

# Some other approaches (and software) for spatial modelling of distance sampling data

Primary reference:

- Miller, D.L. et al. 2013. Spatial models for distance sampling data: recent developments and future directions. *Methods in Ecology and Evolution*. 4:1001-1010

More references at end...

# General formulation<sup>1</sup>

- Point process model
  - Location of animals are a realization of an underlying process with intensity  $D(x,y)$
  - Then, number of animals in an area  $A$  is Poisson( $\lambda$ ) where

$$\lambda = \int_A D(x, y) dx dy$$

i.e. an inhomogeneous Poisson process (IPP)

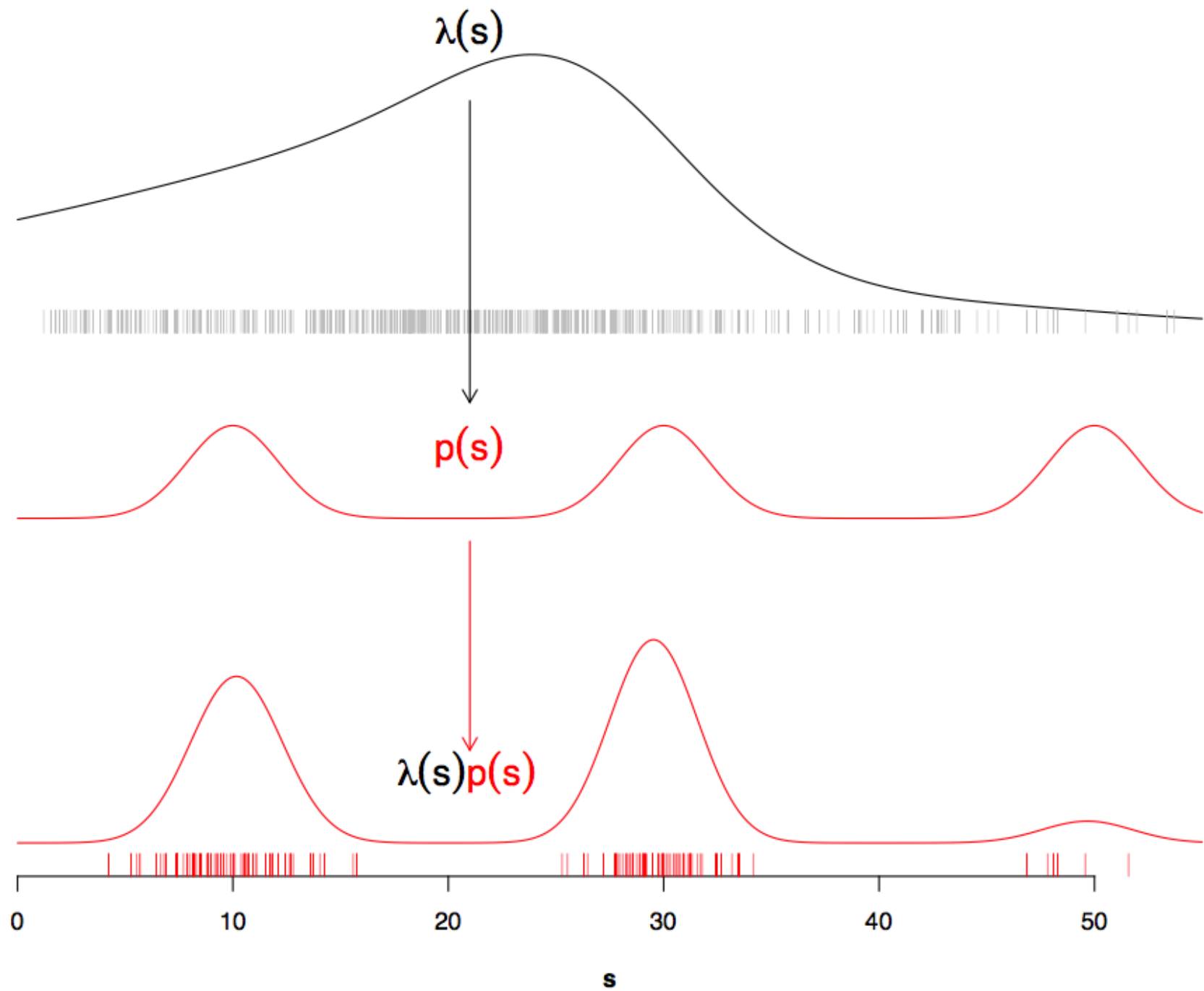
<sup>1</sup>see Hedley (2000) and Johnson et al. (2010)

# Adding uncertain detection

- Let  $g(x,y)$  be the probability of detection of an animal given it is at location  $x,y$
- Detection of animals represents a “thinning” of the IPP, which also yields an IPP, with

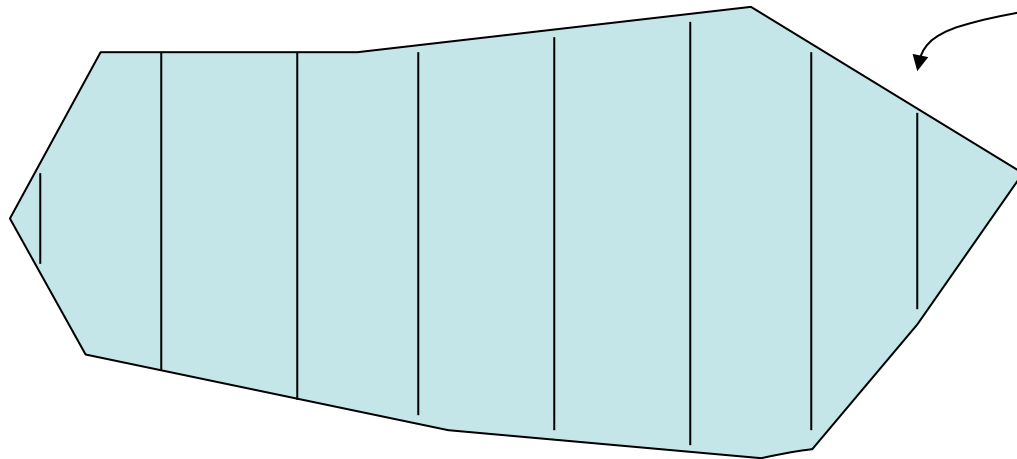
$$\lambda = \int_A D(x, y)g(x, y)dxdy$$

(Can use marked point process framework to deal with animal-level covariates in  $g()$ )



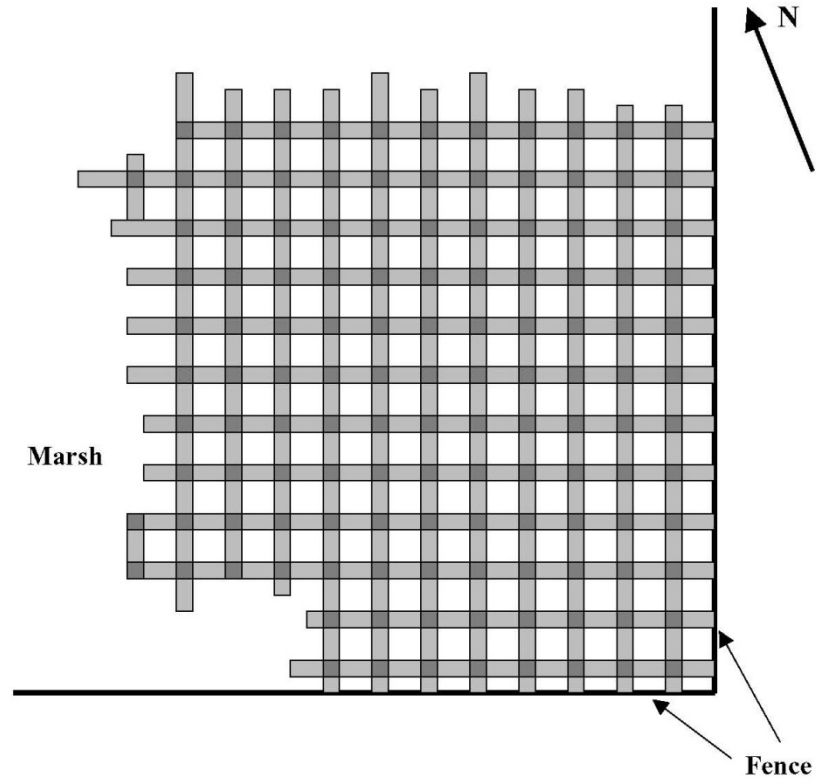
# Full likelihood approach

- Simultaneously estimate parameters of  $D()$  and  $g()$
- Is it worth it? Often little information about  $D()$  contained in the distances (which are used to fit the  $g()$ )



- width of transects small compared with width of study area,
- little information about change in density in the  $x$  direction
- contained in the observed distances from the transect

# Exceptions



- Covered area is a large proportion of study area

# Example Applications

- Hedley (2000)
- Royle et al. (2004) (nicely illustrates lack of information about  $D()$  from the  $g()$ ) – `distsamp` in R (package `unmarked`)  
– see also `gdistsamp` (same package)
- Royle and Dorazio (2008, section 5.5.5)<sup>1</sup> - WinBUGS
- Johnson et al. (2010) – `dspat` in R (DSpat library)
- `inlabru` R package; Yuan et al. (2017) software and training materials at <https://sites.google.com/inlabru.org/inlabru/download>

<sup>1</sup> See also Kéry and Royle 2015. Applied Hierarchical Modelling in Ecology Vol 1.

# Two-stage methods

- First fit  $g()$  using the distances
- Then fit  $D()$  using the locations of observations, and the fitted  $g()$
- Example: method we've been using on this workshop (“Count method” of Hedley (2000), Hedley and Buckland (2004), Hedley et al. (2004))



# Advantages

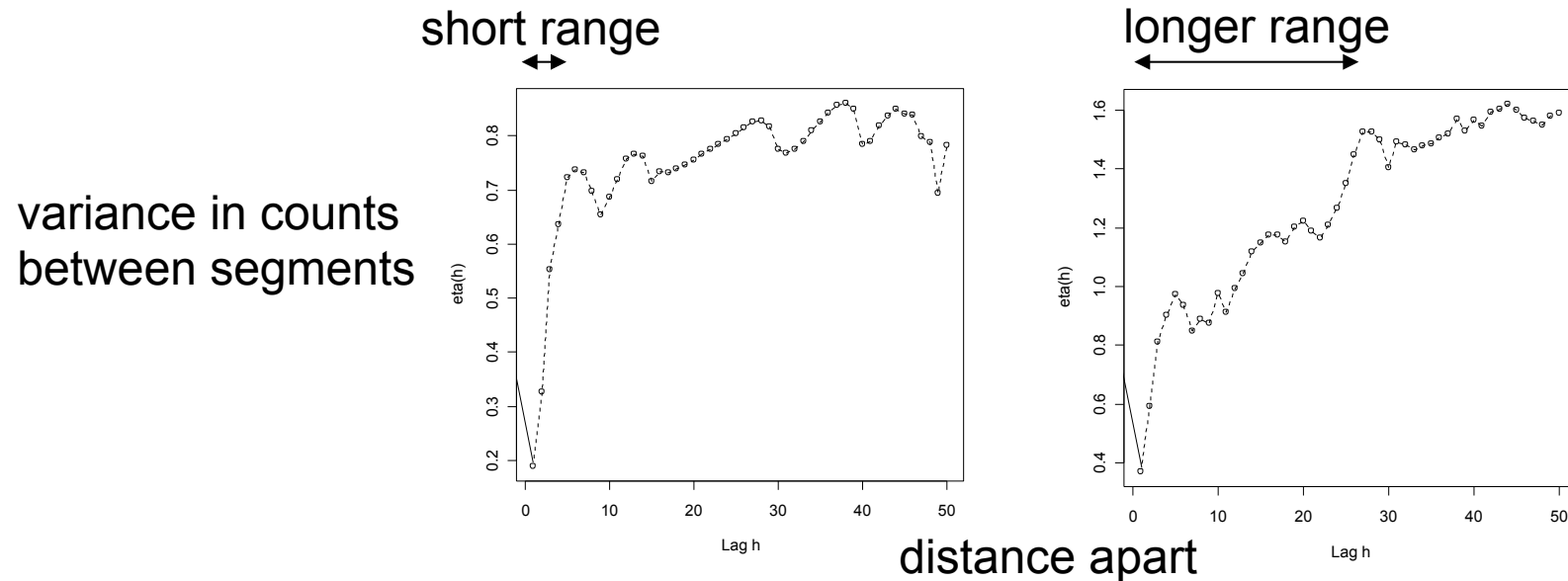
- 2 stage methods in general:
  - Divide and conquer
- Count method:
  - Uses standard, well accepted tools for fitting
  - GLM/GAM is reliable, robust
  - Software available
  - Conceptually simple

# Issues

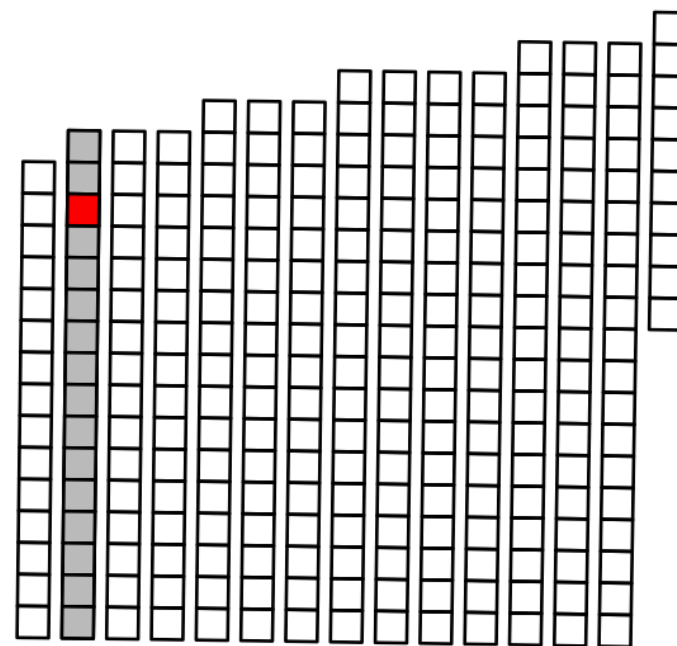
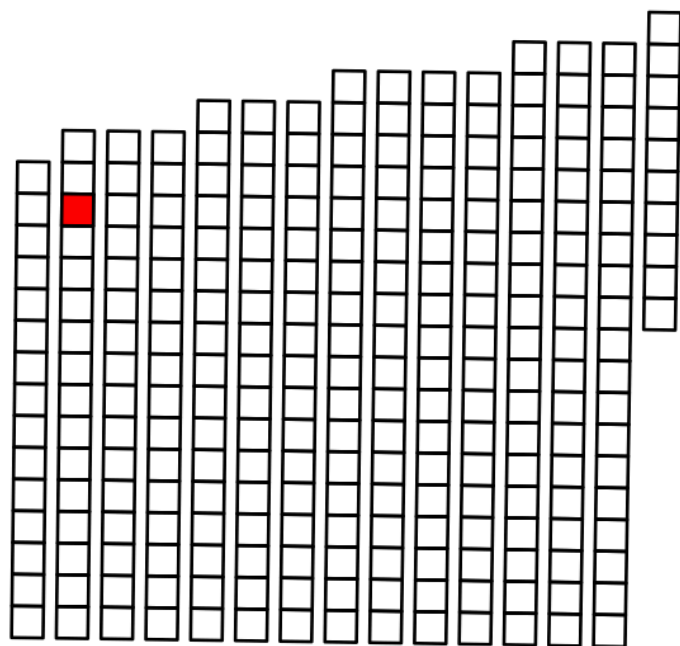
- Residual small-scale spatial clustering
- Extrapolation problems
- Animals in clusters (groups, pods, etc)

# Residual small-scale clustering

- Our models assume large-scale smooth pattern of  $D()$  but there is often residual unexplained variation at a smaller scale



# “Natural” structure



# Solutions

- Better/different models
  - Within GLM/GAM framework (see also next slide):
    - mixed models (GLMM/GAMM) with spatial correlation in the error structure (similar to extensions of kriging)
    - auto-regressive models
    - estimating equations (GEE) with spatial correlation in error structure
  - Extensions/alterations to IPP
    - spatial shot-noise Cox process (Waagepetersen and Schweder 2006)
    - Markov-modulated Poisson process (Skaug 2006)
    - Bayesian tessellations. (Niemi and Fernandez 2010; Kaimi and Fernandez 2008)

# Animals in clusters/groups/pods

- When object detected is a group of animals, can:
  - Model individuals directly, rather than clusters (can use this to indirectly get a density surface of clusters)
  - Model density surface of clusters, and then scale up by mean cluster size
  - Separately model density surface of clusters and density surface of cluster size, then put together (therefore 3 stage modelling – e.g., BWH approach)

# The Future: DenMod

- CREEM + Duke + NOAA + others (US Navy funded)
- Next generation of spatial modelling in Distance
  - New methodology, R packages, practical advice
  - Multiple survey analysis
  - Segment size issues (MMPP etc)
  - Extrapolation
  - Group size uncertainty & more!

# Selected additional references

- Buckland, S.T., D.L. Borchers, A. Johnston, P.A. Henrys and T.A. Marques. 2007. Line transect methods for plant surveys. *Biometrics* 63: 989-998.
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- Hedley, S.L. 2000. Modelling heterogeneity in cetacean surveys. PhD thesis, University of St Andrews. [http://www.creem.st-and.ac.uk/sharon/public\\_html/thesis.pdf](http://www.creem.st-and.ac.uk/sharon/public_html/thesis.pdf)
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- Niemi A. and C. Fernandez. 2010. Bayesian spatial point process modelling of line transect survey data. *Journal of Agricultural, Biological and Environmental Statistics* 15: 327-345.
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*Note: A more complete (but slightly out-of-date) list is contained in Miller et al. (2013).*