Hornsea Project Four

MRSea Baseline Sensitivity Report (Gannet)

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Checked Faye McGinn, Orsted, March 2022
Accepted Hannah Towner-Roethe, Orsted, March 2022
Approved Julian Carolan, Orsted, March 2022

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Revision Summary

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01	23/03/2022	APEM Ltd	Faye McGinn, Orsted	Julian Carolan, Orsted

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Glossary

Term	Definition
Auto-correlation	Data containing systemic variation; for example, spatial variation and is seen by sites close to each other having more similar values.
Bootstrapping	Tests that use random sampling with replacement to assign measures of accuracy to sample estimates.
Bio-season	Bird behaviour and abundance is recognised to differ across a calendar year, with particular months recognised as being part of different seasons. The biologically defined minimum population scales (BDMPS) bio-seasons used in this report are based on those in Furness (2015), hereafter referred to as bio-seasons.
Confidence intervals	Range of values that with a specified certainty contains the true mean of the population that a sample was taken from. For example, 95% confidence intervals states a range of values with a 95% certainty those values contain the population mean.
"Generalised Additive Model" framework	Statistical models to predict relationships between individual predictors and dependent variable following smooth patterns that can be linear or nonlinear.
Hornsea Project Four Offshore Wind Farm	The term covers all elements of the project (i.e. both the offshore and onshore). Hornsea Four infrastructure will include offshore generating stations (wind turbines), electrical export cables to landfall, and connection to the electricity transmission network. Hereafter referred to as Hornsea Four.
MRSea	Statistical package to model spatial count data and predict spatial abundances; developed by the Centre for Research into Ecological and Environmental Modelling (CREEM) specifically for dealing with data collected for offshore wind farm projects.
Orsted Hornsea Project Four Ltd	The Applicant for the proposed Hornsea Project Four Offshore Wind Farm Development Consent Order (DCO).
P-value	A p-value is a measure of the probability that an observed difference could have occurred just by random chance.
Runs Test	A statistical procedure that examines whether a string of data is occurring randomly from a specific distribution.
Zero-inflated data	Count data with excess of zeros.

Acronyms

Term	Definition
1D	One-dimensional
2D	Two-dimensional
ACF	Auto-correlation Function
AFL	Agreement for Lease
ANOVA	Analysis of Variance
CREEM	Centre for Research into Ecological and Environmental Modelling
CReSS	Complex Region Spatial Smoother
CI	Confidence Interval
CRM	Collison Risk Model
CV	Coefficient of Variation
DAA	Developable Area Approach
DCO	Development Consent Order
EIA	Environmental Impact Assessment
EP	Evidence Plan
ES	Environmental Statement
ETG	Expert Topic Group
FFC	Flamborough and Filey Coast
GAM	Generalised Additive Model
GEE	Generalised Estimating Equation
GLM	Generalised Linear Model
GVIFS	Generalised Variance Inflation Factors
KDE	Kernal Density Estimation
MRSea	Marine Renewables Strategic environmental assessment
PEIR	Preliminary Environmental Information Report
RSPB	Royal Society for the Protection of Birds
SALSA	Spatially Adaptive Local Smoothing Algorithm
SD	Standard Deviation
SNCB	Statutory Nature Conservation Bodie
SPA	Special Protection Area
WTG	Wind Turbine Generators

1 Background to MRSea modelling for Offshore Ornithology

1.1.1.1 The MRSea statistical package was developed specifically for analysing offshore ornithological distribution and abundance data collected for offshore wind farm projects, allowing spatially auto-correlated and zero-inflated data to be modelled in a robust method. The package was designed by the Centre for Research into Ecological and Environmental Modelling (CREEM) and uses complex smoothing techniques to model spatial data in a "Generalised Additive Model" (GAM) framework (Scott-Hayward et al. 2014). This allows spatial differences in the density of a species to be understood, as well as allowing the use of environmental variables to predict density.

1.1.1.2 Through the Developable Area Process for Hornsea Four the project area being considered for development reduced from 846 km^2 at Scoping to 468 km^2 for the DCO Application. As the original aerial digital survey data set for offshore ornithology relied on 24 transects across the entire Agreement for Lease (AfL) area plus a 4 km buffer, whilst the final data set relied on 15 across the final array area plus 4 km buffer as submitted in the DCO Application. The Applicant worked with Natural England and the RSPB to consider methods of modelling these data to optimise the baseline characterisation. The use of MRSea for Hornsea Four was proposed and agreed for a limited number of species in consultation with both Natural England and the Royal Society for the Protection of Birds (RSPB), following Natural England's advocation to consider MRSea modelling in their Section 42 responses to the Preliminary Environmental Report. Therefore, the Applicant ran MRSea modelling to characterise the baseline for offshore ornithology for a limited number of species agreed as being appropriate to model (fulmar, gannet, kittiwake, great black-backed gull, guillemot, razorbill and puffin).

1.1.1.3 The Applicant followed the guidance written by CREEM (Scott-Hayward et al. 2017) to undertake the MRSea modelling, though it is recognised that for such a complex model that requires considerable user expertise and multiple testing for it to perform the guidance and advice within it would benefit from updates to allow for consistency in modelling preparation and approaches. The results of the MRSea modelling were then shared with Natural England and the RSPB and agreement reached that the outputs from the modelling were fit for the purpose of defining the baseline and for use in assessing the potential impacts from Hornsea Four on seabirds (ETG#13). The outputs from the MRSea modelling were used to define the final baseline for these species, supplemented with additional data from design-based abundance estimates from apportioned unidentified birds (and corrected for availability bias for auk species). These data were then subsequently used to underpin the impact assessments within **A2.5 Environmental Statement Volume A2 Chapter 5 Offshore and Intertidal Ornithology (APP-017)** and **B2.2: Report to Inform Appropriate Assessment (APP-167** to **APP-178)**.

2 Natural England's Relevant Representations (RR-029) – MRSea Query

2.1.1.1 Following the Hornsea Four DCO Application, Natural England submitted their Relevant Representations (**RR-029**). Comments received related to the preparation and approach used in running the MRSea model for Hornsea Four to define the baseline, which informs the impact assessments undertaken. Further to **RR-029**, Natural England provided the Applicant with an additional review (Scott-Hayward, 2021, not submitted with **RR-029** and presented in **Table 2**). The review was undertaken by the MRSea model developers (Centre for Research into Ecological & Environmental Modelling (CREEM), University of St Andrew's), including retrospective requests for additional screenshots and downloads from the initial model preparation stages of the approach to model building, coding, testing and running stages that are not routinely saved or downloaded due to the scale of such a task. The review requested confirmation of a number of MRSea modelling inputs and outputs that had not been submitted by the Applicant within **A5.5.6 ES Volume A5 Annex 5.6 Offshore Ornithology MRSea Report (APP-079)**.

2.1.1.2 The Applicant is unaware of the specific requests from Natural England to CREEM, which would clarify the basis of the requested review, or why it was felt that this should be concluded post-application and not within the pre-application phase of project development in which to facilitate detailed and timely consideration of the rationale for the review and the subsequent content. At the request of the Applicant Natural England provided supplementary comments specific to MRSea (see **Table 1**).

2.1.1.3 As a consequence of the post-application review of the MRSea model, reports and associated outputs, Natural England have reversed their original position of agreement on the outputs from the MRSea modelling (as concluded from consultation at ETG#13) being used to define the baseline and have not provided opinion on the potential impact levels from Hornsea Four on seabirds as a result, as stated within Natural England's relevant representation (**RR-029**). Natural England's main comments are summarised within the following statements within their Relevant Representations (**RR-029**) on the use of MRSea modelling for Hornsea Four below;

- *'In principle, NE welcome the use of modelling-based approaches to density and abundance estimation, and for the examination of trends in spatial distributions, however these values underpin much of the EIA and RIAA and it is therefore important that there is confidence in the modelling approach.'*; and
- *'Whilst NE remains supportive of using MRSea to produce estimates, the current description and justification for the approach provided here and in Volume A5, Annex 5.6 do not allow appraisal of the relative merits or risks associated with the MRSea approach. We therefore cannot currently have confidence in the density and abundance estimates produced by this method.'*.

3 The Applicant's Response to Natural England's Relevant Representations

3.1.1.1 In response to Natural England's Relevant Representations (**RR-029**) and CREEM review the Applicant agreed to produce a Baseline Sensitivity Report that incorporates all responses and additional information to inform Natural England and the Examining Authority of the progress made on the MRSea modelling queries. Due to the ongoing technical clarifications between CREEM and APEM (one meeting and two telephone conversations and numerous email requests between Feb and March 2022), the Baseline Sensitivity Report is to be submitted in three parts into the examination, as a complete model re-build is proving to be time-consuming and an iterative process requiring clarifications from the model developer. The three parts will provide the following;

- Part 1 - Applicant's response to Natural England and CREEM comments and advice on MRSea approach and methodology. This report provides an account of the Relevant Representations received on MRSea modelling, the consultation process undertaken by the Applicant to resolve any issues and agreed actions and approach to re-run the MRsea model for a single species (gannet). It will also provide initial revised MSRea model outputs from the initial stages of the re-building and testing process (see **Appendix A**);
- Part 2 - Results of the revised MRSea modelling for a single species (gannet) to be presented, with modelling approach, inputs and outputs (where available and / or appropriate) to be inserted to satisfy Natural England with regards to their Relevant Representations on MRsea (**RR-029**); and
- Part 3 - A full comparison between the current MRSea results used to define the Hornsea Four baseline that underpins the impact assessments with the revised MRSea results. This report will set out the implications, if any, of the changes to the baseline characterisation and impact assessments for Hornsea Four for a single species (gannet), with recommendations on how to close out the issues for other species.

3.1.1.2 It is anticipated that Parts 2 and 3 will be ready shortly after Deadline 2 and will then be submitted to Natural England for review. The updated Baseline Sensitivity Report, including Parts 2 and 3 will then be submitted into Examination at Deadline 3, addressing as many of Natural England's comments as is reasonably possible in the short time between Deadline 2 and 3.

4 Baseline Sensitivity Report – Part 1 (Consultation and Agreed Actions)

4.1.1.1 For Part 1 of the Baseline Sensitivity Report the Applicant facilitated a meeting with the MRSea model developers at CREEM, on 20th January 2022, to understand and specific technical aspects of the Natural England review. Following that meeting the Applicant consulted with Natural England to determine, beyond doubt, which aspects of the methodology, preparation and approach used to run MRSea modelling their concerns related to during a meeting on 17th February 2022 and agreed on an approach to resolve the remaining issues. The Applicant agreed with Natural England during this meeting to rerun the MRSea model using a methodology that addressed Natural England's comments for a single species (gannet) in the first instance.

4.1.1.2 Gannet was selected and agreed with Natural England as the most suitable species to undertake initial revised MRSea modelling for, as this species does not require apportionment of unidentified species groups from the raw data and therefore represents the best option to investigate. Should any changes between the current MRSea modelling and revised results be at a level that is judged to be insignificant then additional modelling of other species would not be undertaken following agreement with Natural England.

4.1.1.3 In addition to agreeing to rerun the MRSea model for gannet the Applicant also agreed to provide a further set of clarifications to update Natural England and the Examining Authority on the progress to date on the revised MRSea modelling for a single species (gannet). At the request of Natural England the Applicant also agreed to provide detailed responses to the comments from Natural England in their Relevant Representations (**RR-029**), which are provided in **Table 1**. The Applicant also agreed to provide detailed responses to comments and advice received by the developer of the MRSea model, CREEM, in order to ensure all questions regarding the MRSea modelling process are responded to, which are provided in **Table 2**.

Table 1: Natural England's Relevant Representations comments on MRSea modelling (REP1-029) and Applicant's responses.

Natural England's Comment	Applicant's Initial Response	Agreed Actions and Further Applicant Response
Natural England note that it is implied in Volume A5.1 Offshore and Intertidal Ornithology Baseline Characterisation Report that design-based estimates have been estimated for all species and that additional modelling was undertaken where possible as a supplementary approach. However, MRSea estimates have been used in preference to the design-based methods where sufficient data has allowed models to be fitted (fulmar, gannet, kittiwake, great black-backed gull, guillemot, razorbill and puffin). NE have significant concerns about the suitability of the methods used to analyse the baseline characterisation data to produce the modelled density and abundance estimates in preference to design-based estimates. These are summarised below:	The Applicant and Natural England agreed through the Expert Technical Panel (TPs) that MRSea would be relied upon for all species run through the model and any unidentified birds and correction factors applied to those data. Therefore, in order not to cause confusion the design-based estimates for the key species were not included in the final baseline. For clarity, design-based data were run for all species.	The Applicant agreed with Natural England to rerun the MRSea model using a methodology that addresses Natural England's comments for a single species (gannet) in the first instance. Gannet was selected and agreed with Natural England as the most suitable species to undertake initial revised MRSea modelling for, as this species does not require apportionment of unidentified species groups from the raw data and therefore represents the best option to investigate. On completion of the MRSea modelling design-based abundance estimates for gannet will be supplied alongside revised MRSea abundance estimates at Deadline 3. Should any changes between the current MRSea and revised results be at a level that is judged to be insignificant then additional modelling of other species would not be undertaken following agreement with Natural England.
Natural England note that, despite the scale of the estimates changing, the modelled spatial distributions for each species remain fundamentally the same across all surveys and/or seasons. This appears to be due to the production of a single model for each species and a lack of any temporal flexibility in the spatial parameterisation of the models (e.g. interaction between survey number, latitude and longitude or other selected parameters).	The DAA process ahead of the Hornsea Four DCO Application submission provided for a proactive review of seabird data to reduce the array area and remove WTGs from areas of higher seabird density. When viewing the MRSea outputs for the entire AfL area plus a 4 km buffer it is clearer to see patterns of bird densities both spatially and temporally, which are perhaps less obvious in the reduced size of the final array area assessed and presented in **A2.5 Environmental Statement Volume A2 Chapter 5 Offshore and Intertidal Ornithology (APP-017)**. With regards to the modelling approach and the inclusion of any temporal flexibility in the spatial parameterisation these were considered, though they were not included in the final	Revised MRSea modelling will include the interaction term that allows distributions to vary between months/bio-seasons.

Natural England's Comment	Applicant's Initial Response	Agreed Actions and Further Applicant Response
	model runs as they caused issues with the model fit and ability to run MRSea.	
The rationale for using the model-based approach over design-based estimates has not been addressed and there has been no consideration of model performance and the precision (coefficients of variation CVs) of estimates produced. Despite requests by NE, there has been no comparison between the raw data (i.e. counts and maps showing observations) or design-based estimates with the MRSea modelled estimates (including CVs). Moreover, the estimated relationships with selected covariates are not described and limited model diagnostics are presented.	The Applicant held a meeting with Natural England (ETG#13) to discuss the draft MRSea report and the suitability of the model concluded with agreement from all parties that these data were fit for the purpose of characterising the baseline for Hornsea Four and use in impact assessments. The assumption was therefore taken that any previous requests for additional information were superseded as all queries were discussed and agreed. As agreement was reached that MRSea abundance and density estimates were appropriate for use and no further requests were made ahead of the Application to provide any comparison between the raw data (i.e. counts and maps showing observations) or design-based estimates with the MRSea modelled estimates (including CIs) to use than design-based abundances this was not provided. With regards to the latter point, it was explained during ETG#13 that certain model diagnostics were not downloaded or screenshots taken though explanations as to the decision-making were described and agreed as appropriate. The modelled coefficients for each selected environmental variable in each model were included in the appendix to **A5.5.6 ES Volume A5 Annex 5.6 Offshore Ornithology MRSea Report (APP-079)**, however, further discussion of these relationships could be included in a revised version.	An updated Baseline Sensitivity Report providing design-based abundances estimates and basic dot-density maps with the current MRSea analysis and the revised MRSea analysis for one species (gannet) will be submitted at Deadline 2. This comparison will include consideration of model performance and output precision for the revised MRSea analysis. Additional information on estimated relationships and model diagnostics will be presented for the revised MRSea analysis. Details for an initial run of the model are presented in **Appendix A** of this document.
It also remains unclear how model-based estimates (all bird behaviours) have been treated to derive estimates for specific behaviours (sitting or flying birds) and how subsequent data corrections (apportioning of unidentified birds and adjustment for availability bias) have been applied and Confidence Intervals (CIs) calculated or adjusted. It also appears the Applicant has not reported	The Applicant provided CIs for all data within the Baseline Technical Report for modelled and design-based abundance and density estimates. However, CIs were not calculated for the post-apportioned and corrected datasets. There are some issues with applying or producing CIs retrospectively to modelled or design-based datasets meaning that the accuracy of such CIs may not be as reliable. With regards to the CRM seabird densities, the	The Applicant's position remains as that provided in their initial response.

Natural England's Comment	Applicant's Initial Response	Agreed Actions and Further Applicant Response
CIs associated with density estimates, though they appear to be used in the collision risk modelling.	method to calculate the variation around the mean was agreed with Natural England through the ETGs and relies on the estimation of Standard Deviations (SDs) around the central estimates of the two survey years monthly data.	
Natural England advises that there are several options available to resolve these concerns: A. Provide a robust defence of the adopted modelling approach (see below), including a clear comparison with design-based estimates; B. Revise the modelling approach to address specific issues (in line with CREEM advice), or C. Revert to design-based estimates and use other spatial mapping techniques (e.g. KDE) to illustrate temporal variations in spatial distributions.	The Applicant defends their use of MRSea as agreed in consultation with both Natural England and the Royal Society for the Protection of Birds (RSPB) through the Ornithology Technical Panel meetings (note agreement reached on MRSea use in ETG#13). The Applicant considers Option C to be contrary to all agreements and progress made on matters pertaining to ornithology over the past four years in consultation with Natural England and maintains that the MRSea as presented for baseline characterisation to be robust, using the best evidence available and aligned with agreements from the Statutory Nature Conservation Bodies (SNCBs).	Revised MRSea modelling for gannet is being conducted and will both address the specific issues highlighted in the CREEM advice and also serve to validate the results of the current MRSea results.
6. If Ørsted elect to defend the results of the models used in their assessment, we recommend the following approach is required: • Please provide a more detailed methodology and rationale for the modelling approach ultimately adopted. This should include further clarification on model specification and selection. Selected models should also be described in more detail (illustrating estimated relationships with included covariates) and model diagnostics (e.g. observed vs fitted and cumulative residual plots) presented. • Please provide a full justification for the use of the model-based method over the design-based method. This should include comparisons of modelled spatial distributions with raw data or KDE derived surfaces.	In consideration of the comments received from Natural England and CREEM the Applicant is currently drafting a new Baseline Sensitivity Report in order to provide as much clarity as possible on all points, as described above. The Applicant is also re-running the MRSea model for a single species (gannet) to check on how any slight changes in the model preparation may alter the final outcome of the dataset. The output from the MRSea model is the predicted number of birds within each cell of a user-supplied prediction grid. The area of each cell of the prediction grid is included and forms part of the prediction. The density of birds per grid cell is then calculated by dividing the predicted number of birds in each cell by the area of the grid cell. When using the modelled output to assess abundances and densities	Revised MRSea modelling for gannet is being conducted and will both address the specific issues highlighted in the CREEM advice and also serve to validate the results of the current MRSea results. The Baseline Sensitivity Report will revise the modelling methodology (see **Appendix A**) and results will be presented in an updated Baseline Sensitivity Report at Deadline 3 in a manner that clarifies any outstanding concerns raised.

Natural England's Comment	Applicant's Initial Response	Agreed Actions and Further Applicant Response
It is also requested that the full spatial extent of the modelled surfaces should be presented on maps. Density and population estimates, and associated CIs, should be compared between model- and design-based methods and there should be discussion in relation to the precision of each of the methods based on CVs. • Please also clearly define how population and density estimates were derived (apparently using different approaches) from the modelled surfaces. Confirm whether densities scaled to the relevant area would produce the same populations and associated CIs. Describe how data from cells intersected by the wind farm perimeter or relevant buffer (i.e. part cells of < 1 km^2) have been treated during population and density estimation. • Please provide a description of how populations and densities were apportioned to different behaviours; and • Please clearly describe how Standard Deviations (SDs), CIs and CVs (SD/mean or SE/mean) were estimated using model-based approaches for total populations, densities, apportioned behaviours and corrected apportioned behaviours. Based on discussion with statisticians at CREEM, NE suggests consideration of the following approach for deriving mean abundance and density estimates, and their associated SDs and CIs when bootstrapping is used (applicable to model- or design-based estimates). Apportioning (unidentified birds or behaviours) and application of correction factors (e.g. availability corrections) should be applied to model- or design-based bootstrap sample estimates for each survey. The resultant overall abundance distributions from the samples should be used to derive the means, SDs and CIs. If a mean, SD and CIs are required based on two or more	of smaller areas within the prediction grid, it is assumed that density is constant within each grid cell, and therefore the abundance within a specified area can be readily calculated as the product of the density per grid cell and the area of each grid cell within the specified area. With regards to behaviours, the raw count data (for flying and sitting) were used to split modelled data, which was run with all birds (flying and sitting). See note above regarding why. The process for adjusting data to account for unidentified birds and to account for availability bias are fully described in **A5.5.1 ES Volume A5 Annex 5.1 Offshore and Intertidal Ornithology Baseline Characterisation Report (APP-074)** and follow standard industry methods. CIs were provided for all data presented within the **A5.5.1 ES Volume A5 Annex 5.1 Offshore and Intertidal Ornithology Baseline Characterisation Report (APP-074)** for modelled and design-based abundance and density estimates (prior to any apportionment). However, CIs were not calculated for the post-apportioned and corrected datasets as the approach undertaken for apportionment does not allow robust CIs to be readily calculated. It is not straight forward to run design-based or model-based abundances to include CIs with CVs around apportioned and corrected data. With regards to the Collision Risk Model (CRM) seabird densities, the method to calculate the variation around the mean was agreed with Natural England through the ETGs and relies on the estimation of SDs around the central estimates of the two survey years monthly data.	

Natural England's Comment	Applicant's Initial Response	Agreed Actions and Further Applicant Response
surveys (e.g. from two peak abundance estimates within a season or two densities of birds in flight in a calendar month), the relevant corrected bootstrap samples should be pooled to provide a single sample from which to draw the estimates.		
In essence, a more detailed methodology is required that fully describes the different aspects of the modelling and associated diagnostics in relation to performance. More fundamentally, in order for Natural England to re-appraise our position on the modelling presented, we require a comparison of the model-based estimates with the design-based estimates and modelled spatial distributions against the raw observation data for each survey/month.	As noted above it is not possible to provide all elements of CREEM's requests due to certain aspects not being exported from R during the modelling process. However, the Applicant intends on running a single species (gannet) again following the advice from Natural England and CREEM to present as much additional data as possible and to download or take screenshots of the modelling process, where applicable. This will then be reviewed and issued in a Baseline Sensitivity Report to Natural England. With regards to the latter point, the use of MRSea was agreed through consultation with Natural England (at ETG#13) as being the preferred method to determine the baseline for this project. The change in position post-application is contrary to the agreements in place during the pre-application phase.	Revised MRSea modelling for gannet is being conducted and will both address the specific issues highlighted in the CREEM advice and also serve to validate the results of the current MRSea results. The revised modelling and results will be presented in an updated Baseline Sensitivity Report at Deadline 3 in a manner that clarifies any outstanding concerns raised.
With respect to the CREEM report, as stated in our meeting of 08 December 2021 it was the tone/opinions that did not reflect Natural England's position rather than the technical content. As CREEM are the experts on the MRSea modelling technique, we consider their concerns relating to methodology to be entirely justified and suggest Ørsted should address and/or provide a response to each point raised.	The Applicant has provided responses to the CREEM report (see **Table 2**).	The Applicant has provided responses to the CREEM report (see **Table 2**).

Table 2: CREEM's comments on MRSea modelling and Applicant's responses.

CREEM's Comment	Applicant's Initial Response	Agreed Actions and Further Applicant Response
In general, the overall methods description is poor with some key errors. This suggests that author is not clear on how the methods work or how to adapt them to suit their needs. This is further indicated by including function names rather than the actual methods (for example cv.gamMRSea instead of k-fold cross-validation).	The method section has been reviewed following a conversation between Lindsay Scott-Hayward from CREEM and Tim Kasoar & Sean Sweeney from APEM to understand which description they felt needed clarification. It is the Applicant's opinion is that by including function names in the methods sections it ensures maximum clarity for the reader and enables easy and precise replication. However, the Applicant recognises that statisticians may benefit from being able to see both function names and generic statistical terminology, which will be provided to explain the methods in a manner that allows a clearer understanding for readers with different levels of modelling/statistical expertise.	The Applicant's Baseline Sensitivity Report (Part 2 and 3), to be submitted at Deadline 3, will account for the advice received by CREEM to provide a clearer understanding for readers with different levels of modelling/statistical expertise. Please see **Appendix A** for preliminary outcomes of the application of the advice from CREEM in relation to cross-validation.
There is no description of the sightings data or visual representation of the sightings or transect data for any species which makes it very difficult to pass judgement on model fit and suitability of the analysis.	A review of model fit was undertaken against the raw distribution of species to ensure model fit and suitability of analysis. However, the Applicant recognise that some of these details are not contained within the methods section of the **A5.5.6 ES Volume A5 Annex 5.6 Offshore Ornithology MRSea Report (APP-079)** as the inclusion of such would unnecessarily have increased the volume of the document. These data are available and could be provided as evidence to support the use and suitability of MRSea modelling to define the baseline for Hornsea Four.	The Applicant's Baseline Sensitivity Report (Part 2 and 3), to be submitted at Deadline 3, will allow for comparisons between design-based abundances estimates and basic dot-density maps, the previous iteration of MRSea analysis, and the revised MRSea analysis, all for one species (gannet). This comparison will include consideration of model performance and output precision for the revised MRSea analysis.
In paragraph 2.2.1.4. the authors state that the "CReSS" method incorporates auto-correlation. This is not strictly true, "CReSS" is the name given to the spatial smooth. The R package MRSea has the ability to allow for residual correlation but the user must specify its use via a panel variable.	The Applicant recognise and understand that the "CReSS" method is the name given to the spatial smoother within the MRSea model. Residual autocorrelation within the data was accounted for by specifying a unique transect number as the panel variable. The Applicant recognise that statisticians may benefit from being able to see both function names and generic statistical terminology, which will be provided to explain the methods in a manner that	The Applicant's Baseline Sensitivity Report (Part 2 and 3), to be submitted at Deadline 3, will account for the advice received by CREEM to provide a clearer understanding for readers with different levels of modelling/statistical expertise.

CREEM's Comment	Applicant's Initial Response	Agreed Actions and Further Applicant Response
	allows a clearer understanding for readers with different levels of modelling/statistical expertise.	
In paragraph 2.3.1.3. it is stated that "autocorrelation within the data.". Data correlation is not a problem but residual correlation violates a major assumption of a GLM/GAM. How was residual correlation tested? ACF plot/ Runs Test? Additionally, it seems odd to include month/season in the blocking structure when survey date is already included.	The Applicant can confirm that residual correlation was examined using both ACF plots and Runs Test. For ACF plots residual correlation in the model was examined by ensuring that autocorrelation decays close to zero in a short lag period. For Runs Test residual correlation in the model was examined by interpreting the P value produced to ensure a non-significant value. When running the Runs Test, a significant P value of less than 0.05 was found. This indicated that there was presence of residual correlation within the model, however by specifying an appropriate blocking structure, residual correlation should be corrected for within the model to ensure model p-values and error margins were robust. The appropriateness of the blocking structure was tested using an ACF plot. The absence of the documentation of these tests was brought up during the EP Process with Natural England. The Applicant explained that in relation to the tests referred to above, the outputs were not saved after interrogation. This was due to not having prior knowledge of which outputs would be required at the time of running the model, and these outputs are not provided as automatic outputs or available after models have been run. Due to the stochastic nature of the model fitting process, if the Applicant were to rerun the models this would have produced slightly different outputs, so they could not be provided. Natural England were content with this explanation and the matter was agreed and closed. Month/season is included as a factor to recognise species' migratory patterns and noting that the surveys cover a two-year period, which is therefore distinct from the	An initial re-run of MRSea modelling for gannet has been carried out. The runs test and ACF plot generated as part of the initial process are presented in **Appendix A**. In the revised MRSea model, only survey ID is used within the blocking structure.

CREEM's Comment	Applicant's Initial Response	Agreed Actions and Further Applicant Response
	temporal autocorrelation that results from surveys being close in time.	
It is earlier stated that the blocking structure is included in modelling to account for autocorrelation, why then in paragraph 2.3.1.4 are models re-fitted as GEEs? If a blocking structure was given to MRSea, all standard errors and p-values from the model will be adjusted for the presence of residual correlation. Assuming the GEE has been fitted using an independent working correlation matrix (as opposed to AR(1) for example) and robust standard errors calculated (the default in this scenario) then this part is entirely redundant.	It is not possible for the Applicant to provide all elements of CREEM's requests due to certain aspects not being exported from R during the modelling process. However, the Applicant intends on running a single species (gannet) again following the advice from Natural England and CREEM to present as much additional data as possible and to download or take screenshots of the modelling process, where applicable.	An initial re-run of MRSea modelling for gannet has been carried out as presented in **Appendix A**. Models are no longer refitted as GEES.
This paragraph also states that "The best model can have inaccurate p-values if auto-correlation still exists despite the blocking structure". This is not true if the blocking structure has been specified correctly (and can be checked with a block based ACF plot). Further, MRSea uses a block structure and robust standard errors to account for residual correlation. It does not remove residual correlation as the methods for accounting for it operate solely on the standard errors (not the residuals themselves). In this case any residual correlation will still be present (even after the inclusion of a blocking structure) and an ACF plot would therefore still show the correlation.	It is not possible for the Applicant to provide all elements of CREEM's requests due to certain aspects not being exported from R during the modelling process. However, the Applicant intends on running a single species (gannet) again following the advice from Natural England and CREEM to present as much additional data as possible and to download or take screenshots of the modelling process, where applicable.	An initial re-run of MRSea modelling for gannet has been carried out as presented in **Appendix A**, with robust p-values generated.
The inclusion of a sentence about co-linearity in a paragraph predominantly about residual correlation is confusing. VIFs can be checked up front (prior to any modelling) so collinearity as an issue can be dealt with early on.	The Applicant ensured to check VIFs upfront, before proceeding further with modelling. However, in accordance with best practice, variables showing co-linearity were not removed at that stage and were instead re-assessed after fitting the spatial smooth. As stated above, the Applicant's Baseline Sensitivity Report will provide as much clarity as possible these matters.	An initial re-run of MRSea modelling for gannet has been carried out as presented in **Appendix A**. As per the original MRSea modelling the VIFs are checked upfront, but any co-linearity identified is not dealt with upfront as it is addressed through the model selection process.

CREEM's Comment	Applicant's Initial Response	Agreed Actions and Further Applicant Response
Paragraph 2.3.1.4. states the use of cross validation but only the function name is given and no mention of the type of CV; k-fold. Was it 10-fold cross-validation and did it select folds whilst maintaining the block structure? There is also no mention of how the best model including s(x,y) was chosen and at the end of the paragraph it is then stated that p-values are used for model selection. A look at the results, where there are non-significant p-values would suggest that these have not been used for selection. It would be better to stick to a process and either use k-fold CV for everything (smoothness selection and variable inclusion) or k-fold CV for smoothness and p-values for variable inclusion, whichever you prefer.	It is not possible for the Applicant to provide all elements of CREEM's requests due to certain aspects not being exported from R during the modelling process. However, the Applicant intends on running a single species (gannet) again following the advice from Natural England and CREEM to present as much additional data as possible and to download or take screenshots of the modelling process, where applicable.	An initial re-run of MRSea modelling for gannet has been carried out as presented in **Appendix A**. 10-fold cross validation was used for smoothness selection. P-values were used to consider variable inclusion.
In the methods section, the general models trialled are not specified at all. I would expect a generic equation/paragraph in the methods section stating what is being fitted and to include things like a. Poisson GAM with (over)dispersion and log link b. Discrete covariates (survey or season) c. Quadratic (?) B-splines for the 1D covariates (also allowed as linear?) d. Gaussian (?) radial basis function for the two dimensional smooth of coordinates e. How much flexibility has the user allowed for the B-splines and the spatial smooth – these are user defined. f. Were the discrete variables trialled as interaction terms with the spatial term? Given the 1D variables are all static over time, the only option in the model for a change in distribution over time would be to allow an interaction term of survey or season with s(x,y). Your model selection process would then be used to assess if the inclusion of this term was warranted. Alternatively, if there are computational issues with this, you could fit separate models to each survey. The possibility of a change in	The Applicant will review the methods sections and provide greater input in relation to the points specified above (a to e) to ensure the rationale taken forward for modelling is evidenced. In summary: The initial GLM was a quasipoisson (allowing for oversdispersion) with a log link; survey month or survey season (depending on species) was included as a discrete covariable; b-splines were quadratic (degree = 2); the radial basis function was not specified and therefore the default was used; the maximum number of knots was set to 5 for both 1D and 2D smooths. With regards to point (f) it is not possible for the Applicant to provide all elements of CREEM's requests due to certain aspects not being exported from R during the modelling process. However, the Applicant intends on running a single species (gannet) again following the advice from Natural England and CREEM to present as much additional data as possible and to download or take screenshots of the modelling process, where applicable.	An initial re-run of MRSea modelling for gannet has been carried out as presented in **Appendix A**.

CREEM's Comment	Applicant's Initial Response	Agreed Actions and Further Applicant Response
spatial distribution over time should, at the very least, be discussed.		
Paragraph 2.2.1.4 briefly comments on the use of bootstraps to generate confidence intervals. Presumably this was done using the functionality in MRSea and so is a parametric bootstrap (each bootstrap replicate is based on sampling the model parameters from a multivariate normal). How many bootstraps were used? 500, 1000? Additionally, the glossary definition of "Bootstrapping" in the context of MRSea is incorrect.	The Applicant confirmed 500 bootstraps were used and were carried out using the built-in functionality and accordingly it was a parametric bootstrap. The glossary definition will be updated.	An initial re-run of MRSea modelling for gannet has been carried out as presented in **Appendix A**. This uses 1,000 parametric bootstraps to generate CIs (**Figure 12** and **Figure 13**).
Paragraph 2.3.1.6 describes the calculation of abundance and density estimates. It is not clear how the confidence intervals were calculated and why they were not also presented for the density. The bootstraps can be used to get a set of abundances for each time frame and then as for the cell-based estimates, take the quantiles to get your intervals.	The Applicant agreed that any updated reporting will be modified for clarity. Confidence intervals were generated using the bootstrapping approach as acknowledged in the previous comment. Confidence intervals were not presented for density in order to keep the results concise, though these can be readily calculated from the abundance upper and lower confidence limits if required.	An initial re-run of MRSea modelling for gannet has been carried out as presented in **Appendix A**. This uses 1,000 parametric bootstraps to generate CIs (**Figure 12** and **Figure 13**).
In the results sections, the final model specifications are not given correctly as each one omits the spatial term (which appears to have been selected for in most models) and there is no reason given for why some variables are not in the final model (model selection, collinearity, model fitting issues etc). As mentioned earlier, I would not give R commands as a result in a report. You could try a table with each of the potential variables and give estimated degrees of freedom (or reason for exclusion), and an image of the estimated 1D relationships etc. There is no discussion of the 1D variable relationships and some seem to have excessive flexibility (7df) which is often not warranted in these sorts of settings. Additionally, having fitted two types of model (survey or season) some information about which is the better fitting model would be useful (using say CV scores). If the survey model was best then, being the finer temporal resolution, the season	It is not possible for the Applicant to provide all elements of CREEM's requests due to certain aspects not being exported from R during the modelling process. However, the Applicant intends on running a single species (gannet) again following the advice from Natural England and CREEM to present as much additional data as possible and to download or take screenshots of the modelling process, where applicable.	An initial re-run of MRSea for gannet has been carried out as presented in **Appendix A**. However, further models are planned to be run (if computationally possible) and therefore further discussion of the merits of each model will be presented in the full revised report.

CREEM's Comment	Applicant's Initial Response	Agreed Actions and Further Applicant Response
estimates can be post processed from the predictions/bootstraps.		
Model diagnostics (observed vs fitted and cumulative residuals) were mentioned in paragraph 2.3.1.4 but are not shown/described for any species so the reader has little idea of whether the models are any good. In addition to the diagnostics mentioned, the mean-variance relationship and spatial residuals could/should also be assessed.	The Applicant will provide further detail in the Baseline Sensitivity Report with model diagnostics provided when revising the MRSea modelling for a single species (gannet). However, the Applicant are unable to provide the output diagnostics for the model due to them not being automatically outputted from the current MRSea model when it was run. The Applicant understands that the absence of such diagnostics does not allow for external interpretation of the model. However, the Applicant confirmed that the statisticians did review the diagnostics from the model and were confident with the results produced. It was also recognised that not providing the diagnostics would not lead to the results changing.	An initial re-run of MRSea for gannet has been carried out as presented in **Appendix A**. Additional model diagnostics for this initial re-run have been provided (**Figure 16** to **Figure 18**).
There is no presentation of the spatial uncertainty. It could be shown in the form of plots of coefficient of variation or percentile-based confidence intervals. The bootstraps have been done so it would be easy to calculate either of these for each grid cell.	The Applicant will provide the confidence intervals as requested when revising the MRSea modelling and present this in the Baseline Sensitivity Report.	An initial re-run of MRSea for gannet has been carried out as presented in **Appendix A**. This includes presentation of spatial uncertainty (**Figure 15**).

5 Baseline Sensitivity Report – Part 1 (Methodology for Revised MRSea Modelling)

5.1.1 Data processing & Modelling Approach

5.1.1.1 In line with the approach agreed with Natural England, during the consultation meeting on the 17th February 2022, MRSea analysis was performed *de novo* for gannet following the best practice guidance in Scott-Hayward et al. (2017). The initial stages of the re-building and testing process for the revised MRSea modelling also accounts for the comments provided in the CREEM Statistical Review of Hornsea Project Four: Environmental Statement for Natural England (Scott-Hayward, 2021, comments related to the review presented in **Table 2**).

5.1.1.2 Aerial digital video surveys were conducted by HiDef between April 2016 and March 2018, inclusive. Shapefiles of observations and transect lines from each survey were supplied by HiDef. The footprint of each survey was estimated from the transect line shapefile by assuming a 125m image half-width, as specified by HiDef, and generated using the MMQGIS Create Buffer tool within QGIS (QGIS Version 3.10.5; MMQGIS version 2020.1.16). Observation and transect shapefiles were clipped to the Hornsea Four Agreement for Lease (AfL) area plus 4 km buffer.

5.1.1.3 A regular grid of 1x1km squares covering the Hornsea Four AfL plus 4 km buffer was generated using the "Create grid" tool within QGIS. The transect footprints were intersected with this grid to produce a shapefile of transect segments for each survey.

5.1.1.4 For each transect segment, distance to coast, distance to Flamborough and Filey Coast Special Protection Area (FFC SPA), and depth were calculated within R (R Core Team, 2020) as follows. The distance to coast was measured in kilometres from the centroid of each transect segment to the nearest point on the coast based on a publicly available shapefile of coastlines[1] and using the st_nearest_points function in the sf package (Pebesma, 2018). The distance to FFC SPA was measured in kilometres from the centroid of each transect segment to the centroid of FFC SPA, based on the SPA shapefile available from JNCC (2021). The depth of each transect segment was calculated as the area-weighted mean depth in metres within each transect segment using the OceanWise Bathymetry raster. The coordinates of the centroid of each transect segment in UTM zone 31N (EPSG:32631) were added as variables named "x.pos" and "y.pos".

5.1.1.5 The same approach was taken to assign a distance to coast, distance to FFC SPA, depth, x.pos and y.pos to each grid cell of the 1x1km grid, to be used as the prediction grid.

5.1.1.6 Observations of birds were assigned to each transect segment using a spatial join with the join term set to "nearest". This accommodates minor discrepancies between the observation shapefile and the transect footprints. The number of gannets per transect segment was then extracted and added to the transect shapefile. The survey month was extracted from the date field present within the transect line shapefile, and a field for gannet bio-seasons was created based on the survey month and the definitions of bio-seasons presented in **A2.5 Environmental Statement Volume A2 Chapter 5 Offshore and Intertidal Ornithology (APP-**

[1] https://www.naturalearthdata.com/downloads/10m-physical-vectors/10m-coastline/

017). The transect shapefile was then converted into a data frame for use as input to the subsequent modelling.

5.1.1.7 All subsequent modelling was carried out in R (R Core Team, 2020) using MRSea version 1.3.

5.1.1.8 An initial model run is presented in **Appendix A**. The final results will include more model runs using the same approach.

6 Part 2 - Revised MRSea Results (pending)

7 Part 3 - Comparison of DCO Application and Revised MRSea Results (pending)

8 References

JNCC (2021). Special Protection Areas (SPAs) of Great Britain (including offshore areas): shapefile. Contains public sector data from © JNCC/NE/NRW/NatureScot 2021. Contains OS data © Crown Copyright and database right 2016. Available at https://hub.jncc.gov.uk/assets/20dbc9b4-ceac-4bf2-8763-4ae387fa88c4 [Accessed 03/12/2021].

R Core Team (2020). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL [redacted]

Pebesma, E.J., 2018. Simple features for R: standardized support for spatial vector data. R J., 10(1), p.439.

Scott-Hayward, L.A.S, Mackenzie, M.L., Donovan, C.R., Walker, C.G. and Ashe, E. (2014). Complex Region Spatial Smoother (CReSS). Journal of Computational and Graphical Statistics 23:2, 340-360.

Scott-Hayward et al. (2017) Vignette for the MRSea Package v1.3: Statistical Modelling of bird and cetacean distributions in offshore renewables development areas. Centre for Research into Ecological and Environmental Modelling, University of St Andrews

Scott-Hayward, L.A.S. (2021). Statistical Review of Hornsea Project Four: Environmental Statement for Natural England. CREEM, University of St Andrews.

Appendix A Details of initial revised MRSea re-run for gannet

Introduction

An initial re-run of MRSea has been carried out for gannet. The aim of this re-run is to demonstrate the process and present model details and diagnostics, in order to seek agreement that the broad approach is acceptable and the details presented are appropriate.

As an interim approach, the model has been run using depth as a continuous co-variable. In the final revised report, the aim is to also consider using distance to coast and distance to FFC SPA as continuous variables, although the final model specification will be dependent on the ability to fit the models and the subsequent model selection approach.

Initial Set-up

To assess co-linearity of explanatory variables, Generalised Variance Inflation Factors (GVIFs) are checked at the start of the process (

```
> vif(initial_gannet_model_month_only)
                       GVIF Df GVIF^(1/(2*Df))
mean_depth         4.076740  1        2.019094
as.factor(month)   1.000254 11        1.000012
x.pos              1.356699  1        1.164774
y.pos              4.737407  1        2.176559
```

Figure 1).


```
> vif(initial_gannet_model_month_only)
                       GVIF Df GVIF^(1/(2*Df))
mean_depth         4.076740  1        2.019094
as.factor(month)   1.000254 11        1.000012
x.pos              1.356699  1        1.164774
y.pos              4.737407  1        2.176559
```


Figure 1 – Code snippet showing testing for co-linearity

In this case, the adjusted GVIFs for mean_depth and *y*.pos are both approximately 2 (i.e. the confidence intervals are twice as wide as they would be in the absence of any co-linearity). There is therefore some co-linearity, but as it is relatively small and as *y*.pos will not be modelled in a linear manner, no further action is taken.

In order to fit the model, there needs to be non-zero counts for all levels of categorical variables (in this case month; Figure 2). This is the case and so no action needs to be taken.

```
> checkfactorlevelcounts(factorlist=c("month"), gannet_model_data, gannet_model_data$response)
[1] "month will be fitted as a factor variable; there are non-zero counts for all levels"
> |
```

Figure 2 – Code snippet showing check of non-zero counts for all factor levels.

Generalised Linear Model

A basic Generalised Linear Model (GLM) is run as an initial model (Figure 3).

```
> summary(initial_gannet_model_month_only)

Call:
glm(formula = response ~ mean_depth + as.factor(month) + x.pos +
    y.pos + offset(log(area)), family = "quasipoisson", data = gannet_model_data)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.3446  -0.5503  -0.3312  -0.1479  15.1951

Coefficients:
                      Estimate Std. Error t value Pr(>|t|)
(Intercept)          2.593e+01  3.849e+01   0.674 0.500411
mean_depth           1.738e-02  7.483e-03   2.322 0.020228 *
as.factor(month)Aug  7.038e-01  2.119e-01   3.321 0.000899 ***
as.factor(month)Dec  8.037e-02  2.408e-01   0.334 0.738606
as.factor(month)Feb -1.970e+00  4.973e-01  -3.963 7.43e-05 ***
as.factor(month)Jan -8.908e-01  3.223e-01  -2.764 0.005718 **
as.factor(month)Jul  7.595e-01  2.101e-01   3.616 0.000300 ***
as.factor(month)Jun  8.574e-01  1.964e-01   4.367 1.27e-05 ***
as.factor(month)Mar -5.833e-01  2.904e-01  -2.008 0.044610 *
as.factor(month)May  5.436e-01  2.553e-01   2.129 0.033281 *
as.factor(month)Nov  1.114e+00  2.000e-01   5.572 2.55e-08 ***
as.factor(month)Oct  1.073e+00  2.007e-01   5.346 9.07e-08 ***
as.factor(month)Sep  5.283e-01  2.184e-01   2.419 0.015582 *
x.pos                5.384e-06  4.103e-06   1.312 0.189432
y.pos               -4.706e-06  6.342e-06  -0.742 0.458060
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasipoisson family taken to be 3.693347)

    Null deviance: 14215  on 22396  degrees of freedom
Residual deviance: 13127  on 22382  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 7
```

Figure 3 – Code snippet showing summary of initial GLM

A runs test is carried out on the initial model (Figure 4). From the highly significant p-value, it is evident that there is significant residual correlation within the initial model.

```
> runs.test(residuals(initial_gannet_model_month_only, type = "pearson"), alternative = c("two.sided"))

        Runs Test - Two sided

data:  residuals(initial_gannet_model_month_only, type = "pearson")
Standardized Runs Statistic = -15.162, p-value < 2.2e-16
```

Figure 4 – Code snippet showing runs test

This is further evidenced by non-randomness in the runs profiles (**Figure 5**).

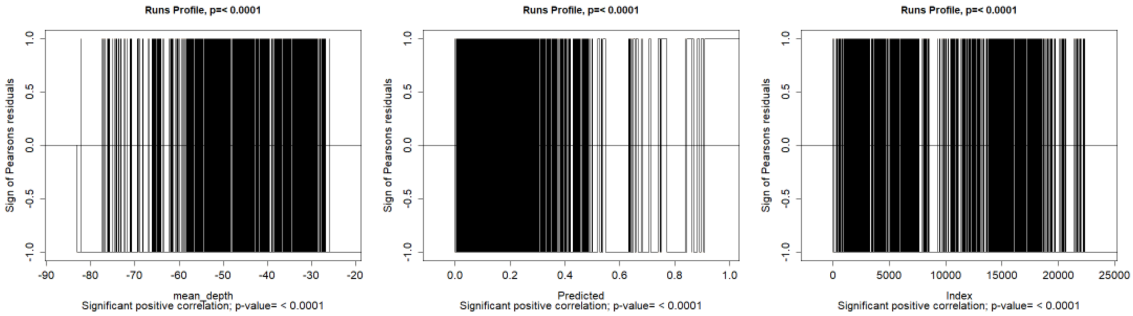

Figure 5 – Runs profile plots. The lines are sequences of positive and negative residuals. In the absence of correlated residuals, the lines would be randomly distributed. Significance of the correlation is also printed beneath each plot.

Therefore, a blocking structure is necessary. Survey ID is specified as the blocking structure – i.e. the model should treat data from within a survey as correlated, but independent between surveys. An Auto-Correlation Function (ACF) plot is used to assess the appropriateness of this blocking structure (**Figure 6**). The mean correlation in residuals (indicated by the red line) and the correlation in residuals within each block (grey lines) both drop to approximately zero, suggesting that the blocking structure specified is appropriate.

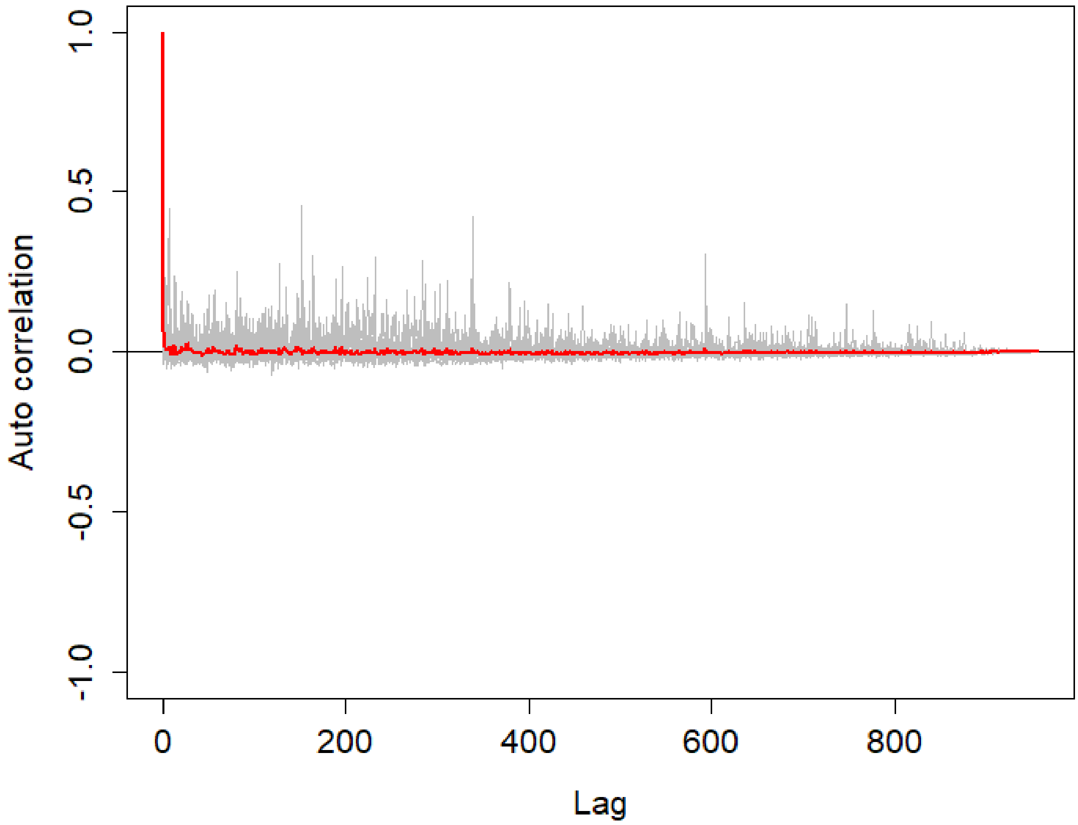

Figure 6 – Auto-correlation Function (ACF) plot. Grey lines are correlation in residuals within each block. Red line is the mean correlation in residual.

Cumulative residuals are calculated (**Figure 7**). The black line shows the modelled cumulative residuals, while the grey line shows what we would expect if the model was correctly fitted. It is evident that there is some systematic over- and under-prediction, especially at shallow water depths. This confirms the need for a more complex model.

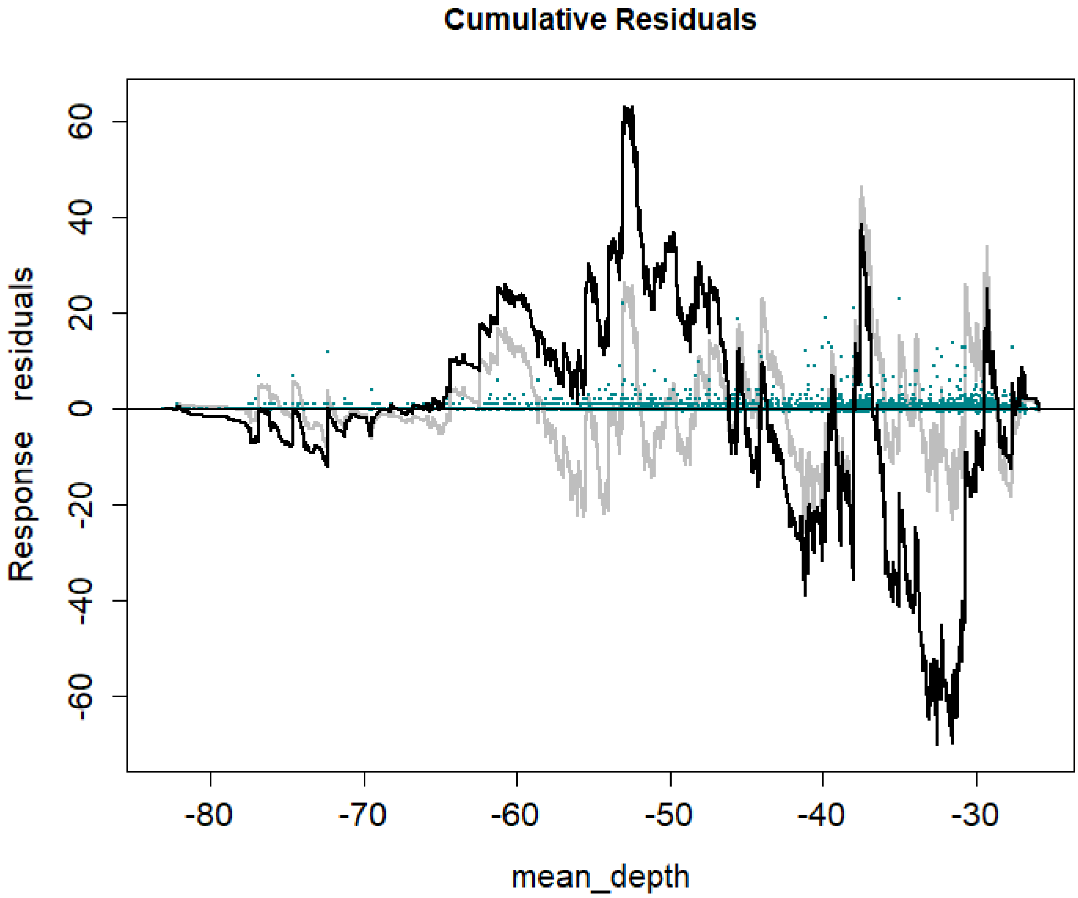

Figure 7 – Cumulative residuals ordered by depth.

Smoothed Model (1D SALSA)

Therefore, with an appropriate blocking structure identified and a clear need for a non-linear model, 1D SALSA is carried out using the parameters specified below (Figure 8). The spline parameters were generated using the built-in function (makesplineParams) and defaults to a degree of two. As the "removal" term was not specified in the runSALSA1D function, all variables were considered with smooth splines (not allowed to be linear or removed). Note that the 1D SALSA routine does not allow for an interaction term to be fitted; an interaction term would be considered as part of the 2D SALSA routine when possible. At this stage, it has not proved possible to fit the 2D SALSA model following the same approach.

```
initial_gannet_model2_month_only <- glm(response ~  as.factor(month) + offset(log(area)),
                                        family = "quasipoisson", data = gannet_model_data)

splineParams<-makesplineParams(data=gannet_model_data, varlist=c('mean_depth'),
                               predictionData=predict_grid_df)

salsa1dlist <-list(fitnessMeasure = "cv.gamMRSea",
                   minKnots_1d = c(1),
                   maxKnots_1d = c(3),
                   startKnots_1d = c(1),
                   degree=c(2),
                   maxIterations = 10,
                   gaps = c(100),
                   cv.opts = list(cv.gamMRSea.seed = 1, K=10))

salsa1doutput_month_only <-runSALSA1D(initialModel=initial_gannet_model2_month_only, salsa1dlist=salsa1dlist,
                                      varlist=c('mean_depth'), factorlist=c("month"),
                                      datain = gannet_model_data,
                                      panelid = gannet_model_data$survey_id,
                                      predictionData = predict_grid_df, splineParams=splineParams)
```

Figure 8 – Code snippet showing setting up of 1D SALSA.

The 1D SALSA function produces many different models and compares them using the specified fitness measure, in this case 10-fold cross validation. The model with the best fit (lowest cross-validation error) is returned as the "best model". A summary of the best model is shown in **Figure 9**.

```
> summary(salsa1doutput_month_only$bestModel)

Call:
gamMRSea(formula = response ~ as.factor(month) + bs(mean_depth,
    knots = splineParams[[2]]$knots, degree = splineParams[[2]]$degree,
    Boundary.knots = splineParams[[2]]$bd) + offset(log(area)),
    family = quasipoisson(link = log), data = gannet_model_data,
    splineParams = splineParams)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.4516  -0.5549  -0.3310  -0.1496  15.2944

Coefficients:
                     Estimate Std. Error Robust S.E. t value Pr(>|t|)
(Intercept)          -1.35964    0.43381     0.65581  -2.073  0.03816 *
as.factor(month)Aug   0.70362    0.21279     0.04754  14.801  < 2e-16 ***
as.factor(month)Dec   0.08018    0.24181     0.02507   3.199  0.00138 **
as.factor(month)Feb  -1.97074    0.49924     0.46694  -4.221 2.45e-05 ***
as.factor(month)Jan  -0.89081    0.32361     0.66571  -1.338  0.18086
as.factor(month)Jul   0.75932    0.21089     0.25308   3.000  0.00270 **
as.factor(month)Jun   0.85698    0.19714     0.39382   2.176  0.02956 *
as.factor(month)Mar  -0.58341    0.29157     0.19183  -3.041  0.00236 **
as.factor(month)May   0.54343    0.25636     0.01247  43.596  < 2e-16 ***
as.factor(month)Nov   1.11423    0.20075     0.20917   5.327 1.01e-07 ***
as.factor(month)Oct   1.06951    0.20154     0.24393   4.384 1.17e-05 ***
as.factor(month)Sep   0.52781    0.21927     0.07488   7.049 1.85e-12 ***
s(mean_depth)1       -0.05313    0.53826     1.01505  -0.052  0.95825
s(mean_depth)2        0.54697    0.37811     0.54395   1.006  0.31464
s(mean_depth)3        1.08409    0.45211     0.89027   1.218  0.22334
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasipoisson family taken to be 3.722853)

    Null deviance: 14215  on 22396  degrees of freedom
Residual deviance: 13126  on 22382  degrees of freedom
AIC:  NA

Max Panel Size = 958; Number of panels = 24
Number of Fisher Scoring iterations: 7
```

Figure 9 – Summary of model identified as the best fitting model through the 1D SALSA algorithm.

An Analysis of Variance (ANOVA) is carried out to test the significance of variables included in the model (Figure 10). As the ANOVA finds both variables to be significant, there is no need to remove either from the model.

```
> anova(salsa1dOutput_month_only$bestModel)
Analysis of 'Wald statistic' Table
Model: quasipoisson, link: log
Response: response
Marginal Testing
Max Panel Size = 958; Number of panels = 24

                  Df      X2 P(>|Chi|)
as.factor(month) 11 2553.23 < 2.2e-16 ***
s(mean_depth)     3   16.95 0.0007228 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Figure 10 – ANOVA of the best fitting model

Ten-fold cross-validation is used to compare the 1D model to the GLM (Figure 11). Although the estimates are similar, the estimated error for the 1D model is lower and therefore that model is a better fit than the GLM.

```
> # 1D model
> cv.gamMRSea(data=gannet_model_data, modelobject = salsa1dOutput_month_only$bestModel, K=10)$delta[2]
[1] 0.4925561
> # intitial model
> cv.gamMRSea(data=gannet_model_data, modelobject = initial_gannet_model_month_only, K=10)$delta[2]
[1] 0.4926745
```

Figure 11 – Code snippets showing cross-validation error estimates for GLM and the best fitting 1D smoothed model

The estimated response (gannets per grid cell) is predicted from the prediction grid. Although largely a 1x1km grid as the prediction grid is cropped to the Hornsea Four AfL plus 4 km buffer, the response is converted to a density by dividing by the area of each grid cell (grid cells on the edge of the prediction grid are <1 km^2; all other cells are exactly 1 km^2; **Figure 12**).

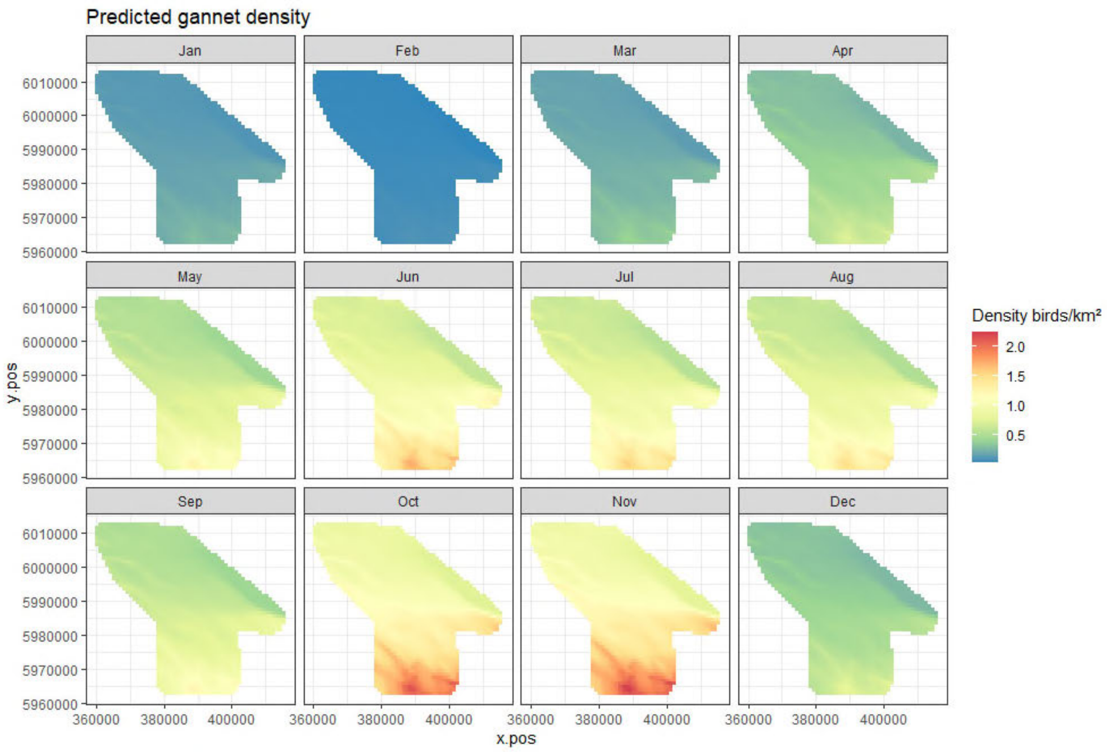

Figure 12 – Predicted gannet density per month

Confidence intervals are estimated using a robust parametric bootstrap with 1,000 bootstraps. The 95% CIs are presented in **Figure 13** and **Figure 14**. Note that the colour scale differs between the mean, lower CI, and upper CI figures.

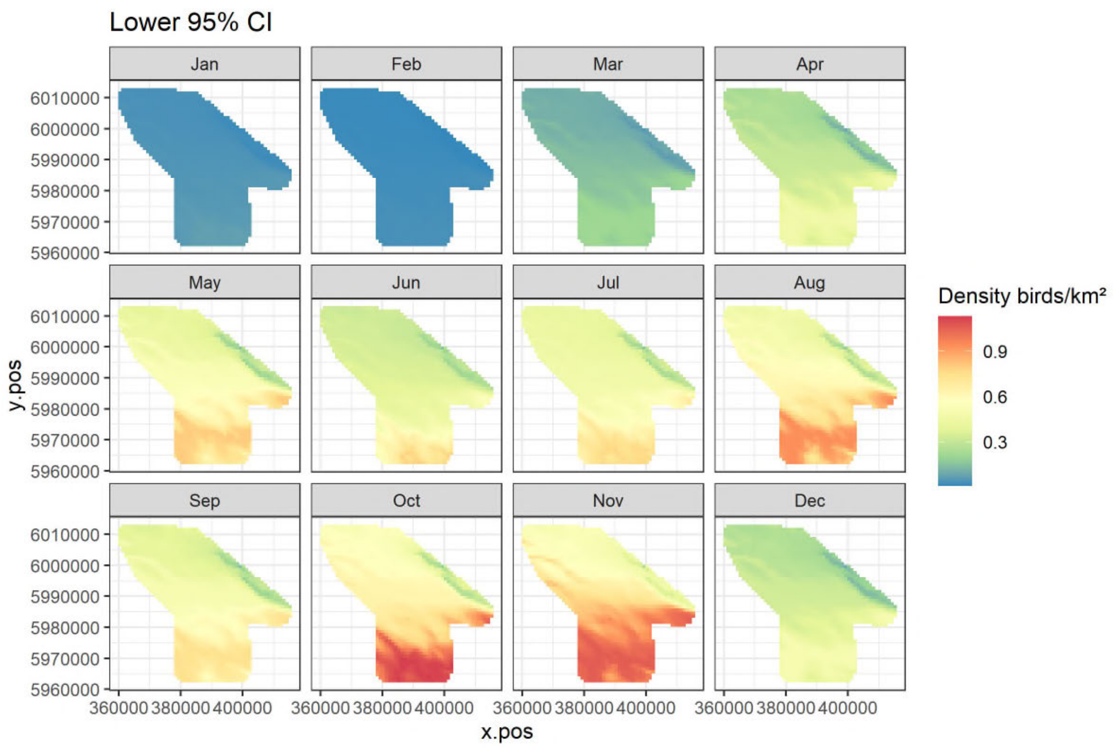

Figure 13 – Lower density estimate from 95% Confidence Intervals

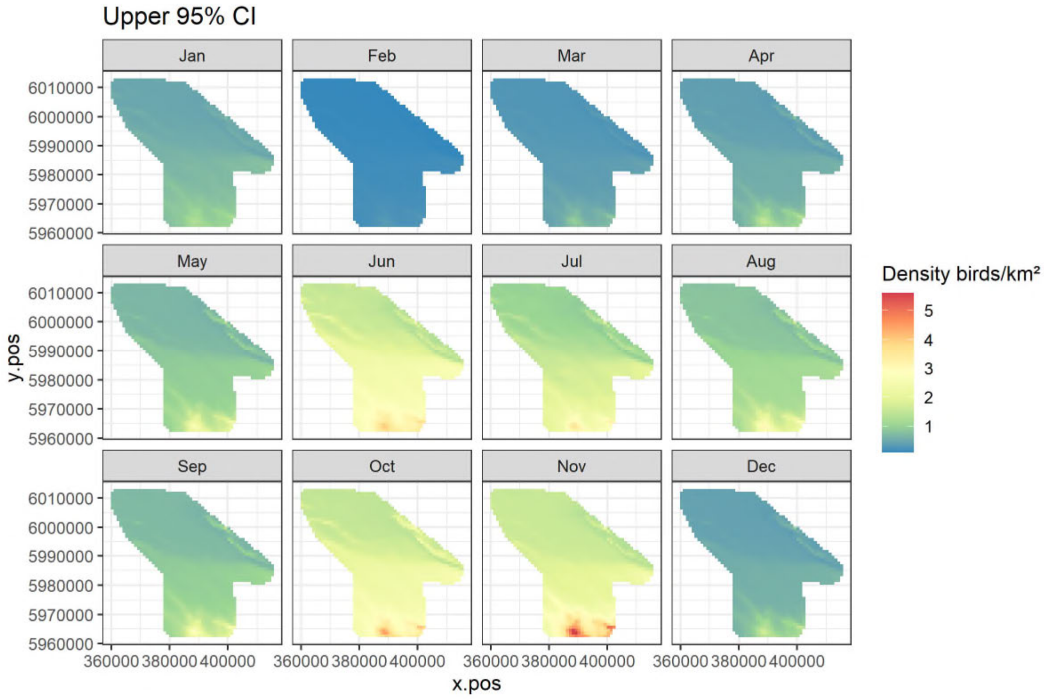

Figure 14 – Upper density estimate from 95% Confidence Intervals

The spatial uncertainty can be visualised as the width of the 95% CI limits (i.e. upper CI minus lower CI; Figure 15).

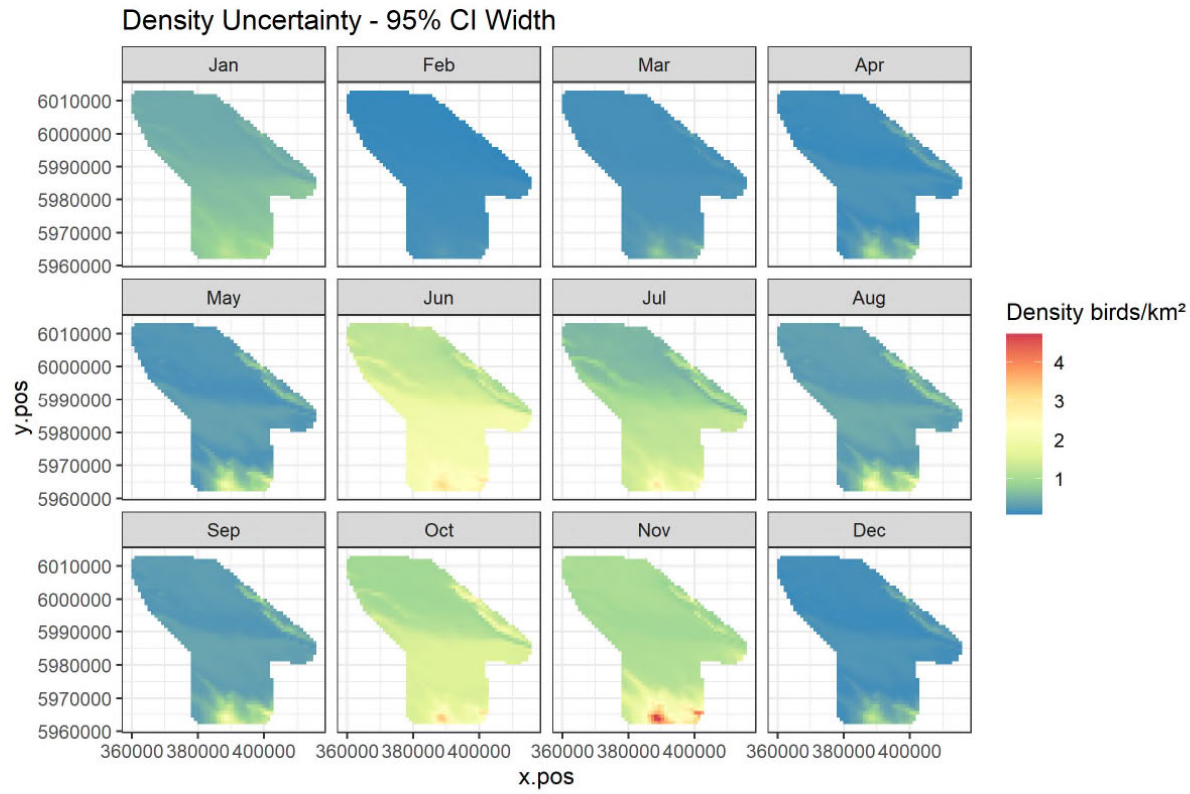

Figure 15 – Spatial uncertainty in model predictions shown as width of 95% CIs for each grid cell.

Model Diagnostics

Additional model diagnostics for the best fitting SALSA 1D model are given in Figure 16 to Figure 18.

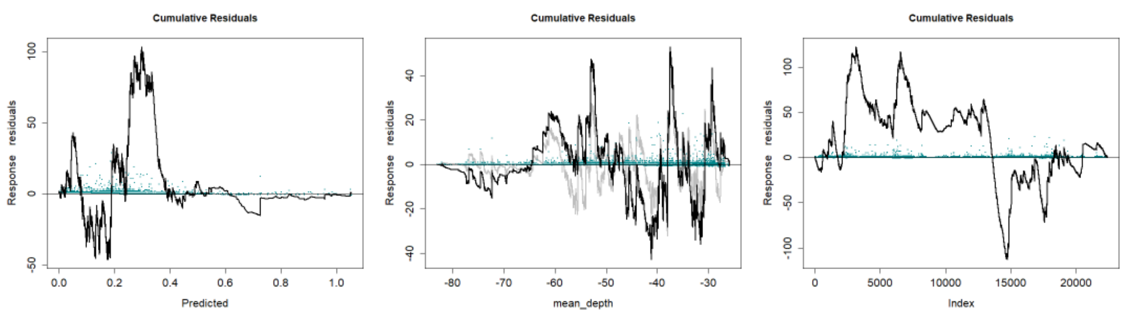

Figure 16 – Cumulative residuals of best fitting 1D smoothed model by predicted value, depth, and index (data order).

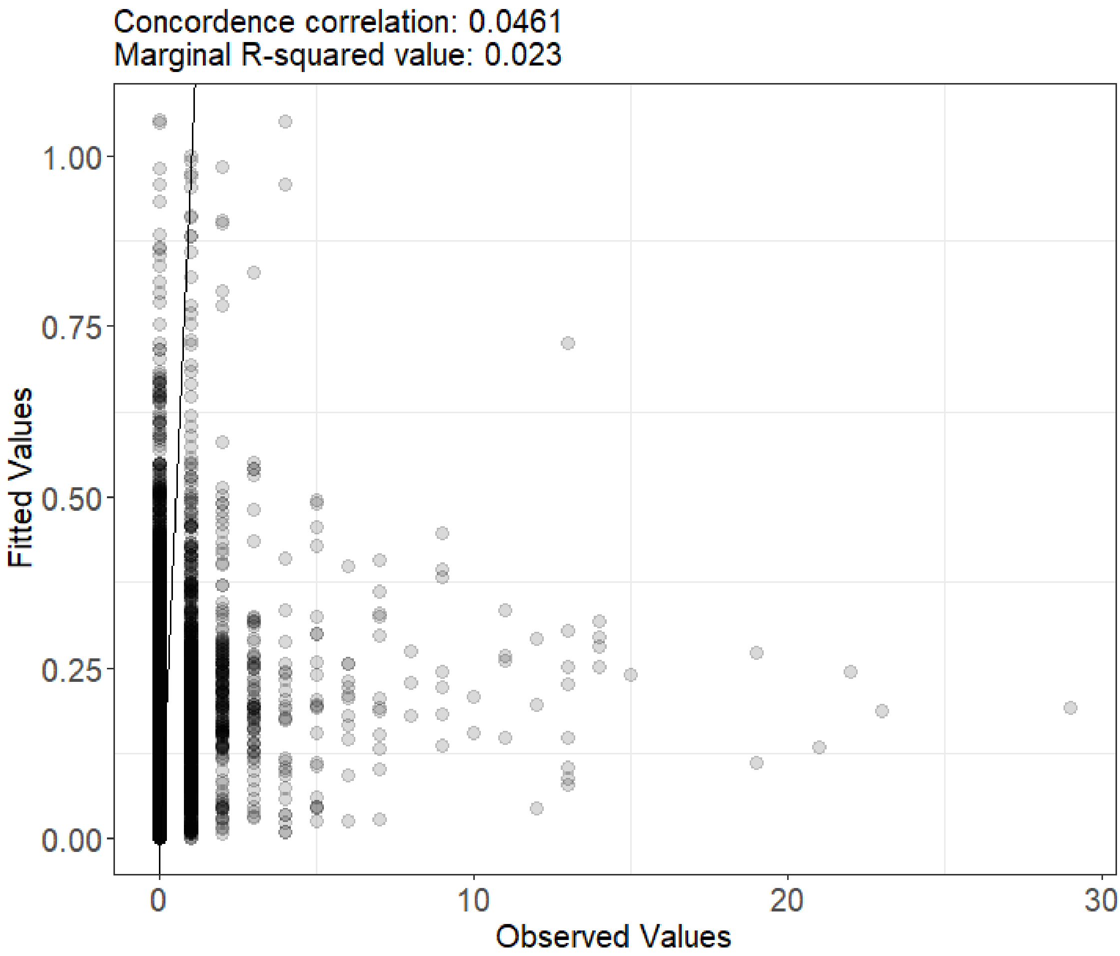

Figure 17 – Observed versus fitted values from best fitting 1D smoothed model.

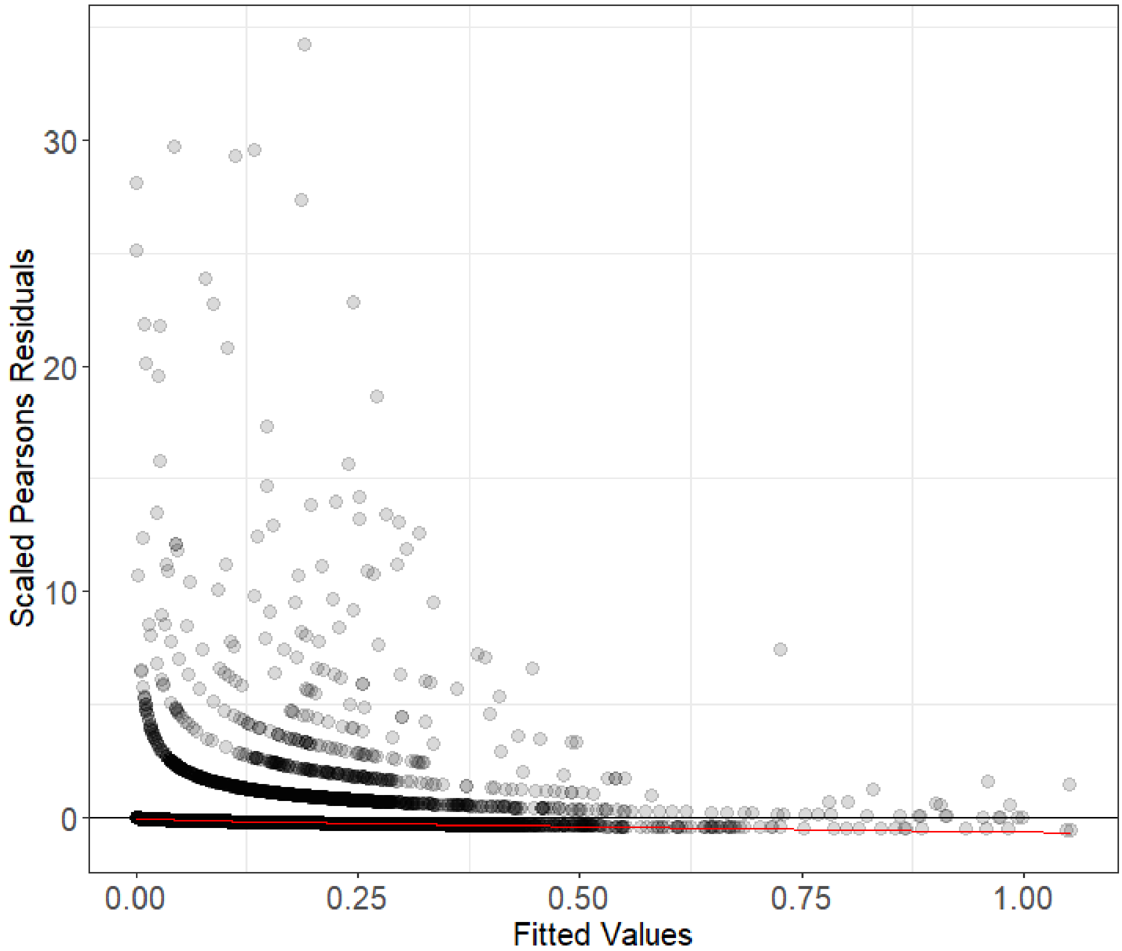

Figure 18 – Scaled Pearson Residuals by fitted value for best fitting 1D smoothed model.