saint-Étienne (C. de la Higuera)
- Germany: Department of Mathematics and Computer Science, University of Bremen (H.-J. Kreowski); Department of Computer Science, University of Dortmund (C. Moraga); Department of Computer Science, Technical University of Dresden (F. Baader); Department of Computer Science, University of Frankfurt (D. Wotschke); Department of Mathematics, University of Freiburg (J. Flum); Department of Computer Science, University of Hamburg (M. Kudlek); Department of Mathematics and Informatics, University of Kassel (F. Otto); Department of Computer Science, University of Magdeburg (J. Dassow); Department of Computer Science, Technical University of Munich (M. Holzer); Department of Computer Science, University of Moniter Science, University of Science, University of Potsdam (H. Bordihn); Department of Computer Science, University of Science, University of Science)
- Hungary: Computer and Automation Research Institute, Hungarian Academy of Sciences (E. Csuhaj-Varjú); Department of Computer Science, University of Szeged (Z. Fülöp)
- India: Department of Mathematics, Chennai Mathematical Institute (R. Siromoney)
- Israel: Department of Computer Science, University of Haifa (S. Wintner)
- Italy: Department of Information Engineering, University of Padua (G. Satta)
- Japan: Department of Computer Science, **University of Electro-Communications** (S. Kobayashi); Department of Information Engineering, **Hiroshima University** (K. Morita); Department of Mathematics, **Kyoto Sangyo University** (M. Ito)

- The Netherlands: Department of Humanities Computing, **University of Groningen** (M.J. Nederhof); Leiden Institute of Advanced Computer Science, **Leiden University** (H.J. Hoogeboom, J. Kleijn); Institute of Linguistics, **Utrecht University** (M. Moortgat)
- Spain: Department of Computer Science, **Pompeu Fabra University** (R. Baeza-Yates)
- Taiwan: Department of Computer Science, National Taiwan University (H.-C. Yen)
- United Kingdom: Department of Computer Science, **University of Hertfordshire** (H. Fernau)
- United States: Department of Mathematical Sciences, **Binghamton University** (F. Guzmán, T. Head); Department of Computer Science, **University of California Santa Barbara** (O. Ibarra); Department of Computer Science, **Earlham College** (J. Rogers); Courant Institute of Mathematical Sciences, **New York University** (M. Mohri); Department of Computer Science, **University of Rochester** (M. Ogihara); Department of Computer Sciences, **University of Texas Austin** (R. Miikkulainen)

3.5 Joint activities organized

The following two events have been co-organized:

- Workshop on Symbolic Networks, in the framework of the European Conference on Artificial Intelligence (ECAI 2004, Valencia, 22 August 2004)
- Pre-Organized Session on Computing with Networks of Evolutionary Processors, in the framework of the 1st International Work-Conference on the Interplay between Natural and Artificial Computation (IWINAC-2005, Las Palmas de Gran Canaria, 15-18 June 2005)

Funding has been recently applied for from the European Science Foundation in order to organize an international symposium on NEPs in Tarragona in March 2006.

3.6 International projects

3.6.1 (URV)

In the field of the project, the following European Union projects are being developed at present:

- 2 Marie Curie MERG (reintegration) grants.
- 1 Marie Curie EIF (intra-European) grant.

Also, an application to the scheme NEST (New and Emerging Sciences and Technologies) on inmune computing is currently under refereeing.

3.6.2 (UPV)

The group has become a member of the European Molecular Computing Consortium.

3.6.3 (UPM)

- INTAS. The following projects are being developed at present: INTAS INNO 182 (collaborating researchers), INTAS YSF 03-55-1696 (principal investigators), INTAS 2000-0626 (collaborating researchers). The topic of these projects is neural networks, data mining and their implementations.
- IST (Information Sciences and Technologies): IST-2001-32008 is being carried out on molecular computing (DNA and membranes). A new project has been recently applied for.

3.7 Summary of journals (+ LNCS) which the researchers of the project published in

Acta Informatica **BioSystems** Bulletin of the EATCS (2) Comparative and Functional Genomics Discrete Applied Mathematics Electronic Notes in Theoretical Computer Science (2) Fundamenta Informaticae (4) Grammars (3) IEEE Transactions on Systems, Man and Cybernetics - Part B: Cybernetics International Journal of Computer Mathematics International Journal of Pattern Recognition and Artificial Intelligence International Journal on Information Theories and Applications Journal of Universal Computer Science Lecture Notes in Computer Science (23) Publicationes Mathematicae Debrecen RAIRO - Theoretical Informatics and Applications (2) Theoretical Computer Science (6) Theory of Computing Systems WSEAS Transactions on Business and Economics

3.8 Summary of conferences which the researchers of the project contributed to

- Second Brainstorming Week on Membrane Computing (Sevilla, Spain, 2-7 February 2004)
 [URV, UPV]
- 10th International Meeting on DNA Computing (DNA 10, Milan, Italy, 7-10 June 2004)
 [URV]
- 5th Workshop on Membrane Computing (WMC 2004, Milan, Italy, 14-16 June 2004)
 [URV, UPV]
- Second International Conference on Information Research, Applications and Education (i.tech 2004, Varna, Bulgaria, 14-24 June 2004) [UPM]

- Grammar Systems Week 2004 (Budapest, 5-9 July 2004) [URV]
- Joint IAPR International Workshops on Structural and Syntactical Pattern Recognition (SSPR 2004) and Statistical Pattern Recognition (SPR 2004) (Lisboa, Portugal, 18-20 August 2004) [**URV**, **UPV**]
- ECAI 2004 Workshop on Symbolic Networks (Valencia, Spain, 22 August 2004) [URV]
- 11th International Conference on Artificial Intelligence. Methodology, Systems, and Applications (AIMSA 2004, Varna, Bulgaria, 2-4 September 2004) [**URV**]
- International Conference on Machines, Computations and Universality (MCU'2004, St. Petersburg, Russia, 21-24 September 2004) [URV]
- 7th International Colloquium on Grammatical Inference (ICGI 2004, Athens, Greece, 11-13 October 2004) [UPV]
- 5th Annual Spanish Bioinformatics Conference (Barcelona, Spain, 29-30 November 2004)
 [UPV]
- Tenth International Workshop on Combinatorial Image Analysis (IWCIA 2004, Auckland, New Zealand, 1-3 December 2004) [URV]
- Third Brainstorming Week on Membrane Computing (Sevilla, Spain, 31 January 4 February 2005) [UPV]
- 2nd International Conference on Information Technology (ICIT 2005, Amman, Jordan, 3-5 May 2005) [UPM]
- Turing Days '05: DNA Computing (Istanbul, Turkey, 13-14 May 2005) [URV]
- 11th International Conference on Automata and Formal Languages (AFL'05, Dobogókö, Hungary, 17-20 May 2005) [URV]
- 11th International Meeting on DNA Computing (DNA 11, London, Canada, 6-9 June 2005) [URV]
- 8th International Work-Conference on Artificial Neural Networks: Computational Intelligence and Bioinspired Systems (IWANN2005, Vilanova i la Geltrú, Spain 8-10 June 2005) [URV]
- First Conference on Computability in Europe: New Computational Paradigms (CiE 2005, Amsterdam, The Netherlands, 8-12 June 2005) [URV]
- Pre-Organized Session on Computing with Networks of Evolutionary Processors, 1st International Work-Conference on the Interplay between Natural and Artificial Computation (IWINAC-2005, Las Palmas de Gran Canaria, Spain, 15-18 June 2005) [URV]
- 10th International Conference on Implementation and Application of Automata (CIAA 2005, Nice, France, June 27-29 2005) [UPV]

- Third International Conference on Information Research, Applications and Education (i.tech 2005, Varna, Bulgaria, 27-30 June 2005) [UPM]
- Fifth International and Interdisciplinary Conference on Modeling and Using Context (CONTEXT 05, Paris, France, 5-8 July 2005) [URV]
- First International Workshop on Developments in Computational Models (DCM, Lisboa, Portugal, 10 July 2005) [URV]
- 6th Workshop on Membrane Computing (WMC 2005, Vienna, Austria, 18-21 July 2005)
 [URV, UPV]
- 3rd International Workshop on Logic and Communication in Multi-Agent Systems (LCMAS 2005), Nineteenth International Joint Conference on Artificial Intelligence (IJCAI-2005, Edinburgh, United Kingdom, 1 August 2005) [URV]
- 10th Conference on Formal Grammar and 9th Meeting on Mathematics of Language (FG-MOL 2005, Edinburgh, United Kingdom, 5-7 August 2005) [URV]
- 4th International Conference on Artificial Immune Systems (ICARIS-2005, Banff, Canada, 14-17 August 2005) [URV]
- VIIIth European Conference on Artificial Life (ECAL 2005, Canterbury, United Kingdom, 5-9 September 2005) [URV]
- International Conference on Artificial Neural Networks (ICANN 2005, Warsaw, Poland, 11-15 September 2005) [URV]
- First Conference on Algebraic Informatics (Thessaloniki, Greece, 20-23 October 2005) [URV]