

Carole KNIBBE

36 years old

Born Dec. 5th, 1980 in Hoorn (Netherlands)

French citizenship

Associate Professor

Université Lyon 1, France

Computer Science Department

LIRIS Laboratory (UMR CNRS 5205)

INRIA Beagle Team



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Education and job history

Université Lyon 1, Lyon, France

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| 2015 - Present | Head of the Beagle-Liris team (10 members), a subset of the INRIA Beagle team. |
| 2010 - Present | Member of the INRIA Beagle team. |
| 2007 - Present | Associate Professor in the Computer Science Department and in the LIRIS laboratory. |

Université Paris 5, Paris, France

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| 2006-2007 | Post-doctoral Fellow in the Laboratoire de Génétique Moléculaire Evolutive et Médicale (Microbiology laboratory, INSERM U571, Faculté de Médecine Necker), with François Taddéi. |
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National Institute for Applied Sciences (INSA), Lyon, France

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| 2006 | PhD in Computational Biology, INSA-Lyon.

Thesis : <i>Structuration des génomes par sélection indirecte de la variabilité mutationnelle – une approche de modélisation et de simulation</i> . Supervisors : Jean-Michel Fayard (Biosciences dept) and Guillaume Beslon (Computer Science dept). |
| 2003 | MSc in Computational Biology. Highest honors, top of the year.

Thesis: <i>Evolution structurelle des génomes bactériens – une approche computationnelle</i> . Supervisors: Jean-Michel Fayard and Guillaume Beslon. |

Research themes

I build mathematical and computational models of biological systems, with applications in molecular evolution, and, more recently, in lipid metabolism.

Publications

International journals :

- C. Rocabert, **C. Knibbe**, J. Consuegra, D. Schneider, G. Beslon. (2017). Beware Batch Culture: Seasonality and Niche Construction Predicted to Favor Bacterial Adaptive Diversification. *PLoS Computational Biology*, in press.
- P. Biller, L. Gueguen, **C. Knibbe**, E. Tannier. (2016). Breaking good: accounting for fragility of genomic regions in rearrangement distance estimation. *Genome Biology and Evolution*, 8(5): 1427-1439.
- S. Fischer, S. Bernard, G. Beslon, **C. Knibbe**. (2014). A model for genome size evolution. *Bulletin of Mathematical Biology* 76(9):2249-2291.
- B. Batut, **C. Knibbe**, G. Marais, V. Daubin. (2014). Reductive genome evolution at both ends of bacterial population size spectrum. *Nature Reviews Microbiology* 12(12):841-850.
- B. Batut, D.P. Parsons, S. Fischer, G. Beslon, **C. Knibbe**. (2013). *In silico* experimental evolution: a tool to test evolutionary scenarios. *BMC Bioinformatics* 14(S15):S11.
- T. Hindré, **C. Knibbe**, G. Beslon, D. Schneider. (2012). New insights into bacterial adaptation through in vivo and in silico experimental evolution. *Nature Reviews Microbiology* 10:352–365.
- G. Beslon, D. P. Parsons, Y. Sanchez-Dehesa, J.-M. Pena, **C. Knibbe**. (2010). Scaling laws in bacterial genomes: A side-effect of selection of mutational robustness? *Biosystems* 102:32–40.
- C. Knibbe**, J.M. Fayard, G. Beslon. (2008). The topology of the protein network influences the dynamics of gene order: From Systems Biology to a systemic understanding of evolution. *Artificial Life* 14(1):149–156.
- C. Knibbe**, O. Mazet, F. Chaudier, J.-M. Fayard, G. Beslon (2007). Evolutionary coupling between the deleteriousness of gene mutations and the amount of non-coding sequences. *Journal of Theoretical Biology* 244(4):621–630.
- C. Knibbe**, A. Coulon, O. Mazet, J.-M. Fayard, G. Beslon (2007). A long-term evolutionary pressure on the amount of non-coding DNA. *Molecular Biology and Evolution* 24(10):2344–2353.

International conferences with peer-reviewed proceedings :

- P. Biller, **C. Knibbe**, G. Beslon, E. Tannier. (2016). Comparative genomics of artificial life. In L. Bienvenu and N. Jonoska (ed.), *CiE 2016 (Computability in Europe)*, Paris, France, volume 9709 of Lecture Notes in Computer Science, Springer, pp. 35-44.
- C. Knibbe**, D.P. Parsons. (2014). What happened to my genes? Insights on gene family dynamics from digital genetics experiments. In *ALIFE 14 (14th Intl. Conf. on the Synthesis and Simulation of Living Systems)*, Sayama, H. et al. (ed.) New York, NY. MIT Press, Cambridge, Massachusetts, pp. 33-40.
- G. Beslon, B. Batut, D. Parsons, D. Schneider, **C. Knibbe**. (2013). An alife game to teach evolution of antibiotic resistance. In *European Conference on Artificial Life*, Taormina. pp. 43-50. MIT Press.
- D.P. Parsons, **C. Knibbe**, G. Beslon. (2012). The Paradoxical Effects of Allelic Recombination on Fitness. In *Artificial Life XIII*, East Lansing, Michigan (USA). ISBN 978-0-262-31050-5. 2012.
- D.P. Parsons, **C. Knibbe**, G. Beslon. (2011). Homologous and nonhomologous rearrangements: Interactions and effects on evolvability. In *European Conference on Artificial Life (ECAL)*, T. Lenaerts, M. Giacobini, H. Bersini, P. Bourguin, M. Dorigo, R. Doursat ed. Paris. pp. 622-629. MIT Press.

C. Knibbe, D.P. Parsons, G. Beslon. (2011). Parsimonious modeling of scaling laws in genomes and transcriptomes. In *European Conference on Artificial Life (ECAL)*, T. Lenaerts, M. Giacobini, H. Bersini, P. Bourguine, M. Dorigo, R. Doursat ed. Paris. pp. 414-415. MIT Press .

D.P. Parsons, **C. Knibbe**, G. Beslon. (2010) Importance of the rearrangement rates on the organization of transcription. In *Artificial Life*, MIT Press ed. Odense, Denmark. pp. 479-486. ISBN 978-0-262-29075-3.

G. Beslon, Y. Sanchez-Dehesa, D.P. Parsons, J.M. Pena, **C. Knibbe**. (2009). Scaling Laws in Digital Organisms. In *Proc. Information Processing in Cells and Tissues (IPCAT'09)*, Ascona, Switzerland. pp. 111-114.

Book chapters:

C. Knibbe. (2013). L'évolution expérimentale in silico. In *Modéliser et simuler - Epistémologies et pratiques de la modélisation et de la simulation - Tome 1*, edited by F. Varenne and M. Silberstein, Editions Matériologiques, ISBN: 978-2-919694-19-8, pp. 581–610.

G. Beslon et C. Knibbe. (2010). Petits bricolages en évolution. In *Des mondes bricolés? Arts et sciences à l'épreuve de la notion de bricolage*, édité par F. Odin and C. Thuderoz, Presses Polytechniques et Universitaires Romandes, ISBN: 978-2-88074-901-9.

Workshops, other conferences :

C. Rocabert, C. Knibbe, J. Consuegra, D. Schneider & G. Beslon (2016). « In Silico Experimental Evolution Highlights the Influence of Environmental Seasonality on Bacterial Diversification ». *2nd EvoEvo Workshop, (Satellite workshop of CCS2016)*, Septembre 2016, Amsterdam, The Netherlands.

P. Biller, E. Tannier, G. Beslon, C. Knibbe (2016). In silico experimental evolution provides independent and challenging benchmarks for comparative genomics (titre court: Comparative genomics on artificial life). In *Journées ouvertes en Biologie, Informatique et Mathématiques (JOBIM) 2016*, June 2016, Lyon, France.

B. Batut, G. Beslon & C. Knibbe (2016). « Unexpected genome inflation and streamlining in variable environments ». In *Journées ouvertes de Biologie Informatique & Mathématiques (JOBIM) 2016*, June 2016, Lyon, France.

C. Rocabert, C. Knibbe, G. Beslon. (2015). Towards an Integrated Evolutionary Model to Study Evolution of Evolution. In *EvoEvo Workshop (Satellite workshop of ECAL 2015)*, 24 July 2015, York (UK).

S. Fischer, S. Bernard, G. Beslon, C. Knibbe (2013). Genome size evolution: challenging intuition with modelling. In *International Conference on Stochastic Models in Ecology, Evolution and Genetics*, Angers, 9-13 décembre 2013.

B. Batut, M. Dumond, G. Marais, G. Beslon & C. Knibbe (2012). « Simulating evolutionary scenarios to test whether they can induce reductive evolution ». *SMBE 2012 : Society for Molecular Biology and Evolution*, June 26th, 2012, Dublin, Ireland.

S. Fischer, C. Knibbe, S. Bernard, G. Beslon (2011). Unravelling laws of genome evolution with both mathematical and individual-based models. *8th European Conference on Mathematical and Theoretical Biology (ECMTB 2011)*, Krakow, Poland, June 2011.

D.P. Parsons, C. Knibbe, G. Beslon (2010). Influence of the rearrangement rates on the organization of genome transcription, In *Integrative Post-Genomics 2010*, Lyon, France.

D.P. Parsons, C. Knibbe, G. Beslon. (2010). Influence of the rearrangement rates on the organization of genome transcription. In *JOBIM 2010*, Montpellier, France.

D.P. Parsons, G. Beslon, C. Knibbe, Y. Sanchez-Dehesa, J.M. Pena. (2009). Evolution of scaling laws in artificial regulation networks. In *Integrative Post-Genomics 2009*, Lyon, France. p. 22.

G. Beslon, S. Franceschelli, C. Knibbe. (2008). Petits bricolages en évolution. In "*Génies de la Bricole et du Bricolage, tribute to Claude Lévy-Strauss*", Lyon, France.

G. Kaneko, C. Knibbe, G. Beslon. (2007). Effect of bottlenecks on genome size: Investigations by digital genetics. In *Integrative Post-Genomics 2007*, Lyon, France.

Software

- **Aevol (Artificial EVOLution)**: an individual-based simulator of genome evolution. About 50 000 lines of C++ code. GPL license. Available either as a Debian package or via the aevol website (<http://aevol.inrialpes.fr/>). Currently used by Inserm U10001 microbiology laboratory (Paris), and by researchers from the universities of York (UK), Manchester (UK), Valencia (Spain) and New-Foundland (Canada).
- **Tewep (Transposable Elements Within Expanding Populations)**: an individual-based simulator of transposable element proliferation in expanding populations. About 4 000 lines of C++ code, under development. Joint work with population geneticist Matthieu Boulesteix (Laboratoire de Biométrie et Biologie Evolutive, Lyon).
- **Evo2Sim**: Within the context of the European project "EvoEvo" and of Charles Rocabert's PhD thesis, we have developed a multi-scale evolutionary model which takes into account the (ultra-fast) dynamics of metabolic networks, the (fast) dynamics of gene regulatory networks, the (medium to slow) dynamics of resources in the ecosystem and the (slow) evolutionary dynamics of genes and genome structure.
- **Simuscale**: prototype of an individual-based simulator of cell populations where cells have an internal circuitry and can exchange molecular signals, move, grow, divide and die. Joint work with Samuel Bernard (Institut Camille Jordan and Inria "Dracula" team, Lyon). Simuscale's development is now being carried on by Inria Dracula team.

Student supervision

PhD theses

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| 2008 – 2011 | David Parsons, "Indirect selection in Darwinian Evolution: Mechanisms and Implications". Joint supervision with Guillaume Beslon (LIRIS). Thesis defended on December 8th, 2011, INSA-Lyon. |
| 2010 – 2013 | Stephan Fischer, "Modélisation de l'évolution de la taille des génomes et de leur densité en gènes par mutations locales et grands réarrangements chromosomiques". Joint supervision with Guillaume Beslon (LIRIS) and Samuel Bernard (ICJ). Thesis defended on December 2 nd , 2013, INSA-Lyon. |
| 2011 - 2014 | Bérénice Batut, "Etude de l'évolution réductive des génomes bactériens par expériences d'évolution in silico et analyses bioinformatiques". Joint supervision with Gabriel Marais (LBBE) and Guillaume Beslon (LIRIS). Thesis defended on November 21st, 2014, INSA -Lyon. |

2013 - Present Charles Rocabert, "Studying evolution of bacterial micro-organisms by computer simulation approaches". Joint supervision with Guillaume Beslon (LIRIS).

MSc theses

2011 Bérénice Batut: "Quand l'évolution darwinienne réduit la complexité: Etude de l'évolution réductive de certains génomes bactériens par expériences d'évolution *in silico*". Full supervision.

2014 Mathias Millet: "Artificial chemistries: on the influence of parameters on evolution of populations". Joint supervision with Hédi Soula (Inserm Carmen, Lyon).

2015 Alice Joffard: "Modélisation et simulation de la dynamique des éléments transposables lors d'une expansion géographique". Joint supervision with Matthieu Boulesteix (Laboratoire de Biométrie et Biologie Evolutive, Lyon).

2016 Nicolas Comte: "Evolution expérimentale in silico : production de benchmarks pour les méthodes d'inférence phylogénétique". Joint supervision with Eric Tannier (Laboratoire de Biométrie et Biologie Evolutive, Lyon) and Guillaume Beslon.

Other internships

2011 Mathilde Dumond (undergraduate student in Biology, ENS), « Modélisation de l'évolution structurelle de génomes bactériens dans différents contextes environnementaux ».

2012 Houleymatou Baldé (undergraduate student in Computer Science, Université Lyon 1), « Conception et réalisation d'un formulaire en ligne pour la saisie des paramètres du simulateur aevol ».

2016 Tom Dusséaux (graduate student in Computer Science, Université Lyon 1): "Un nouveau mapping du génotype au phénotype pour aevol".

Awarded grants and participation to research projects

2011-2012 Principal investigator for a collaborative two-year project awarded by the French CNRS: "Analyze, simulate and experiment bacterial genome evolution". Coordination of 5 partners from Microbiology, Mathematics, Bioinformatics and Computer Science with a total budget of 50 000 euros.

2014-2016 Principal investigator for a two-year technological grant awarded by the Inria Institute. Coordination of a small development team for the aevol software.

2013-2016 Member of the European project Evoevo (<http://www.evoevo.eu/>, EVLIT call of the FP7 program). Joint project with Utrecht University (Netherlands), University of Valencia (Spain), Université Joseph Fourier (Grenoble, France), University of York (UK).

Implication in the research community

Responsibilities inside the LIRIS laboratory:

2015 - Present Head of the Beagle-Liris team.
2015 - Present Member of the laboratory council.

Examination committees for PhD theses:

2009 External examiner for the PhD thesis of Anton Crombach, Utrecht University, Netherlands.
2014 External examiner for the PhD thesis of Antoine Frénoy, Université Paris Descartes, Paris, France.
2016 External examiner for the PhD thesis of Gael Jalowicki, University College Dublin, Ireland.

Hiring committees and grant committees:

2007-2010 Head of the grant committee of the Rhône-Alpes Institute for Complex Systems (IXXI), which awards about 100 000 euros per year to interdisciplinary, exploratory research projects.
2010-2012 Vice-Head of the grant committee of the Rhône-Alpes Institute for Complex Systems (IXXI).
2014 Member of the expert panel to hire an Associate Professor in the Biosciences department of the National Institute for Applied Sciences (INSA), Lyon.
2016 Member of the expert panel to hire an Associate Professor in the Medicine Department of Université Paris Diderot, 2016.
2016 - Present Member of the Technological Grants Committee of Inria Rhône-Alpes, Grenoble.

Organization of international conferences :

Scientific chair of ECAL 2017 (European Conference on Artificial Life), which will take place in Lyon in september 2017.

Program committees of international conferences :

- PC member of ECCB 2012 (European Conference on Computational Biology)
- PC member of ECCB 2014 (European Conference on Computational Biology)
- PC member of ALIFE 2014 (International Conference on the Synthesis and Simulation of Living Systems)
- PC member of ECAL 2015 (European Conference on Artificial Life)
- PC member of ALIFE 2016 (International Conference on the Synthesis and Simulation of Living Systems)
- Reviewer for ECCB 2016 (European Conference on Computational Biology)

Invited talks:

- Inria TAO team, "Lessons from the evolution of artificial genomes", Orsay, February 2007.
- Laboratoire Matière et Systemes Complexes, "Lessons from the evolution of artificial genomes", Paris, April 2007.
- Séminaire de Modélisation du Vivant (Semovi), "Evolvability, robustness and genome structure: where is the link?", Lyon, June 2007.
- Santa Fe Institute (USA), "How the topology of the protein network influences the evolution of genome structure in artificial organisms", Santa Fe, USA, July 2007.
- Advanced School on Biodiversity and biological resources, "Evolution of evolution : molecular mechanisms, models and virtual experiments", Lyon, June 2008.

- Bioinformatics group, Utrecht University, "Evolution in action: robustness and evolvability in digital genomes and gene networks", Utrecht (Pays-Bas), April 2009.
- York Centre for Complex Systems, "Evolution in action: robustness and evolvability in digital genomes and gene networks", York, UK, November 2009.
- EvoLyon 2009 conference, "Robustesse et évolutivité des génomes", Lyon, November 2009.
- Ecole thématique interdisciplinaire d'échanges et de formation en biologie de Berder 2012, "Evolution réelle de génomes artificiels, ou évolution artificielle de génomes réels ?", Berder, 2012.
- Journée de bilan du RTRA Finovi, "PEACE: Parallel Experimental and Computational Evolution of virulence in Legionella pneumophila", June 2013.
- EvoLyon 2013 conference, "L'évolution expérimentale in silico", Lyon, November 2013.
- Laboratoire Interdisciplinaire de Physique, "Computational and mathematical models for the evolution of genomic architecture... or: How really bad our intuition is, when genome evolution is concerned", Grenoble, September 2014.
- International conference on Theoretical Approaches for the Genome and the Proteome, "What happened to my genes? Insights on gene family dynamics from digital genetics experiments", Chambéry, December 2014.
- Center for Research and Interdisciplinarity, Université Paris Descartes, "Genome size evolution: challenging intuition with modelling", Paris, November 2014.
- Workshop of the International Laboratory EvoAct (Evolution in action) "Modeling regulation and metabolism in MISEEM (Multi-scale In Silico Experimental Evolution Model)", Autrans, April 2016.
- Séminaire de Modélisation du Vivant (Semovi), "Insights on genome dynamics from in silico experimental evolution and mathematical modelling", Lyon, September 2016.
- Jacques Monod conference on "Evolutionary Genomics and Systems Biology: Bringing Together Theoretical and Experimental Approaches", "Genome evolution: challenging intuition with modelling and simulation", Roscoff, October 2016.

Teaching

About 200 hrs per academic year.

Undergraduate level:

Lectures and labs of Algorithmics and procedural programming

Labs on Web programming

Graduate level:

Labs on Web programming

Lectures and labs on Object-Oriented Programming

Lectures and labs on Bioinspired computing

Lectures and labs on Scientific methods and research ethics

Coordination of the Computer Science part of the Bioinformatics Master Program of Université Lyon 1