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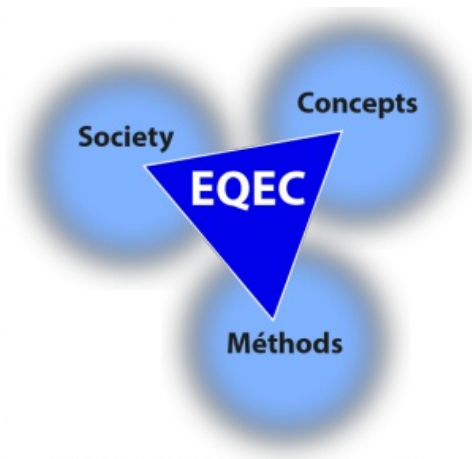
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Our research activities, focused on interspecific interactions (community ecology), aim to better understand the ecological and evolutionary processes structuring species assemblages and biodiversity at different temporal and spatial scales. Our team addresses these major issues using contrasting biological models (communities of large African mammals, insects, microbiota, plants) from 3 complementary angles:

- Our work is strongly anchored in the conceptual framework of evolutionary biology by studying (i) the diversity of adaptive responses implemented by organisms to selective pressures in their environment, (ii) their consequences on population demography and ultimately (iii) the dynamics and composition of species communities.
- Our research is closely linked to societal issues of biodiversity conservation and management by integrating both the functioning of socio-ecological systems and the context of climate change. We conduct experimental studies, manage and ensure the long-term monitoring of several community observation networks.
- Methodological issues also occupy a central place in our team, with the development of new tools for statistical processing and modeling of ecological data. This activity leads to the development of methods and software that we develop and distribute freely.

Research programs



Functioning of African savanna communities

The Hwange LTSER (Long-Term Socio-Ecological Research site in [Zimbabwe](#) ↗

hosts a long-term interdisciplinary research program that focuses on the functioning of plant and animal communities within the Hwange National Park and the interactions between this protected area and humans living in its periphery. Based on this program, three axes are developed: (1) studying the population dynamics of elephants, exploring their impact and that of management policies on the socio-ecosystem functioning; (2) Understanding the extent to which interactions within and between trophic levels are sensitive to management actions (e.g. sport hunting, water management) and climate change; (3) Decoding human ecology and human-wildlife coexistence mechanisms towards integrated conservation and sustainable functioning of the socio-ecosystem.

This research is complemented by more recent works in the Hluhluwe-iMfolozi Park and in the Madikwe reserve in South Africa, which focus on the role of environmental conditions on the hunting success of large African carnivores. We work in close collaboration with the IRL (International Research Lab)

[Rehabs](#) ↗

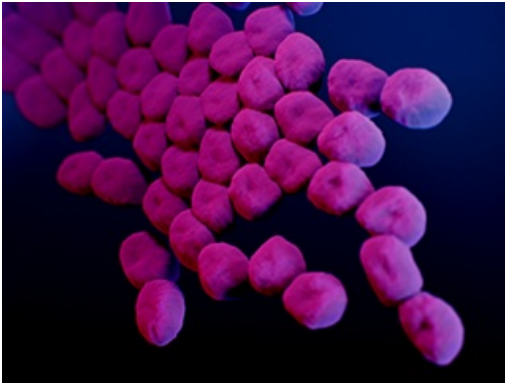
Involved group members : Alice Bernard, Laura Lacomme, Aïssa Morin, Lisa Nicvert, Elie Pedarros, Yolán Richard, Marion Valeix*



Masting and the community dynamics of seed consumers

Masting is a reproductive strategy often encountered in perennial plants, characterized by fructifications highly fluctuating in time and being synchronized at the population level. The seeds produced that way constitute a pulsed resource with a strong impact on the eco-evolutionary dynamics of seed-consuming communities and forest regeneration. Our lack of knowledge of this system still impedes our understanding of the dynamics of temperate forest ecosystems and its future in the context of climate change. Our work carried out on oak forests aims to better understand (i) the proximal causes of masting, (ii) the mechanisms underlying the coexistence of species competing for such highly fluctuating resource and (iii) the co-evolution of consumer exploitation strategies for the fluctuating resource and forest tree fruiting strategies. On the basis of the results obtained, scenarii will be proposed on the future of forest regeneration under climate change, that may serve forest management.

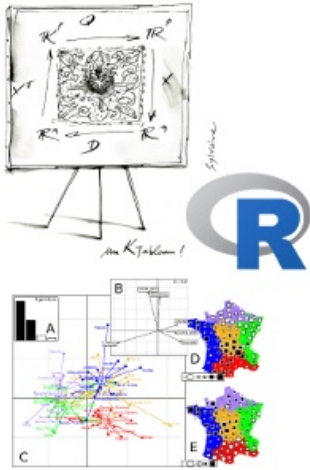
Involved group members : Marie-Claude Bel-Venner*, Emilie Fleurot, Léa Keurinck, Jean Lobry, Samuel Venner



The spread of antibiotic resistance genes in bacteria

Antibiotic resistance is recognized as one of the greatest current threats to human health, and the mobile genetic elements (MGEs) that circulate in bacterial populations and communities are the main vehicles. To understand the dynamics and diversity of MGEs in bacterial pangenomes and the emergence of antibiotic resistance genes, we propose to go beyond the framework of conventional genomics by considering pangenomes as complex ecological communities. In the Ab-One program, we mobilize the concepts and tools developed in community ecology based on an integrative approach (monitoring of bacterial populations/communities evolving in contrasting environments -One-Health approaches-, pan-genomic analyses, experimentation in molecular and cellular microbiology, mathematical modelling). This program is currently focused on the dynamics of MGEs in *Acinetobacter baumannii*, an antibiotic-resistant microorganism classified as a priority by the WHO. Other more general approaches will illustrate the relevance of this new conceptual framework to understand the dynamics and diversity of MGEs in bacterial pangenomes. This program, co-piloted by our team and a team from CIRI (Horigene) involves the participation of 9 organizations (6 from Lyon -LBBE, CIRI, MMSB, HCL, LEM, VetAgro Sup-, Institut Pasteur (Paris), LMGM (Toulouse), Robert Koch Institute (Germany)).

Involved group members : Stéphane Dray, Rémi Tuffet, Samuel Venner*



Statistical analysis of ecological data

Understanding the structure and dynamics of species assemblages, and the processes behind them, requires collecting data that are becoming increasingly complex owing to the sophisticated technological developments made available for their acquisition (e.g. GPS, loggers, satellite imagery, molecular data). We are developing new methods for analysing such data, that provide new insights into the ecological processes at work in communities. Multivariate analysis methods allow the analysis of spatial structures, accounting for various information on species (functional traits, morphology, phylogeny), the spatio-temporal variation of species-environment relationships or the multifaceted perception of the protected human-environment relationship. We also model multi-omics' dose-response data within communities in order to better understand the Adverse Outcome Pathway (AOP) and to better appreciate the risks to the environment. These methodological innovations are made available to the scientific community through the development, distribution and maintenance of software (libraries for the R language: `ade4`, `adegraphics`, `adephylo`, `ade4TkGUI`, `nlstools`, `fitdistrplus`, `DRomics`, `seqinr`).

Involved group members: Marie Laure Delignette-Muller, Stéphane Dray*, Jean Lobry, Jean Thioulouse.

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