MACIS

Minimisation of and Adaptation to Climate change Impacts on biodiverSity

Deliverable 3.4:
Report on improved method for reserve selection

Specific targeted research project (STREP)

Contract period 01 November 2006 – 31 October 2008
Contract no. 044399 (SSPI) MACIS

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Improved methods for conservation planning

Systematic conservation planning is a young field, constantly developing quantitative techniques and computerized tools to identify cost-efficient conservation priority areas (Cabeza and Moilanen, 2001; Pressey et al 2007). The science behind it has addressed important problems, and is slowly influencing practice. Next developmental avenues should move from representing static biodiversity patterns to including the protection of processes and acknowledging the dynamic nature of biodiversity. Additionally, the approaches need to better anticipate the various ways in which humans are modifying the planet at ever faster rates. Climate change, rapidly altering the quantity, quality and distribution of suitable areas for many species (e.g. IPCC 2007) remains as one of the biggest challenges to conservation planning (Pressey et al 2007). The need for a change in paradigm is pressing, as many species seem to be shifting their ranges due to climate change (Parmesan 2007).

Some species, even if currently protected, will persist only if they can colonize new (protected) areas, although often their dispersal abilities might not be enough in so disturbed and fragmented landscapes, and may thus require corridors and stepping stones between protected areas. In other cases, species might persist in areas where they can retain parts of their ranges. Araújo et al. (2004) showed that common conservation planning approaches do not capture such retention and connection areas, and that new tools are needed for biodiversity conservation in a rapidly changing world. Such advances will perhaps be the main focus of conservation planning in the coming years.

There has been a recent effort to develop conservation planning tools to account for forecasted changes in species distributions (Williams et al 2005; Hannah et al 2007). These studies identify minimum sets of areas that protect occurrences of the species currently and as forecasted according to particular models and emission scenarios. But models for forecasting biodiversity responses include a wide range of assumptions and limitations. They seldom deal with migration processes, the dynamics of population at the retracting edge, the potential of adaptation or species' interactions (Thuiller et al 2008). Additionally, even similar modeling approaches making use of the same predictor variables can result in very different predictions. Studies have shown how the variability of the predictions can be as high between different emission scenarios as between different niche-based models (Thuiller et al 2006). Further, there is not even agreement in predictions from different climatic models providing the estimates for the predictors of the biological models. I uncertainty has become an issue in forecasting biodiversity responses to climate change, it should definitely be acknowledge when planning conservation areas. With this project we wanted to emphasize that one may not want to rely fully on future projections when setting conservation priorities, especially if this can compromise current levels of protection

We developed a new conservation planning tool to be implemented in the public Zonation software (Moilanen and Kujala 2006, 2008; http://www.helsinki.fi/bioscience/consplan/), which is particularly well suited for the analysis of large GIS-based raster grid data sets that describe the distributions of many biodiversity features (Kremen et al. 2008; Leathwick et al. 2008). Zonation offers several alternatives for valuing biodiversity when planning areas, and for exemplification, here we concentrate on what is referred to as Core Area Zonation . With this alternative, the landscape s hierarchically classified, showing the areas from less to more value retaining the core (percentage of current distribution with highest occurrence values) of as many species as possible (fig 1).

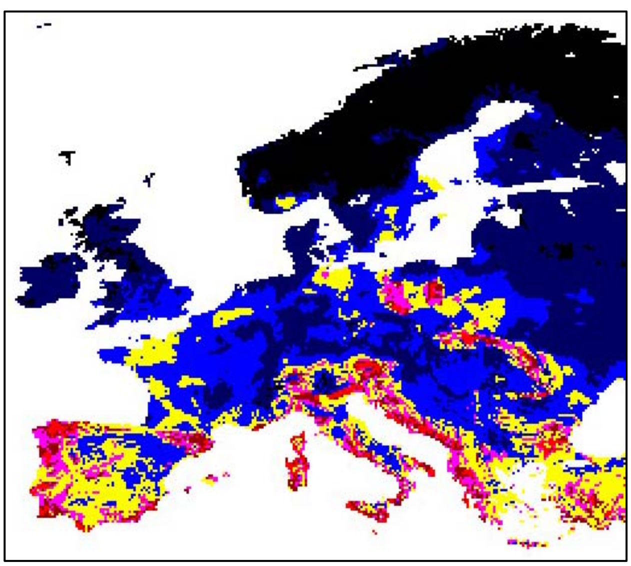

Figure 1
Example showing the importance of the European landscape retaining the distribution of European amphibians and reptiles at present. The method removes the sites of less biodiversity contribution, one by one, until no more sites can be removed, while trying to retain the best parts of each species distribution until the end. The last 10% of sites removed (red) show then the top conservation priorities, that would protect an even proportion of the distribution of all species

As with similar approaches accounting for climate change, the features to be retained include the present and the forecasted distributions of all species, but also connectivity between important present core areas and future core areas (e.g. Hannah et al). We account for present and future simply by including both distributions in the prioritization analysis. We propose a standardized way of accounting for (i) connectivity from present to future distribution areas, and importantly (ii) uncertainty about climate change and its influence on species distribution projections. The inclusion of these components is implemented so that it can be computed even for very large data sets including distributions defined on multi-million element grids.

Connectivity

Connectivity from present to the future was implemented via the “species interactions” technique of Zonation, which allows calculation of connectivity between two distributions (Moilanen and Kujala 2008; Rayfield et al., submitted). This technique essentially weights the local quality of one distribution by metapopulation-type connectivity to another distribution. This approach has been applied to compute the required connectivity between two species, for instance, predator and prey (Rayfield et al). In a climate change context, we apply the same approach to compute the connectivity for each species between present and future.

Two types of connectivity are important when thinking of climate change. In first place, it is important to identify source sites, i.e. areas that are of high habitat quality today, and that contain a large number of species, that are well connected to future suitable areas, i.e. from where dispersal to future distribution areas would be easiest. This is computed as the connectivity from present to future(see fig 2). The second connectivity refers to stepping stones, areas perhaps not yet suitable today, which will help species reach the core areas of their future distributions. This connectivity is computed as the connectivity from good future areas to the present.

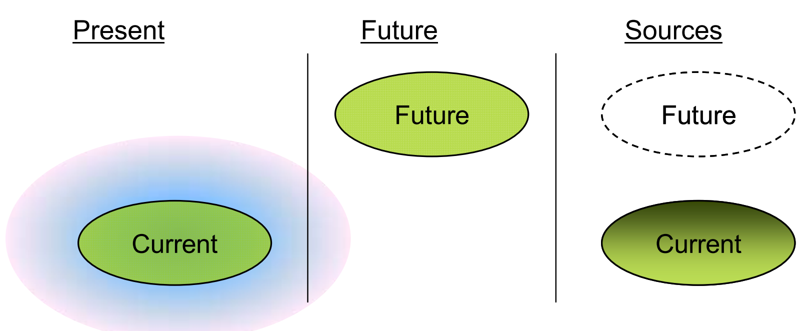

Figure 2. Illustration of the concept of source, here defined as areas of the current distribution that are within colonizing distance from future suitable areas. The area in blue shades represents the dispersal likelihood. The dark green area at the source panel represents areas of the current distribution most valuable as sources

We denote S_{ij} as the source and SS_{ij} as the stepping-stone value for a species *i* in a site *j.* The equation below expresses mathematically the computation of this values, with P_{ij} and F_{ij} representing the probability of occurrence of species *i* in site *j* at present and future, respectively. β_i is a parameter modeling the spatial scale of dispersal for species *i*. Thus, the source value for species *i* in grid cell *j* depends on the local probability of occurrence, the dispersal ability of the species, and the distance of between the focal cell and all other cells where the species is predicted to occur in the future, weighted by the future probability of occurrence:

$$S_{ij} = P_{ij} \min\left\{1.0, \frac{\sum_{n=1}^{N} \exp(-\beta_i d_{in}) F_{in}}{\max \sum_{n=1}^{N} \exp(-\beta_i d_{in}) F_{in}}\right\}$$

Locations with high S_{ij} have both a high probability of occurrence of species *i*, and that species is within the dispersal distance to a relatively high number of sites with high probability of occurrence for species *i* in the future.

Similarly, stepping-stone value can be defined as:

$$SS_{ij} = F_{ij} \min\left\{1.0, \frac{\sum_{n=1}^{N} \exp(-\beta_i d_{in}) P_{in}}{\max \sum_{n=1}^{N} \exp(-\beta_i d_{in}) P_{in}}\right\}$$

Uncertainty

We denote the present, future, source and stepping stone distributions by P_{jsm}, F_{jsm}, S_{jsm} and SS_{jsm}, where *j* is index for species, *s* is index for emission scenario and *m* is index for habitat modeling method. Each of these distributions is a rectangular grid with the value for each grid cell representing the predicted probability of occurrence of the species, conditional on emission scenario and model. Our aggregate best prediction for a species, assuming emission scenario *s*, is the (cell-specific) mean across different models: using the present distribution as example $P^{*}_{js}=E_m[P_{jsm}]$, where $E_m[]$ represents expected value taken across models m. Another quantity needed below is the (cell-specific) standard deviation of predictions across models, denoted by $\sigma_m[P_{jsm}]$. This quantity represents prediction uncertainty for the species at a location.

We accounted for uncertainty in predictions in two ways. First, we emphasize those parts of species distributions where high occurrence levels for the species are relatively certain. We do this using an uncertainty analysis technique called distribution discounting, which penalizes predicted occurrence levels according to the amount of uncertainty in the prediction (Moilanen et al. 2006). In essence, a multiple of the standard error of prediction across models is subtracted from the mean prediction. We set $P_{js}(\alpha)= P^{*}_{js}-\alpha\sigma_m[P_{js}]$, where α is a parameter called the horizon of uncertainty (Moilanen et al. 2006). Our base-analysis used α=1, corresponding to subtracting one standard deviation off the mean (fig 3).

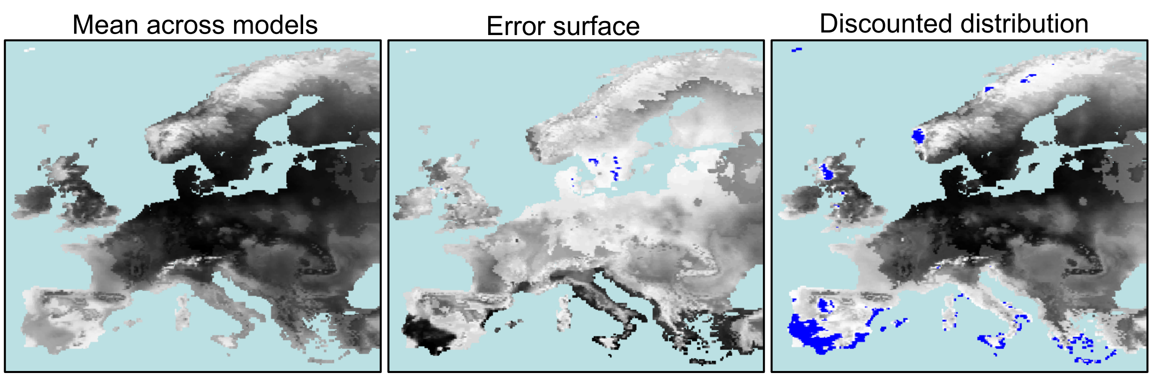

Figure 3. Exemplification of the distribution discounting using the current distribution of one amphibian species. The left panel shows in dark colours areas where the mean occurrence probability across four different model types (ANN, CTA, GLM, GAM) is high. The middle panel shows in dark, areas where models disagree, i.e. the error can be high. The panel on the right shows the discounted means, reflecting areas of high probability of occurrence and high certainty

It is clear though, that there is more uncertainty than that due to the habitat modelling approach. Future predictions include the greatest uncertainty about the future degree of climate change, and the connectivity distributions include additional uncertainty about dispersal distances and colonization success. When maximizing protection both at present and in future, ignoring these uncertainties, we are trading-off protection level at present, and overall we can capture less of the current biodiversity value in protected areas. Figure four shows that when equal priority is given to present and future, we are protecting 10% less biodiversity at present, for an uncertain high protection in the future.

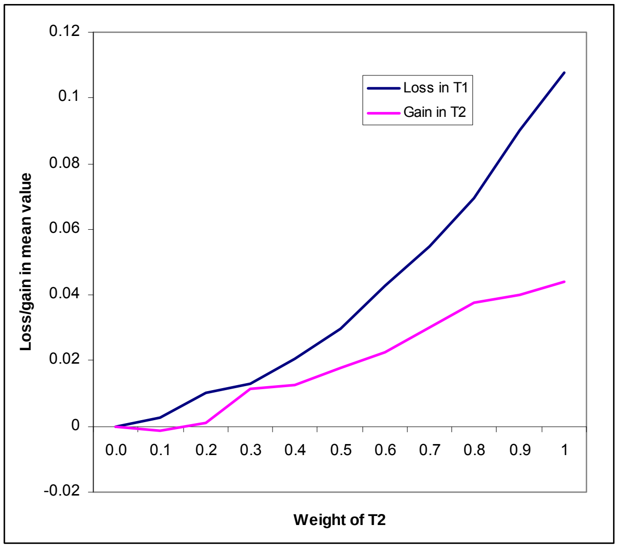

Figure 4. Curves showing the percentage loss of protection value at present (blue line) and the percentage gain in future conservation value (pink line) when increasing weight is given to future projections. With weight of one, uncertainty about the future is disregarded, thus present and future distributions are treated as equally valuable. The curves are done using the same example of amphibian and reptile species, for emission scenario A1.

We thus suggest that as a second uncertainty consideration, we give highest overall weight to the present distributions, and weight the future distributions and connectivity distributions relatively less, depending on risk aversion. Denoting by $w(D)$ the weight given for a particular kind of a distribution D, considerations of uncertainty suggest that $w(P_{js}) > w(S_{js}) \geq w(F_{js}), > w(S_{js})$. Alternatively, optimal weighting can be assessed by exploring the trade-offs, or by assigning a maximum tolerance level for loss of protection at present. Below, figure 5 shows visually how the solutions change spatially when different weight is given to Future and to Sources

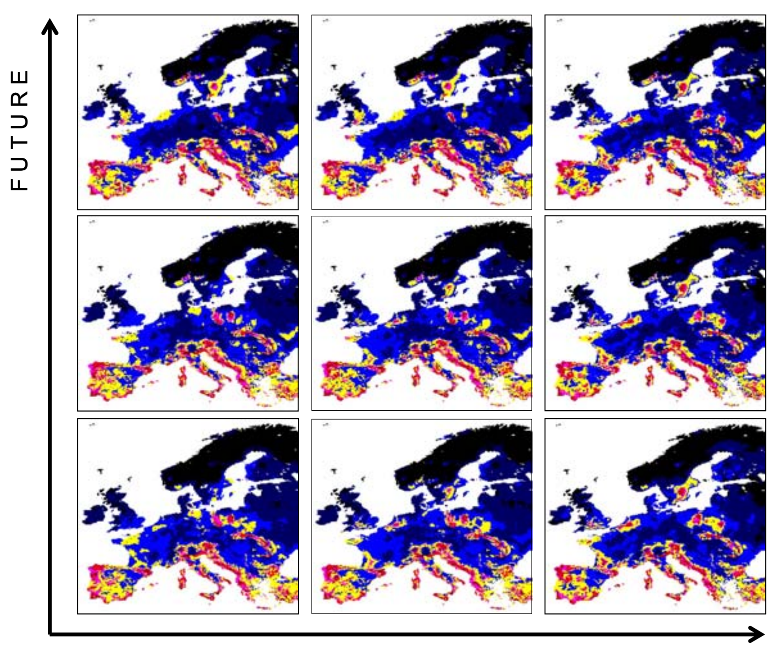

Figure 5. Ranking of conservation priorities, when different weight is given to future distributions and sources. The bottom left panel is includes only the present distributions. Although the main picture is similar note, for example, some differences in UK and Scandinavia. These results are for emission scenario A1.

Cores, Sources and sinks

Once the desired weighting is applied, conservation priorities are identified. From figures such as Fig. 5, though, it cannot be assessed which of the top 10% areas are important sources, important cores or important stepping stones. Such classification may be important for scheduling actions, as present cores and sources may require more urgent action, while the protection of future areas not yet suitable may necessitate different management approaches. The role of each of the priority areas can be identified based on a comparison of cell ranks in different Zonation analyses. We denote by $rank_i\{D\}$, the rank of cell i in an analysis using distributions D. For example, $rank_i\{P, F\}$ indicates an analysis using present and future distributions but no connectivity components. We use the following conditions to identify different types of areas:

Area type	identification condition
Present core area	$rank_i\{P\} > rank_i\{P, F, C_P, C_F\}$
Future core area	$rank_i\{F\} > rank_i\{P, F, C_P, C_F\}$
Dispersal source	$rank_i\{P, C_P\} > rank_i\{P, F, C_P, C_F\}$
Stepping stone	$rank_i\{P, F, C_P, C_F\} > rank_i\{P, F, C_P\}$

Emission scenarios

We suggest that analyses would be done separately for each emission scenario. No averaging across emission scenarios is recommended, because the scenarios are mutually exclusive and cannot happen simultaneously. Nonetheless, we recommend a sensitivity analysis to estimate potential conservation losses if one scenario was used to identify priority areas but another scenario would take place. Another option is to identify those areas that maximize biodiversity conservation across all scenarios. Catering for all emission scenarios simultaneously of course implies that solution quality may be reduced from the perspective of any single emission scenario.

Data used in the examples

All data used here to exemplify the conservation planning methods is from Araújo et al (2006), where 143 amphibian and reptile species were modelled with four species–climate envelope techniques (artificial neural networks, generalized linear models, generalized additive models, and classification tree analyses). In favor of clarity, we only used future distributions that were projected for emission scenario A1 for 2050. Cabeza et al (in prep) is currently comparing conservation priorities for different scenarios

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