

Charles ROCAERT, Ph.D.

Evolutionary and Systems Biology, Computational and Mathematical Biology

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EDUCATION AND RESEARCH PROJECTS

Postdoctoral Research Fellow, Balazs Papp laboratory

Since 2018 (Szeged, Hungary)

- **Supervisor:** Dr. Balázs Papp.
- **Studying the conservation of metabolic levels across mammalian species (1 manuscript in preparation):** Development of [MetEvolSim](#), a Python package to simulate the evolution of metabolic concentrations in SBML kinetic models (**MCMC simulations, ODE numerical solving, numerical integration, parallel computing**). Thermodynamics-based flux balance analysis (**mTOW on Recon 1 model, optimization, parallel computing**).
- **Analyzing phenotypic noise in compensatory evolution:** Analysis of a multi-dimensional Calmorph dataset from several knock-out Yeast strains under compensatory evolution (**statistical analysis, GLM, non-linear transformations, linear algebra**).
- **Proficient in agile management/dev methods:** Initiated an agile-based management in the team.

Postdoctoral Research Fellow, INRIA (project-team Beagle)

2019-2020 (Lyon, France)

- **Supervisor:** Prof. Guillaume Beslon.
- **Impact of an evolvable phenotypic noise on the adaptation rate of complex organisms (1 publication in Evolution):** Development of a quantitative genetics and computational framework (**mathematical modeling, agent-based simulations, HPC**).

Ph.D. Research, INRIA Rhône-Alpes, INSA-Lyon, LIRIS UMR-CNRS-5205

2013-2017 (Lyon, France)

- **Subject:** « Studying the evolution of bacterial micro-organisms by modeling and numerical simulation approaches » (defended on Nov. 17th, 2017).
- **Supervisors:** Prof. Guillaume Beslon and Dr. Carole Knibbe.
- **Studying the emergence of metabolic cross-feeding and stable bacterial diversification (1 publication in PLoS Computational Biology):** Development of [Evo²Sim](#), a C++ simulation software of bacterial evolution in realistic experimental setups (**agent-based simulations, ODE numerical solving, graph theory, HPC**).
- **Studying the evolution of bacterial genetic regulation:** Evolutionary simulations of realistic bacterial genetic regulation networks with Evo²Sim.
- Member of the inter-disciplinary European project EvoEvo: **wrote 8 deliverables, developed official website** (www.evoevo.eu).
- Organizing committee of the 14th European Conference on Artificial Life ([ECAL 2017](#)), Lyon, France.

Other research projects

- **Integrating road network topology for modeling human-mediated dispersal in terrestrial landscapes (1 manuscript under review at Methods in Ecology and Evolution + 1 in preparation):** Development of [MoRIS](#) software in collaboration with LEHNA UMR-CNRS-5023, Université de Lyon, LIRIS UMR-CNRS-5205 (Lyon, France), and University of Lausanne (Lausanne, Switzerland). MoRIS is a spatially explicit and mechanistic stochastic jump model to simulate HMD in terrestrial landscapes through road network (**agent-based simulations, data-based optimization, graph theory, HPC on the IN2P3 computing center**).

M.Sc. Computational and Mathematical Biology, Université de Lyon

2011-2013 (Lyon, France)

- With honors (1st/101).

B.Sc. Computational and Mathematical Biology, Université de Lyon

2008-2011 (Lyon, France)

- With honors.

SUPERVISION OF STUDENTS

Co-supervisor of Aymeric Bonnamour (Master 1, Université de Lyon, France).

2019

- **Subject:** « Combining landscape genetics and numerical simulation to understand how humans disperse invasive species on a landscape scale ».

TEACHING EXPERIENCE

Tutoring (middle school, high school)

Since 2018 (San Francisco, USA)

- **Mathematics (~150h/year):** 6th to 12th grades (French mathematics curriculum)

Graduate Department, INSA de Lyon

2014-2016 (Lyon, France)

- **Genetic algorithms and project management (16h/year):** 4th year students of Bioinformatics and Modeling program (project management, graph theory, optimization algorithms, Python programming).

Undergraduate Department, INSA de Lyon

2014-2016 (Lyon, France)

- **C/C++ programming (52h/year):** 3rd year students of Bioinformatics and Modeling program (C/C++ programming basics, object-oriented programming, project management).

SOFTWARE AND NUMERICAL TOOLS

MetEvolSim

MetEvolSim is a Python package providing numerical tools to simulate the long-term evolution of metabolic abundances. MetEvolSim takes as an input any SBML metabolic network model, as soon as kinetic parameters and initial metabolic concentrations are specified, and a stable steady-state exists.

- Developed by **C. Rocabert**, G. Boross and B. Papp.
- **Github:** <https://github.com/charlesrocabert/MetEvolSim>.

Evo²Sim

Evo²Sim is 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. The software is designed to perform *in silico* experimental evolution experiments, that mimic real experimental evolution protocols.

- Developed by **C. Rocabert**, C. Knibbe and G. Beslon, under the European project EvoEvo (www.evoevo.eu).
- **Github:** <https://github.com/charlesrocabert/Evo2Sim>.

σFGM

σFGM is a numerical solver for Fisher's geometric model, with evolvable phenotypic noise.

- Developed by **C. Rocabert**, G. Beslon, C. Knibbe and S. Bernard.
- **Github:** <https://github.com/charlesrocabert/SigmaFGM>.

MoRIS

MoRIS software (Model of Roads of Invasive Spread) is a spatially explicit spread model designed to simulate invasive species dispersal by transport, at local to regional spatial scales.

- Developed by **C. Rocabert**, J. M.W. Gippet and S. Fenet.
- **Github:** <https://github.com/charlesrocabert/MoRIS>.

COMPUTER SKILLS

- **Programming languages:** C/C++, Python, Bash, R.
- **Developing tools:** CI/CD (Github Actions, Github project management tools), VCS (svn, git), Build and Packaging (autotools, Cmake, Pypi), Debug (gdb, Valgrind), Profiling and Code Optimization (Intel-Advisor, OSX-Instruments), Documentation (Doxygen, LaTeX, Github), Parallel computing and HPC (TBB, OAR, regular user of the computing farm IN2P3, <https://cc.in2p3.fr/>).
- **Scientific tools and visualization:** R, GSL, numpy, scipy, pygmo, cma, cobrapy, optlang, matplotlib, ggplot, tidyverse, SBML, Copasi, libroadrunner, Tellurium.
- **Web:** HTML, CSS, SQL, Hugo, WordPress, Bootstrap.

GRANTS AND AWARDS

- **2019-2020:** INRIA@SiliconValley postdoctoral grant (1.5 year funding).
- **2015:** Grant (€5,000) from the Institute of Complex Systems (Lyon, France) to develop MoRIS.
- **2013-2017:** INRIA PhD fellowship funded by the European project EvoEvo (www.evoevo.eu).
- **2011-2013:** Merit scholarship (€200/month), granted by CROUS, Lyon, France.
- **2011:** Merit scholarship (€2,000), granted by Université de Lyon, France.

IMPLICATION IN THE RESEARCH COMMUNITY

- **2017:** Reviewer for BioSystems international journal.
- **Sept. 2017:** Organizing committee of the 14th European Conference on Artificial Life, Lyon, France.
- **2013-2016:** Development and management of the website of the European project EvoEvo (www.evoevo.eu, EVLIT call of the FP7 program).

PUBLICATIONS

- 2 articles published in high-impact peer-reviewed journals (*PLoS Computational Biology*, *Evolution*),
- 1 manuscript under review (*Methods in Ecology and Evolution*),
- 2 manuscripts in preparation,
- 9 presentations and posters in international conferences with peer-reviewed proceedings and workshops (France, UK, Netherlands).
- 8 deliverables for the European project EvoEvo.

International journals

- **C. Rocabert**, G. Beslon, C. Knibbe, S. Bernard **(2020)**. Phenotypic Noise and the Cost of Complexity. *Evolution*, 74(10), 2221-2237.
- **C. Rocabert**, C. Knibbe, J. Consuegra, D. Schneider and G. Beslon **(2017)**. Beware Batch Culture: Seasonality and Niche Construction Predicted to Favor Bacterial Adaptive Diversification. *PLoS Computational Biology*, 13(3), e1005459.

Pre-prints

- **C. Rocabert**, S. Fenet, B. Kaufmann, J.M.W. Gippet **(2020)**. Integrating road network topology for modelling human-mediated dispersal in terrestrial landscapes (under review at *Methods in Ecology and Evolution*).

International conferences with peer-reviewed proceedings

- **C. Rocabert**, C. Knibbe, J. Consuegra, D. Schneider and G. Beslon **(2017, September)**. Environmental seasonality drives digital populations towards stable cross-feeding. In *Proceedings of ECAL 2017 conference. 14th European Conference on Artificial Life* (Lyon, France).
- J. M.W. Gippet, S. Fenet, A. Dumet, B. Kaufmann and **C. Rocabert (2016, August)**. MoRIS: Model of Routes of Invasive Spread. Human-mediated dispersal, road network and invasion parameters. In *Proceedings of IENE 2016 conference. 5th International Conference on Ecology and Transportation: Integrating Transport Infrastructures with Living Landscapes* (Lyon, France).
- J. M.W. Gippet, **C. Rocabert**, S. Fenet, A. Dumet and B. Kaufmann **(2015, July)**. Modeling and evaluating human-mediated dispersal mechanisms at landscape scale: a study of road network and invasion parameters for *Lasius neglectus* ants invasive species. In *Proceedings of World Conference on Natural Resource Modeling* (Bordeaux, France).

Workshops, other conferences, poster communications

- O. Liska, G. Boross, **C. Rocabert**, M. Faragó, B. Szappanos, B. Papp **(2020, February)**. Principles of metabolome conservation in mammals. *Evolutionary Systems Biology, Wellcome Genome Campus* (Cambridge, UK).
- **C. Rocabert**, G. Beslon et C. Knibbe and S. Bernard **(2019, December)**. Phenotypic Noise and the Cost of Complexity. *EvoLyon 2019* (Lyon, France).

- **C. Rocabert**, S. Bernard, G. Beslon and C. Knibbe **(2017, November)**. Phenotypic Noise and the Cost of Complexity. *SMBE conference, Approches Interdisciplinaires pour l'Évolution Moléculaire* (Lyon, France).
- **C. Rocabert**, C. Knibbe, J. Consuegra, D. Schneider and G. Beslon **(2016, September)**. In Silico Experimental Evolution Highlights the Influence of Environmental Seasonality on Bacterial Diversification. In *the Second EvoEvo Workshop. Satellite workshop of CCS2016* (Amsterdam, Netherlands).
- **C. Rocabert**, C. Knibbe, J. Consuegra, D. Schneider and G. Beslon **(2016, April)**. In Silico Experimental Evolution Highlights the Influence of Environmental Seasonality on Bacterial Diversification. In *EvoAct: Evolution in action with living and artificial organisms conference* (Autrans, France).
- **C. Rocabert**, C. Knibbe, J. Consuegra, D. Schneider and G. Beslon **(2016, March)**. Environmental Driving of Bacterial Diversification in In Silico Experimental Evolution. In *Evolutionary systems biology: from model organisms to human disease workshop*, (Cambridge, UK).
- **C. Rocabert**, C. Knibbe and G. Beslon **(2015, July)**. Towards a Integrated Evolutionary Model to Study Evolution of Evolution. In *the First EvoEvo Workshop, Satellite Workshop of ECAL 2015* (York, UK).

Publicly available scientific reports

- G. Beslon and **C. Rocabert (2015)**. EvoEvo Deliverable 2.8: Integrated evolutionary model. *[Research Report] INRIA Grenoble - Rhône-Alpes*.
- G. Beslon and **C. Rocabert (2015)**. EvoEvo Deliverable 2.6 : Realistic-network model. *[Research Report] INRIA Grenoble - Rhône-Alpes*.
- G. Beslon and **C. Rocabert (2015)**. EvoEvo Deliverable 2.4 : Population model. *[Research Report] INRIA Grenoble - Rhône-Alpes*.
- G. Beslon and **C. Rocabert (2015)**. EvoEvo Deliverable 2.2 : Genome-network model. *[Research Report] INRIA Grenoble - Rhône-Alpes*.
- G. Beslon and **C. Rocabert (2015)**. EvoEvo Deliverable 2.7: Specifications of the integrated evolutionary model. *[Research Report] INRIA Grenoble - Rhône-Alpes*.
- G. Beslon, C. Knibbe and **C. Rocabert (2014)**. EvoEvo Deliverable 2.5 : Specifications of the realistic network model. *[Research Report] INRIA Grenoble - Rhône-Alpes*.
- G. Beslon, P. Hogeweg, C. Knibbe, **C. Rocabert** and S. Stepney **(2014)**. EvoEvo Deliverable 2.3: Specifications of the population model. *[Research Report] INRIA Grenoble - Rhône-Alpes*.
- G. Beslon, P. Andrews, C. Knibbe and **C. Rocabert (2014)**. EvoEvo Deliverable 2.1: Specifications of the genome-network model. *[Research Report] INRIA Grenoble - Rhône-Alpes*.