



Community Ecology for 21st Century (from genes to ecosystems)

Évora, 17th-19th of October 2016



Workshop 1 – Introduction to Ecological Network Analysis

A. Jesús Muñoz Pajares graduated in Biochemistry from the University of Granada (Spain) in 2006 and finished his PhD on the evolution of a pollination-generalist plant species in 2013. Currently, he works in CIBIO-InBIO being part of the PLANTBIO group. He is interested in evolutionary biology, particularly in the genetic consequences of ecological interactions, adaptation and colonization on recent speciation processes.

Abstract: Complex systems can be described and quantified on the basis of their interactions using networks, that is, any set of elements connected by links. Most ecological issues can be represented and analysed using the universal properties of networks. For example, using these techniques, researchers are able to better understand evolutionary relationships and pathogens propagation, but also to predict the consequences of changes in trophic relationships of food webs and pollination interactions. Thus, network analyses constitute a useful set of tools that may improve the amount of information obtained from ecological data. In this workshop we will briefly introduce the theoretical background of networks and will exemplify the analysis of different ecological datasets by means of the most widely used R packages.



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Workshop II – Introduction to Invasive Species Modelling

Joana Vicente is a post-doc at Research Center in Biodiversity and Genetic Resources (CIBIO), with a background on fundamental and applied research on ecological modelling of biodiversity geographic patterns, landscape ecology, environmental changes, and alien invader species. More specifically predicting isolated and synergic impacts of multi-scale environmental changes in the spread of biological invasions in heterogeneous landscapes, ecosystems and landscape functioning using both static and dynamic modelling techniques.

Abstract: The introduction and the expansion of non-native species, mainly as result of human action from trading of species to landscape-management, often have profound consequences for the invaded ecosystems and thereby for provision of valuable ecosystem services. Depending on their effects on ecosystem structure and function, invasions can affect a single ecosystem service, or can have significant effects on multiple services. Effective approaches to improve multi-scale management of invasions are thus needed, not only to anticipate future invasions and their impacts on ecosystems and their services, but also in mitigation of such impact in areas already invaded and where invasive species may play many roles in local social-ecological systems. To address the combined effects of these various factors, we will apply a methodological framework based on multi-model inference to identify areas of possible conflict between ecosystem services and alien invasive plants, considering interactions between landscape invasibility and species invasiveness.



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Workshop II – Introduction to Dynamic Modelling in Community Ecology

Rita Bastos is a PhD student, with Degree in Biology (University of Trás-os-Montes e Alto Douro) and Master in Applied Ecology (University of Coimbra). The main areas of expertise are ecological modeling, biostatistics and spatial ecology, directed to the management and conservation of target ecosystems and endangered species. Currently has been exploring new approaches in combining different modeling methodologies, such as system dynamics, species distribution models and individual-based models with focus on environmental impact assessment and biodiversity conservation.

Abstract: Through this workshop, participants will have the opportunity to contact with dynamic modelling approaches and develop a simple application in System Dynamics, directed to the scope of Community Ecology. The combination of mechanistic and correlative modelling approaches will be used to predict the response of community indicators' response at higher levels of the system, highlighting the integration of the outputs with Geographic Information Systems, following a modelling protocol known as Stochastic Dynamic Methodology.



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Workshop IV – Introduction to Bioinformatics as Applied to Community Ecology Data

John Archer. MSc in Software Engineering with Distinction (2001, Faculty of Computer Science, University of Liverpool, UK), PhD in Bioinformatics (2008, Department of Computational and Evolutionary Biology, University of Manchester, UK), post-doctoral researcher (2008-2013, University of Manchester, UK), post-doctoral researcher (2013-2014, Liverpool School of Tropical Medicine, UK) and senior bioinformatician (2014 – present, University of Porto). I use my background in software engineering to develop solutions to problems faced when analysing next generation sequence, specifically in relation to mapping, storage, assembly and variant detection. Tools that I have developed are currently used both within research and clinical based settings. My academic activities include lecturing on next generation sequencing, programming and general bioinformatics topics.

Abstract: Within many research areas, such as transcriptomics, the millions of short DNA fragments produced by current sequencing platforms need to be assembled into contig sequences before they can be utilized. Despite recent advances in assembly software, characterizing sequence diversity within data derived from sources harbouring isoform variation remains challenging. This is because current approaches fail to identify all variants present, e.g. reference based assembly, or they create chimeric contigs within which relationships between co-evolving sites and other evolutionary factors are disrupted, e.g. de Bruijn based assembly. In this workshop we will apply current methods of assembling read data as well as a more novel hybrid method designed to overcome some of the problems associated with more traditional approaches.