



## PÔLES TECHNIQUES

### PÔLE INFORMATIQUE

**MIELE Vincent**

### INGÉNIEUR DE RECHERCHE

CNRS

📍 43 bd du 11 novembre 1918  
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](#) ↗

@

[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

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

> 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-
- > [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 :**

- > 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



- › 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, ENS Lyon, Deep learning for camera traps, 2021
- › Julien Bonnier, M2 BEE, reconnaissance des pollens, 2021
- › Giuseppe Capizzi, M2 Data Science, Machine learning for botanics, 2020-21
- › Christophe Botella, Post Doc, Graph embeddings, 2020-21
- › Thibault Genissel, 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, 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, Software Engineer  
[INRIA Bamboo](#)   
, 2013-2014
- › Thomas Bigot, Software Engineer  
[ANR Ancestrome](#)   
, 2013-2015
- › Mathilde Boutigny, M1 Ingénieur, Développement du  
[package kisssplice2reftranscriptome](#)   
, 2014
- › Alice Julien, 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, CDD ANR, 2010-11(C++ development manager)
- › Marie Jorandon, M1 INAPG, Etude statistique de données NGS sur l'espace des nucléosomes, 2009
- › Laurent Modolo, L3 UCBL Bio, Packaging d'une application de recherche de motifs, 2008



> [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](#)

*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 Clermond-Ferrand  
Master Applied Mathematics - University of Clermont Auvergne

