

Multiple covariate distance sampling (MCDS)

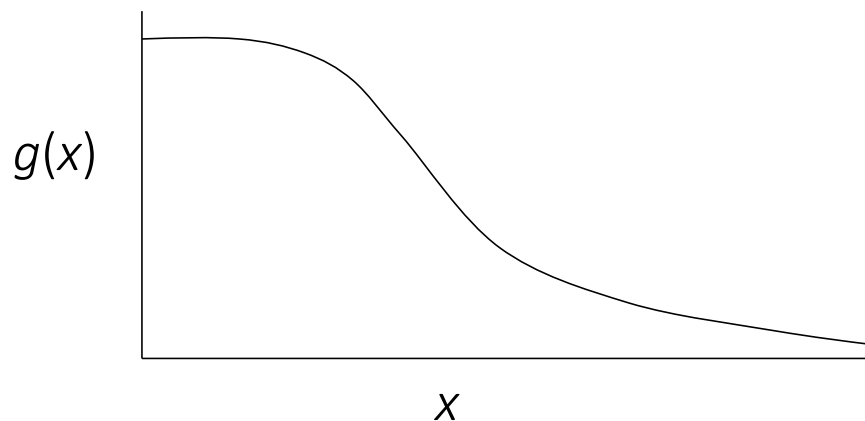
- Aim: Model the effect of additional covariates on detection probability, in addition to distance, while assuming probability of detection at zero distance is 1
- References:
 - Marques (F) and Buckland (2004) Covariate models for the detection function. Chapter 3 in Buckland *et al.* (eds). Advanced Distance Sampling.
 - Marques (T) *et al.* (2007) Improving estimates of bird density using multiple covariate distance sampling. The Auk 127: 1229-1243.
 - Section 5.3 of Buckland *et al.* (2015) Distance Sampling: Methods and Applications

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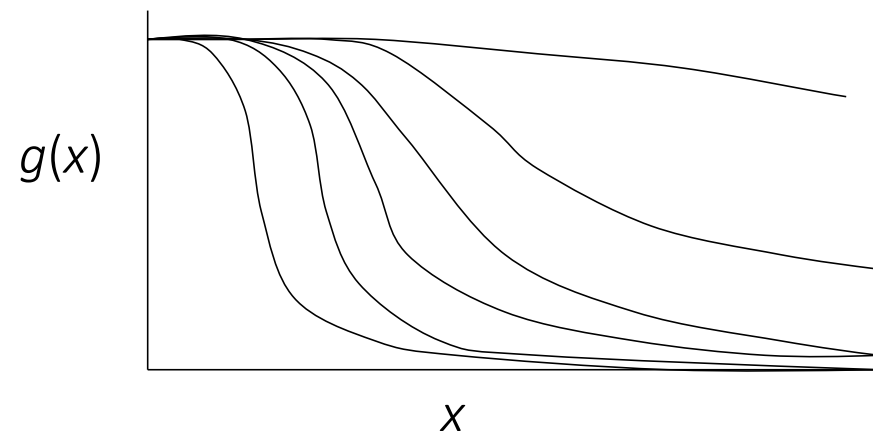
- Why additional covariates?
- Multiple covariate models
- Estimating abundance
- MCDS in the `Distance` package
- Complications
 - Clustered populations
- MCDS analysis guidelines

Why additional covariates?

In conventional distance sampling (CDS) analysis all factors affecting detectability, except distance, are ignored



In reality, many factors may affect detectability



Sources of heterogeneity:

Object : species, sex, cluster size

Effort: observer, habitat, weather

Examples of heterogeneity 1

Effect of time of day on Rufous Fantail birds in Micronesia (point transects). Ramsey et. al. 1987. Biometrics 43:1-11

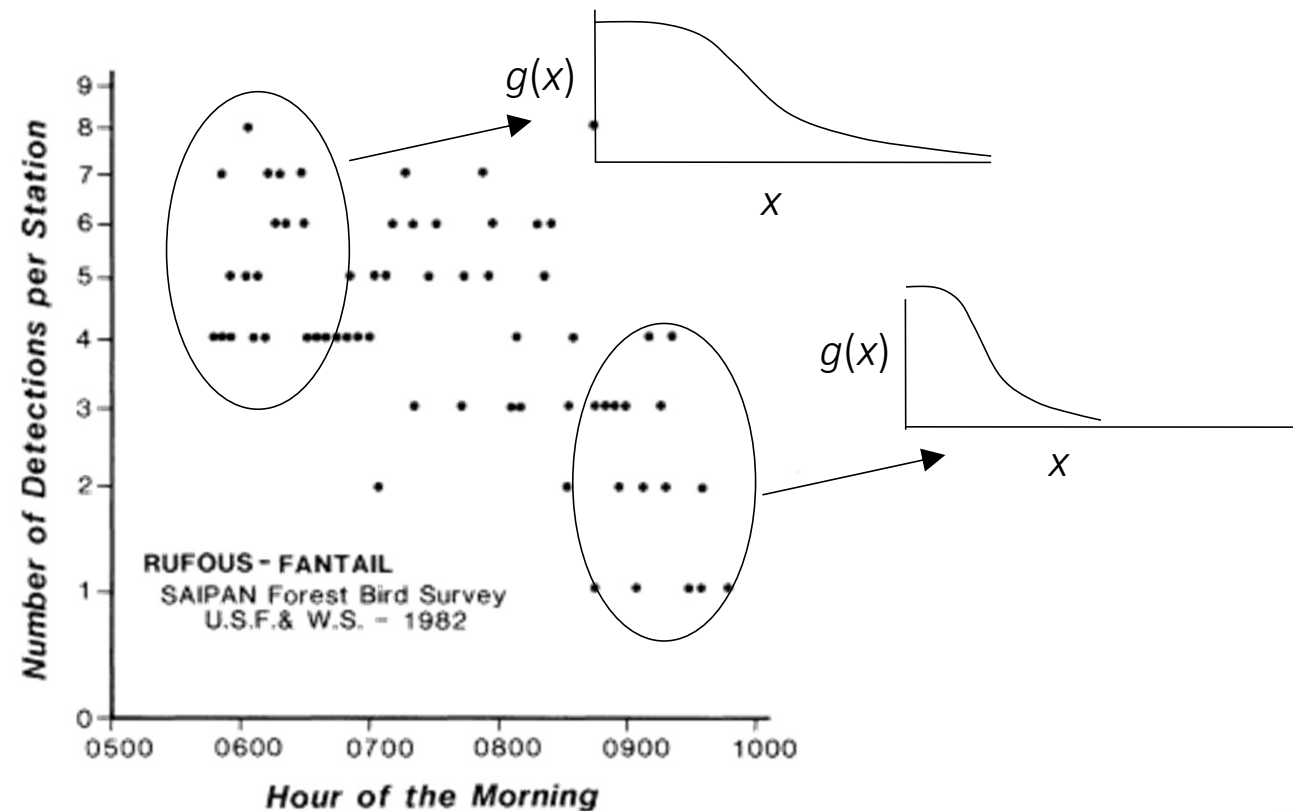


Figure 1. Station counts of Rufous Fantails on Saipan appear higher in the early morning hours than in the late morning ($n = 64$, $r = -.60$).

Examples of heterogeneity 2

Effect of sea state (and other covariates) on sea turtles in the Eastern Tropical Pacific (shipboard line transects). Beavers and Ramsey, 1998, J. Wildl. Manage. 63: 948-957

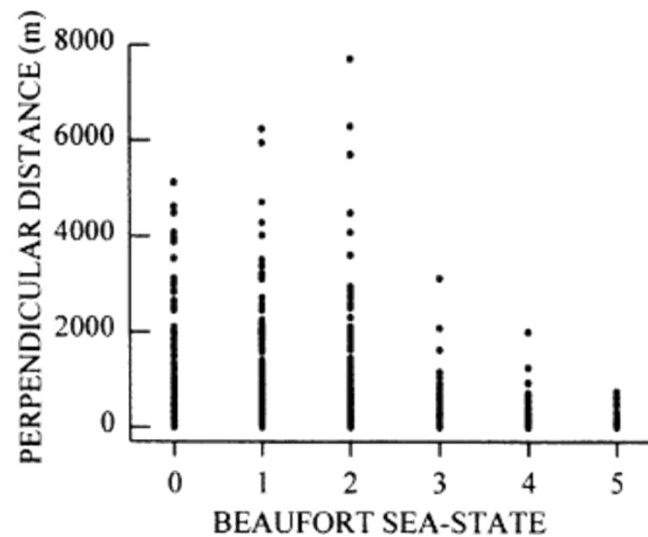
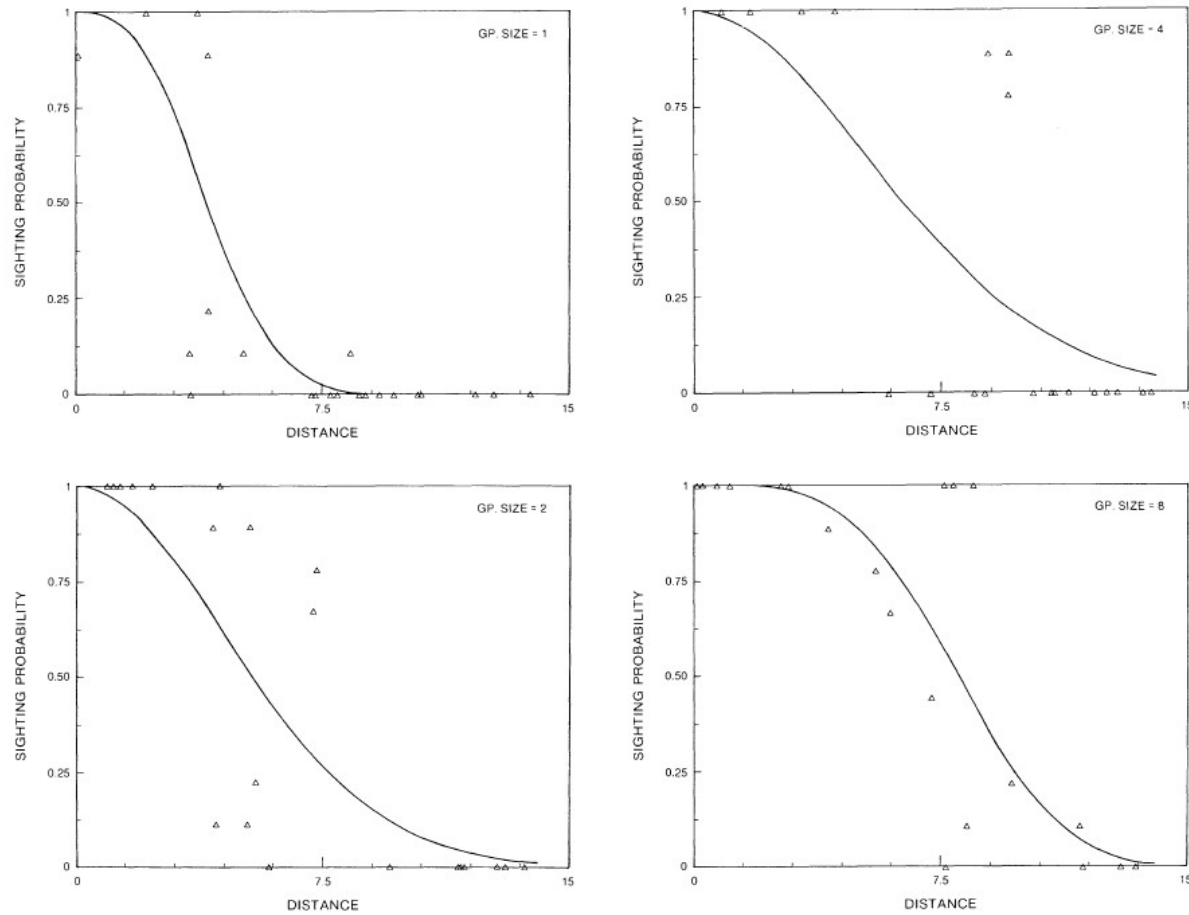


Fig. 2. Covariates of air temperature, sea surface temperature, and Beaufort sea-state plotted against unadjusted, ungrouped perpendicular sighting distances (m) of sea turtles in the eastern tropical Pacific, 1989–90.

Examples of heterogeneity 3

Effect of cluster size on beer can detectability. Otto and Pollock, 1990, Biometrics 46: 239-245



Why worry about heterogeneity?

In CDS, we use models that are pooling robust, so why worry about heterogeneity?

- *Pooling robustness works* for all but extreme levels of heterogeneity
- Potential bias if density is estimated at a 'lower level' than detection function (e.g. density by geographic region, detection function pooled)
- Could potentially increase precision of detection function estimate
- Interest in sources of heterogeneity in their own right (e.g. group size)

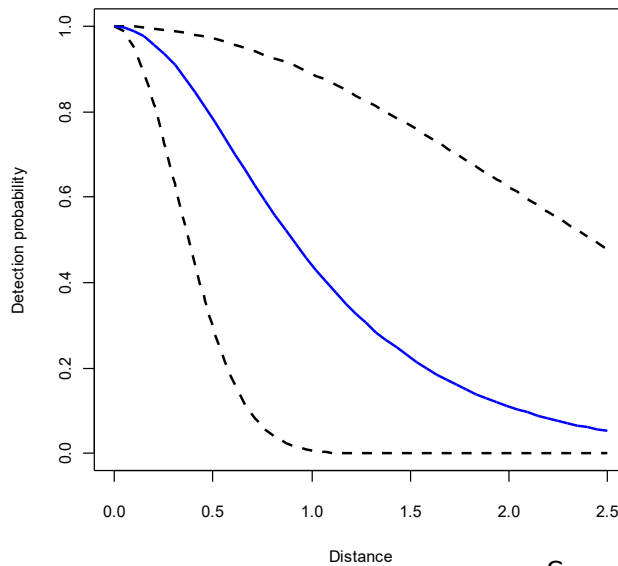
Pooling robustness

Individuals can have quite different detection functions, but this produces little bias (up to a point!)

‘Pooling robustness’ = robust to pooling of multiple detection functions

e.g. Simulation study (unpublished) Truth = 1000 animals

Detection functions for min, max and mean exposure



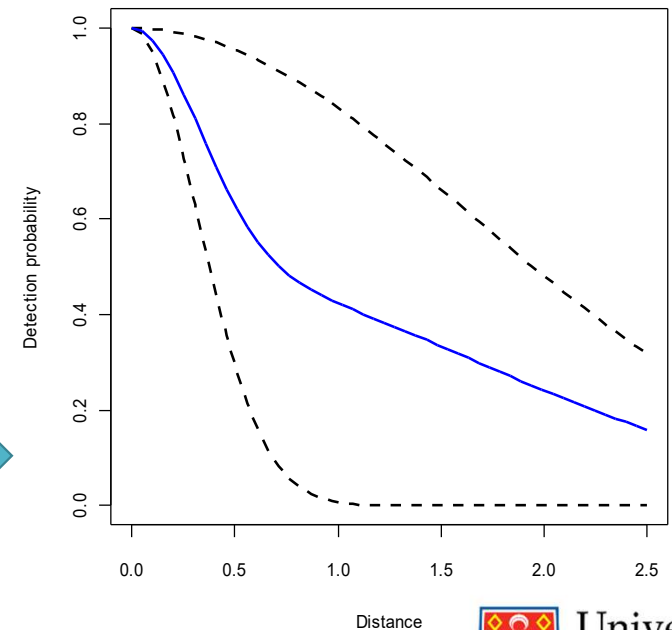
Scenario 1: animals have a gamma distribution of detection functions between min and max shown.

Mean estimate from simulation: 984 animals (SE 2.3). Bias -1.6%

Scenario 2: half of animals have max detection function, half have minimum.

Mean estimate from simulation: 976 animals (SE 2.7). Bias -2.4%

Detection functions for min, max and mean exposure



Dealing with heterogeneity

Stratification

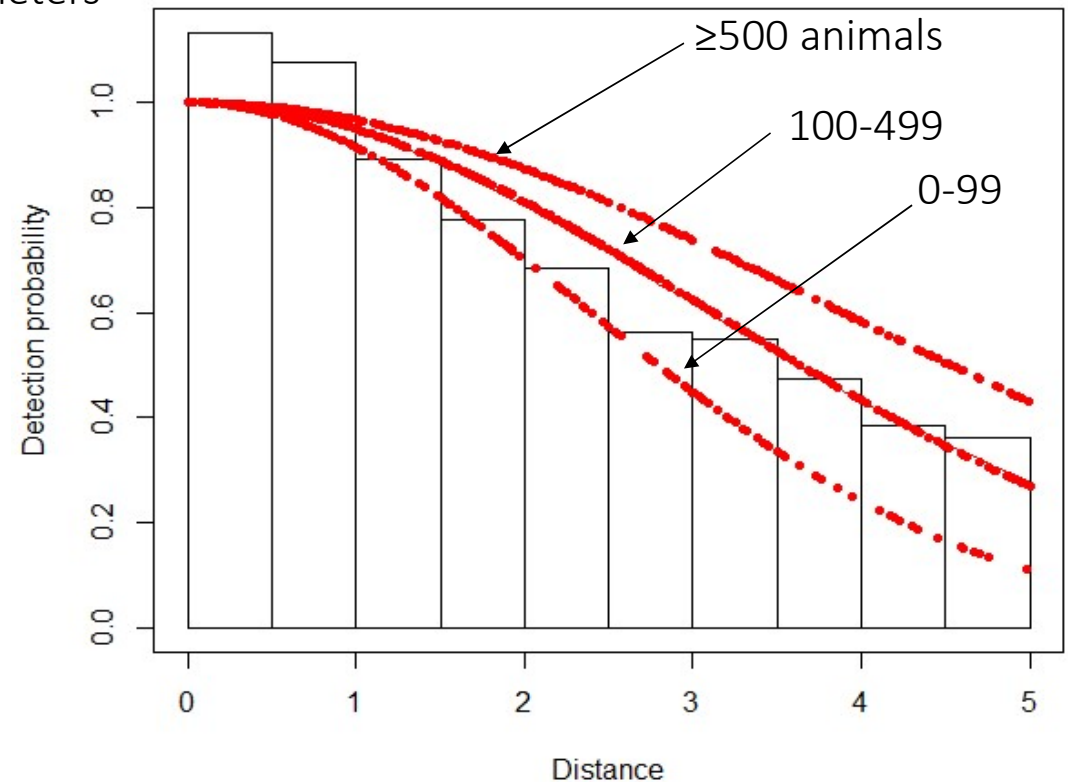
Requires estimating separate detection function parameters for each stratum,

- often not possible due to lack of data

Model as covariates in detection function

Allows a more parsimonious approach:

- can model effect of numerical covariates
- can 'share information' about detection function *scale* parameter between covariate levels



Multiple covariate models

- Recap of CDS models

$g(x)$ = Pr[animal at distance x is detected]

$$= k(x) \left[1 + \sum_{j=1}^m a_j p_j(x_s) \right] / c$$

Key function

j^{th} series adjustment term

Scaling constant to ensure $g(0) = 1$

CDS models continued

Key functions

Shape parameter

Hazard rate $k(x) = 1 - \exp\left[-\left(\frac{x}{\sigma}\right)^{-b}\right]$

Half-normal $k(x) = \exp\left(\frac{-x^2}{2\sigma^2}\right)$

Uniform $k(x) = 1$

Scale parameter

Series adjustments

Cosine $\cos(j\pi x_s)$

Polynomial x_s^j

Hermite poly. $H_j(x_s)$

x_s are scaled distances

Modelling with covariates

$g(x, z) = \text{Pr}[\text{animal at distance } x \text{ and covariates } z \text{ is detected}]$

Assume the covariates affect the *scale* of the key function, not its *shape*. So choose key functions with a scale parameter

Let $\sigma(z) = \exp\left(\beta_0 + \sum_{j=1}^J \beta_j z_j\right)$

e.g. Hazard rate $k(x, z) = 1 - \exp\left[-\left(\frac{x}{\sigma(z)}\right)^{-b}\right]$

Half normal $k(x, z) = \exp\left(\frac{-x^2}{2\sigma(z)^2}\right)$

k is used here to denote the “key” function

Modelling with covariates

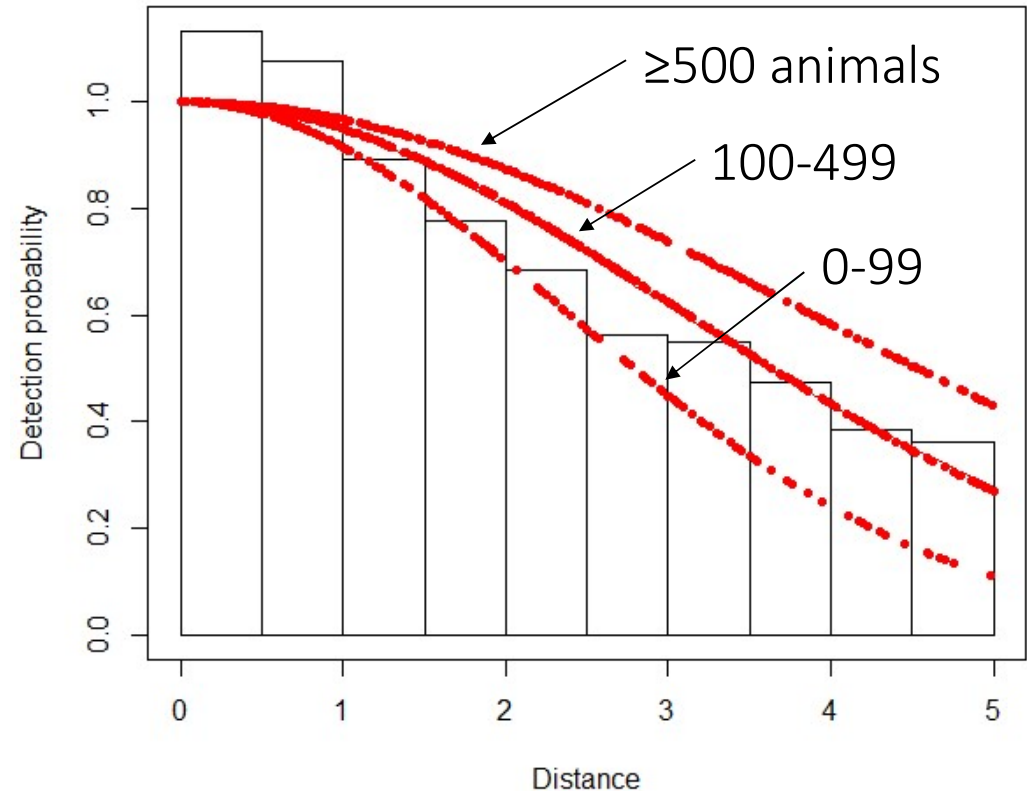
Example: Dolphin tuna vessel data

Model: half-normal, with no adjustments

Covariate: cluster size as factor (3 levels)
with dummy variables, s_{d1} and s_{d2}

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

$$\sigma(s) = \exp(\beta_0 + \beta_1 s_{d1} + \beta_2 s_{d2})$$



Estimating abundance without covariates using Horvitz-Thompson estimator

$$\frac{2wL}{A} = \frac{a}{A} = \Pr(\text{my tree in sampled area})$$

$$\hat{N} = \sum_{i=1}^n \frac{1}{\Pr[\text{animal included}]} = \sum_{i=1}^n \frac{1}{\left[\frac{2wL\hat{P}_a}{A} \right]} = \frac{nA}{2wL\hat{P}_a}$$

Recall that $f(x)$ = pdf of observed x 's $= \frac{g(x)}{\int g(x)dx} = \frac{g(x)}{\mu} = \frac{g(x)}{wP_a}$

Because $g(0)=1$ by assumption, then $f(0) = g(0)/\mu = 1/\mu = 1/wP_a$

Remember:
 x 's are the distances
 and $P_a = \mu/w$

$$\text{So } \hat{N} = \frac{nA}{2wL\hat{P}_a} = \frac{nA}{2L} \cdot \hat{f}(0)$$

Estimating abundance with covariates

$$\hat{N} = \sum_{i=1}^n \frac{1}{Pr[animal\ included]} = \sum_{i=1}^n \frac{1}{\left[\frac{2wL\hat{P}_a(z_i)}{A} \right]} = \frac{A}{2wL} \sum_{i=1}^n \frac{1}{\hat{P}_a(z_i)}$$

$$\text{Now } f(x|\mathbf{z}) = \frac{g(x,\mathbf{z})}{\int g(x,\mathbf{z})dx} = \frac{g(x,\mathbf{z})}{\mu(\mathbf{z})} = \frac{g(x,\mathbf{z})}{wP_a(\mathbf{z})}$$

Because $g(0,\mathbf{z})=1$ by assumption, then $f(0|\mathbf{z}) = g(0,\mathbf{z})/\mu(\mathbf{z}) = 1/\mu(\mathbf{z}) = 1/wP_a(\mathbf{z})$

So

$$\hat{N} = \frac{A}{2wL} \sum_{i=1}^n \frac{1}{\hat{P}_a(0|\mathbf{z}_i)} = \frac{A}{2L} \sum_{i=1}^n \hat{f}(0|\mathbf{z}_i)$$

Note similarity to CDS estimator

MCDS in Distance

In ds command, specify covariates in formula argument

```
ds(data, key, formula)
```

E.g. `ds(data=Dolphin, key="hn", formula=~size.class)`

Covariate type:

- Factor covariates classify the data into distinct classes or levels. Can be numerical or text. One parameter per factor level.
- Non-factor (i.e., continuous) covariates must be numerical (integer or decimal). One parameter per covariate + 1 for the intercept.

Complication: Clustered populations

When cluster size is a covariate:

- Distance recognizes cluster size because column is called `size` (i.e. reserved word)

E.g. `ds (data=Dolphin, key="hn", formula=~size)`

$$\hat{N}_{group} = \sum_{i=1}^n \frac{1}{Pr[group\ i\ included]} \quad \hat{N} = \sum_{i=1}^n \frac{size\ of\ group\ i}{Pr[group\ i\ included]}$$

Estimate of group size is given by $\hat{E}[s] = \frac{\hat{N}}{\hat{N}_{group}}$

MCDS analysis guidelines

Choose covariates that are:

- independent of distance
- not strongly correlated with each other

Specifying the model:

- factor covariates generally harder to fit
- check convergence and monotonicity
- add only one covariate at a time
- where necessary, use starting values and bounds for parameters
- consider reducing the truncation distance, w , if more than 5% of the $P_a(z_i)$ are <0.2 , or if any are less than 0.1