



## Programme & Abstracts

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# **ABOUT TiBE 2015**

## ABOUT TiBE 2015

The current unprecedented rates of biodiversity loss, from genes and species to communities and ecosystems, have been related to the effects of multi-scale environmental changes. The Earth's biosphere is currently experiencing exceptionally high rates of ecosystem degradation and species extinction, largely due to human activities and other anthropogenic pressures on the global environment. This rapid decline of biodiversity has been recognized at several scales and across regions, and has been widely discussed for at least two decades in the scientific community. It is nowadays considered one of the most important themes of the environmental sustainability agenda, particularly since reductions in current species diversity can lead to profound alterations in the functioning of ecosystems well as in the resulting societal benefits.

The TiBE 2015 conference, organized by CIBIO-InBIO's Predictive Ecology (PRECOL) and Applied Ecology (APPLECOL) groups, will provide a broad perspective on recent advances in the study of the ecological impacts of social and economic drivers, land-use dynamics, biological invasions, species range and niche dynamics, genetic structure and flow, and other dimensions of change in ecosystems, landscapes and their biodiversity. Furthermore the conference will allow a direct link with applied ecology including: i) the detection, interpretation and forecast of changes in a given territory; ii) the anticipation of trends in the patterns of drivers of ecological change, and the early detection of biodiversity responses and ecosystem changes; and iii) the support to model-assisted frameworks for cost-efficient conservation and monitoring.

The program will include four scientific sessions, each with a plenary conference by an invited international expert and several communications proposed by the conference participants. The four sessions will address biological invasions, land use changes and social transitions as key drivers of global biodiversity change, as well as range and niche dynamics as processes involved in species' responses to global change drivers. The various presentations will cover a wide range of ecosystem types, taxonomic groups, theoretical approaches, methods and tools that are being used to tackle the key societal challenge of biodiversity decline and depletion of ecosystem services worldwide.

We hope you have a nice time at Vairão and wish you a fruitful scientific discussion!



# PROGRAMME

# PROGRAMME

## Day 1 - Monday | June 1, 2015

8:30 - 9:30 | Registration

9:30 - 9:45 | Opening session, by [Nuno Ferrand de Almeida](#), CIBIO-InBIO Director

### THEME 1 - BIOLOGICAL INVASIONS

9:45 - 10:45 | Plenary session

***Invasion science for society: tree invasions in South Africa as a case study***

[David Richardson](#)

10:45 - 11:15 | Oral presentations (12'+3' discussion)

***The world spread of fire ants - an example from French Guyana***

Eduardo Fox

***Angler's behavior as a vector of freshwater invasive species***

Filipe Banha et al.

11:15 - 11:45 | Coffee break

11:45 – 13:00 | Oral presentations (12'+3' discussion)

***Top-down regulation of estuarine phytoplankton by an invasive bivalve***

Jacinto Cunha et al.

***An improved multi-scale modelling framework to guide management of plant invasions in a transboundary context***

João Martins et al.

***Use and persistence of empty bivalve shells in a freshwater system***

Martina Ilarri et al.

***The unacknowledged trilemma of invasive species eradication***

Pedro Bingre and Luís Reino

***Reassembly of an aquatic community after drought: different resilience capacity by native and invasive species***

Ronaldo Sousa et al.

13:00 - 14:30 | Lunch

## THEME 2 - LAND USE CHANGE

14:30 - 15:30 | **Plenary session**

*Land use change, habitat change and consequences for biodiversity and ecosystem functions*

[Peter Verburg](#)

15:30 - 16:00 | **Oral presentations** (12'+3' discussion)

***A framework for efficient monitoring of riverscape's priority bryophyte diversity***

Ana Paula Portela et al.

***Differential movement of a forest carnivore within habitat heterogeneity and road influence: consequences for genetic structuring***

Filipe Carvalho et al.

16:00 - 16:30 | **Coffee break**

16:30 - 17:30 | **Oral presentations** (12'+3' discussion)

***From conservation genetics to conservation genomics of northern Madagascar lemurs***

Jordi Salmons and Lounès Chikhi

***Demographic inference using genetic data from a single individual: separating population size variation from population structure***

Lounès Chikhi et al.

***Responses of São Tomé's endemic-rich bird assemblage to land-use change: the need to acknowledge complexity***

Ricardo Lima et al.

***Landscape dynamics in mediterranean oak forests under global change: disentangling the role of anthropogenic and environmental drivers across species***

Vanda Acácio et al.

18:00 - 18:45 | **Poster presentations** (3' each)

19:00 | **Dinner at CIBIO-InBIO with multinational foods and drinks**

All participants are kindly invited to bring some food/drinks!

## Day 2 - Tuesday | June 2, 2015

### Theme 3 - SOCIOECOLOGICAL DRIVERS

9:30 - 10:30 | Plenary session

***Social drivers and regime shifts in tropical forest landscapes***

[Christian Kull](#)

10:30 - 11:00 | Oral presentations (12'+3')

***Biodiversity patterns of legume trees from the miombo and mopane woodlands of Mozambique in relation to fire frequency***

Luís Goulão

***Integrating resilience-based indicators of forest ecosystem services in a DPSIR framework – a review***

Ana Sofia Vaz et al.

11:00 - 11:30 | Coffee break

11:30 - 12:45 | Oral presentations (12'+3')

***Integrating concepts and indicators for a more effective assessment of high nature value***

Ana Teresa Novais et al.

***Hotspots of invasiveness of three acacia species in northern Portugal: a probabilistic overview of climate change effects***

Diogo Alagador and Joana Vicente

***The role of herbivores in the conservation of endemic heathlands in Galicia (NW Spain)***

Jaime Fagúndez

***Evaluating the regional cumulative impact of wind farms on birds: how can spatially-explicit dynamic modelling improve impact assessments and monitoring?***

Rita Bastos et al.

***Demographic bottleneck in two arboreal primates: a consequence of forest exploitation***

Tânia Minhós et al.

12:45 - 14:30 | Lunch

## Theme 4 - SPECIES' RANGE AND NICHE DYNAMICS

14:30 - 15:30 | Plenary session

***Contributions of life-history traits, niche variation, anthropogenic land use and historical factors to range and niche dynamics of invading species***

[Diederik Strubbe](#)

15:30 - 16:00 | Oral presentations (12'+3')

***Modelling invasions for managing impacts***

Mário Santos et al.

***Modeling the effects of temperature and salinity variations on the shore crab *Carcinus maenas****

Allan Souza et al.

16:00 - 16:30 | Coffee break

16:30 - 18:00 | Oral presentations (12'+3')

***Modeling the genetic consequences of social structure***

Bárbara Parreira and Lounès Chikhi

***Genetic inbreeding and neighbour vegetation cover drive drought-induced forest die-off***

Cristina García and Francisco Lloret

***Dispersal ability determines the scaling properties of species abundance distributions: a case study using data on arthropods from the Azores archipelago***

Luís Borda de Água et al.

***The importance of shallow areas as nursery grounds for the recruitment of juveniles of the blue crab *Callinectes sapidus rathbun, 1896****

Marcos Alaniz Rodrigues et al.

***Survey on effective factors in population's distribution and abundance of *Tatera indica* in Sistan, southeastern of Iran***

Saeed Mohammadi and Ali Sabaghzadeh

***The role of fish in the conservation of freshwater mussels***

Vanessa Modesto et al.

18:00 | Closing session



# ABSTRACTS

# ABSTRACTS

## Plenary Sessions

### DAY 1 - MONDAY | JUNE 1, 2015

#### THEME 1 - BIOLOGICAL INVASIONS

9:45 - 10:45 | Plenary session

#### ***Invasion science for society: tree invasions in South Africa as a case study***

[David Richardson](#)<sup>1</sup>

<sup>1</sup> Centre for Invasion Biology, Department of Botany & Zoology, Stellenbosch University, South Africa

Trees have increased in importance as invasive species over the last few decades. Because of their large size, their disproportionate influence on ecosystem processes, their many uses for humans, and because most tree introductions are intentional, tree invasions pose particularly challenging problems for managers of natural resources in many parts of the world.

South Africa is probably the “tree invasions capital of the world”. Hundreds of tree species have been introduced over the last three centuries and many species have become invasive. An initial wave of introductions, comprising especially species of *Acacia*, *Eucalyptus* and *Pinus*, resulted in widespread invasions with major impacts. Species from many other tree genera were introduced much more recently and many of these are also invading.

This talk reviews recent work undertaken at the Centre for Invasion Biology to understand the patterns and processes of tree invasions and to inform management and remediation efforts. Examples of studies on different tree species are reviewed to show the diversity of methods and approaches followed to shed light on the “nuts and bolts” of these invasions with respect to: introduction pathways; establishment; expansion and spread; and impacts. New approaches to improve management are also discussed. These include studies to improve our ability to prevent new introductions, optimize control procedures, restore ecosystems following invasion and control, and to monitor spread and the efficiency of control.

## THEME 2 - LAND USE CHANGE

14:30 - 15:30 | Plenary session

***Land use change, habitat change and consequences for biodiversity and ecosystem functions***

[Peter Verburg](#)<sup>1</sup>

<sup>1</sup> VU University, Amsterdam, The Netherlands

Land use change directly and indirectly changes habitat conditions affecting both biodiversity and ecosystem services. While land use change is commonly associated with loss of habitat in reality different changes in land use have different consequences and trade-offs between ecosystem services. No simple generalisations can be made and impacts are dependent on the scale of analysis. This presentation will provide examples of analysis of the impact of land use ranging from the global to the European to the local scale. New methods to analyse trade-offs can help land use planning and management.

## DAY 2 - TUESDAY | JUNE 2, 2015

### THEME 3 - SOCIOECOLOGICAL DRIVERS

9:30 - 10:30 | Plenary session

***Social drivers and regime shifts in tropical forest landscapes***

[Christian Kull](#)<sup>1</sup>

<sup>1</sup> Institute for Geography and Sustainability, University of Lausanne, Switzerland

What are the social drivers of global biodiversity change? In tropical forest landscapes, diverse processes are reshaping forest landscapes, causing deforestation, afforestation, and reforestation. These include economic exploitation, demographics, local and national policies, and the global circulation of ideas, capital, species, and people. The conjuncture of different drivers in different geographic contexts leads to different outcomes. I review examples from Madagascar, Costa Rica, and South East Asia, and then consider whether the concept of 'regime shift' (which is increasingly used in systems ecology and resilience studies) can be productively applied to such social processes.

## THEME 4 - SPECIES' RANGE AND NICHE DYNAMICS

14:30 - 15:30 | Plenary session

***Contributions of life-history traits, niche variation, anthropogenic land use and historical factors to range and niche dynamics of invading species***

[Diederik Strubbe](#)<sup>1,2</sup>

<sup>1</sup> University of Antwerp, Evolutionary Ecology Group, Belgium, <sup>2</sup> Ghent University, Terrestrial Ecology Unit, Belgium

Climate change, anthropogenic habitat alteration and the introduction of non-native species interact to reshape global patterns of species diversity. Forecasts of how biodiversity is likely to respond to these drivers are paramount for devising and implementing mitigation strategies. Yet, current methods attempting to predict species range dynamics assume that species realized niches remain conserved across space and time. Therefore, to formulate robust predictions, a better understanding of driver determining the degree of niche conservatism is required. Here, I will discuss four key issues where understanding is not all it should be. (1) There is little knowledge on which species traits and life-history characteristics that influence niche (and thus range dynamics). (2) Species may not represent ecological and evolutionary units. (3) Anthropogenic land habit conversion may overrule species climatic constraints. (4) Historical processes such as propagule pressure and residence time should be account for when evaluating niche and range dynamics of invasive species.

# ABSTRACTS

## Oral Communications

### DAY 1 - MONDAY | JUNE 1, 2015

#### THEME 1 - BIOLOGICAL INVASIONS

10:45 – 11:00 | Oral presentation

##### ***The world spread of fire ants - an example from French Guyana***

Eduardo Fox<sup>1</sup>

<sup>1</sup> University of Lausanne, DEE

Fire ants are aggressive stinging insects from South America which have spread around the world via marine commerce, mainly from the US. The fire ants are rated among the top 100 most dangerous invasive species by the IUCN, because of massive disequilibria and social damage caused into regions where they have been introduced. In their native range, fire ants can also become a nuisance, particularly in the Amazon forest. Based on recently obtained data, the ultramarine European territory of French Guyana has likely become a source of invasive fire ant populations, namely of a subspecies of *Solenopsis saevissima*. Specimens collected from Guadeloupe in the Antilles were initially assigned to *S. nr saevissima*, yet further morphological and chemical analyses have enabled assigning them to a well-studied, unicolonial population of *S. saevissima* that infests French Guyana, mainly causing issues at Kourou and Cayenne. The recently invaded territory is an island, and ants likely arrived by vessels coming from mainland French Guyana to the port of Jarry. The ecological impact of fire ants in islands has been previously reported as greatly damaging. Assigning the origin and approximate date of this spread may help prevent partially the damage and preclude similar future invasions.

11:00 – 11:15 | Oral presentation

##### ***Angler's behavior as a vector of freshwater invasive species***

Filipe Banha<sup>1</sup>, António Diniz<sup>2</sup> and Pedro M. Anastácio<sup>1</sup>

<sup>1</sup> MARE – Marine and Environmental Sciences Centre, Departamento de Paisagem, Ambiente e Ordenamento, Escola de Ciências e Tecnologia, Universidade de Évora, <sup>2</sup> Departamento de Psicologia, Escola de Ciências Sociais, Universidade de Évora, Colégio Pedro da Fonseca

Anglers are a recognized vector for invasive fauna, with both intentional and accidental introductions reported worldwide. The purpose of this study was to investigate the Iberian freshwater angler's habits related to biological invasions, using an international and bilingual

survey in Spain and Portugal. Our results showed that anglers have a great mobility, with no differences between countries in distances traveled to the fishing locations. The majority of anglers fish during consecutive days and visit several places. Yet, angler's activity patterns throughout the year were not similar. For both countries, the preferred fish species were invasive and its introductions were reported more often than native species. The categorical motivations chosen for introductions were country dependent. A low number of anglers use live bait, sometimes invasive species, and discharges of unused bait in the water are very frequent. Our findings on angler's behaviors, practices, mobility and activity may be used to model invasion risks and also to improve governmental agencies monitoring and awareness programs.

11:30 - 11:45 | **Oral presentation**

***Top-down regulation of estuarine phytoplankton by an invasive bivalve***

Pedro Morais<sup>1,2</sup>, Cátia Luís<sup>1</sup>, Jacinto Cunha<sup>2</sup>, Iolanda Rocha<sup>2</sup>, Ester Dias<sup>2</sup>, José Carlos Antunes<sup>2,3</sup> and Ronaldo Sousa<sup>2</sup>

<sup>1</sup> CIMA- Centro de Investigação Marinha e Ambiental, Universidade do Algarve, <sup>2</sup> CIIMAR- Centro Interdisciplinar de Investigação Marinha e Ambiental, Universidade do Porto, <sup>3</sup> Aquamuseu do Rio Minho, Vila Nova de Cerveira

Several invasive bivalves can disrupt established processes in pelagic and benthic realms. The Asian clam *Corbicula fluminea* is one of such species; however, the extent of its impact on ecosystem functions are still speculative and remain to be quantified. Thus, one of our goals was to investigate if *C. fluminea* can exert a significant top-down control upon estuarine phytoplankton and how it varies between blooming and non-blooming periods. A Latin-square design experiment was conducted with nine 1 m<sup>3</sup> tanks, paved with sediment, and three *C. fluminea* densities (0, 100 and 2000 ind. m<sup>-2</sup>), during a blooming and a non-blooming period. Samples were collected every hour throughout the first 12 hours, and subsequently at every 12h, for a total of 48h. During phytoplankton blooming, *C. fluminea* exerted a significant top-down control on estuarine phytoplankton and a similar grazing pressure upon all size classes. For example, 8 hours after the beginning of the experiment, just 1% of the initial phytoplankton abundance remained in the 2000 ind. m<sup>-2</sup> treatment. Apparently, during the non-blooming period, *C. fluminea* has the potential to delay the spring bloom, and a consequently cascading effect upon other trophic levels may occur by increasing the chances of resource mismatch.

11:45 - 12:00 | **Oral presentation**

***An improved multi-scale modelling framework to guide management of plant invasions in a transboundary context***

João Martins<sup>1</sup>, Renato Henriques<sup>2</sup>, Elizabeth Marchante<sup>3</sup>, Hélia Marchante<sup>3,6</sup>, Paulo Alves<sup>1</sup>, David M. Richardson<sup>4</sup>, Mirijam Gaertner<sup>4</sup>, João Honrado<sup>1,5</sup> and Joana Vicente<sup>1</sup>

<sup>1</sup> CIBIO-InBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva-, Universidade do Porto, <sup>2</sup> Earth Sciences Department, University of Minho, <sup>3</sup> Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, <sup>4</sup> Centre for Invasion Biology, Department of Botany and Zoology, Stellenbosch University, <sup>5</sup> Faculdade de Ciências, Universidade do Porto, Portugal, <sup>6</sup> Departamento de Ambiente, Escola Superior Agrária do Instituto Politécnico de Coimbra

Invasion by exotic species threatens biodiversity conservation, promoting impacts ranging from local to global scales and affecting many features of ecosystems and human health. To understand and manage invasions, reliable frameworks for modelling drivers and spatial patterns of invasion are needed.

This work presents a multiscale spatial modelling framework, incorporating state of the art techniques such as Multimodel Inference and Ensemble Modelling to overcome some barriers to spatial modelling of invasions, such as lack of absence records and few registered occurrences. The framework is demonstrated with *Hakea sericea* Schrad, a Proteaceae shrub native to Australia and invasive in several regions. Two study areas were considered: the regional scale included Portugal and Galicia, and the local scale included the Minho region in northern Portugal. For the regional scale relative importance of sets of climate, landscape and geology predictors was evaluated, while at the local scale importance of each environmental predictor was assessed. The potential distribution of *H. sericea* was projected for both scales. Results indicate climate and landscape features as the most important determinants of the regional distribution of the species. A geological variable, related to the presence of schist lithology, was primarily important for predicting local scale distribution.

12:00 - 12:15 | **Oral presentation**

***Use and persistence of empty bivalve shells in a freshwater system***

Martina Ilarri<sup>1,2</sup>, Allan Tainá de Souza<sup>1</sup>, Vanessa Modesto<sup>1</sup>, Lúcia Guilhermino<sup>1,2</sup> and Ronaldo Sousa<sup>3</sup>

<sup>1</sup> Interdisciplinary Centre of Marine and Environmental Research (CIIMAR/CIMAR), University of Porto, <sup>2</sup> ICBAS-UP - Abel Salazar Biomedical Sciences Institute, University of Porto, <sup>3</sup> CBMA – Centre of Molecular and Environmental Biology, Department of Biology, University of Minho

Bivalve shells can potentially alter the aquatic community, especially in the benthic domain. Little is known about the influence of different shell morphologies and origins on the associated fauna. The present study aimed at studying how empty shells of four bivalves (*Anodonta anatina*, *Corbicula fluminea*, *Potomida littoralis*, *Unio delphinus*) influence the macrozoobenthic community and how long they can persist in the aquatic system, namely the Minho River (NW Iberian Peninsula). Comparisons among individual species and between different scenarios (before and after *C. fluminea* invasion) were performed. Our results indicated that the macrozoobenthic community did not vary among treatments (with the exception of species richness that was higher in the native species), and that almost no

differences were detected comparing the before and after invasion scenarios, despite the dissimilarities (size and morphology) between species. Furthermore, the shell decay rates were significantly different among species, with the invasive species *C. fluminea* showing a slower decay when compared to the natives *U. delphinus* and *A. anatina*. Due to the high *C. fluminea* population density, the amount of shells present on the river bottom nowadays is presumably higher than before its invasion, with the empty shells of this species partially replacing the shells of native species (in terms of density and biomass) as a physical and persistent substratum to the associated fauna.

12:15 - 12:30 | **Oral presentation**

***The unacknowledged trillema of invasive species eradication***

Pedro Bingre<sup>1</sup> and Luís Reino<sup>2</sup>

<sup>1</sup> Escola Superior Agrária de Coimbra, Coimbra, Portugal, <sup>2</sup> CIBIO-InBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva, Universidade do Porto, Portugal

Invasive alien species have been considered an environmental problem by scientists, civil society and governments for half a century. Within the European Union laws and policies have been enacted both to combat invasions already present and to prevent the occurrence of newer ones. While most of these initiatives prioritize the elimination of allochthonous taxa that caused objective damages either in the autochthonous biodiversity or in the economic infrastructure, some of them focus on purging exotic species for no other reason than freeing the landscape from non-native plants or animals and to restore ecosystems to its supposedly pristine condition. This latter option implies an ethical judgement that should be acknowledged. Facing a biological invasion, societies must choose one of the following three options: eradicate the invasive species, explore it (whenever feasible), or disregard it. To eradicate an exotic harmless species (however abundant it might be in the area) implies allocating technical resources that might be better put to use in the preservation of indigenous species; to explore it or to disregard it implies to renounce the ideal of restoring the pristineness of landscapes. Since every one of these alternatives is suboptimal in ethical terms, this choice constitutes a deontological trillema.

12:30 - 12:45 | **Oral presentation**

***Reassembly of an aquatic community after drought: different resilience capacity by native and invasive species***

Ronaldo Sousa<sup>1,2</sup>, Allan Tainá de Souza<sup>2</sup> and Martina Ilarri<sup>2</sup>

<sup>1</sup> CBMA – Centre of Molecular and Environmental Biology, Department of Biology, University of Minho, Portugal, <sup>2</sup> Interdisciplinary Centre of Marine and Environmental Research (CIIMAR/CIMAR), University of Porto

Extreme climatic events are predicted to increase in frequency and intensity due to global warming but their ecological legacies are poorly studied, particularly how they may reassemble aquatic communities. In this study a long data set (from 2004 to 2014) assessing the dynamics of a molluscan community provided us with an opportunity to show the consequences of the

2005 supra-seasonal drought on this faunal group. The resulted effects of this disturbance were responsible for significant alterations in the molluscan community with several native species (mainly native gastropods and sphaeriids) declining precipitously after 2006, whereas the invasive species *Corbicula fluminea* rapidly recovered from this disturbance. Given the low resilience shown by several native species they are threatened with local extinction. We conclude that extreme climatic events can be responsible for drastic changes in the structure of aquatic communities and that long term data sets are essential to fully understand the community changes and ecosystem functioning.

## THEME 2 - LAND USE CHANGE

15:30 - 15:45 | **Oral presentation**

### ***A framework for efficient monitoring of riverscape's priority bryophyte diversity***

Ana Paula Portela<sup>1,2</sup>, Bruno Marcos<sup>2</sup>, Helena Hespanhol<sup>2</sup>, Rubim Silva<sup>1,2</sup>, João Honrado<sup>1,2</sup> and Cristiana Vieira<sup>2</sup>

<sup>1</sup> Faculdade de Ciências, Universidade do Porto, Portugal, <sup>2</sup> CIBIO-InBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva, Universidade do Porto, Portugal

Freshwater biodiversity is among the most threatened worldwide, hence conservation planning and monitoring are urgent needs. The objective of this work was to develop a framework for efficient monitoring network of high conservation-interest bryological communities in riverscapes of Northern Portugal.

A three step modelling approach was employed: (1) community-level modelling approach using biomod2 to produce a spatially-explicit model of community types (2) Zonation software to spatialize conservation priority for bryophyte communities with high conservation value; and (3) a monitoring network using “sampling” package based on unequal-probability, random sampling and priority ranking. Four sampling strata were employed and obtained through the intersection of two criteria: (i) protection status of the areas (ii) presence of potential impacts from fragmenting infrastructures.

We obtained the potential distribution of fluvial bryophyte communities allowing the spatial conservation prioritization across the territory and hence developing a network to monitor conflicts between priority conservation areas and human impact.

We demonstrated the usefulness of modelling techniques to assist the development of efficient monitoring networks at regional scales. The need for monitoring schemes that are not limited to protected areas and individual impact assessments, but, instead, are based on a comprehensive cumulative vision of the impacts, is evident.

15:45 - 16:00 | **Oral presentation**

***Differential movement of a forest carnivore within habitat heterogeneity and road influence: consequences for genetic structuring***

Filipe Carvalho<sup>1</sup>, Rafael Carvalho<sup>1</sup>, António Mira<sup>1</sup> and Pedro Beja<sup>2,3</sup>

<sup>1</sup> CIBIO-InBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva, Universidade de Évora, Portugal <sup>2</sup> EDP Biodiversity Chair, CIBIO-InBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva, Universidade do Porto, Portugal, <sup>3</sup> CIBIO-InBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva, Universidade do Porto, Portugal

Landscape functional connectivity of a species depends on its behaviour and movement ability and influences its persistence in human-modified landscapes. Nonetheless, the effects of functional connectivity loss by small forest carnivores are poorly understood. This study combines movement and genetic data to assess the effects of roads and habitat heterogeneity on the functional connectivity of the common genet in a forest-agricultural landscape, in southern Portugal. Specifically, we aim to : i) use path-level analysis to model landscape functional connectivity and assess the main environmental factors influencing it; ii) combine roadkills, radiotracking and genetic analysis to infer crossing events and dispersal effectiveness. Landscape connectivity was favoured by large forest patches, and near riparian areas providing corridors within open agricultural land highly resistant to genet movement. Roads reduced connectivity by dissecting forest patches, but had less effect on riparian corridors due to crossing structures. The combined sources of information suggested that the motorway allowed high gene flow, despite the roadkills and the constraints to adult movements. Low traffic volume, numerous crossing structures, ability to overcome obstacles, high population sizes on both sides of the motorway, and the absence of territorial constraints to effective migration potentially originated our results. Our study provides important clues to mitigate road effects on the landscape functional connectivity of small forest carnivores.

16:30 - 16:45 | **Oral presentation**

***From conservation genetics to conservation genomics of northern Madagascar lemurs***

Jordi Salmona<sup>1</sup> and Lounès Chikhi<sup>1,2,3</sup>

<sup>1</sup> Instituto Gulbenkian de Ciência, Portugal, <sup>2</sup> CNRS, Université Paul Sabatier, ENFA, France, <sup>3</sup> Université de Toulouse, France

Madagascar is one of the hottest biodiversity hotspot and it faces critical deforestation and poaching rates. As such it represents a conservation priority. It is increasingly recognized that ancient climatic changes have influenced temperate and tropical species alike. However, in many regions it is difficult to disentangle anthropogenic from climatic effects. Madagascar represents an exception for such a large island, as it was colonized only recently by humans (4-5000yBP). It is thus a very good model to study the Holocene demographic history of endemic species. Our ongoing research focuses on three lemur genera (*Propithecus*, *Lepilemur* and *Microcebus*) from northern Madagascar and uses a comparative and multidisciplinary approach combining ecological field data, remote sensing tools, genetic and genomic data to model recent and ancient forest changes and population demography. After estimating population sizes, and sampling exhaustively populations from these species, we aim at bringing together traditional genetic (microsatellites and mt-DNA) and genomic (RAD-seq) data within a

single framework. We will present preliminary results on the recent natural history of lemurs populations and insights on the relative effects of human and environmental (past climatic) factors. While answering these questions is very challenging, the incorporation of genomic data provides accuracy not reachable just a few years ago.

16:45 - 17:00 | **Oral presentation**

***Demographic inference using genetic data from a single individual: separating population size variation from population structure***

Olivier Mazet<sup>1</sup>, Willy Rodriguez<sup>1</sup>, Lounès Chikhi<sup>2,3</sup>

<sup>1</sup> Institut de Mathématiques de Toulouse, Université de Toulouse & CNRS, France, <sup>2</sup> CNRS, Université Paul Sabatier, ENFA, France, <sup>3</sup> Instituto Gulbenkian de Ciência. Portugal

Genomic data represent opportunities for population genetics research. However, the increase in genetic information also represents new statistical challenges. For instance, recent work has shown that structured populations generate signals of population size change under various sampling schemes. As a consequence it is difficult to determine the extent to which the demographic histories reconstructed for many species are robust to confounding factors such as population structure, sampling schemes, mutation models etc. Given that genomic data will necessarily increase the precision of parameter estimates, it is important to identify meaningful models before estimating parameters. We found that it is possible to use genomic data from a single diploid individual to perform precise parameter estimation and model choice. We analysed one model of instantaneous population size change and Wright's n-island model and determined when data were generated by one or the other model. To do that we used the coalescent theory to re-derive the distribution of coalescence times under the two models for a sample of size two, and used a maximum likelihood approach to estimate the parameters of these models. We then validated a model rejection procedure based on the Kolmogorov-Smirnov test, and a model choice procedure based on the AIC.

17:00 - 17:15 | **Oral presentation**

***Responses of São Tomé's endemic-rich bird assemblage to land-use change: the need to acknowledge complexity***

Ricardo Faustino de Lima<sup>1</sup>, Martin Dallimer<sup>2</sup>, Philip W. Atkinson<sup>3</sup> and Jos Barlow<sup>4</sup>

<sup>1</sup> Ce3C - Centre for Ecology, Evolution and Environmental Changes, Lisbon University, Portugal, <sup>2</sup> Sustainability Research Institute, University of Leeds, United Kingdom, <sup>3</sup> British Trust for Ornithology, United Kingdom, <sup>4</sup> Lancaster Environment Centre, Lancaster University, United Kingdom

Land-use change is a major driver of the ongoing extinction crisis, but the processes through which it acts on biodiversity are complex and often remain poorly understood. We used the endemic-rich avifauna of São Tomé Island (São Tomé and Príncipe, central Africa) as a case study to assess the responses of biodiversity to land-use change. We sampled bird assemblages in 220 point counts, stratified across region and land-use type, and examined changes in species richness, composition and structure. Species richness at the point level decreased with land-use intensification, but a higher dissimilarity between points meant that

these land-uses had and overall higher species richness. Endemics dominated in less intensive land-uses, although many occurred across all land-uses. Non-endemics were clearly dependent on the more intensive land-uses. Our results show that species richness concealed a major shift towards an endemism impoverished avifauna. We advocate for the use of multiple metrics to gain a better understanding of complex biodiversity dynamics.

17:15 - 17:30 | **Oral presentation**

***Landscape dynamics in Mediterranean oak forests under global change: disentangling the role of anthropogenic and environmental drivers across species***

Vanda Acácio<sup>1</sup>, Francisco Moreira<sup>1</sup>, Filipe Dias<sup>1</sup>, Filipe Xavier Catry<sup>1</sup>

<sup>1</sup> Centro de Ecologia Aplicada Prof. Baeta Neves, Instituto Superior de Agronomia, Universidade de Lisboa

In recent years, several fast-changing drivers have been associated with a generalized oak forest loss in Iberian Peninsula, including land abandonment, wildfires and drought-induced mortality. We used data from national forest inventories and multimodel inference to disentangle the role of wildfires, slope, climatic and anthropogenic variables on evergreen and deciduous oak landscape dynamics in Portugal for the period 1966-2006. Land abandonment with depopulation was the dominant trend in cork oak land cover changes, which followed a dual path: the land was afforested in steeper areas, or colonized by shrubs in isolated areas with frequent wildfires and increasing warm periods. Land management intensification at gentle slopes and changes to cork oak dominated areas were the dominant trends in holm oak land cover changes, occurring mostly in peripheral populations in the westernmost range margins of the species distribution area. Changes in deciduous oak forests showed a dominant trend of land abandonment with shrub encroachment, in which wildfires and competition with shrubs seem to have hindered oak forest recovery. Furthermore, increasing dry periods were associated with the replacement of deciduous oak forests by forest species better adapted to more xeric conditions. Results are discussed in the context of current global change.

**DAY 2 - TUESDAY | JUNE 2, 2015****THEME 3 - SOCIOECOLOGICAL DRIVERS**

10:30 - 10:45 | **Oral presentation**

***Biodiversity patterns of legume trees from the Miombo and Mopane woodlands of Mozambique in relation to fire frequency***

Natasha Ribeiro<sup>1</sup>, Luís Goulão<sup>2</sup> and Ana Isabel Ribeiro-Barros<sup>2</sup>

<sup>1</sup> Faculty of Agronomy and Forestry, Eduardo Mondlane University, Mozambique, <sup>2</sup> Tropical Research Institute, Portugal

The Miombo-Mopane woodlands is considered one of the five ecozones (together with Amazonia, Congo, New Guinea and the North American deserts) with irreplaceable species endemism. From the environmental point the woodlands are determinant for energy, carbon and water balance. At the socio-economic level, they are key providers of goods and services, supporting the livelihoods of millions of people in the region. The woodlands are also very important to the national economies as they provide timber for exportation. The ecological dynamics of Miombo-Mopane is strongly influenced by a combination of climate, disturbances (e.g. drought, fire, grazing and herbivory primarily by elephants) and human activities. Growing population in the region over the last 20-25 years has resulted in increased woodlands degradation and deforestation. Slash and burn agriculture and charcoal production are the major causes of forest loss and degradation in the ecoregion. Additionally, the region is experiencing several major investments in mining, commercial agriculture and infrastructure, which have further increased the pressure on the woodlands. In this presentation we will discuss the impact of fire on legume trees from the miombo (Niassa National Reserve, north Mozambique) and mopane (Limpopo National Park, south Mozambique) and its implications for conservation programs.

10:45 - 11:00 | **Oral presentation**

***Integrating resilience-based indicators of forest ecosystem services in a DPSIR framework – a review***

Ana Sofia Vaz<sup>1,2</sup>, Carlos Vila-Viçosa<sup>1,2</sup>, Antonio J. Muñoz-Pajares<sup>1</sup>, Joana Vicente<sup>1</sup> and João P. Honrado<sup>1,2</sup>

<sup>1</sup>CIBIO-InBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva, Universidade do Porto, Portugal, <sup>2</sup>Faculdade de Ciências, Universidade do Porto, Portugal

Forests face several pressures (namely climate and land use changes, and biological invasions) which induce shifts in ecosystem functioning, threatening the provision of goods and services needed for human well-being. Understanding the relations between drivers and pressures that impact on forest ecosystem services (ES), and how these relations are modulated by societal

responses, are major sustainability challenges. Resilience-based research has been proposed as a new paradigm for these challenges, considering the ability of ecosystems to resist and recover from impacts, to absorb disturbances and to maintain core ecosystem functions. Yet, robust frameworks that allow the operationalization of resilience-based approaches to address forest ES are underexplored. Based on a literature review, this study identifies a preliminary set of indicators which have been used to assess the general and specified resilience of worldwide forest ES. Indicators are organized following the categories of the DPSIR (Drivers-Pressures-State-Impacts-Responses) framework, adapted whenever necessary. Through an explicit linkage with resilience thinking, this study identifies the drivers and pressures of ES in several forest types, along spatial and temporal scales, identifying resilience approaches behind such assessments. We argue that integrating resilience-based indicators in a DPSIR framework provides a useful management tool for supporting solutions regarding common socio-ecological problems.

11:30 - 11:45 | **Oral presentation**

***Integrating concepts and indicators for a more effective assessment of high nature value forests***

Ana Teresa Novais<sup>1</sup>, João Carlos Martins Azevedo<sup>2</sup> and Ângela Lomba<sup>1</sup>

<sup>1</sup> CIBIO-InBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva, Universidade do Porto, Portugal, <sup>2</sup> CIMO – Centro de Investigação da Montanha, Portugal

Forests are important providers of ecosystem services (ES) and goods. Whilst maintaining and promoting forest resilience and multifunctionality has been highlighted as essential for many EU political commitments, EU forests have been under several threats, mostly derived from changes of land uses and forest management regimes, known to have profound impacts on forest structure and associated biodiversity.

The High Nature Value (HNV) indicator, defined in the context of the Rural Development Programs (RDPs), comprises the identification and evaluation of forests that support high levels of biodiversity in Europe. Whilst EU-level guidelines and strategies to map and assess HNV areas have already been provided, the identification of suitable, spatially explicit indicators is a challenge yet to tackle.

Here, built on a comprehensive meta-analysis of published research, a preliminary framework of spatially-explicit indicators to assess HNV forests is proposed. Also, such indicators are analysed in their ability to express the natural value of forests and distinct levels of ecosystem services and goods provision, in the broad context of the implementation of RDPs across EU.

11:45 - 12:00 | **Oral presentation**

**Hotspots of invasiveness of three acacia species in northern Portugal: a probabilistic overview of climate change effects**

Diogo Alagador<sup>1</sup> and Joana Vicente<sup>2,3</sup>

<sup>1</sup> CIBIO-InBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva, Universidade de Évora, Portugal, <sup>2</sup> CIBIO-InBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva, Universidade do Porto, Portugal, <sup>3</sup> Faculdade de Ciências, Universidade do Porto, Portugal

The impacts of invasive species over socio-economic and ecological equilibria have instigated many conservation projects to run in the recent decades. However, given the dynamics that characterize current and (much likely) future environments, those effects tend to be more unpredictable and challenging to anticipate. Climate change and depletion of native habitats will prompted such invasion processes and therefore the identification of the areas predicted to be highly impacted by these synergistic effects is of paramount importance in order to plan effective measures on them.

In this study we introduce a framework aiming to pinpoint the areas more likely to facilitate the establishment of populations of three highly invasive *Acacia* species (*A. dealbata*, *A. melanoxylon* and *A. longifolia*) in Northern Portugal, from current time into 2050, under climate change scenarios. The framework, established around optimization and network theories, uses environmental suitability predictions and probabilities of successful dispersal to evaluate the likely persistence of each species independently, each combination of two species and the three species altogether (hotspots of invasiveness) across the focal region. The identification of such areas is controlled by amount area to prospect or by a given accepted predictive uncertainty.

The framework is flexible to be extended to any region and to integrate several concerns likely to impact species range adaptations in the coming decades. It offers practitioners a support tool to identify the areas where conservation measures should be taken to minimize socio-economic and ecological drawbacks from species invasions.

12:00 - 12:15 | **Oral presentation**

**The role of herbivores in the conservation of endemic heathlands in Galicia (NW Spain)**

Jaime Fagúndez<sup>1</sup>

<sup>1</sup> Department of Animal and Plant Biology and Ecology, Faculty of Science, University of A Coruña, Spain

Heathlands are one of the most valuable ecosystems throughout Western Europe, holding a great diversity of organisms and ecological interactions. In Galicia, NW Iberian Peninsula, large areas are covered by heathlands, where the main dependent trophic chain is the interaction between the heathland vegetation, the wild ponies, and its predator, the wolf. This complex system has persisted relatively unchanged for thousands of years in Galicia, but is now threatened mainly by the abandonment of traditional management practices. I studied the effect of different grazing systems (ponies, cattle, abandonment) and intensities on habitat quality in terms of species richness and diversity, and vegetation structure, in the particular *Erica mackayana*-dominated heathlands in northern Galicia. Vegetation height and

homogeneity was higher in abandoned areas. Ungrazed areas also showed lower species richness and diversity, while those areas heavily grazed by cattle had lower occurrences of rare and endemic species. Our results suggest that the presence of wild ponies play a key role in the maintenance of wet heathlands and habitat quality, a result of the particular vegetation pattern developed by horse grazing, in which mounds of gorse and heather alternate with narrow paths with low herbaceous cover. Preserving these wild populations is needed for heathland conservation.

12:15 - 12:30 | **Oral presentation**

***Evaluating the regional cumulative impact of wind farms on birds: how can spatially-explicit dynamic modelling improve impact assessments and monitoring?***

Rita Bastos<sup>1</sup>, Ana Pinhaños<sup>2,3</sup>, Mário Santos<sup>1</sup>, Rui F. Fernandes<sup>2,3</sup>, Joana Vicente<sup>2,3</sup>, Francisco Morinha<sup>1</sup>, João P. Honrado<sup>2,3</sup>, Paulo Travassos<sup>1</sup>, Paulo Barros<sup>1</sup>, João Alexandre Cabral<sup>1</sup>

<sup>1</sup> Laboratory of Applied Ecology, CITAB – Centre for the Research and Technology of Agro-Environment and Biological Sciences, University of Trás-os-Montes e Alto Douro, Portugal, <sup>2</sup> CIBIO-InBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva, Universidade do Porto, Portugal, <sup>3</sup> Faculdade de Ciências, Universidade do Porto, Portugal

Eurasian Skylark (*Alauda arvensis*) is very susceptible to the negative effects of wind farms. In North Portugal, this evidence is particularly severe due to Skylark preference for mountain breeding habitats where most wind farms are located. This study aims to develop and test a methodology to evaluate the cumulative impacts of wind farms on wildlife, by quantifying local and regional consequences on birds using Skylark as a test species. We propose a spatially-explicit dynamic approach that combines the results from multiple modelling techniques under a common framework, which includes: modelling the local impact of wind farms (in terms of collision mortality) on the Skylark population dynamics, determining the actual and future Skylark breeding distribution across the North of Portugal, integrating the above contributions in an emergent spatially-explicit representation to capture regional ecological cumulative consequences. The distribution area of Skylark breeding populations was predicted to decrease around 4.5% throughout 15 years, as result of the scenario of climate and land cover changes. When combined with a drastic increase of Skylark global mortality (approximately 184%), induced by all wind farms of the study region, the above trend contributes to an intensification of the regional cumulative impact from 1.2% to 3.7% of the total estimated breeding individuals. The proposed modelling framework represents a step forward in evaluating the multi-scale cumulative consequences of wind farms on vulnerable birds.

12:30 - 12:45 | Oral presentation

**Demographic bottleneck in two arboreal primates: a consequence of forest exploitation**

Tânia Minhós<sup>1,2</sup>, Lounès Chikhi<sup>2,3</sup>, Cláudia Sousa<sup>4,5</sup>, Luis M. Vicente<sup>6</sup>, Maria Ferreira da Silva<sup>7,8</sup>, Rasmus Heller<sup>2,9</sup>, Catarina Casanova<sup>1</sup> and Michael W. Bruford<sup>7</sup>

<sup>1</sup> CAPP - Centro de Administração e Políticas Públicas e Instituto Superior de Ciências Sociais e Políticas da Universidade de Lisboa, Portugal, <sup>2</sup> Instituto Gulbenkian de Ciência, Portugal, <sup>3</sup> CNRS, EDB (Laboratoire Evolution et Diversité Biologique), France, <sup>4</sup> Department of Anthropology, Faculdade de Ciências Sociais e Humanas, Universidade Nova de Lisboa, Portugal, <sup>5</sup> Centre for Research in Anthropology, Portugal, <sup>6</sup> Centre for Environmental and Marine Studies, Departamento de Biologia Animal, Faculdade de Ciências, Universidade de Lisboa, Portugal, <sup>7</sup> Organisms and Environment Division, Cardiff School of Biosciences, UK, <sup>8</sup> CIBIO-InBIO – Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva, Universidade do Porto, Portugal, <sup>9</sup> Department of Biology, University of Copenhagen, Denmark

The rapid pace of forest degradation stands as a major challenge to the ability of forest dwelling primates to adapt to changes in their habitat. We used microsatellite data to compare the demographic history and genetic structure of two sympatric primates—the Western black-and-white colobus (*Colobus polykomos*) and Temmick’s red colobus (*Procolobus badius temminckii*)—in the fragmented Cantanhez National Park, which is one of the last pockets of forest in Guinea Bissau. We did not detect a strong genetic substructure in neither taxon, but rather a fine-spatial genetic structure for *P. b. temminckii* only. Moreover, we detected a strong and recent demographic bottleneck for both species, which we inferred to have resulted from the anthropogenic exploitation of forest resources in the last centuries. The very low estimated effective population sizes for both primates and the known demographic tendencies indicate that they are under imminent risk of extinction in the park, and by extension in Guinea Bissau, if urgent action is not taken. The stronger bottleneck in *P. b. temminckii* and the fact that this species is absent from the most degraded forests in the park, suggest that *P. b. temminckii* is particularly susceptible to human disturbance.

## THEME 4 - SPECIES' RANGE AND NICHE DYNAMICS

15:30 - 15:45 | **Oral presentation**

### **Modelling invasions for managing impacts**

Mário Santos<sup>1</sup>, Rita Bastos<sup>1</sup>, Joana Vicente<sup>2,3</sup>, Uta Berger<sup>4</sup>, Britaldo Silveira Soares Filho<sup>5</sup>, Hermann Rodrigues<sup>5</sup>, Joaquim Alonso<sup>6</sup>, Carlos Guerra<sup>7</sup>, João Martins<sup>2</sup>, João Honrado<sup>2,3</sup>, João Alexandre Cabral<sup>1</sup>

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The mobility of our societies accelerates the global redistribution of species and consequently biological invasions contribute to environmental changes affecting biodiversity, ecosystem functioning, and associated services. The complex nature of these processes and their interactions often result in non-linear and emergent properties of the ecosystems, which cannot be decoded by classical modelling approaches. New spatiotemporal approaches have been developed over the last decade which explicitly address species responses, taking into account landscape heterogeneity. They include individual-based models (IBMs), stochastic dynamic models (StDM), statistical species distribution models (SDMs), and complex cellular automata models (CA) coupled with geographic information systems (GIS). This communication reviews these recent spatiotemporal modelling approaches applied to predicting and management, with a focus on biological invasions. Based on case samples of prominent biological invasions, we discuss the concepts, requirements, and potential outcomes of such approaches and describe the ecological relevance of applications, along with specific advantages and drawbacks.

15:45 - 16:00 | **Oral presentation**

### **Modeling the effects of temperature and salinity variations on the shore crab *Carcinus maenas***

Allan T. Souza<sup>1,2</sup>, João Carlos Marques<sup>3</sup> and Irene Martins<sup>3</sup>

<sup>1</sup> CIMAR/CIIMAR – Centro Interdisciplinar de Investigação Marinha e Ambiental, Universidade do Porto, <sup>2</sup> ICBAS – Instituto de Ciências Biomédicas de Abel Salazar, Universidade do Porto, Portugal, <sup>3</sup> IMAR – CMA, Institute of Marine Research - Centre for Sea and Environment, Department of Life Sciences, University of Coimbra, Portugal

Despite of the IPCC predictions about the temperature rising in the near future and the global awareness about this issue, there are only few studies that use these predictions to simulate the effects of climate change on the population dynamics of estuarine crustaceans. In this context, the present study aimed at assessing the effects of temperature and salinity variations on the population dynamics of the shore crab *Carcinus maenas* in an important nursery area for the species within its indigenous range of occurrence. This aim was achieved by modeling the dynamics of *C. maenas* population in Minho estuary (Portugal). The model focused only on

subadults and adults inhabiting the estuary, but it also accounted for the two stages of *C. maenas* development, namely, the planktonic and benthic phases, that occurs at the sea and within the estuary respectively. Linear regressions between the observed and the predicted density of subadults (ANOVA:  $F = 10.66$ ;  $p < 0.01$ ), females (ANOVA:  $F = 17.41$ ;  $p < 0.01$ ), males (ANOVA:  $F = 17.38$ ;  $p < 0.01$ ) and the total estuarine population (ANOVA:  $F = 8.77$ ;  $p < 0.05$ ) were significant, which accounted for the accuracy of the model to describe *C. maenas* population dynamics, and, thus, used to simulate the effects of climatic changes on the crab population. Results suggest that *C. maenas* is more sensitive to oscillations on temperature than on salinity. Temperature rises of up to 2°C causes increases on the population density of *C. maenas* from Minho estuary, whilst further temperature increase leads to a noticeable decrease on shore crab density (up to 60%). Assuming a temperature rise of 2°C in the next decades, simulations indicate that *C. maenas* density will continuously increase. Due to the voracious and generalist feeding behavior of the species, a *C. maenas* population increase will probably have significant effects on the estuarine community in the studied area.

16:30 - 16:45 | **Oral presentation**

***Modeling the genetic consequences of social structure***

Bárbara Parreira<sup>1,2</sup> and Lounès Chikhi<sup>1,3</sup>

<sup>1</sup>Instituto Gulbenkian de Ciência, Portugal, <sup>2</sup>Departamento de Biologia Vegetal, Faculdade de Ciências, Universidade de Lisboa, Portugal, <sup>3</sup>CNRS, EDB - Laboratoire Evolution et Diversité Biologique, France

In nature mammalian populations often consist of small age-structured units where a limited number of individuals monopolize reproduction and exhibit complex mating strategies. Despite its ubiquity, social structure is usually ignored in most population genetics models. Here, we use a new individual-based simulation framework to simulate genetic and demographic data under some of the most common mating strategies found in mammals. We model populations as networks of social groups among which individuals from one or both sexes can move.

Our results show that social structure produces high levels of genotypic diversity in the form of outbreeding even though we do not model explicit inbreeding avoidance, tolerance or preference behaviours. Also sampling strategies that ignore this level of structure or only include reproductive individuals can generate spurious signals of random-mating, in agreement with empirical studies. Moreover, our simulations suggest that sociality maximizes diversity in relation to what theory predicts for random-mating populations, which contradicts the belief that social groups are necessarily subject to strong genetic drift and at high risk of inbreeding depression. This new framework may thus represent a valuable tool to give insights about the rate at which diversity is being lost in natural endangered populations, which is important for their management.

16:45 - 17:00 | **Oral presentation**

***Genetic inbreeding and neighbour vegetation cover drive drought-induced forest die-off***

Cristina García<sup>1</sup> and Francisco Lloret<sup>2,3</sup>

<sup>1</sup> CIBIO-InBIO – Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva, Universidade do Porto, Portugal, <sup>2</sup> CREAF, Spain, <sup>3</sup> Unitat d'Ecologia, Department of Biologia Animal, Biologia Vegetal i Ecologia, Universidad Autònoma Barcelona, Spain

Drought-induced episodes of forest die-off are being reported worldwide. Individual affectation obeys to several ecological factors, but the contribution of within population genetic diversity has not been explicitly assessed. Here we report the role of ecological, phenotypic and genetic factors in determining the response of *Juniperus phoenicea* trees to prolonged drought conditions inhabiting a semi-arid shrubland in central Spain. We correlated individual inbreeding (F) and kinship among neighbours with remaining plant green canopy and crop size. We found that F was negatively correlated with plant performance, whereas mean kinship was not. Healthier canopy also tended to correspond with large plants and neighbourhoods dominated by trees and shrubs, suggesting facilitation interactions. Accordingly, the probability of being heavily damaged increased linearly with F, and individuals growing in open habitats with F values > 0.60 only have 15% chance of remaining unaffected after a period of prolonged drought. This study shows empirically that in addition to ecological drivers, the ability of plant populations to confront the new conditions imposed by climate change would be determined by its standing genetic diversity. Thus, the understanding of phenomena such as drought-induced forest die-off needs incorporate the contribution of genetic background on population responses.

17:00 - 17:15 | **Oral presentation**

***Dispersal ability determines the scaling properties of species abundance distributions: a case study using data on arthropods from the Azores archipelago***

Luís Borda de Água<sup>1</sup>, Paulo A. V. Borges<sup>2,3</sup> and Henrique Pereira<sup>1,4,5</sup>

<sup>1</sup> REFER Biodiversity Chair, CIBIO-InBIO – Centro de Investigação em Biodiversidade e Recursos Genéticos-Rede de Investigação em Biodiversidade e Biologia Evolutiva, Portugal, <sup>2</sup> cE3c – Centre for Ecology, Evolution and Environmental Changes, Portugal, <sup>3</sup> Azorean Biodiversity Group and Universidade dos Açores - Departamento de Ciências Agrárias, Portugal, <sup>4</sup> German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Germany, <sup>5</sup> Institute of Biology, Martin Luther University Halle-Wittenberg, Germany

We used data on arthropods collected in the Azores (i) to test whether a pattern on the scaling properties of the moments of the species abundance distributions previously observed for tropical tree species also holds for arthropods, (ii) to test predictions obtained with spatially explicit computer simulations on the rate of change of species abundance distributions as a function of sample size, and (iii) to forecast the evolution of the species abundance distribution for sample sizes hitherto not obtained. The moments of the species abundance distributions of arthropods have a pattern similar to that observed for tropical tree species, therefore, we conjecture that this is a general pattern in ecology. In agreement with computer simulations, the shape of species abundance distributions of high and low dispersal ability species evolve at different paces when sample size increases; low dispersal ability species reveals a bump for intermediate abundance classes earlier than the distributions of high dispersal ability species. Projections of the distributions for sample sizes for two and for times larger of those already sampled revealed the same trend and show that considerable more

data is required to observe transitions in the shape of the distributions as predicted by simulation models.

17:15 - 17:30 | Oral presentation

***The importance of shallow areas as nursery grounds for the recruitment of juveniles of the blue crab *Callinectes sapidus* rathbun, 1896***

Marcos Alaniz Rodrigues<sup>1</sup>, Vinícius Mendes Ruas<sup>1</sup> and Fernando D’Incao<sup>1</sup>

<sup>1</sup> Universidade Federal do Rio Grande, Brazil

The recruitment is a critical phase on the life cycle of the blue-crab *Callinectes sapidus*. With this study we determined concentration areas of blue-crab juveniles on two estuaries of Southern Brazil in order to determine preference areas for settlement and establishment of juvenile populations. Samplings were conducted for 18 months, with bottom trawl in two depths for four places in each estuary, along with environmental parameters. Data were analyzed by multiple regression and repeated-measures ANOVA, to verify possible relations between CPUA and environmental data, and to estimate the relation between abundance by size of class, depths and sampling places. The response pattern appears to be similar for settling of juveniles on both estuaries, and juveniles seems to concentrate more on areas with a greater amount of organic matter, and significantly more on margins than in deep areas. On both estuaries, two peaks of entrance of juveniles were found, with the first occurring at the beginning of autumn, and the second during winter. These peaks can be related to anomalous increasing of temperature, and delays on the reproductive cycle. The internal areas of estuaries are determinant for the correct settling of blue crabs, thus increasing the concern for its protection.

17:30 - 17:45 | Oral presentation

***Survey on effective factors in population’s distribution and abundance of *Tatera indica* in Sistan, southeastern of Iran***

Saeed Mohammadi<sup>1</sup> and Ali Sabaghzadeh<sup>1</sup>

<sup>1</sup> Department of Environmental Sciences, Faculty of Natural Resources, University of Zabol, Iran

Distribution of species may be related to environmental independent variables that the importance of different variables depending on the biology and ecology of species. Studies in relation to many species have shown that always several key variables have the greatest impact on pattern of distribution species. Thus, identifying factors affecting species play a role in managing and reducing the threats to these species. Indian Gerbil (*Tatera indica* Hardwicke, 1807) is from Muridae family and Gerbillinae subfamily. Habitat range of this species involves arid and semi -arid areas. The species has been listed in IUCN at the lowest level of concern (Lc). In this study effective factors on the habitat suitability of *T. indica* were identified in Sistan region. Field studies were conducted at five different sampling stations in Zabol during spring 2013. Seven environmental variables including the percentage of vegetation cover, soil, gravel cover (<0/2 mm diameter), the percentage of cover of Tamarix species (*Haloxylon* sp), the percentage of coverage of *Desmatchia-Bipinata* and cover of *Salsola aucheri* and distance from water resources in the 60 plots of presence/absence were performed and analyzed by binary logistic regression analysis. The results showed that the variables of soil cover, cover gravel and the coverage percentage of *Desmatchia-Bipinata* and distance from water resources have important role ( $P < 0.05$ ) in relation to the distribution of *T. indica* in Sistan.

17:45 – 18:00 | **Oral presentation**

***The role of fish in the conservation of freshwater mussels***

Vanessa Modesto<sup>1</sup>, Martina Ilarri<sup>1,2</sup>, Allan Tainá de Souza<sup>1</sup> and Ronaldo Sousa<sup>1,3</sup>

<sup>1</sup> *Interdisciplinary Centre of Marine and Environmental Research (CIIMAR/CIMAR),*

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*CBMA – Centre of Molecular and Environmental Biology, Department of Biology, University of Minho, Portugal*

Coextinctions received virtually no attention in conservation studies so far, despite their relevance. Freshwater mussels are one of the most threatened faunal groups on Earth. Several mussel species present complex life cycles, spending one phase of their development as a parasite in fishes. Hence, one can assume that changes in fish populations may significantly impact mussels' conservation. We performed a literature survey aiming to revise the relationship between fishes and freshwater mussels and the main human impacts affecting the interaction between them. Overall, an increase trend in the number of publications was observed in the last years with most of them being performed in North America (69%). The majority of studies were performed in the mussels' native range of occurrence (99%), with 84% mussels being classified as generalists in terms of fish hosting. Most specialist mussels in fish hosting are listed as vulnerable or endangered (55%). On the other hand, the studies performed in laboratory accounted for 83% of the total, indicating a scarcity in field studies. Very few studies addressed the main threats to the mussel-fish interaction, impeding the application of species conservation and restoration plans. Therefore, our results expose that there is a long path still needing to be fulfilled in order to discover the more appropriate conservation measures to mussels and their freshwater fish hosts, with critical demand of information from areas other than North America and Europe.

# ABSTRACTS

## Poster Presentations

**DAY 1 - MONDAY | JUNE 1, 2015 | 18:30 - 19:15**

***Facilitation in the low intertidal: effects of an invasive species on the structure of an estuarine macrozoobenthic assemblage***

Adriana Novais<sup>1</sup>, Allan Tainá de Souza<sup>2</sup>, Martina Ilarri<sup>2,3</sup>, Cláudia Pascoal<sup>1</sup>, Ronaldo Sousa<sup>1,2</sup>

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The Asian clam *Corbicula fluminea* (Müller, 1774) has been recognized as one of the most important invasive alien species in aquatic ecosystems and may have significant ecological and economic impacts. Recently, the presence of *C. fluminea* was associated with changes in benthic and epibenthic fauna. In this study, we aimed to understand the mechanisms underlying the effects of *C. fluminea* on an estuarine macrozoobenthic assemblage using a manipulative experiment. We used 5 different treatments: control, rock, closed, live and open, which were placed in a low sandy intertidal soft bottom area in the Minho estuary (NW Iberian Peninsula) for 2 months. We found that the presence of live and open empty shells of *C. fluminea* had positive effects on the density, biomass and species richness of macrozoobenthos, specifically on species belonging to Annelida, Mollusca and Crustacea. Our results may be explained by 2 main mechanisms: (1) the production of feces and pseudofeces by *C. fluminea*, which increases organic matter content and food resources for some macrozoobenthic species; and (2) ecosystem engineering activities by *C. fluminea*, which can create conditions for the establishment of other species via shell production and bioturbation in the sediments.

***Interaction between an invasive and a native amphipod species***

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The aim of this study was to analyze the interactions between two freshwater amphipods *Echinogammarus meridionalis*, native in Portugal, and *Crangonyx pseudogracilis*, a smaller invasive species recently found in Portugal. *Echinogammarus meridionalis* is usually found in rivers, lakes and fresh water and *Crangonyx pseudogracilis* inhabits a wide variety of aquatic habitats including lakes, permanent and temporary ponds, rivers, streams and even interstitial habitats.

In a 7 days experiment we used plastic cups on 8 different treatments with each species isolated and combining them in a cup. Preconditioned alder leaves circles were used as food in some treatments. Consumption rates of conditioned leafs were significantly higher for *E. meridionalis* when compared with *C. pseudogracilis*. The cumulative consumptive effect of the native species and the invasive species was not different from the effect of just the native. The overall proportion of dead vs. live individuals in the end of the experiment was dependent on the species. The presence or absence of food, and the conjunction of this factor with the non-native amphipod presence did not affect survival of the native species. However, the native species presented a much higher overall mortality than the invasive species.

***Crowned sifaka (Propithecus coronatus) mitochondrial genetic diversity in a fragmented landscape***

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*Propithecus coronatus* is an endangered diurnal lemur living in a large but highly fragmented region, in the north-est of Madagascar. It is thought to have undergone a population decline of  $\approx 50\%$  in the last decades and it is threatened by habitat fragmentation and deforestation due to anthropogenic activities logging and fire).

We conducted the first genetic study on this species across most of its range, by sequencing the D-loop of 125 individuals from 14 study sites. The main goals were to assess genetic diversity and differentiation within and among populations. We also used the Extended Bayesian Skyline Plot (EBSP) approach to reconstruct the demographic history of the species.

We detected a moderate level of haplotype diversity (0.853) and low nucleotide diversity (1.21%), compared to other lemur species of the same genus but labeled as critically endangered.

Despite the high level of habitat fragmentation of this region,  $\Phi_{ST}$ , isolation by distances and haplotype network did not show strong patterns of genetic differentiation among study sites. Given that structure effect may confound demographic inference based on the EBSP, we used four different sampling strategies before applying this approach.

The results, although exhibiting large confidence intervals, did not suggest any population size change.

***Towards the conservation of bottlenose dolphin of Sado estuary, a highly human-impacted environment***

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The bottlenose dolphin (*Tursiops truncatus*) is catalogued as a high priority species under the EU Habitats Directive requiring the designation of Special Areas of Conservation. The status of the species is the consequence of a variety of human-related impacts among which pollution appears to be particularly significant. The Sado population inhabits a degraded and polluted estuarine environment and it is one of the few resident populations in Europe and the last one in Portugal. Dedicated research has revealed long-term site fidelity, an ageing population, high calf/juvenile mortality and a declining population with less than 30 individuals today. The Sado population is under a *Conservation Action Plan* coordinated by the ICNF. A multidisciplinary approach combining molecular, ecotoxicological, and environmental data, with new analytical methods is being developed. It will allow us to better understand the genetic diversity and the demographic history of the Sado population and its relationship with other bottlenose dolphins. The genetic and ecotoxicological results will be crucial to identify threats and promote effective conservation of the last Sado dolphins, as well as to elucidate the general processes that may explain the genetic diversity in similar environments, thus contributing to conservation of the species at a broader scale.

***Alien Reptiles on the Mediterranean Islands: which and where?***

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Biological invasions are one of the major causes of biodiversity loss. The Mediterranean basin has a long history of human-biota interaction which makes it a good model to study these phenomena, being islands the systems more vulnerable to invasion. Here we present an on-going project focused on the reptile fauna of the Mediterranean Islands. The conservation significance of this group is double-fold: on one hand reptiles are among the most widely introduced vertebrates; on the other hand, some species are threatened by biological invasions. Ecological modelling will be used to assess the biogeographical pattern of alien reptiles, namely, 1) to identify potential alien reptile species and their colonization patterns; 2) to assess the factors more important to introduction and establishment disentangling them from natural biogeographic factors; and 3) to identify which islands are more prone to be invaded. A large database, with information on 90 reptiles distribution in > 900 Mediterranean

Islands and their native status as well as human activities, land use and geographical features, will be integrated to achieve the objective. It is expected to create a general framework for the Mediterranean to be applied in management policies of the countries with more number of islands (Spain, Italy, Croatia and Greece) or, even at the European level.

***Genetic variation and differentiation in the northern rufous mouse lemur (*Microcebus tavaratra*) in the loky-manambato region (northern Madagascar)***

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Population genetic studies provide information on the recent evolution of species, as well as their response to natural or anthropogenic pressures. *Microcebus tavaratra* is a mouse lemur living in the fragmented forests of northern Madagascar for which we genotyped 149 individuals, sampled across 11 forests of the Loky Manambato region. In total, 15 microsatellite markers were used to quantify the genetic diversity and differentiation across the region. In particular, we wanted to determine whether patterns of genetic differentiation correlated with fragment size, geographic distance and relative position to the main river crossing the region, the Manankolana (known to play a role in the genetic structure of the golden-crowned sifaka, a lemur endemic of that region). The results suggest that the species exhibits a high level of genetic diversity across all forest patches and patterns of isolation by distance (IBD). However, we could not detect any difference between the two sexes and could not correlate the population structure and IBD signals to the river or any particular landscape feature. More research is currently carried out to reconstruct the demographic history of the species and determine whether it can explain the spatial patterns uncovered here.

***Isolation by ecology drives the geographic distribution of the genetic variation of a generalist insect-pollinated herb across elevational gradients***

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The isolation by distance model (IBD) predicts that genetic differentiation among populations increases with geographic distance, yet empirical studies show that a variety of ecological, geographic, and historical factors might erase the outcome of the geographic distance on the

spatial distribution of the genetic variation. This might be particularly the case of natural species confined to narrow, but highly heterogeneous, distribution ranges such as those observed across elevational gradients. Here, we aim to investigate the contribution of different environmental and historical factors in shaping spatial genetic patterns at increasing spatial scales in the mountainous

Generalist entomophilous herb, *Erysimum mediohispanicum*. Specifically we evaluated six competing models that put forward the role of the geographic distance, local environmental factors –including biotic interactions–, the presence of barriers to gene flow, and phylogeographic patterns. Overall, after controlling by the geographic distance, climatic variables showed the strongest effect on genetic distances at most geographic scales. Pollinator assemblage had mixed effects on genetic diversity, with pollinator diversity showing a positive effect and large bees abundance having a negative one. Our results highlight the importance of biological interactions to explain geographic patterns in plant population genetics and the potential impact of pollinator decline on generalist pollination systems.

### ***Assessment of High Nature Value farmlands in space and time: the case-study of Entre-Douro-e-Minho region***

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Agricultural landscapes are known to cover ca. 50% of EU, with farmers currently managing a vast territory. Often related to high levels of biodiversity, extensive farming practices have been shaping the EU countryside for centuries. However, due to the agricultural polarization, i.e. the intensification of intensively managed farmlands and growth of urban areas, and agricultural abandonment of marginal areas, agrobiodiversity has been severely affected.

EU policies have been converging with nature conservation and the sustainable use of agro-ecosystems. In such context, the High Nature Value farmlands (HNVf) concept was devised to define landscapes where extensive agriculture is still dominant, characterized by a high proportion of natural and/or semi-natural vegetation, often associated with small-scale landscape features.

Here, we implement a recently proposed spatially-explicit approach to assess High Nature Value farmlands in space and time, using the Entre-Douro-e-Minho region as test site. Indicators expressing landscape elements, the extensive character of agricultural practices and crop diversity for two distinct years were derived from available datasets for 1990 and 2007, and then used to assess the extent of HNVf for both periods. HNV farmlands dynamics between 1990 and 2007 were then assessed and outcomes analysed in the context of recent environmental change.

***Global patterns and predictors of fish species richness in estuaries***

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Knowledge of global patterns of biodiversity and regulating variables is indispensable to develop predictive models. We used predictive modelling to investigate the variation in fish species richness (*S*) between estuaries worldwide. Such models should assist in assessing future changes in ecosystem structure and function as a result of environmental changes. A worldwide database was compiled on the fish assemblage composition and environmental characteristics of estuaries. Generalized Linear Models quantified how variation in *S* among estuaries relates to historical events, energy dynamics and ecosystem characteristics, while controlling for sampling effort. At the global extent, *S* differed among marine biogeographic realms and continents and increased with sea surface temperature, terrestrial net primary productivity and connectivity with the marine ecosystem (open vs. temporarily open estuaries). At smaller extents (within realms or continents), other characteristics were also important in predicting *S*, which increased with estuary area and continental shelf width. Results suggest that *S* in an estuary is defined by predictors that are spatially hierarchical. At a global spatial extent, *S* is influenced by the broader distributions and habitat use patterns of marine and freshwater species that can colonize estuaries, which are in turn governed by history contingency, energy dynamics and productivity. *S* is also influenced by regional and local parameters that can further affect community colonization in an estuary including the connectivity with the marine habitat, and, over smaller spatial extents, the size of these habitats. Patterns of *S* in estuaries seem to reflect from global to local processes acting on community colonization.

***A computer program to simulate complex demographic histories***

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SINS (Simulating INdividuals in Space) is a computer program designed to simulate complex demographic histories using a spatial framework, similar to the SPLATCHE2 software but with a forward approach instead. SINS is thus slower but provides more realistic scenarios. With SINS, space is divided into layers, which are themselves subdivided into demes that harbour male and female individuals. Each deme is characterized by values which define the maximum population size (*K*) and the difficulty to move into that deme (*F*). SINS allows the user to simulate (1) variable *K* and *F* maps across time and space, (2) population expansions from multiple sources, (3) contractions and habitat fragmentation, (4) sex-biased admixture and competition between populations from two or more layers corresponding to the same geographical space, (5) short distance sex-biased migration and (6) variance in reproductive success in males and females. The program uses an individual-based approach to simulate forward in time several types of molecular markers (sequences, SNPs and microsatellites) and

genetic objects (X and Y chromosomes, autosomes and mitochondrial DNA). Being able to simulate population structure and at the same time sample the whole population allows SINS to be applied to many species and evolutionary questions.

***Habitat selection of oceanic-tagged blue and mako sharks***

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Habitat selection depends not only on biotic factors such as prey availability and predator avoidance, but also on environmental features, such as temperature and dissolved oxygen, which control metabolic processes. At higher temperatures, a faster metabolism consequently accelerates the aerobic processes increasing oxygen demand. Blue and mako sharks are top predators, which have high (albeit different) oxygen requirements due to the active foraging behaviour. However, preliminary results here presented suggest blue sharks are tolerant to oxygen minimum zones (OMZ), while makos do not seem to enter the OMZ. The latter are endothermic sharks, therefore the higher aerobic metabolism seems to restrict their habitat to more oxygenated zones. This study also suggests sharks tend to follow temperature isoclines, as sharks dive deeper when the isocline is also deeper and shallower when the isocline is shallower. Additionally, there seems to be a trend for sharks to move vertically within zones where chlorophyll is more abundant. Our data suggests on future climate change scenarios mainly the habitat of mako sharks may be compressed, increasing the susceptibility to surface fisheries and likely leading to stronger declines.



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