

# Hierarchical models for wildlife transect surveys

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# Outline

- Design-based inference

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- Hierarchical modeling roadmap

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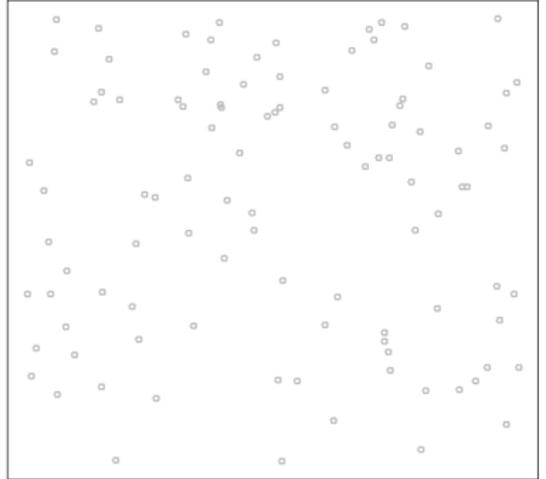
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- Seal example

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- Hierarchical modeling roadmap
- Simulations
- Seal example
- Extensions and future work

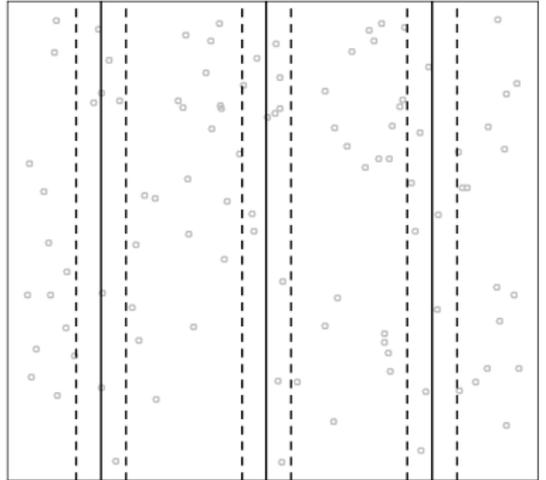
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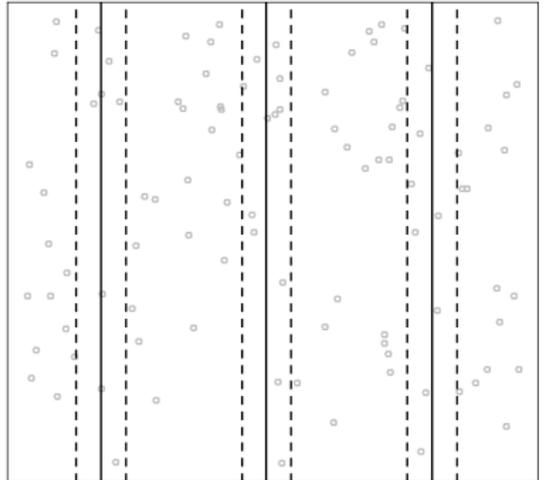
Design-based  
estimator

$$\hat{N} = \frac{n}{P_a}$$

$N$  = Abundance

$n$  = # of animals  
counted

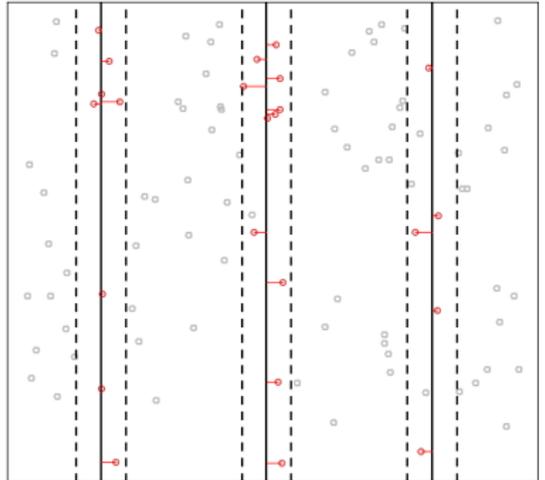
$P_a$  = proportion of  
area sampled



# Design-based inference

If all animals are not detectable in our strip, we need to estimate detection probability,  $P_d$ .

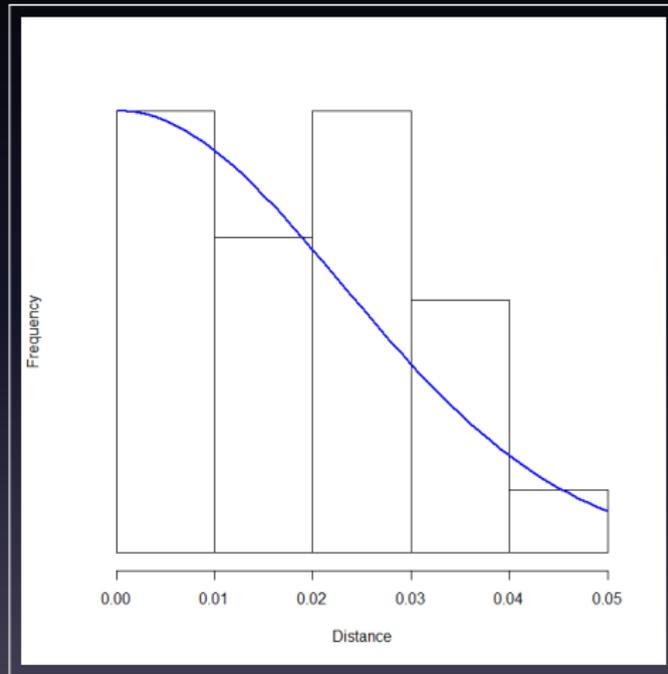
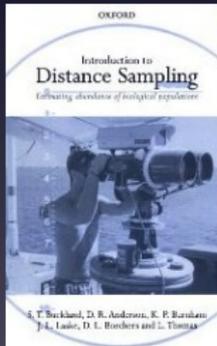
⇒ One approach:  
relate detectability to  
distance from transect  
line



# Design-based inference

Distance estimator  
(design-based)

$$\hat{N} = \frac{n}{P_a \hat{P}_d}$$



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Large improvements to design-based abundance estimators over the last few decades

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- Requires preset sampling design
- Requires static population
- Difficult to incorporate spatial or temporal autocorrelation

# Model-based inference

## Challenges with wildlife surveys

- Weather and logistics often influence where sampling occurs
- Abundance isn't static in time or space



# Model-based inference

Conceptualize data collected as having arisen from two conceptually distinct processes, providing a model for each:

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Need to estimate the parameters of each model and predict abundance over a surface!

# Model-based inference

Types of model-based analyses for animal transect data

## Thinned point process

- Hedley and Buckland (2004)
- Johnson et al. (2010), R package `dspat`

## Highfaluutin Poisson GLMM

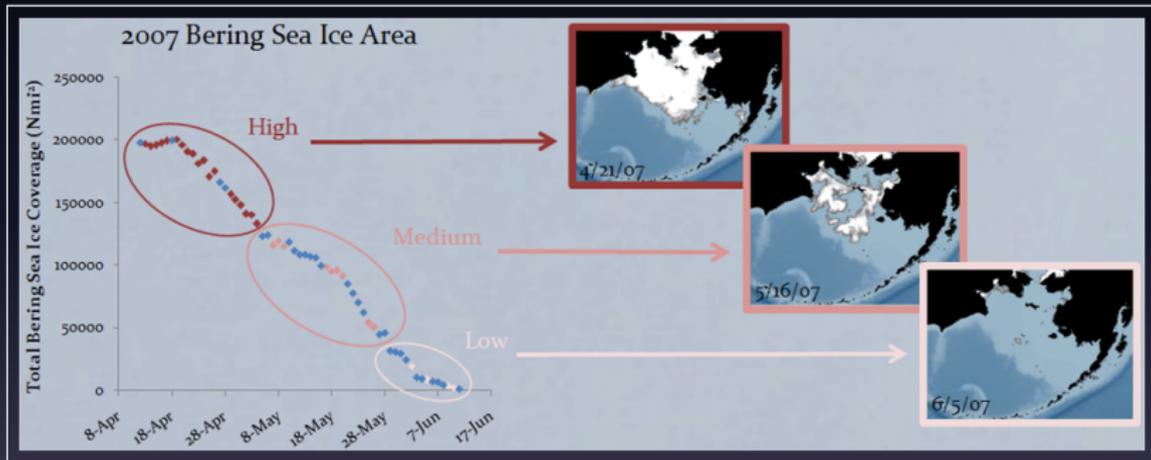
- Moore and Barlow (2011)
- Chelgren et al. (2011)

## Data augmentation

- Royle and Dorazio (2008)
- Schmidt et al. (2011)
- †Conn et al. (2012), R package `HierarchicalDS`

†Accounts for double observers

# Introduction



# Introduction

An additional challenge: Partial observability and errors in species assignment

Obs1	Obs2	Distance	Group size
Bearded	Bearded	1	2
Bearded	0	5	1
Bearded	Unknown	1	2
Unknown	Unknown	2	3
Unknown	Unknown	4	8
0	Spotted	4	1
Spotted	Bearded	2	2



Spotted seal



Bearded seal

# Introduction

## Model-based approaches to estimation

- Inference based on *prediction* (e.g. on spatial surface)
- Sampling design can focus on minimizing prediction error (regular placement of transects) but not strictly necessary
- Hierarchical extensions possible (spatial, temporal variation in abundance)
- Separation of process and observation models lends itself to modular approach to model building

# Introduction

## Goals for modeling

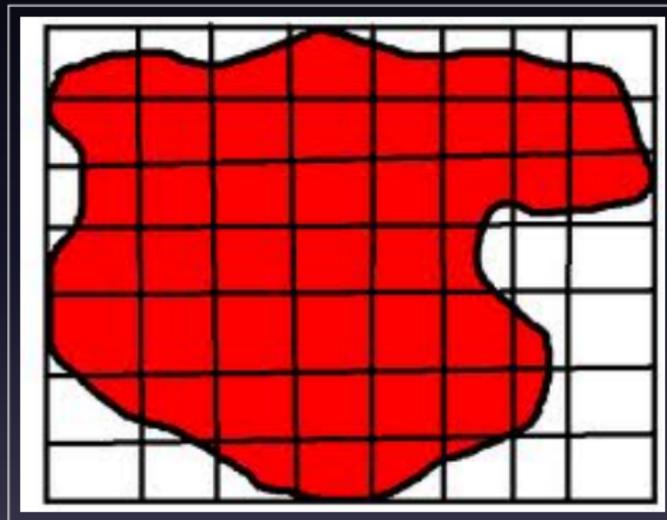
Develop hierarchical framework for line transect sampling that permits

- Straightforward inclusion of temporal/spatial effects on abundance
- Multiple observers with possible observer dependence
- Estimation of individual covariate distributions (e.g. group size)
- Possible extensions for species misidentification/partial observation

# Math

Start by discretizing  
time & space

Let  $D_1, D_2, \dots, D_S$   
form a partition of  
some area of interest,  
 $D$ .



# Math

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- 2 Abundance in a specific transect/grid cell combination  
(Local abundance model)
- 3 Observations in a particular cell at a particular time  
(Observation model)

# Math: Process model

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⇒ Assume that abundance is Poisson distributed, and work with the log of abundance intensity,  $\nu_{st}$ :

$$G_s \sim \text{Poisson}(\lambda_s),$$

$$\lambda_s = A_s \exp(\nu_s)$$

where  $\lambda_s$  gives abundance intensity in cell  $s$ , and  $A_s$  gives area of cell  $s$  proportional to mean cell area

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⇒ How does  $\nu$  change over time and space?

# Math: Process model

One possibility (implemented in R package *hierarchicalDS*!)

$$\nu \sim \text{Normal}(\mathbf{X}\boldsymbol{\beta} + \boldsymbol{\eta}, \tau_\nu^{-1}), \text{ where}$$

$\mathbf{X}$  gives a design matrix,

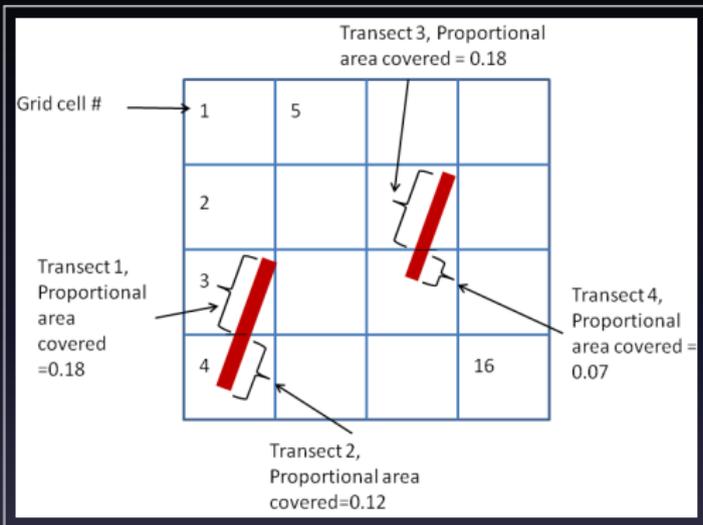
$\boldsymbol{\beta}$  is a vector of regression coefficients,

$\boldsymbol{\eta}$  is a vector of spatially structured random effects (stay tuned),  
and

$\tau_\nu$  is the precision associated with overdispersion relative to the Poisson distribution.

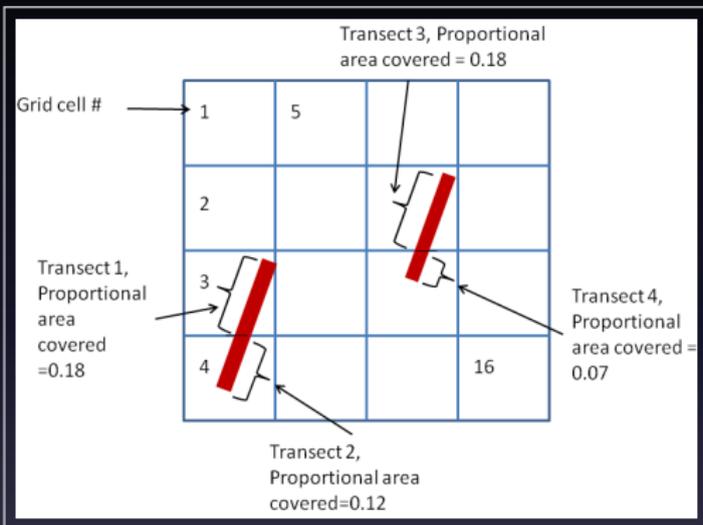
Other possibilities: cellular automata, resource selection models

# Math: Local abundance model



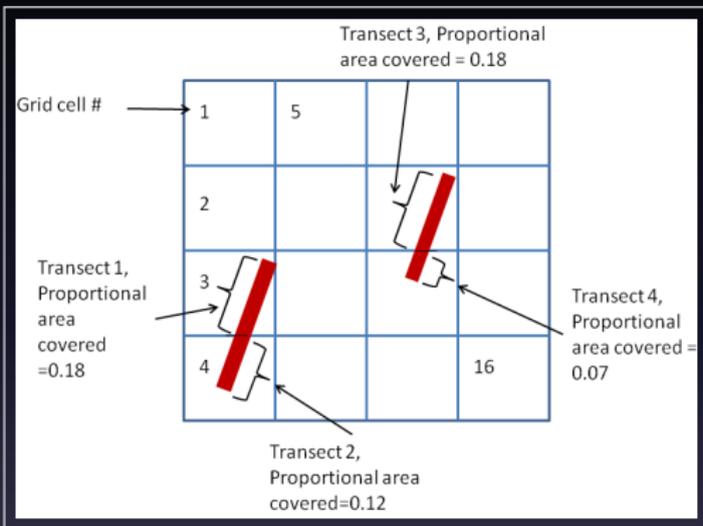
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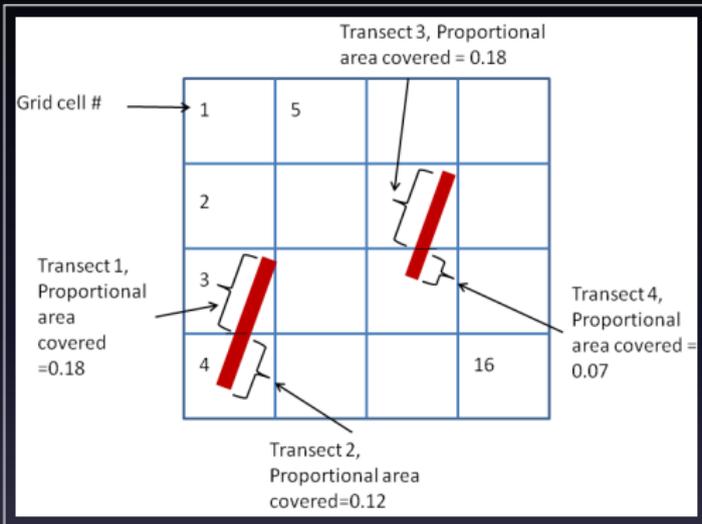
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(Note that  $P_{st}$  could also be modified to incorporate availability!)

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- Data augmentation with RJMCMC (e.g. Durban and Elston JABES 2005)  
⇒ Model unobserved animals & their covariates probabilistically

# Math: Observation model (Data, finally!)

Link and Barker (2010) suggest the following observation model likelihood for distance data:

$$[G_j^{\text{obs}} | G_j, p_{ij}] = \binom{G_j}{G_j^{\text{obs}}} \prod_{i=1}^{G_j} p_{ij}^{Y_{ij}} (1 - p_{ij})^{(1 - Y_{ij})},$$

where

$p_{ij}$  is the probability of observing group  $i$  while surveying transect  $j$

$G_j$  is the number of animal groups in transect  $j$

$G_j^{\text{obs}}$  is the number of observed groups in transect  $j$

# Math: Observation model (Data, finally!)

For us,  $p_{ij}$  is the probability that a group of animals is seen by *at least* one observer. With two observers (and a probit link function):

$$\text{probit} \begin{pmatrix} p_{ij1} \\ p_{ij2} \end{pmatrix} = \begin{bmatrix} \tilde{Y}_{ij1} \\ \tilde{Y}_{ij2} \end{bmatrix} \sim \text{MVN} \left( \begin{bmatrix} \mathbf{X}_{ij1}^{\text{det}} \boldsymbol{\beta}^{\text{det}} \\ \mathbf{X}_{ij2}^{\text{det}} \boldsymbol{\beta}^{\text{det}} \end{bmatrix}, \begin{bmatrix} 1 & \rho_{ij} \\ \rho_{ij} & 1 \end{bmatrix} \right),$$

$$Y_{ijk} = 1 \text{ iff } \tilde{Y}_{ijk} > 0,$$

$$p_{ij} = \int_0^\infty \int_0^\infty \text{MVN} \left( \begin{bmatrix} x \\ y \end{bmatrix}; \begin{bmatrix} \mathbf{X}_{ij1}^{\text{det}} \boldsymbol{\beta}^{\text{det}} \\ \mathbf{X}_{ij2}^{\text{det}} \boldsymbol{\beta}^{\text{det}} \end{bmatrix}, \begin{bmatrix} 1 & \rho_{ij} \\ \rho_{ij} & 1 \end{bmatrix} \right) dx dy$$

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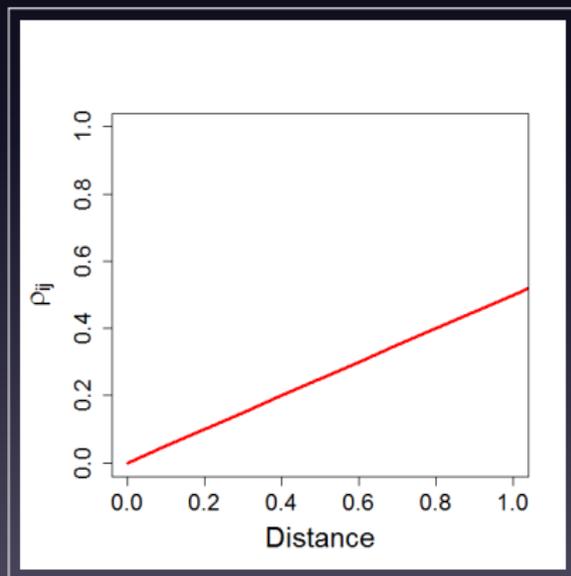
In HierarchicalDS,

discrete distance:

$$\rho_{ij} = \frac{(d_{ij} - 1)}{\max(d_{ij} - 1)},$$

continuous distance:

$$\rho_{ij} = \frac{d_{ij}}{\max(d_{ij})}.$$



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$$[\boldsymbol{\beta}^{\text{det}} | \dots] = \text{Normal} \left( (\mathbf{X}'\mathbf{X})^{-1} \mathbf{X}'\tilde{\mathbf{Y}}, (\mathbf{X}'\mathbf{X})^{-1} \right).$$

# Math: Covariate models

## Individual covariate pdfs, $g(\theta)$ , in HierarchicalDS

- Poisson
- Poisson-lognormal mixture
- Zero-truncated Poisson
- Zero-truncated Poisson-lognormal mixture
- Categorical
- Normal

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Other parameters updated via Gibbs or Metropolis-Hastings steps

# RJMCMC Algorithm

$Y_1$	$Y_2$	$\tilde{Y}_1$	$\tilde{Y}_2$	Distance	Species	Gr size
1	1	2.3	2.0	1	A	2
1	0	1.0	-0.4	3	A	1
1	1	0.6	0.3	4	A	1
0	0	-0.5	-0.8	3	A	2
0	0	-1.2	-1.6	5	A	1

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0	0	-3.7	-2.8	5	A	1

Well great, but how does this work in practice?

- 1 Simulated data, no spatial structure
- 2 Known population of golf tees (no spatial structure)
- 3 Simulated data (Matern process), spatial structure

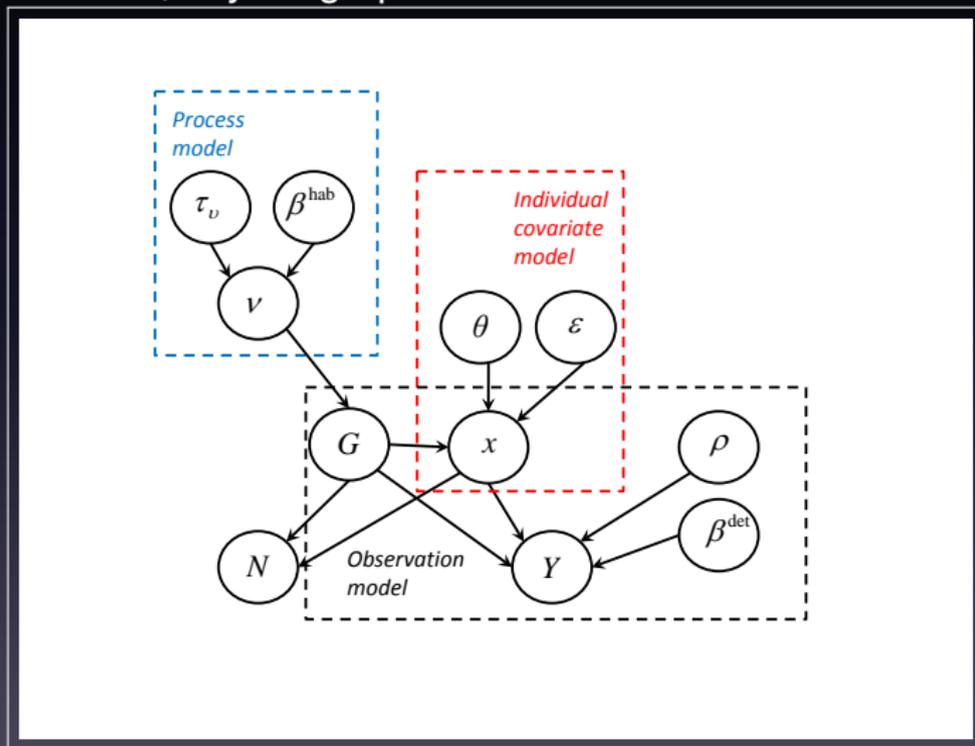
# Simulated data: no spatial structure

## Simulation study

- Simulated data for two species: (a) linearly increasing trend in abundance as a function of a covariate, and (b) abundance as a quadratic function of a covariate.
- Group size simulated from a zero-truncated Poisson distribution
- Detection probability a function of observer (categorical), distance (categorical; 5 bins), group size (continuous), and species (categorical).
- Correlation in probit-scale responses of each observer linearly increasing from 0 to a maximum of 0.5 as a function of distance
- Two MCMC chains of length 270,000 with first 20,000 of each discarded as burnin

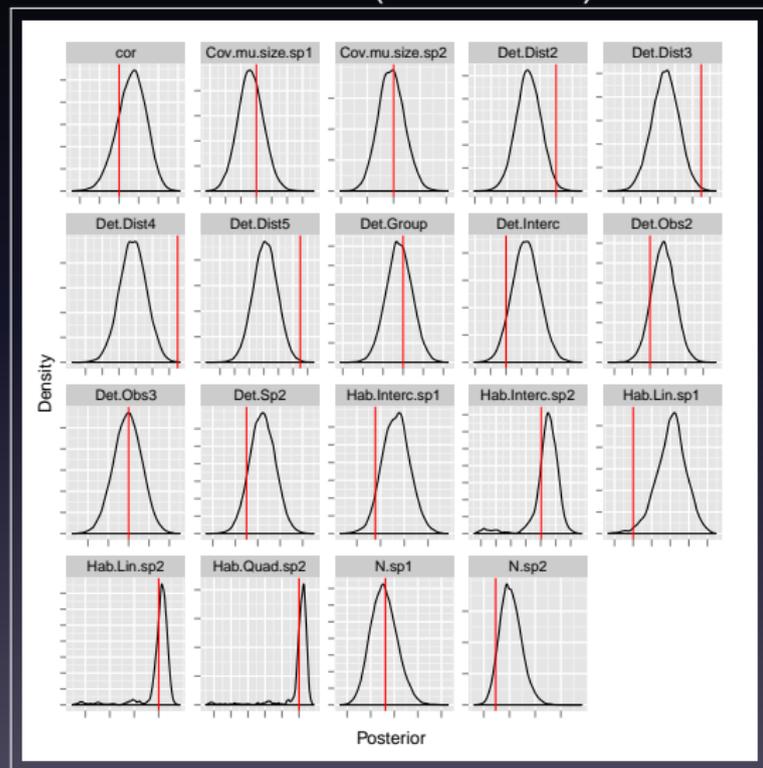
# Simulated data: no spatial structure

Directed, acyclic graph



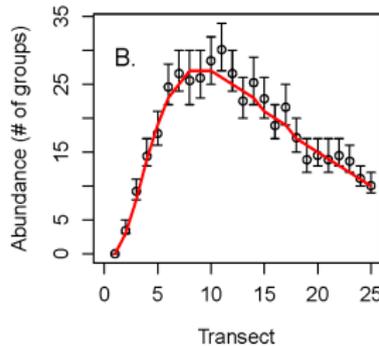
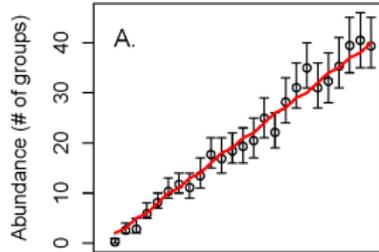
# Simulated data: no spatial structure

Results: Posteriors (truth in red)



# Simulated data: no spatial structure

Results: Abundance by transect



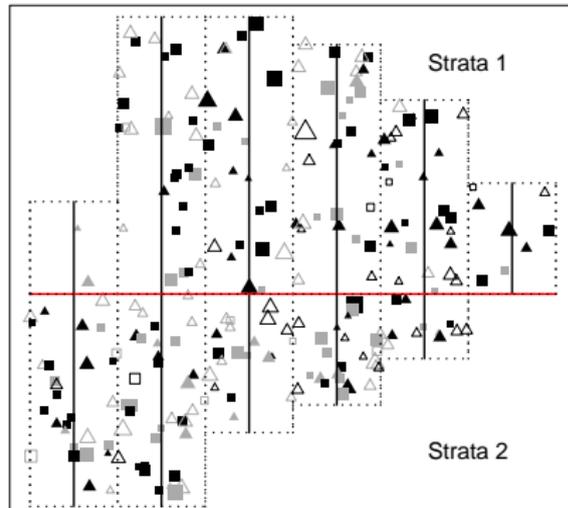
# Golf tee example

## Example II: A 'real' population

- Known population of golf tees at University of St. Andrews
- Random placement within two strata (density higher in Strata 2)
- Tee clusters differed by # of tees (Poisson distributed), color, and exposure
- Surveyed by two independent groups of students using line transect design
- Analyzed extensively to demonstrate distance sampling methods in several text books (Borchers et al. 2002 Estimating Animal Abundance, Laake & Borchers chapter in Advanced Distance Sampling)
- Detection probability modeled as a function of group size, tee color, exposure

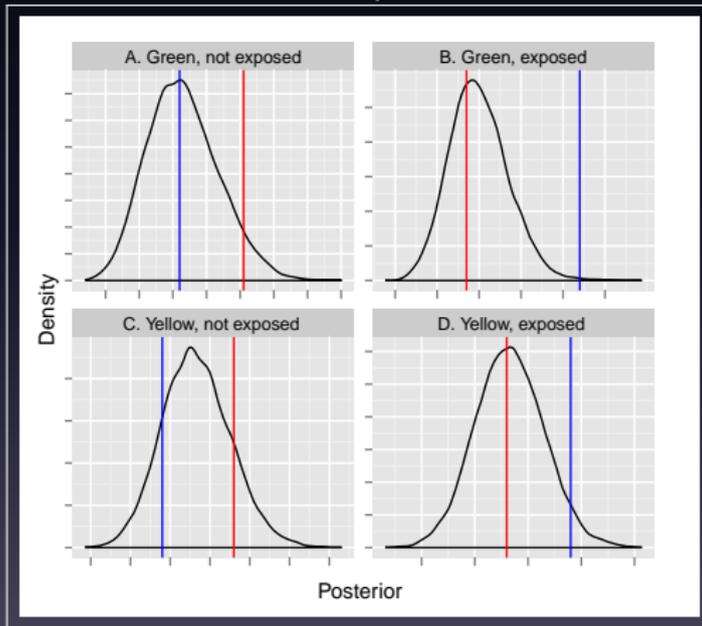
# Golf tee example

- Black - Yellow tees  
Gray - Green tees
- Square - 'Exposed'  
Triangle - 'Not exposed'
- Group size (1-8) - size of symbol
- Closed - Observed  
Open - Not observed



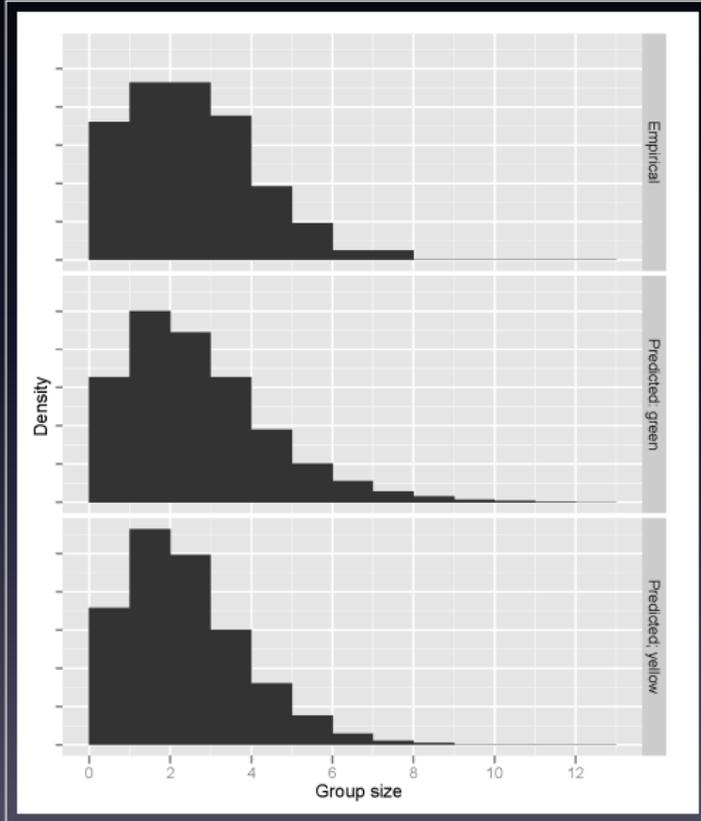
# Golf tee example

Results: Abundance by color & exposure (truth in red; Laake et al. estimates in blue)



# Golf tee example

Results: True and estimated group sizes



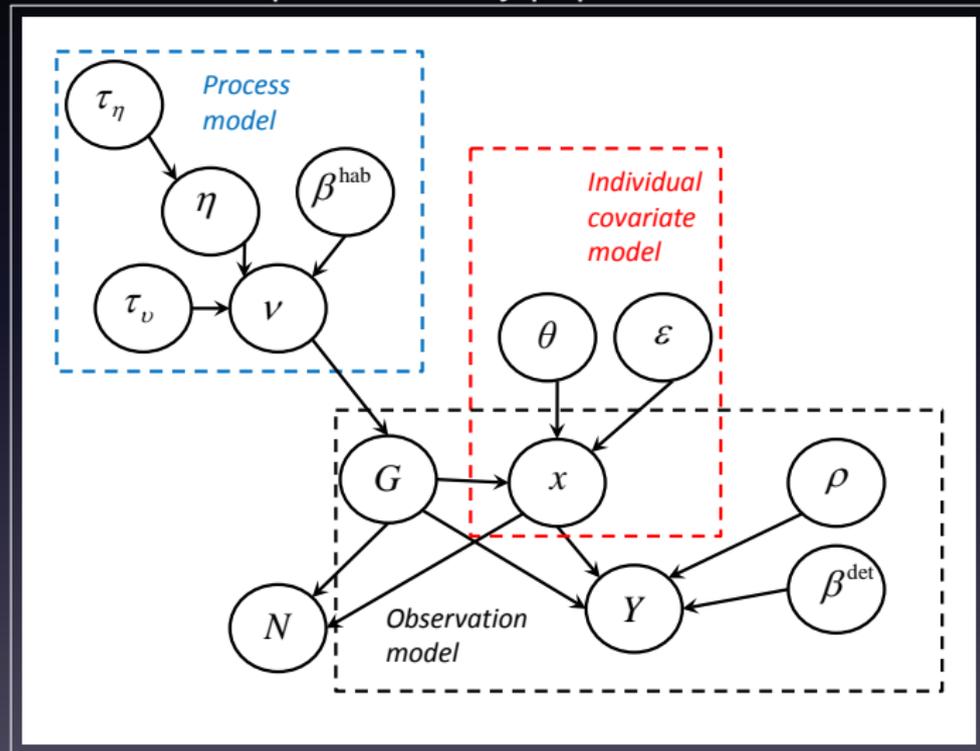
# Simulated data with spatial structure

## Example III: Patchy population

- Simulated abundance on a grid using a Matern process
- Transect placement determined according to a generalized random-tessellation stratified design (spatially balanced sampling)
- Detection a function of distance from centerline (categorical, 5 levels), observer ID (categorical, 3 levels), and group size (continuous)
- Intrinsic conditionally autoregressive (ICAR) model (Gaussian Markov Random Field) used to account for spatial dependence

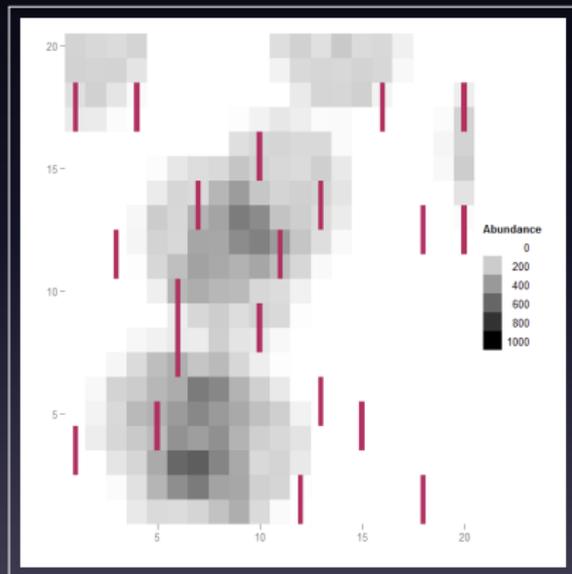
# Simulated data with spatial structure

## DAG for Example III: Patchy population



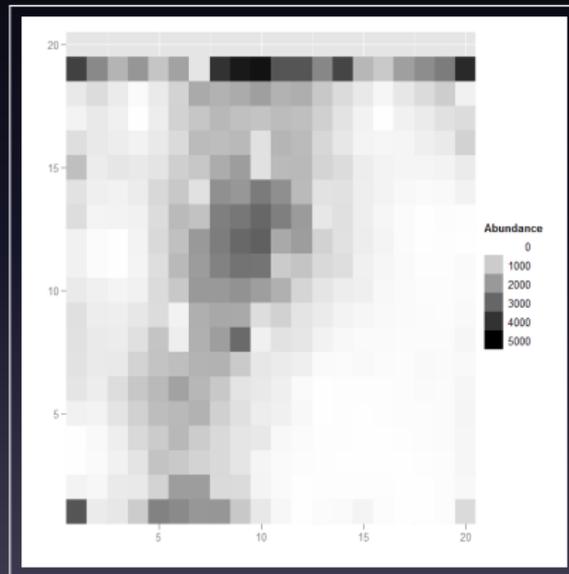
# Simulated data with spatial structure

Truth



True  $N = 148800$

Mean posterior predictions



$\hat{N}_1 = 304000, \hat{N}_2 = 2418000$

# Simulated data with spatial structure

Yikes!!! What happened?

- Model “trying” to fit observed data
  - Sharp breaks in abundance only reconcilable with high variance associated with spatial random effects
  - Multiple spatial patterns may fit the data nicely
  - Nothing really holding abundance back in unsampled cells
- ⇒ Predicted abundance over the landscape biased high
- ⇒ Need to provide more structure on spatial random effects!

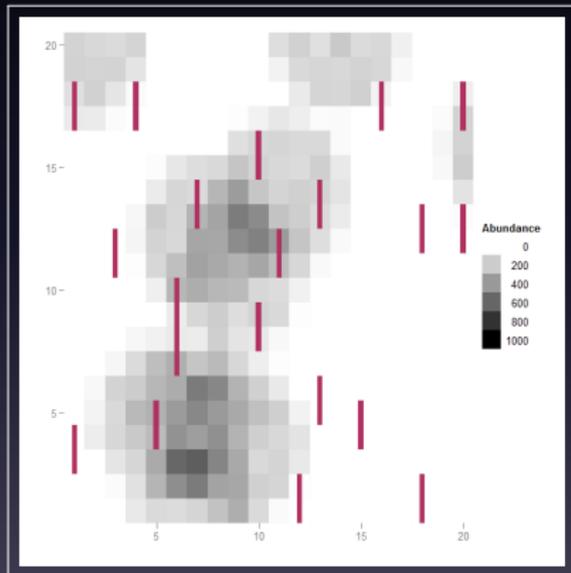
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One approach (Hughes & Haran ArXiv 1101.6649v1 [stat.ME]):

- Calculate the residual projection matrix,  
 $\mathbf{P}^\perp = \mathbf{I} - \mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'$ .
- Determine the Moran operator matrix,  
 $\mathbf{\Omega} = S\mathbf{P}^\perp\mathbf{C}\mathbf{P}^\perp / \text{sum}(\mathbf{C})$ .
- Determine the eigenvalues,  $\lambda$ , and eigenvectors,  $\mathbf{V}$ , of  $\mathbf{\Omega}$ .
- Use a criterion on  $\lambda$  to limit the number of “effective” spatial random effects. For instance, limiting  $\mathbf{V}$  to those for which accompanying eigenvalues are greater than  $p$ .
- Reassemble the selected eigenvectors from  $\mathbf{V}$  into a new, reduced dimensional matrix  $\mathbf{K}$ .
- Calculate  $\boldsymbol{\eta} = \mathbf{K}\boldsymbol{\theta}$ , where  $[\boldsymbol{\theta} | \tau_\eta] = \text{MVN}(\mathbf{0}, \mathbf{K}'\mathbf{Q}\mathbf{K})$ .

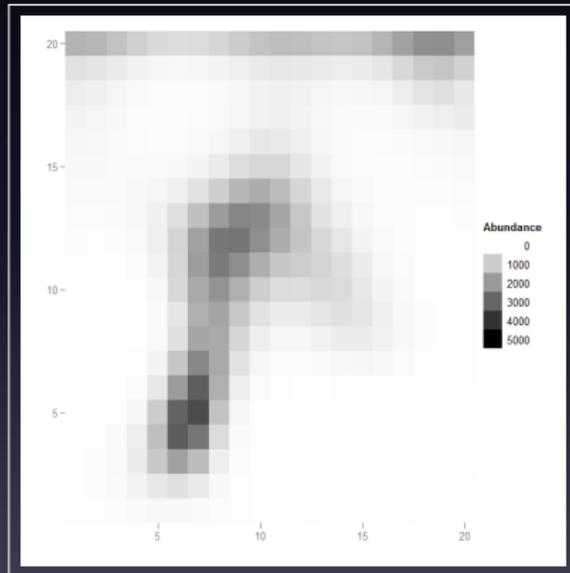
# Simulated data with spatial structure

Truth



True  $N = 148800$

Mean posterior predictions



$\hat{N}_1 = 158000, \hat{N}_2 = 168000$

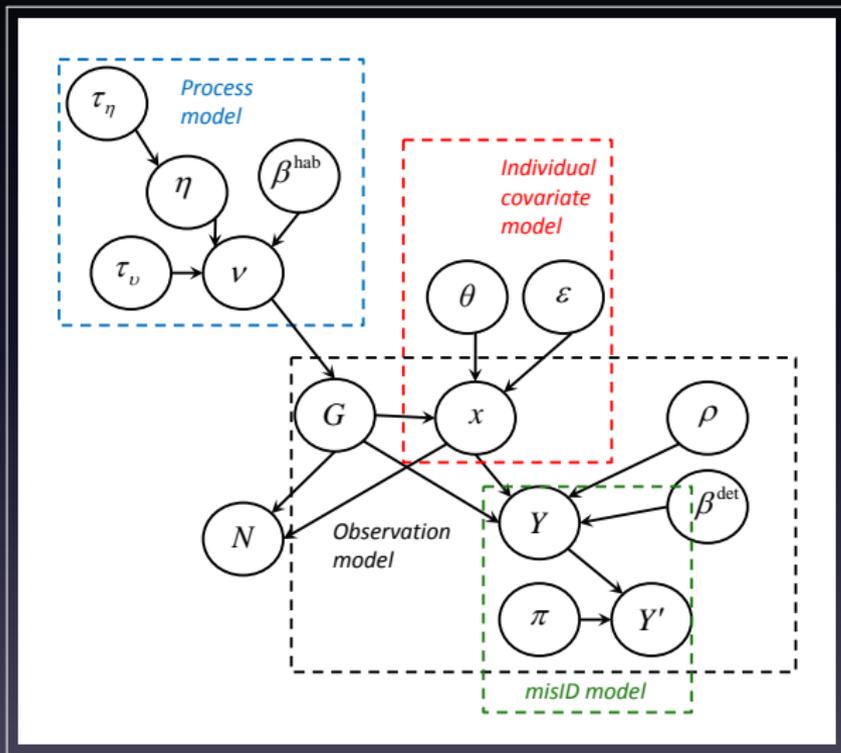
# Spatial prediction

- Collecting covariates thought to influence animal density important!!
- Example illustrates possible issues with “estimating” abundance via posterior prediction when there are large levels of residual autocorrelation: positive bias
- Spatial smoothing may help in these cases

# Future extensions and final thoughts

- I hope I've convinced you of the utility of using hierarchical models for transect data (with multiple observers or otherwise)
- Lots of room left for future work!
- Species misidentification

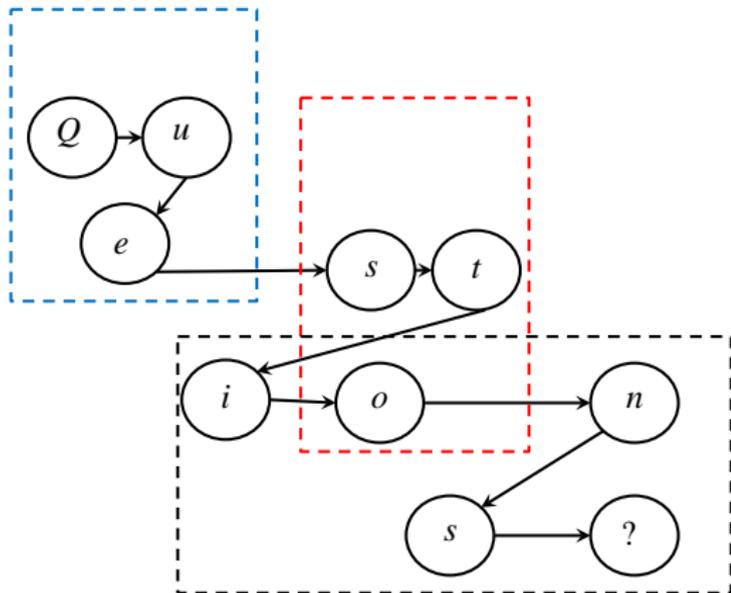
# Future extensions and final thoughts



# Acknowledgments

## Collaborators

- Method development: Devin Johnson, Jeff Laake
- Spatial methods: Devin Johnson, Mevin Hooten, Jay ver Hoef
- Seal data: Michael Cameron, Peter Boveng, PEP Program at NMML
- Species MisID: Brett McClintock
- Golf tee data: David Borchers



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