

# Testing the accuracy of species distribution models using species records from a new field survey



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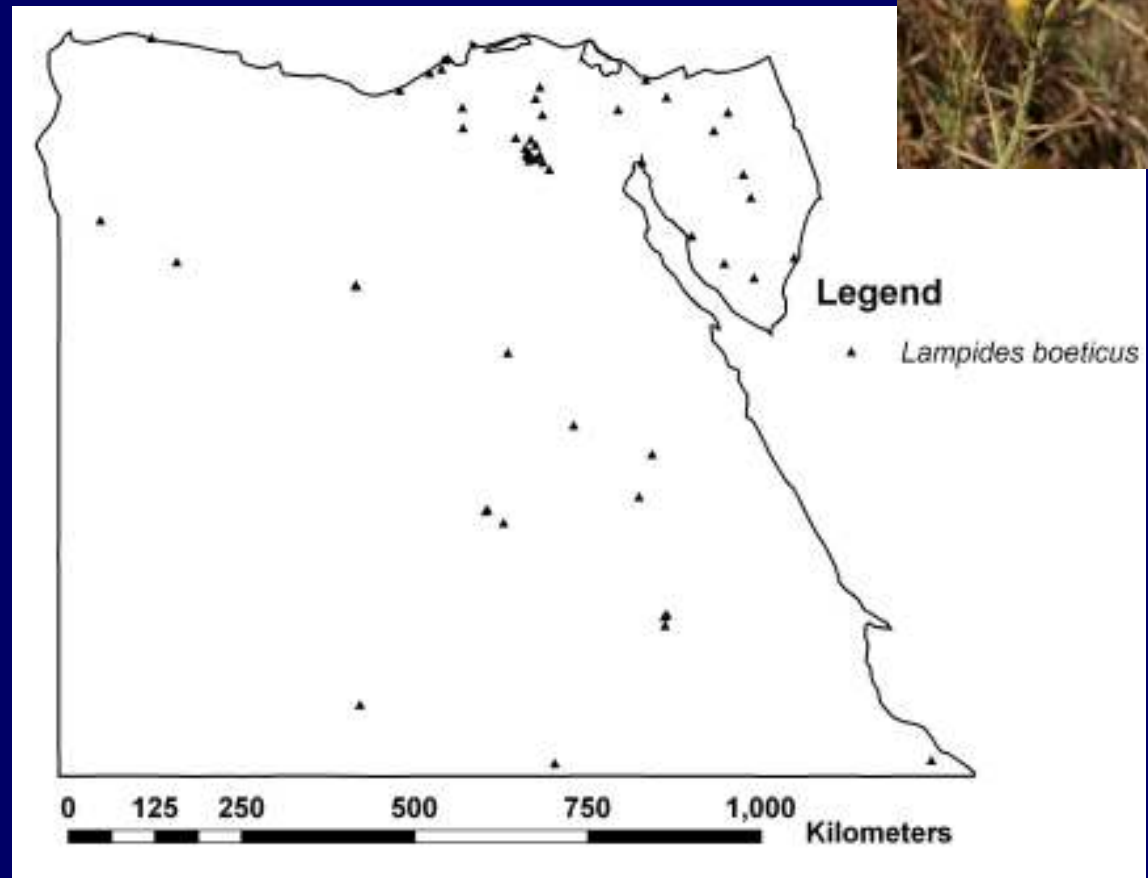
# Outline

- Species distribution models
- Museum data
- Evaluating distribution models
- Variation in model accuracy among species
- Egypt field survey
- Results



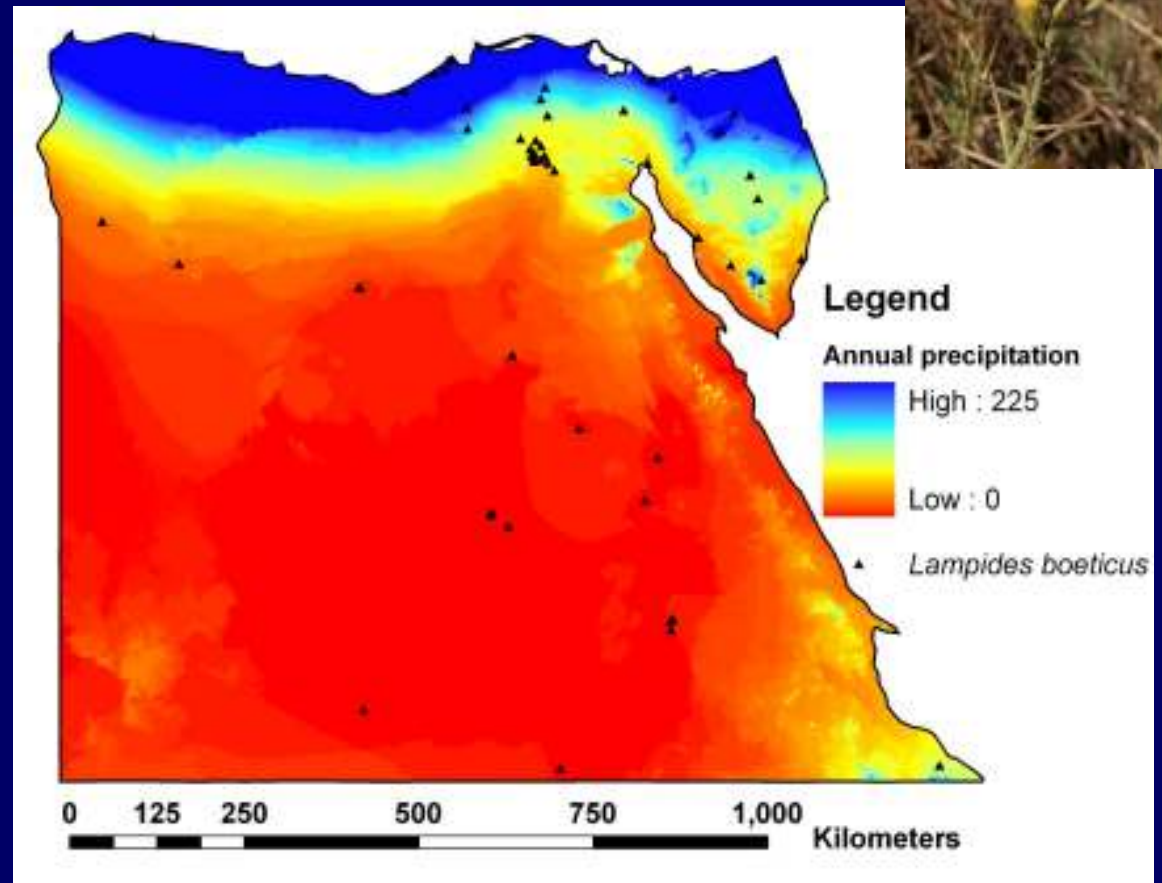
# Species distribution models

- Recorded occurrences



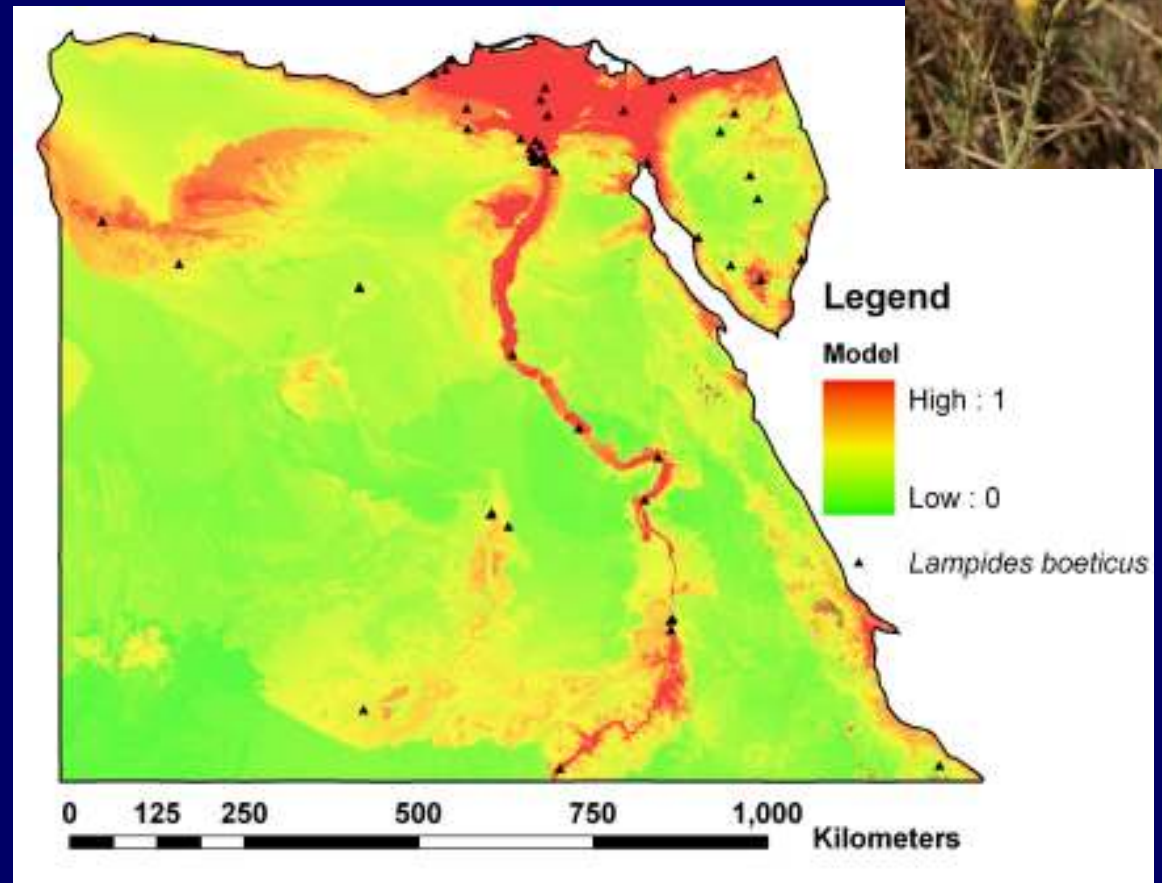
# Species distribution models

- Environmental variables



# Species distribution models

- Model prediction



# Applications of SDMs

- Conservation planning, e.g. protected areas (Thorn et al., 2009, *Div & Distns*; Newbold et al., 2009, *J Biogeog*)
- Finding new populations of species (Raxworthy et al., 2003, *Nature*)
- Predicting impacts of climate change & land-use change (Thomas et al., 2004, *Nature*)
- Ecological/evolutionary questions (Peterson et al., 1999, *Science*; Eaton et al., 2008, *Biol J Linnean Soc*)



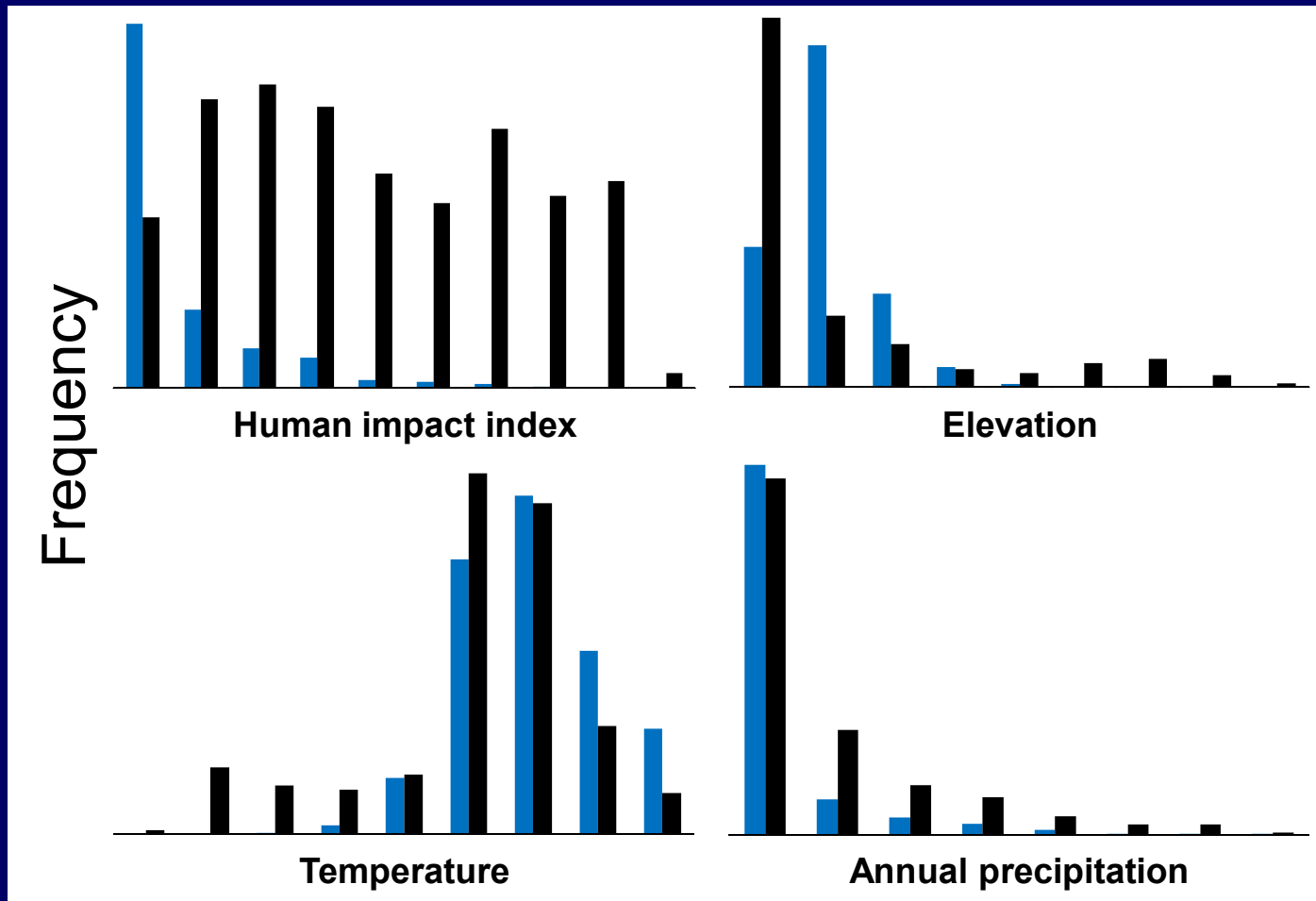
# Museum data

- Valuable source of species records
- Errors
- Biases:
  - Spatial
  - Temporal
  - Taxonomic
- Environmental bias → Poor distribution models
- BioMAP data for Egypt



# Bias in BioMAP butterflies data

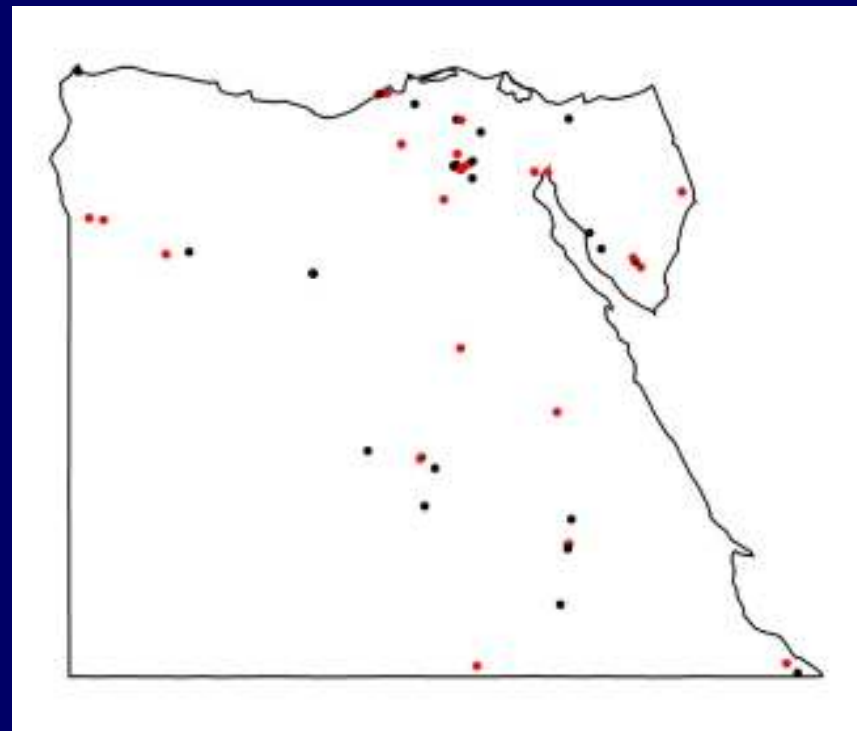
Black bars = butterfly sites; blue bars = all grid cells





# Evaluating distribution models

- Common practice is to divide sightings of species for model development and evaluation
- Gives over-optimistic estimates of accuracy with biased data
- Better to collect new data



# Methods

- Developed distribution models for Egyptian reptile & amphibian ( $n = 20$ ), butterfly ( $n = 10$ ) and mammals ( $n = 4$ )
- Environmental variables - temperature, rainfall, elevation, habitat
- Compared 2 methods of model evaluation: 1) Dividing BioMAP records into 2 halves; 2) Collecting new data
- AUC statistic



# Methods

- Field surveys May-July 2007 and 2008
- Impossible to survey randomly
- Sampled as many habitats as possible
- 21 sites
- 4 walking transects at each site



# Model accuracy

- Species detectability:                    1001      1100
  - Species missed                            1100      0001
  - Less complete distribution data        1000      0101
- Outcome depends on probability of occurrence ( $\Psi$ ) and probability of detection ( $p$ )
  - 0000      1010
  - 1111      1000
  - 1110      0001
  - 1000      0011
- Modelled  $\Psi$  and  $p$  using maximum likelihood
  - 1100      1001
  - 1001      1111
  - 1111      1010

# Model accuracy

- Species characteristics:
  - Niche breadth
  - Range size
  - Migratory behaviour
  - Mobility
- Tested the effect of range size and mobility
- For tests of other characteristics, see Newbold et al., 2009, Biodiv & Conserv



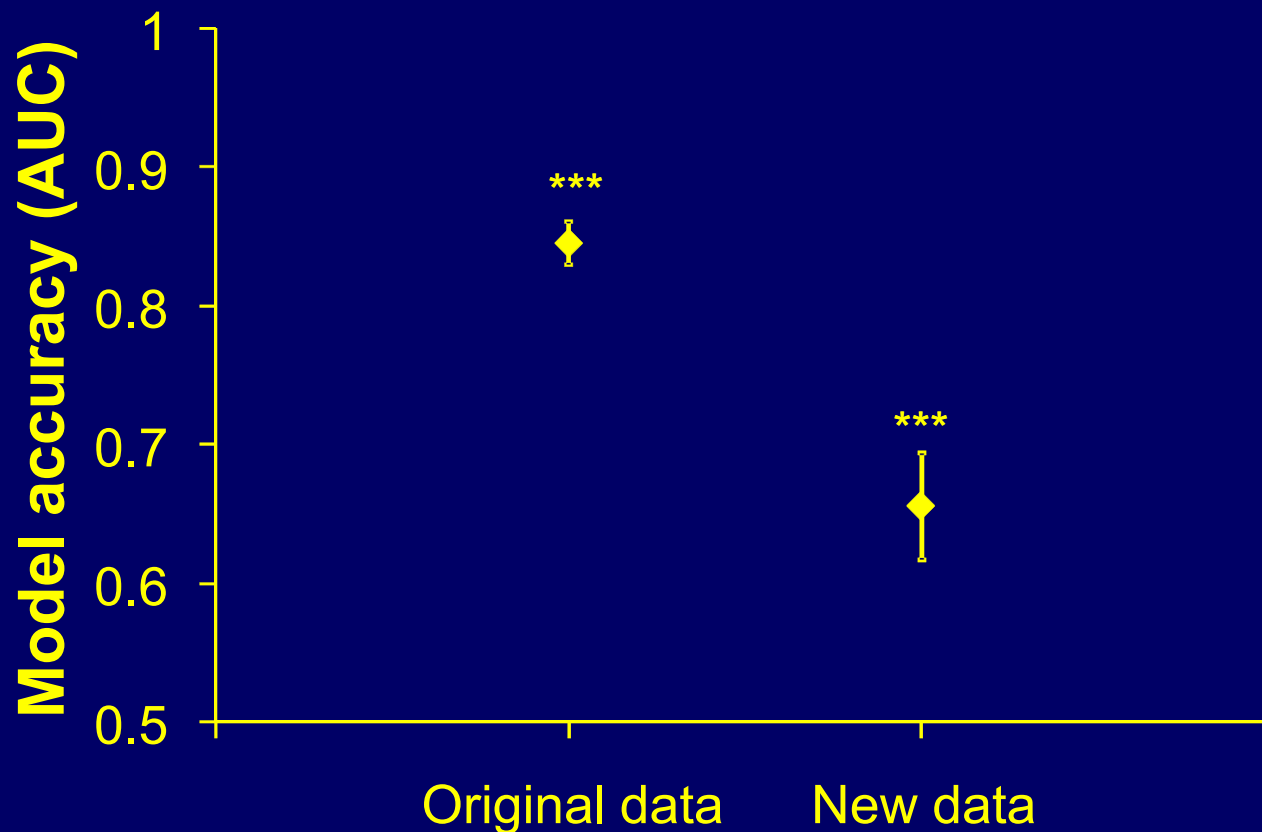
# Results

- Detection probabilities ranged from  $< 0.001$  to c. 0.75
- Snakes, mammals and migrant butterflies had low detectability
- Lizards, most butterflies and the Dorcas gazelle (faeces and tracks) were highly detectable



# Results

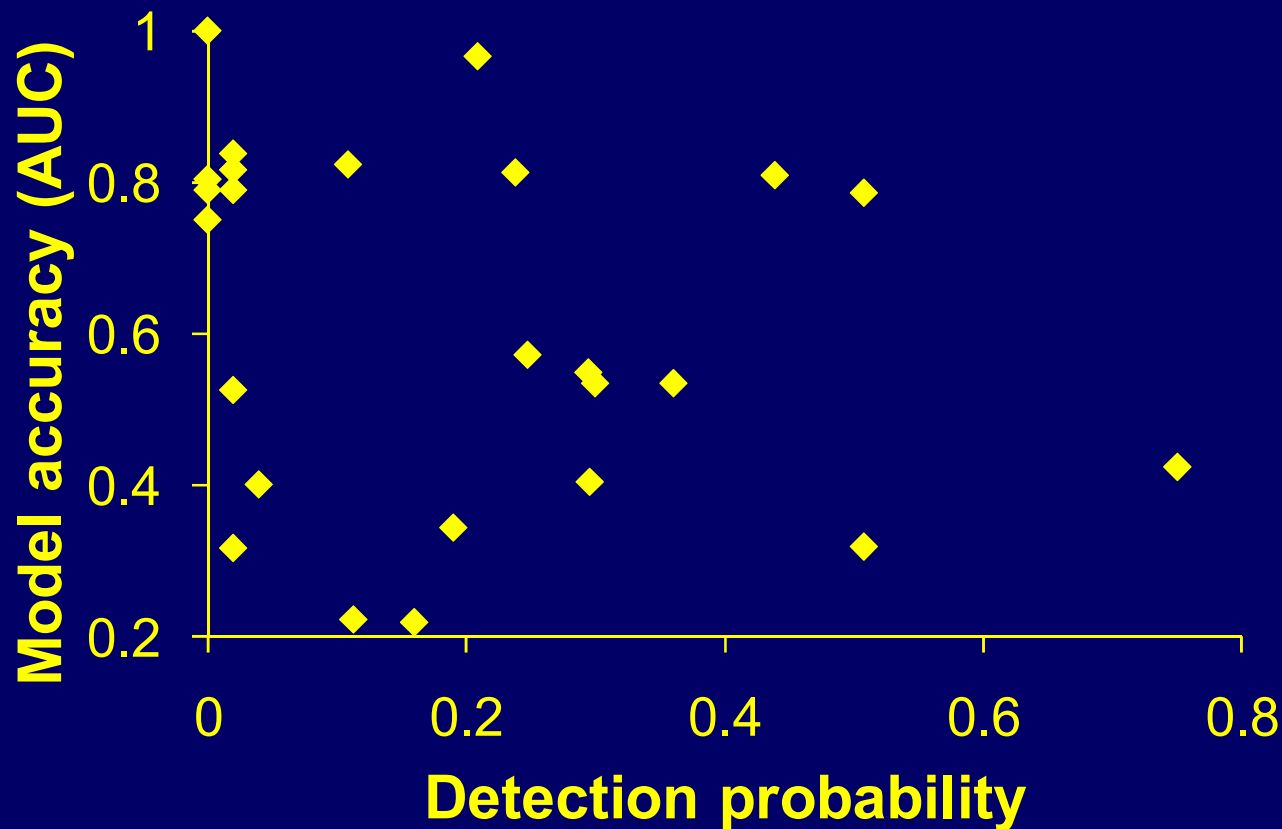
- Estimates of model accuracy lower using new data
- But both estimates were sig. better than random



\*\*\*One-sample t-test: sig. better than random (AUC = 0.5)  $p < 0.001$

# Results

- Model accuracy was not related to detection probability

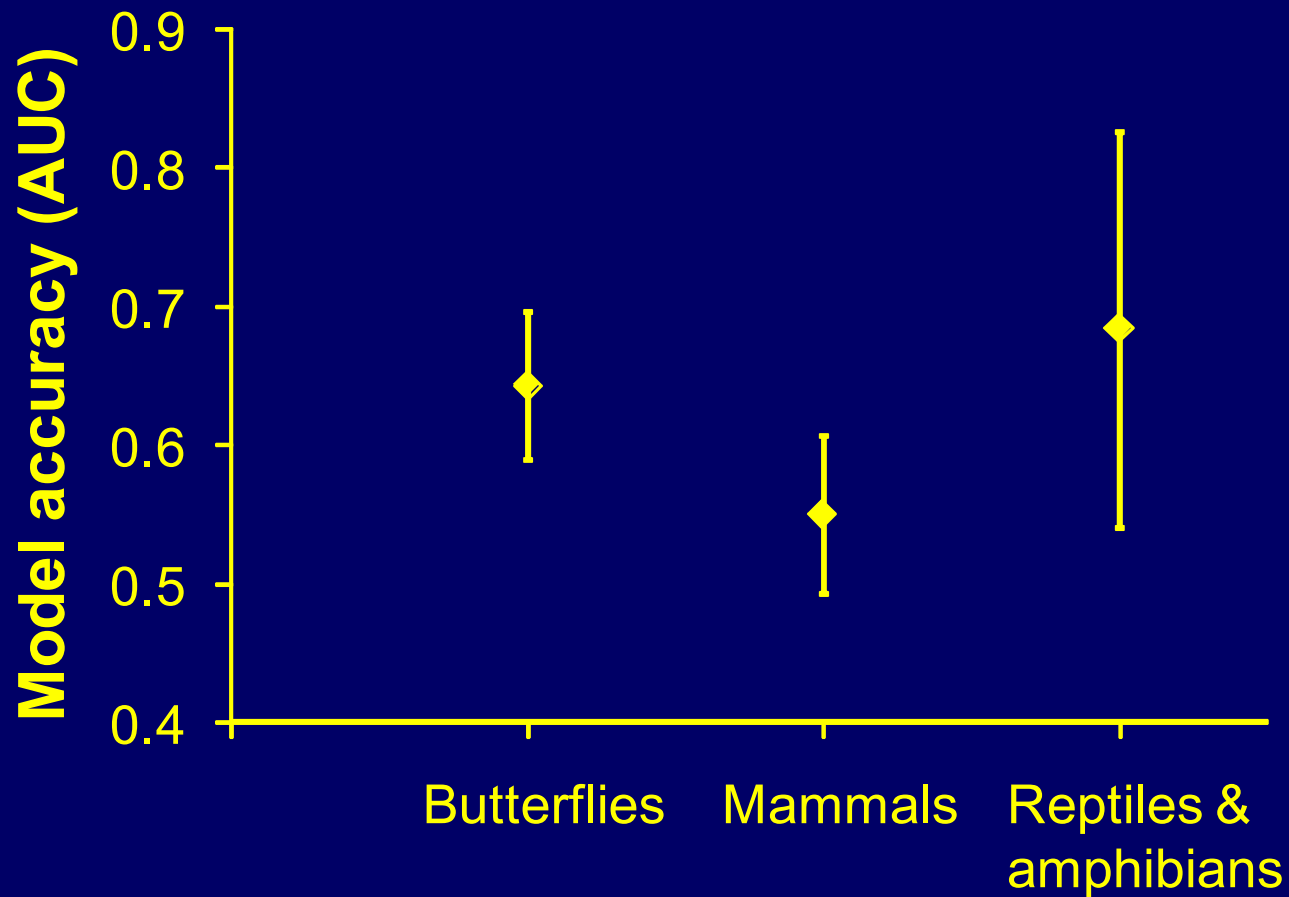


Spearman's rank correlation:  $r_s = -0.294$ ,  $n = 25$ ,  $P = 0.154$



# Results

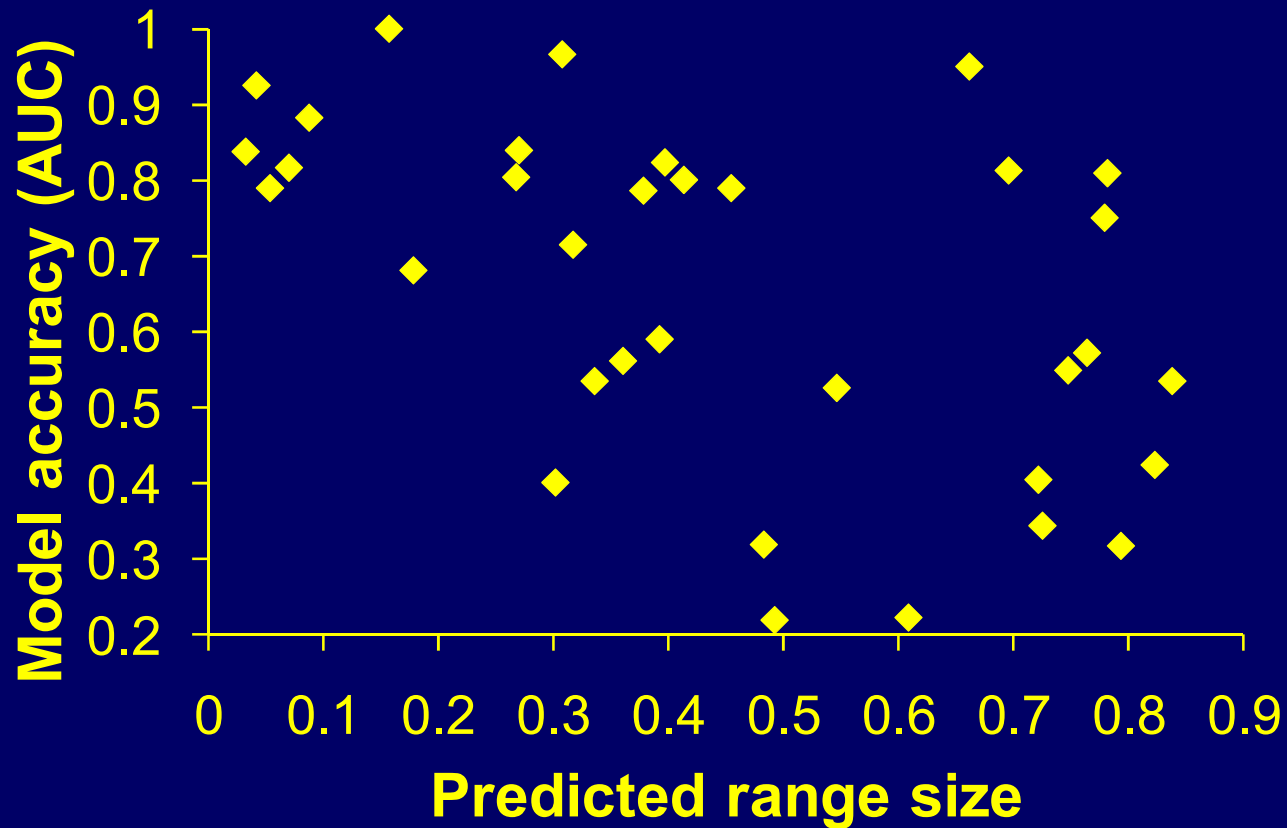
- Model accuracy didn't vary among taxonomic groups



Sum of AIC weights = 0.172

# Results

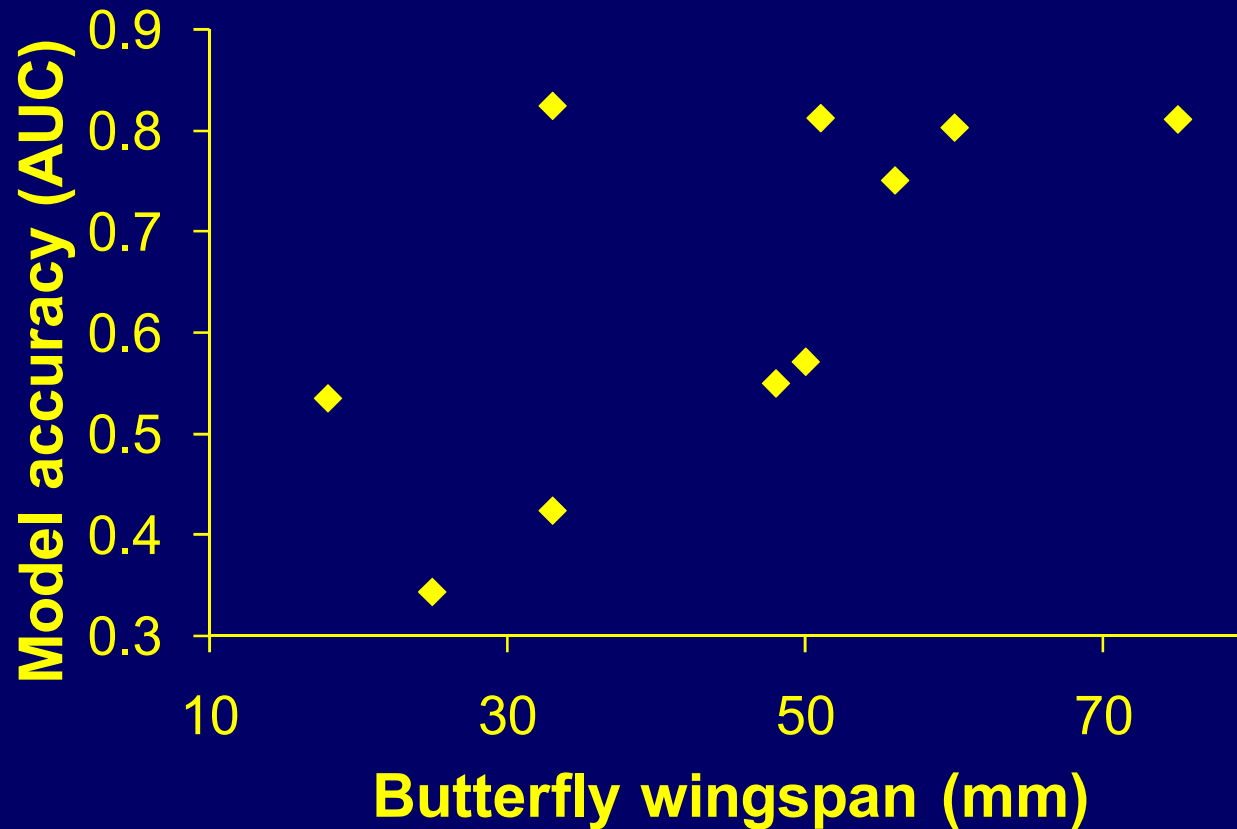
- Species with larger ranges had less accurate models



Sum of AIC weights = 0.952

# Results

- Larger butterflies had more accurate models
- Detectability or mobility?



Pearson's correlation test:  $r = 0.652$ ,  $n = 10$ ,  $p = 0.041$

# Conclusions

- Species distribution models were generally very accurate
- Important to collect new field data to validate models
- Model accuracy not related to detectability
- But did vary among species
- Reveals differences among species in response to environment



# Acknowledgements

- Rashed Refaey, Ahmed Refaey & other field guides
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The University of  
Nottingham



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# Methods

$$L = \left[ \psi^{n_t} \prod_{t=1}^{t=4} p^{n_t} (1-p)^{n_t-n_t} \right] \times \left[ \psi \prod_{t=1}^{t=4} (1-p) + (1-\psi) \right]^{N-n_t}$$

- $\Psi$  = probability of occurrence
- $p$  = probability of detection
- $t$  = transect number
- $n_t$  = number of sites at which the species was detected on transect  $t$
- $n_t$  = number of sites at which species was recorded on one transect
- $N$  = total number of sites
  
- $\Psi$  and  $p$  were estimated by maximum likelihood