

ANNE SIEGEL CURRICULUM VITAE

Name, Surname: SIEGEL, Anne **URL:** <http://www.irisa.fr/dyliss/anne.siegel>
Nationality: French **Date of birth:** 21/07/1975

EDUCATION

2008: habilitation from University Rennes (FR), with a **double degree in Computer Science and Mathematics**.

2000: PhD from Aix-Marseille University (FR), in **Discrete mathematics & Foundations of computer science**

1997: laureate of the **aggregation of mathematics**

ACADEMIC POSITIONS

2010: **director of research (CNRS) in computer science** at IRISA, the joint CNRS, Inria and University **laboratory of computer science in Rennes**

Between 2002 and 2010: **research scientist (CNRS) in computer science** at IRISA.

RESEARCH TOPICS

Research field: bioinformatics, systems biology, automatic logical reasoning

Contributions: 60 publications (journal paper and conferences), transversally to theoretical computer science, knowledge representation, bioinformatics and mathematics, for a total number of 1800 citations (google h-index: 18).

Supervision of graduate students: 10 ph-D students, 10 post-docs and engineers.

SERVICE TO THE COMMUNITY & SCIENTIFIC LEADERSHIP

Institutional boards: (i) **National evaluation board of INRIA** (2008-11, 2015-present). (ii) **National board of CNRS for research evaluation** (2010-12)

Leader of the Dyliss research group ([www](http://www.dyliss.fr)), (6 permanent researchers from Inria, 10 PhD students & post-docs). The group develops formal systems techniques based on logical programming constraints to interpret large-scale cellular observation datasets.

Founder of a national working group on the symbolic study of dynamical systems involved in biology ([www](http://www.dyliss.fr)).

Selection of International collaborations: T. Schaub (University of Potsdam, Germany) [5 joint publications. 1 co-supervised PhD student.], J. Saez-Rodriguez, chair of systems biology at RWTH-Aachen university, Germany [5 joint publications.], A. Maass (University of Chile) [3 joint publications and 1 co-supervised PhD student].

2010-2014: **Scientific coordinator** of the research project Biotempo ([www](http://www.dyliss.fr))

Since 2012: **scientific board of the Idealg project - PIA** ([www](http://www.dyliss.fr)). Responsible for the systems biology task (0.9M€).

Participation to scientific projects: TGF-SysBio (Plan cancer), Mecagenotox (Anses), IDEALG (PIA).

Guest presentations (selection). Keynote speaker at **MCU'2015, PRIB'2013, CIBB'2013**. **Invited survey speaker** **ECCB workshop** (2014, France), **CSL/LICS workshop** (Austria, 2014), **Numeration conference** (Netherlands, 2010); **Conference on aperiodic Order** (UK, 2009). **50 seminar talks**.

A SELECTION OF PUBLICATIONS

- [1] S. Videla, J. Saez-Rodriguez, C. Guziolowski, A. Siegel caspo: a toolbox for automated reasoning on the response of logical signaling networks families , *Bioinformatics*, 2017.
- [2] S. Prigent, C. Frioux, S. M. Dittami , (...) T. Tonon, A. Siegel, Meneco, a Topology-Based Gap-Filling Tool Applicable to Degraded Genome-Wide Metabolic Networks, *Plos Computation Biology*, 2017.
- [3] P. Bordon, M. Latorre, M.-P. Cortes, M. Gonzalez, S. Thiele, A. Siegel, A. Maass, D. Eveillard, Putative bacterial interactions from metagenomic knowledge with an integrative systems ecology approach. *Microbiology open*, 2015.
- [4] S. Thiele, L. Cerone, J. Saez-Rodriguez, A. Siegel, C. Guziolowski, S. Klamt. Extended notions of sign consistency to relate experimental data to signaling and regulatory network topologies. *BMC Bioinformatics*, 2015.
- [5] S. Prigent, G. Collet, (...) , A. Siegel, T. Tonon (2014), The genome-scale metabolic network of *Ectocarpus siliculosus* (EctoGEM) : a resource to study brown algal physiology and beyond, *the Plant Journal*, 2014
- [6] C. Guziolowski, S. Videla, F. Eduati, S. Thiele, A. Siegel and J. Saez-Rodriguez. Exhaustively characterizing feasible logic models of a signaling network using Answer Set Programming. *Bioinformatics*. 2013
- [7] J. Bourdon, D. Eveillard, A. Siegel. Integrating quantitative knowledge into a qualitative gene regulatory network. *PLoS Computational Biology* 2011

ETAT-CIVIL

Née en 1975.

Mariée. Quatre enfants (nés en 1999, 2002, 2006, 2011).

CURSUS ET TITRES UNIVERSITAIRES

- 2010 Directrice de Recherche DR2, Informatique, IRISA, Rennes
2009 Qualification professeur en informatique (CNU 27) et en mathématiques (CNU 25)
2008 HDR, Univ. Rennes 1, spécialités Mathématiques et Informatique.
Analyse de systèmes dynamiques par discrétisation. Exemples d'applications en théorie des nombres et en biologie moléculaire. Rapporteurs : Marie-Pierre Béal, Hidde De Jong, Boris Solomyak, Alejandro Maass
2006 Chargée de Recherche 1ère classe au CNRS
01/2002 Chargée de recherche 2ème classe au CNRS, section 07 (informatique), IRISA, Rennes
09/2001 Maître de conférences en mathématiques, affectée à l'IRMAR, Rennes
12/2000 Doctorat de l'université de la Méditerranée, Mathématiques Discrètes et Fondements de l'Informatique. Directeur de thèse : Pierre Arnoux. Rapporteurs : A. Fathi & F. Parreau
1998-2001 Allocataire de Recherche Moniteur, IML, Université de la Méditerranée
1997 Agrégation de mathématiques
1997 DEA de mathématiques de l'université de Lyon
1994-1998 Ecole Normale Supérieure de Lyon, spécialité mathématiques

RESPONSABILITÉS

Instances nationales

- 2015-19 Commission d'évaluation de l'INRIA. Membre nommée.
2010-12 Comité national du CNRS, section 01 (mathématiques et interactions). Membre nommée.
2008-11 Commission d'évaluation de l'INRIA. Membre élue.

Animation de la recherche

- 2014-.. Création et co-animation du groupe de travail BIOS "modélisation symbolique des systèmes biologiques" communs aux GDR BIM - Bioinformatique Moléculaire et au GDR IM - Informatique Mathématique.

Responsabilités scientifiques

- 2012-.. **Responsable Equipe Dyliss** (IRISA & Inria) [<http://www.irisa.fr/dyliss/>]
une vingtaine de membres (8 permanents, 6 doctorants, 4 post-doc. ou ingénieurs).
2011-20 **ANR Idealg**, membre du conseil scientifique, co-responsable du workpackage 4, Inv. Avenir Bioresources et biotech. (11M ?)
2012-21 Co-responsable ligne de recherche **Ciric-Omics Integrative center**, Centre INRIA au Chili. (équipe associée INRIA France/Chili IntegrativeBioChile).
2010-14 **ANR Biotempo**, Coordinatrice du projet de recherche, ANR blanc Informatique.

Egalité femmes-hommes

- 2017-.. Coordination du groupe de travail "égalité femmes-hommes" de l'Irisa - Inria Rennes
2016-.. Comité parité-égalité INRIA. Responsable du groupe de travail "recrutement des chercheurs"

Instances locales

- 2016-.. Conseil de laboratoire de l'IRISA. Membre élue.
2013-15 Conseil de centre Inria Rennes Bretagne Atlantique. Membre nommée.
2012-15 Conseil scientifique de la génopole BioGenOuest.
2012-16 Commission des thèses de mathématiques du réseau Bretagne-Pays de la Loire.
2003-08 Conseil de laboratoire de l'IRISA. Membre élue.

Comités d'experts, de sélections, jurys

- ERA-CAPS* Panel committee of the Europe-USA Call Strengthening Transnational Research in Molecular Plant Sciences
Divers International Israel Science Foundation - FP7-people-Cofund. - NWO (netherlands).
H CERES Bioinformatique-Institut Curie (présidente, 11/2017) - LIFL-LAGIS (2013).
Plan cancer/biologie des systèmes Présidence comité (10/2017) - Membre comité (2014).
ANR Expertise de dossiers : informatique, biologie, mathématiques (2013. 2014).
Divers France ARP Mermed (2014)

Organisation de conférences, rencontres, école jeunes chercheurs...

- 2014 Théorie des réseaux booléens et leurs applications en biologie, Nice.
- 2013 Workshop "integrative omics", Pucon, Chili.
- 2012 Ecole jeunes chercheurs en Informatique-Mathématiques, Rennes.
- 2007-10 Journées satellites de la conférence JOBIM.
- 2010 Workshop Franco-Chinois *Substitutive Tiling and Fractal Geometry*, Chine, 2010.
- 2009 Session *Numération*, rencontres de l'arithmétique-informatique, Octobre 2009, Lyon
- 2009 Conférence *Numeration : Mathematics and Computer Science*, 2009, CIRM, Marseille.
- 2004-07 Projet VicAnne. Coordination de l'organisation d'ateliers sur les réseaux biologiques.
- 2002-09 Séminaire de bioinformatique de l'IRISA.
- 2002-09 Journées thématiques de bioinformatique, animation de Ouest-Génopele.

Comités de sélections

- Directeur de recherche (4)** DR Inria, 2016 & 2017
DR CNRS, Section 01 (mathématiques), 2011 & 2012.
- Chargé de recherche (7)** CR1 Inria (2017), Inria Nice (2015), Concours CR1/CR2 CNRS section 01 (2011&2012), Inria Grenoble (2010), Inria Lille (2009 & 2010)
- Professeur (6)** UPMC (2 postes en biologie des systèmes, 2016) - Lille (informatique, 2015) - Angers (informatique, 2015) - Bordeaux (informatique, 2014) - Lille (informatique, 2012).
- Maitre de Conférence (6)** Orsay (informatique, 2014) - Rennes (informatique, 2013) - Nantes (informatique, 2012) - Lille (bioinformatique, 2010) - Lyon (biologie, 2009) - Rennes (biologie, 2009).
- Ingénieur de Recherche (1)** INRA (2016)

Jurys de thèse

- Jurys thèse (19)** M. Manceny (Informatique, Evry, 2006) - G. Kervizic (biologie, Brest, 2009) - C. Friguet (biologie, Rennes, 2010) - I. Ndiaye (automatique, Nice, 2010. *rapporteuse*) - G. Espinoza (mathématiques, Univ. Chile & Univ. Nice, 2010. *rapporteuse*) - N. Loira (informatique, Univ. Bordeaux, 2012. *rapporteuse*) - S. Thiele (informatique, Univ Potsdam, 2012. *rapporteuse*) - M. Noulal (informatique, ENS Lyon, 2012, *présidente*) - P. Vanier (informatique, Univ. Marseille, 2013. *présidente*) - F. Nguema-Ndong (mathématiques, Poitiers, 2013. *présidente*) - T. Jolivet (informatique. Univ. Paris Diderot, 2013) - M. Folschette (bioinformatique, Nantes, 2014. *rapporteuse*) - B. Le Gloannec (informatique, Orléans, 2014. *présidente*) - Vu Nguyen (bioinformatique, Bordeaux, 2015. *rapporteuse*) - N. Mobilia (informatique, Grenoble, 2015. *présidente*) - A. Rougny (informatique, Paris Sud, 2016. *rapporteuse*) - M. Morterol (informatique, Paris Sud, 2016 *rapporteuse*) - P. Traynard (Informatique, ENS&Inria, 2017) - J. Mercier (Biologie, Evry, 2017. *rapporteuse*)
- Jurys HDR (4)** O. Dameron (Rennes, 2016) - A. Chateau (Montpellier, 2016 *rapporteuse*) - M. Elati (Evry, 2016 *rapporteuse*) - E. Remy (Evry, 2016 *présidente*).

Relecture d'articles

TCS - Advances in Math - Annales Institut Fourier - BMC bioinformatics - PLOS CB - Journal of Mathematical Biology - Genome Biology - Nature - DCDS - ...

FORMATION

Encadrement thèses

- **Thèses soutenues (8)**
 - V. Picard (2012-15, ENS Rennes), professeur en classes préparatoires.
 - S. Prigent (2011-14, MENRT), chargé de recherches à l'Inra.
 - S. Videla (2011-14, ANR Biotempo), année sabbatique après avoir obtenu un poste de chercheur en Argentine.
 - A. Aravena (2010-13, financement Chili), enseignant-chercheur en Turquie.
 - O. Abdou-Arbi (2010-13, MENRT) Enseignant-chercheur. Université de Maradi, Niger.
 - C. Guziolowski (2006-09, Financement ministère affaires étrangères) Maitre de conférence/chaire CNRS, Ecole centrale Nantes.
 - P. Blavy (2006-09). Ingénieur de recherche, INRA.
 - P. Veber (2004-07). Ingénieur de Recherche. LBBE. CNRS.
- **Thèse en cours (3)** J. Laniau (2013-2017, Inria-cordi. soutenance prévue le 23/10/17) - V. Delannée (2014-2017, ANSES-région - soutenance prévue le 8/11/2017) - C. Frioux (2015, Inria-Cordi).
- **Thèses qui démarreront en octobre 2018 (3)** M. Louarn (Inria-Inserm) - M. Wery (CIFFRE Sanofi) - M. Conan (Université Rennes 1, école doctorale biologie).

Encadrement post-doc et ingénieurs (9)

S. Blachon (2008-09, post-doc Inria) - T. Baumuratova (2008-09, post-doc ANR SITCON) - S. Thiele (2012-13, post-doc Inria) - G. Collet (2012-14, CDD ANR IDEALG) - O. Quenez (2013, CDD ANR FATINTEGGER) - C. Bettembourg (2014-15, post-doc ANR MIRNADAPT). - C. Trottier (2015-2017, ANR IDEALG) - M. Chevallier (2014-18, ADT Inria + Projet régional Ecosyst) - M. Aite (2015-19, ADT Inria+ ANR Idealg) - P. Vignet (2016-2018, Plan Cancer TGFSysBio).

Enseignements

- 2014-17 Cours de Master 2 bioinformatique (Rennes). *Biologie des systèmes*.
2017 Ecole Jeunes chercheurs *Modélisation des systèmes biologiques* (Porquerolles).
2014 Representing streams II (Lorentz center, Leiden, Pays-Bas). *Symbolic dynamics & tilings*
2013 Ecole Jeunes chercheurs *Modélisation des systèmes biologiques* (Porquerolles).
2011-13 Jury du concours commun de recrutement des ENS (informatique-mathématiques).
2012 Ecole Jeunes chercheurs en Informatique Mathématique (Rennes). *Systèmes dynamiques*.
2011 Ecole Systèmes Complexes (Rennes). *Biologie des systèmes*.
2008-10 Cours de Master 2 bioinformatique (Rennes). *Biologie des systèmes*.
2009 Ecole Internationale CANT'09 (Liege, Belgique). *Dynamique symbolique*.
2005 Formation interne Inria (Liffré) *Biologie des systèmes*
2004 Université d'été Sciences math. & modélisation (Bordeaux, 2004). *Dynamique du nombre d'or*
1998-02 Licence Mathématiques.

VIE SCIENTIFIQUE

Collaborations internationales

- Allemagne* ASP-BASED KNOWLEDGE REPRESENTATION FOR SYSTEMS BIOLOGY. Informatique (Univ. Potsdam). Egide Procope (2011-12). Visite : 2012, 2013. Co-encadrement de thèse.
Chili BIOLOGIE DES SYSTÈMES, MÉTHODES PROBABILISTES. Mathématiques (CMM, Univ. Chile). Inria-Conycit (2011). Equipe associée Inria (2011-13). CIRIC-omics (2011-21, **Coordinatrice**). Visites : 2012, 11, 08, 05. Co-encadrement thèse.
Japon NUMBER THEORY AND DISCRETE DYNAMICAL SYSTEMS. Mathématiques (Univ. Nagoya & Kanazawa). Egide Sakura (2007-08). Visites : 2008, 09, 11.
UK INFERENCE OF SIGNALING NETWORK WITH ASP. Bioinformatique (EBI, Cambridge). Visite : 2013.
Autriche FRACTALS ET NUMÉRATION. Mathématiques (Univ. Leoben). ANR FAN (2013-16). Egide Amadeus (2008-09 & 2011-12, **coordinatrice**). Visites : 2008, 09, 12.
Autres invitations *Chine*. Math. Univ. Canton (2009 & 10). *USA*. Math. Univ North Texas (2000). *Finlande*. Informatique, Turku (1999)

Participation à des projets scientifiques

- Info.* ALGAE IN SILICO, Inria Project Lab (2015-2018) - BIOTEMPO, ANR blanc (2011-14). IRISA. **Coordinatrice** - CIRIC-OMICS, CORFO (Chili)/Inria (2012-22. **Co-responsable ligne de recherche "Omics")** - QUANTOURSIN, PEPS CNRS (2009-11). IRISA. **Coordinatrice**. - MOCA, ARC INRIA (2005-07, Inria Contraintes) - MATHRESOGEN, ACI IMPBio (2003-06). IRMAR, Rennes. **Responsable locale**.
Biologie TGFSYSBIO, Plan Cancer (2015-2018) - MECAGENOTOX, ANSES (2013-2017) - SAMOSA, ANR Bioadapt (2014-2017) - IDEALG, Inv. avenir (2011-21. Stat. Bio. Roscoff. **Responsable WP4**) - FATINTEGER, ANR blanc agro (2012-15. INRA PEGASE. Rennes. **Responsable locale**.) - MIRNADAPT, ANR blanc bioinfo (2012-15. INRA IGEPP. Rennes) - SITCON, ANR Biosys. (2006-09. Inst. Curie. **Responsable locale**) - VICANNE, ACI IMPBio (2003-06. Bordeaux, **coordinatrice actions d'animation**).
Math. FAN, ANR Internationale (2013-16. LIAFA. Paris Diderot) - SUBTILE, ANR blanc (2009-12. IML. Marseille) - LAREDA, ANR blanc (2007-10. Greyc. Caen) - DYCONUM. ANR jeunes chercheurs (2006-09. LIAFA. Paris-Diderot. **Responsable locale**) - NUMERATION, ACI Interfaces (2003-06, LIAFA).

Conférences invités, prix

- LPMNR - **Best Student Paper award** (07/2017).
- Conference Machine, Complexity Universality (MCU). Chypres (09/2015). **Invited conference**
- Workshop on Logical Modeling and Analysis of Cellular Networks (associated with ECCB 2014), Strasbourg (09/2014). **Invited conference**.
- Workshop on Logic and Systems Biology (associated with CSL/LICS 2014), Vienna (07/2014). **Invited conference**.
- CIBB *Computational Intelligence Methods for Bioinformatics and Biostatistics* & PRIB *International Conference on Pattern Recognition in Bioinformatics*, Nice (06/2013). **Keynote speaker**.
- CMSB - *Computational Methods in Systems biology* 2012. London. **Best paper award**.
- *Numeration*, Leiden, Netherlands (06/2010), **Invited conference**.
- *Aperiodic Order*, Leicester, UK (09/2009) **Invited conference**.

Publications dans des revues ou conférences

- Biologie systèmes / méthodes* / PLOS Comp Bio - Bioinformatics - BMC Systems Biology - BMC Bioinformatics - BMC Genomics - CMSB - IEEE TCBB - Jour. Royal Soc. interface - Biosystems - CIBB - ECCS
Informatique Theoretical Computer Science - Knowledge Reasoning - ICLP - LPNMR - WORDS - VMCAI
Mathématiques Adv. in Math - Bull. LMS - Mémoire SMF - Jour. Number Theory - Ann. Institut Fourier - Erg. Th. Dyn. Sys. - Trans. AMS - Acta Arith.
Biologie/modèles Plant Journal - Frontiers - Jour. Theor. Bio. - OMICS - Mol. Rep. Dev.

4. Production Scientifique

Edition d'ouvrages

- E1. B. Adamczewski, A. Siegel, W. Steiner (2009). *Présentation de "Numeration : Mathematics and Computer Science" (CIRM, 2009)*. Actes des rencontres du CIRM. Vol. 1 no. 1. p. 1-2.
- E2. Journées Montoises d'Informatique Théorique 2006 (2009). Theoretical Informatics and Applications, Vol 42 (3). D. Caucau and A. Siegel, guest editors.
- E3. N. Pytheas-Fogg (2002). *Substitutions in Dynamics, Arithmetics and Combinatorics*. Lectures Notes in Mathematics 1794, Springer-Verlag. V. Berthé, S. Ferenczi, C. Mauduit and A. Siegel, editors.

Chapitres dans des ouvrages

- B1. S. Akiyama, M. Barge, V. Berthé, J.-Y. Lee, A. Siegel (2015) *On the Pisot substitution conjecture*. Mathematics of Aperiodic order. J. Kellendonk, D. Lenz, J. Savinien (ed.). Progress in Mathematics Volume 309. Birkhaeuser. p.33-72
- B2. T. Schaub, A. Siegel, S. Videla (2014). *Reasoning on the Response of Logical Signaling Networks with ASP*, Chapter of *Logical Modeling of Biological Systems*, ed. by Luis Farinas del Cerro, Katsumi Inoue, John Wiley and Sons.
- B3. V. Berthé, A. Siegel, J. Thuswaldner (2011). *Tilings, substitutions and Rauzy fractals : effectivity and complexity*, Chapter of *Combinatorics, Automata and Number Theory*, Cambridge University Press.
- B4. V. Berthé and A. Siegel (2002). Basic notions on substitutions. In N. Pytheas-Fogg, *Substitutions in Dynamics, Arithmetics and Combinatorics*. Lectures Notes in Mathematics 1794, Springer-Verlag, 1–34 (chapter 1).
- B5. A. Siegel (2002). Spectral theory and geometric representation of substitutions. In N. Pytheas-Fogg, *Substitutions in Dynamics, Arithmetics and Combinatorics*. Lectures Notes in Mathematics 1794, Springer-Verlag, 2002, pp. 199–252 (Chapter 7).

Revue internationale à comité de lecture

- J1. S. Videla, J. Saez-Rodriguez, C. Guziolowski, A. Siegel (2017) *caspo : a toolbox for automated reasoning on the response of logical signaling networks families* BIOINFORMATICS.
- J2. S. Prigent, C. Frioux S.M. Dittami, S. Thiele, A. Larhlimi, G. Collet, F. Gutknecht, J. Got, D. Eveillard, J. Bourdon, F. Plewniak, T. Tonon, A. Siegel (2017). *Meneco, a Topology-Based Gap-Filling Tool Applicable to Degraded Genome-Wide Metabolic Networks*. PLOS COMPUTATIONAL BIOLOGY.
- J3. V. Picard, A. Siegel, J. Bourdon (2017) *A Logic for Checking the Probabilistic Steady-State Properties of Reaction Networks* JOURNAL OF COMPUTATIONAL BIOLOGY
- J4. V. Delanné S. Langouet-Prigent, N. Théret, A. Siegel (2017) *A modeling approach to evaluate the balance between bioactivation and detoxification of MeIQx in human hepatocytes* PEERJ
- J5. F. Gondret, A. Vincent, M. Houé-Bigot, A. Siegel, S. Lagarrigue, D. Causeur, H. Gilbert, I. Louveau (2017) *A transcriptome multi-tissue analysis identifies biological pathways and genes associated with variations in feed efficiency of growing pigs* BMC GENOMICS
- J6. V. Picard, O. Mulner-Lorillon, J. Bourdon, J. Morales, P. Cormier, A. Siegel, R. Bellé (2016). *Model of the delayed translation of cyclin B maternal mRNA after sea urchin fertilization* MOLECULAR REPRODUCTION AND DEVELOPMENT.
- J7. Loic Paulevé, Max Ostrowski, Torsten Schaub, Anne Siegel, Carito Guziolowski (2016) *Boolean Network Identification from Perturbation Time Series Data combining Dynamics Abstraction and Logic Programming*, BIOSYSTEMS.
- J8. V. Acuna, A. Aravena, C. Guziolowski, D. Eveillard, A. Siegel and A. Maass (2016). *Deciphering transcriptional regulations coordinating the response to environmental changes*. BMC BIOINFORMATICS
- J9. F. Gondret, A. Vincent, M. Houé-Bigot, A. Siegel, S. Lagarrigue, I. Louveau and D. Causeur (2016), *Molecular alterations induced by a high-fat high-fiber diet in porcine adipose tissues : variations according to the anatomical fat location*, BMC GENOMICS
- J10. P. Bordon, M. Latorre, M.-P. Cortes, M. Gonzalez, S. Thiele, A. Siegel, A. Maass, D. Eveillard (2015), *Putative bacterial interactions from metagenomic knowledge with an integrative systems ecology approach*. MICROBIOLOGY OPEN.
- J11. S. Videla, I. Konokotina, L. G. Alexopoulos, J. Saez-Rodriguez, T. Schaub, A. Siegel and C. Guziolowski (2015) *Designing experiments to discriminate families of logical models*. FRONTIERS BIOENG. BIOTECH.
- J12. S. Thiele, L. Cerone, J. Saez-Rodriguez, A. Siegel, C. Guziolowski, S. Klamt (2015) *Extended Notions of Sign Consistency to Relate Experimental Data to Signaling and Regulatory Network Topologies*, BMC BIOINFORMATICS
- J13. Valérie Berthé, Jérémie Bourdon, Anne Siegel, Timo Jolivet (2015) *A combinatorial approach to products of Pisot substitutions*. ERGODIC THEORY AND DYNAMICAL SYSTEMS.
- J14. S. Prigent, G. Collet, S. M. Dittami, L. Delage, F. Ethis de Corny, O. Dameron, D. Eveillard, S. Thiele, J. Cambefort, C. Boyen, A. Siegel, T. Tonon (2014), *The genome-scale metabolic network of Ectocarpus siliculosus (EctoGEM) : a resource to study brown algal physiology and beyond*, THE PLANT JOURNAL

- J15. S. Videla, C. Guziolowski, F. Eduati, S. Thiele, M. Gebser, J. Nicolas, J. Saez-Rodriguez, T. Schaub, A. Siegel (2014) *Learning Boolean logic models of signaling networks with ASP* (2014). THEORETICAL COMPUTER SCIENCE.
- J16. S.M. Dittami, T. Barbeyron, C. Boyen, J. Cambefort, G. Collet, L. Delage, A. Gobet, A. Groisillier, C. Leblanc, G. Michel, D. Scornet, A. Siegel, J.E. Tapia and T. Tonon (2014). *Genome and metabolic network of "Candidatus Phaeoamarinobacter ectocarpi" Ec32, a new candidate genus of Alphaproteobacteria frequently associated with brown algae*, FRONTIERS IN GENETICS, section Systems Biology.
- J17. S. Laurent, A. Richard, O. Mulner-Lorillon, J. Morales, D. Flament, V. Glippa, J. Bourdon, P. Gosselin, A. Siegel, P. Cormier, R. Bellé (2014) *Modelisation of the regulation of protein synthesis following fertilization in sea urchin shows requirement of two processes : a destabilization of eIF4E :4E-BP complex and a great stimulation of the 4E-BP-degradation mechanism, both rapamycin-sensitive* FRONTIERS IN GENETICS section Systems Biology
- J18. P. Blavy, F. Gondret, S. Lagarrigue, J. Van Milgen and A. Siegel (2014). *Using a large-scale knowledge database on reactions and regulations to propose key upstream regulators of various sets of molecules participating in cell metabolism* BMC SYSTEMS BIOLOGY
- J19. O. Abdou-Arbi, S. Lemosquet, J. Van Milgen, A. Siegel and J. Bourdon (2014). *Exploring metabolism flexibility in complex organisms through quantitative study of precursor sets for system outputs*. BMC SYSTEMS BIOLOGY.
- J20. V. Berthé, T. Jolivet and A. Siegel (2014). *Connectedness of fractals associated with Arnoux-Rauzy substitution*. Special issue of the RAIRO-THEORETICAL INFORMATICS AND APPLICATIONS dedicated to the "Journées Montoises d'Informatique Théorique 2012".
- J21. C. Guziolowski, S. Videla, F. Eduati, S. Thiele, A. Siegel and J. Saez-Rodriguez (2013). *Exhaustively characterizing feasible logic models of a signaling network using Answer Set Programming*. BIOINFORMATICS.
- J22. R. Kaminski, T. Schaub, A. Siegel and S. Videla (2013). *Minimal Intervention Strategies in Logical Signaling Networks with Answer Set Programming*. ICLP - 29TH INTERNATIONAL CONFERENCE ON LOGIC PROGRAMMING. THEORY AND PRACTICE OF LOGIC PROGRAMMING 13 (Special Issue 4-5). 675-690.
- J23. V. Berthé, T. Jolivet, A. Siegel (2012). *Substitutive Arnoux-rauzy sequences have pure discrete spectrum* UNIFORM DISTRIBUTION THEORY 7(1).
- J24. J. Bourdon, D. Eveillard, A. Siegel (2011). *Integrating Quantitative Knowledge Into a Qualitative Gene Regulatory Network*. PLOS COMPUTATIONAL BIOLOGY, 7(9) e1002157.
- J25. V. Berthé, A. Siegel, W. Steiner, P. Surer, J. Thuswaldner (2011). *Fractal tiles associated with shift radix systems* ADVANCES IN MATHEMATICS.
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- C1. C. Frioux T. Schaub, S. Schellhorn, A. Siegel, P. Wanko, Hybrid Metabolic Network Completion, LPNMR 2017 (International Conference on Logic Programming and Nonmonotonic Reasoning, Logic Programming and Nonmonotonic Reasoning, 10377, Springer, p. 308 ?321.
- C2. V. Picard, J. Bourdon, A. Siegel, A logic for Checking the Probabilistic Steady-State Properties of Reaction Networks, IJCAI-BAI 2015 BIOINFORMATICS AND ARTIFICIAL INTELLIGENCE Argentina.
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- C9. V. Berthé, J. Bourdon, T. Jolivet and A. Siegel (2013). *Generating discrete planes with substitutions*. WORDS - 9TH INTERNATIONAL CONFERENCE ON WORDS.
- C10. S. Videla, C. Guziolowski, F. Eduati, S. Thiele, N. Grabe, J. Saez-Rodriguez and A. Siegel (2012). *Revisiting the Training of Logic Models of Protein Signaling Networks with a Formal Approach based on Answer Set Programming*. CMSB - COMPUTATIONAL METHODS IN SYSTEMS BIOLOGY. London. **Best paper award**.
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- C12. S. Lemosquet, O. Abdou-Arbi, A. Siegel, J. Guinard-Flament, J. Van Milgen, J. Bourdon, A generic stoichiometric model to analyse the metabolic flexibility of the mammary gland in lactating dairy cows (2010). in MODELLING NUTRIENT DIGESTION AND UTILIZATION IN FARM ANIMALS, Wageningen Academic Publishers , 2010
- C13. S. Blachon, A. Siegel, O. Radulescu (2009). *Relate inter-patient gene copy numbers variations with gene expression via gene networks in Ewing sarcoma*, BIOMEDICAL INFORMATICS AND INTELLIGENT METHODS IN THE SUPPORT OF GENOMIC MEDICINE Workshop, AIAI 2009, Greece. CEUR Workshop Proceedings vol. 475.

- C14. C. Guziolowski, J. Gruel, O. Radulescu and A. Siegel (2009). *Curating a large-scale regulatory network by evaluating its consistency with expression datasets*, CIBB 2008 - COMPUTATIONAL INTELLIGENCE METHODS FOR BIOINFORMATICS AND BIOSTATISTICS. Peer-reviewed selected papers. Lecture Notes in Computer Science, 5488, Springer-Verlag, p.144-155, 2009
- C15. A. Siegel, M. Le Borgne, O. Radulescu, C. Guziolowski, P. Veber (2007). *Qualitative response of interaction networks : application to the validation of biological models*. Minisymposium *New research in bioinformatics*. ICIAM - 6TH INTERNATIONAL CONGRESS ON INDUSTRIAL AND APPLIED MATHEMATICS. Zurich. PPAM, Volume 7, Issue 1, p 1121803-1121804.
- C16. P. Arnoux, V. Berthé, and A. Siegel (2006). *Finiteness properties for Pisot S-adic tilings* JOURNÉES MONTTOISES D'INFORMATIQUE THÉORIQUE.
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- C18. A. Siegel, *Spectral theory for dynamical system arising from substitutions* (2003). EWM, K. Dajani, J. Von Reis (eds.), CWITract, Marseille, 2003.

AUTRES COMMUNICATIONS

Communication à des congrès, symposium en mathématiques (sans actes)

Numeration, Kyoto, Japon (06/2012) - *The Mathematics of Aperiodic Order*, Corea (10/2010) - *Numeration*, Leiden, Neitherlands (06/2010, **Invited conference**) - *Aperiodic Order*, Leicester, Great-Britain (09/2009, **Invited conference**) - *Fractals and Tilings*, Strobl, Austria (07/2009) - *Number Theory and Ergodic Theory*, Kanazawa, Japan (04/2008) - *Systèmes Dynamiques, Automates et Algorithmes, GT SDA2*, Paris (10/2007) - *Numeration*, Graz, Autriche (04/2007) - *International Conference on Probability and Number Theory*, Japan (05/2005) - *Numeration Tilings and Substitutions*, Grenoble (03/2005) - *Number Theoretic Algorithms and Related Topics* Strobl, Austria (10/2004) - *Aperiodic Order : Dynamical Systems, Combinatorics and Operators*, Banff, Canada (04/2004). EWM (European Women in Mathematics), Marseille (11/2003). *Forum des jeunes mathématiciennes et des jeunes informaticiennes* Paris (03/2002). *Systèmes dynamiques-l'odyssée dynamique*, CIRM (02/2001) - *Fourth international joint meeting of the AMS and SSM* Denton, Texas (05/1999).

Communication à des congrès, symposium en bioinformatique (sans actes)

ECMTC - european conference on mathematical and theoretical biology, Nottingham, UK (07/2016) - *Integrative biology*, Lille (12/2015) - *Journées de l'axe analyse structurale et métabolomique de BioGenOuest*, Nantes (12/2015) - *Théorie des réseaux booléens et leurs applications en biologie*, Nice (11/2015) - *Logical Modeling and Analysis of Cellular Networks*, Strasbourg/ECCB 2014 (09/2014). **Invited conference** - *Logic and Systems Biology*, Vienna/CSL/LICS 2014 (07/2014). **Invited conference** - *CIBB Computational Intelligence Methods for Bioinformatics and Biostatistics & PRIB International Conference on Pattern Recognition in Bioinformatics*, Nice (06/2013) **Keynote speaker**.

Séminaires

Systèmes biologiques Sanofi (Gentilly, 01/17) - CMM (Chile, 11/2016) - Frei Berlin Univ. (10/2015) - CMM (Chile, 11/2014) - FRUMAM, Marseille (10/2014) - LINA, Nantes (07/2014) - LRI, Orsay (06/2014) - EBI, Cambridge, UK, (02/2013) - Inria Sophia Antipolis (02/2013, 02/2010) - Info, Univ. Evry (01/2013) - CMM, Univ. Chile (11/2012) - Station Bio. Roscoff (05/2010 ; 10/2008) - CAREN, Rennes (03/2010) - Math, Orsay (04/2009) - LSNC, Toulon (12/2007) - Math, Nice (03/2007).

Géométrie discrète, numération LIRMM, Montpellier (02/2006) - LIAFA, Paris VII (02/01) - IGM, Marne la vallée (12/2000) - Info, Amiens (03/1998).

Systèmes dynamiques symbolique, numération, pavages Orsay (01/2015) - Leoben, Austria (10/2012) - LATP, Marseille (01/2010, 10/1997, 03/1999, 04/2000) - Grenoble (11/2009) - IRMAR, Rennes (02/2008, 02/2005, 11/2001) - Orsay (05/2006, 06/2001) - ENS Lyon (04/2006) - Neuchâtel (01/2006) - TU Wien (11/2005) - Brest (11/2004) - Dijon (03/2001) - Montpellier (03/01) - Paris VI (11/2000) - Ecole polytechnique (11/2000) - Bordeaux (10/2000) - Turku (09/1998) - IML, Marseille (04/1998, 04/2000)

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1. D. Eveillard, P. Vandenkoornhuysse, Anne Siegel (2016, to appear), *L'écologie des systèmes*, LES BIG DATA À DÉCOUVERT
2. M. Taghipoor, S. Lemosquet, J. van Milgen, A. Siegel, D. Sauvart, F. Gondret (2016, to appear), *Modélisation de la flexibilité métabolique : vers une meilleure compréhension des capacités adaptatives de l'animal*, INRA PRODUCTION ANIMALE
3. T. Schaub and A. Siegel (2010) *Testing, Diagnosing, Repairing, and Predicting from Regulatory Networks and Datasets* ERCIM NEWS (82)

4. A. Siegel, C. Guziolowski, P. Veber, O. Radulescu, M. Le Borgne (2007) *Optimiser un plan d'expérience à partir de modèles qualitatifs ?*, BIOFUTUR (275).
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6. A. Siegel, *Fractals a la carte* (2004) TANGENTE, Hors Série 18 Les fractales
7. A. Siegel. *Répétitions dans les figures géométriques*. (2002) *Quadrature* 34.