



PÔLES TECHNIQUES

PÔLE INFORMATIQUE

MIELE Vincent

INGÉNIEUR DE RECHERCHE

CNRS

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69622 VILLEURBANNE cedex (<http://maps.google.com/maps?q=43%20bd%20du%2011%20novembre%201918+69622+%20VILLEURBANNE%20cedex>)

📞 330472448544

@ Courriel

I am working in

[CNRS](#) ↗

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[Biometry and Evolutionary Biology Lab \(https://lbbe.univ-lyon1.fr\)](https://lbbe.univ-lyon1.fr)

. With a background in mathematics and computer science, I am involved in projects in ecology, on two main axes :

ecological networks : analysing original datasets, proposing new methodological developments and helping non specialists (see

this ["quick tips" paper](#) ↗

);

image, ecology & deep learning : as a leader of the **imaginecology initiative** (see

[imaginecology website](#) ↗


), developing computer vision pipelines and sharing knowledge with other ecologists.

SELECTED WORK

[Projet JENGA](#) ↗

[Projet DeepFaune](#) 



For a complete list, I am almost 100% degooglized, but you can still have a look at [my scholar profile](#) 

- › Noa Rigoudy, the DeepFaune consortium, Bruno Spataro, Vincent Miele, Simon Chamaillé-Jammes, *The DeepFaune initiative: a collaborative effort towards the automatic identification of the French fauna in camera-trap images*,

[Preprint bioRxiv](#) ↗

(2022)

- › Vincent Miele, Stéphane Dray et Olivier Gimenez, *Images, écologie et deep learning*,

[Regards sur la biodiversité, Société Française d'Écologie et d'Évolution](#) ↗

(2021)

- › Vincent Miele, Gaspard Dussert, Bruno Spataro, Simon Chamaillé-Jammes, Dominique Allainé & Christophe Bonenfant, *Revisiting giraffe photo-identification using deep learning and network analysis*.

[Methods in Ecology and Evolution](#) ↗

(2021)

[Preprint bioRxiv](#) ↗

/ Media coverage :

[France 3](#) ↗

,

[RFI](#) ↗

- › Christophe Botella, Stéphane Dray, Catherine Matias, Vincent Miele, Wilfried Thuiller, *An appraisal of graph embeddings for comparing trophic network architectures*.

[Methods in Ecology and Evolution](#) ↗

(2021)

- › Vincent Miele, Catherine Matias, Marc Ohlmann, Giovanni Poggiato, Stéphane Dray, Wilfried Thuiller, *Quantifying the overall effect of biotic interactions on species communities along environmental gradients*.

[Preprint HAL](#) ↗

(2021)

- › Vincent Miele, Catherine Matias, Stéphane Robin & Stéphane Dray, *Nine Quick Tips for Analyzing Network Data*.

[PLoS Comp. Biology](#) ↗

(2019)

- › Catherine Matias & Vincent Miele, *Statistical clustering of temporal networks through dynamic a stochastic block model*.

[Journal of the Royal Statistical Society : Series B](#) ↗

(2016)

[Arxiv](#) ↗

COMMITTEE/JURY/PROJECT MEMBER

Project member :



> [ANR EcoNet 2019-2024](#) 

> ANR FuturePred 2019-2022

> ANR Horizon 2018-2022

> ANR Colib'read 2012-2016

> ANR Ancestrome 2011-2016

> ANR NeMo 2007-2011

Board member

> [GdR EcoStat](#) 

2019-

> CNRS AISSAI (AI for Science, Science for AI) 2022-

> [IXXI](#) 

2021-

> [Groupe Calcul](#) 

2009-2017

> [LyonCalcul](#) 

(co-founder) 2012-2016

> [CCIS/COCIN \(CNRS\)](#)

2012-2015

> [SMAI MAIRCI](#) 

2013-2015

Reviewer :

- > [Journal of Statistical Software](#) 
- > [Annals of statistics](#) 
- > [Journal of The Royal Society Interface](#) 
- > [Journal of the American Statistical Association](#) 
- > [PLoS Biology](#) 
- > [PCI Ecology](#) 
- > [The American Naturalist](#) 
- > [Biology Letters](#) 
- > [Scientific Reports](#) 
- > [Science Advances](#) 
- > [IEEE Transactions on Signal and Information Processing over Networks](#) 
- > [Frontiers in Ecology and Evolution](#) 
- > [Biological reviews](#) 
- > [Mammalian Biology](#) 
- > [PLoS ONE](#) 
- > [Bioinformatics](#) 
- > [TCBB](#) 

Jury member :

- > INRA IRE01, 2022 (président)
- > HCERES MISTEA, 2020
- > INRA IRE01, 2018 (président)
- > UGA IGE, 2017
- > CNRS IR43, 2017
- > INRA CEI, 2017
- > CNRS IE 13INSMI03, 2013
- > INRA IRE12, 2012
- > INRA IRE05, 2011
- > INRA IRE01, 2009

> CNRS IE 155, 2008

Organizing committee :

> [imaginecology workshop](#) 

, Novembre 2020

> ANF

[R pour le calcul](#) 

, Octobre 2015

> Ecole Rhône-Alpes ARC6

[Découverte du calcul](#) 

, Septembre 2013

> [Mini-Symposium SMAI 2013](#) 

MAT4NET Mathématiques pour l'analyse de grands réseaux, Juin 2013

> ANF

[Programmation hybride](#) 

, Octobre 2012

> [CEMRACS](#) 

, Méthodes numériques et algorithmes pour architectures hautes performances, Summer 2012 (le reportage de France3

[ici](#) 

)





> Journées du groupe Calcul , November 2010.

> Le coté Calcul de Jobim , June 2009.

> Mathematics for Biological Networks , December 2007

> European Conference on Computational Biology, September 2003

Here (c) means "co-supervision"

- › Elias Chetouane, M2 Informatique et Données, Deep learning for camera traps, 2022
- › Marine Desprez (c), Post Doc, Machine learning in ecology, 2022
- › Bastien Payre, M2 Maths en action, Deep learning et séquences d'images, 2021
- › Nathan Levray, M2 Maths en action, Higher order networks, 2021
- › Noa Rigoudy (c), ENS Lyon, Deep learning for camera traps, 2021
- › Julien Bonnier (c), M2 BEE, reconnaissance des pollens, 2021
- › Giusseppe Capizzi, M2 Data Science, Machine learning for botanics, 2020-21
- › Christophe Botella (c), Post Doc, Graph embeddings, 2020-21
- › Thibault Genissel (c), ENS Lyon, Réseaux de contact entre ongulés, 2020
- › Gaspard Dussert, ENSTA, imaginecology, 2019
- › Claire Gayral, M2 Maths en action, Algorithme EM classifiant dans dynSBM, 2018
- › Gonché Danesh (c), M2 Bioinformatique, Simulation de HTT, 2017
- › Florent Tessier, M2 Bioinformatique, Génomique comparative du manchot, 2015
- › Mamadou Dione, M2 Mathématiques, Etude de la température corporelle des marmottes en lien avec les conditions climatiques, 2014
- › Camille Marchet (c), Software Engineer
[INRIA Bamboo](#) 
, 2013-2014
- › Thomas Bigot (c), Software Engineer
[ANR Ancestrome](#) 
, 2013-2015
- › Mathilde Boutigny, M1 Ingénieur, Développement du
[package kisssplice2reftranscriptome](#) 
, 2014
- › Alice Julien (c), Software Engineer
[INRIA Bamboo](#) 
, 2012-2013
- › Patrick Tran Van, L3 UCBL, Intégration de programmes de calcul dédiés aux NGS dans le système GALAXY, 2012
- › Vincent Lanore, M1 ENS Info, Hybrid parallel computing applied to DNA processing, 2011
- › Aurélie Siberchicot (c), CDD ANR, 2010-11 (C++ development manager)
- › Marie Jorandon, M1 INAPG, Etude statistique de données NGS sur l'espacement des nucléosomes, 2009
- › Laurent Modolo, L3 UCBL Bio, Packaging d'une application de recherche de motifs, 2008

> [deepfaune](#) 

Automatic identification of the French fauna in camera-trap images

Collaboration with Simon Chamailé-Jammes et Bruno Spataro

> [econetwork](#) 

A collection of advanced tools, methods and models for the analysis of ecological networks,

Collaboration with EcoNet group

> [queyras](#) 

A minimal deep learning image classifier, implemented in the french Alps with R and Keras

> [dynsbm](https://lbbe.univ-lyon1.fr/dynsbm) (<https://lbbe.univ-lyon1.fr/dynsbm>)

Dynamic stochastic block models,

Collaboration with C.Matias

> [HiFiX](#)

+

[SiLiX](#)

Ultra-fast + High Fidelity Clustering of sequences

efficient parallel algorithms + network science.

Collaboration with L.Duret, D.Kahn, V.Daubin & S.Penel

Ingénieur Mathematics and Modelling - Polytech Clermont-Ferrand
Master Applied Mathematics - University of Clermont Auvergne

