

Hierarchical models for wildlife transect surveys

Paul B. Conn

NOAA National Marine Mammal Laboratory

Seattle, Washington

Email: paul.conn@noaa.gov

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Outline

- Design-based inference

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- Hierarchical modeling roadmap

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- Simulations

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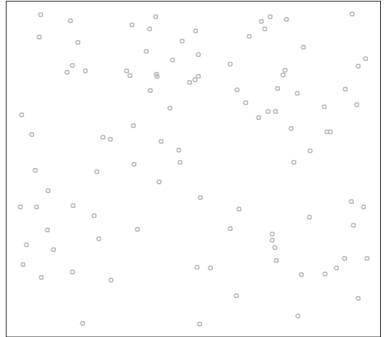
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- Simulations
- Seal example

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- Simulations
- Seal example
- Extensions and future work

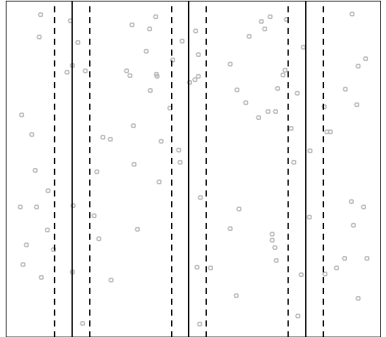
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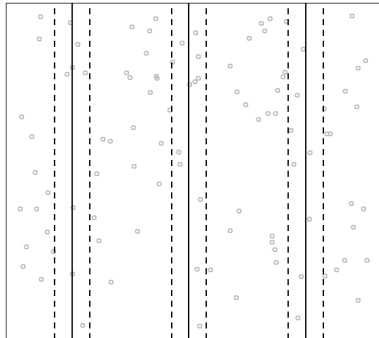
Design-based
estimator

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

N = Abundance

n = # of animals
counted

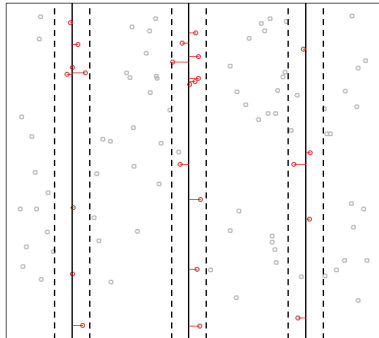
P_a = proportion of
area sampled



Design-based inference

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

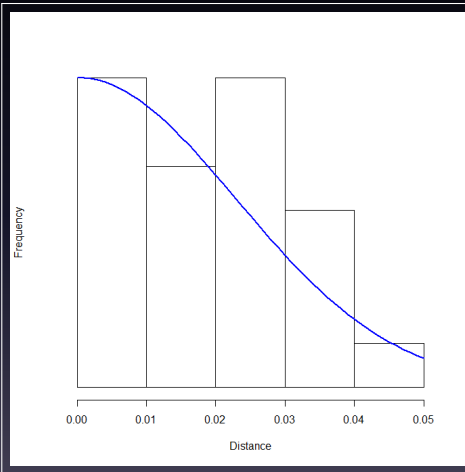
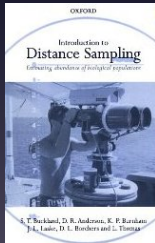
⇒ One approach:
relate detectability to
distance from transect
line



Design-based inference

Distance estimator
(design-based)

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



Design-based inference

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

- Account for multiple covariates influencing detection probability

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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:

- **Process model** Describes how abundance or a surrogate (density, abundance intensity) varies over time or space

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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`

Highfalutin Poisson GLMM

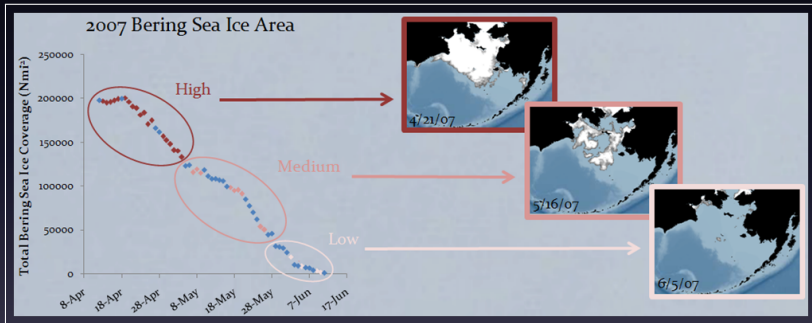
- Moore and Barlow (2011)
- Chelgren et al. (2011)

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

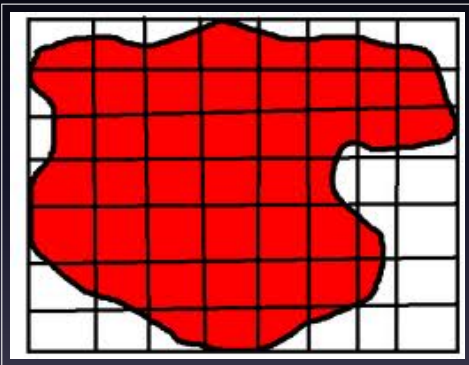
Develop hierarchical framework for line transect sampling that permits

- 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

Consider separate processes for:

- 1 Spatial and temporal dynamics of abundance at cell level
(Process model)

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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

Group abundance (G_s) is difficult to work with

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

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

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

where λ_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 ν change over time and space?

Math: Process model

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

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

\mathbf{X} gives a design matrix,

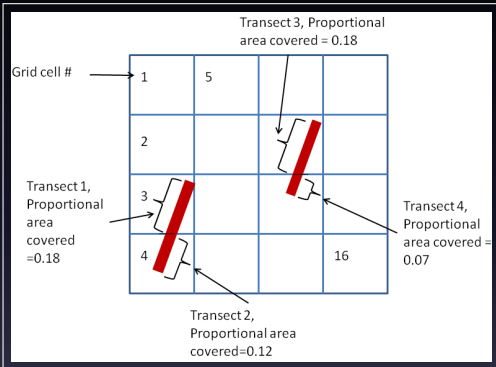
β is a vector of regression coefficients,

η is a vector of spatially structured random effects (stay tuned),
and

τ_ν is the precision associated with overdispersion relative to the Poisson distribution.

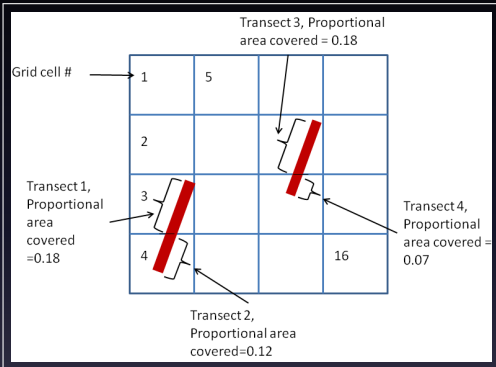
Other possibilities: cellular automata, resource selection models

Math: Local abundance model



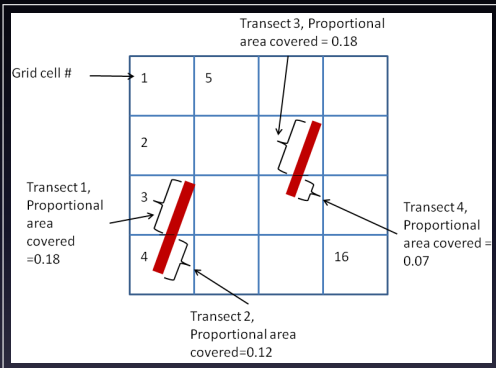
- Data are partitioned into grid cell/transect combinations

Math: Local abundance model



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- Area surveyed in each transect used to scale λ_s to the actual area surveyed $\lambda_{st} = P_{st}\lambda_s$

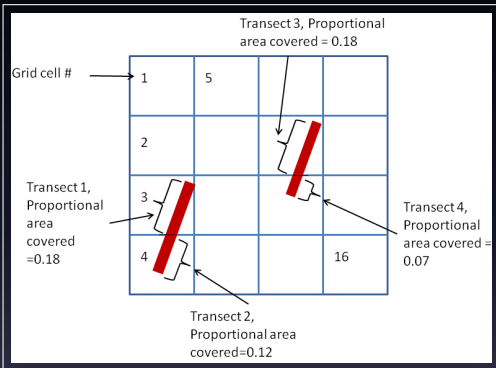
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- Posterior predictions can be generated for areas of cells not sampled:

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

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For areas of cells that *are* sampled, update abundance based on a whole bunch of things (this is where the rubber meets the road):

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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^{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):

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

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

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

Math: Observation model (Data, finally!)

Observer dependence: $\rho_{ij} = f(\text{distance})$, with y-intercept constrained to be 0 [the point independence assumption], and maximum ≤ 1 .

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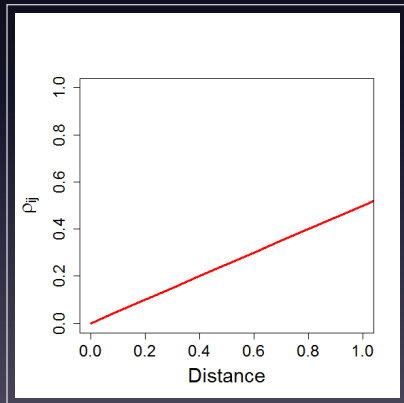
In HierarchicalDS,

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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$$\tilde{Y}_{ijk} \sim \text{Normal} \left([\mathbf{X}^{\text{det}} \boldsymbol{\beta}^{\text{det}}]_{ijk}, 1 \right)$$

where $\tilde{Y}_{ijk} < 0$, while $\tilde{Y}_{ijk} > 0$ if $Y_{ijk} = 1$. \Rightarrow Simulate $\tilde{\mathbf{Y}}$ directly using truncated normal pdfs.

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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

Math: Estimation

RJMCMC algorithm:

- 1 Update (add or subtract) latent animals

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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	-1.0	-1.8	4	A	1
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

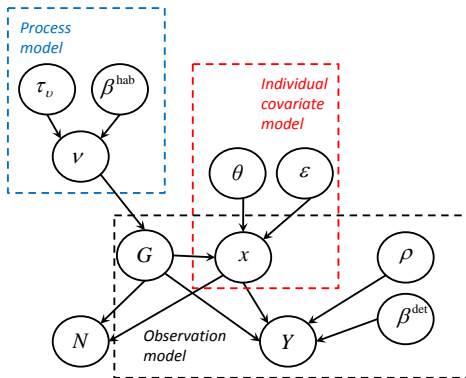
Simulated data: no spatial structure

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

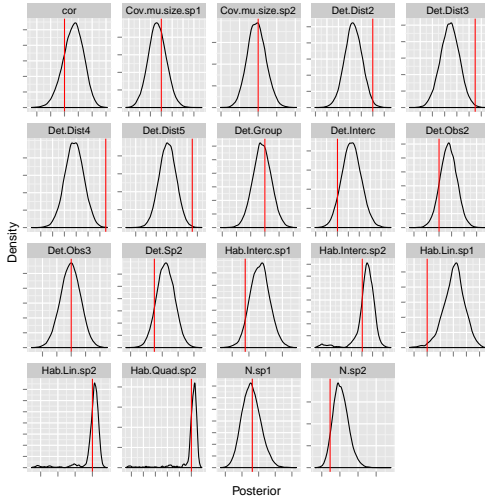
Simulated data: no spatial structure

Directed, acyclic graph



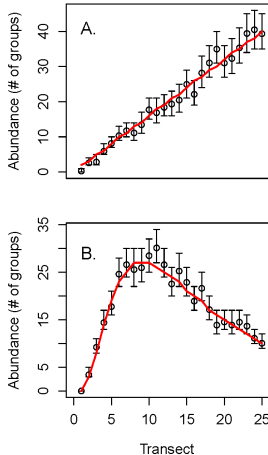
Simulated data: no spatial structure

Results: Posteriors (truth in red)



Simulated data: no spatial structure

Results: Abundance by transect



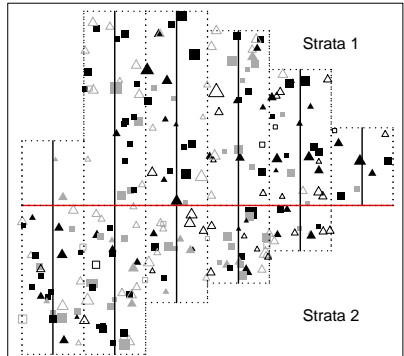
Golf tee example

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

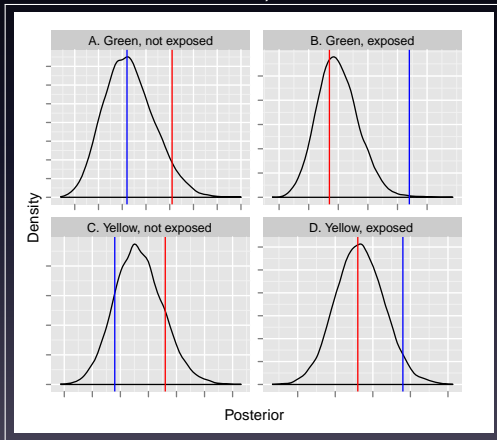
Golf tee example

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



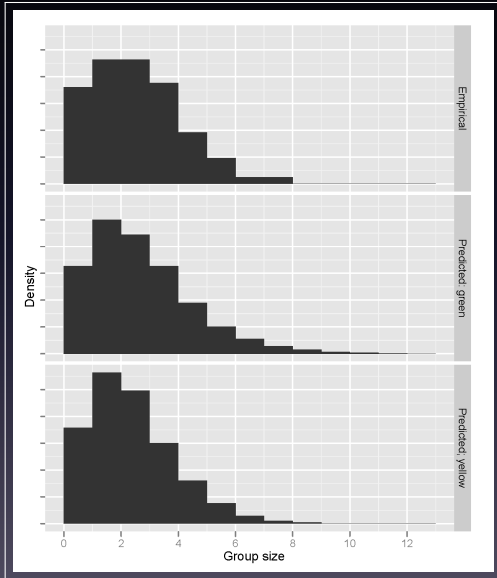
Golf tee example

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



Golf tee example

Results: True and estimated group sizes



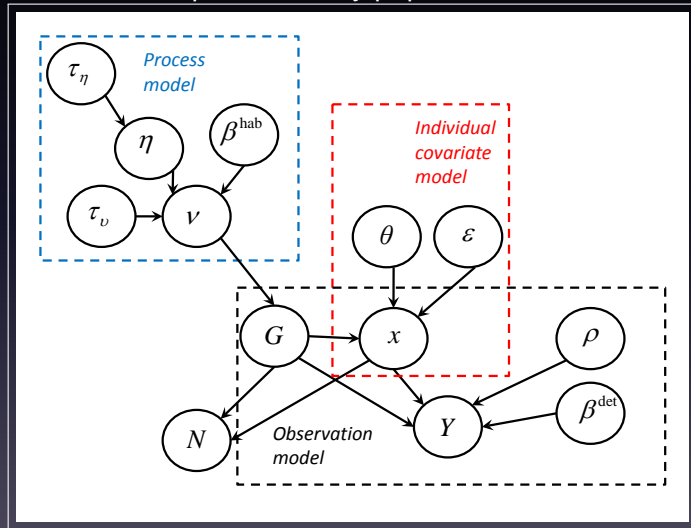
Simulated data with spatial structure

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

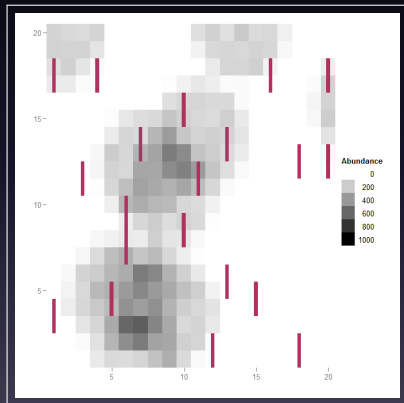
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DAG for Example III: Patchy population



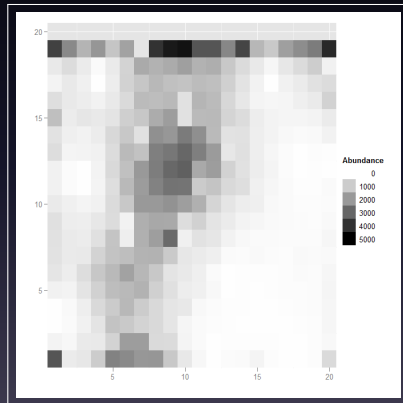
Simulated data with spatial structure

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!

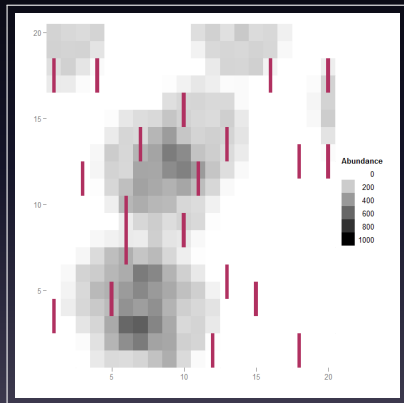
Simulated data with spatial structure

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, λ , and eigenvectors, \mathbf{V} , of $\mathbf{\Omega}$.
- Use a criterion on λ 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 $[\boldsymbol{\theta} | \tau_\eta] = \text{MVN}(\mathbf{0}, \mathbf{K}'\mathbf{Q}\mathbf{K})$.

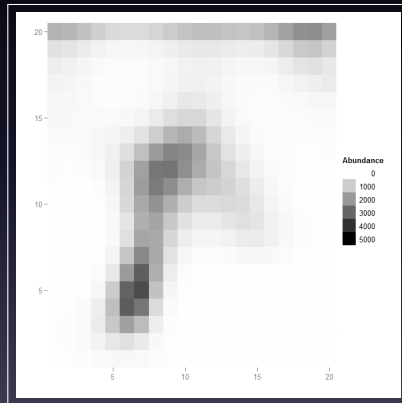
Simulated data with spatial structure

Truth



True $N = 148800$

Mean posterior predictions



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

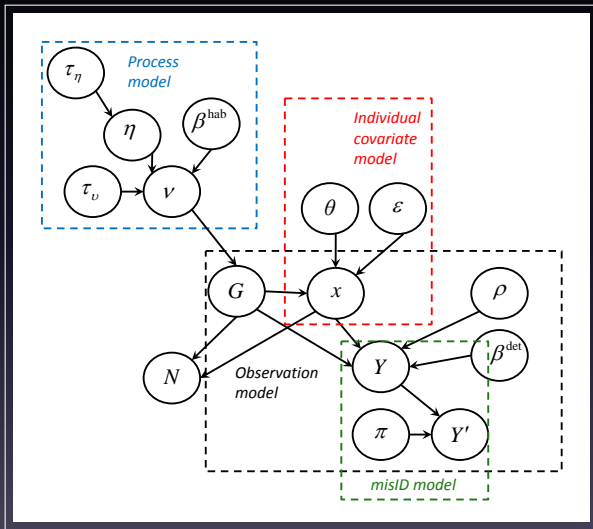
Spatial prediction

- 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

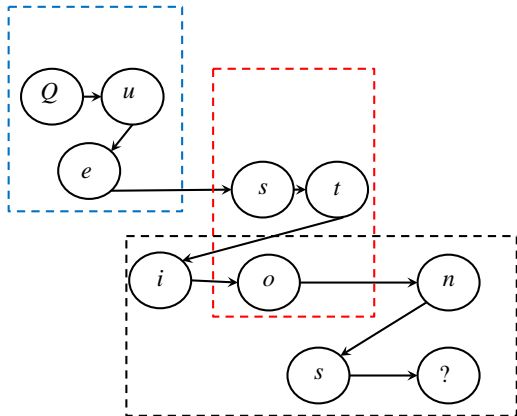
Future extensions and final thoughts



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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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