

Blerina SINAIMERI

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INRIA–Grenoble
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Research interests

Ecological Networks, Cophylogeny, Next Generation Sequencing, Graph Theory.

Academic appointments

- 10/2015– CHARGÉE DE RECHERCHE
INRIA Grenoble - Rhône-Alpes
European Research team in Algorithms and Biology, Formal and Experimental (ERABLE) team
computational biology, algorithms, evolution, cophylogeny
- 07/2019–07/2020 VISITING RESEARCHER
LUISS – Libera Università Internazionale degli Studi Sociali Guido Carli
ecological networks, coevolution, algorithms
- 01/2018–03/2018 VISITING RESEARCHER
Computer Science Department, Sapienza University of Rome.
cophylogeny, algorithms, graph theory
- 02/2012–09/2015 POSTDOC
INRIA Grenoble - Rhône-Alpes – ERABLE team
Computational biology, algorithms, (co)-evolution, cophylogeny
- 02/2010–02/2012 POSTDOC
Computer Science Department, Sapienza University of Rome.
algorithms, graph theory, complexity

Education

- 22/01/2010 PH.D. IN COMPUTER SCIENCE, (EVALUATION : OUTSTANDING)
Sapienza University of Rome – Computer Science Department – Rome – Italy
Thesis: “Structures of diversity”
- 5/07/2006 LAUREA DEGREE IN COMPUTER SCIENCE, (SUMMA CUM LAUDE)
Sapienza University of Rome – Computer Science Department – Rome – Italy

Qualifications

- 2015 French Qualification for the position of Associate Professor (“maître de conférences”) in Computer Science and Applied Mathematics.

Awards

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

Research visits

- jul. 2019 LUISS – Libera Università Internazionale degli Studi Sociali Guido Carli, Rome, Italy (1 year).
- mar.2019 Instituto Superior Técnico de Lisboa (IST), Universidade de Lisboa, Lisbon, Portugal (2 weeks).
- sep.2018 Instituto Superior Técnico de Lisboa (IST), Universidade de Lisboa, Lisbon, Portugal (1 week).
- apr.2018 Instituto Superior Técnico de Lisboa (IST), Universidade de Lisboa, Lisbon, Portugal (2 weeks).
- jan.2018 Computer Science Department, Sapienza University of Rome, Italy (3 months).
- jul.2017 Instituto Superior Técnico de Lisboa (IST), Universidade de Lisboa, Lisbon, Portugal (10 days).
- sep. 2016 Dept. of Mathematics and Computer Science, Università degli Studi di Palermo, Italy (1 week).
- mar.2016 Instituto de Matemática e Estatística Universidade de São Paulo (USP), Brasil (1 week).
- feb.2015 Instituto de Matemática e Estatística Universidade de São Paulo (USP), Brasil (1 week).
- mar.2014 Instituto de Matemática e Estatística Universidade de São Paulo (USP), Brasil (1 week).
- mar.2014 Laboratório Nacional de Computação Científica, Petrópolis, Brasil (1 week).
- apr.2013 Laboratório Nacional de Computação Científica, Petrópolis, Brasil (1 week).
- apr.2013 Centro de Modelamiento Matemático de la Universidad de Chile, Santiago, Chile (1 week).
- jan.2013 Instituto de Engenharia de Sistemas e Computadores (INESC), Lisbon, Portugal (1 week).

Professional Responsibilities

I. Evaluation Committees

- 2020 Member of the INRIA national commission for the recruitment of 3 Chargée de recherche (CR).
- 2019-2023 Elected Member of the Inria Evaluation Committee – The Evaluation Committee is a largely autonomous committee composed of selected Inria scientists and outside experts. It is at the forefront of scientific assessment at the Institute. It constitutes the core of recruitment assessment committees, which also include outside experts nominated by general management, and of internal promotion committees. In cooperation with the Research Department, it coordinates the external evaluation of Inria project teams in each field of research. (For more information see <https://www.inria.fr/institut/organisation/instances/commission-d-evaluation>)
- 2018 Member of the commission for the recruitment of 1 *Maître de Conférences* in Computer Science for the Laboratory of Plant Genome and Development (Laboratoire Génome et Développement des plantes) at the University of Perpignan, France.

II. Ph.D. Committees

- 2019 Member of the jury of the Ph.D. thesis defense of Aikaterini Karanasiou, Ph.D. in Computer Science, Control and Geoinformation (Ph.D. Thesis Title “Robustness in Directed Graphs”).
- 2019 Member of the jury of the Ph.D. thesis defense of Pierre Marijon, Ph.D. in Bioinformatics (Ph.D. Thesis Title “Novel components at the periphery of long read genome assembly tools”).
- 2016 Referee of the Ph.D. Thesis of Nilakanta Paudel, Doctoral Thesis in Mathematics, University Roma 3 (Ph.D. Thesis Title “Graph Algorithms for Analytics and Security”).
- 2016 Member of the supervision committee (*Comité de suivi de la thèse*) of Wandrille Duchemin (Ph.D. Thesis Title “Phylogénie des dépendances et dépendances des phylogénies dans les gènes et les génomes”). The objective of the supervision committee is to monitor the progress of research work and the professional project of the doctoral student.
- 2015 Member of the supervision committee (*Comité de suivi de la thèse*) of Bastien Cazaux (Ph.D Thesis Title “Approximation of superstring, indexation and genome assembly”).

Research projects and Grants

I. Grant as Principal Investigator

2016–2017 Iceberg – “Integrating Cophylogeny in the analysis of ecological networks”,
Funding: Project founded by LBBE, 5K Euro.
Role: **Principal investigator**

II Grants as Investigator

- 2016–2020 ASTER – “Algorithms and software for third generation RNA sequencing”,
Funding: Project founded by the French National Research Agency (ANR-16-CE23-0001), 562K Euro.
Role: **Work Package Leader**
- 2015–2017 “Mathematical tools to analyse the arms race between organisms and their parasites”,
Funding: Project founded by the The Royal Society, 13K Euro.
Role: **Investigator**
- 2012–2015 “SISYPHE: Species Identity and SYmbiosis Formally and Experimentally explored”,
Funding: Project founded by the European Research Council (ERC) Advanced Grant, (ERC-AG-PE6-ERC) 2,3M Euro.
Role: **Investigator**
- 2012–2016 Colib’read – “Methods for efficient detection of biological information from non assembled HTS data.”,
Funding: Project founded by the French National Research Agency (ANR12-BS02-0008), 362K Euro.
Role: **Investigator**
- 2008–2010 “Compression limits in combinatorics and computational complexity”,
Funding: Project founded by the Progetti Universitari 2007, Sapienza University of Rome, Italy 40K Euro.
Role: **Investigator**

Editorial Duties

- I am a member of the Program Committee for *CIAC* 2021 (12th International Conference on Algorithms and Complexity). I was a member of the Program Committee for *SeqBIM* 2019 (Sequences en Bioinformatique, Mathematiques, Bioinformatique), *WABI* 2019 (19th Workshop on Algorithms in Bioinformatics), *IWOCA* 2019 (30th International Workshop on Combinatorial Algorithms) and *WALCOM* 2016 (10th International Workshop on Algorithms and Computation).
- I have refereed papers for the following journals and conferences:
 - **International journals:** *Algorithmica*, *Bioinformatics*, *BMC Bioinformatics*, *Journal of mathematical Biology*, *Molecular Ecology*, *IEEE Transactions on Computational Biology and Bioinformatics*, *Algorithms for Molecular Biology*, *BMC Genomics*, *Current Zoology*, *Discussiones Mathematicae Graph Theory*, *Theoretical Computer Science*, *ACM Journal on Experimental Algorithmics*, *Journal of Applied Mathematics and Computing*, *Discrete Mathematics*, *Discrete Applied Mathematics*, *European Journal of Combinatorics*, *Journal of Combinatorial Optimization*, *Discrete Mathematics*, *Algorithms and Applications*, *Information Processing Letters*, *ARS Combinatoria*.
 - **International conferences:** *WABI* 2013, 2014, 2015, 2016, 2017, 2018, 2019 *RECOMB* 2013, 2015, 2017, *RECOMG-CG* 2017, 2019, *MFCS* 2019, *CPM* 2019, *IWOCA* 2019, *CIAC* 2013, 2015, 2018, *WALCOM* 2014, 2016, 2018, *ESA* 2013, *WG* 2016, 2017, *WADS* 2013, *SODA* 2011.

Lectures and Seminars in International Institutes and Conferences

I. Invited Lectures

- mar. 2018 “Reconciling phylogenetic trees”, Information and Decision Support Systems Lab of INESC-ID, Lisbon, Portugal.
- sep. 2016 “Algorithmic issues in cophylogenetic analysis”, Department of Mathematics and Computer Science, Università degli Studi di Palermo, Italy.

- 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, France.
- dec. 2013 "Combinatorial biology: a mathematical exploration of species interaction", Epoka Univ., Tirana, Albania.
- nov. 2012 "Rainbow Graph Splitting", Séminaire de théorie des graphes, LIMOS, Clermont-Ferrand, France.
- sept. 2010 "Structures of Diversity", 12th Italian Conference on Theoretical Computer Science (ICTCS2010), Camerino, Italy.

II. Presentations in Internationals and National Conferences and Workshops (with selection committee)

- jul. 2019 AmoCoala: Towards a more realistic model for cophylogeny reconstruction via an approximate Bayesian computation, ISMB/ECCB (The 27th Conference on Intelligent Systems for Molecular Biology and the 18th European Conference on Computational Biology, Basel, Switzerland (video of the talk: <https://www.youtube.com/watch?v=bg77fS1FCyk>).
- jun. 2017 Modélisation de la (co)-évolution des espèces, Journée Scientifique de la Faculté des Sciences et technologies de l'UCBL, Lyon, France.
- jul. 2015 Cophylogeny Reconstruction via an Approximate Bayesian Computation, (**Jobim 2015**), Clermont-Ferrand, France.
- mar. 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.
- sept. 2014 Navigating in a sea of repeats in RNA-seq without drowning, 14th Workshop on Algorithms in Bioinformatics (**WABI 2014**), Wroclaw, Poland.
- mar. 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.
- sept. 2010 L(2,1)-labeling of oriented planar graphs, accepted at the 12th Italian Conference on Theoretical Computer Science (**ICTCS 2010**), Camerino, Italy.

Outreach Activities

I am very interested in public dissemination of science and I have been involved in a range of educational activities for different audiences.

2018 Participation at the Fête de la Science of Inria. The topic of the workshop was "Marcher avec Darwin". More information about this event may be found at this address: <http://www.inria.fr/centre/grenoble/actualites/fete-de-la-science-les-coulisses-du-numerique>. Audience: 10 - 16 years old students.

2017 Participation at the Fête de la Science of Inria. The topic of the workshop was "Mythes et idées fausses sur 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>. Audience: 10 - 16 years old students.

- 2016 Participation at the Conference “Girls and mathematics: an enlightening equation!” (see <https://filles-et-math.sciencesconf.org/program>). Audience: 15 - 18 years old students.
- 2016 Participation as invited speaker at the “Journées Nationales de l’APMEP (Association des Professeurs de Mathématiques de l’Enseignement Public)” in Lyon. The title of the presentation “Une exploration mathématique de l’évolution et des interactions des espèces.” These are events, organized each year by a region in France, where the participants (usually high school teachers) are invited, through conferences and workshops, to reflect on their teaching profession.
- 2016 Participation as invited speaker at the *Conférences ISN et enseignement* organized of INRIA. These are series of conferences on computer science, approached from a scientific, technological or societal point of view: current research, computer concepts, tools and applications, impacts and societal debates, to accompany the teaching of computer science in high school. 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>. Audience: 10 - 16 years old students.

Spoken Languages

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

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

RECMETRICS

- Software developed in Python for computing different reconciliation metrics. It also contains a module in R that offers the possibility to systematically compare and visualize whole collections of reconciliations between a specified pair of host and symbiont trees.
- Package website can be found here: <https://team.inria.fr/erable/en/team-members/blarina-sinaimeri/reconciliation-distances/>
- License: CeCILL

Scientific Publications

The following publications are in chronological order. Except for the cases where my name appears in bold, the authors are in alphabetical order. In the latter case, the first authors are indicated by a “*”.

I. Refereed International Journals

- 1 T. Calamoneri, M. Gastaldello, A. Mary, M.-F. Sago, B. Sinaimer, Algorithms for the quantitative Lock/Key model of cytoplasmic incompatibility, **Algorithms for Molecular Biology**, (to appear).
- 2 Y. Wang, A. Mary, M.-F. Sagot and B. Sinaimer, Cappybara: equivalence CLASS enumeration of coPhylogenY event-BASed ReconciliAtions, **Bioinformatics**, 2020, (to appear) doi.org/10.1093/bioinformatics/btaa498
- 3 V. Acuña, R. Grossi, G. Italiano, L. De Lima, R. Rizzi, G. Sacomoto, M.-F. Sagot and B. Sinaimer. On Bubble Generators in Directed Graphs, **Algorithmica**, 82(4): 898-914, 2020.
- 4 T. Calamoneri, A. Monti and B. Sinaimer; Co-divergence and tree topology, **Journal of Mathematical Biology**, Vol. 79, Issue 3, pp 1149–1167, 2019.
- 5 L. Urbini, **B. Sinaimer**, 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**, 16(3): 738-748, 2019.
- 6 K. Huber, V. Moulton, M.-F. Sagot, B. Sinaimer: Exploring and Visualising Spaces of Tree Reconciliations, **Systematic Biology**, 68 (4), 607-618, 2019.
- 7 A. Monti and B. Sinaimer, On variants of Vertex Geography on undirected graph, **Discrete Applied Mathematics**, 251: 268–275, 2018.
- 8 K. Huber, V. Moulton, M.-F. Sagot, B. Sinaimer: Geometric medians in reconciliation spaces of phylogenetic trees, **Information Processing Letters**, 136, 96-101, 2018.
- 9 L. Lima*, **B. Sinaimer***, 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.
- 10 T. Calamoneri, B. Sinaimer, Pairwise Compatibility Graphs: A Survey. **SIAM Review** 58(3): 445–460, 2016.
- 11 C. Baudet*, B. Donati*, **B. Sinaimer***, 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.
- 12 B. Donati, C. Baudet, **B. Sinaimer**, P. Crescenzi and M.-F. Sagot, EUCALYPT: Efficient tree reconciliation enumerator, **Algorithms for Molecular Biology** 10(3), 2015.
- 13 T. Calamoneri, A. Frangioni and B. Sinaimer, Pairwise Compatibility Graphs of Caterpillars, *The Computer Journal* 57(11), 1616–1623, 2014.
- 14 T. Calamoneri, R. Petreschi and B. Sinaimer, Pairwise compatibility property of some superclasses of threshold graphs, **Discrete Mathematics, Algorithms and Applications (DMAA)**, 5(2), 2013.
- 15 T. Calamoneri, E. Montefusco, R. Petreschi and B. Sinaimer, Exploring Pairwise Compatibility graphs, **Theoretical Computer Science** 468: 23–36, 2013.
- 16 T. Calamoneri and B. Sinaimer, L(2,1)-labeling of oriented planar graphs, **Discrete Applied Mathematics** 161(12): 1719–1725, 2013.
- 17 T. Calamoneri, D. Frascaria and B. Sinaimer, All graphs with at most seven vertices are Pairwise Compatibility Graphs, **The Computer Journal** 56(7): 882–886, 2013.
- 18 A. Monti and B. Sinaimer, Rainbow Graph Splitting, **Theoretical Computer Science** 412(39): 5315–5324, 2011.
- 19 Z. Füredi, I. Kantor, A. Monti and B. Sinaimer, On Reverse-Free Codes and Permutations, **SIAM Journal on Discrete Mathematics** 24(3): 964–978, 2010.
- 20 J. Körner, G. Simonyi and B. Sinaimer, On types of growth for graph-different permutations, **Journal of Combinatorial Theory Series A** 116: 713–723, 2009.
- 21 J. Körner and B. Sinaimer, On cancellative set families, **Combinatorics, Probability and Computing**, 16(4): 767–773, 2007.

II. Refereed International Conference

- 22 V. Acuña, R. Grossi, G. Italiano, L. De Lima, L. Pepé Sciarria, M.-F. Sagot and B. Sinaimeri. A family of tree-based generators for bubbles in directed graphs, 31rd International Workshop on Combinatorial Algorithms, IWOCA 2020 , Bordeaux, France, June 8-10, 2020.
- 23 V. Acuña, R. Grossi, G. Italiano, L. De Lima, R. Rizzi, G. Sacomoto, M.-F. Sagot and B. Sinaimeri. On Bubble Generators in Directed Graphs, 43rd International Workshop on Graph-Theoretic Concepts in Computer Science, **WG 2017**, Eindhoven, The Netherlands, June 21-23, 2017.
- 24 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.
- 25 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.
- 26 T. Calamoneri, M. Gastaldello, A. Mary, M.-F. Sago, B. Sinaimeri: On Maximal Chain Subgraphs and Covers of Bipartite Graphs. **ICTCS 2016**, 286–291, 2016.
- 27 L. Bulteau, G. Sacomoto and B. Sinaimeri, Computing an Evolutionary Ordering is Hard, **LAGOS 2015**, VIII Latin-American Algorithms, Graphs and Optimization Symposium, Brazil 2015.
- 28 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, **WABI 2014**, 14th Workshop on Algorithms in Bioinformatics, LNCS vol.8701 ,82–96, Wroclaw, Poland 2014.
- 29 Tiziana Calamoneri, Blerina Sinaimeri: Relating threshold tolerance graphs to other graph classes,**ICTCS 2014**, 16th Italian Conference on Theoretical Computer Science, Perugia, Italy 73-79, 2014.
- 30 T. Calamoneri, R. Petreschi and B. Sinaimeri, On relaxing the constraints in Pairwise Compatibility graphs, **WALCOM 2012**, In: Md. S. Rahman and S.-i. Nakano (Eds.), LNCS vol. 7157,124–135, Springer, Berlin, 2012.
- 31 Z. Füredi, I. Kantor, A. Monti and B. Sinaimeri, On Reverse-Free Codes and Permutations, **EuroComb 2011**, Electronic Notes in Discrete Mathematics vol. 38, 383–387, Budapest, 2011.

III. Other Publications

- 32 B. Sinaimeri, L. Urbini, C. Matias and M. F. Sagot, AmoCoala: Towards a more realistic model for cophylogeny reconstruction via an approximate Bayesian computation, **ISMB/ECCB** (The 27th Conference on Intelligent Systems for Molecular Biology and the 18th European Conference on Computational Biology, poster session, Basel, Switzerland.
- 33 C. Baudet*, B. Donati*, B. Sinaimeri*, L. Urbini*, P. Crescenzi, C. Gautier, C. Matias and M.-F. Sagot, Understanding coevolution through cophylogeny methods, **EMOTIONS 2014**, Ecological and molecular modelling of infections, poster session, Lyon, France.
- 34 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, **WABI 2013**, 13th Workshop on Algorithms in Bioinformatic, poster session, Sophia Antipolis, France.
- 35 T. Calamoneri, R. Petreschi and B. Sinaimeri, On relaxing the constraints in Pairwise Compatibility graphs, accepted at **GA 2011**, Graph and Algorithms 2011, Workshop colocated with ICALP 2011, Zürich, Switzerland.
- 36 T. Calamoneri and B. Sinaimeri, Labeling of oriented planar graphs, accepted at **CTW2011**, 10-th Cologne-Twente Workshop on graphs and combinatorial optimization, 93–96, Frascati, Italy.
- 37 T. Calamoneri and B. Sinaimeri, L(2,1)-labeling of oriented planar graphs, accepted at **ICTCS 2010**, 12th Italian Conference on Theoretical Computer Science, Camerino, Italy (short abstract).
- 38 B. Sinaimeri, Structures of Diversity, 2010, Ph.D. thesis.

IV. Research Reports and Publications under Review

- 40 Y. Wang, A. Mary, M.-F. Sagot and B. Sinaimeri, Lazy listing of equivalence classes – A paper on dynamic programming and tropical circuits, (submitted).
- 41 B. Sinaimeri, L. Urbini, C. Matias and M.-F. Sagot, AMOCOALA: A more realistic cophylogeny model, (submitted).
- 42 T. Calamoneri, A. di Mambro and B. Sinaimeri, Comparing related trees, (submitted).

Teaching in Italy and International Institutes

During my career I have taught a number of courses at various levels, including: Network Algorithms for Molecular Biology, Advanced Algorithms, Discrete Mathematics, Algorithms and Data Structures, Combinatorics, Programming etc. I have taught in Italy (Sapienza University of Rome) and in France (Université Lyon 1, École Normale Supérieure de Lyon (ENS), Institut National des Sciences Appliqués de Lyon (INSA)). I have taught in Italian, English and French.

- 2020, Spring – “*Advanced Algorithms*”, Master of “*Bioinformatique et Modélisation*” (M2), Dep. Biologie, Univ. Claude Bernard – Lyon 1, Lyon, France. The course provides an introduction to basic algorithms in bioinformatics. It includes algorithms on strings, introduction to data structures (hashing functions, Bloom filters, Burrows-Wheeler Transform) and main algorithmic techniques: Greedy, Divide and Conquer, Dynamic Programming and Backtracking.
- 2018, Fall – “*Computational Complexity*”, Master of “*Bioinformatique et Modélisation*” (M1), Institut National des Sciences Appliqués (INSA), Lyon, France. The course provides an introduction to computational complexity, including how most decision problems are uncomputable, hardness and completeness, and reductions; approximation algorithms and parameterized complexity.
- 2018, Spring – “*Advanced Algorithms*”, Master of “*Bioinformatique et Modélisation*” (M1), (M1), Dep. Biologie, Univ. Claude Bernard – Lyon 1, Lyon, France.
- 2017, Fall – “*Discrete Mathematics*”, Master of “*Bioinformatique et Modélisation*” (M1) , Institut National des Sciences Appliqués (INSA), Lyon, France.
- 2017, Spring – “*Advanced Algorithms*”, Master of “*Bioinformatique et Modélisation*” (M1), Dep. Biologie, Univ. Claude Bernard – Lyon 1, Lyon, France. 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 – “*Network Algorithms for Molecular Biology*”, Master of “*Informatique*” (M2), École Normale Supérieure de Lyon (ENS), Lyon, France.
- 2016, Fall – “*Discrete Mathematics*”, Master of “*Bioinformatique et Modélisation*” (M1), Institut National des Sciences Appliqués (INSA), Lyon, France.
- 2016, Spring – Teaching Assistant, “*Biostatistiques/Bioinformatique*”, Licence 2, Dep. Biologie, Univ. Claude Bernard – Lyon 1, Lyon, France. 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 – “*Discrete Mathematics*”, Master of “*Bioinformatique et Modélisation*” (M1), Institut National des Sciences Appliqués (INSA), Lyon, France.
- 2015, Fall – “*Network Algorithms for Molecular Biology*”, Master of “*Informatique*” (M2), École Normale Supérieure de Lyon (ENS), Lyon, France. 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. Different networks were considered in the context of genomics, transcriptomics, metabolism and (co)-evolution. The course included also a introduction to enumeration (listing) algorithms.
- 2015, Spring – Teaching Assistant, “*Biostatistiques/Bioinformatique*”, Licence 2, Dep. Biologie, Univ. Claude Bernard – Lyon 1, Lyon, France. 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 was 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.

- 2014, Fall – “*Discrete Mathematics*”, Master of Bioinformatique et Modélisation (M1), Institut National des Sciences Appliqués (INSA), Lyon, France. The course provided an introduction to graph theory and graph algorithms. It covered: 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).
- 2014, Fall – “*Discrete Mathematics*”, Dep. Biologie, Univ. Claude Bernard – Lyon 1, (M1), Lyon, France.
- 2013, Fall – “*Discrete Mathematics*”, Master of Bioinformatique et Modélisation (M1), Institut National des Sciences Appliqués (INSA), Lyon, France.
- 2012, Fall – “*Discrete Mathematics*”, Master of Bioinformatique et Modélisation (M1), Institut National des Sciences Appliqués (INSA), Lyon, France.
- 2011, Spring – Teaching Assistant, “*Algorithms and Data Structures II*” course, Department of Computer Science, Sapienza University of Rome (L3). The course covered some of the main algorithmic techniques: Greedy, Divide and Conquer, Dynamic Programming and Backtracking. The emphasis was put on the definition and the rigorous proof of the properties of the concepts presented (algorithms and data structures). The techniques presented were illustrated by numerous example problems that are also important for their intrinsic interest.
- 2009, Spring – Teaching Assistant, “*Combinatorics*” course (L2), Department of Computer Science, Sapienza University of Rome. The course provided an introduction to basic definitions and classical results in Graph Theory. It covered: 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 – Tutor, “*Programming I*” course (L1). Department of Computer Science, Sapienza University of Rome. The course introduced fundamental data structures and algorithms. The main topics included 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 consisted in helping the students with practicals/assignments concerning the implementation of data structures and algorithms using the C programming language.
- 2005, Fall – Tutor, “*Laboratory of Programming Languages II*” (L1), Department of Computer Science, Sapienza University of Rome. This was a project-oriented course on fundamental concepts of programming and problem-solving. The course emphasized good programming designs, coding, and debugging techniques. The tutoring consisted in helping and supervising the students as concerns the design and implementation of the main project of the course using the C programming language.

Supervision of Ph.D. and graduate students

During my career I have co-advised 2 Ph.D. and 9 graduate students as follows:

I. Ph.D. Students

current Yishu Wang, Ph.D. Thesis title “Algorithmic investigation of the dynamics of species interactions”, (co-supervisor), University Lyon I, Lyon. This supervision was in collaboration with M.-F. Sagot (Directeur de recherche - INRIA, ERABLE) and Mario Figueiredo (Full professor at IST, Lisbon, Portugal).

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 (Directeur de recherche - INRIA, ERABLE) and C. Matias (Directeur de recherche - CNRS, ERABLE).

II. Master Students

2018 Yishu Wang, Master 2 in Computer Science, Master Thesis title “Exploring the solution space of phylogenetic tree reconciliations”, (co-advisor), École Normale Supérieure de Lyon (ENS), Lyon. This supervision was in collaboration with M.-F. Sagot.

- 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 (Directeur de recherche - CNRS).
- 2015 Virginie Jouffret, Master 1 in Bioinformatics. Master 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).
- 2015 Henri Dupoy, Master 1 in Bioinformatics. Master 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.
- 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-advisor), University Lyon I. This supervision was in collaboration with M.-F. Sagot.

III. B.Sc. Students

- 2018 Angelo di Mambro, B.Sc. in Computer Science, Thesis title: “Analysis and comparison of phylogenetic tree distances”, (co-advisor) Sapienza University of Rome. This supervision was in collaboration with Prof. T.Calamoneri (Associate professor, CS Dep. Sapienza University of Rome).
- 2012 Laurent Feuilloley, B.Sc. in Bioinformatics, title “Algorithmic aspects of the Mod/Resc problem”, (co-advisor), University Lyon I. This supervision was in collaboration with M.-F. Sagot.
- 2011 Dario Frascaria, B.Sc. in Computer Science, “Analysis of pairwise compatibility graphs with few vertices”, (co-advisor) Sapienza University of Rome. This supervision was in collaboration with T.Calamoneri.
- 2010 Stefano D’Epifanio, B.Sc. in Computer Science, “L(2,1)-labeling of oriented cacti”, (co-advisor) Sapienza University of Rome. This supervision was in collaboration with T.Calamoneri.