Arnaud Becheler - Software Engineer (Genetics)

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♒ February 6th, 1990 🏴 French 🎓 Ph.D.

Education

Université Paris-Sud, Paris-Saclay, France
Ph.D., Population Genetics (December 2014 – June 2018)
Fields: Genetics and Coalescence Theory, Applied Mathematics, Statistics.

Université de Montpellier, France
MSc, Biodiversity, Ecology and Evolution (2013/2014)
Ranked 6/17

Universidad de Salamanca, Espagne
MSc, Biodiversity and Terrestrial Ecosystems (2012/2013)

Université de Bordeaux, France
BSc, Biodiversity of Organisms and Ecosystems (2011/2012)
Major of the promotion

Industry Experience

Designing a synthetic genetic system to enable breeding of in-game artificial-intelligent characters with unique personality, genome, bionics, colors and complexion.
Software Engineer (Genetics). July 2022 – May 2023.
Irreverent Labs (Bellevue, WA, USA).

Research Experience

Does genetic structure detected under the Multi-Species Coalescent Model reflect cryptic species divergence or population structure in geographically widespread putative taxa?
Post-doctoral contract. July 2018 – July 2022.
University of Michigan (Ann Arbor, MI, USA).
Principal Investigator: Dr. Lacey Knowles (Ecology and Evolutionary Biology Department).

Environmental demogenetic models for biological invasion processes, application to the invasion of Vespa velutina.
Ph.D. Student December 2014 – June 2018.
Supervisor: Dr. Stéphane Dupas, (Laboratory EGCE, Gif-sur-Yvette, France).
Co-supervisor: Dr. Camille Coron, (Laboratoire de Mathématiques d'Orsay).

Limits of genome-scans for detecting loci under selection in autogamous species.
Master 2, internship. 2014, 6 months, CBGP (Montpellier, France).
Supervisors: Miguel Navascuès, Renaud Vitalis.

Softwares

The Quetzal framework - Tools for spatial coalescence simulations. Open source project.
Maintainer and developer.
C++ genetic components, C++ programs and Python library for simulation of genetic data in spatially explicit landscapes and inference with Machine Learning.
⊙ Github Organization.

(Pre) Publications	de Navascués, M, **Becheler, A**, Gay, L, Ronfort, J., Loridon, K., Vitalis, R. (2021). Power and limits of selection genome scans on temporal data from a selfing population. *Peer Community Journal.* 📄 Access the article.
	Becheler, A., & Knowles, L. L. (2020). Occupancy spectrum distribution: application for coalescence simulation with generic mergers. *Bioinformatics.* 📄 Access the article.
	Becheler, A., Coron, C., & Dupas, S. (2019). The Quetzal Coalescence Template Library: A C++ programmers resource for integrating distributional, demographic and coalescent models. *Molecular Ecology Resources.* 📄 Access the article.
	Becheler A., Moritz C., Sukumaran J. & Knowles, L. L. (in preparation, 12 pages). Cryptic species or populations? Testing competing hypotheses from the multispecies coalescent.
	Becheler A., Moritz C., Sukumaran J. & Knowles, L. L. (in preparation, 2 pages). *Quetzal-EGGS, Quetzal-CRUMBS, Quetzal-NEST and Decrypt: resources for simulating, inferring and testing the geography of divergence.*
Presentations & Posters	*Modèle de démogénétique environnementale pour l'étude des processus d'invasion biologique.* Séminaire IDEEV, Mars 2018.
	Modèle de démogénétique environnementale pour l'étude des processus d'invasion biologique. Rencontre de la Chair de Modélisation Mathématique pour la Biodiversité, Février 2018.
	Study of recent coalescence events in contemporaneous landscapes : C++ template library for Approximate Bayesian Computation. 3rd BeNeLuxFra Student Symposium, Juillet 2017, Lille (France).
	Demogenetic Model for Invasive Processes (poster). JOBIM 2017, Juillet 2017, Lille (France).
Conference Organization	*Ecosystems dynamics: Stakes, data and models.* Research Program 2019 – Pascal Institute, Université Paris-Saclay. **Organization:** Stéphane Dupas , Camille Coron, **Arnaud Becheler**, Adelaïde Olivier. Concepts et modern approaches in modelisation and statistical analyses. 1 week summer school, 3 weeks research.
	Species delimitation. Workshop 2020 – University of Michigan. **Organisation:** Lacey L. Knowles, **Arnaud Becheler**. The MultiSpecies Coalescent model and its applicability for species delimitation. Presentation of DECRYPT and DELINEATE. Impact of assumption violation and sampling scheme on species delimitation.
Mentoring	Florence Jornod (2016) **Simulating gene genealogies in landscapes for studying biological invasions.** MSc thesis. Master 1 Biologie Informatique Bioinformatique, Université Paris-Diderot (France). Mentoring quota 100%.
Languages & Skills	French (native) , English (advanced), Spanish (avanced), German (basic). C++, Python, R, LaTeX, Git, Github, Docker, DAGMan, HTCondor.