Project

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Notes

There is still a significant amount of work I wish to complete before submission for the interim deadline. Namely:

Code explanation if required.

Additional survey regions, designs and densities tests to ensure code can handle different designs

Proper comparison of models via coefficients of variation, bias, mean standard errors and standard deviation of estimates

Perform model checking for both ds and dsm model, via gam.check, residuals, modelling residuals by GAM

Potential example of use by simulation of making predictions outside survey area based on distance data.

Abstract

Introduction

The purpose of this report is to detail to extensions made to the dsims R package and conduct analysis to compare the abundance estimates generated through a design based approach, distance sampling, and a model based approach, density surface modelling. This will allow researchers the opportunity to use the best possible model to fit the circumstances of their own study.

main objective is that the use of density surface modelling can be extended beyond the original survey area while distance sampling is more restricted in this approach. The simulations of different designs can be used to evaluate the how well these extended areas can be modelled without the requirement to sample there, potentially allowing for the survey design to be optimised to allow the maximum area to be estimated within a given accuracy.

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.

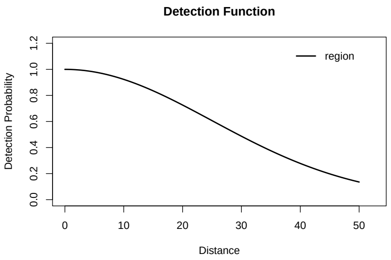
Distance sampling can therefore be thought of as a method of plot sampling, with the additional factor of not every animal on the plots being observed. For this, the plots in line transect sampling are rectangles of dimension $2wl$, where l is the length of a given transect and may change between transects 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.

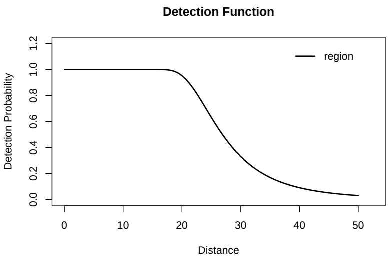
Detection function

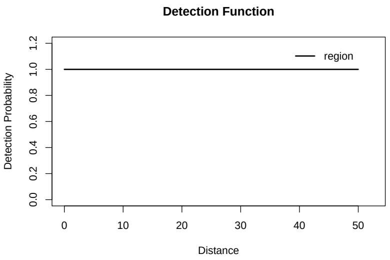
To take into account the fact that not all animals or clusters within each transect are observed, the probability of detecting an animal with a transect must be estimated. This is done by using the distances to the animals observed, x for line transects and r for point transects, to fit a detection function $g(x)$, 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 know 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 on which gives high precision, although high precision should not outweigh the need for the other properties to be satisfied.

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 be 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. 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 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, using AIC as the default. 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

Density Surface Modelling

This sections contains material base on D.L.Miller et al 2013 In order to construct a density surface model, initial 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 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 is 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 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 2 w x 2 w 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.

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 convariate 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 estinator 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 jth segment and s_{jr} is the size of the rth 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:

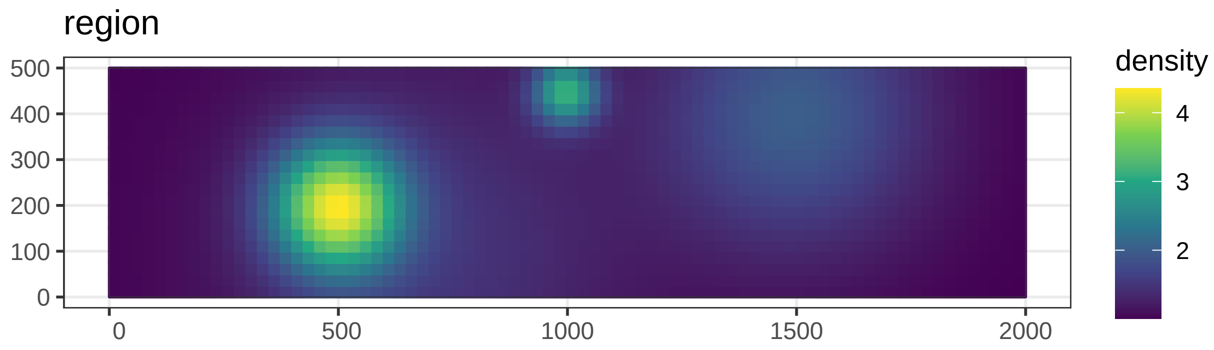
$$\mathbb{E}(\hat{N_j}) = A_j exp[\beta_0 + \sum_k f_k(z_{jk})]$$

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.

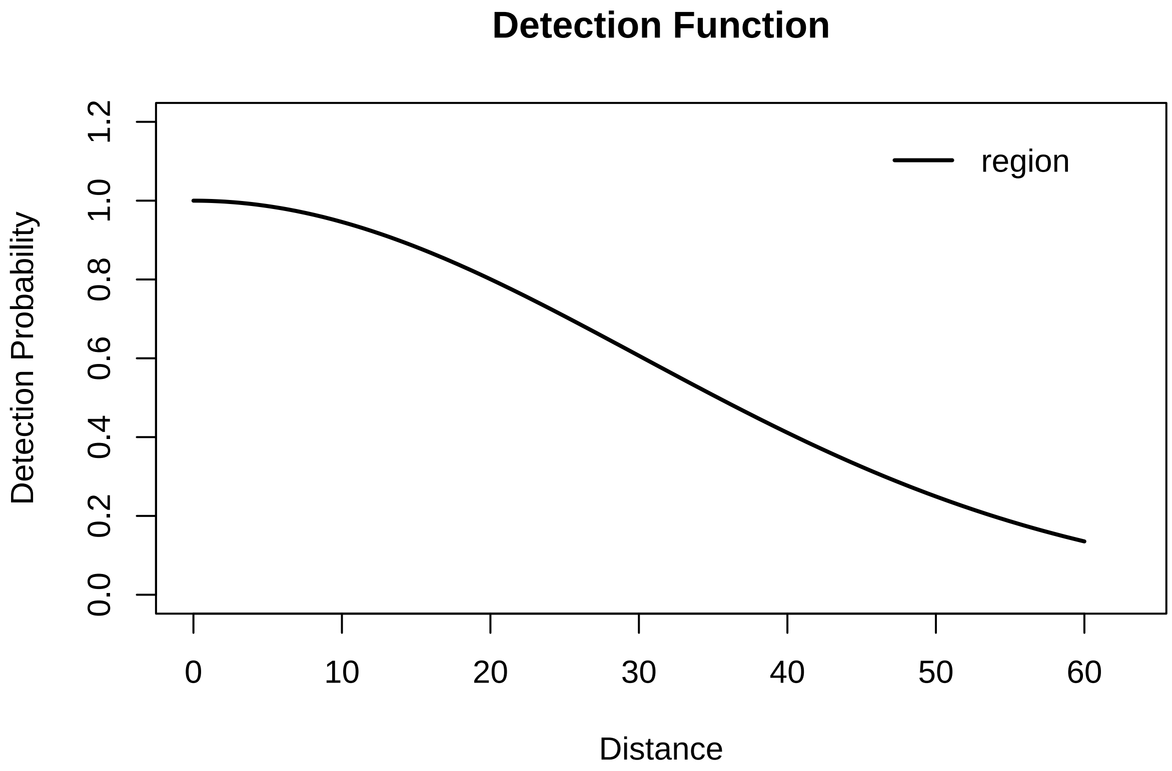
To allow for a DSM to predict abundance, a series of prediction cells must be defined. These are not necessarily restricted to just the original study region, allowing for regions outside the study area to be predicted over. Each of the prediction cells must include the same covariates as specified in 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.

Modelling

The simulation was initially tested using the default region generated by dsims 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 with relatively gently gradients.

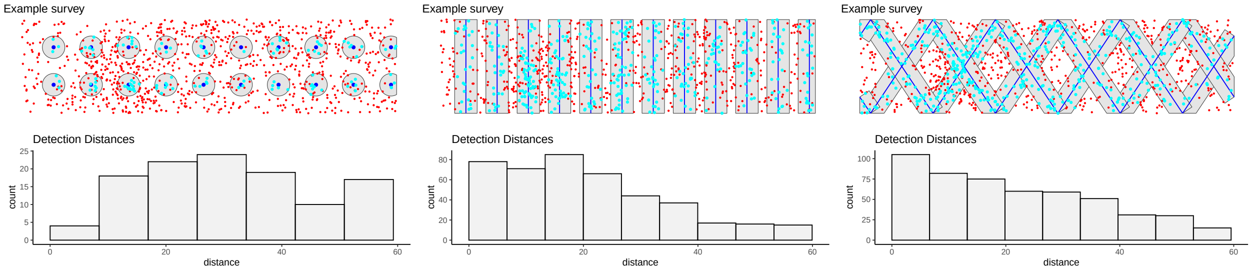


A population description was then constructed based on this density surface with a true population of 1000. A detection function was then defined as a half normal with scale parameter of 30 for both designs, producing the following detection function:



A prediction grid is then constructed across the study region and is identical for each simulation iteration, with the resolution of the grid set at the truncation distance of the design. As Miller et al 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.

The simulation loop then begins. For each iteration, a new survey constructed. From this, the observation data and segmented data is extracted. An example survey for each of the designs is displayed below:



In the case of line transect designs, the transects are split to allow them to be modelled as points. Each transect 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. For Point transect designs, each point is treated as its own segment.

The polygons of each segment is then created using the st_buffer command (sf package, ref required), using w 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 study region, to ensure only areas within the study region are counted towards segment area. Failure to do this results in the areas of each segment being larger than they are in the survey, and as a result the dsm abundance estimate is smaller than true, since the prediction grid is only over the survey area. Once the segment areas have been calculated, they 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.

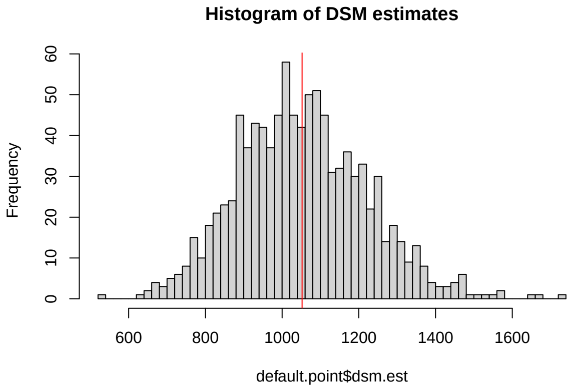
Based on this data, both a distance sampling model and density surface model are constructed, with the dsm modeling the counts against the smooth of spatial locations using a tweedie error distribution. In the smoothed term, the degrees of freedom is restricted to the total number of transects. The abundance estimates are extracted from both models and stored alongside the prediction variance and deviance explained from the dsm model.

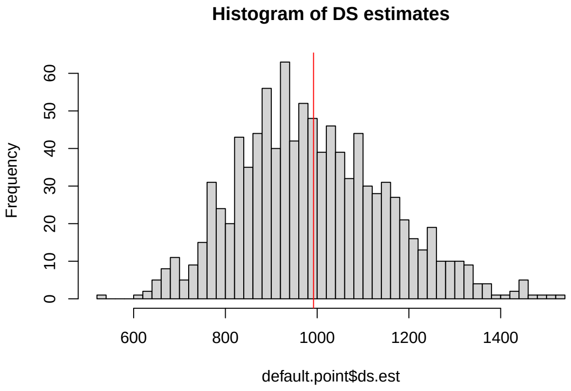
Results

Having completed 1000 bootstrap 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.

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:





These plots show somewhat similar data since both estimates are generated by the same data set. If we now compare the means and 95% confidence intervals:

```
## [1] 1052.032
## [1] 992.0967
```

```
## [1]  722.3986 1381.6645
```

```
## [1]  674.1186 1310.0748
```

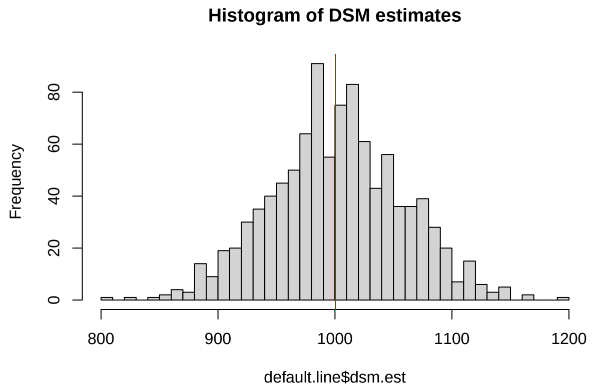
It can be seen that the mean of the dsm estimates appears to similar to the true population of 1000 while the distance sampling method is closer. Examining the confidence intervals for both methods, the interval for the dsm model is in this case slightly wider than that of the ds model, indicating it is slightly less accurate in the case of this region and density surface however this effect is very small.

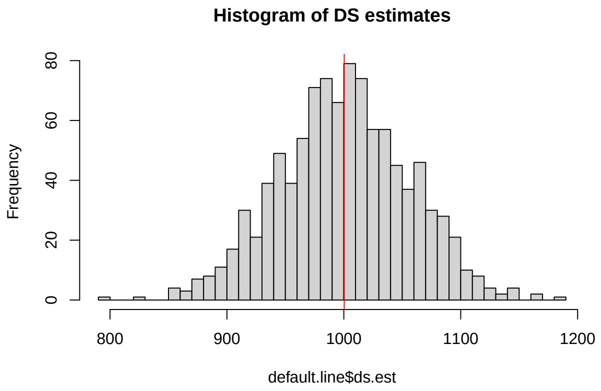
Next, we can evaluate how many times the true abundance, was within the 95% CI for every model computed.

With truth being in the 95% CI `1000` times out of 1000, we can conclude that the model is particularly good and containing truth within its estimated confidence interval. However, this could be due the the variance in each model being quite large resulting in wide confidence intervals.

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:





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 means for each set of estimates to be:

```
## [1] "Mean of DSM estimates and associated 95% CI"
```

```
## [1] 1002.038
## [1]  890.8191 1113.2573
```

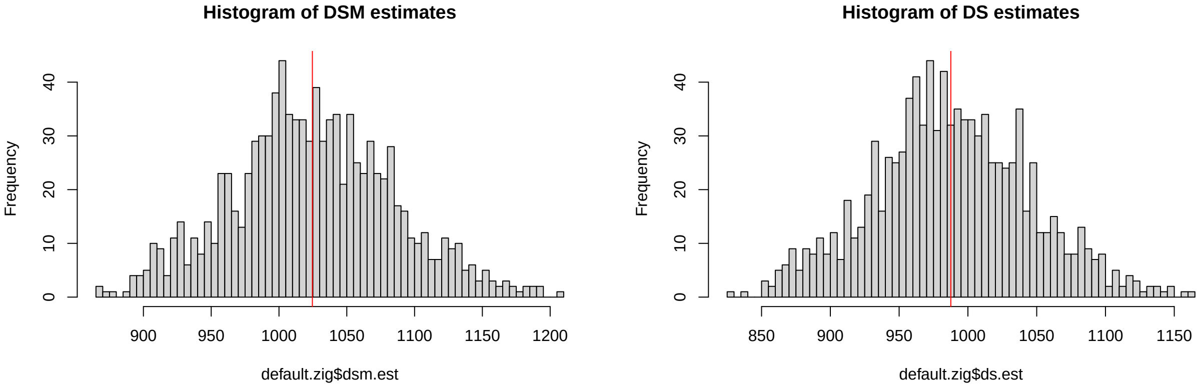
```
## [1] "Mean of DS estimates and associated 95% CI"
```

```
## [1] 1000.358
```

```
## [1]  890.8782 1109.8380
```

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:



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 for each set of estimates to be:

```
## [1] "Mean of DSM estimates and associated 95% CI"
```

```
## [1] 1024.619
```

```
## [1]  913.4002 1135.8384
```

```
## [1] "Mean of DS estimates and associated 95% CI"
```

```
## [1] 987.576
```

```
## [1]  878.0961 1097.0559
```

conclusion