Biomathematics and Statistics Scotland

Refinements of tern *Sterna sp*. tracking data modelling (Phase 1)
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In addition to this report, there are ancillary files associated with this project:

(i) Spreadsheet files of grid predictions
(ii) R code for bootstrapping and modified code for fitting the final model and for prediction

1. Introduction

The Joint Nature Conservation Committee (JNCC) is currently working with the four Statutory Nature Conservation Bodies (SNCBs) to identify important marine areas around the UK that are used by terns *Sterna sp.* during the breeding season. This is to inform the identification of areas that may be suitable for designation as marine Special Protection Areas (SPAs) under the EC Birds Directive (2009/147/EC).

Previous work undertaken developed a weighted logistic regression modelling approach to analyse JNCC tern tracking data for the four larger species of terns (Arctic, common, Sandwich and roseate terns). This was developed in two phases: Phase 1 developed individual site-specific models (Brewer *et al*. 2012a) while Phase 2 developed generic models which, in theory, could be applied to any colony which had the requisite covariate data (Brewer *et al*. 2012b). Subsequent to this, some refinements were made in relation to the candidate covariate data set for the Phase 1 models (Brewer *et al*. 2012c; Potts *et al*. 2013) which addressed some issues previously identified in the earlier work.

For the Phase 1 models, both Generalised Linear Models (GLMs) and Generalised Additive Models (GAMs) were run and several model selection methods were used. As this resulted in several model outputs, JNCC wanted to further refine the approach, incorporating a clear rationale behind the choice of final models which will be used to underpin any boundary delineation of any possible SPAs. This report describes these further refinements to the Phase 1 models.

2. Methods

We followed the methodology described in the report for Phase 1 (Brewer *et al*., 2012a) and the report on additional work for the Coquet colony (Potts *et al*., 2012). As in Potts *et al*. (2012) we fitted models excluding data points with extreme values of SST (for April this is interpreted as less than 6°C, for May as less than 8°C, and for June as less than 9.3°C) and chlorophyll concentrations, slope and wave and current shear stresses were log-transformed. Where necessary, a small constant was added to variables prior to log transformation to avoid taking logs of zero values. Before making the final predictions data points with values of log chlorophyll greater than 2.5 were also excluded.

For some colonies it was not possible to use all the covariates due to large amounts of missing data, especially close to the coast. For Mull and Leith the chlorophyll and SST variables had to be excluded. For North Norfolk chlorophyll in April and the SST variables were removed. Sand was excluded for Mull, Larne Lough, Forvie and North Norfolk. There was no salinity data for North Norfolk. The chlorophyll and SST variables also had to be omitted for sandwich terns at Forvie, Larne Lough and Cemlyn since most of the recorded tracks fell in the coastal strip where chlorophyll was missing and SST was either missing or classified as an outlier due to negative values. In the case of sandwich terns at Cemlyn spring_front and summ_front were also excluded. For sandwich terns at the Farne Islands SST was omitted.

100 bootstrap samples were formed by sampling with replacement from the tracks. In each case a sample of control tracks was taken by resampling with replacement from the 12 control tracks. The number of times each variable was selected in the model with minimum AIC was counted.

We use bootstrapping as a way to inform our confidence in the model predictions and based on the bootstrapping results we consider a shortlist of possible models that have low AIC. Note that running an exhaustive search of models to find those with the lowest AIC would be prohibitive given the size of the data set and the number of variables. It would be possible to do this on the shortlist of variables, for example using the R package MuMIn, but this leads to a very large number of models with very similar AIC values. A rule of thumb is that two models are essentially indistinguishable if the difference in their AICs is less than 2 (Burnham and Anderson, 2002). We therefore aimed instead to find a model that is parsimonious, biologically realistic and with an AIC value close to the minimum.

As such, we use the minimum AIC model, but where this model includes covariates which are either selected < 50% of the time in our bootstrapping and/or have biological ranking of > 5 (ranks provided by JNCC), we investigate whether their removal provides an equivalent model (i.e. the AIC difference is <2). If so, we choose to use the model which contains frequently selected and/or high ranking variables rather than the model with the lowest AIC. Models containing distance to colony only are presented for comparison purposes.

Because chlorophyll and SST covariates have a much higher proportion of values that are missing (in the case of SST, missing after removal of outliers), in cases where the potential lowest AIC models did not involve the SST and/or chlorophyll variables, the stepwise search was rerun with the exclusion of these variables to ensure a more reliable AIC statistic based on a more complete data set. Note that AIC models cannot be compared with those obtained previously because they are based on a different data set but the AIC was recalculated for the previous minimum AIC model (which might be different from the new minimum AIC model using the data set excluding chlorophyll and SST covariates).

Note that the AIC printed out in R is incorrect in a weighted analysis; AIC was therefore calculated by adding two times the number of parameters to the residual deviance.

Some small modifications were made to the code for making predictions. To calculate preference the odds ratio, or equivalently the exponential transformation of the linear predictor, is adjusted by multiplying by the number of controls per observation. Previously, this was done by just taking a value of 12. However, due to control points falling on land and missing covariate data there are not always 12 controls per observation so this has now been replaced by the actual value from the data set that was used to fit the final model. This addresses one of the reviewers' comments on the previous work of Brewer *et al*. (2012a). Confidence intervals for preference are constructed using a normal approximation by taking an exponential transformation of the predictions plus or minus 1.96 times the standard error. This is then multiplied by the number of controls per observation. Confidence limits for usage are then calculated by rescaling the confidence limits in the same way that the predictions were rescaled, i.e. by dividing first by distance to colony and then by the sum of the predictions.

3. Results

The final models are presented in the Appendix. Results from the bootstrapping exercise and the shortlisted models are shown in the tables below.

Arctic terns

Coquet

Table 1. Frequency with which covariates were selected for 100 bootstrap samples for Arctic terns at the Coquet colony, using all candidate covariates.

Variable	Count
dist_col	99
chl_june	62
ss_current	55
bathy_1sec	52
sal_spring	50
sst_april	46
chl_may	42
dist_shore	41
sal_summ	40
sst_may	38
strat_temp	29
sst_june	28
spring_front	27
ss_wave	27
sand	23
chl_apr	20
summ_front	11
slope_1s_deg	10
northness_1s	8
eastness_1s	4

Table 2. Shortlisted models and AIC statistics for Arctic terns at the Coquet colony; the proposed final model is indicated in bold.

Terms	AIC
dist_col, chl_june, bathy_1sec, sst_may, ss_current	416.47
dist_col, chl_june, bathy_1sec, sst_may	417.84
dist_col, chl_june, bathy_1sec, ss_current	416.91
dist_col, chl_june, bathy_1sec	**416.63**
dist_col	418.38

The model obtained by the stepwise search for a minimum AIC model included distance to colony, chlorophyll concentration in June, bathymetry, sea surface temperature in May and shear stress current and had an AIC value of 416.47. The bootstrapping shows that this includes the four most frequently selected covariates but also one (SST in May) which was only selected 38% of the time. Only one of the covariates (ss_current) had a rank >5. When only one of SST May or ss_current is removed, the change in AIC value is <2 but is greater than the change when both are removed together. Thus, the final model contained distance to colony, chlorophyll concentration in June and bathymetry.

Farne Islands

The minimum AIC model contains distance to colony, salinity in spring and probability of a summer front. As this model did not include chlorophyll or SST variables and these have a lot of missing data compared to others we ran the model selection with these covariates removed as candidates (Tables 3 and 4). For comparison the minimum AIC model before excluding SST and chlorophyll variables is also shown.

Table 3. Frequency with which covariates were selected for 100 bootstrap samples for Arctic terns at the Farnes colony, using covariates excluding SST and chlorophyll.

Variable	Count
dist_col	73
dist_shore	42
sal_spring	41
sand	37
strat_temp	30
sal_summ	28
bathy_1sec	27
spring_front	27
ss_current	22
ss_wave	22
summ_front	11
eastness_1s	8
slope_1s_deg	8
northness_1s	6

Table 4. Shortlisted models and AIC statistics for Arctic terns at the Farnes colony; the proposed final model is indicated in bold.

Terms	AIC
dist_col, spring_front	185.62
dist_col, sal_spring, summ_front	186.58
dist_col, sal_spring	**185.67**
dist_col, summ_front	186.55
dist_col	187.9

The minimum AIC model contains distance to colony and probability of a spring front (AIC =185.62). Removing spring front (because it is selected <50% and has a rank >5) increases the AIC >2. The previous minimum AIC model containing distance to colony, salinity spring and summ_front has an AIC of 186.58 which is an increase of <2. If sum_front is removed (because it is selected <50% and has a rank >5), then the AIC is 185.67, while if sal_spring is removed (because it is selected <50%), the AIC is 186.55. As salinity in spring has a lower rank (more biologically plausible) than either spring_front or summ_front, and is selected more frequently , the final model chosen therefore contained distance to colony and salinity in spring.

Outer Ards

Table 5. Frequency with which covariates were selected for 100 bootstrap samples for Arctic terns at the Outer Ards colony, using all candidate covariates.

Variable	Count
dist_col	74
dist_shore	58
chl_apr	57
chl_june	46
sal_spring	44
chl_may	28
sal_summ	27
ss_wave	24
strat_temp	24
sst_april	21
bathy_1sec	19
sand	17
sst_june	17
summ_front	15
sst_may	11
eastness_1s	8
ss_current	6
spring_front	5

northness_1s	1
slope_1s_deg	1

The minimum AIC model found by the stepwise search involves distance to colony and chlorophyll concentration in June which are the first and fourth most frequently selected covariates in the bootstrap samples. As this does not include SST variables and as there are a lot of missing data for these variables compared to others, we ran model selection when SST variables were removed as candidates. In this case, the minimum AIC model contains distance to colony and shear stress current; removing shear stress current (because it has a rank of 7 and is selected <50%) increases the AIC by >2. The original minimum AIC model when SST variables are included is shown for comparison. If chlorophyll in june was removed (because it was selected <50% of the time), the AIC is reduced by <2, but is still much greater than that of the model containing dist_col and ss_current. Thus our final model is dist_col, ss_current.

Table 6. Shortlisted models and AIC statistics for Arctic terns at the Outer Ards colony when SST variables are excluded; the proposed final model is indicated in bold.

Terms	AIC
dist_col, ss_current	**114.53**
dist_col, chl_june	123.39
dist_col	121.41

Common terns

Coquet

Table 7. Frequency with which covariates were selected for 100 bootstrap samples for common terns at the Coquet colony, using all candidate covariates.

Variable	Count
dist_col	90
chl_june	71
sst_april	61
bathy_1sec	58
summ_front	37
chl_may	36
sal_spring	36
sand	34
dist_shore	33
sst_june	31
ss_wave	29
strat_temp	27
ss_current	24
sst_may	20
sal_summ	19
chl_apr	17
slope_1s_deg	14
spring_front	11
eastness_1s	2
northness_1s	2

Table 8. Shortlisted models and AIC statistics for common terns at the Coquet colony; the proposed final model is indicated in bold.

Terms	AIC
dist_col, chl_june, bathy_1sec, sst_april, sst_june	317.9
dist_col, chl_june, bathy_1sec, sst_april	**318.48**
dist_col	326.84

The model obtained by the stepwise search for a minimum AIC model included distance to colony, chlorophyll concentration in June, bathymetry, sea surface temperature in April and sea surface temperature in June and had an AIC value of 317.9. All of these have a rank <5, and all except SST_june are selected >50% of the time in the bootstrap samples (Table 7). When SST_june is removed, the difference in AIC is <2. Thus, the final model contained distance to colony, chlorophyll concentration in June, bathymetry and sst_april.

Larne Lough

Table 9. Frequency with which covariates were selected for 100 bootstrap samples for common terns at the Larne Lough colony, using all candidate covariates.

Variable	Count
dist_col	99
bathy_1sec	96
ss_wave	68
dist_shore	67
sal_summ	34
chl_apr	31
sal_spring	28
spring_front	22
sst_june	22
strat_temp	19
northness_1s	15
slope_1s_deg	15
sst_may	14
chl_june	13
eastness_1s	13
ss_current	9
chl_may	7
sst_april	5
summ_front	2

The minimum AIC model includes distance to colony, distance to shore and bathymetry. As this model did not include either SST or chlorophyll variables, both of which have extensive missing data, we ran model selection when these variables were removed (to obtain more accurate estimates of AIC) (Table 10).

Table 10. Shortlisted models and AIC statistics for common terns at the Larne Lough colony with chlorophyll and SST variables excluded; the proposed final model is indicated in bold.

Terms	AIC
dist_col,dist_shore,bathy_1sec,slope,ss_wave	90.104
dist_col,dist_shore,bathy_1sec,ss_wave	92.53
dist_col,dist_shore,bathy_1sec,slope	**90.369**
dist_col,dist_shore,bathy_1sec	93.743
dist_col	117.55

In this case, the minimum AIC model contains distance to colony, distance to shore, bathymetry, slope and shear stress wave. Removing shear stress wave (because it has a rank of 10) increases the AIC by <2 but removing slope (rank of 9) increases it by more than 2. Removing both (which would be the original minimum AIC model) increases the AIC value by >2. The final model chosen therefore includes distance to colony, distance to shore, bathymetry and slope.

Mull

Table 11. Frequency with which covariates were selected for 100 bootstrap samples for common terns at the Mull colony, using available covariates.

Variable	Count
dist_col	100
slope_1s_deg	83
eastness_1s	70
dist_shore	68
strat_temp	23
ss_wave	21
sal_summ	19
bathy_1sec	17
sal_spring	14
ss_current	14
northness_1s	12
summ_front	12

Table 12. Shortlisted models and AIC statistics for common terns at the Mull colony; the proposed final model is indicated in bold.

Terms	AIC
dist_col, dist_shore, eastness, slope	282.88
dist_col, dist_shore, slope	**283.94**
dist_col, dist_shore, eastness	287.85
dist_col, dist_shore	289.52
dist_col	290.24

For common terns at Mull, it was decided to remove SST and Chlorophyll as candidate covariates at the outset due to the high amount of missing data. The minimum AIC model contains distance to colony, distance to shore, eastness and slope, all of which were selected in >50% of the bootstrap samples. When eastness is removed (because it has a rank >5), the difference in AIC is <2. When slope is removed (because it has a rank >5), the difference in AIC is >2. Equally, removing both eastness and slope together also increases the AIC by >2. Therefore, the final model selected contains distance to colony, distance to shore and slope.

Leith

Table 13. Frequency with which covariates were selected for 100 bootstrap samples for common terns at the Leith colony, using available covariates.

Variable	Count
dist_col	100
dist_shore	95
bathy_1sec	90
spring_front	81
slope_1s_deg	80
sal_spring	63
sal_summ	42
summ_front	34
ss_current	31
sand	30
northness_1s	11
ss_wave	10
eastness_1s	8
strat_temp	4

Table 14. Shortlisted models and AIC statistics for common terns at the Leith colony; the proposed final model is indicated in bold.

Terms	AIC
dist_col, slope_1s_deg, sal_spring, dist_shore, bathy_1sec, spring_front	653.98
dist_col, slope_1s_deg, sal_spring, dist_shore, bathy_1sec	**655.46**
dist_col, sal_spring, dist_shore, bathy_1sec, spring_front	656.46
dist_col,dist_shore,sal_spring,bathy_1sec	658.61
dist_col	685.82

For common terns at Leith, SST and Chlorophyll were removed as candidate covariates at the outset due to the high amount of missing data. The minimum AIC model contains distance to colony, distance to shore, salinity in spring, bathymetry, slope and probability of a spring front, all of which were selected >50% in the bootstrap samples. Removal of the probability of a spring front (rank of 8) increases the AIC by <2, while removal of slope (rank of 9) increases the AIC >2. Removal of both together increases the AIC by >2. Thus the final model contains dist_col, slope_1s_deg, sal_spring, dist_shore and bathy_1sec.

North Norfolk

Table 15. Frequency with which covariates were selected for 100 bootstrap samples for common terns at the Blakeney colony, using available covariates.

Variable	Count
bathy_1sec	68
dist_shore	57
strat_temp	57
dist_col	55
chl_june	38
ss_wave	36
ss_current	31
chl_may	28
spring_front	21
slope_1s_deg	18
summ_front	15
eastness_1s	12
northness_1s	12

Table 16. Shortlisted models and AIC statistics for common terns at the Blakeney colony; the proposed final model is indicated in bold.

Terms	AIC
dist_col, ss_wave	**52.191**
dist_col	58.261

For common terns at Blakeney, Chl_apr and the three SST variables were removed at the outset as candidate covariates due to extensive missing data. The minimum AIC model includes distance to colony and shear stress wave. This was chosen as the final model since the removal of shear stress wave (because it was selected <50% of the time and has a rank of 7) increases the AIC by > 2.

Cemlyn

Table 17. Frequency with which covariates were selected for 100 bootstrap samples for common terns at the Cemlyn colony, using all available covariates.

Variable	Count
dist_col	100
sal_spring	84
spring_front	31
bathy_1sec	27
chl_may	27
sst_may	23

summ_front	22
strat_temp	18
sal_summ	15
chl_apr	14
dist_shore	14
northness_1s	14
chl_june	12
ss_wave	12
eastness_1s	11
sst_april	11
ss_current	10
sst_june	3

The minimum AIC model found by a stepwise search involves distance to colony and salinity in spring. As this model did not include either SST or chlorophyll variables, both of which have extensive missing data, we also ran model selection when these variables were removed (to obtain more accurate estimates of AIC). Re-running the models with chlorophyll and SST variables excluded (Table 18) gives a minimum AIC model that contains distance to colony, salinity in spring and spring_front. Removal of spring_front (because it has a rank of 9) increases the AIC by <2. Therefore we chose this as the final model. Thus, regardless of whether SST and Chlorophyll covariates are candidate covariates, the final model is dist_col, sal_spring.

Table 18. Shortlisted models and AIC statistics for common terns at the Cemlyn colony excluding chlorophyll and SST variables; the proposed final model is indicated in bold.

Terms	AIC
dist_col, sal_spring, spring_front	66.622
dist_col, sal_spring	**67.157**
dist_col	79.044

Roseate terns

Coquet

Table 19. Frequency with which covariates were selected for 100 bootstrap samples for roseate terns at the Coquet colony, using all candidate covariates.

Variable	Count
sst_may	98
dist_col	83
dist_shore	80
chl_may	61
chl_june	55
sst_april	41
sal_spring	39
ss_wave	37
summ_front	37
spring_front	36
ss_current	36
sst_june	30
sal_summ	28
chl_apr	26
bathy_1sec	22
slope_1s_deg	21
strat_temp	18
sand	15
eastness_1s	9
northness_1s	5

Table 20. Shortlisted models and AIC statistics for roseate terns at the Coquet colony; the proposed final model is indicated in bold.

Terms	AIC
dist_col, sst_may, chl_june	**94.027**
dist_col	124.53

The model obtained by the stepwise search for a minimum AIC model included distance to colony, sea surface temperature in May and chlorophyll concentration in June and has an AIC of 94.027. This contains the top first, second and fifth most frequently selected covariates in the bootstrap samples all of which were selected >50% in the bootstrap samples and all have a rank ≤5.

Sandwich terns

Coquet

The model obtained by the stepwise search for a minimum AIC model included distance to shore, distance to colony, chlorophyll concentration in April and chlorophyll concentration in June.

As no SST variables were selected, the AIC statistics were recalculated excluding the SST variables from the list of candidate covariates, giving a more complete data set.

Table 21. Frequency with which covariates were selected for 100 bootstrap samples for Sandwich terns at the Coquet colony, excluding SST variables.

Variable	Count
ss_wave	65
bathy_1sec	62
dist_col	62
chl_may	48
strat_temp	44
chl_june	39
ss_current	39
dist_shore	36
sal_summ	22
sand	19
summ_front	19
sal_spring	18
chl_apr	16
slope_1s_deg	16
eastness_1s	13
spring_front	12
northness_1s	10

Table 22. Shortlisted models and AIC statistics for Sandwich terns at the Coquet colony; the proposed final model is indicated in bold.

Terms	AIC
dist_col, dist_shore, chl_may	280.26
dist_col, dist_shore	**280.44**
dist_col, chl_may	304.47
dist_col	319.30
dist_col, dist_shore, chl_apr, chl_june	282.31
dist_col, dist_shore, chl_june	280.36
dist_col, dist_shore, chl_apr	282.38

The minimum AIC model now involves dist_col, dist_shore and chl_may. If chl_may is excluded (because it is selected <50% in the bootstrap models), the difference in AIC is <2 but if dist_shore (selected <50% in the bootstrap models) is excluded the difference is >2. Removing both increases the AIC >2. Therefore the model containing distance to colony and distance to shore was chosen as the final model. For comparison the minimum AIC model before excluding SST variables is also shown.

Farne Islands

For sandwich terns at the Farne Islands it was decided to remove SST as candidate covariates at the outset due to the high amount of missing data. The minimum AIC model then includes dist_col, dist_shore, bathy_1sec, summ_front, spring_front. As this does not involve any of the chlorophyll variables these were also excluded.

Table 23. Frequency with which covariates were selected for 100 bootstrap samples for Sandwich terns at the Farnes colony, excluding SST and chlorophyll variables.

Variable	Count
dist_shore	96
dist_col	85
sal_spring	69
summ_front	65
spring_front	63
bathy_1sec	49
eastness_1s	47
strat_temp	28
sal_summ	20
ss_wave	20
ss_current	17
northness_1s	11
slope_1s_deg	3

Table 24. Shortlisted models and AIC statistics for Sandwich terns at the Farnes colony excluding chlorophyll and SST variables; the proposed final model is indicated in bold.

Terms	AIC
dist_col, dist_shore, sal_spring	**68.169**
dist_col,dist_shore,bathy_1sec,summ_front,spring_front	68.727
dist_col,dist_shore,bathy_1sec,summ_front	72.087
dist_col,dist_shore,bathy_1sec,spring_front	72.532
dist_col,dist_shore,bathy_1sec	70.842
dist_col	143.66

The model with the minimum AIC involves the three variables selected most frequently in the bootstrap samples (distance to colony, distance to shore and salinity in spring; Table 23). These variables also all have a rank <5. Therefore we chose the minimum AIC model as our final model. For comparison the original minimum AIC model when chlorophyll was included is also shown, together with the results of removing spring_front and summ_front from this model (as they have rank>5).

Larne Lough

Table 25. Frequency with which covariates were selected for 100 bootstrap samples for sandwich terns at the Larne Lough colony, using available covariates.

Variable	Count
dist_col	98
sal_spring	80
sal_summ	60
dist_shore	57
eastness_1s	52
ss_wave	42
bathy_1sec	41
ss_current	37
strat_temp	34
slope_1s_deg	25
summ_front	12
northness_1s	11

Table 26. Shortlisted models and AIC statistics for Sandwich terns at the Larne Lough colony; the proposed final model is indicated in bold.

Terms	AIC
dist_col, dist_shore, sal_spring	**49.493**
dist_col	68.63

SST and Chlorophyll were removed at the outset as candidate covariates due to the high amount of missing data The minimum AIC model involves distance to colony, distance to shore and salinity in spring. All of these covariates were selected >50% in the bootstrapping samples and all have a rank of <5. Therefore we use the minimum AIC model as our final model.

Forvie

Table 27. Frequency with which covariates were selected for 100 bootstrap samples for sandwich terns at the Forvie colony, using available covariates.

Variable	Count
ss_current	67
ss_wave	54
strat_temp	53
dist_col	46
slope_1s_deg	44
sal_spring	43
bathy_1sec	37

dist_shore	27
spring_front	22
sal_summ	18
northness_1s	12
eastness_1s	3

Table 28. Shortlisted models and AIC statistics for Sandwich terns at the Forvie colony; the proposed final model is indicated in bold.

Terms	AIC
bathy_1sec,ss_current,strat_temp	89.376
bathy_1sec, strat_temp	**90.462**
strat_temp	169.78
ss_current,strat_temp	162.58
dist_col	201.07

SST and Chlorophyll were removed as candidate covariates at the outset due to the high amount of missing data. The minimum AIC model involves temperature stratification, shear stress current and bathymetry (Table 28). Dropping shear stress current (because it has a rank >5) increases the AIC by <2. Removing bathymetry (because it was selected <50% of the time) and removing both together results in increases in AIC of much greater than two. Therefore the final model chosen contains bathymetry and strat_temp.

Cemlyn

Table 29. Frequency with which covariates were selected for 100 bootstrap samples for sandwich terns at the Cemlyn colony, using available covariates.

Variable	Count
dist_col	100
dist_shore	91
sal_spring	82
ss_wave	49
bathy_1sec	35
ss_current	35
sal_summ	30
eastness_1s	28
slope_1s_deg	25
northness_1s	18
strat_temp	16
sand	8

Table 30. Shortlisted models and AIC statistics for Sandwich terns at the Cemlyn colony; the proposed final model is indicated in bold.

Terms	AIC
dist_col, dist_shore, sal_spring	**297.53**
dist_col	414.09

SST and Chlorophyll were removed as candidate covariates at the outset due to the high amount of missing data. The minimum AIC model found by a stepwise search includes distance to colony, distance to shore and salinity in spring. This includes the three variables most frequently selected in the bootstrap samples and all three variables have a rank <5 (Table 29). Therefore we use the minimum AIC model as our final model.

North Norfolk

Table 31. Frequency with which covariates were selected for 100 bootstrap samples for sandwich terns at the Scolt Head and Blakeney colonies, using available covariates.

Variable	Count
dist_col	100
dist_shore	93
ss_wave	71
bathy_1sec	56
chl_june	56
ss_current	23
chl_may	16
summ_front	15
slope_1s_deg	11
northness_1s	10
spring_front	9
strat_temp	9
eastness_1s	5

Table 32. Shortlisted models and AIC statistics for Sandwich terns at the Scolt Head and Blakeney colonies; the proposed final model is indicated in bold.

Terms	AIC
dist_col, dist_shore, chl_may,ss_wave,bathy_1sec,northness	371.82
dist_col, dist_shore, chl_may,ss_wave,bathy_1sec	372.11
dist_col, dist_shore, chl_may,bathy_1sec,northness	385.18
dist_col, dist_shore,ss_wave,bathy_1sec,northness	372.87
dist_col, dist_shore, chl_may,bathy_1sec	388.22
dist_col, dist_shore,ss_wave,bathy_1sec	**373.44**
dist_col, dist_shore,bathy_1sec,northness	385.95
dist_col, dist_shore, bathy_1sec	389.38
dist_col	402.89

For Sandwich terns at North Norfolk, chl_may and chl_june retained but chl_apr and the three SST variables were removed as candidate covariates due to extensive missing data. The minimum AIC model involves distance to colony, distance to shore, chl_may, bathymetry, shear stress wave and northness. Of these, distance to colony, distance to shore and bathymetry have ranks <5 as well as being selected >50% of the time in the bootstrap samples. The remaining three variables (northness, chl_may and ss_wave were removed in varying combinations as follows.

Removal of northness (because rank>5 and selected only 10% of the time), increases the AIC by <2

Removal of ss_wave (because it has a rank >5) leads to an increase in the AIC of >2.

Removal of chl_may (because it is selected <50% in the bootstrap samples) leads to an increase in the AIC of <2.

Removal of both northness and ss_wave increases the AIC by >2

Removal of both northness and Chl_may concentration together increases the AIC by <2.

Removal of both ss_wave and Chl_may increases the AIC by >2.

Removal of all three of these covariates (northness, ss_wave and Chl_may) leads to an increase in AIC >2.

The final model therefore contains distance to colony, distance to shore, bathymetry and shear stress wave.

4. Discussion

It is clear that distance to colony is a key variable for all four species. However, there are many different combinations of other variables that result in models with similar AIC statistics. It is not therefore possible to choose a model on the basis of statistical criteria alone. Biological plausibility, covariate data quality and the number of covariates in the model must also be taken into consideration.

Confidence intervals (or more correctly, prediction intervals) have been added for usage predictions at individual grid cells. They should be interpreted carefully. For example, it would not be valid to sample from these intervals from neighbouring grid cells (if, say, you wanted to try to generate a distribution of possible usage surfaces) independently, as this would ignore the correlations between them. Because of the way the usage predictions are calculated – via scaling the expected usage scale to sum to one – it would not be possible for all “true” values to be at the lower limits of the intervals for all cells. However, the range of the interval for any one cell does reflect the uncertainty associated with the likely usage for that cell; it is perfectly valid to say that if two cells (neighbouring or not) have non-overlapping prediction intervals, that their relative usage patterns are likely to be quite different.

Usage predictions can only ever inform us about relative rather than absolute usage, because the total number of birds and foraging trips is unknown. Some covariates tend to have missing data close to the shore, where predicted values tend to be higher. The constraint on the sum of the usage values (they need to sum to 1) means that the decision whether or not to include these covariates (and hence whether or not to include some grid points) has a considerable impact on the absolute usage values at the remaining locations.

References

Brewer M.J., Potts J.M., Duff E.I. & Elston D.A. (2012a). To carry out tern modelling under the Framework Agreement C10-0206-0387. Contract Report to JNCC, March 2012.

Brewer, M.J., Potts, J. M., Duff, E. I. & Elston, D. A. (2012b). *Prediction of new colonies – seabird tracking data (under Agreement C10-0206-0387)*. Contract Report to JNCC, November 2012.

Burnham K.P. and Anderson D.R. (2002). Model selection and multimodel inference: a practical information-theoretic approach. Second Edition. Springer-Verlag, New York.

Potts J.M., Brewer M.J., Duff E.I. & Elston D.A. (2012). Additional Work Coquet Colony - Seabird Tracking Data (Under Agreement C10-0206-0387). Contract Report to JNCC, December 2012.

Potts, J. M. Brewer, M.J., Duff, E. I. & Elston, D. A. (2013). *Additional Work Other Colonies – Seabird Tracking Data (Under Agreement C10-0206-0387).* Contract Report to JNCC, March 2013

Appendix – Results from final models

Arctic terns

Coquet

```
Call:

glm(formula = formula.glm, family = "binomial", data = 
complete.data.to.analyse,

    weights = weights)


Deviance Residuals: 

     Min        1Q    Median        3Q       Max  

-0.85148  -0.03867  -0.01614  -0.00686   1.96794  


Coefficients:

            Estimate Std. Error z value Pr(>|z|)    

(Intercept) -3.74101    1.14187  -3.276  0.00105 ** 

dist_col    -0.22098    0.03844  -5.748 9.01e-09 ***

chl_june     1.52928    0.61138   2.501  0.01237 *  

bathy_1sec  -0.03583    0.01658  -2.161  0.03073 *  

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1 


(Dispersion parameter for binomial family taken to be 1)


    Null deviance: 567.8  on 48994  degrees of freedom

Residual deviance: 446.4  on 48991  degrees of freedom

AIC: 56.677


Number of Fisher Scoring iterations: 8
```

```
Single term deletions


Model:
SEARCH_FORAGE ~ dist_col + chl_june + bathy_1sec
           Df Deviance     AIC    LRT  Pr(>Chi)
<none>          446.40  56.677
dist_col    1   502.54 110.821 56.143 6.737e-14 ***
chl_june    1   452.62  60.899  6.222   0.01262 *
bathy_1sec  1   451.32  59.596  4.918   0.02657 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Farne Islands

```
Call:
glm(formula = formula.glm, family = "binomial", data = 
complete.data.to.analyse,
    weights = weights)


Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.86809  -0.05086  -0.02434  -0.00821   1.64252


Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) 5218.74154 2703.57704   1.930   0.0536 .
dist_col      -0.27067    0.06501  -4.163 3.14e-05 ***
sal_spring  -148.81638   77.08026  -1.931   0.0535 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 225.63  on 18129  degrees of freedom
Residual deviance: 181.50  on 18127  degrees of freedom
AIC: 15.951

Number of Fisher Scoring iterations: 8

Single term deletions

Model:
SEARCH_FORAGE ~ dist_col + sal_spring
           Df Deviance    AIC    LRT  Pr(>Chi)
<none>          181.50 15.951
dist_col    1   222.68 55.131 41.181 1.388e-10 ***
sal_spring  1   185.78 18.228  4.278   0.03861 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Outer Ards

```
Call:
glm(formula = formula.glm, family = "binomial", data = 
complete.data.to.analyse,
    weights = weights)

Deviance Residuals: 
     Min        1Q    Median        3Q       Max  
-0.56403  -0.03132  -0.01698  -0.00930   1.49448  
```

```
Coefficients:

            Estimate Std. Error z value Pr(>|z|)

(Intercept)  -1.5888     0.4782  -3.323 0.000891 ***

dist_col     -0.1074     0.0386  -2.782 0.005404 **

ss_current    0.9347     0.2974   3.143 0.001674 **

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1


(Dispersion parameter for binomial family taken to be 1)


    Null deviance: 168.74  on 28704  degrees of freedom

Residual deviance: 132.71  on 28702  degrees of freedom

AIC: 6


Number of Fisher Scoring iterations: 7


Single term deletions


Model:

SEARCH_FORAGE ~ dist_col + ss_current

           Df Deviance    AIC     LRT  Pr(>Chi)

<none>          132.71  6.000

dist_col    1   142.47 13.760  9.7597 0.0017838 **

ss_current  1   145.58 16.877 12.8768 0.0003327 ***

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Common terns

Coquet

```
Call:

glm(formula = formula.glm, family = "binomial", data = 
complete.data.to.analyse,

    weights = weights)


Deviance Residuals:

     Min        1Q    Median        3Q       Max

-0.84174  -0.04193  -0.01357  -0.00597   2.18484


Coefficients:

             Estimate Std. Error z value Pr(>|z|)

(Intercept) -16.10658    8.08069  -1.993   0.0462 *

dist_col     -0.23875    0.04914  -4.858 1.18e-06 ***

chl_june      2.96525    0.71404   4.153 3.28e-05 ***

bathy_1sec   -0.05218    0.02168  -2.407   0.0161 *

sst_april     1.42391    1.13830   1.251   0.2110

---

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


(Dispersion parameter for binomial family taken to be 1)


    Null deviance: 419.47  on 30090  degrees of freedom

Residual deviance: 315.51  on 30086  degrees of freedom

AIC: 24.16


Number of Fisher Scoring iterations: 8
```

```
Single term deletions


Model:
SEARCH_FORAGE ~ dist_col + chl_june + bathy_1sec + sst_april
           Df Deviance    AIC    LRT  Pr(>Chi)
<none>          315.51 24.160
dist_col    1   354.26 60.907 38.746 4.827e-10 ***
chl_june    1   334.00 40.651 18.490 1.708e-05 ***
bathy_1sec  1   322.04 28.692  6.531    0.0106 *
sst_april   1   317.24 23.887  1.727    0.1888
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Larne Lough

```
Call:
glm(formula = formula.glm, family = "binomial", data =
complete.data.to.analyse,
    weights = weights)


Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.15117  -0.02196  -0.01042  -0.00254   1.46547


Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   0.219939   0.350330   0.628  0.53013
dist_col     -0.447394   0.141211  -3.168  0.00153 **
dist_shore    0.543190   0.175945   3.087  0.00202 **
bathy_1sec    0.029170   0.009754   2.991  0.00278 **
slope_1s_deg  0.643094   0.215508   2.984  0.00284 **
```

```
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 225.15  on 20886  degrees of freedom
Residual deviance: 135.60  on 20882  degrees of freedom
AIC: 21.742

Number of Fisher Scoring iterations: 9

Single term deletions

Model:
SEARCH_FORAGE ~ dist_col + dist_shore + bathy_1sec + slope_1s_deg
             Df Deviance    AIC    LRT  Pr(>Chi)
<none>            135.60 21.742
dist_col      1   165.83 49.974 30.233 3.832e-08 ***
dist_shore    1   149.03 33.176 13.434 0.0002471 ***
bathy_1sec    1   146.38 30.525 10.783 0.0010241 **
slope_1s_deg  1   146.41 30.552 10.811 0.0010092 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’
```

Mull

```
Call:
glm(formula = formula.glm, family = "binomial", data =
complete.data.to.analyse,
    weights = weights)
```

```
Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.80213  -0.05173  -0.02954  -0.01408   1.79362

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.15095    0.39513  -5.444 5.22e-08 ***
dist_col     -0.15681    0.03051  -5.140 2.74e-07 ***
dist_shore    0.44728    0.22412   1.996    0.046 *
slope_1s_deg  0.37390    0.16686   2.241    0.025 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 343.39  on 24995  degrees of freedom
Residual deviance: 290.05  on 24992  degrees of freedom
AIC: 23.381

Number of Fisher Scoring iterations: 7

Single term deletions

Model:
SEARCH_FORAGE ~ dist_col + dist_shore + slope_1s_deg
             Df Deviance    AIC    LRT  Pr(>Chi)
<none>             290.05 23.381
dist_col      1   332.88 64.217 42.835 5.955e-11 ***
dist_shore    1   293.88 25.215  3.834   0.05023 .
```

```
slope_1s_deg  1   295.88 27.218  5.837   0.01570 *

---

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Leith

```
Call:

glm(formula = formula.glm, family = "binomial", data = 
complete.data.to.analyse,

    weights = weights)


Deviance Residuals: 

     Min        1Q    Median        3Q       Max  

-0.87894  -0.04421  -0.02148  -0.00626   2.01090  


Coefficients:

               Estimate Std. Error z value Pr(>|z|)    

(Intercept)  -724.88210  173.46644  -4.179 2.93e-05 ***

dist_col       -0.21052    0.03190  -6.600 4.11e-11 ***

bathy_1sec      0.02702    0.01430   1.890  0.05870 .  

dist_shore     -0.29079    0.10753  -2.704  0.00684 ** 

sal_spring     20.65795    4.94687   4.176 2.97e-05 ***

slope_1s_deg    0.19393    0.09322   2.080  0.03750 *  

---

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


(Dispersion parameter for binomial family taken to be 1)


    Null deviance: 827.65  on 71868  degrees of freedom

Residual deviance: 684.95  on 71863  degrees of freedom

AIC: 64.331
```

```
Number of Fisher Scoring iterations: 8


Single term deletions


Model:
SEARCH_FORAGE ~ dist_col + bathy_1sec + dist_shore + sal_spring +
    slope_1s_deg
             Df Deviance     AIC    LRT  Pr(>Chi)
<none>            684.95  64.331
dist_col      1   771.89 149.272 86.941 < 2.2e-16 ***
bathy_1sec    1   688.86  66.237  3.906  0.048123 *
dist_shore    1   692.95  70.331  8.000  0.004679 **
sal_spring    1   703.52  80.905 18.574 1.634e-05 ***
slope_1s_deg  1   689.48  66.865  4.534  0.033225 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

North Norfolk

```
Call:
glm(formula = formula.glm, family = "binomial", data =
complete.data.to.analyse,
    weights = weights)


Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.61454  -0.04248  -0.00542  -0.00114   1.43657


Coefficients:
            Estimate Std. Error z value Pr(>|z|)
```

```
(Intercept)  -5.7088     1.9965  -2.859 0.004245 **
dist_col     -0.4754     0.1411  -3.368 0.000756 ***
ss_wave       1.6119     0.5377   2.998 0.002721 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 140.86  on 1677  degrees of freedom
Residual deviance:  70.39  on 1675  degrees of freedom
AIC: 23.722

Number of Fisher Scoring iterations: 9

Single term deletions

Model:
SEARCH_FORAGE ~ dist_col + ss_wave
         Df Deviance    AIC    LRT  Pr(>Chi)
<none>        70.390 23.722
dist_col  1  107.710 59.043 37.321 1.002e-09 ***
ss_wave   1   83.832 35.164 13.442 0.0002461 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Cemlyn

```
Call:
glm(formula = formula.glm, family = "binomial", data = 
complete.data.to.analyse,
    weights = weights)
```

```
Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.07366  -0.01345  -0.00090   0.00000   0.70942

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -3888.3222  1662.6491  -2.339  0.01935 *
dist_col       -0.8143     0.2602  -3.130  0.00175 **
sal_spring    113.2631    48.4294   2.339  0.01935 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 133.968  on 17923  degrees of freedom
Residual deviance:  70.025  on 17921  degrees of freedom
AIC: 6

Number of Fisher Scoring iterations: 10

Single term deletions

Model:
SEARCH_FORAGE ~ dist_col + sal_spring
           Df Deviance    AIC    LRT  Pr(>Chi)
<none>          70.025  6.000
dist_col    1  133.795 67.770 63.770 1.398e-15 ***
sal_spring  1   82.282 16.258 12.258 0.0004634 ***
```

```
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Roseate terns

Coquet

```
Call:

glm(formula = formula.glm, family = "binomial", data =
complete.data.to.analyse,

    weights = weights)


Deviance Residuals:

     Min        1Q    Median        3Q       Max

-1.53683  -0.01548  -0.00773  -0.00275   1.02255


Coefficients:

             Estimate Std. Error z value Pr(>|z|)

(Intercept) -79.24111   15.12793  -5.238 1.62e-07 ***

dist_col     -0.21202    0.06481  -3.271  0.00107 **

chl_june      1.80816    0.76466   2.365  0.01805 *

sst_may       8.13432    1.61721   5.030 4.91e-07 ***

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1


(Dispersion parameter for binomial family taken to be 1)


    Null deviance: 252.02  on 24787  degrees of freedom

Residual deviance: 116.16  on 24784  degrees of freedom

AIC: 20.371


Number of Fisher Scoring iterations: 8
```

```
Single term deletions


Model:
SEARCH_FORAGE ~ dist_col + chl_june + sst_may
         Df Deviance    AIC    LRT  Pr(>Chi)
<none>        116.16 20.371
dist_col  1   130.84 33.047 14.677 0.0001276 ***
chl_june  1   121.78 23.991  5.620 0.0177522 *
sst_may   1   158.51 60.713 42.343 7.661e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Sandwich terns

Coquet

```
Call:
glm(formula = formula.glm, family = "binomial", data =
complete.data.to.analyse,
    weights = weights)


Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.05409  -0.01070  -0.00040  -0.00001   2.22121


Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.36765    0.22314   1.648   0.0994 .
dist_col    -0.08129    0.01918  -4.238 2.26e-05 ***
dist_shore  -0.51050    0.08622  -5.921 3.20e-09 ***
---
```

```
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 633.94  on 60582  degrees of freedom
Residual deviance: 370.50  on 60580  degrees of freedom
AIC: 54.926

Number of Fisher Scoring iterations: 10

Single term deletions

Model:
SEARCH_FORAGE ~ dist_col + dist_shore
           Df Deviance     AIC    LRT  Pr(>Chi)
<none>          370.50  54.926
dist_col    1   399.27  81.692 28.766 8.169e-08 ***
dist_shore  1   444.59 127.019 74.093 < 2.2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Farne Islands

```
Call:
glm(formula = formula.glm, family = "binomial", data = 
complete.data.to.analyse, 
    weights = weights)

Deviance Residuals: 
     Min        1Q    Median        3Q       Max  
-0.59796  -0.00012   0.00000   0.00000   1.31009  
```

```
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.071e+04  7.877e+03  -2.629  0.00857 **
dist_col    -4.124e-01  1.267e-01  -3.255  0.00114 **
dist_shore  -1.958e+00  4.476e-01  -4.374 1.22e-05 ***
sal_spring   5.904e+02  2.246e+02   2.629  0.00857 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 239.571  on 16692  degrees of freedom
Residual deviance:  75.787  on 16689  degrees of freedom
AIC: 8.5126

Number of Fisher Scoring iterations: 12

Single term deletions

Model:
SEARCH_FORAGE ~ dist_col + dist_shore + sal_spring
           Df Deviance    AIC    LRT  Pr(>Chi)
<none>          75.787  8.513
dist_col    1   95.045 25.770 19.258 1.142e-05 ***
dist_shore  1  114.678 45.404 38.891 4.481e-10 ***
sal_spring  1   85.096 15.821  9.308  0.002281 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Larne Lough

```
Call:

glm(formula = formula.glm, family = "binomial", data =
complete.data.to.analyse,

    weights = weights)


Deviance Residuals:

    Min       1Q   Median       3Q      Max

-0.6976   0.0000   0.0000   0.0000   0.6006


Coefficients:

              Estimate Std. Error z value Pr(>|z|)

(Intercept) -4677.4679  1896.8897  -2.466   0.0137 *

dist_col       -0.4314     0.1898  -2.273   0.0230 *

dist_shore     -3.3519     1.3220  -2.535   0.0112 *

sal_spring    133.8926    54.2826   2.467   0.0136 *

---

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


(Dispersion parameter for binomial family taken to be 1)


    Null deviance: 210.722  on 29785  degrees of freedom

Residual deviance:  53.631  on 29782  degrees of freedom

AIC: 8.4867


Number of Fisher Scoring iterations: 13


Single term deletions
```

```
Model:

SEARCH_FORAGE ~ dist_col + dist_shore + sal_spring

           Df Deviance    AIC    LRT  Pr(>Chi)

<none>          53.631  8.487

dist_col    1   82.807 35.663 29.176 6.609e-08 ***

dist_shore  1   68.722 21.578 15.091 0.0001024 ***

sal_spring  1   69.594 22.450 15.964 6.457e-05 ***

---

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Forvie

```
Call:

glm(formula = formula.glm, family = "binomial", data =
complete.data.to.analyse,

    weights = weights)


Deviance Residuals:

     Min        1Q    Median        3Q       Max

-1.12046  -0.00006   0.00000   0.00000   0.93901


Coefficients:

            Estimate Std. Error z value Pr(>|z|)

(Intercept)  4.05603    1.06717   3.801 0.000144 ***

strat_temp  -2.37559    1.02867  -2.309 0.020922 *

bathy_1sec   0.26172    0.05121   5.111 3.21e-07 ***

---

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


(Dispersion parameter for binomial family taken to be 1)
```

```
    Null deviance: 341.802  on 30188  degrees of freedom
Residual deviance:  83.686  on 30186  degrees of freedom
AIC: 7.8467

Number of Fisher Scoring iterations: 11

Single term deletions

Model:
SEARCH_FORAGE ~ strat_temp + bathy_1sec
           Df Deviance    AIC    LRT  Pr(>Chi)
<none>          83.686  7.847
strat_temp  1   97.424 19.584 13.737 0.0002102 ***
bathy_1sec  1  165.952 88.112 82.265 < 2.2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Cemlyn

```
Call:
glm(formula = formula.glm, family = "binomial", data = 
complete.data.to.analyse,
    weights = weights)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.54047  -0.02339  -0.00045  -0.00001   1.45597

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.717e+03  3.857e+02  -4.450 8.58e-06 ***
```

```
dist_col    -2.770e-01  5.345e-02  -5.182 2.19e-07 ***
dist_shore  -3.661e-01  6.925e-02  -5.287 1.24e-07 ***
sal_spring   5.001e+01  1.124e+01   4.451 8.53e-06 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 665.34  on 9505  degrees of freedom
Residual deviance: 319.00  on 9502  degrees of freedom
AIC: 71.516

Number of Fisher Scoring iterations: 10

Single term deletions

Model:
SEARCH_FORAGE ~ dist_col + dist_shore + sal_spring
           Df Deviance     AIC    LRT  Pr(>Chi)
<none>          319.00  71.516
dist_col    1   418.97 169.481 99.965 < 2.2e-16 ***
dist_shore  1   363.02 113.531 44.015 3.259e-11 ***
sal_spring  1   381.47 131.983 62.468 2.709e-15 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

North Norfolk

```
Call:
glm(formula = formula.glm, family = "binomial", data =
complete.data.to.analyse,
```

```
    weights = weights)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.27057  -0.04867  -0.01660  -0.00522   2.01131

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -4.18978    0.89194  -4.697 2.64e-06 ***
dist_col    -0.17373    0.03497  -4.968 6.76e-07 ***
dist_shore   0.09494    0.04269   2.224   0.0262 *
bathy_1sec   0.05937    0.02918   2.034   0.0419 *
ss_wave      1.15652    0.24792   4.665 3.09e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 620.00  on 17989  degrees of freedom
Residual deviance: 390.39  on 17985  degrees of freedom
AIC: 59.696

Number of Fisher Scoring iterations: 8

Single term deletions

Model:
SEARCH_FORAGE ~ dist_col + dist_shore + bathy_1sec + ss_wave
           Df Deviance     AIC    LRT  Pr(>Chi)
```

```
<none>          390.39  59.696
dist_col    1   471.30 138.599 80.903 < 2.2e-16 ***
dist_shore  1   395.72  63.026  5.330   0.02096 *
bathy_1sec  1   394.66  61.965  4.268   0.03883 *
ss_wave     1   419.77  87.075 29.378 5.954e-08 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```