

Project

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2022-03-23

Contents

1	Abstract	3
2	Introduction	4
3	Background research	5
3.1	Detection function	6
3.2	Distance Sampling Simulations	6
3.3	Density Surface Modelling	9
4	Simulation extentions	11
5	Modelling - Default Region	13
5.1	Results	15
6	Modeling - North Sea	19
6.1	Non-Stratified Designs	20
6.2	Stratified Designs	26
7	Modeling - Buckland 2015 Example	33
7.1	Results - Random Parallel Line	35
7.2	Results - Systematic Parallel Line	36
7.3	Results - Zigzag Line	36
8	Modeling - Variance estimation tests	38

9 Modeling - North Sea Predictions outside study area:	39
9.1 Results	40
10 Discussion	41
References	42

1 Abstract

2 Introduction

The aim of this report is to detail to extensions made to the *dsims* R package through the inclusion of density surface modelling (dsm) simulations. Analysis will be undertaken to compare the abundance estimates generated through a design based approach, distance sampling, and the model based approach, density surface modelling, to ensure the validity of the new method. By including the model based approach, this will allow researchers the opportunity to run simulations on distance sampling designs while allowing abundance estimations for specific regions to be generated through the density surface model. This ability to predict abundance estimates over very specific regions is a key reason for the inclusion of dsm, alongside the potential for more accurate error estimation than the existing methods used by distance sampling models. A variety of different simulations will be carried out to establish in which scenarios the

3 Background research

Informed from Buckland et al. (2015) One of the key aims in areas of applied ecological research is to determine the abundance of a particular population of interest, such as in a periodic way to monitor its development over time and determine changes, or to evaluate the potential effect of a new factor, such as a human disturbance. The size of the population can determine the importance of any new factors, with a smaller populations more under threat from a given factor compared to an abundant one. One option for determining a populations size is to count every single individual, known as a census, similar to the UK completing a Census of its population every 10 years. However, in the natural world, this is only realistically possible in the simplest instances and therefore a different approach must be used. Researches often use some form of sampling method to conduct a sample of the target population and draw conclusions for the overall population based on this sample.

The two most common methods of sampling for ecological populations are Mark-recapture and distance sampling, where information on the detectability of animals comes from the capture histories of individuals or the distances at which observations are made respectively. Mark and recapture methods, while important, are not the focus of this report and hence will not be further discussed.

Distance sampling was first introduced by Buckland et al. (1993) and includes a variety of techniques such as line and point transect sampling, which can then be used to estimate animal abundance using information on the distances to the individuals or clusters observed. The underpinning theory is that if the probability of animal detection can be estimated based on the sample observed, this can allow for estimates on how many animals were not observed and can therefore correct the abundance estimates to take this information into account.

The two simple techniques of distance sampling are, as mentioned above, line transect sampling and point transect sampling, with subsequent more complex techniques being extensions of these in one aspect or another. Line transect sampling consists of a set of lines being placed over a study area by some predetermined method, for example systematic with regular spacing between each or randomly generated. The observer moves along each line, known as a transect, looking for animals or animal groups, referred to as clusters. These are defined by Buckland et al. (2015) as “a group of animals with a well defined location for the group centre.” For any animal or cluster the observer detects at they make their way along each transect, the observer estimates or calculates the perpendicular distance x of the animal or cluster from the nearest point of the line. For point transect sampling, the transects are a set of points placed over the study area, with different placement methods available as with line transects, however, most common is a systematically spaced grid. At each point, the observer records any individuals or clusters observed from the point, along with the distance r from the point at which the observation was made.

Distance sampling can therefore be thought of as a method of plot sampling, with the additional factor of not every animal on the plots being observed. For this, the plots in line transect sampling are rectangles of dimension $2wl$, where l is the length of a given transect and may change between transects depending on the survey design and area shape, and w is the truncation distance. This is the distance from the line, beyond which observations

are not recorded if the truncation distance is determined prior to the study. However, if the truncation distance is determined during the analysis phase, then this is the distance beyond which the observations are excluded from the analysis. For the plots in point transect sampling, these are circles of area πw^2 with the plot radius w being the truncation distance.

3.1 Detection function

To take into account the fact that not all animals or clusters within each transect are observed, the probability of detecting an animal with a transect must be estimated. This is done by using the distances to the animals observed, x for line transects and r for point transects, to fit a detection function $g(x)$, defined as ‘the probability of detecting an animal that is distance x ($0 \leq x \leq w$) from the line.’ This can be similarly defined as $g(r)$ for point transects where r ($0 \leq r \leq w$) is the distance from the point. The normal technique is to assume that all animals on the point or line are definitely observed, such that $g(0) = 1$. Several detection functions can be defined by the user and a model selection criteria can be used to select the most appropriate for the data. However, all good detection function models share a set of properties, namely, they should have a shoulder, be non-increasing, be model robust, have pooling robustness and be efficient. A shoulder is when the probability of detection remains close to 1 as distance from the transect increases, before decreasing at a later point. Non-increasing suggests that the probability of detection at a far distance should not exceed the probability at any shorter distance from the transect. Model robustness is necessary as the true function is never known and as such, any models must be flexible to allow a range of different profiles to be modelled. Pooling robustness is a property whereby it is assumed that the model will not be affected if any covariates which influence detection are not included in the model, however these can be included through the use of multi-covariate detection functions, part of Multiple-covariate distance sampling (MCDS). Efficiency informs that should all other factors be equal, a preferable model is one which gives high precision, although high precision should not outweigh the need for the other properties to be satisfied.

3.2 Distance Sampling Simulations

All the material in this section is based on Buckland et al. (2015). Prior to the simulation for a particular design being run, a number of objects must first be defined. The first object is the study region, this can either be the default generated by R or user defined from a shapefile. Following this, a spatial distribution or density surface must be defined, from which animal locations can be generated based on the population description. The desired population size can be user defined and set for a series of simulations or be generated based on the spatial distribution supplied by the user. The desired truncation distance must then be defined and based on this an appropriate design can be generated.

The main considerations when constructing the design are the type, either line or point transects and the desired number or length of transects. If line transects are used, the design angle may be altered from its default of 0. A further parameter that must be set is whether plus or minus sampling should be used. Plus sampling is where the transects

extend beyond the survey region into a buffer zone of distance w from the edge, however only observations within the survey region are recorded. With minus sampling, transects end at the edge of the study region and do not extend beyond. Minus sampling will be used for all simulations throughout the remainder of this report. This is because in reality, most studies conduct minus sampling due to the additional cost associated with running a plus sampling survey, in addition to the fact that *dsims* does not support plus sampling simulations at the present time. Based on the design, a set of survey transects can be generated, during which the detection process is simulated. The user can then define a detection function, based on either a half normal ('hn'), hazard rate ('hr') or uniform distribution ('uf') with a defined scale parameter and the desired truncation distance w , examples of which can be seen in Figure 1 below:

Therefore for an animal at distance x from the closest transect the probability of the animal being detected is given by the detection function evaluated at x , provided x is less than or equal to w . The distance data generated during the survey is then analysed to estimate the abundance N of the study area, with options available for several models to be analysed for each set of distance data, with a model selection criteria used to select the best, with AIC being the default.

At this stage, the encounter rate variance estimator can be specified, with a comprehensive summary of the various estimators found within Fewster et al. (2009). Unfortunately, not all of the estimators mentioned within Fewster et al. (2009) are currently compatible with the survey realisations produced by *dsims*, with those not compatible being 'R4,' 'S1,' 'S2' and 'O1.' The default estimator is 'R2' for line transects and 'P3' for point transects and unless otherwise stated, these were used within all simulations conducted in this report. Fewster et al. (2009) does however recommend the 'O2' estimator when using systematic parallel line transects, which will be investigated later in this report.

These operations are then repeated the specified number of times, say R , for each density and design, to obtain a set of simulations of animal distribution and survey design, alongside a corresponding set of estimates \hat{N} of N . Typical values for R are between 100 and 1000. In the case where the design is intrinsically selected by the user, as opposed to randomised, the exact same design will be used for all R simulations

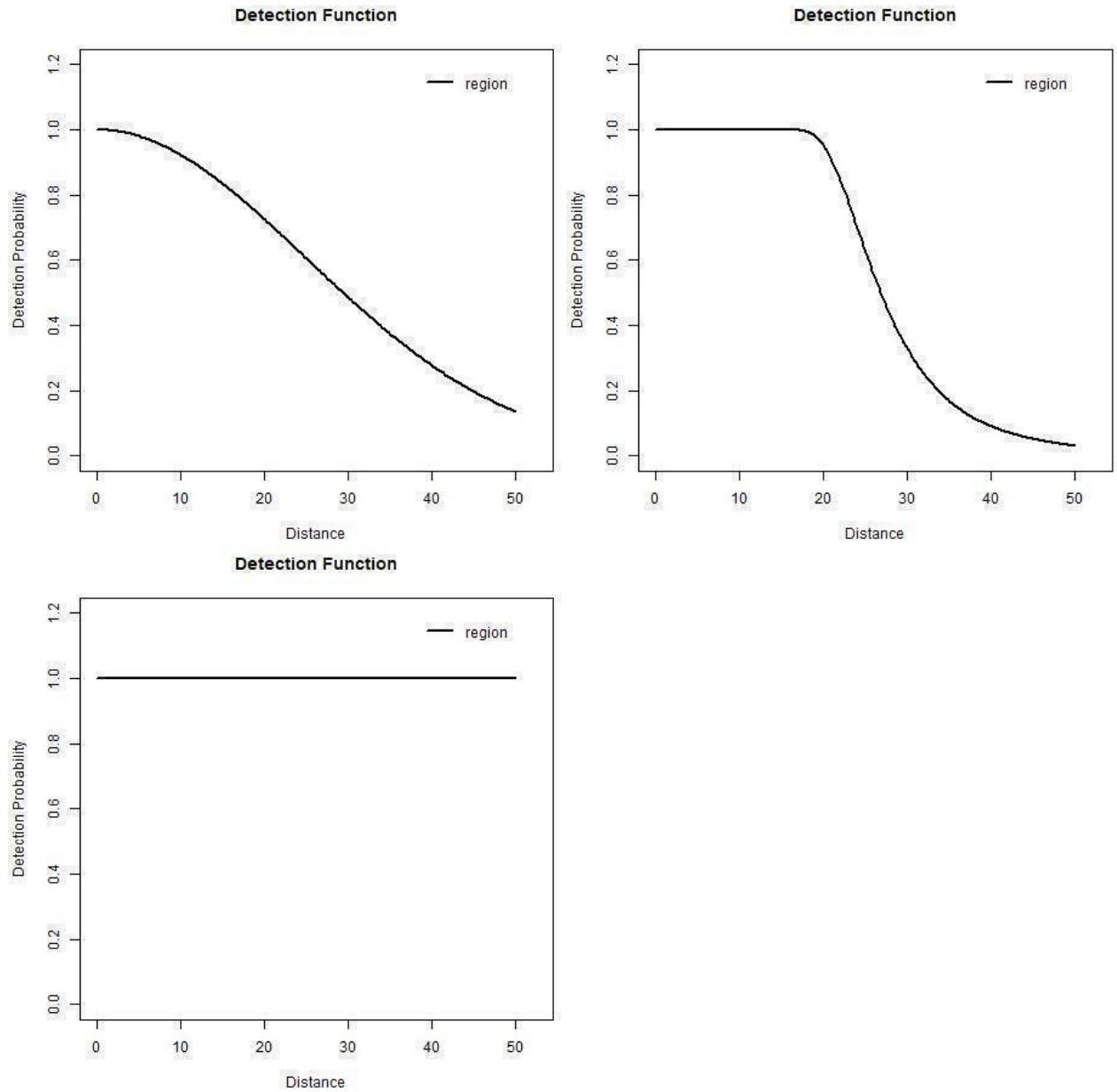


Figure 1: Examples of different detection functions: Left: Half Normal, Middle: Hazard Rate, Right: Uniform

3.3 Density Surface Modelling

This section contains material based on Miller et al. (2013). In order to construct a density surface model, initially the approach must be decided upon. The choice is between using a two stage approach, whereby the detection function is fitted first then subsequently fitting a spatial model, while the one stage approach leads to estimating the detection and spatial parameters simultaneously. Miller et al. (2013) states that ‘Generally, very little information is lost by taking the two stage approach’ as transect width is comparably smaller than that of the study region, therefore, provide the population does not differ spatially within the transect, no information is lost by the two stage approach. This may lead to issues occurring where the density of the species has significant variability at the transect level. However, one drawback of the two stage model is that, to accurately evaluate the model uncertainty, the uncertainty in both the detection function and the spatial models should be suitably combined. For the remainder of this report only the two stage approach will be discussed. Initially, the detection function must be fitted, with the specification being the same as mentioned in the distance sampling section above. Following this, the density surface model can be fitted. To enable this to occur, the data must be separated into segments. This is easily done for point transects with each point being a segment however it is more complicated for line transects. With line transects, they must be split up into J segments of length l_j . It is normally from the segments to be approximately square, with dimensions of $2w \times 2w$ where w is the truncation distance of the design. From here, the segment areas enter the model as part of an offset, to allow for non-constant segment areas. This leads the line transect segments to have an area of $2wl_j$ and the point transect segments with an area of πw^2 . In the model, the counts or abundances are using a generalised additive model (GAM) using the sum of the smoothed covariates.

3.3.1 Response models

The model used when the count per segment is used as the response is:

$$\mathbb{E}(n_j) = \hat{p}_j A_j \exp[\beta_0 + \sum_k f_k(z_{jk})]$$

Where f_k are the smoothed functions of the covariates and β_0 is the intercept term. By multiplying the segment area A_j by the estimated probability of detection p_j this gives the effective area of the segment, acting as an offset to account for different segment areas. Where distance is the only covariate in the detection function, p_j is constant across all segments and therefore $\hat{p}_j = \hat{p} \forall j$. The distribution of n_j can then be modeled using an overdispersed Poisson, Negative binomial or Tweedie distribution.

An alternative to using this is to use abundance estimates for each segment generated by distance sampling as the response. To do this, the response n_j is replaced by an estimator of the abundance in each section, \hat{N}_j where this is defined as:

$$\hat{N}_j = \sum_{r=1}^{R_j} \frac{s_{jr}}{\hat{p}_j}$$

Where R_j is the number of observations in the j th segment and s_{jr} is the size of the r th group observed, with this being 1 if only individuals are observed. As identified by Buckland et al. (2015), this is an Horvitz–Thompson-like estimator of the segment abundance, allowing for covariates to be included through \hat{p}_j . The fitted model then becomes:

$$\mathbb{E}(\hat{N}_j) = A_j \exp[\beta_0 + \sum_k f_k(z_{jk})]$$

Where the model follows the same three distributions as before. The main difference between these models is that the offset is now the physical area of each segment, as opposed to the effective area in the first model for n_j .

To allow for a DSM to predict abundance, a series of prediction cells must be defined. These are not necessarily restricted to just the original study region, allowing for regions outside the study area to be predicted over. Each of the prediction cells must include the same covariates as specified in the dsm, including the area of each cell. Predictions can then be made for the abundance in each cell and by summing these over the whole region, an overall abundance estimate can be obtained. The size of the prediction cells may be specified by the user, however cells ‘smaller than the resolution of the spatially referenced data’ do not have an influence on the abundance estimates produced by dsm.

4 Simulation extentions

Within the *dsims* package Marshall (2021), the current simulation is set-up as explained within the the Distance Sampling Simulations section above. To allow for the inclusion of Density surface modelling within the simulation, a number of changes and additions were required to be made to ensure the compatibility of the two approaches within the simulation. This was a major focus of this project and was where a large portion of time was spent testing to ensure the generality of the code for future use. The initial setup required is the same as with the existing simulation. Namely, the study region, density surface, population and detection function are required. In addition to this, the design in question should also be specified, with any of the choices provided by *dsims* available.

Prior to the simulation beginning, the prediction grid required by the dsm is constructed across the study region, with the resolution of the grid set at half the truncation distance of the design. As Miller et al. (2013) noted, smaller cells sizes could be used but there is a limit since using cells smaller than the spatial data resolution will not have an effect on the abundance estimates provided by dsm, and there is also the computational increase resulting from smaller cell sizes. This can be specified prior to the simulation as it is only dependant on the study region and will not change between iterations of the simulation. Existing code to construct this prediction grid can be found in Souchay (2020) and this was used in early testing and simulations. However, it was noted that some of the R packages used in this code are due to be retired at the end of 2023, namely the *rgeos* package Bivand and Rundel (2021) . Therefore, the decision was made to rewrite this code using the far more widely used Simple Feature (sf) package Pebesma (2022). The prediction grid is currently setup to create the grid over the entire study region, to allow for a comparison with the distance sampling approach. However, this is not a restriction and any prediction grid could be specified, including areas outside of the study region. This would allow for simulations to predict the abundance on areas not specifically studied in the survey, which the distance sampling approach cannot do without increasing the size of the study region itself. This offers a distinct advantage for dsm over the distance sampling approach, however it may be possible to generate unrealistic abundance estimates if the gradient of the density surface is steep near the boundary. This effect will be tested later in this report.

The simulation loop then begin, running for the number of iterations specified within the simulation object. For each iteration, a new survey constructed. From this, the observation data and segmented data is extracted and linked. To do this, a function *generate.dsm.data* was written, taking the study region, survey and type of transects as inputs. This function first extracts the observation data from the survey. Subsequently, the transects are split into the segments required by the dsm approach, using a function *to_segments* which was written for this explicit purpose, taking the same inputs as *generate.dsm.data*.

For Point transect designs, each point is treated as its own segment however, in the case of line transect designs, the lines are split to allow them to be modelled as points. Each line is split into segments of approximate length $2w$ with w being the truncation distance, as suggested by Miller et al. (2013) and each segment assigned its own unique sample label. Subsequently, the length of each segment is recorded as the segments effort value and

the centre of the segment as its location. Polygons of each segment are then created using *st_buffer*, with w being used as the distance. This leads to squares of approximately $2w * 2w$ for line transects and circles of radius w for points. These allow the area of each segment to be calculated, a requirement for the dsm model. This is calculated using *st_area*, on the intersection between the polygons and the outer boundary of the study region. This ensures only areas within the study region are counted towards segment area and internal strata boundary's do not split segments. Failure to do this results in the areas of some segments being larger than they are in the survey, and as a result the dsm abundance estimate is smaller, since the prediction grid is only over the survey area.

Once the segment areas have been calculated, the segments can be linked to the observation data by allocating each observation to the nearest segment and giving this the respective segments sample label in the observation data, overwriting the original allocation. Additionally, the coordinate reference system of the observation data is set as that of the segments to ensure consistency when using different reference systems to the default.

Based on this data, both a distance sampling model and density surface model are constructed, with the dsm modeling the counts against the smooth of spatial locations using a tweedie error distribution. The formulas for both could be changed to include environmental or other covariates such as strata, allowing for different detection functions to be fit to each strata. In the smoothed term, the degrees of freedom is restricted to the total number of transects. The limit for this is the number of segments in the model, which in the case of point transects is the total number of transects. While this could be far larger for line transects, this would increase the computational requirements beyond a reasonable level and not offer a significant improvement for this increase. The abundance estimates are extracted from both models and stored alongside other values from each including the standard errors and confidence intervals for each model.

5 Modelling - Default Region

The simulation was initially tested using the default region generated by *dsims* Marshall (2021) with a truncation distance of 60. Both point and line transect designs were run with an aim of 25 and 12 samplers for the respective designs. A basic test density was then constructed for the region with high and low spots as seen below in Figure 2 with relatively gently gradients.

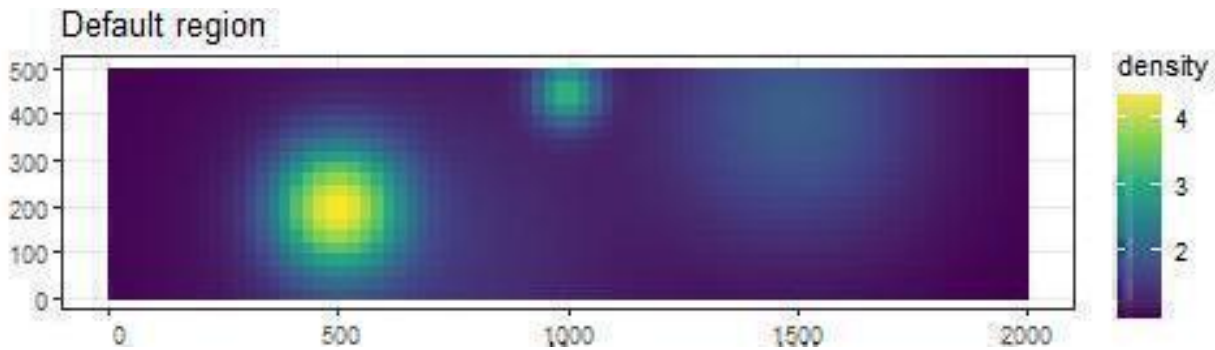


Figure 2: Density surface used for the Default region

A population description was then constructed based on this density surface with a true population of 1000. A detection function was then defined as a half normal with scale parameter of 30 for both designs, producing the detection function seen in Figure 3:

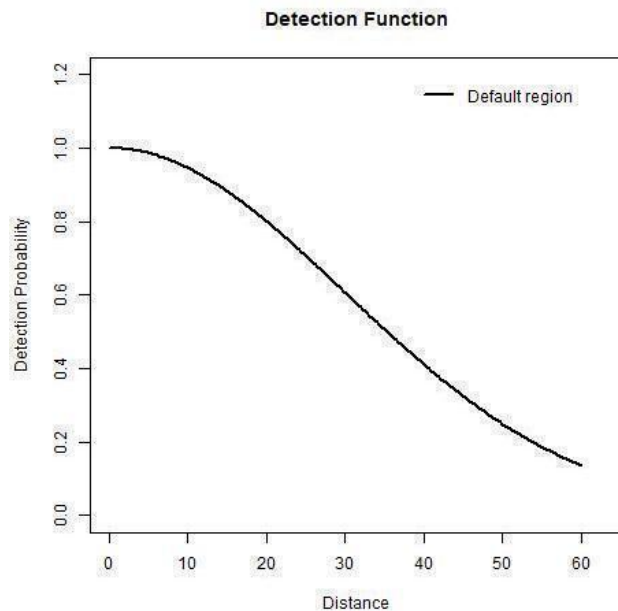


Figure 3: Detection function for the default region, a half normal with scale parameter of 30

An example survey for each of the designs is displayed below in Figure 4.

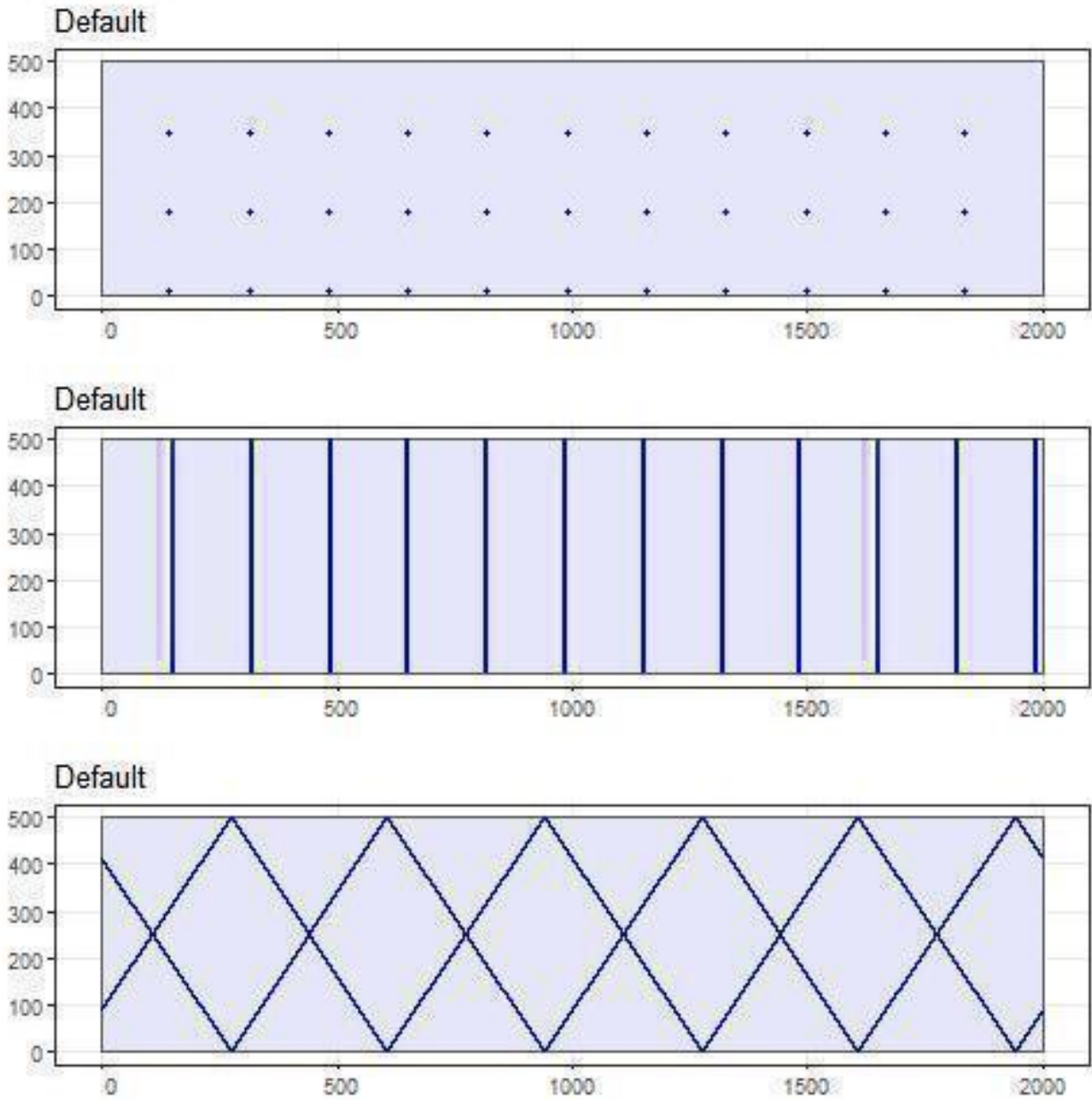


Figure 4: Example Surveys for the default region. Top: Point Transect design, Middle: Parallel line design, Bottom: Zigzag line design

5.1 Results

Having completed 1000 simulations for both the distance sampling and density surface models with each design, we can now examine and compare these to give us an insight into the circumstances under which a particular model is better of worse than the other.

5.1.1 Default Region Point design

For the initial default region with the point transect design, the histograms of both the distance sampling and dsm abundance estimates are displayed below in Figure 5:

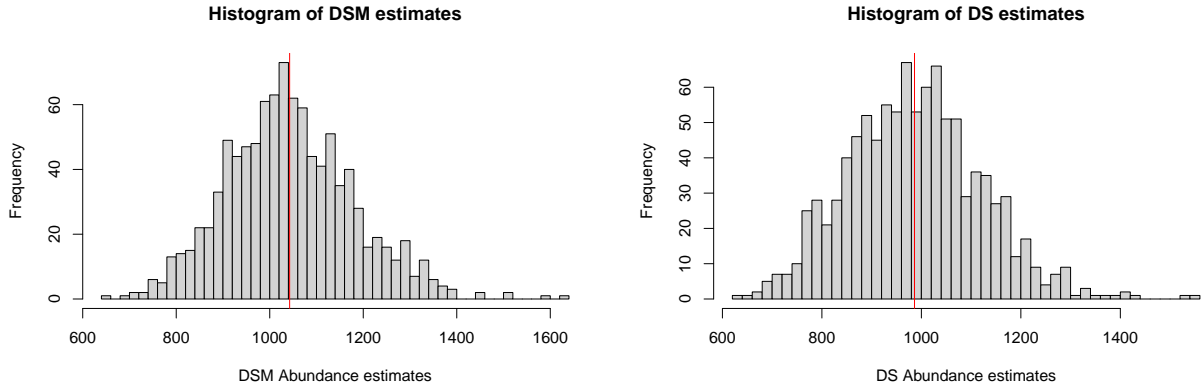


Figure 5: Histograms of Point Design estimates for Default region

These plots show somewhat similar data since both estimates are generated by the same data set. If we now compare the means of the two approaches, the mean of DSM estimates was 1042.55 and the mean of DS estimates was 986.21. It can be seen that the mean of the DSM estimates appears a good distance from the true population of 1000 while the distance sampling method is closer.

Table 1: Default region results - Point

Statistic	Point Design	
	DSM results	DS results
Mean	1050.3465198	989.0635222
Bias	5.0346520	-1.0936478
Mean Std error of estimates	160.7477256	152.7249734
Std Dev of estimates	167.6863061	156.2742970
Mean CV	0.1545738	0.1556531
Confidence Interval Coverage	0.9210000	0.9480000

Table 1 above provides statistics which allow us to compare the variability of the models as well as their ability to capture truth within their confidence intervals. We see in this

case that the DSM method has a slightly larger positive bias than that of the DS method, indicating the DS method produced more accurate results in this case. This trend continues with the Mean Standard errors and estimate standard deviations being similar but again the DS method producing a smaller error. The DSM does produce a smaller Coefficient of variation, however the difference is marginal. Next, we can evaluate how many times the true abundance was within the 95% CI for every model computed. The results show that truth was captured by the CI with a probability of above 0.9 for both models, with the DS again performing better at 0.948 compared with 0.921 for the DSM method.

5.1.2 Default region parallel Line design

Now examining the results of the line transect design, on the same density surface, we see the histograms of the two estimates below in Figure 6:

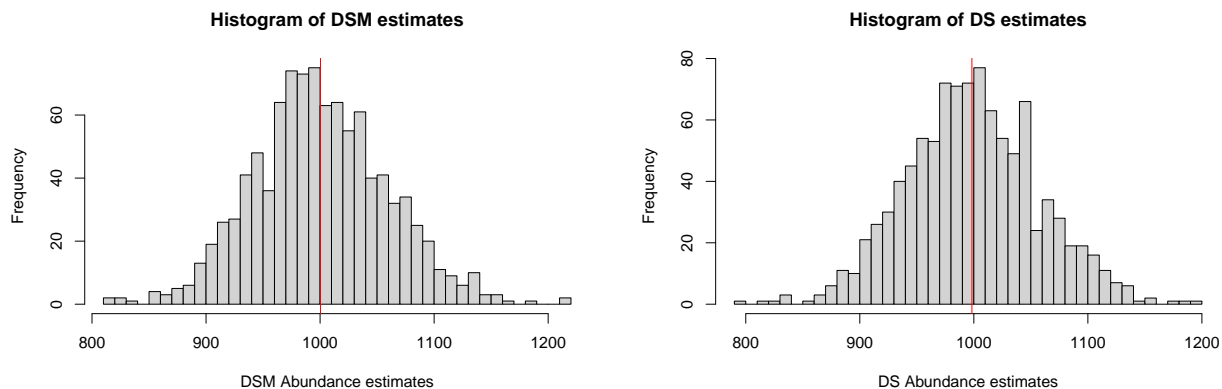


Figure 6: Histograms of Line Design estimates for Default region

These plots are very similar to their point transect counterparts, with the mean for each signified by the red line appearing very close to truth. Investigating this further, we find the mean of DSM estimates to be 1000.35 and the mean of DS estimates to be 998.31. These estimates are both very close to the true value, possibly as a result a large portion of the survey area being covered by the transects.

From table 2 above, it can be observed that in this case, the DSM method overall performed better than the DS method, having a slightly smaller bias as well as a dramatically smaller mean standard error and mean coefficient of variation. However, for the DS method, the standard deviation of the estimates is markedly less than the mean standard error, indicating this method provides better precision than the standard errors suggest. This is also the case with the DSM method however the difference is far smaller. The DS method also has a higher probability of truth being contained within its confidence intervals, at 0.999 compared to 0.972.

Table 2: Default region results - Line

Statistic	Parallel Line Design	
	DSM results	DS results
Mean	1000.3464022	998.3144253
Bias	0.0346402	-0.1685575
Mean Std error of estimates	68.9012076	106.1785893
Std Dev of estimates	58.8779025	57.5569613
Mean CV	0.0689178	0.1064057
Confidence Interval Coverage	0.9720000	0.9990000

5.1.3 Default region Zigzag Line design

Now examining the results of the zigzag line transect design, on the same density surface, we see the histograms of the two estimates below in Figure 7 :

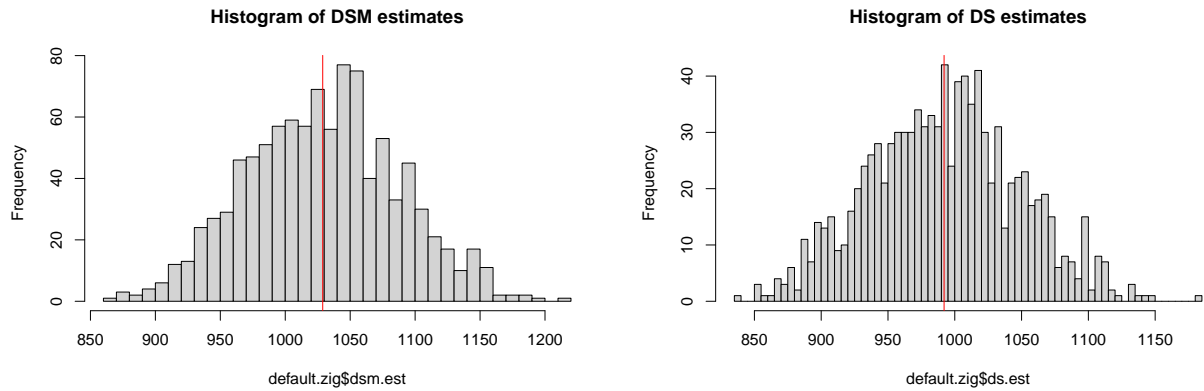


Figure 7: Histograms of Zigzag Design estimates for Default region

These plots differ slightly to their point and parallel line counterparts, with the mean appearing further away from truth than previously, however there is a known error in the code that may cause this and is being investigated. Investigating this further, we find the means of DSM estimates to be 1028.85 and the mean of DS estimates to be 991.99. These estimates are both very close to the true value, possibly as a result a large portion of the survey area being covered by the transects.

Table 3: Default region results - Zigzag

Statistic	Zigzag Line Design	
	DSM results	DS results
Mean	1028.8483718	991.9923373
Bias	2.8848372	-0.8007663
Mean Std error of estimates	70.4895927	90.2284558
Std Dev of estimates	58.3785323	55.9582394
Mean CV	0.0685151	0.0907944
Confidence Interval Coverage	0.9680000	0.9970000

From Table 3, despite the known issue, the DSM model performs relatively well, having a reasonably small bias. The mean standard error is in fact lower than that of the DS model, indicating higher precision on average across the models, with the standard deviation of the estimates being lower in both cases, suggesting greater precision for both modes than the standard errors imply. The mean coefficient of variation is slightly lower for the DSM model however the confidence interval coverage is higher with the DS model, indicating truth has a higher probability of being captured within the models confidence interval.

6 Modeling - North Sea

Having gone through the process and results for the default region produced by *dsims*, a more complex example was created to further test the capabilities of the simulations with a real world example. This region will be in the area of the North sea off the east coast of the UK. As this would likely be a shipborne or airborne study, point transects are not realistic in this scenario, however they will be included for completeness. To assess the performance of both the distance sampling and density surface modelling approaches, point and line transect designs will be examined. These will be two point transect designs and four line transect designs, with one of each type using a stratified design with the region split in two. The standard designs will be compared first before examining the stratified designs. All designs used a truncation distance of 10 with the number of transects varying between the point and line transect designs. This difference is ensure the covered area of each study is similar to allow the results to be compared, as well as ensure sufficient observations to fit the detection function can be obtained. The density maps for stratified and non-stratified will be different to justify the use of different strata and examine the models ability to pick this up. These density surfaces can be seen in Figure 8 below.

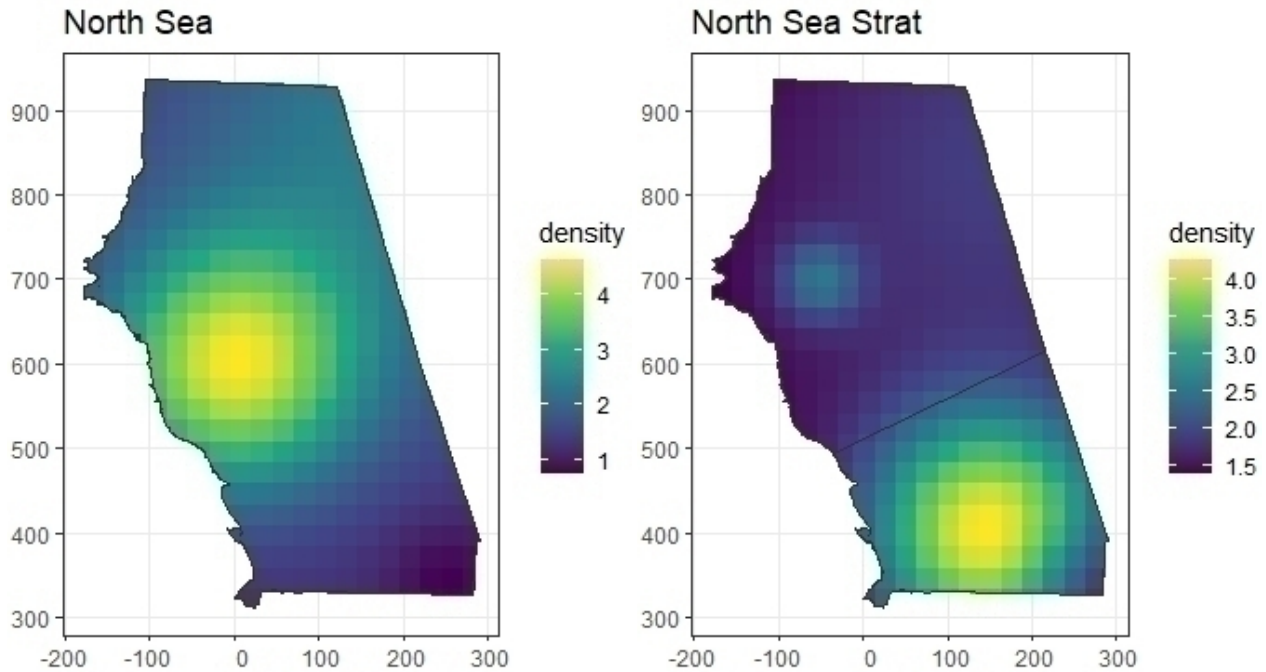


Figure 8: Density surfaces for the basic and stratified North Sea regions

As before, the detection function was kept identical between each design for both stratified and non-stratified. In this case it was a Half Normal detection function with a scale parameter of 5, which can be seen in Figure 9 below:

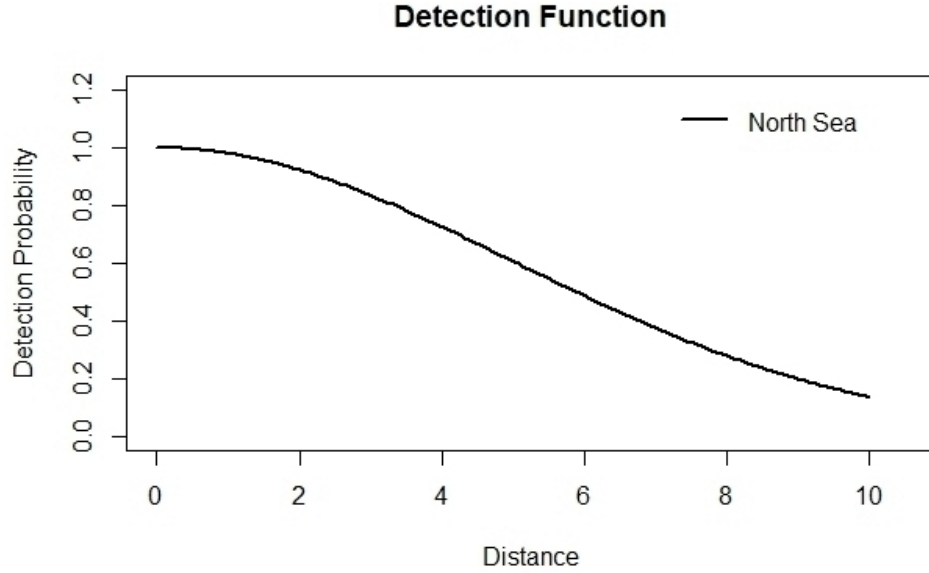


Figure 9: Plot of the detection function used in both the basic and stratified North Sea regions: A half Normal with scale parameter 5 and truncation 10

6.1 Non-Stratified Designs

The point transect designs aimed for 70 samplers and the line transects for 25 samplers. The standard line designs consisted of a systematic parallel line design with transects perpendicular to the coast and a zigzag line design originating in the North of the region. An example of each design can be seen in Figure 10 below:

The simulation was run 5000 times with the dsm model using a tweedie error distribution and the only covariates being spatial coordinates.

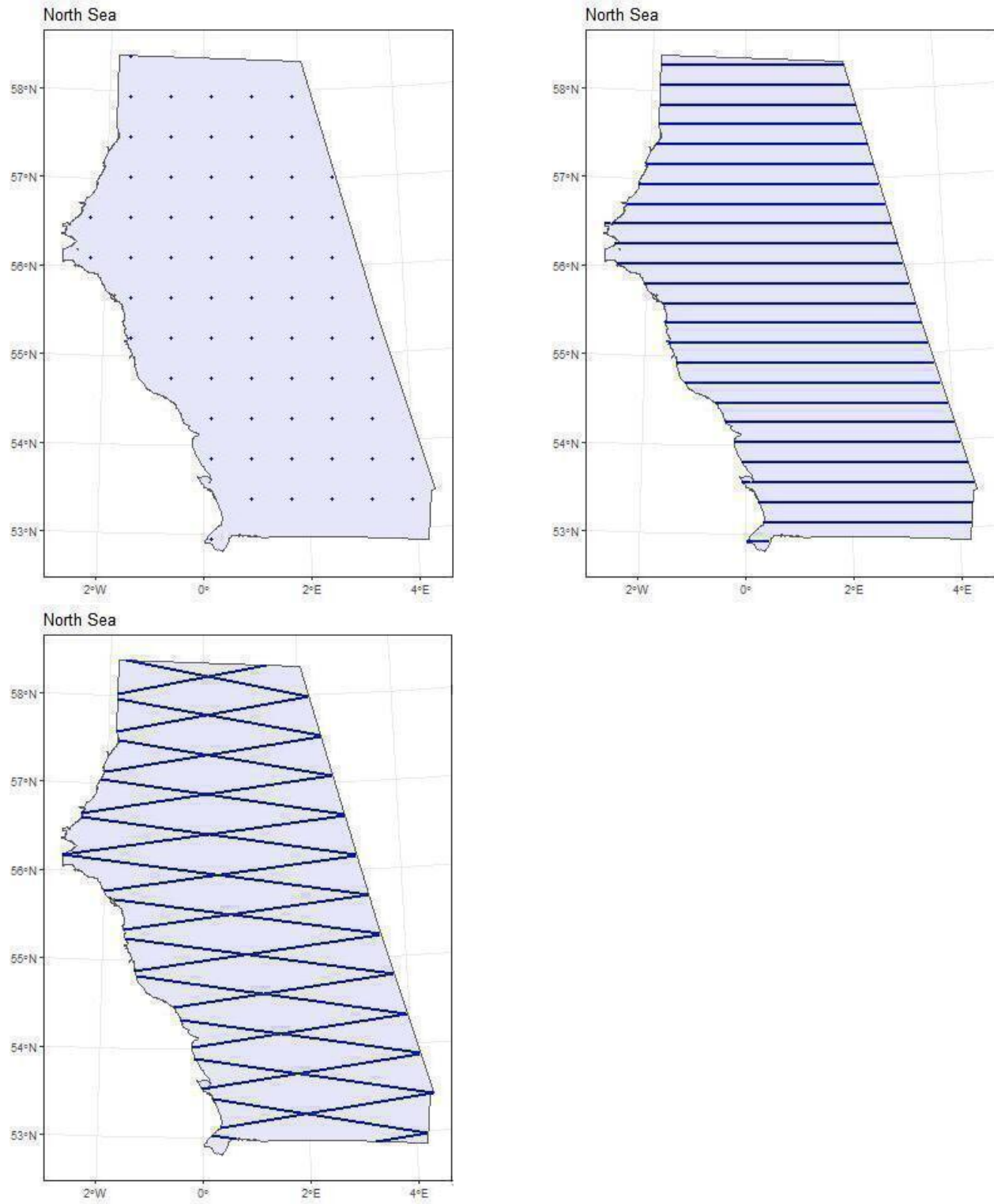


Figure 10: Examples of surveys for the North Sea region. Top Left: Point Transect design, Top Right: Parallel line design, Bottom Left: Zigzag line design

6.1.1 Non Stratified Results - Point Design

For the point transect design, the histograms of the abundance estimates from each simulation run are displayed below in Figure 11:

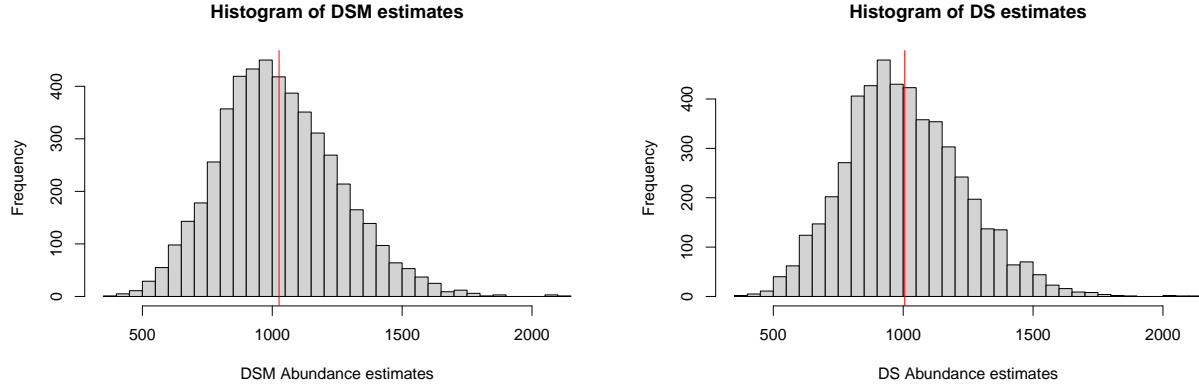


Figure 11: Histograms of the abundance estimates for the North Sea region using a point transect design

These plots suggest both methods are relatively good at estimating the true abundance of 1000, with both methods appearing to overestimate, with the DSM method overestimating slightly more than the DS method. There also appears to be a slight right skewness to both plots which will be looked at analytically. Investigating the means further, we find the mean of DSM estimates to be 1026.21 and the mean of DS estimates to be 1005.97. These estimates are both close to the true abundance, with the overestimation present as mentioned above. Overall, it was found that the estimates produced by DSM were greater than those produced by DS from the same survey data 92.8 % of the time, indicating it is highly likely DSM will produce an estimate greater than that of DS. A Wilcoxon test was performed on both sets of estimates with the alternative being that DSM was greater than DS.

This returned a p-values of 0 indicating at any significance level, the null hypothesis of the estimates being zero is rejected in favour of the alternate, that the DSM estimates are greater than those of DS. If we now compare the other variables extracted from the models in the below, we can examine the accuracy and variability of each method:

From the results table above, it can be observed that in this case, the DS method overall performed better than the DSM method, having a smaller bias as well as higher confidence interval converge, despite having a smaller Mean Std error. Additionally, the standard deviation of the estimates is slightly less for the DS method, however both methods do a relatively good job at estimating this. Additionally, we observe from the skewness statistics that both methods returned a positive statistic indicating the right-skewed as identified above, which suggests the right tail is longer and this is supported by some of the estimates being over 2000, with the maximums for DSM and DS being 2113.2 and 2112.52 respectively.

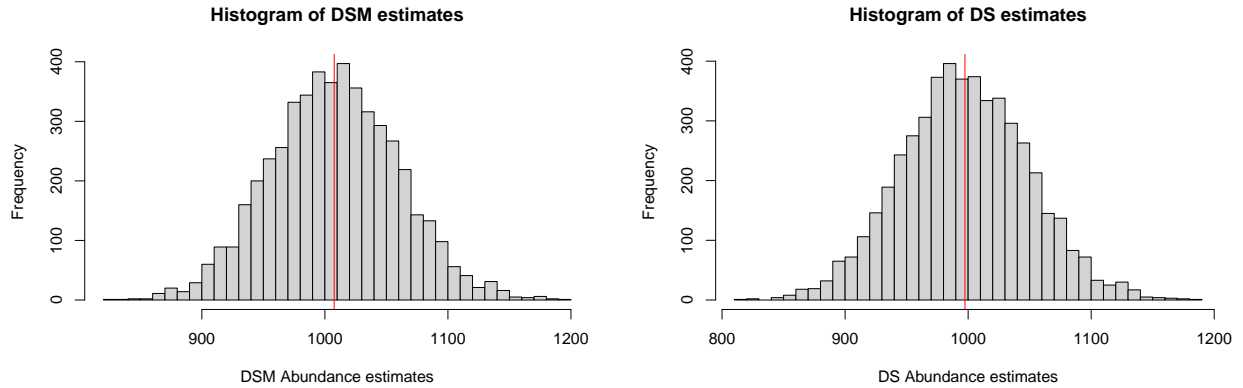
Table 4: North Sea Non-Stratified results - Point

Statistic	Point Design	
	DSM results	DS results
Mean	1026.2081430	1005.9650684
Bias	2.6208143	0.5965068
Mean Std error of estimates	234.5771639	234.0227893
Std Dev of estimates	230.8981167	226.7679405
Mean CV	0.2321996	0.2362012
Confidence Interval Coverage	0.9484000	0.9582000
Estimate Skewness	0.4034455	0.4097919
Estimate Kurtosis	3.2729606	3.3024713

The kurtosis figures for both methods are greater than 3, indicating we would expect more frequent outliers than a normal distribution. While the Mean CV for the DSM method is lower, the difference is marginal and does not out-way the bias or variance issues of this method. Overall this clearly seems to be a case where the DS method performs better than the DSM estimation method.

6.1.2 Non Stratified Results - Parallel Line Design

Now examining the results of the line transect design, on the same density surface, we see the histograms of the two estimates below:



These plots are very similar to their point transect counterparts, with the mean for each signified by the red line appearing very close to truth. However, there appears to be less skewness for these than is present with the point transect results. Investigating this further, we find the mean of DSM estimates to be 1007.57 and the mean of DS estimates to be 997.41. These estimates are very close to the true Overall, it was found that the estimates produced by DSM were greater than those produced by DS from the same survey data 100 % of the time, indicating it is highly likely DSM will produce an estimate greater than that of DS. A Wilcoxon test was performed on both sets of estimates with the alternative being that DSM

was greater than DS.

This returned a p-values of 0 indicating at any significance level, the null hypothesis of the estimates being zero is rejected in favour of the alternate, that the DSM estimates are greater than those of DS. Examining the other statistics extracted from the simulation.

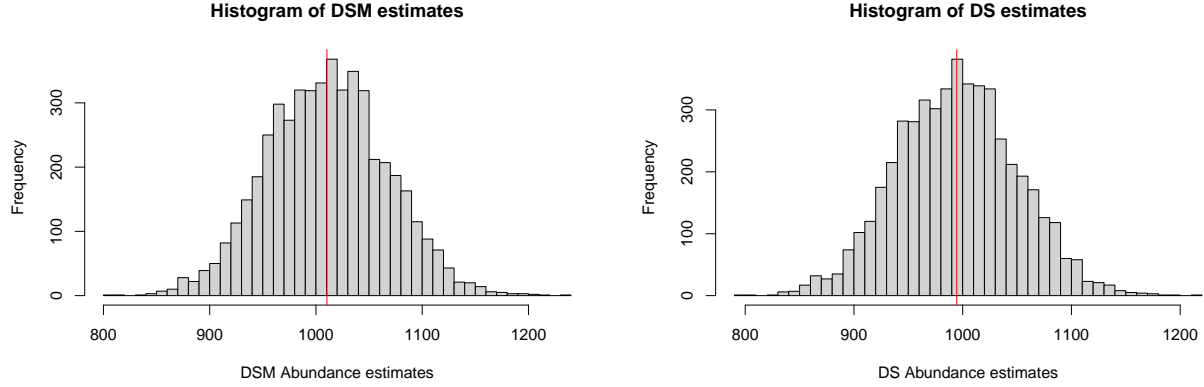
Table 5: North Sea Non-Stratified results - Line

Statistic	Parallel Line Design	
	DSM results	DS results
Mean	1007.5691041	997.4080181
Bias	0.7569104	-0.2591982
Mean Std error of estimates	61.0407009	86.7850841
Std Dev of estimates	51.8726020	51.7437163
Mean CV	0.0606351	0.0870698
Confidence Interval Coverage	0.9748000	0.9996000
Estimate Skewness	0.0607668	0.0591685
Estimate Kurtosis	3.0058358	2.9856027

From the results table above, it can be seen that in this case, the performance of both models was similar and each performed well in different areas compared to the each other. The mean estimate was again a slight overestimation and as a result, bias was slightly higher for DSM, however this difference was comparatively small. The Mean Std errors were lower for DSM and far closer to the Std Dev of the estimates, highlighting the better error estimation of DSM. However the Std Dev of the estimates was slightly smaller for the DS approach. The DS method also has a higher probability of truth being contained within its confidence intervals, at 0.9996 compared to 0.9748, however this difference is likely due to the higher Std errors from the DS method wideing the confidence interval. Despite this, both methods achieved truth in their confidence intervals over the 95% significance level. The skewness scores for both are very similar and suggest again a slight right skew however this is very small. The kurtosis scores are very close to 3, suggesting the kurtosis is very similar to that of a normal distribution. In the Jarque-Bera test for normality, DSM and DS estimates return p-values of 0.2139247 and 0.2275685 respectively. These indicate we can not reject the null hypothesis that these estimates are normally distributed. Overall, while the mean estimate appears in favour of the DS method, the DSM approach can be said to have performed better in this simulation, due to the small bias, lower Mean Std error and coefficients of variation.

6.1.3 Non Stratified Results - Zigzag Line Design

Now examining the results of the zigzag line design, on the same density surface, we see the histograms of the two estimates below:



These plots are very similar to their point transect counterparts, with the mean for each signified by the red line appearing very close to truth. However, there appears to be less skewness for these than is present with the point transect results. Investigating this further, we find the mean of DSM estimates to be 1010.34 and the mean of DS estimates to be 994.51. These estimates are very close to the true Overall, it was found that the estimates produced by DSM were greater than those produced by DS from the same survey data 99.96 % of the time, indicating it is highly likely DSM will produce an estimate greater than that of DS. A Wilcoxon test was performed on both sets of estimates with the alternative being that DSM was greater than DS.

This returned a p-values of 0 indicating at any significance level, the null hypothesis of the estimates being zero is rejected in favour of the alternate, that the DSM estimates are greater than those of DS. Examining the other statistics extracted from the simulation.

Table 6: North Sea Non-Stratified results - Zigzag

Statistic	Parallel Line Design	
	DSM results	DS results
Mean	1010.3404728	994.5099646
Bias	1.0340473	-0.5490035
Mean Std error of estimates	61.1878286	81.8307222
Std Dev of estimates	55.9827256	55.3082445
Mean CV	0.0606281	0.0823353
Confidence Interval Coverage	0.9660000	0.9950000
Estimate Skewness	0.0640797	0.0614198
Estimate Kurtosis	2.9645959	2.9557928

From the results table above, it can be seen that in this case, the performance of both models was similar and each performed well in different areas compared to the each other. The mean estimate was again a slight overestimation and as a result, bias was slightly higher for DSM, however this difference was comparatively small. The Mean Std errors were lower for DSM and far closer to the Std Dev of the estimates, highlighting the better error estimation of DSM. However the Std Dev of the estimates was slightly smaller for the DS

approach. The DS method also has a higher probability of truth being contained within its confidence intervals, at 0.995 compared to 0.966, however this difference is likely due to the higher Std errors from the DS method wideing the confidence interval. Despite this, both methods achieved truth in their confidence intervals over the 95% significance level. The skewness scores for both are very similar and suggest again a slight right skew however this is very small. The kurtosis scores are very close to 3, suggesting the kurtosis is very similar to that of a normal distribution. In the Jarque-Bera test for normality, DSM and DS estimates return p-values of 0.1585816 and 0.1694159 respectively. These indicate we can not reject the null hypothesis that these estimates are normally distributed. Overall, while the mean estimate appears in favour of the DS method, the DSM approach can be said to have performed better in this simulation, due to the small bias, lower Mean Std error and coefficients of variation.

6.2 Stratified Designs

For the stratified designs, it was decided to split the region into two strata, a large northern strata ‘North’ and a smaller southern strata ‘South’ to test how the simulation and both methods cope with a stratified design, alongside ensuring th . The point transect designs aimed for 60 samplers, with 30 in each strata, and the line transects for 25 samplers with 10 in the North strata and 15 in the South strata. The standard line designs consisted of a systematic parallel line design with transects perpendicular to the coast for both the North and South Stratum. The zigzag line design selected has the transects in the North strata originating in the North of the Strata, with a design angle of 90° , while in the South Strata, transects originate on the Western boundary with a design angle of 0° . An example of each design, including the point design, can be seen in Figure 12 below:

The simulation was run 5000 times with the dsm model using a tweedie error distribution and the only covariates being spatial coordinates.

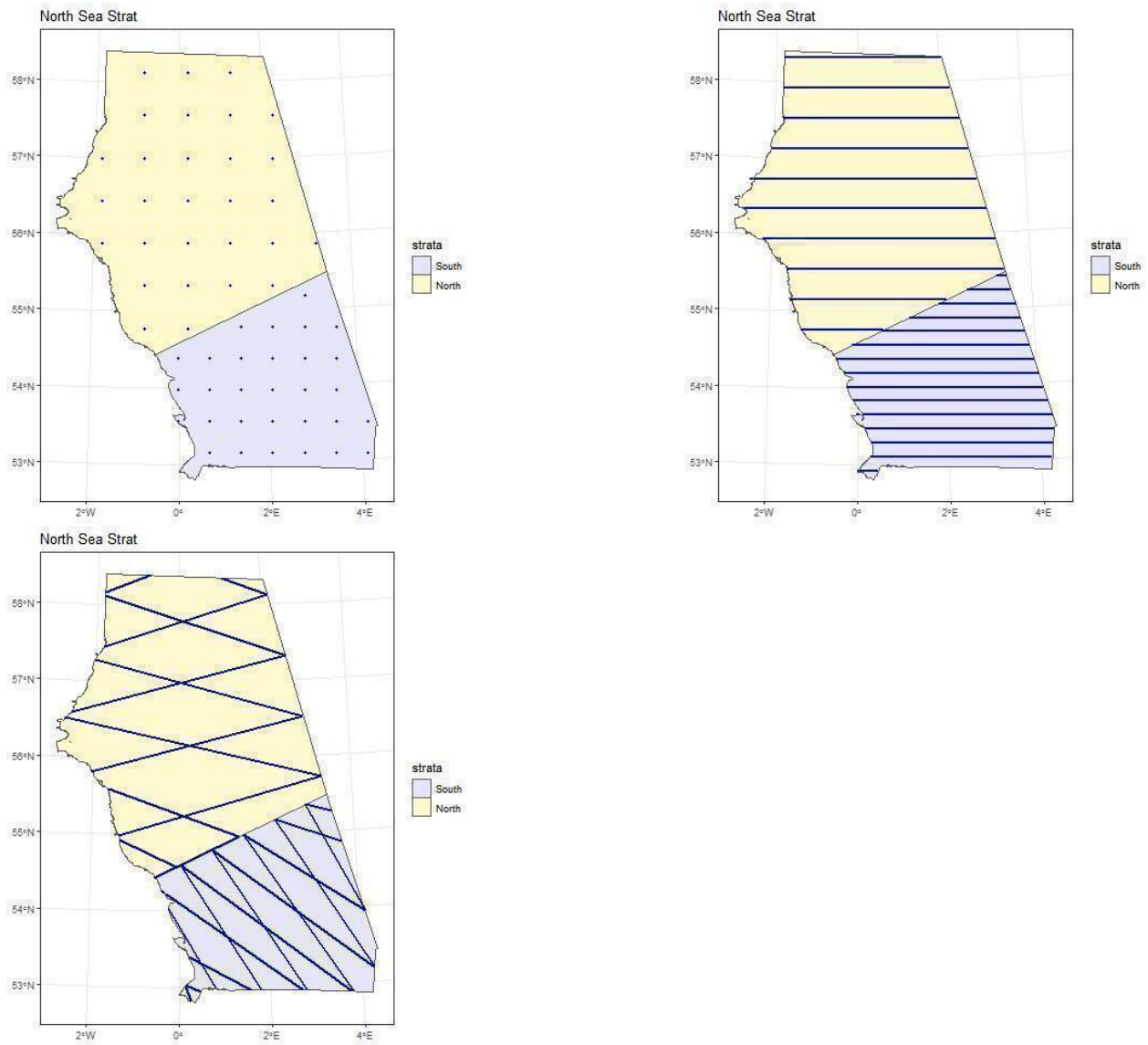


Figure 12: Example surveys for each Stratified Designs. Top Left: Point Transect design, Top Right: Parallel line design, Bottom Left: Zigzag line design

6.2.1 Stratified Results - Point Design

For the point transect design, the histograms of the abundance estimates from each simulation run are displayed below in Figure 13:

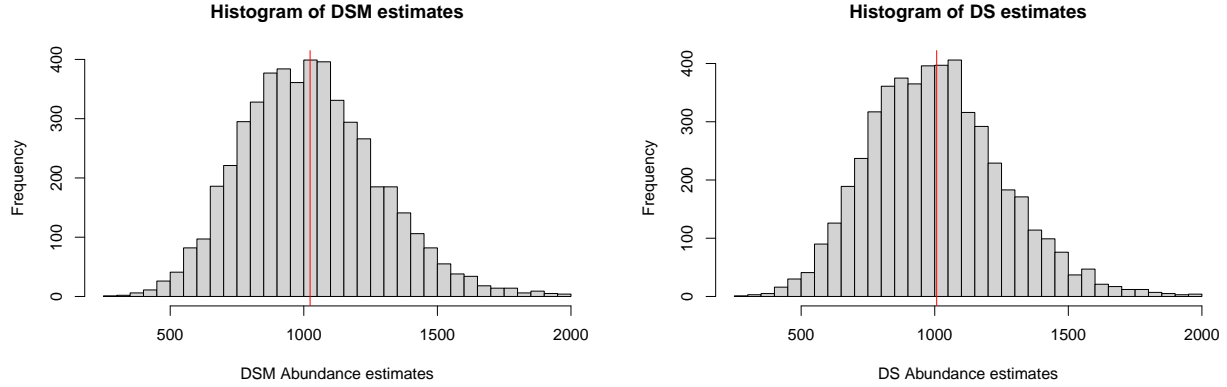


Figure 13: Histograms of Point Design abundance estimates for Stratified North Sea Region

These plots suggest both methods are relatively good at estimating the true abundance of 1000, with both methods appearing to overestimate, with the DSM method overestimating slightly more than the DS method. There again appears to be a slight right skewness to both plots which will be looked at analytically below. Investigating the means further, we find the mean of DSM estimates to be 1023.56 and the mean of DS estimates to be 1007.28. These estimates are both close to the true abundance, with the overestimation present as mentioned above and to a very similar level to the Non-Stratified point results. Overall, it was found that the estimates produced by DSM were greater than those produced by DS from the same survey data 74.08 % of the time, indicating it is highly likely DSM will produce an estimate greater than that of DS. A Wilcoxon test was performed on both sets of estimates with the alternative being that DSM was greater than DS.

This returned a p-values of 0 indicating at any significance level, the null hypothesis of the difference between the DSM and DS estimates being zero is rejected in favour of the alternate, that the DSM estimates are greater than those of DS. If we now compare the other variables extracted from the models below, we can examine the accuracy and variability of each method:

From Table 7 above, it can be observed that in this case, the DS method overall performed better than the DSM method, having a smaller bias as well as higher confidence interval coverage, despite having a smaller Mean Std error. Additionally, the standard deviation of the estimates is slightly less for the DS method, however both methods do a relatively good job at estimating this. Additionally, we observe from the skewness statistics that both methods returned a positive statistic indicating the right-skewed as identified above, which suggests the right tail is longer and this is supported by some of the estimates being close to 2000, with the maximums for DSM and DS being 1979.15 and 1990.98 respectively.

Table 7: North Sea Stratified results - Point

Statistic	Point Design	
	DSM results	DS results
Mean	1023.5635274	1007.2782907
Bias	2.3563527	0.7278291
Mean Std error of estimates	256.9842564	253.9268810
Std Dev of estimates	253.8727239	250.7267820
Mean CV	0.2558409	0.2569336
Confidence Interval Coverage	0.9500000	0.9534000
Estimate Skewness	0.4033869	0.4093011
Estimate Kurtosis	3.2215680	3.2570919

The kurtosis figures for both methods are greater than 3, indicating we would expect more frequent outliers than a normal distribution. In the Jarque-Bera test for normality, DSM and DS estimates return p-values of 0 and 0 respectively. These indicate we can reject the null hypothesis that these estimates are normally distributed, therefore our use of the Wilcoxon test above is justified. While the Mean CV for the DSM method is lower, the difference is marginal and does not out-way the bias or variance issues of this method. Overall this clearly seems to be a case where the DS method performs better than the DSM estimation method.

6.2.2 Stratified Results - Parallel Line Design

Now examining the results of the line transect design, on the same density surface, we see the histograms of the estimates below in Figure 14:

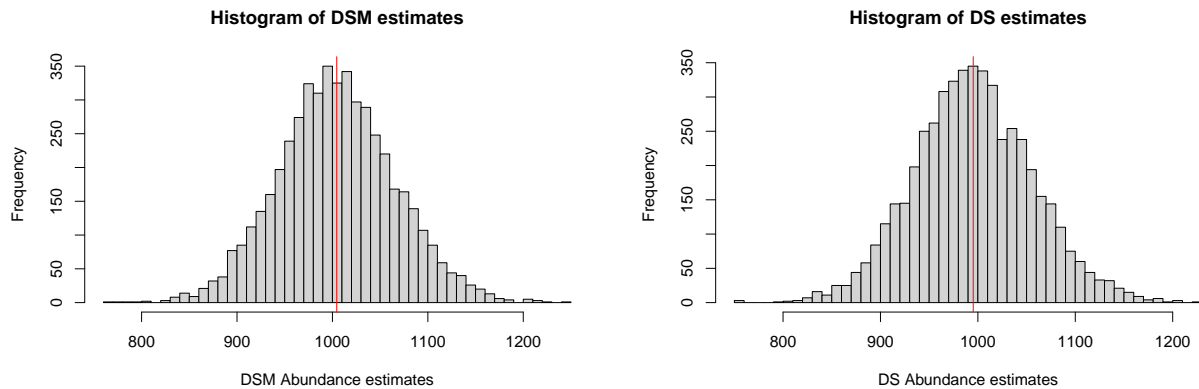


Figure 14: Histograms of Parallel Design estimates for North Sea Region

These plots are similar to their point transect counterparts, with the mean for each signified by the red line appearing very close to truth. However, there appears to be less skewness for

these than is present with the point transect results, exhibiting a slightly sharper point at the mean. Investigating this further, we find the mean of DSM estimates to be 1004.53 and the mean of DS estimates to be 995.22. These estimates are very close to the truth, with DSM again overestimating in comparison to DS. Overall, it was found that the estimates produced by DSM were greater than those produced by DS from the same survey data 81.86 % of the time, indicating it is highly likely DSM will produce an estimate greater than that of DS. A Wilcoxon test was performed on both sets of estimates with the alternative being that DSM was greater than DS. This returned a p-values of 0 indicating at any significance level, the null hypothesis of the difference between the DSM and DS estimates being zero is rejected in favour of the alternate, that the DSM estimates are greater than those of DS. Examining the other statistics extracted from the simulation.

Table 8: North Sea Stratified results - Line

Statistic	Parallel Line Design	
	DSM results	DS results
Mean	1004.5256879	995.2226076
Bias	0.4525688	-0.4777392
Mean Std error of estimates	69.2225719	70.0728537
Std Dev of estimates	61.0506879	61.0934785
Mean CV	0.0689899	0.0704740
Confidence Interval Coverage	0.9710000	0.9720000
Estimate Skewness	0.0779817	0.0779652
Estimate Kurtosis	3.1668925	3.1843860

From Table 8 above, it can be seen that in this case, the performance of both models was very similar throughout all areas, with the exception being the mean estimates and bias. The mean estimate for DSM was again a slight overestimation and as a result, bias was positive, while DS underestimated by almost the same amount, leading to an almost identical but negative bias. The Mean Std errors and Std Deviation of estimates were slightly lower for DSM, however the difference in both cases is very small. The Mean CV for each method is very similar, being slightly in favour of the DSM method although the difference is negligible. The DS method has a slightly higher probability of truth being contained within its confidence intervals, at 0.972 compared to 0.971, however this small difference is likely due to the slightly higher Std errors from the DS method widening the confidence interval. Despite this, both methods achieved truth in their confidence intervals over the 95% significance level. The skewness scores for both are very similar and suggest again a slight right skew however this is small. The kurtosis scores are close to 3 but larger, suggesting the distribution of the estimates are is similar to that of a normal distribution, with a slight trend towards a leptokurtic distribution. In the Jarque-Bera test for normality, DSM and DS estimates return p-values of 0.0043605 and 0.0023014 respectively. These indicate we can reject the null hypothesis that these estimates are normally distributed and our use of the Wilcoxon test above is justified, since the normality assumption would have been violated for a parametric test. Overall, while the mean estimate appears in favour of the DS method,

the DSM approach can be said to have performed better in this simulation, due to the small bias, lower Mean Std error and coefficients of variation.

6.2.3 Stratified Results - Zigzag Line Design

Unfortunately, for the stratified zigzag design, an error intermittently occurred within the simulation which caused the fitting of the density surface model to fail. Upon further inspection, this error did not occur within any of the code written as part of this project. After consultation with L Marshall, the author of the *dsims* package, it was determined the error likely occurred as a result of how some of the survey realisations within *dsims* were constructed. This likely led to issues with the coordinates for the transects and segments, with this not being an issue within the DS model however the density surface model would not accept these, resulting in the error. It is outside the scope of this project to investigate the root cause of this error, therefore L Marshall was notified of the bug and given access to the code to determine the root cause. As mentioned, this error occurred intermittently, resulting in a full set of 5000 iterations not being completed in a single run. However, multiple runs were completed with the exact same conditions until a total of 5000 were completed, with these results being examined below. Examining these results, we see the histograms of the two abundance estimates below in Figure 15:

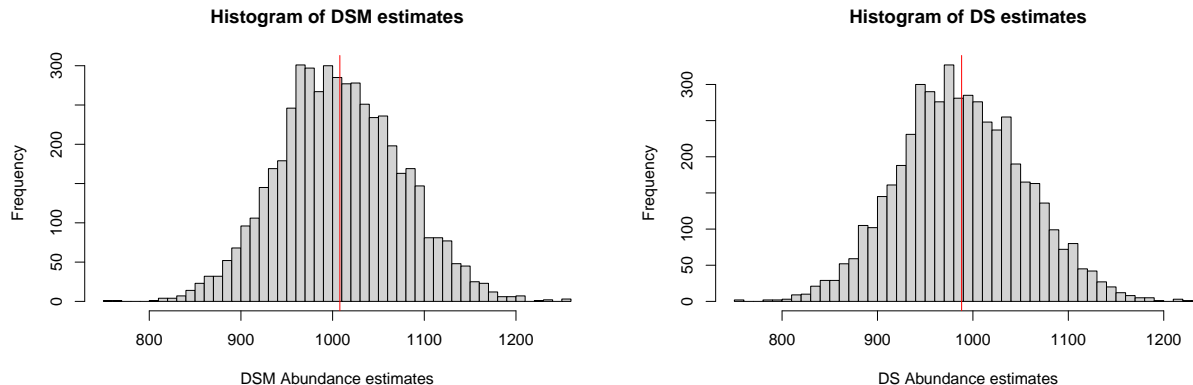


Figure 15: Histograms of Abundance estimates generated by a zigzag line design for the Stratified North Sea region.

These plots are very similar to their point transect counterparts, with the mean for each signified by the red line appearing very close to truth. However, there appears to be less skewness for these than is present with the point transect results. Investigating this further, we find the mean of DSM estimates to be 1007.89 and the mean of DS estimates to be 988.17. These estimates are very close to the true Overall, it was found that the estimates produced by DSM were greater than those produced by DS from the same survey data 99.46 % of the time, indicating it is highly likely DSM will produce an estimate greater than that of DS. A Wilcoxon test was performed on both sets of estimates with the alternative being that DSM was greater than DS.

This returned a p-values of 0 indicating at any significance level, the null hypothesis of the estimates being zero is rejected in favour of the alternate, that the DSM estimates are greater than those of DS. Examining the other statistics extracted from the simulation.

Table 9: North Sea Non-Stratified results - Zigzag

Statistic	Parallel Line Design	
	DSM results	DS results
Mean	1007.8906091	988.1679758
Bias	0.7890609	-1.1832024
Mean Std error of estimates	71.3800598	71.1709390
Std Dev of estimates	66.5563054	65.6280487
Mean CV	0.0709281	0.0721369
Confidence Interval Coverage	0.9634000	0.9666000
Estimate Skewness	0.1105532	0.1130020
Estimate Kurtosis	2.9413753	2.9488149

From the results in Table 9 above, it can be seen that in this case, the performance of both models was similar and each performed well in different areas compared to the each other. The mean estimate was again a slight overestimation and as a result, bias was slightly higher for DSM, however this difference was comparatively small. The Mean Std errors were lower for DSM and far closer to the Std Dev of the estimates, highlighting the better error estimation of DSM. However the Std Dev of the estimates was slightly smaller for the DS approach. The DS method also has a higher probability of truth being contained within its confidence intervals, at 0.9666 compared to 0.9634, however this difference is likely due to the higher Std errors from the DS method wideing the confidence interval. Despite this, both methods achieved truth in their confidence intervals over the 95% significance level. The skewness scores for both are very similar and suggest again a slight right skew however this is very small. The kurtosis scores are very close to 3, suggesting the kurtosis is very similar to that of a normal distribution. In the Jarque-Bera test for normality, DSM and DS estimates return p-values of 0.0042941 and 0.0037219 respectively. These indicate we can not reject the null hypothesis that these estimates are normally distributed. Overall, while the mean estimate appears in favour of the DS method, the DSM approach can be said to have performed better in this simulation, due to the small bias, lower Mean Std error and coefficients of variation.

7 Modeling - Buckland 2015 Example

For our next set of simulations to examine the capabilities of the DSM approach in respect to the DS method, I will revisit the the example simulation provided in Section 2.5.2 of Buckland et al. (2015) and use both a DS and DSM approach to repeat these simulations. It must be noted that the original analysis was part of a survey design case study by Laura Marshall and used the R package *DSsim* Marshall (2020) . For the purpose of this study, each of the designs and simulations will be translated into the *dsims* Marshall (2021) package used throughout the remainder of the simulations to ensure comparability with the DSM approach developed. All details from the original designs will be kept constant, with the population being fixed at 1500 individuals and using a truncation distance of 1000m. For each of the surveys, a half-normal detection function with a scale parameter of 500 will be assumed. The density surfaced used is displayed below alongside the detection function in Figure 16.

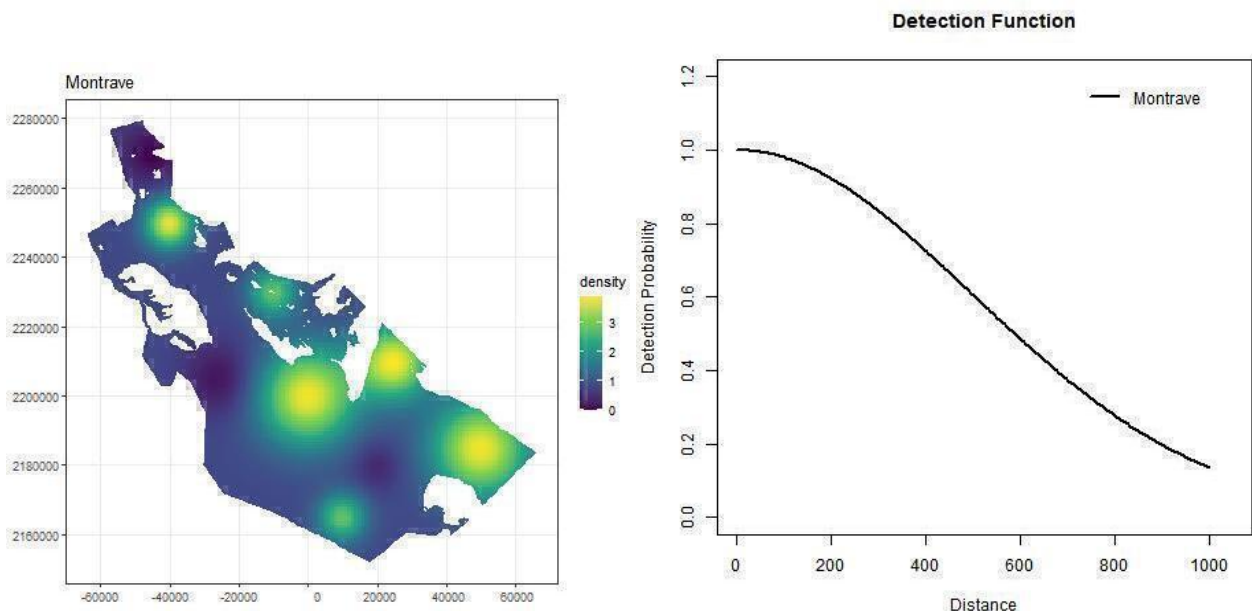


Figure 16: Density surface and detection function for Buckland 2015 example

By using this study region, it is possible to verify the simulation method developed for DSM can be run on study regions with internal holes, such as islands on a seaborne survey. The three different designs will be used, being the same as those tested in the case study in Buckland et al. (2015). These will be a systematic parallel line design, a random parallel line design and a zigzag design. Examples of each design are displayed in Figure 17 below:

As with each of the simulations run as part of the North Sea section, 5000 iterations will be run for each design. While this is different from the 100 iterations originally conducted, the increase in the number of iterations will increase the reliability of the results.

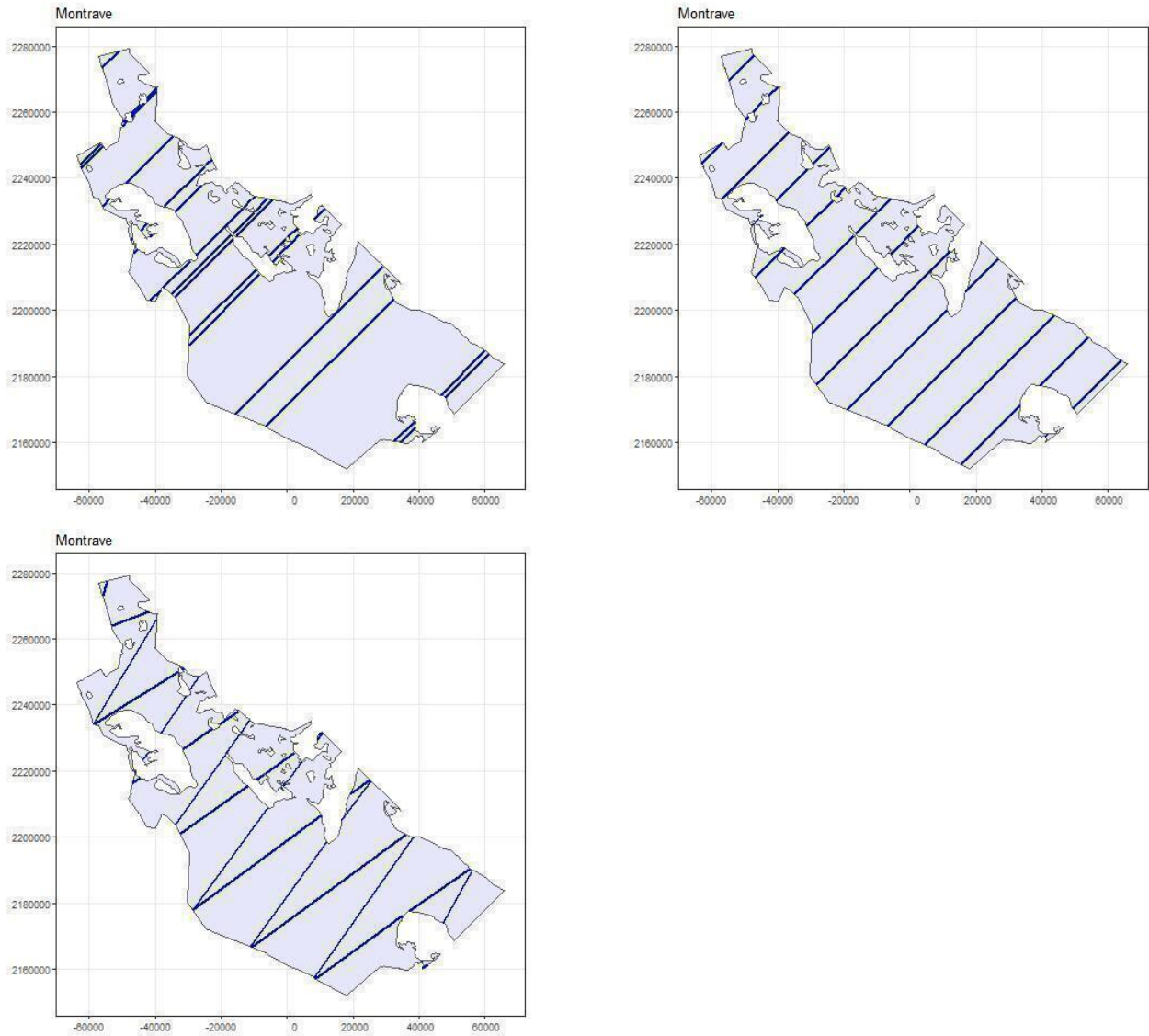


Figure 17: Example surveys for each Design: Top Left: Random Parallel Line, Top Right: Systematic Parallel line, Bottom Left: Zigzag line

7.1 Results - Random Parallel Line

We can now examine the results of the Random parallel line design by initially plotting histograms of the estimates from both the DS and DSM methods below in Figure 18:

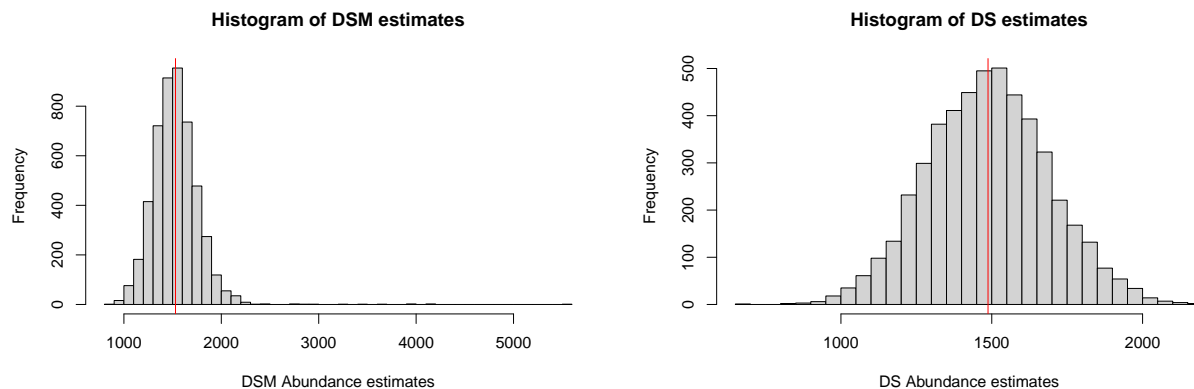


Figure 18: Histograms of Random Parallel Line Design estimates for Buckland 2015 example region

While the plot for the DS estimates appears similar to those we have seen before, the estimates for the DSM method appear markedly different. This is due to the presence of very extreme overestimates with the largest estimate being 5552, over 3 times the true population. It initially appears that the majority of the DSM estimates are centred around the true population of 1500, however this will be investigated further below. As with the previous simulations, it was found that the estimates produced by DSM were greater than those produced by DS from the same survey data 61.68 % of the time, indicating it is likely DSM will produce an estimate greater than that of DS. A Wilcoxon test was performed on both sets of estimates with the alternative being that DSM was greater than DS.

This returned a p-values of $6.5547013 \times 10^{-84}$ indicating at any significance level, the null hypothesis of the difference between the estimates being zero is rejected in favour of the alternate, that the DSM estimates are greater than those of DS.

Table 10: Buckland 2015 example results - Random Line

Statistic	Random Parallel Line Design	
	DSM results	DS results
Mean	1529.7525902	1487.6347184
Bias	1.9835060	-0.8243521
Mean Std error of estimates	175.4654981	196.5362110
Std Dev of estimates	238.4670400	201.3611866
Mean CV	0.1139636	0.1334070
Confidence Interval Coverage	0.8880000	0.9420000
Estimate Skewness	2.4886720	0.0578036
Estimate Kurtosis	31.3798293	2.9516809

In Table 10 above, we can see the various statistics extracted during the course of the simulations. As we have seen throughout this report, the mean for the DSM is a slight overestimates and the DS is a slight underestimates. This is transferred into the bias, with the DSM having a positive bias and DS having a negative bias, however both of these are below the 5% level so no concerns are raised for either method. Unfortunately, there are major concerns regarding the Mean Std errors of the estimates, which are the estimator of the Std deviations. For both methods, it can be seen that they are underestimates of the Std deviations and very severely in the case of the DSM method. This is problematic as not capturing all of the variance can lead to the results assuming they are more accurate than they actually are. These underestimations of variance are translated into the confidence interval coverage, where both fail to contain truth at the 95% confidence level. Additionally, the skewness and kurtosis statistics are very different for the DSM method, likely as a result of the extreme overestimations produce by some survey realisation. Overall, it could be concluded that in this scenario, the DS method performed better, by virtue of underestimating the variance less and having less extreme estimates, however neither method should be considered adequate in this case.

7.2 Results - Systematic Parallel Line

Moving on the systematic parallel line design, histograms of the abundance estimates are plotted below in Figure 19.

7.3 Results - Zigzag Line

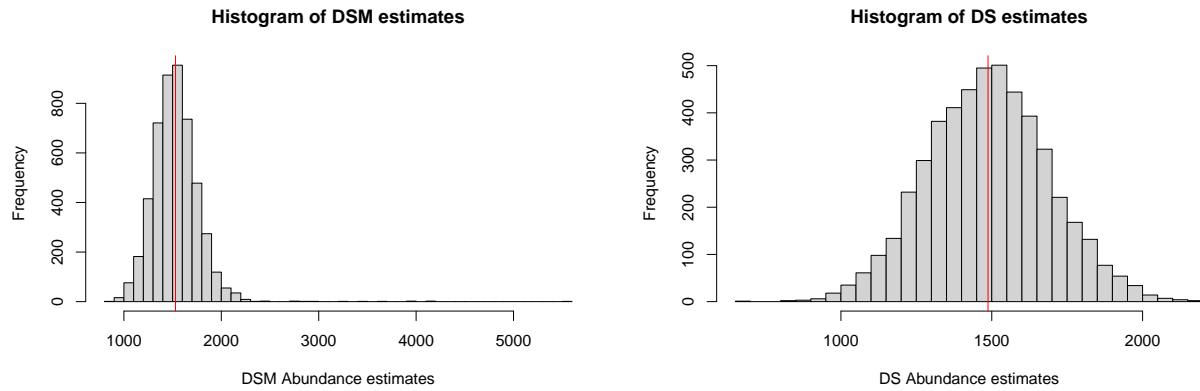


Figure 19: Histograms of Systematic Parallel Line Design estimates for Buckland 2015 example region

Table 11: (#tab:histMontline, fig.cap)Buckland 2015 example results - Parallel Line

Statistic	Systematic Parallel Line Design	
	DSM results	DS results
Mean	1537.3035256	1497.1665768
Bias	2.4869017	-0.1888949
Mean Std error of estimates	167.4557120	217.2829383
Std Dev of estimates	162.7215057	157.1575653
Mean CV	0.1093682	0.1455074
Confidence Interval Coverage	0.9516000	0.9912000
Estimate Skewness	0.1282707	0.1328383
Estimate Kurtosis	2.9807139	2.9845720

Table 12: Buckland 2015 example results - Zigzag Line

Statistic	Zigzag Line Design	
	DSM results	DS results
Mean	1535.8679659	1490.9859160
Bias	2.3911977	-0.6009389
Mean Std error of estimates	154.0152961	201.4087609
Std Dev of estimates	149.6840030	142.3056900
Mean CV	0.1005728	0.1353724
Confidence Interval Coverage	0.9488000	0.9936000
Estimate Skewness	0.1562206	0.0825283
Estimate Kurtosis	3.1318763	3.0696502

8 Modeling - Variance estimation tests

Table 13: North Sea Line transect results with "R2" encounter rate variance estimator

Statistic	"R2" estimator	
	DSM results	DS results
Mean	1006.7220521	995.6210343
Bias	0.6722052	-0.4378966
Mean Std error of estimates	61.0404014	86.8150325
Std Dev of estimates	53.7859543	53.9502032
Mean CV	0.0606838	0.0872327
Confidence Interval Coverage	0.9720000	1.0000000
Estimate Skewness	0.1327232	0.1219796
Estimate Kurtosis	2.7373307	2.7587752

Table 14: North Sea Line transect results with "O2" encounter rate variance estimator

Statistic	"O2" estimator	
	DSM results	DS results
Mean	1010.3458147	999.7456113
Bias	1.0345815	-0.0254389
Mean Std error of estimates	61.2120362	61.4284279
Std Dev of estimates	50.8573841	50.9772744
Mean CV	0.0606361	0.0615026
Confidence Interval Coverage	0.9780000	0.9780000
Estimate Skewness	0.0790554	0.0745994
Estimate Kurtosis	2.9569733	2.9480249

Table 15: North Sea Line transect results with "O3" encounter rate variance estimator

Statistic	"O3" estimator	
	DSM results	DS results
Mean	1009.8269117	998.6522485
Bias	0.9826912	-0.1347752
Mean Std error of estimates	61.1646292	60.8111562
Std Dev of estimates	51.1835571	50.8538331
Mean CV	0.0606222	0.0609604
Confidence Interval Coverage	0.9760000	0.9780000
Estimate Skewness	0.0176335	0.0567768
Estimate Kurtosis	3.0051147	3.0335553

9 Modeling - North Sea Predictions outside study area:

As mentioned within the simulation etentions section, the prediction grid for DSM is not limited to the area of the study region, it can be smaller or larger and does not even need to include any part of the study region. However, predicting populations outside of the original study region may be subject to large variations dependant on the gradient of the density surface at the edge of the region. This will be tested by using the same North Sea region we have explored before, however with two very contrasting density surfaces to show the two extremes of what could happen in this scenario. As this simulation will focus on predicting the abundance outside of the study region, the estimates from the DS method will not be compared here as the predictions will be made over a far larger area. As a simple example, the prediction grid used will be based on the bounding box of the North Sea region, in essence a large rectangle encompassing the entirety of the region.

The two contrasting density surfaces can be seen in Figure 20

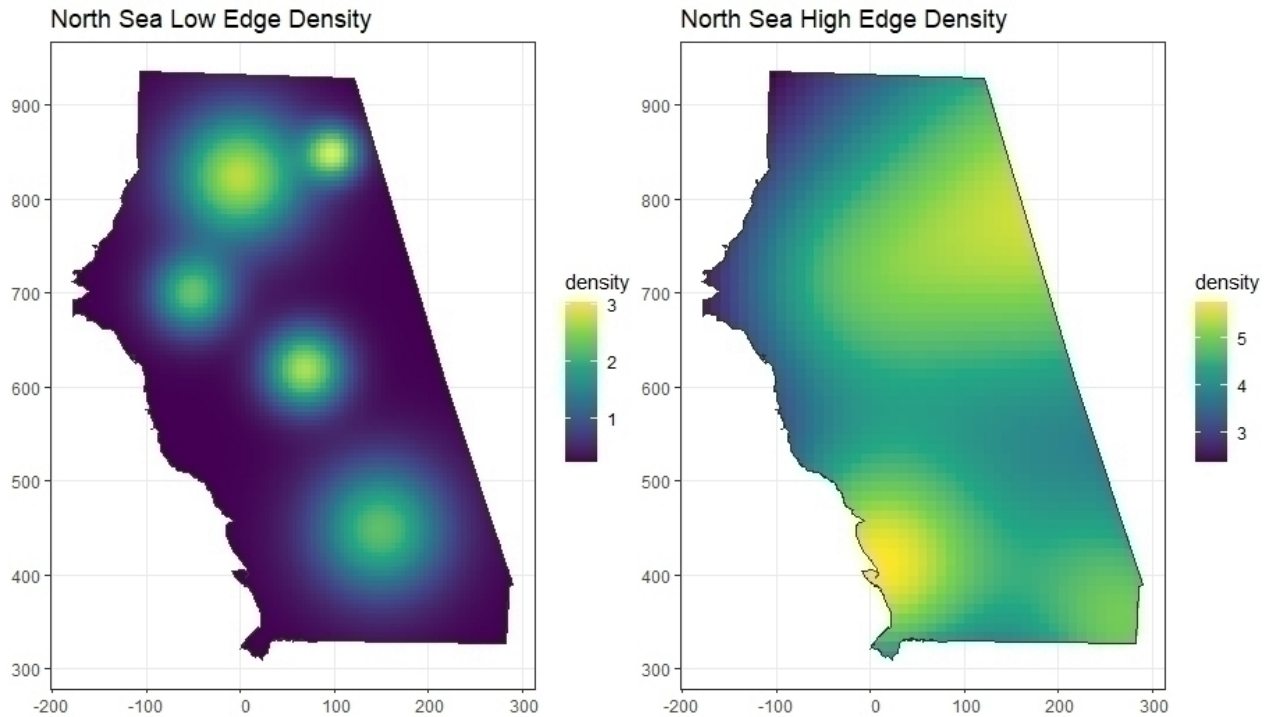


Figure 20: Density surface and detection function for Montrave region

In a slight difference to the original simulations, the number of transects was reduced to 20 to reduce the amount of area covered by each study. All other aspects of the original simulation were kept the same, with the detection function being the same half normal function with a scale parameter of 5 with a truncation distance of 10 seen in Figure 9.

9.1 Results

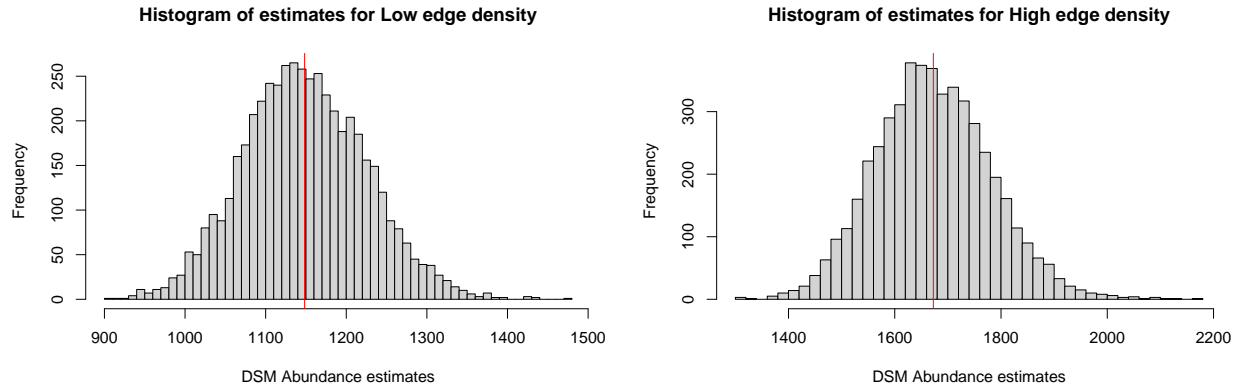


Figure 21: Histograms of DSM abundance estimates for the North Sea region when predicting outside the study region using different density surfaces

Table 16: North Sea region with different densities when predicting outside the study region

Statistic	DSM results	
	Low Edge Density	High Edge Density
Mean	1148.3549197	1672.6246878
Mean Std error of estimates	82.8996866	125.3147025
Std Dev of estimates	75.9493672	108.5915038
Mean CV	0.0722341	0.0749656
Estimate Skewness	0.1509434	0.2247339
Estimate Kurtosis	3.0347758	3.2674359

10 Discussion

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