3rd Lab Retreat – Araújo & Rahbek Labs

Convento da Arrábida, Portugal, 19-13 October 2009

Center for Macroecology and Evolution

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PARTICIPANTS

1. Miguel Araújo (research professor)
2. Neil Burgess (professor)
5. Hans Henrik Bruun (associate professor)
4. Jack Hayes (professor)
5. Carsten Rahbek (professor)
6. Diogo Alagador (PhD student)
7. Márcia Barbosa (Post doc)
8. Michaek Krabbe Borregaard (PhD student)
9. Mar Cabeza (Post doc)
10. Emilio Civantos (Post doc)
11. Carlos Dommar (Post doc)
12. Susanne Fritz (Post doc)
13. Raúl García (PhD student)
14. Bjørn Hermansen (GIS technician)
15. Christian Hof (PhD student)
16. Knud Jønsson (Post doc)
17. Peter Søgaard Jørgensen (PhD student)
18. Lauri Laanisto (Post doc)
19. Irina Levinsky (PhD student)
20. Mariana Munguía (PhD student)
21. David Nogués (Post doc)
22. Isaac Pozo (GIS Technician)
23. Anders P Tøttrup (Post doc)
24. Maria Triviño (PhD student)

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Monday
12h30 – Arrival and check in
13h30 – Lunch
15h50 – Miguel Araújo & Carsten Rahbek, Welcoming
16h – Diogo Alagador, Aligning species with protected areas: a probabilistic approach under climate change
17h – Emilio Civantos, Evaluating possible impacts of biodiversity and land use changes on human social systems
18h – Mar Cabeza, Some thoughts on protected area effectiveness
19h30 – Dinner
21h – Niel Burgess, The world's protected area network: progress towards meeting international conservation targets

Tuesday
7h – Breakfast
9h– David Nogués-Bravo, Species' geographical ranges: physiology, dispersal and environment matters
10h– A. Márcia Barbosa, Distinguishing the roles of history and environment in generating common distribution patterns among Mediterranean vertebrates: consequences for conservation
11h – Irina Levinsky, Phylogenetic signals in traits, dispersal ability and changes in climatically suitable ranges of African starlings
12h – Lunch
15h – Peter Søgaard Jørgensen, Multiple drivers of environmental change effect on European bird populations' temporal trends
16h – Anders P. Tøttrup, Modelling future non-breeding distributions of European waterbirds under climate change
17h –Raúl García-Valdes, Metapopulation-based forecasting of forest response to climate change
19h – Dinner
21h – Hans Henrik Bruun, I want a new community ecology (and macroecology): one based on species' traits

Wednesday
9h – Maria Triviño, Exploring and assessing the effects of climate change on Iberian vertebrate species
10h – Christian Hof, Global change impacts on the world's amphibians
11h – Susanne Fritz, Global mammalian extinction risk: why and where being bad is bad / Global amphibian species richness and phylogenetic diversity
12h – Lunch
14h –Lauri Laanisto, Intraspecific niche plasticity in *Aextoxicon punctatum*
15h – Carlos J. Dommar D'Lima, The role of niche conservatism and niche adaptation in changing environments
16h – Michaek Krabbe Borregaard, Range-diversity plots: separating the maths from the biology
19h – Dinner
21h – Jack Hayes, A physiologist's view of the metabolic theory of ecology: new paradigm or much ado about nothing?

Thursday
Day off including a walk in the "Mata do Solitário" (The woodland of the lonely)

Friday
9h – Mariana Munguía-Carrara, Why were mammals from North America better colonizers than South American ones during the Great American Biotic Interchange?
10h - Knud A Jønsson, Islands: the beginning of the colonization road for a major passerine bird radiation
11h – Isaac Pozo, Ibiodat A tool for homogenizing and geo-referencing taxonomic data
11h30 – Bjørn Hermansen, How to Describe and Evaluate Data Quality in Digital Maps
12h – Check out
13h – Departure to Lisbon

EVENING TALKS

I want a new community ecology (and macroecology): one based on species' traits

Hans Henrik Bruun

I address a number of interwoven questions: Can community assembly be predicted from functional traits? (alpha and beta niches) Is 'limiting similarity' or 'limiting dissimilarity' the rule? Or, in other words, are co-existing species less or more functionally similar than one should expect from chance alone? Likewise, are co-existing species less or more phylogenetically related than under randomness? Has Darwin's old contention that more closely related organisms compete more intensely become justified by later empirical data? Are alpha and beta niches often contingent so that included species are favoured under the more optimal environmental conditions? Can regional species pools be forecast from climate-related traits? (gamma niches) Are gamma (climatic) niches always discrete (not contingent)? These are - from my perspective - the most burning questions in contemporary community ecology. I have a strong feeling that the answering these questions will have repercussions in macroecology and evolutionary biology.

The world's protected area network: progress towards meeting international conservation targets

Niel Burgess

The world's network of protected areas has been established over the past 100 years to cover more than 113,000 sites and 12% of the worlds land surface. Protected areas are thus the most important conservation mechanism in the world. In order to further promote the development of the global protected area network, the Convention of Biological Diversity has established a series of targets for the establishment of protected areas on land and in the sea. Progress towards achieving these 2010 (land) and 2012 (sea) targets will be assessed in a meeting of the Convention of Biological Diversity at Nagoya in Japan in 2010. This paper will present recent analysis of progress towards achieving various targets, and will make some projections of how long it will take to meet the targets, and assess if the targets are meaningful in any case.

A physiologist's view of the metabolic theory of ecology: new paradigm or much ado about nothing?

Jack Hayes

The metabolic theory of ecology is claimed to be one of the most significant breakthroughs in ecology in the last 20 years. For example, some claim that it is as fundamental to ecology as genetics is to evolutionary biology or as the ideal gas law is to chemistry. The 'theory' has also been sharply criticized by others who consider it a hypothesis soundly refuted by data. Which of these perspectives will prove correct is a major question facing ecologists of the 21st century. The original impetus for the metabolic theory of ecology comes from physiological ecology, especially animal physiological ecology. The metabolic theory of ecology attempts to link the scaling of metabolic rate with size and temperature to many other (ecological) processes. I will present a historical perspective on scaling and power laws in physiological ecology and on the physiological underpinnings of the theory. Next I will discuss how the model has been tested with both physiological and then ecological data. Lastly I will consider whether the metabolic theory is a good first order approximation in need of second order refinements or whether a better fundamental theory is needed.

RESEARCH TALKS

Aligning species with protected areas: probabilistic a approach under climate change

Diogo Alagador
Gap analysis is an established conservation procedure that identifies species, habitats or ecosystems in more urgency for in-situ protection, by crossing biological distribution with protected area cover. Whilst being straightforward in implementation it entangles some degree of arbitrariness when dealing with uncertainty behind protected area assignment: non-informed threshold values are commonly used to decide about local protection status. We suggest a probabilistic framework to deal with the problem, using a simple and intuitive protocol, based on statistical theory, to assess spatial protection levels of biological elements. We demonstrate the principles behind our approach and explore its ability to be used in a static and dynamic perspective of conservation, using consensual predictions of plant species distributions in Iberian Peninsula for present time and 2080, assuming a changing climate. We found that the estimated current representation of species in protected areas and its trend in a climatically changed future are highly affected by the mapping rules used. These results address the need to work on more robust approaches to deal with inevitable uncertainties.

Distinguishing the roles of history and environment in generating common distribution patterns among Mediterranean vertebrates: consequences for conservation

A. Márcia Barbosa
Species distributions are shaped by both historical factors (related with past climate and dispersal routes) and environmental constraints (including ecological interactions and tolerances to climate and to human pressure). Their effects are hard to disentangle and, indeed, historical and ecological biogeography have often been studied separately. However, distinguishing and accounting for both effects is important to design conservation strategies that will remain relevant in the face of global change. Inferences about the future evolution of species distributions must take into account the weight of historical factors in shaping the present distributions. Chorotypes are groups of significantly similar distribution patterns and can simplify the analysis of important biodiversity patterns when many species are involved. Species may share a common distribution area mainly due to historical reasons (e.g., shared glacial refuges and dispersal history), or mainly due to similar environmental constraints (e.g., requirement for abundant rainfall). Significant congruence between the phylogeographic structures of species belonging to the same chorotype would corroborate a historical origin of the common distribution pattern; conversely, a lack of similarity in phylogeographic structures within a chorotype would indicate the predominance of environmental causes behind the distribution pattern, which would be more appropriately explained through environmental models. This work aims to search for chorotypes of terrestrial vertebrates in the Mediterranean Basin, to perform comparative phylogeography and distribution modelling of species within these chorotypes, and to try and discern between the roles of history and environment in shaping current distribution patterns. The results can be used to predict species' responses to changes in environmental (whether climatic or anthropogenic) conditions, and to design conservation strategies accordingly.

Range-diversity plots: separating the maths from the biology

Michaek Krabbe Borregaard
Species richness patterns are generated by the overlapping ranges of species, and thus the ranges of species and the richness of sites on a domain are closely connected. In a recent paper, Arita et al. (2008) developed a novel way of visualizing this dependence, by combining richness values and range sizes in 'range-diversity' plots. These plots communicate more information than plots of ranges or richness values alone, and could be used for testing hypotheses on ecological patterns such as Rapoport's rule. However, range-diversity plots are not intuitively easy to interpret. The point patterns observed in these plots are shaped by mathematical constraints, in that only some areas of the plots represent permissible combinations of range sizes and richness values. Though Arita et al. (2008) develop some of these structural constraints explicitly, it is an open question whether the remaining patterning can be attributed strictly to biological processes. To answer this question, we applied their approach to a dataset on the birds of South America and demonstrated a further set of mathematical constraints affecting the plots. A simple null model, based on the assumption that frequency distributions of richness and range size values constrain the possible parameter space, seems to explain most of the pattern in range-diversity plots. However, even after accounting for these constraints some characteristic pattern remains.

Some thoughts on protected area effectiveness

Mar Cabeza
Protected areas cover twelve percent of the Earth's terrestrial surface. These lands are critical for biodiversity conservation, yet they are insufficient. They are inefficient in covering biodiversity, and importantly, they are also ineffective in protecting biodiversity within them in the long term. Population declines in African reserves as well as ongoing illegal deforestation in protected areas worldwide indicate that reserves are not functioning. Part of the problem stems from a history of ad-hoc decisions in protected-area designation. This has motivated extensive advances in the science of reserve-network design. Nevertheless, a substantial gulf remains between what is moving research versus what practitioners claim to require. With this talk I want to address a number of questions related to protected-area effectiveness by presenting several ongoing projects. First, I will show results of a review suggesting that while conservation-planning researchers seem to be obsessed with connectivity, practitioners believe that connectivity is not a major problem but instead, other issues are more pressing. Among these, law enforcement, corruption and lack of resources often result in protected area failures. I will discuss whether these issues may, and should, be incorporated in the reserve design process. I will conclude with a discussion on measures of reserve effectiveness, while presenting some starting projects in Madagascar.

Evaluating possible impacts of biodiversity and land use changes on human social systems

Emilio Civantos

Our ability to understand and predict how biodiversity and ecosystems will respond to the ongoing environmental change is still limited. Simulation models have become important tools to assess the consequences of global change for ecosystems and the goods and services that they provide to human populations. The impacts of environmental change on ecosystem goods and services (EGS) can thus be assessed using an Agent Based Modelling approach (ABM). However, before assessing socio-economic and environmental impacts that can be simulated as output from the ABM, EGS indicators have to be identified and defined. This should include human-orientated indicators, biophysical indicators of landscape quality, as well as multiple-species assessment of land-use change scenarios. We primarily focus on ecosystem goods and services related to the conservation of biodiversity at the level of species and habitats. For instance, modelling animal and plant species will help to understand the effect of human land use decisions on the ecosystem. This should include the different potential land uses, along with differing management practises. This means that we should be able to look at the interaction between land uses and the different needs that species have at different times of their lives. This strategy will result in a comprehensive and integrated assessment of global change impacts not only on biodiversity per se but also on the services it provides and, hence, facilitates the analysis of the impacts on society, economy and environment.

The role of niche conservatism and niche adaptation in changing environments

Carlos J. Dommar D'Lima

Niche conservatism is the tendency of organisms to retain ancestral ecological characteristics – that is both habitat (i.e. abiotic environmental component such as temperature, geographical height, depth in the water column, etc.), and ecological roles (that is the biotic environment defined by the intra- and interspecific ecological interaction). Adaptation to new niches can be the outcome of severe changes in (biotic and/or abiotic) environment, radiation to empty niches, etc. However, in the environment changing scenario, whether a lineage conserves a niche or can adapt to new niches may depend upon diverse characteristics such as life-history (capability to develop new adaptive traits or behaviours), the nature of the environmental change (rate of change, severity of change), the availability of other niches, etc. On the other hand, such selection of habitat/role is usually both density- and frequency-dependent in ecological setups; frequency-dependence selection is best tackled within a game theoretical paradigm. In this framework one can define strategies (e.g. to invade or to conserve), a constrained strategy set (given by capabilities of the organism to face the changes), and per capita fitness (growth rates), and thus, investigate the dynamic of the community structure using a evolutionary game approach. The idea is to develop such theory in close connection with real data and make predictions of evolutionary trajectories in systems of particular interest to the lab.

Metapopulation-based forecasting of forest response to climate change

Raúl García-Valdes

The effects of climate change on species distributions have been a central issue in ecology and biogeography in the last years. So far mostly bioclimatic envelope models have been used, showing drastic changes in suitable areas for many species. These models, however, have received some criticism because they do not include population and metapopulation dynamics. We developed a Spatial Patch Occupant Model (SPOM) for 16 species of trees in Spain. We used a binomial function that measures the probability of local colonizations and extinctions including both: the metapopulation approach, considering the distances from already occupied sites to the later colonized, and the bioclimatic envelop approach, including two environmental variables: Average Annual Temperature and Total Annual Precipitation. We parameterized the model with data from the Second and Third Spanish Forest Inventory, where more than 70000 sites on a 1x1 km. grid in all Spanish forests were surveyed twice, in 1990 and 2000. Using a Metropolis-Hastings (M-H) Markov chain Monte Carlo numerical algorithm we estimated the parameters that were later used to simulate these species dynamics in two different theoretical climate change scenarios and one no climate change scenario.

Global change impacts on the world's amphibians

Christian Hof

Amphibians are declining globally with a rate exceeding that of any other vertebrate group. In addition to habitat destruction, fragmentation and the spread of the parasitic chytrid fungus Batrachochytrium dendrobatidis, the impact of climate change presents a major threat to amphibians across the globe. Moreover, the interactions among these different pressures impose even greater threats for amphibian populations and species, as well as challenges for scientists and conservationists aiming to project and protect amphibian diversity. Here, I attempt to quantify global changes in climatic suitability for the world's amphibians using 14 global circulation models, three carbon emission scenarios and three climate envelope modelling algorithms. I identify the regions with the most dramatic changes in climatic suitability and evaluate model uncertainty. Finally, I aim to put the results of the climate models into a broader picture, with particular focus on recent studies projecting the spread of the parasitic chytrid fungus.

Global mammalian extinction risk: why and where being bad is bad / Global amphibian species richness and phylogenetic diversity

Susanne Fritz
The talk will be in two parts: First I will present part of my PhD work on extinction risk in mammals, then ongoing work from my postdoc at the CME. 1 - Why are some species more threatened than others? Which biological traits play a role in determining extinction risk, and how do they interact with anthropogenic traits? Finally, what are the consequences of phylogenetic and trait selectivity on extinction risk? Using a global mammalian trait dataset and phylogeny, I investigated the impact of species traits on extinction risk as estimated by the IUCN Red List 2007, both globally and on a regional scale. My results reveal strong geographical variation in the influence of traits on risk: notably, larger species are at higher risk only in tropical regions. I then related these patterns to current and recent-historical human impacts across the globe using spatial modelling. For example, the body-mass results apparently reflect historical declines of large species outside the tropics, due to large-scale land conversion. I also investigated global patterns of threatened species and estimated the impact on phylogenetic and trait diversity if all threatened species went extinct. Due to the selective loss of large species, phylogenetic diversity would be much less affected than the variety in body mass. If body mass diversity in mammals correlates with functional diversity, the consequences for ecosystem functioning could be severe. 2 - The underlying phylogenetic diversity can provide information about the history of the species in a place, and it may be important to conserve areas of outstanding phylogenetic diversity in terms of protecting feature and functional diversity as well as evolutionary history. I combine a global species distribution dataset for amphibians with a phylogeny compiled from taxonomic and molecular sources, to identify regions with unusually high and low phylogenetic diversity for their species richness. I also present conservation implications, and ideas how to use the data to identify centres of diversification and diversity maintenance.

Islands: the beginning of the colonization road for a major passerine bird radiation

Knud A Jønsson
A central paradigm in island biogeography is the uni-directional "downstream" colonization of islands from continents (source to sink) based on the assertion that less diverse island communities are easier to invade than the biologically more diverse continental communities. However, several cases of reverse "upstream" colonizations (from islands to continents) have recently been documented, challenging the traditional view, although most cases have simply been a matter of one or a few species within large island radiations back-colonizing the mainland. Thus, in terms of colonization directionality, "upstream" colonization remains the exception to the rule. Here we use molecular phylogenetic data, divergence time estimates and lineage diversity distributions to reconstruct origin, pattern and tempo of speciation within a widespread and species-rich (> 700 species) passerine bird radiation (core Corvoidea). Our analyses demonstrate that the origin of this radiation dates back to the late Eocene/Oligocene and was centered in the emerging proto-Papuan archipelago. Our findings demonstrate that contrary to previous island biogeography dogma, islands may in fact be the beginning of the colonization road for a major songbird radiation that subsequently invaded all other continents. That reverse colonization may be the rule rather than the exception alters widely held perceptions of the role of dispersal and establishment in biogeography.

Multiple drivers of environmental change effect on European bird populations' temporal trends

Peter Søgaard Jørgensen
One of the often implicitly assumed notions in conservation biology is that populations that are exposed to multiple and more severe agents of environmental change should be in a less favourable state than those that are exposed to fewer and less severe changes, all other things being equal. Across Europe several nation wide populations of birds are showing differing quantitative and qualitative temporal trends in size between countries. With the increasing amount of available environmental data (especially land use and climate data) from mainly the breeding range we can begin to look at correlations at a national scale between multiple environmental factors and population trends. Do populations that are exposed to more severe habitat decline and climate change do worse than those that experience mainly one of the two agents? How do different migratory routes and e.g. the differential poaching pressures experienced along each one of them play in? What are the effects from different wintering ranges between populations and species of the same breeding habitat? And what are the general patterns within countries and on a continental scale? These are all some of the questions that I will try to address in the thesis.

Intraspecific niche plasticity in *Aextoxicon punctatum*

Lauri Laanisto
Niche models usually consider niches as static entities that show no spatial flexibility at intraspecific levels. However, recent advances in experimental and field biology have demonstrated that there is a certain variation in niches, which reflect the varying preferences of the species throughout their geographic range. The idea of niche plasticity (also called niche variability; niche flexibility, niche width) could help to explain both species biogeographic and coexistence patterns. This knowledge is also worth to take into account when modelling niche dynamics from climate change perspective. Aextoxicon punctatum, ("Olivillo"), is an Chile endemic and relict evergreen broadleaf tree that dominates in very different climatic conditions. We hypothesize that in order for this species to dominate in such a wide range (from latitudes 30-43oS), it has to comprise significant niche plasticities, especially taking into account that it is at least 55 million year old relict species. For example, one of the most remarkable abilities of Olivillo seems to be its capability of growing under very varying rainfall conditions (from 2000 mm/y to 150 mm/y), and this could be due to the capability of some populations of compensating water shortage with fog water uptake.

Phylogenetic signals in traits, dispersal ability and changes in climatically suitable ranges of African starlings

Irina Levinsky

Phylogenies contain intriguing information on the evolution of species' niches and traits. Here, a new molecular phylogeny of African starlings (Sturnidae) is used to search for phylogenetic signals in species specific traits and in changes in climatically suitable ranges over time. I collected data on the traits of 55 African starling species; measures of body mass and habitat preference were obtained from the literature, while dispersal abilities were calculated from wing length. Current and last glacial maximum climatically suitable ranges were modelled using climatic envelope models. Traits and changes in size and position of species' ranges were then related to the phylogeny to test for phylogenetic clustering.

Why were mammals from North America better colonizers than South American ones during the Great American Biotic Interchange?

Mariana Munguía-Carrara

After the Panaman Isthm land connection in America (2.5 mya), a great number of north-american mammal genera crossed the land-bridge separating the northern and southern parts of the continent; this process of mixing of otherwise isolated faunas is know as the Great American Biotic Interchange (GABI). In contrast to this massive movement of taxa from the north to the south, a reduced number of genera from South America were reported to successfully colonize North America. Two main explanations for this asymmetrical pattern in the interchange of the two faunas have been hypothesized: 1) the land size area available for their ancestors to evolve in; 2) climate of those migrating southward would then be able to occupy much of South America because they were able tolerate moist tropical forest against the challenge of northward migrants who had little prospect of penetrating beyond Central America because they were specialized for tropical environments. Here, we test, for the first time, the latter hypothesis that the reported asymmetry during the GABI might have been due to differences in the availability of suitable environment in both sides of the continent. Using hindcasting of bioclimate envelopes extant American mammal genera from Plioscene, we found that the total area of suitable available bioclimatic envelopes for colonization in the receiver continent was greater for North American mammals than it was for the South American counterparts. Although other factors might have contributed to the asymmetry in the colonization patterns during the GABI, we are able to demonstrate including fossil data validation, that the availability of habitat for colonization provides a parsimonious and testable explanation for the reported pattern.

Species' geographical ranges: physiology, dispersal and environment matters

David Nogués-Bravo
The factors that shape geographical ranges of species have long fascinated ecologists and biogeographers, and unveiling them is of utmost importance for assessing the potential impacts of global change in species distributions and extinctions. Empirical studies on limiting factors of geographical ranges, and implicitly species niches, have often correlated the distribution of species with current environmental conditions such as climate, soil or land-uses. On the contrary, theoretical studies on geographical ranges and their limiting factors have focused on biotic parameters as physiological tolerances of species to the environment, dispersal abilities or species interactions. Following these theoretical assumptions, then the size of geographical ranges should be partly explained by the interplay between the geographical extent of environmental conditions and species-specific physiological tolerances to those environmental conditions and dispersal abilities respectively. Herein we test this idea for European trees using information about the distribution of environmental condition in Europe, tree-specific physiological tolerances to environment and dispersal abilities.

Modelling future non-breeding distributions of European waterbirds under climate change

Anders P. Tøttrup
Climate change models on species distributions have so far mainly been conducted on breeding ranges in terrestrial habitats, ignoring the non-breeding distributions of species as well as species' depending on marine environments. In temperate and arctic birds, the vast majority of species are migratory occupying and depending on at least two geographical areas for successful completion of their annual cycle. Waterbirds are typically characterized by being numerically abundant, long lived and feed at a variety of trophic levels. As such, waterbirds are likely to be very responsive to changes in their environment. Generally, waterbirds overwintering in northern Europe are expected to move their occurrence north-eastward under large-scale climatic changes tracking their climate-niche. Using Species Distribution Modeling I aim to determine the large-scale environmental factors most important for current non-breeding distributions of waterbirds and predict future geographical distributions and spatial abundance patterns of individual species. Distribution and abundance data are available in unique spatiotemporal time series from northern Europe (1987-2008). Models based on the distribution in the late 1980's will be evaluated with patterns seen in the 2000's.

Exploring and assessing the effects of climate change on Iberian vertebrate species

Maria Triviño

Habitat loss and habitat degradation are the main causes of species extinction. However, there are already substantial evidences that climate change is affecting ecosystems and is expected to be the main threat in the near future. Future impacts of climate change on biodiversity have been explored using niche models but more ecologically realistic models are starting to be developed. These developments include moving from statistical towards mechanistic approaches. BIOMOVE is a software in line with these new advanced approaches. BIOMOVE models vegetation dynamics by incorporating physiological and demographic processes of plant functional types. Nevertheless, a missing element is including plant-animal interactions. I will explore ways of integrating these interactions focusing on vertebrates. In order to achieve this aim I will first identify species which strongly depend on vegetation and identify causes for this dependence such as feeding, nesting, breeding, escaping predators and so on. I will present different alternatives for including these interactions in BIOMOVE in the Arrábida meeting for further discussion. I will also discuss how to combine or differentiate direct or indirect (via vegetation changes) climate change impacts on vertebrates. Eventually I will hope to assess the risk of extinction of Iberian vertebrate species using this approach.

TECHNICAL UPDATE

Ibiodat – A tool for homogenizing and geo-referencing taxonomic data

Isaac Pozo
Often taxonomic data are located in specimen collections, museum records, and to a lesser extent on digitalized data bases. These data typically contain incorrect taxonomic references and inaccurate geographical locations. The problem in taxonomic references often comes from changes in the nomenclature of species (group aggregations, new species, etc). Problems in geo-referencing come from inaccuracies in the capture location, use of old locality names, etc. To solve these problems we developed a software application called IBIODAT (Application for Normalizing of Taxonomic Collections) under the scope of the project IBERIA GAP. This application enables the checking and correction of already digitalized collections and also provides a tool for digitizing and geo-referencing old collections. All the outputs of the application follow the formats of the international standards for digitalization of taxonomic collections (Darwin Core, GIBIF). The application is available for free and can be downloaded on the web page of the project IBERIA GAP.

How to Describe and Evaluate Data Quality in Digital Maps

Bjørn Hermansen
Lots of papers and articles have been written about how to measure and how to improve data quality. At the same time still more data sets with poor or unknown quality are produced. To be able to discuss how to describe and perhaps quantify data quality, it is essential off course to define the main components of the quality concept. This is done with focus on vector map data and a few suggestions concerning practical solutions are presented.