



Hierarchical spatial modelling for applied population and community ecology

Jeffrey W. Doser, Marc Kéry,
Gesa von Hirschheydt

24-27 June 2024





Spatial hierarchical distance sampling models

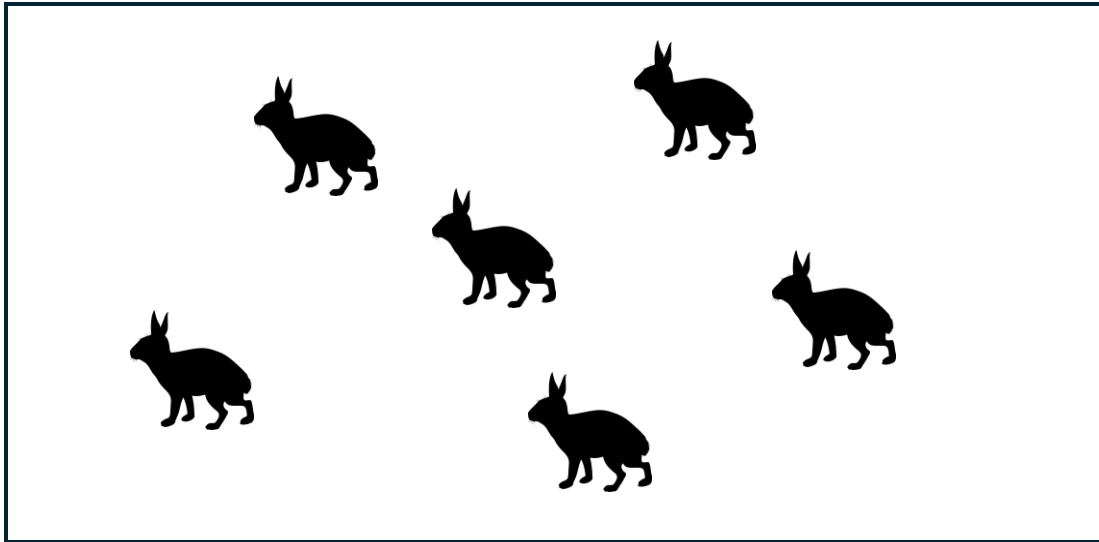
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Objective: Estimate population abundance (N)

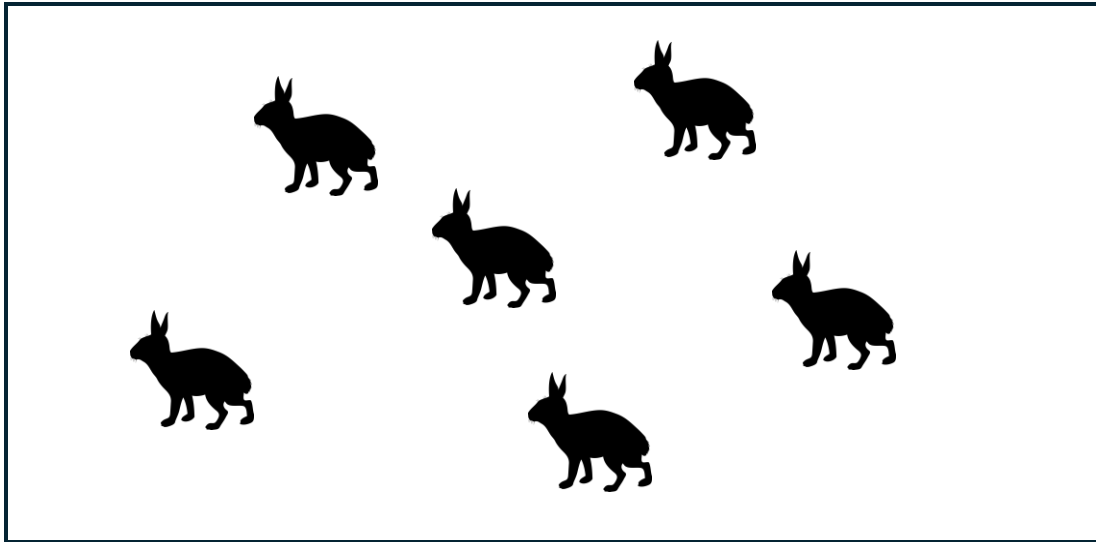
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Population

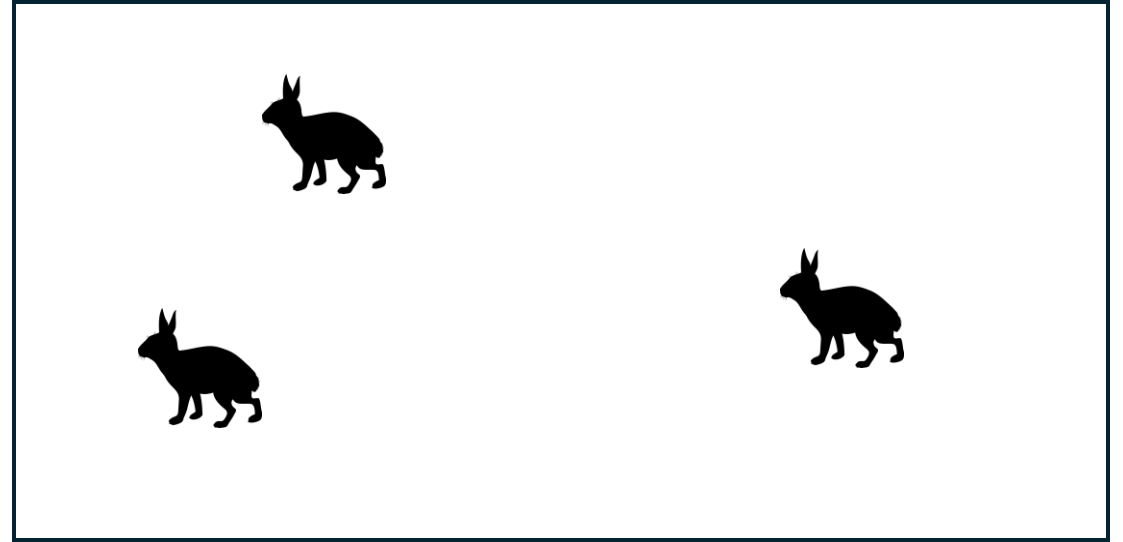


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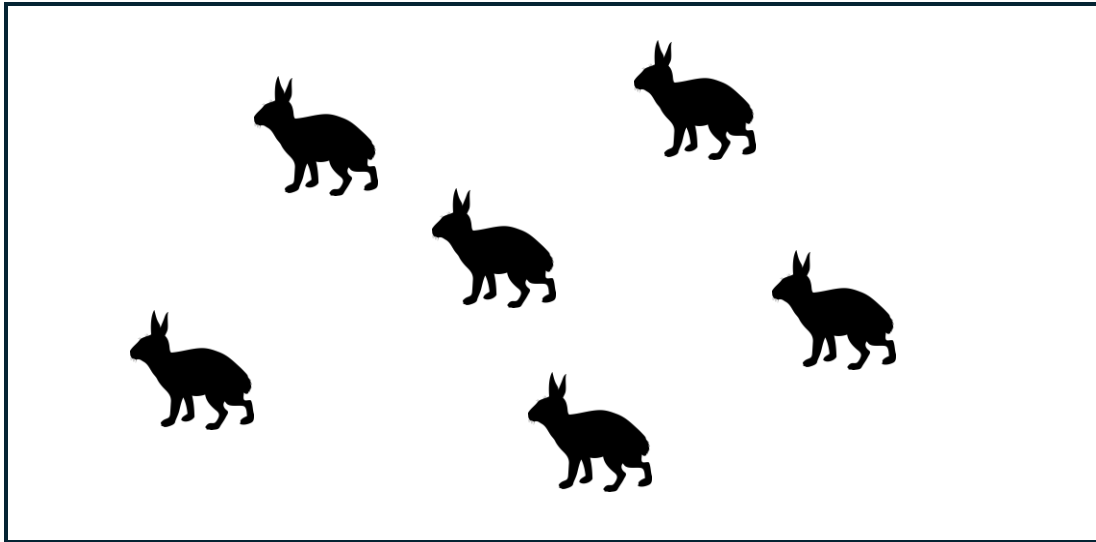


Sample

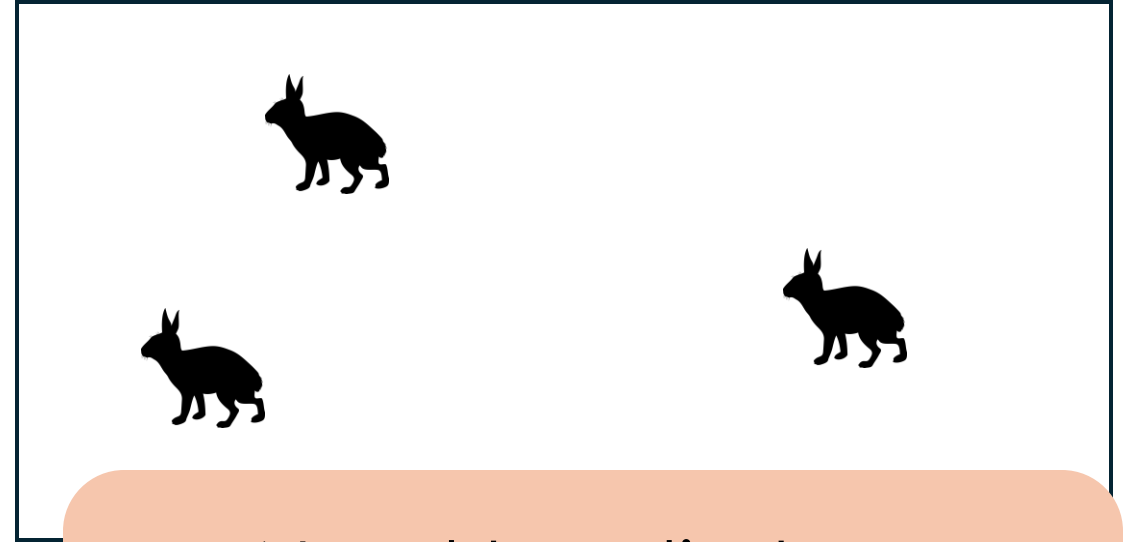


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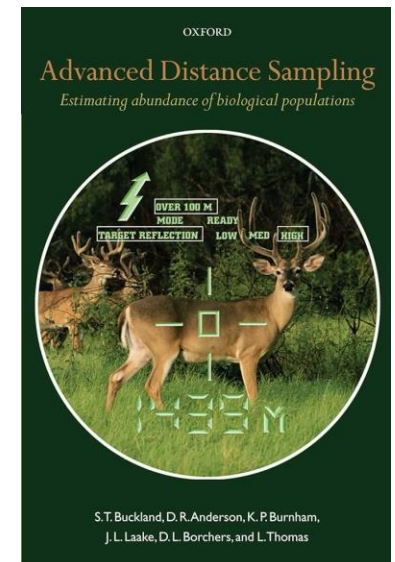
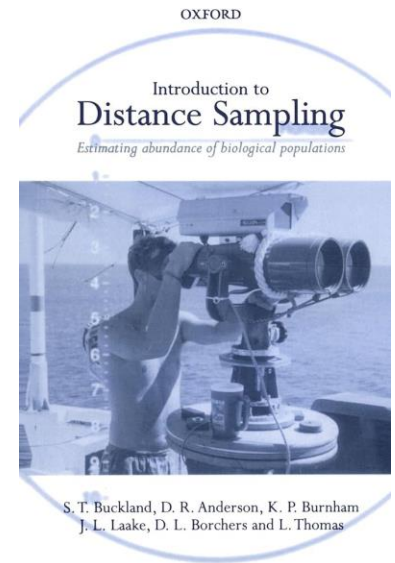
Sample



Need to adjust our abundance estimate by our **detection probability**

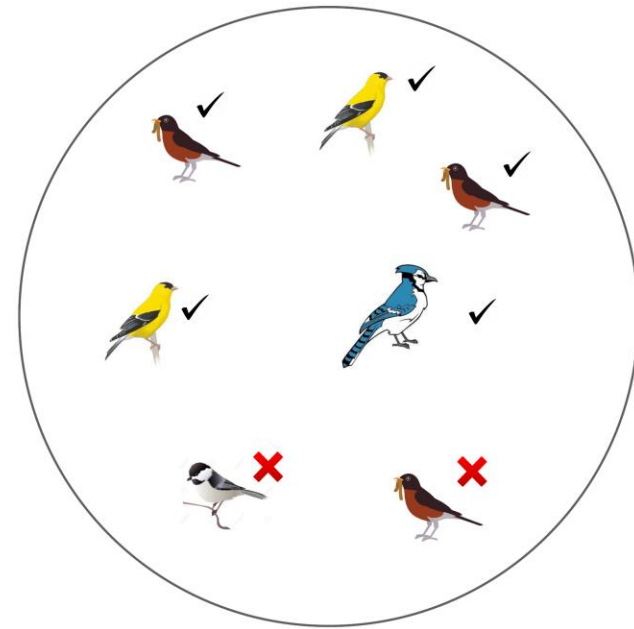
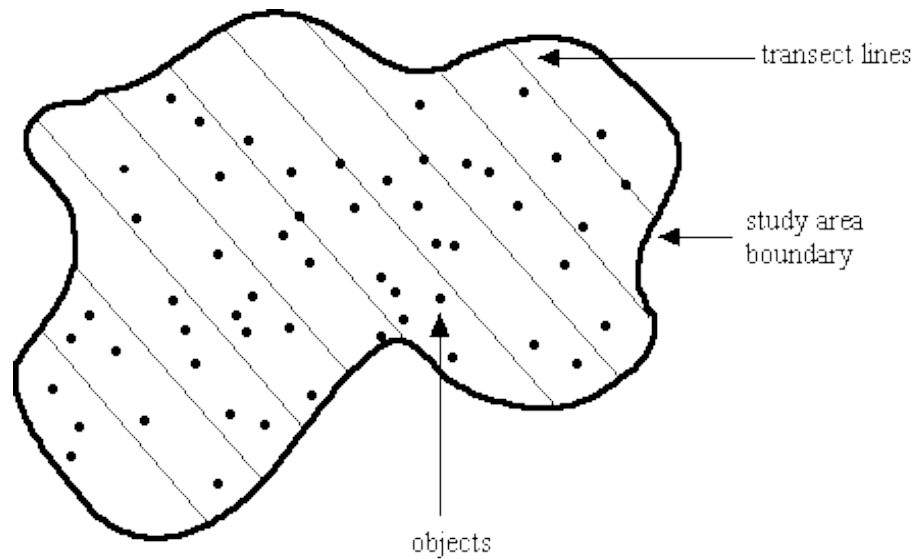
Distance sampling

- A specialized protocol to estimate abundance/density while accounting for imperfect detection.
- **Fundamental concept:** use information on the observed distances of animals to estimate detection probability.
- One of the most common methods in ecology for density/abundance estimation.
- Two major "flavors" of distance sampling
 1. Conventional distance sampling
 2. Hierarchical distance sampling (and related approaches)



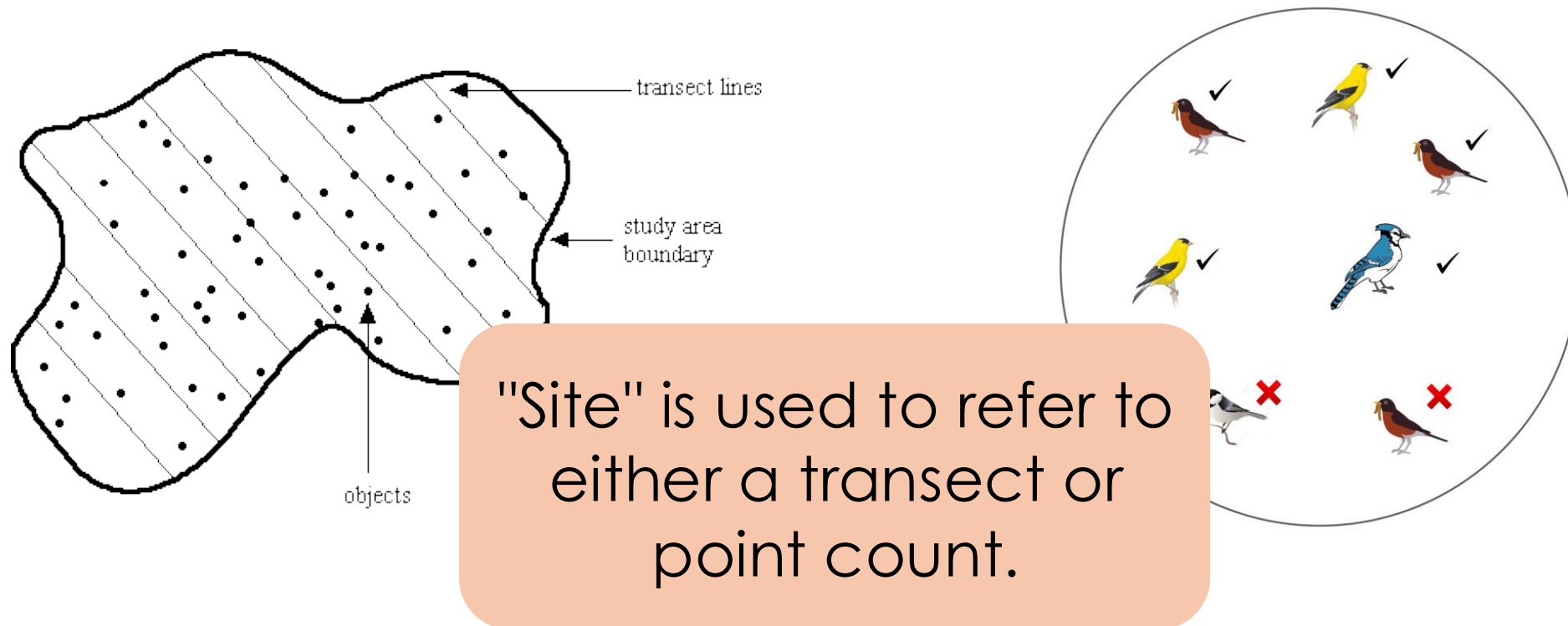
Distance sampling data collection

- A population is surveyed using a line transect or point transects (i.e., point counts).
- Observer records the distance to each individual observed.



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Distance sampling data collection

- Line transects or point counts are performed at a set of $j = 1, 2, \dots, J$ sites.
- Distances can be recorded in one of two ways:
 - Continuous distance measurement to each individual
 - Assign each individual to a distance bin

Distance sampling data collection

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 - Continuous distance measurement to each individual
 - Assign each individual to a distance bin

For analysis in `spAbundance`, we will always work with binned data (which can be derived from continuous measurements after data collection).

Continuous vs. Binned distances

Continuous

Site	Distance (m)
1	100
1	122
1	30
2	18
3	7
4	53
4	47

Continuous vs. Binned distances

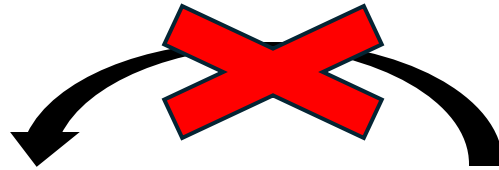
Continuous

Site	Distance (m)
1	100
1	122
1	30
2	18
3	7
4	53
4	47

Binned

Site	Distance bin (m)
1	100-150
1	100-150
1	25-50
2	0-25
3	0-25
4	50-100
4	25-50

Continuous vs. Binned distances



Continuous

Site	Distance (m)
1	100
1	122
1	30
2	18
3	7
4	53
4	47

Binned

Site	Distance bin (m)
1	100-150
1	100-150
1	25-50
2	0-25
3	0-25
4	50-100
4	25-50



Binned distance sampling data

Site	Distance bin (m)
1	100-150
1	100-150
1	25-50
2	0-25
3	0-25
4	50-100
4	25-50



Site	0-25m	25-50m	50-100m	100-150m
1	0	1	0	2
2	1	0	0	0
3	1	0	0	0
4	0	1	1	0

Binned distance sampling data

This is the format of distance sampling data we need for spAbundance.

Site	Distance bin (m)
1	100-150
1	100-150
1	25-50
2	0-25
3	0-25
4	50-100
4	25-50



Site	0-25m	25-50m	50-100m	100-150m
1	0	1	0	2
2	1	0	0	0
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4	0	1	1	0

Key distance sampling concepts

- Detection probability decreases as the distance of an individual from the observer increases.

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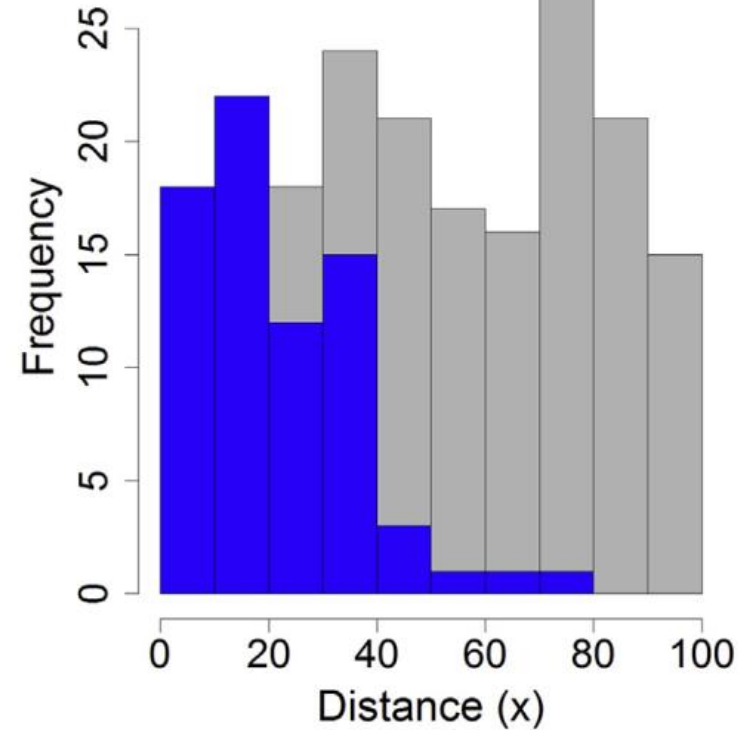
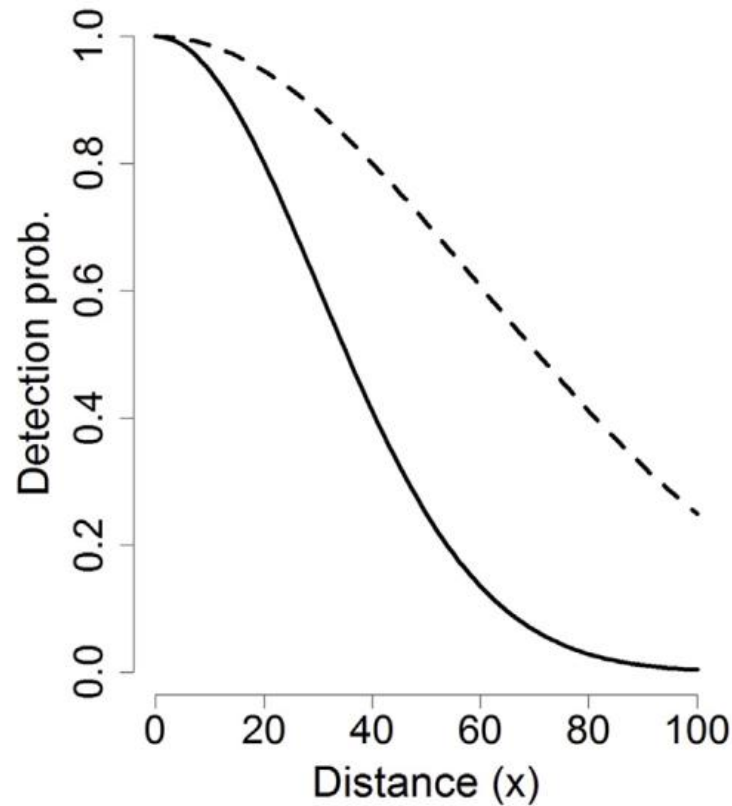
- Detection probability decreases as the distance of an individual from the observer increases.
- $E(n) = p * N$
 - n = sample count
 - N = true abundance
 - p = detection probability (the probability an individual in the population appears in our sample)

Key distance sampling concepts

- Detection probability decreases as the distance of an individual from the observer increases.
- $E(n) = p * N$
 - n = sample count
 - N = true abundance
 - p = detection probability (the probability an individual in the population appears in our sample)
- Detection probability p is determined by two components:
 - Detection function
 - Distribution of individuals in space with respect to the observer

Key distance sampling concepts

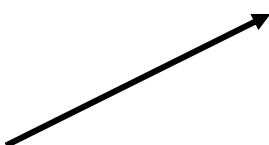
Detection probability decreases as distance from observer increases



Detection probability in distance sampling

$$\bar{p} = \int_0^B g(x)[x]dx$$

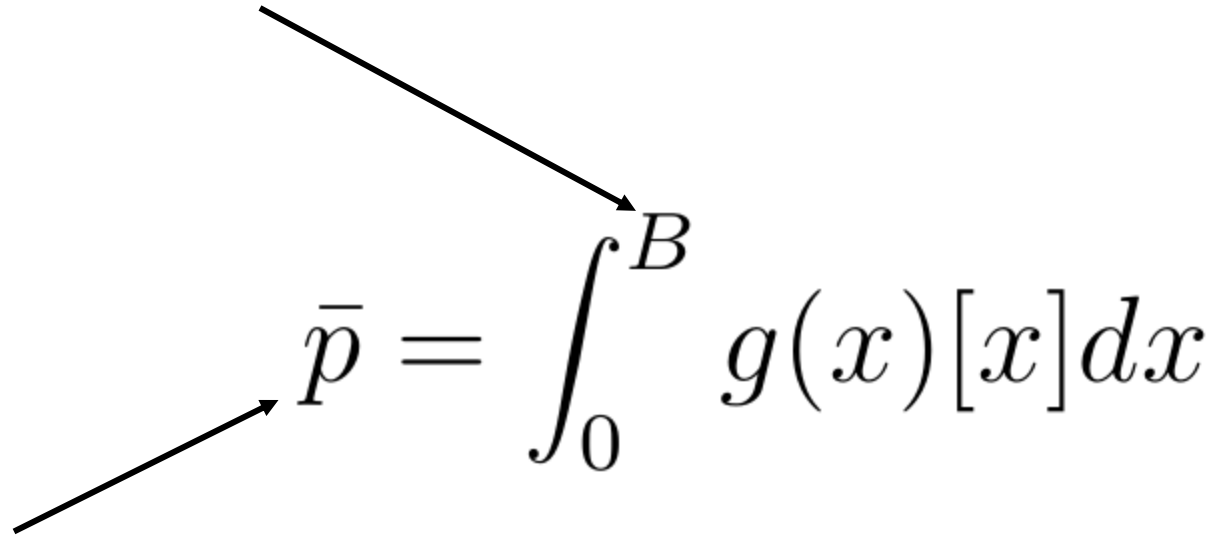
Detection probability in distance sampling


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Average
detection
probability

Detection probability in distance sampling

Maximum detection distance



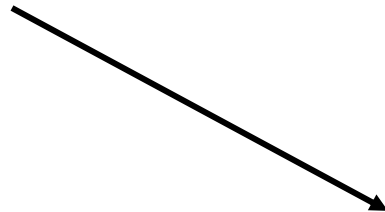
The diagram illustrates the components of the distance sampling formula. An arrow points from the text "Maximum detection distance" to the upper limit B of the integral. Another arrow points from the text "Average detection probability" to the symbol \bar{p} on the left side of the equation.

$$\bar{p} = \int_0^B g(x)[x]dx$$

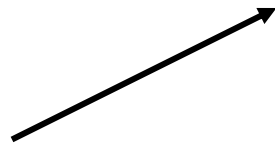
Average
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Detection probability in distance sampling

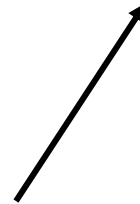
Maximum detection distance



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Average
detection
probability



Probability of detecting
an individual at distance
 x , given it is there.

Detection probability in distance sampling

Maximum detection distance

A probability distribution that determines the probability an individual occurs at distance x .

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Detection function $g(x)$

- More formally, $g(x) = Pr(\text{detect} \mid x)$
- Distance sampling requires $g(0) = 1$ (there are models to relax this assumption, but not in `spAbundance`).
- $g(x)$ must be a monotonic decreasing function (i.e., starts at 1, then continuously decreases towards 0).
- Common detection functions:
 - Half normal
 - Negative exponential
 - Hazard rate (not available in `spAbundance`)

Detection functions $g(x)$

Half normal

$$g(x; \sigma) = \exp\left(-\frac{x^2}{2\sigma^2}\right)$$

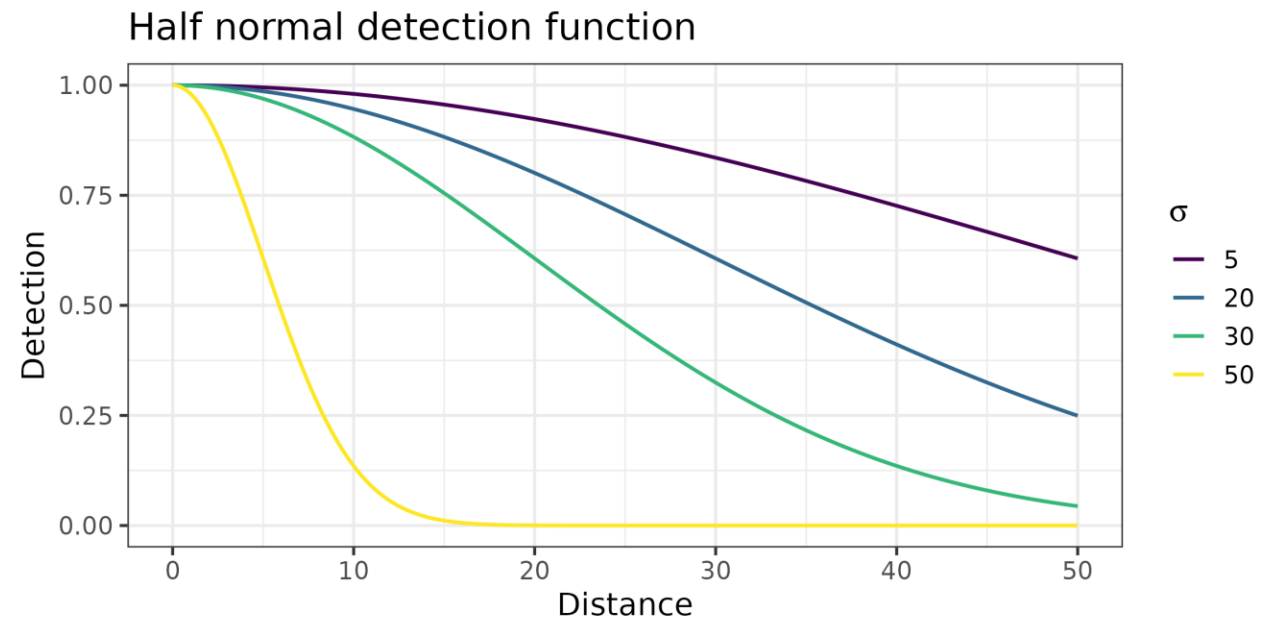
Negative
exponential

$$g(x; \sigma) = \exp\left(-\frac{x}{\sigma}\right)$$

σ is a scale parameter that takes positive values. It controls the shape of the detection curve.

Detection functions

- The average detection probability p is equal to the area under the detection curve!
- We can estimate other effects of covariates on detection using a GLM framework with the scale parameter σ .
- What link function makes sense for modeling σ as a function of covariates?



Detection probability in distance sampling

Maximum detection distance

A probability distribution that determines the probability an individual occurs at distance x .

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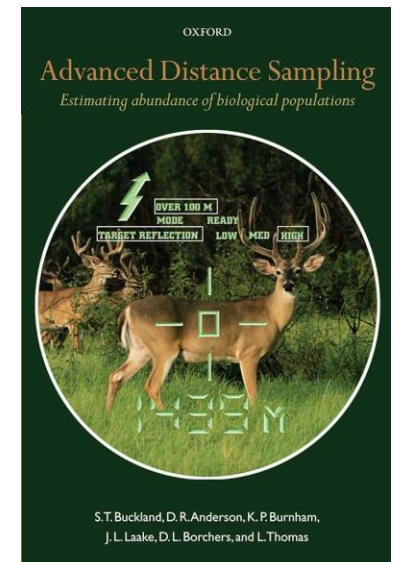
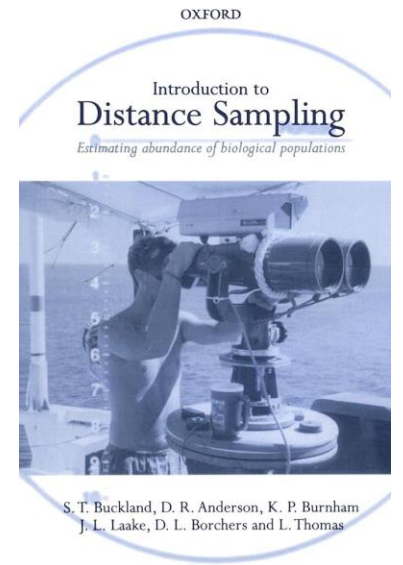
Probability distribution of individual distances

- Most distance sampling approaches assume individuals are uniformly distributed across the line transect rectangle/point count circle.
- Uniformity can also be induced by design (i.e., randomly locating transects).
- This results in $[x]$ taking the following forms:

$$\text{Line transects: } [x] = \frac{1}{B}$$

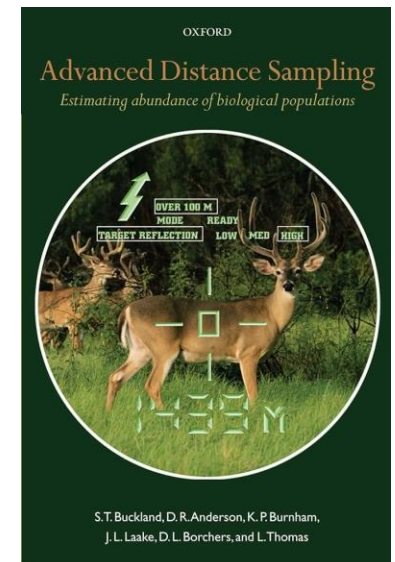
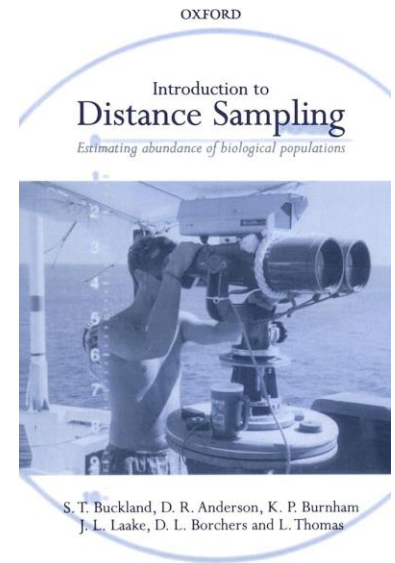
$$\text{Point counts: } [x] = \frac{2x}{B^2}$$

Conventional Distance Sampling



Conventional Distance Sampling

- Long history of development.
- Focus is on estimating abundance/density in an area of interest, not on spatial variation in abundance.
- Assumes abundance is constant across all transects.
- Can model detection probability with many covariates (sometimes called *multiple covariate distance sampling*).



Hierarchical distance sampling (HDS)

- Allows density/abundance to vary across transects (sites) using a GLM approach.
- Based on a similar hierarchical framework to occupancy models, N-mixture models.
- Similar approach:
 - Density surface modelling (Hedley and Buckland 2004; Miller et al. 2013)

Ecology, 85(6), 2004, pp. 1591–1597
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MODELING ABUNDANCE EFFECTS IN DISTANCE SAMPLING

J. ANDREW ROYLE,^{1,4} DEANNA K. DAWSON,² AND SCOTT BATES³

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This is the approach implemented in spAbundance.

MODELING ABUNDANCE EFFECTS IN DISTANCE SAMPLING

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Hierarchical distance sampling

- As with N-mixture models, our HDS model is split into two components:

Process model

Model for the true abundance/density and how it varies spatially.

Observation model

Model that relates our imperfect observations to the true abundance/density.

HDS process model

$$N_j \sim \text{Poisson}(\mu_j A_j)$$

$$\log(\mu_j) = \boldsymbol{x}_j^\top \boldsymbol{\beta}$$

HDS process model

True abundance at site j


$$N_j \sim \text{Poisson}(\mu_j A_j)$$

$$\log(\mu_j) = \mathbf{x}_j^\top \boldsymbol{\beta}$$

HDS process model

True abundance at site j

An offset to convert μ to
abundance per unit area
(density)



$N_j \sim \text{Poisson}(\mu_j A_j)$

$$\log(\mu_j) = \mathbf{x}_j^\top \boldsymbol{\beta}$$

HDS process model

True abundance at site j

An offset to convert μ to
abundance per unit area
(density)



The diagram illustrates the HDS process model. It features three main components: a title 'HDS process model' at the top left, a central equation, and three explanatory text blocks with arrows pointing to parts of the equation. The text 'True abundance at site j ' has an arrow pointing to N_j in the equation $N_j \sim \text{Poisson}(\mu_j A_j)$. The text 'An offset to convert μ to abundance per unit area (density)' has an arrow pointing to A_j in the same equation. The text 'Expected abundance (or abundance per unit area) at site j ' has an arrow pointing to μ_j in the equation $\log(\mu_j) = \mathbf{x}_j^\top \boldsymbol{\beta}$.

$$N_j \sim \text{Poisson}(\mu_j A_j)$$

$$\log(\mu_j) = \mathbf{x}_j^\top \boldsymbol{\beta}$$

Expected abundance
(or abundance per
unit area) at site j

HDS process model

True abundance at site j

An offset to convert μ to
abundance per unit area
(density)

$$N_j \sim \text{Poisson}(\mu_j A_j)$$

$$\log(\mu_j) = \mathbf{x}_j^\top \boldsymbol{\beta}$$

Expected abundance
(or abundance per
unit area) at site j

Covariates
(including an
intercept)

Covariate
effects

Spatial HDS process model

$$N_j \sim \text{Poisson}(\mu_j A_j)$$

$$\log(\mu_j) = \mathbf{x}_j^\top \boldsymbol{\beta} + w_j$$

$$\mathbf{w} \sim \text{Multivariate Normal}(\mathbf{0}, \tilde{\mathbf{C}}(d, \phi, \sigma^2))$$

Spatial HDS process model

$$N_j \sim \text{Poisson}(\mu_j A_j)$$

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For spatial models, we use our usual NNGP approach. All of our previous discussion on spatial models applies!

HDS observation model

- For HDS, we use "binned" distance sampling data.
- If you collected continuous distances, you should just bin the data. There is minimal loss of information.
- $k = 1, 2, \dots, K$ distance bins.
- $y_{j,k}$ = number of individuals observed at site j in distance bin k

$\mathbf{y}_j = [y_{j,1}, y_{j,2}, \dots, y_{j,K}]$

		k \longrightarrow			
j	Site	0-25m	25-50m	50-100m	100-150m
	1	0	1	0	2
	2	1	0	0	0
	3	1	0	0	0
	4	0	1	1	0

HDS observation model

- For our observation model (likelihood) we will use the **multinomial distribution**.
- For our context, the multinomial distribution distributes the N_j individuals across the distance bins, assigning each individual to only one bin.
- However, we need to also have an "unobserved" bin.

HDS observation model

Site	0-25m	25-50m	50-100m	100-150m
1	0	1	0	2
2	1	0	0	0
3	1	0	0	0
4	0	1	1	0

$$\mathbf{y}_j = [y_{j,1}, y_{j,2}, \dots, y_{j,K}]$$

Site	True (unobserved) abundance
1	5
2	2
3	1
4	4

$$N_j$$

HDS observation model

Site	0-25m	25-50m	50-100m	100-150m	Unobserved
1	0	1	0	2	2
2	1	0	0	0	1
3	1	0	0	0	0
4	0	1	1	0	2

$$\mathbf{y}_j^* = [y_{j,1}, y_{j,2}, \dots, y_{j,K}, y_{j,K+1}]$$

Site	True (unobserved) abundance
1	5
2	2
3	1
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$$N_j$$

HDS observation model

Site	0-25m	25-50m	50-100m	100-150m	Unobserved
1	0	1	0	2	2
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3	1	0	0	0	0
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Site	True (unobserved) abundance
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$$\mathbf{y}_j^* = [y_{j,1}, y_{j,2}, \dots, y_{j,K}, y_{j,K+1}]$$

$$N_j$$

$$\mathbf{y}_j^* \sim \text{Multinomial}(N_j, \boldsymbol{\pi}_j^*)$$

$$\boldsymbol{\pi}_j^* = [\pi_{j,1}, \pi_{j,2}, \dots, \pi_{j,K}, \pi_{j,K+1}]$$

HDS observation model

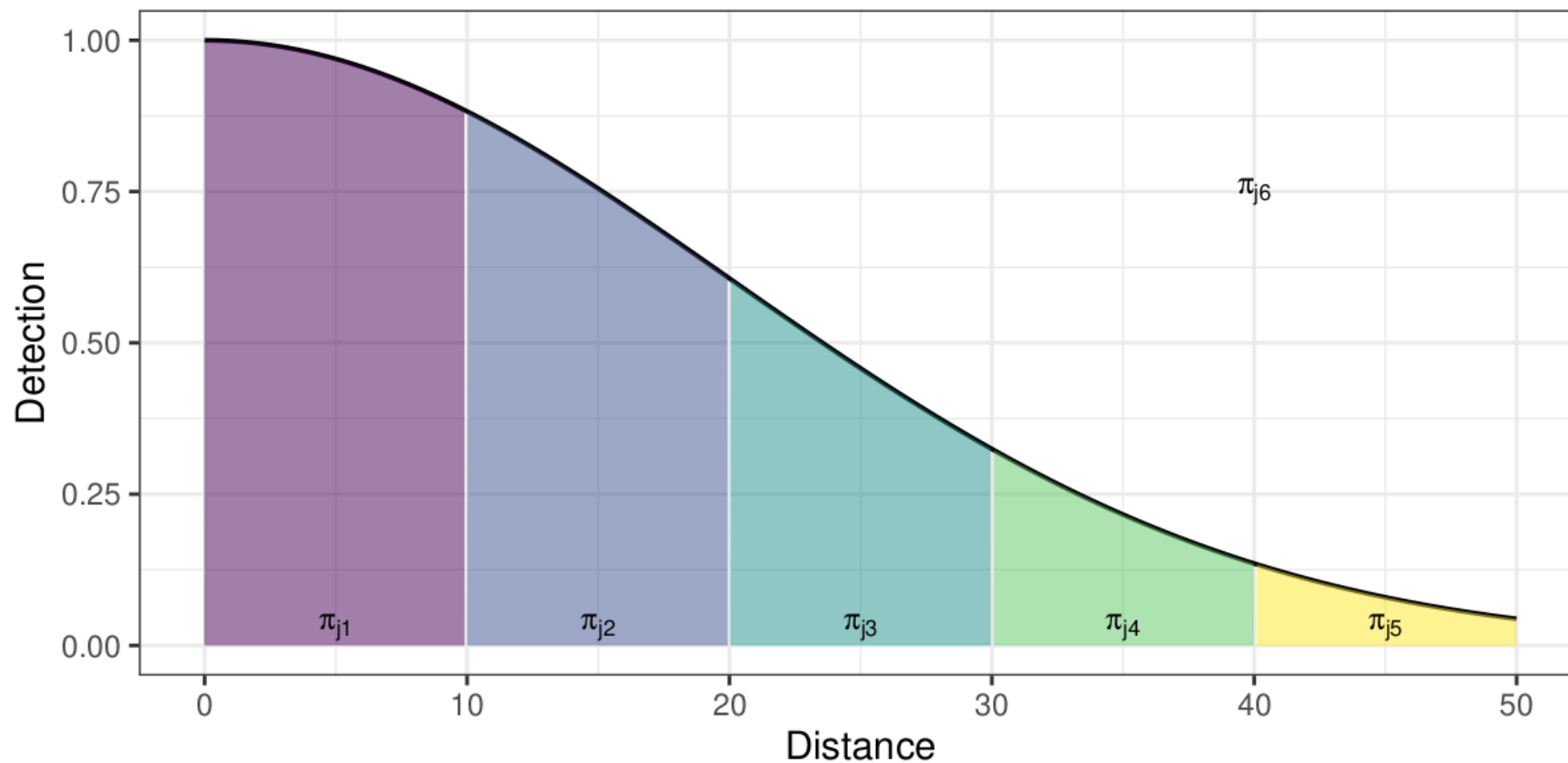
$$\mathbf{y}_j^* \sim \text{Multinomial}(N_j, \boldsymbol{\pi}_j^*)$$

$$\boldsymbol{\pi}_j^* = [\pi_{j,1}, \pi_{j,2}, \dots, \pi_{j,K}, \pi_{j,K+1}]$$

- $\pi_{j,k}$ is the probability of detecting an individual in the k th distance band at site j .
- $\pi_{j,K+1}$ is the probability of not detecting an individual at site j .

Multinomial cell probabilities visually

$K = 5$ distance bands



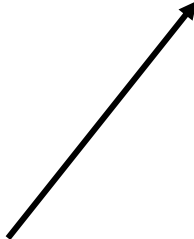
HDS observation model

$$\pi_{j,k} = \bar{p}_{j,k} \cdot \psi_k$$

HDS observation model

$$\pi_{j,k} = \bar{p}_{j,k} \cdot \psi_k$$

Probability of of detecting an individual at site j in distance band k, given the individual is there



HDS observation model

Probability an individual occurs in distance band k

$$\pi_{j,k} = \bar{p}_{j,k} \cdot \psi_k$$

Probability of detecting an individual at site j in distance band k, given the individual is there

HDS observation model

$$\pi_{j,k} = \bar{p}_{j,k} \cdot \psi_k$$

Upper distance limit for band k



$$\bar{p}_{j,k} = \int_{b_k}^{b_{k+1}} g(x)[x]dx$$

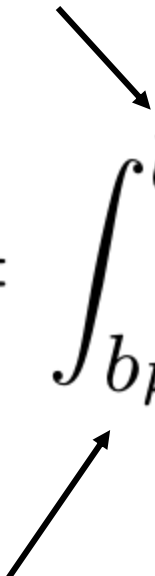


Lower distance limit for band k

HDS observation model

$$\pi_{j,k} = \bar{p}_{j,k} \cdot \psi_k$$

Upper distance limit for band k


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Lower distance limit for band k

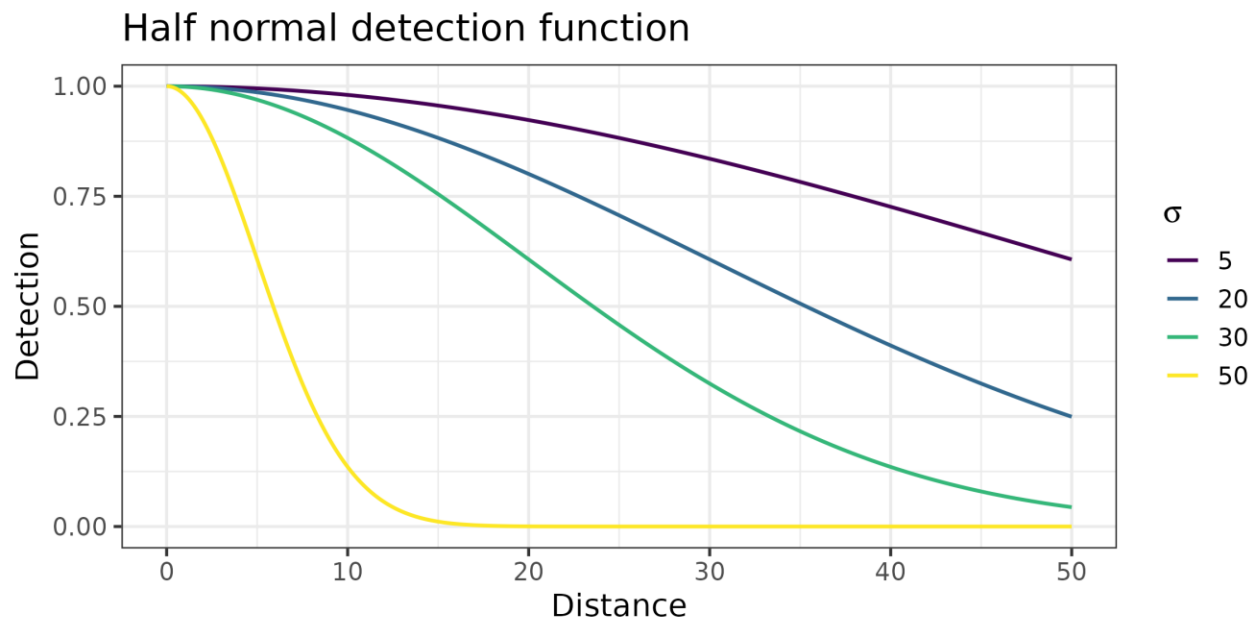
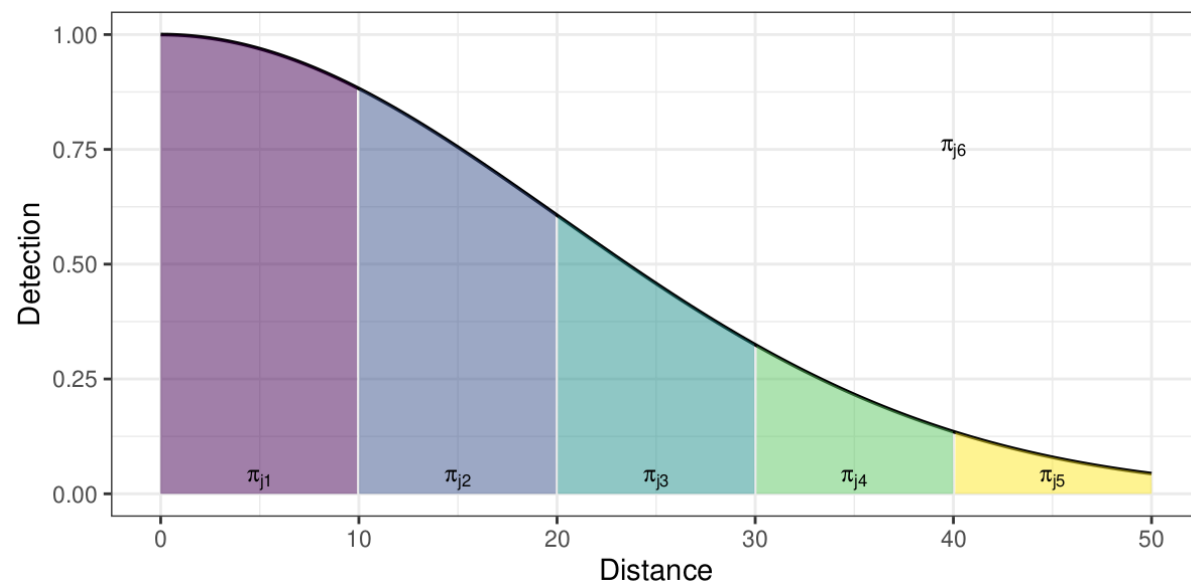
Line transects

$$\psi_k = \frac{b_{k+1} - b_k}{B}$$

Point counts

$$\psi_k = \frac{b_{k+1}^2 - b_k^2}{B^2}$$

Cell probabilities depend on σ



$$\log(\sigma_j) = \mathbf{v}_j^\top \boldsymbol{\alpha}$$

Spatial HDS: putting it all together

spAbundance also supports
negative binomial

$$N_j \sim \text{Poisson}(\mu_j A_j)$$

$$\log(\mu_j) = \mathbf{x}_j^\top \boldsymbol{\beta} + w_j$$

$$\mathbf{w} \sim \text{Multivariate Normal}(\mathbf{0}, \tilde{\mathbf{C}}(d, \phi, \sigma^2))$$

$$\mathbf{y}_j^* \sim \text{Multinomial}(N_j, \boldsymbol{\pi}_j^*)$$

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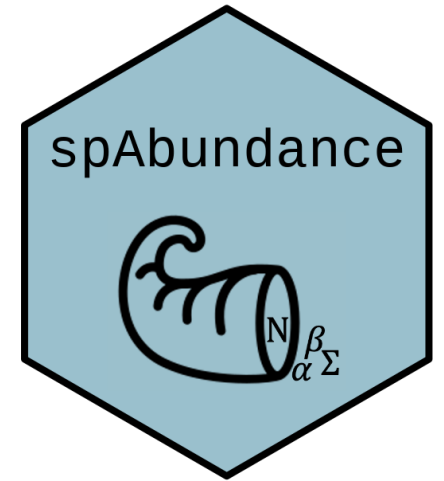
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$$\log(\sigma_j) = \mathbf{v}_j^\top \boldsymbol{\alpha}$$


Fitting hierarchical distance sampling models in spAbundance

- Non-spatial models: `DS ()`
- Spatial models: `spDS ()`
- Family argument can be Poisson or NB (aiming to have zero-inflated Poisson in the future)
- Detection function (`det.func`) can be either half-normal or negative exponential.
- Supports both circular (point count) transects and linear transects via the `transect` argument.



A note on what we mean by "spatial hierarchical distance sampling"

- Hierarchical distance sampling allows for abundance to vary across transects (sites) but not within a transect.
- When we fit a spatial model, we still assume abundance is uniform within a transect/site. We account for spatial autocorrelation across transects/sites.
- This differs from "spatial distance sampling" in Section 9.8 of Kéry and Royle (2015), in which the objective is to account for within-transect spatial variation in abundance.



Exercise: Estimating density of an island endemic

13-spatial-hds-issj.R

