

Curriculum Vitae

BLERINA SINAIMERI

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Citizenship: Albanian
Date of Birth: 08/07/1981
Place of Birth: Tirana, Albania
Date of CV: May 2018

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Research interests

Computational Biology, Graph Algorithms, Combinatorics and its application to Theoretical Computer Science.

Education/Experience

oct.2015 - **Researcher**, (CR) INRIA (Erable Team).
jan. 2018 - mar. 2018 - **Visiting Researcher**, Sapienza University of Rome, CS Department.
feb. 2012 – sept. 2015 **Post-doc**, INRIA (Bamboo Team).
dec. 2009 – dec. 2011 **Post-doc**, Sapienza University of Rome, CS Department.
feb. 2010 **Ph.D. in Computer Science**, Sapienza University of Rome.
Advisor: J. Körner.
Thesis: “Structures of Diversity”.
jul. 2006 **Laurea degree in Computer Science**, (with Honors), Sapienza University.

Awards

sept. 2010 Winner of the **2010 Italian Chapter EATCS Award** for the best Ph.D. thesis in theoretical computer science.
may 2009 **Best PhD Student paper of the year**, CS Department, Sapienza University of Rome.

Publications and Preprints

Except for the cases in bold, the authors are in alphabetical order. In the latter case, the first authors are indicated by a “*”.

Peer-reviewed journals

1. L. Urbini, B. Sinaimeri, C. Matias and M.-F. Sagot, Exploring the Robustness of the Parsimonious Reconciliation Method in Host-Symbiont Cophylogeny, **IEEE/ACM Transactions on Computational Biology and Bioinformatics**, (to appear).
2. K. Huber, V. Moulton, M.-F. Sagot, B. Sinaimeri: Geometric medians in reconciliation spaces of phylogenetic trees, **Information Processing Letters**, 136, 96-101.

3. L. Lima, B. Sinaimeri, G. Sacomoto, H. Lopez-Maestre, C. Marchet, V. Miele, M.-F. Sagot, V. Lacroix: Playing hide and seek with repeats in local and global de novo transcriptome assembly of short RNA-seq reads. **Algorithms for Molecular Biology** 12(1): 2:1-2:19, 2017.
4. T. Calamoneri, B. Sinaimeri, Pairwise Compatibility Graphs: A Survey. **SIAM Review** 58(3): 445–460, 2016.
5. C. Baudet*, B. Donati*, **B. Sinaimeri***, P. Crescenzi, C. Gautier, C. Matias and M.-F. Sagot, Co-phylogeny Reconstruction via an Approximate Bayesian Computation, **Systematic Biology** 64 (3), 416–431, 2015.
6. B. Donati, C. Baudet, **B. Sinaimeri**, P. Crescenzi and M.-F. Sagot, EUCALYPT: Efficient tree reconciliation enumerator, **Algorithms for Molecular Biology** 10(3), 2015.
7. T. Calamoneri, A. Frangioni and B. Sinaimeri, Pairwise Compatibility Graphs of Caterpillars, **The Computer Journal** 57(11), 1616–1623, 2014.
8. T. Calamoneri, R. Petreschi and B. Sinaimeri, Pairwise compatibility property of some superclasses of threshold graphs, **Discrete Mathematics, Algorithms and Applications (DMAA)**, 5(2), 2013.
9. T. Calamoneri, E. Montefusco, R. Petreschi and B. Sinaimeri, Exploring Pairwise Compatibility graphs, **Theoretical Computer Science** 468: 23–36, 2013.
10. T. Calamoneri and B. Sinaimeri, L(2,1)-labeling of oriented planar graphs, **Discrete Applied Mathematics** 161(12): 1719–1725, 2013.
11. T. Calamoneri, D. Frascaria and B. Sinaimeri, All graphs with at most seven vertices are Pairwise Compatibility Graphs, **The Computer Journal** 56(7): 882–886, 2013.
12. A. Monti and B. Sinaimeri, Rainbow Graph Splitting, **Theoretical Computer Science** 412(39): 5315-5324, 2011.
13. Z. Füredi, I. Kantor, A. Monti and B. Sinaimeri, On Reverse-Free Codes and Permutations, **SIAM Journal on Discrete Mathematics** 24(3): 964–978, 2010.
14. J. Körner, G. Simonyi and B. Sinaimeri, On types of growth for graph-different permutations, **Journal of Combinatorial Theory Series A** 116: 713–723, 2009.
15. J. Körner and B. Sinaimeri, On cancellative set families, **Combinatorics, Probability and Computing**, 16(4): 767–773, 2007.

Peer-reviewed conferences with proceedings

1. T. Calamoneri, M. Gastaldello, A. Mary, M.-F. Sago, B. Sinaimeri, On Maximal Chain Subgraphs and Covers of Bipartite Graphs, 27th International Workshop on Combinatorial Algorithms **IWOCA 2016**, Helsinki, Finland, August 17–19, 2016.
2. L. Urbini, B. Sinaimeri, C. Matias and M.-F. Sagot, Robustness of the Parsimonious Reconciliation Method in Cophylogeny, Algorithms for Computational Biology, Third International Conference, **AICoB 2016**, 119–130.
3. L. Bulteau, G. Sacomoto and B. Sinaimeri, Computing an Evolutionary Ordering is Hard, VIII Latin-American Algorithms, Graphs and Optimization Symposium (**LAGOS 2015**), Brazil.

4. G. Sacomoto, **B. Sinaimeri**, C. Marchet, V. Miele, M-F. Sagot and V. Lacroix, Navigating in a sea of repeats in RNA-seq without drowning, 14th Workshop on Algorithms in Bioinformatics (**WABI 2014**), Wroclaw, Poland.
5. Tiziana Calamoneri, Blerina Sinaimeri: Relating threshold tolerance graphs to other graph classes ,16th Italian Conference on Theoretical Computer Science (**ICTCS 2014**), Perugia, Italy 73-79, 2014.
6. T. Calamoneri, R. Petreschi and B. Sinaimeri, On relaxing the constraints in Pairwise Compatibility graphs, In: Md. S. Rahman and S.-i. Nakano (Eds.), (**WALCOM 2012**), LNCS vol. 7157,124–135, Springer, Berlin (2012).
7. Z. Füredi, I. Kantor, A. Monti and B. Sinaimeri, On Reverse-Free Codes and Permutations, Electronic Notes in Discrete Mathematics vol. 38, 383–387, (**EuroComb 2011**) Budapest, (2011) (extended abstract).

Peer-reviewed conferences without proceedings

1. C. Baudet*, B. Donati*, B. Sinaimeri*, L. Urbini*, P. Crescenzi, C. Gautier, C. Matias and M.-F. Sagot, Understanding co-evolution through co-phylogeny methods, **Poster Session**, Ecological and molecular modelling of infections (**EMOTIONS 2014**), Lyon, France.
2. V. Lacroix, A. Julien-Laferrière, G. Sacomoto, M.-F. Sagot, B. Sinaimeri and A. Trindade, De novo identification of repeats in RNA-seq: a de Bruijn graph based approach, **Poster Session**, 13th Workshop on Algorithms in Bioinformatics (**WABI 2013**), Sophia Antipolis, France.
3. T. Calamoneri, R. Petreschi and B. Sinaimeri, On relaxing the constraints in Pairwise Compatibility graphs, accepted at Graph and Algorithms 2011 (**GA 2011**), Workshop colocated with ICALP 2011, Zürich, Switzerland.
4. T. Calamoneri and B. Sinaimeri, Labeling of oriented planar graphs, accepted at the 10-th Cologne-Twente Workshop on graphs and combinatorial optimization (**CTW2011**) 93–96, Frascati, Italy.
5. T. Calamoneri and B. Sinaimeri, L(2,1)-labeling of oriented planar graphs, accepted at the 12th Italian Conference on Theoretical Computer Science (**ICTCS 2010**), Camerino, Italy (short abstract).

Research Reports and Publications under Review

1. K. Huber, V. Moulton, M.-F. Sagot, B. Sinaimeri: Exploring and visualizing spaces of tree reconciliations (submitted).
2. T. Calamoneri, M. Gastaldello, A. Mary, M.-F. Sago, B. Sinaimeri, Enumerating Maximal Chain Subgraphs and Covers of Bipartite Graphs (submitted).
3. T. Calamoneri, A. Monti and B. Sinaimeri, Reconciling phylogenetic trees: extreme cases (submitted).
4. L. Urbini, B. Sinaimeri, C. Matias and M.-F. Sagot, AMOCOALA: Inferring event frequencies in a cophylogeny model with multiple association. (paper in preparation).
5. C. Baudet and A. Mary and M.-F. Sagot and B. Sinaimeri, A simpler model for the cophylogeny reconstruction problem (paper in preparation).

6. B. Sinaimeri, Structures of Diversity, 2010, Ph.D. thesis.

Invited talks

- dec. 2015 Dealing with repeats in RNA-seq: algorithmic challenges, Dipartimento di Ingegneria Civile e Ingegneria Informatica Università di Roma "Tor Vergata", Rome, Italy.
- dec. 2015 Algorithmic issues in cophylogenetic analysis, LIRMM, Montpellier, France.
- june 2015 Alternative splicing and RNA-seq data: the repeats' challenge, Computer Science Department Sapienza University of Rome, Rome, Italy.
- dec. 2014 Structures of Diversity – what's new?, Séminaire Graphes et structures discrètes, École normale supérieure de Lyon.
- dec. 2013 Combinatorial biology: a mathematical exploration of species interaction, scientific divulgation talk at the Computer Engineering Department of Epoka University, Tirana, Albania.
- nov. 2012 Rainbow Graph Splitting, graph theory seminar, LIMOS, Clermont-Ferrand, France.
- sep. 2010 Structures of Diversity, at the 12th Italian Conference on Theoretical Computer Science (ICTCS2010), Camerino, Italy.

Other Talks

- jun. 2017 Modélisation de la (co)-évolution des espèces , Journée Scientifique de la Faculté des Sciences et technologies de l'UCBL.
- jul. 2015 Cophylogeny Reconstruction via an Approximate Bayesian Computation, (**Jobim 2015**), Clermont-Ferrand, France.
- march 2015 On Phylogenetic Trees and Forests: Analysing Inter-specific Interactions in Ecological Networks Through Algorithmic Lens, LNCC Petropolis, Brazil.
- dec. 2014 Dealing with repeats in RNA-seq, Journées COMATEGE-SeqBio (**SeqBio2014**), Montpellier, France.
- set.2014 Navigating in a sea of repeats in RNA-seq without drowning, 14th Workshop on Algorithms in Bioinformatics (**WABI 2014**), Wroclaw, Poland.
- march 2014 Algorithmic issues in cophylogenetic analysis, WBA 2014 - Workshop in Bioinformatics and Algorithms, Institute of Mathematics and Statistics of the University of São Paulo-IME-USP.
- jul. 2014 Navigating in a sea of repeats in RNA-seq without drowning, ABS4NGS seminars, Lyon, France.
- apr. 2013 Combinatorial aspects of (co)-phylogenies, Centro de Modelamiento Matemático de la Universidad de Chile, Chile.
- dec. 2011 On relaxing the constraints in Pairwise Compatibility graphs, accepted at Graph and Algorithms 2011 (**GA 2011**), Workshop colocated with ICALP 2011, Zürich, Switzerland.
- jul. 2011 Labeling of oriented planar graphs, accepted at the 10-th Cologne-Twente Workshop on graphs and combinatorial optimization (**CTW2011**) 93–96, Frascati, Italy.
- sep. 2010 L(2,1)-labeling of oriented planar graphs, accepted at the 12th Italian Conference on Theoretical Computer Science (**ICTCS 2010**), Camerino, Italy.

Teaching

- 2018 Spring Teaching “*Advanced Algorithms*”, Master of “*Bioinformatique et Modélisation*” (4BIM), Institut National des Sciences Appliqués (INSA), Lyon, France - (8 HETD). The course covers graph traversals (BFS and DFS), greedy algorithms to find MST (Kruskal’s algorithm and Prim’s algorithm) and introduction on approximation algorithms.
- 2017 Fall Teaching “*Discrete Mathematics*”, Master of “*Bioinformatique et Modélisation*” (4BIM), Institut National des Sciences Appliqués (INSA), Lyon, France - (8 HETD). The course provides an introduction to graph theory and graph algorithms. It covers: Basic definitions in Graph Theory (directed and undirected graphs, basic terminology, paths and circuits, trees and their properties, rooted trees, spanning trees, etc.), Graph traversals (BFS and DFS), Shortest paths in weighted graphs (Dijkstra’s algorithm).
- 2017 Spring Teaching “*Advanced Algorithms*”, Master of “*Bioinformatique et Modélisation*” (4BIM), Institut National des Sciences Appliqués (INSA), Lyon, France - (8 HETD). The course provides an introduction to random graph models graph for analysing real networks. It covers: Basic definitions in Graph Theory (directed and undirected graphs, basic terminology, paths and circuits, trees and their properties, etc.), Erdős-Renyi model for generating random graphs, random generation of graphs with specified degree sequence (matching algorithm, switching algorithm).
- 2016 Fall Teaching “*Network Algorithms for Molecular Biology*”, Master of “*Informatique*” (M2), École Normale Supérieure de Lyon (ENS), Lyon, France - (8 HETD). The course aims to explore the algorithmic approach in analysing "complex systems" in biology, and to bring students near to the particular challenges of modeling living systems.
- 2016 Fall Teaching “*Discrete Mathematics*”, Master of “*Bioinformatique et Modélisation*” (4BIM), Institut National des Sciences Appliqués (INSA), Lyon, France - (8 HETD).
- 2016 Spring - Teaching Assistant, “*Biostatistiques/Bioinformatique*”, Licence 2, Dep. Biologie, Univ. Claude Bernard – Lyon 1, Lyon, France - (17h). The content of this course is a mix between mathematics, computer science and biology. It offers an introduction to the study of different characteristics of the result of sequencing a DNA fragment. I am responsible for the practice work in which the goal is to provide students with knowledge on the basic tools in such a biological context as well as on their application through the use of real datasets.
- 2015 Fall Teaching “*Discrete Mathematics*”, Master of “*Bioinformatique et Modélisation*” (4BIM), Institut National des Sciences Appliqués (INSA), Lyon, France - (8 HETD).
- 2015 Fall Teaching “*Network Algorithms for Molecular Biology*”, Master of “*Informatique*” (M2), École Normale Supérieure de Lyon (ENS), Lyon, France - (8 HETD).
- 2015 Spring - Teaching Assistant, “*Biostatistiques/Bioinformatique*”, Licence 2, Dep. Biologie, Univ. Claude Bernard – Lyon 1, Lyon, France - (17h).
- 2014 Fall Teaching “*Discrete Mathematics*”, Master of “*Bioinformatique et Modélisation*” (4BIM), Institut National des Sciences Appliqués (INSA), Lyon, France - (8 HETD).
- 2014 Fall Teaching “*Discrete Mathematics*”, Master 2, Université Lyon I, Lyon, France - (9 HETD).
- 2013 Fall Teaching “*Discrete Mathematics*”, Master of Bioinformatique et Modélisation (4BIM), Institut National des Sciences Appliqués (INSA), Lyon, France - (8 HETD).
- 2012 Fall Teaching “*Discrete Mathematics*”, Master of Bioinformatique et Modélisation (4BIM), Institut National des Sciences Appliqués (INSA), Lyon, France - (8 HETD).

- 2011 Spring Teaching Assistant for the “*Algorithms and Data Structures II*” course, Department of Computer Science, Sapienza University of Rome - (24 HETD). The course covers some of the main algorithmic techniques: Greedy, Divide and Conquer, Dynamic Programming and Backtracking. The emphasis is put on the definition and the rigorous proof of the properties of the concepts presented (algorithms and data structures). The techniques presented are exemplified by numerous example problems that are also important for their intrinsic interest.
- 2009 Spring Teaching Assistant for “*Combinatorics*” course, Department of Computer Science, Sapienza University of Rome - (24 HETD). The course provides an introduction to basic definitions and classical results in Graph Theory. It covers: Basic concepts in graph theory (connectivity, distance, circuits, paths, classic counting methods), Trees (spanning trees, Cayley’s theorem on the number of spanning trees, Prüfer’s code, permutations, cyclic decomposition of permutations), Coloring and Ramsey Theory (Mantel-Turán Theorem, Sperner Theorem, Erdős-Ko-Rado Theorem), Counting Techniques (inclusion-exclusion technique and its application to the number of permutations without a fixed point and Euler’s function).
- 2007 Fall Teaching Assistant for “*Programming I*” course. Department of Computer Science, Sapienza University of Rome - (24 HETD). The course introduces fundamental data structures and algorithms. The main topics include data structures such as arrays, linked lists, stacks, queues, graphs, and trees, and algorithms such as those that are used for list manipulation, sorting, searching, and tree traversals. The tutoring consists in helping the students with practicals/assignments concerning the implementation of data structures and algorithms using the C programming language.
- 2004 Spring Tutor for “*Laboratory of Programming Languages II*”, Department of Computer Science, Sapienza University of Rome - (24 HETD). This is a project-oriented course on fundamental concepts of programming and problem-solving. The course emphasizes good programming designs, coding, and debugging techniques. The tutoring consists in helping and supervising the students as concerns the design and implementation of the main project of the course using the C programming language.

Students advised

- 2018 Yishu Wang, Master 2 in Computer Science, Master Thesis title “Exploring the solution space of phylogenetic tree reconciliations”, (co-adviser), École Normale Supérieure de Lyon (ENS), Lyon. This supervision was in collaboration with M.-F. Sagot. The work consisted in developing algorithms for clustering the optimal reconciliation in the copyhygen event based method.
- 2018 Angelo di Mambro, B.Sc. in Computer Science, Thesis title: “Analysis and comparison of phylogenetic tree distances”, (co-adviser) Sapienza University of Rome. This supervision was in collaboration with Prof. T.Calamoneri. The work consisted in developing and implementing different phylogenetic distances and studied the correlation between them.
- 2018 Mattia Gastaldello, Ph.D. in Bioinformatics. Thesis title “Algorithms and models for complex problems in biology”, (co-advisor), University Lyon I and Sapienza University of Rome. This supervision is in collaboration with M.-F. Sagot and T. Calamoneri. The work is centred around the design of models and algorithms for the study of symbiotic interactions among species. The biological questions we plan to tackle often lead to NP-hard problems. Hence, the design of exact, approximate, and probabilistic algorithms is

an important issue of this project. These algorithms must be able to deal with a large dimension of the data in input and at the same time a huge number of solutions. To this purpose, we aim to apply data mining techniques to extract useful information from the input and output.

- 2017 Laura Urbini, Ph.D. in Bioinformatics. Thesis title “Models and algorithms for the study of symbiotic interactions”, (co-adviser), University Lyon I and University Paris Diderot. This supervision is in collaboration with M.-F. Sagot and C. Matias. The goal of this research project is the design of new algorithms and models with the aim to better understand species interactions and their evolution. In particular, we would like to refine the current model used for this problem, including more biological information and making it more realistic. The design of likelihood-based approaches is another important point of the project. An advantage of these methods is the fact that they remove the subjective step of cost parameter choice and rely instead on a simultaneous inference of parameter values and events. We will be particularly interested in ABC (Approximate Bayesian Computation) methods.
- 2016 Nina Paffoni, Master 1 in Bioinformatics. Thesis title “ Integrating cophylogeny information within ecological networks studies”, (co-advisor), University Lyon I. This supervision is in collaboration with S. Dray. The work consists in developing methods for analyzing ecological networks that incorporate the information on the cophylogeny of species that could affect their interactions. In particular we consider how different parameters measured on ecological networks are related with the patterns of coevolving interactions.
- 2015 Virginie Jouffret, Master 1 in Bioinformatics, expected graduation July 2015. Thesis title “Distances for phylogenetic trees: a comparative study”, (co-advisor), University Lyon I. This supervision is in collaboration with A. Mary (Associate professor in ERABLE). The work consists in analysing different tree comparison methods with particular focus on edit distances and matrix distances. The most efficient algorithms for the distances considered will be implemented. Moreover, it is planned a comparative analysis on the distribution and the power of these distances to discriminate among different trees.
- 2015 Henri Dupoy, Master 1 in Bioinformatics, expected graduation July 2015. Thesis title “Exact algorithms for covering problems: an application to *Wolbachia* infection and cytoplasmic incompatibility”, (co-advisor), University Lyon I. This supervision is in collaboration with A. Mary. The work consists in the design of efficient exact algorithms for a new model (known as quantitative model) for the problem of inferring the minimum genetic architecture explaining a host manipulation called cytoplasmic incompatibility caused by *Wolbachia*, in particular in arthropods. This is modelled as the problem of a minimal cover of the edges of a bipartite graph with chain graphs.
- 2014 Laura Urbini, Master 2 in Bioinformatics. Master Thesis title “Statistical and algorithmic method for the cophylogeny analysis of host/parasite systems: a case study on *Wolbachia*-arthropod trees”, (co-adviser), University Lyon I. This supervision was in collaboration with M.-F. Sagot. The work consisted mainly in the design and development of statistical and combinatorial methods for analysing host/parasite systems based on their phylogenetic information. The algorithms developed were fast in practice and thus able to handle large datasets. The algorithms allowed to start studying the large dataset of *Wolbachia* and their arthropod hosts.

- 2014 Beatrice Donati, Ph.D. in Bioinformatics, Thesis title “Graph models and algorithms in (co)evolutionary contexts” (co-advisor) University Lyon I and University of Florence. This supervision was in collaboration with M.-F. Sagot and P. Crescenzi. The work I supervised was mainly related to the use of combinatorics and statistical techniques to model phylogenetic information, and in particular to investigate the interactions among different organisms at a phylogenetic level. I co-authored with B. Donati 2 (out of the 3) papers related to her Ph.D. work.
- 2012 Laurent Feuilloley, B.Sc. in Bioinformatics, Thesis title “Aspects algorithmiques du problème Mod/Resc”, (co-adviser), Université Lyon I. This supervision was in collaboration with Prof. M.-F. Sagot. The work consisted in designing more efficient algorithms for the problem of inferring the minimum genetic architecture explaining a host manipulation called cytoplasmic incompatibility caused by *Wolbachia* in particular in arthropods. This problem corresponds to enumerating minimum biclique edge covers in a bipartite graph. The algorithms implemented for solving it had a better performance in practice compared to the existing ones. Moreover, extensions of the model that take into account gene expression and lead to a different computational problem were also considered and efficient algorithms designed.
- 2011 Dario Frascaria, B.Sc. in Computer Science, Thesis title: “Analysis of pairwise compatibility graphs with few vertices”, (co-adviser) Sapienza University of Rome. This supervision was in collaboration with Prof. T.Calamoneri. The work consisted in developing and implementing an algorithm for recognizing pairwise compatibility graphs (PCG). The motivation for introducing this class of graphs came from a computational biology problem. Until now, there is no polynomial time algorithm for recognizing PCGs, and there is evidence for believing it is an NP-hard problem. The algorithm has a good performance for small size graphs presenting some particular structure. The results of this work were published in *The Computer Journal*.
- 2010 Stefano D’Epifanio, B.Sc. in Computer Science, Thesis title: “ $L(2,1)$ -labeling of oriented cacti”, (co-adviser) Sapienza University of Rome. This supervision was in collaboration with Prof. T.Calamoneri. The work consisted in developing and implementing a branch and bound algorithm for finding an $L(2,1)$ -labeling for oriented planar graphs. The $L(2,1)$ -labeling problem is a well-known one in graph theory, connected to the frequency assignment problem of wireless networks. The algorithm implemented had a good performance for small size graphs and helped in obtaining some interesting results for the class of oriented cactus graphs. The project included also a graphical user interface.

Funded Projects

- 2016 – 2017 PI: “Integrating Cophylogeny in the analysis of ecological networks”, inter-departmental project of LBBE.
- 2012 – 2013 Member of the research project: “SISYPHE”, ERC Advanced Grant, sole partner Bamboo team.
- 2000 – 2006 Member of the research project: “Compression limits in combinatorics and computational complexity”. Funded by the Italian Ministry of University and Research.

Refereeing Activities

- I was a member of the Program Committee for *WALCOM* 2016 (10th International Workshop on Algorithms and Computation).
- I have refereed papers for the following journals and conferences:
 - **International journals:** *Molecular Ecology* 2017, *Algorithms for Molecular Biology* 2016, *Discussiones Mathematicae Graph Theory* 2016, *Theoretical Computer Science* 2016, *ACM Journal on Experimental Algorithmics* 2015, *Theoretical Computer Science* 2015, *Current Zoology* 2015, *Journal of Applied Mathematics and Computing* 2014, *Discrete Mathematics* 2014, *European Journal of Combinatorics* 2014, *Journal of Combinatorial Optimization* 2014. *Discrete Mathematics, Algorithms and Applications* 2014. *Theoretical Computer Science* 2015, 2014, *ARS Combinatoria* 2013, *Theoretical Computer Science* 2013.
 - **International conferences:** *WABI* 2013, 2015, 2016, 2017, *RECOMB* 2015, *CIAC* 2015, *WABI* 2014, *WALCOM* 2014, *CIAC* 2013, *ESA* 2013, *RECOMB* 2013, *WADS* 2013, *SODA* 2011.

Popularization

- 2017 Participation at the Fête de la Science of Inria. The topic of the workshop was “Wrong ideas and myths in science”. More information may be found at this address: <http://www.inria.fr/centre/grenoble/actualites/fete-de-la-science-les-coulisses-du-numerique>.
- 2017 Presentation within the context of a stage, organised by ENS de Lyon, for high school girls with the aim of discovering computer science.
- 2016 Participation at the Conference “Girls and mathematics: an enlightening equation!” (see <https://filles-et-math.sciencesconf.org/program>).
- 2016 Participation at the “Journées Nationales de l’APMEP” in Lyon (as a speaker) The Title of the presentation " Une exploration mathématique de l’évolution et des interactions des espèces."
- 2016 Participation at the Conférences ISN et enseignement 2016 of INRIA. The video of the talk can be found at this address: https://www.canal-u.tv/video/inria/modelisation_de_l_evolution_des_especes.24863
- 2015 Participation at the Fête de la Science of Inria. The title of the workshop presented was: “Du passé au présent : explorons l’évolution”. More information may be found at this address: <http://www.inria.fr/centre/grenoble/actualites/fete-de-la-science-les-coulisses-du-numerique>.

Spoken Languages

Albanian (native language), Italian (fluent), English (fluent), French (intermediate).

Programming Languages C, Pascal, Java, HTML, SQL, Lisp, ML, Assembler.

Released Softwares and Tools

COALA

- Software web site: <http://coala.gforge.inria.fr/>
- Software developed in Java which implements an ABC method for estimating the frequency of the cophylogenetic events (cospeciation, duplication, host switch, and losses) which could explain the patterns observed between a pair of phylogenetic trees (host and parasite, for instance).
- License: CeCILL

EUCALYPT

- Software web site: <http://eucalypt.gforge.inria.fr/>
- Software developed in Java which implements a polynomial-delay algorithm for enumerating all solutions for the Cophylogeny reconciliation problem. It also offers the possibility of counting the total number of solutions without enumerating and of randomly sampling the space of solutions.
- License: CeCILL