

# Hierarchical modeling of resource utilization using MCMC

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## Predicting resource selection / use at multiple scales

### Theory

- Animals select / use resources at multiple-spatial scales (Johnson 1980)

### The disconnect ...

- Common approach cannot be used for prediction
  - Compositional analysis (Aebischer et al. 1993)
    - » multi-scale approach to date

### Introduction

However, we need to predict habitat use probabilities and display them spatially to aid decision making ...

Maps of predicted habitat use aid policy decisions ...

## Data and modeling approaches for multivariate predictive habitat models

- Presence and absence data
    - True absence is difficult to document
      - Temporal and spatial scale
      - Probability of detection required
      - Examples
  - Presence only data (radio-telemetry)
    - Ecological Niche Factor Analysis (Hirzel et al. 2002) – empirical, multivariate normality
    - Mahalanobis distance (Clarke 1993) – empirical, multivariate normality
    - Habitat Suitability Index – hypotheses validated with data
- \*\*\*\* These do not allow for a measure of habitat availability, and apart from Mahalanobis distance, do not allow for model selection

## Logistic Regression

- Allows for model selection and incorporation of model uncertainty
- Provides a measure of habitat availability
- Habitat at points of presence compared to “absence” points
- Some key assumptions:
  - Occurrences are rare or clumped
  - Data are not autocorrelated (Keating and Cherry 2004)

## Hierarchical Logistic Regression

- Frequentist hierarchical models are not easily modeled, covariance estimation is complicated
- Frequentist Logistic regression assumes multivariate normality

### Utility of Bayesian logistic regression for modeling habitat: Philosophical and practical reasons

See Hierarchical Bayesian Modeling Group at Warnell for more info:  
<http://fisher.forestry.uga.edu:9673/bayes/seminar>

- Explicit estimation of uncertainty, important to decision analysis (i.e. cost – benefit analysis) – parameters are random variables (AIC is also)
- Use prior information in posterior distribution (if you have prior info)
- Intuitive probability
  - not the probability that if an experiment were repeated, 95% of the time the mean would be in range..... (gasp)
- Update information over time as more data become available
- No assumption of multivariate normality

### Simulation of parameter distributions using Markov Chain Monte Carlo Techniques

- Why use Markov Chain Monte Carlo and what the heck is it?
- A way of obtaining probability values from complex integrals (area under the curve)
- Stochastic process, an ordered collection of random variables (random walk)
- $Pr(X_{t+1} = x_{t+1} | X_t = x_t, X_{t-1} = x_{t-1}, \dots, X_0 = x_0) = Pr(X_{t+1} = x_{t+1} | X_t = x_t)$
- Each value in a Markov Chain depends only on the previous value
- The probability of getting from one value in a chain to any of the previous values is equal (irreducibility)

### Modeling process of one MCMC simulation

- 1) Select 1 random presence point from point cloud per location per season & 1 random absence point = simulation dataset (fixed)
- 2) 10,000 iterations of the Metropolis Hastings (MH) algorithm
  - each MH iteration updates the posterior distribution of the betas, based on an acceptance criteria
- 3) Result is a posterior distribution of beta estimates and deviance or AIC

## Radio-telemetry data

- Presence-only data
- Telemetry error

More chance animal is pin-pointed when the standard deviation of field – measured telemetry error is used instead of the 95% error ellipse (based on Kenow et al. 2001)

- Usually autocorrelated to some degree
  - Assumption of location independence based on traversal of home range is subjective
    - Where you are always depends on where you were unless it's been a really long time (or you can drive a car)

## Objectives

- **Construct and validate predictive bear habitat models & maps for central Georgia**
- Identify areas for habitat management & possible reintroduction
- Incorporate telemetry error uncertainty
- Model presence only habitat data
- Condition the probability of habitat use at the location scale by the probability of habitat use at the home range scale

## METHODS

### Telemetry error estimation

- 6 Collar beacon study – 100 locations per observer from 4 distance intervals
- Observer bias – general linear model (SAS 2001)

### Incorporation of error in location estimates

(Kenow et al. 2001)

- Standard error of bearing error (12.2 deg)
- Simulated a random normal distribution of bearings about the estimated bear location to produce points (SAS code from White and Garrott 1990)

### Criteria for location error

- Bearings within 15 minutes or less, within 2 km
- *Evaluation of systematic errors – future analysis*

### Candidate model subset

Took top-ranked single level variable models for combined variable models

#### Location level (home range use = random)

1.	cut, hardwood, cypress, county rd. density
2.	cut, cypress, county rd. density
3.	cut, hardwood, county rd. density

#### Home range level (locations = random)

1.	cut, agri, hardwood, highway density
2.	cut, hardwood, highway density
3.	cut, hardwood

#### 4. Null model – intercept only model (no selection)

- **Model presence only habitat data without autocorrelation**
  - One point per season per bear for each simulation run of the logistic regression model
  - Compile simulation traces for final stats over 300 simulations
  - For each 1 location point per bear randomly selected within season, a home range “absence” point is selected at random and a study area (home range “absence”) point is selected
  - Idea is that when few location points are selected for a long time period, autocorrelation is minimized and absence can be inferred
- Condition the probability of habitat use at the location scale on the presence of a home range

### Challenges to using this technique

- 300 simulations per model = ~ 88 HOURS!
- Using 24 computers in forestry to run these suckers
- I run 50 simulations for each model on 6 computers and compile the traces later with another python program (C. Fannesbeck)
- Databases of points are large and hard to sample
- We did not feed in point data for home range and study area
- We sample from the multinomial distribution of habitat types and the distribution of continuous variables by habitat type (Python code is about 350 lines long)

See [www.python.org](http://www.python.org) for python programming

## Results Example

RANK	model	name	mean	lower 95%	upper 95%	2.50%	50%	97.50%	variance	mc error
1	HR_MG	AIC	282.835	239.172493	320.63607	240.4501	282.5732	322.1554451.5115	0.01735	
1	HR_MG	gamma0	0.405546	-0.15926163	0.97250874	-0.15519	0.404057	0.9769680.082661	0.000235	
1	HR_MG	GOF	DIC					279.1535		
1	HR_MG	hr_ag	-3.465606	-3.84748307	1.14747027	-49.4191	-1.01999	0.41564159.1306	0.0103	
1	HR_MG	hr_cut	-0.018716	-1.30732694	1.6188194	-1.35475	0.168662	1.57787112.97713	0.002941	
1	HR_MG	hr_hwdmx	0.041665	-1.2595268	1.3238878	-1.29217	0.054096	1.293810.433581	0.000538	
1	HR_MG	hr_hwyhr	-2.010274	-4.55785658	0.34199831	-4.73035	-1.92423	0.2115971.517824	0.001006	
2	HR_MA	AIC	287.5613	244.5818405	321.686638	246.2655	288.7303	323.9064401.5583	0.016362	
2	HR_MA	Gamma0	0.251505	-0.25933233	0.77055424	-0.26164	0.250578	0.7682890.068719	0.000214	
2	HR_MA	GOF	DIC					279.4991		
2	HR_MA	hr_cut	0.247123	-1.22599343	1.65008848	-1.28294	0.278967	1.5996190.530027	0.000594	
2	HR_MA	hr_hwdmx	0.213387	-1.11339931	1.44949527	-1.16349	0.247827	1.4076710.424097	0.000532	
2	HR_MA	hr_hwyhr	-2.172298	-4.65556733	0.10206862	-4.81473	-2.0818	-0.022031.467815	0.000989	
3	LMG_HRMG	AIC	288.6929	240.7222824	330.426605	242.4488	289.1486	332.4108527.1909	0.018747	
3	LMG_HRMG	gamma0	0.527354	-0.1580494	1.2444948	-0.12744	0.51108	1.2820530.125667	0.000289	
3	LMG_HRMG	GOF	DIC	282.9890124						
3	LMG_HRMG	hr_ag	-2.561707	-3.29928324	0.65134399	-9.92326	-1.14834	0.35090891.75428	0.007821	
3	LMG_HRMG	hr_cut	-0.071992	-1.92792973	2.58471536	-1.95601	0.212952	2.55902526.1327	0.004174	
3	LMG_HRMG	hr_hwdmx	0.067542	-1.60239802	1.65481144	-1.67499	0.098385	1.5983530.682822	0.000675	
3	LMG_HRMG	hr_hwyhr	-2.114815	-4.93430898	0.41960114	-5.07745	-2.01016	0.3008071.844359	0.001109	
3	LMG_HRMG	l_cntyhr	-0.804932	-2.97889273	1.32302339	-3.02964	-0.77775	1.2757661.184689	0.000889	
3	LMG_HRMG	l_cut	-0.707059	-4.12187501	3.44328433	-4.45638	-0.16904	3.19387743.261	0.00537	
3	LMG_HRMG	l_cypr	-0.371767	-2.74359671	2.35193437	-2.76241	-0.23933	2.33497813.82882	0.003036	
3	LMG_HRMG	l_hwdmx	0.105042	-2.37056572	2.56477778	-2.2908	0.08451	2.6564551.556889	0.001019	

### Predictive habitat maps

$$p(\text{use}) = \frac{1}{(1 + \exp(\logit\_p))} \quad p = \text{inv logit}(\beta_0 + \beta_i X_i) \quad \beta_0 = (\gamma_{00} + \gamma_{0i})$$

p(use) calculated for each pixel in ArcView or GIS using map calculator

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