Integrated modeling of range shifts of highly dispersive animals under climate change

Expert workshop, 2-5 September 2008
Centre for Biodiversity Conservation – Conference Room, Kirstenbosch, Cape Town

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1 Record of workshop

Background

Conservation measures to maximise the adaptation of species to environmental change need to be based on robust and regularly updated science. Global change scientists therefore have a great responsibility to be rigorous as possible in their approach, as well as proactive in communicating their results to planners, managers, and policymakers -- not just to other researchers.

Conservation planners have expressed frustration to the global change ecology community that existing models of species range shifts under climate change are usually based on overly simplistic assumptions about species distribution. There is an urgent need to improve the basis of species range shift modeling by using population and behavioural data to inform spatial models or, as Steve Willis of Durham University puts it, “putting biology into climate modeling.”

Models integrating biogeographic and demographic approaches are a significant advance on first-generation bioclimatic envelope models. One such model explored in some depth here is the emerging programme BioMove, developed to model plant range shifts using dispersal, fecundity and survivorship matrices. Other approaches include the Migrate software used by Durham University global change biologists and a variety of supportive mapping tools like MaxEnt.

A workshop was held in early September 2008 with global change ecologists from South Africa, Australia, the UK and Swaziland to focus attention on the ways in which BioMove and other modeling approaches could be adapted for highly dispersive animals, such as birds and bats. Although our initial hope was to use the workshop to test and refine a first adaptation of BioMove for animals, this proved to be overly optimistic as the initial programming to do this was judged to need in advance significant conceptual inputs from animal ecologists. The workshop thus aimed to provide these inputs as a first step, and to produce a collaborative paper on dynamic species range modeling as a way to integrate biogeography, demography, behaviour and climate tolerances.

Financing and acknowledgments

The workshop was hosted by the South African National Biodiversity Institute’s (SANBI’s) Climate Change and BioAdaptation Division, and financed largely through a bilateral research collaboration agreement between South Africa and Australia, via the Australian Department of Climate Change and the Western Australian Department of Environment and Conservation (DEC). Further in-kind support for travel was provided by The Royal Society (UK) through a Joint Project Grant to Durham University for collaboration with SANBI, and by participants themselves (some through their institutions). The organisers warmly thank Richard McKellar of DEC for encouragement and facilitating financial support. We also thank Res Altwegg, Ian Davies, and Danni Guo for essential technical/conceptual inputs, and Lynn Havinga, Deryck de Witt, Nawaal Titus, Ilhaam La Guma, and cleaner Thembakazi Gqabuza for administrative or logistical help.

Introduction, aims and objectives

The main aim of the workshop was to advance conceptually the use of modeling tools, in particular the package 'BioMove,' for projecting the range shifts of mobile animals under environmental change, and thereby to improve significantly the reliability of climate change projections for such animals within southern Africa and elsewhere.

Participants (Annex 1) introduced their own research interests and expectations of the meeting. This included several brief, informal research presentations by Guy Midgley (SANBI), Steve Willis (Durham), Lesley Gibson (DEC), Lynda Chambers (Australian Bureau of Meteorology), and Ara Monadjem & Peter Taylor (Bat Atlas of Southern Africa) to set the scene for the groups’ work on habitat suitability / niche modeling and/or data collection. Additional short presentations were given by Phil Hockey (FitzPatrick Institute) to highlight the complexity of birds’ movement strategies, by Res Altwegg (SANBI) on demographic modeling and the use of two-sex models, and by Bernard Coetzee (PhD student) on ensemble modeling and consensual prediction of the effectiveness of South Africa’s Important Bird Area network under climate change.

The phrase “highly dispersive animals” was clarified as simply “dispersing at multiple life stages,” unlike sessile plants which can only disperse at the propagule stage. For simplicity, we initially consider animals which may disperse simply after birth or between breeding events. Yet movement patterns of birds and other animals can be highly variable and complex (including nomadism, migration, residency and many variations on these themes). Indeed, one working group concluded that more sophisticated tools specific for migratory animals will be needed, as so many birds in Europe and elsewhere have simple or complex migration patterns – and African bird migration patterns are equally or more complex.

Data limitations and needs

Attention needs to be paid (and investment made) to improving, securing and continuing the datasets needed for more accurate animal species range modeling – including those on demography, niche requirements, phenology, behaviour and physiology. Southern hemisphere datasets are usually highly imperfect -- spatially or taxonomically incomplete, undigitized, institutionally insecure, with short or broken time series. While it is sometimes possible to take crude first steps at animal range modeling, it is therefore difficult to attach confidence limits, especially given the natural environmental stochasticity and aridity of much of the south. Investment is urgently needed from major donors to collate, secure, and further develop long-term environmental observation datasets on biodiversity and climate change. But even in the northern hemisphere, data access and intellectual property issues between institutions often severely constrain the use of appropriate datasets for these purposes. Given the urgency of climate change vulnerability and adaptation work, these obstacles need rapid attention.

Key questions

- What are the essential differences between plants and animals affecting modeling?
- What different movement strategies do birds have? What sorts of animals will first have their ranges influenced by climate change?
- What predictions can we make to inform patterns of conservation resource allocation?
- What are the thermal and moisture tolerances of animal species in different habitats and of different life histories? Are birds and bats generically different in these ways?
- How can we use population parameters of species to predict declines or increases in certain parts of shifting ranges? Which parameters are most important and ‘do-able’?

The discussion emphasized a point made by both Steve Willis and Bernard Coetzee: “climate modeling needs more ecology, not more maths.”

Bioclimatic niches and their use in next-generation dynamic range modeling

Guy Midgley sketched the modeling tool ‘BioMove’ conceptually for the group. BioMove defines two types of range-shift response to climate change -- inside or outside potential bioclimatic range -- then links this response to population responses. For plants, this means modeling the response of different life stages: seeds, juveniles, subadults, and adults. The model identifies areas of maximum population growth or productivity, scales seed production or fecundity more generally
against environmental quality, and allows population structure and mortality bottlenecks to be identified. It essentially converts spatial shifts to projections of demographic rates.

**Key questions about BioMove**

Q. Can BioMove incorporate density-dependent processes? A. Yes. It also allows incremental (annual) climate envelope shifts and investigation of changing mortality patterns. BioMove also allows modeling of background biomass (grass, trees etc) which help drive fire, shading-specific mortality and so on. It simulates the background habitat.

Q. Can it incorporate competition? A. Yes, it incorporates shading. But this is not easy to adapt to animal competition – this is enormously more complex. We can introduce masks that can accelerate mortality.

Q. Doesn’t this imply the need for two interacting models? A. Yes, this is possible. We could introduce things like “a facilitating food resource,” in place of plant functional types, to accelerate population growth rather than shading to reduce or zero it. We can scale areas of suitability.

Q. Do new habitats just appear instantaneously? A. No, they have their own demographics built in. In theory, this is completely scale-free, although in practice, scaling up makes dispersal less relevant.

Q. What language is BioMove written in? A. It was originally coded in C++ but was put into Lamos by Ian Davies (ANU) overnight.

Q. Can BioMove handle the directionality of dispersal? A. Yes, in the “decision to settle” term. Dispersal is then simulated and compared to observed dispersal. Every time step allows life stages to disperse, so the computational requirements are immense.

The data requirements to parameterize BioMove and related models are less onerous than we think, as Res Altwegg outlined in his presentation on demographic modeling inputs to spatial modeling. We can make generalizations, based on our field knowledge of species. One can explore the sensitivity of different life stages to climate in species of different life-history strategies.

Phil Hockey emphasized the different “buffering” effects of different habitats. forests (and therefore forest birds) are highly buffered, open airspace is completely un-buffered, and savannas and deserts somewhere in between. He asked if we couldn’t use a 3D matrix of this issue to predict responses, to avoid case-by-case modification of each species. He also noted that those species which have moved already, for whatever reason, are innately mobile habitat generalists, but habitat specialists are forced to stay where they are.

Models need to start 30 years ago to calibrate the model according to where species are today. We can do this by constructing qualitative matrices of habitat use, then select suites of species and code different layers into BioMove. The Angolan Free-tailed Bat was mentioned to illustrate – it inhabits hot climates, is widespread and well-known physiologically. We now find colonies cropping up in Durban and elsewhere. (Is this drought? Or a species previously undetected?)

The two key demographic issues needing attention in BioMove's adaptation to animals are (A) dispersal – differing natal and breeding dispersal (decision to leave, probability of settling) and (B) survivorship. Birds and bats are similar here: there are cave-dwelling, tree-dwelling, and house-dwelling bats, similar to the associations of many birds. The model discussions discussed so far work well for bats. It was agreed that we could potentially try BioMove out on invasive species -- for example, on common starlings where the introduction events and dates are well known?

Metapopulation model dispersal functions may be relevant here, commented Dave Hole; Illka Hanski’s research group has surely done bird metapopulation modeling. (Apparently not, but they have of course worked on other highly mobile vertebrates and invertebrates as well as plants – see [http://www.helsinki.fi/science/metapop/Study_organisms.htm](http://www.helsinki.fi/science/metapop/Study_organisms.htm).) Are there ways we can build on their insights, or incorporate them?
Phil Hockey presented life history variables for which we have basic information on a number of southern African species. He argued the difficulty of generalizing, e.g. from aerial insectivores. Ten aerial insectivores have not shifted their range while eleven have. We need to generate predictions on which species may move their ranges first, and to where. These can be soon tested. Swifts are moving now, but African green pigeons may not move for 200 years. These assessments are based on comparison of the 1978 *Roberts' Birds of Southern Africa* (the first time range maps were published) with the 1997 SABAP1, supported by documentary evidence from the published literature and other sources. He urged that Penn Lloyd be consulted on the autocorrelations between life history traits. The 2005 *Roberts' Birds of Southern Africa* database has data for

- Body mass (most species)
- Mating system (most species)
- Nest dispersion (most species)
- Clutch size – brood frequency (most or many species)
- Movement pattern (many species)
- Habitat occupancy (most species)
- Breeding performance (some species)

**Model development challenges**

On Wednesday morning, Guy recapped the previous day’s interactive software session with new flow charts of the parameterization of BioMove/Lamos (below) and handling of target species.

**Parameterising target species**

- Determine species demography
  - # life stages/max rate of transition/max mortality/max fecundity/
  - Seed life history

- Determine species fire response
  - per life stage – killed/re-sprouter set back

- Determine species light response
  - 3 life stages and germination

- Determine species dispersion
  - (kernels/long distance)

- Determine species bioclimate
  - transition/fecundity/survival

**Plant functional types**

**Target species (ghost)**

- Update drivers – Masks/Habitat suitability

- Determine population structure of FFTs in each cell
  - Fire module
    - Fecundity
    - Dispersal

- Grow population, structure and biomass according to habitat suitability and competition (transition/mortality/seed production)

- Determine population structure in each cell

- Fire – yes – release stored seed
  - kill/set back resprouters

- Disperse seed
  - update dormant and active pools
  - Germinate available seed
  - Age seed pools

- Grow population according to habitat suitability
  - (transition/mortality/seed production)
Yvonne Collingham at Durham has also done this with Migrate – she has parameterized dispersal functions using butterflies. It was agreed that we need to be careful about trying to ‘run before we can walk’ with taking on too many or too complex species to model, especially species with multiple life-history stage dispersal events.

**A research agenda**

A sensible research agenda to extend BioMove (and other tools) involves three or more steps:

1. Theoretical development – started at this workshop
2. Case studies
3. Gap analysis – highlights research gaps, sensitivities etc

**What are the take-home (theoretical development) messages from this workshop?** We have development needs in the following prioritized areas for animal modeling:

<table>
<thead>
<tr>
<th>Challenge</th>
<th>Priority</th>
<th>Do-ability / Approach</th>
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<tbody>
<tr>
<td>1. Dispersal of multiple life-stages</td>
<td>Highest</td>
<td></td>
</tr>
<tr>
<td>2. Active re-dispersal guided by choice of habitat quality</td>
<td>High</td>
<td>Very good information needed to parameterize – see density dependence theory for plants</td>
</tr>
<tr>
<td>3. Dispersal triggered by density?</td>
<td>High</td>
<td></td>
</tr>
<tr>
<td>4. Fecundity (step change)</td>
<td>For noting</td>
<td>For noting</td>
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<tr>
<td>5. Dynamic resource dependence (niche specialization)</td>
<td>Medium?</td>
<td>Tough unless done through PFT analogue</td>
</tr>
<tr>
<td>6. Masks (e.g. roost sites)</td>
<td>For noting</td>
<td>For noting – check use of masks as positive and negative drivers</td>
</tr>
<tr>
<td>7. Sex ratio</td>
<td>Medium</td>
<td>Easy? Specified life stages</td>
</tr>
<tr>
<td>8. Disturbance functions – NB drought which can force birds to occupy new ranges temporarily or permanently</td>
<td>Low? (Pathogens, e.g. Phytophthora – wildfire analogy)</td>
<td>Easy? Cookie cutter – or is this captured through average habitat suitability? Drought disturbance has been shown to increase dispersal distance</td>
</tr>
<tr>
<td>9. Model a separate strongly interacting species</td>
<td>Low – useful future direction</td>
<td>Difficult – e.g. pine bark beetle- key predator/competitor (PVA applications)</td>
</tr>
<tr>
<td>10. Nomadic species</td>
<td>High SA &amp; Aus, low in Europe</td>
<td>Special case of re-dispersal – difficult to handle in BioMove as these are driven by sub-annual processes</td>
</tr>
<tr>
<td>11. Migration</td>
<td>Low</td>
<td>Model as independent species? Model winter/summer separately</td>
</tr>
<tr>
<td>12. Other mating / breeding systems</td>
<td>Low</td>
<td>Relevant only for some species at tail end of process (esp for red data species, declining populations – effective sex ratio). Treat as minimum population size per cell switching on breeding</td>
</tr>
</tbody>
</table>
Planned activities – a way forward

1. Opinion piece (possible journals *J Biogeography, Ecography, Global Ecology and Biogeography, Diversity and Distributions, TREE*) - clear comparison with plant approach

2. Plan collaboration, develop funding strategy for Biomove and macroecological study

3. Explore macroecological similarities and differences (birds, bats, continents) separate funding strategy

4. Select case studies, compile data for target species and background vegetation structure

5. Prioritize “plant-like sparrows” -- or endemics (to model entire range) – data rich species include most of those at Koeberg

6. Identify bird/plant relationships, elaborate and record data availability for different functional types.

7. Refine instructions for the initial adaptation of BioMove – core group

8. Schedule meetings and training (with Ian Davies)

9. Run simulations

10. Refine adaptation of BioMove

11. Identify gaps and obtain data

Species selection, key products and collaborative teams

Working groups developed shortlists of species for initial BioMove extension. For simplicity, these were chosen on the basis of the following basic criteria:

- Availability of historical data
- Resident, not nomadic
- Good distribution data for entire range and widespread (min 30-50 occurrence units)
- Relatively generalist
- No water or seabirds
- Not specialist colonial (e.g. bald ibis, karst cave-dwelling bats) – generalist colonials (e.g. fruit bats, weavers) are okay. Specialists are possible, if we have spatial datasets (mask) on occupied and unoccupied sites (caves, ledges, cliffs, etc)
- Availability or guessability of demographic parameters (survivorship, reproduction and age at first breeding)
- Reasonable dispersal estimates

A Durham PhD student has just finishing modeling breeding occurrence of bird species in Europe and non-breeding occurrence in Africa.

Candidate bird species:

Southern Africa:
Expanding species (11, including 2 dependent on alien plantations)
- Southern Grey-Headed Sparrow
- Fork tailed Drongo
- Black Sunbird
- Crested Barbet
- Swainsons Spurfowl
- Tambourine Dove – uses invaded watercourses
- Streakyheaded Seedeeater
- Acacia Pied Barbet – well documented
- African Goshawk – breeding in unnatural habitats (competing local hypotheses!)
Black Sparrowhawk – breeding in unnatural habitats – competing hypotheses!
Hadeda Ibis – well documented, both demographic and distributional – very easy to look at
gap filling at fine scales.

Contracting species (209 identified as priority atlas species by Richard Dean 2006). Permission to
model these species based on this shortlist has been sought from Richard and two reminders sent
– he appears to be out of office, and is anyway retired.

**Europe:**
Expanding species (14)
- Cetti’s Warbler – not already done with Migrate by Yvonne C
- Dartford Warbler – already done with Migrate by Yvonne C at fine scale w Chris Thomas
- Collared Dove – but maybe no link to CC
- Green Woodpecker
- Great Spotted Woodpecker
- Nuthatch
- Black Redstart
- Little Owl
- Firecrest
- Siskin
- Scarlet Rosefinch
- Cirl Bunting
- Hawfinch – poorly documented but range has increased most
- Short-toed Creeper

Contracting species (5)
- Red-backed Shrike - migrant
- European Roller – migrant
- Pied Flycatcher – migrant
- Lesser Spotted Woodpecker
- Ortolan Bunting

**Australia:**
Lynda Chambers and Lesley Gibson used the New Atlas (Birds Australia data) to select species
according to distributions that were restricted to the south-west of Western Australia. The
exceptions are Hooded Plover (found throughout southern Australia), Australian Ringneck (near
continental) and Blue-winged Kookaburra (restricted to northern tropical areas). Water and
seabirds were excluded, as were species with low reporting rates or very restricted distributions.
The 11 species selected during this first draft cover a range of guilds (including parrots, pigeons,
fairy-wrens, honeyeaters and kingfishers). Comparisons between the distribution of the species
during the two Atlas periods (1977-1981 and 1998-2001) divided the species into those that have
experienced significant regional variation in distribution (no change in reporting rate) to no change
regionally (with change in reporting rate). Further work is required to determine which of the
species have sufficient demographic and dispersal information.

Discussions are needed to identify potential Australian bat species.

**Candidate southern African bat species:**
Ara Monadjem and Peter Taylor chose the following 27 species based on application of the above
criteria to the database of the new Bat Atlas of Southern Africa:

- *Cistugo lesueri*
- *Cistugo seabrae*
- *Epomophorus angolensis*
- *Epomophorus anselli*
- *Epomophorus crypturus*
- *Epomops dobsonii*
- *Hypsugo anchietae*
- *Laephotis angolensis*
<table>
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<tr>
<th>Species</th>
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<tr>
<td>Laephotis botwanae</td>
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<td>Laephotis namibensis</td>
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<tr>
<td>Lissonycteris goliath</td>
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<tr>
<td>Mimetillus thomasi</td>
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<tr>
<td>Miniopterus fraterculus</td>
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<tr>
<td>Mops niveiventer</td>
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<tr>
<td>Myonycteris relicta</td>
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<tr>
<td>Neoromicia cf. melckorum</td>
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<tr>
<td>Neoromicia zuluensis</td>
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<tr>
<td>Nycteris thebaica</td>
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<tr>
<td>Nycteris woodi</td>
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<tr>
<td>Pipistrellus rusticus</td>
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<tr>
<td>Plerotes anchietae</td>
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<tr>
<td>Rhinolophus capensis</td>
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<tr>
<td>Rhinolophus denti</td>
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<tr>
<td>Rhinolophus sakejiensis</td>
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<tr>
<td>Sauromys petrophilus</td>
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<tr>
<td>Scotophilus leucogaster</td>
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<tr>
<td>Mops condylurus</td>
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**Text box – Workshopped notes on the Opinion piece**

Scope of the paper: This is how far we’ve come with bioclimatic envelopes, this is where we need to go with animals. Direction – what’s the next step? How do we implement it? BioMove not to be mentioned too explicitly – only an example of a tool.

Existing manuscript on BioMove is just a software-release paper – BioMove with a (plant) case study – it is at an advanced stage, awaiting Ian Davies’ inclusion of a tutorial and parameterization.

“Bioclimatic modeling – the next step?”
“Moving towards dynamic species range modeling in the context of climate change”

- Don’t limit to BioMove
- Don’t limit to animals
- Emphasize potential for hypothesis testing in gcb
- Adding biology back into climate modeling! (Steve)
- Respond to literature observations that models are not reliable
- Improve basis for conservation resource allocation – policy and planning relevance
- Relationship between complexity and scale (decreasing scale, increasing complexity)
- Put in more mechanisms, but need to know more about mechanisms
- Downside – need more data, meet more stumbling blocks
- Upside – can do more sensitivity analyses, can produce more and better policy relevant info
Integrated modeling of range shifts of highly dispersive animals under climate change

Invitation to an expert workshop, 2-5 September 2008
Centre for Biodiversity Conservation – Conference Room, Kirstenbosch, Cape Town

PROPOSED AGENDA

Tuesday, 2 September, 2008

13:00 Welcome luncheon

13:45 Introduction to the workshop, initial aims and objectives – Phoebe Barnard & Guy Midgley

Getting to know each other: Informal presentations (SANBI, Durham, Australia, Bat Atlas):
- species geographic range data collection;
- habitat suitability (niche) modeling;
- modeling of range shifts – Presenters from SANBI, Durham, Australia, Bat Atlas

Expectations, desired outcomes and possible products (facilitator: Phoebe Barnard)

17:30 Depart for pub / supper etc

Wednesday, 3 September, 2008

09:00 Background: Bioclimatic niches and their potential use in “next generation” dynamic range shift modelling – Guy Midgley (vegetation) and Dave Hole/ Steve Willis (birds)

Interactive working session (facilitator: Res Altwegg) – Deriving bioclimatic envelopes and “response curves” for bird and bat data, addressing non-climate determinants of range.

Preparatory work on datasets will be done by Danni Guo.

Suggested presenters: Guy Midgley/Danni Guo
Lynda Chambers/ Lesley Gibson
Dave Hole/ Steve Willis

13:00 Light lunch

14:00 Demographic modeling concepts – matrix modeling and issues in estimating demographic rates – Res Altwegg

Discussion – how can range data be augmented for next-generation dynamic range shift modeling? (facilitator: Guy Midgley)

17:30 Depart for pub / supper etc

Thursday, 4 September, 2008

09:00 Introducing the Biomove concept – Guy Midgley
All participants load Biomove on their computers and experiment with sensitivity of output to input variation (facilitator: Guy Midgley)

13:00  Light lunch
Discussion: Conceptual changes needed to apply BioMove to animals and identification of projects to test the approach (facilitator: Guy Midgley)

17:00  Group supper at Silvertree Restaurant

Friday, 5 September, 2008

09:00  Way forward to addressing the dynamic range modeling approach to niche projections - identify key products, collaborative teams (facilitator: Phoebe Barnard)

13:00  Lunch and end of meeting
Hike Kirstenbosch Forest up Skeleton Gorge or cable car trip up Table Mountain

MAP OF KIRSTENBOSCH NATIONAL BOTANICAL GARDEN
Workshop is in Conference Room, Centre for Biodiversity Conservation
Climate Change and Bioadaptation Division offices are in upper south wing, Kirstenbosch Research Centre (tel 021 799 8895 – secretary Lynn Havinga)

Main Kirstenbosch Gate
3 Annex - Presentations

1. SANBI (Guy Midgley)
2. Durham University (Steve Willis)
3. Australian Bureau of Meteorology (Lynda Chambers)
4. Western Australia Dept of Environment & Conservation (Lesley Gibson)
6. Clarifying movement patterns and ranges of southern African birds (Phil Hockey)
7. Ensemble model application: birds, IBAs and climate change (Bernard Coetzee)
8. Flow chart: BioMove parameterization (Guy Midgley)

All presentations are available on request from the convenors.
## Annex - Participants and contacts

<table>
<thead>
<tr>
<th>NAME</th>
<th>CONTACTS</th>
<th>RESEARCH &amp; PERSONAL WEB LINKS</th>
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</table>
| Dr. Res Altwegg       | South African National Biodiversity Institute, Kirstenbosch Research Centre, P/Bag X7, Claremont 7735, Cape Town, SA Phone: +27 (0) 21 799 8809, Fax: +27 (0) 21 797 6903, altwegg@sanbi.org | [http://web.uct.ac.za/depts/stats/adu/staff/glcres.html](http://web.uct.ac.za/depts/stats/adu/staff/glcres.html) (former postdoc page with publications list updated to 2007 – new page on SANBI site is not up yet)  
[http://www.sanbi.org/frames/gcrg.htm](http://www.sanbi.org/frames/gcrg.htm) (this website in active development – new one soon) |
| Dr Phoebe Barnard    | Birds & Environmental Change Partnership Climate Change and BioAdaptation Division, South African National Biodiversity Institute, Kirstenbosch Research Centre, P/Bag X7, Claremont 7735, Cape Town, SA Phone: +27 (0) 21 799 8722, Fax: +27 (0) 21 799 8705, barnard@sanbi.org | [http://www.sanbi.org/frames/gcrg.htm](http://www.sanbi.org/frames/gcrg.htm) (this website in active development – new one soon)  
[http://www.fitzpatrick.uct.ac.za/docs/climate.html](http://www.fitzpatrick.uct.ac.za/docs/climate.html)  
[http://www.fitzpatrick.uct.ac.za/docs/phoebe.html](http://www.fitzpatrick.uct.ac.za/docs/phoebe.html) |
| Mr Bernard Coetzee    | PhD student and SANBI research affiliate, SA Environmental Observation Network student network; recently WWF Climate Project, Fiji and SANBI research affiliate, pwc0etzee@gmail.com | [http://academic.sun.ac.za/cib/team/students/bernard/bernard.htm](http://academic.sun.ac.za/cib/team/students/bernard/bernard.htm)  
[http://www.saeon.ac.za/eNewsletter/archives/April%202006/saeon-networks](http://www.saeon.ac.za/eNewsletter/archives/April%202006/saeon-networks)  
[http://www.sciencemag.org/cgi/content/citation/321/5887/340b](http://www.sciencemag.org/cgi/content/citation/321/5887/340b)  
| Dr Danni Guo          | Spatial Modeler Climate Change and BioAdaptation Division, South African National Biodiversity Institute, Kirstenbosch Research Centre, P/Bag X7, Claremont 7735, Cape Town, SA Phone: +27 (0) 21 799 8691, Fax: +27 (0) 21 799 8705, guo@sanbi.org | [http://www.sanbi.org/frames/gcrg.htm](http://www.sanbi.org/frames/gcrg.htm) |
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[http://www.fitzpatrick.uct.ac.za/docs/phil.html](http://www.fitzpatrick.uct.ac.za/docs/phil.html) |
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[http://www.fitzpatrick.uct.ac.za/docs/doug.html](http://www.fitzpatrick.uct.ac.za/docs/doug.html) |
<p>| Dr Guy Midgley        | Chief Director, Climate Change and BioAdaptation Division, Kirstenbosch Research Center, South African National Biodiversity Institute, P/Bag X7 Claremont | <a href="http://www.sanbi.org/frames/gcrg.htm">http://www.sanbi.org/frames/gcrg.htm</a> |</p>
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