

Biomathematics and Statistics Scotland

**Refinements of tern *Sterna sp.* tracking data
modelling (Phase 2)
(Under Agreement C10-0206-0387)**

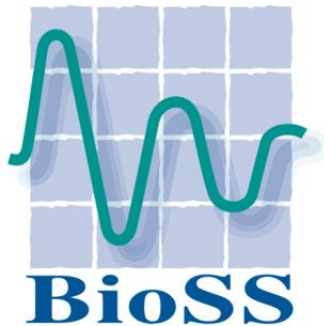
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CONTENTS	PAGE
1. Introduction	3
2. Methods	4
3. Results	6
4. Discussion	22
5. Appendix	24

In addition to this report, there are ancillary files associated with this project:

- (i) Spreadsheet files of grid predictions
- (ii) R code for cross-validation, fitting the final model and prediction

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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 dataset for the Phase 1 models (Brewer *et al.* 2012c; Potts *et al.* 2013a) 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 (Potts *et al.* 2013b). In light of the results from Potts *et al.* (2013b), here we describe how the candidate covariates used for the Phase 2 models were revisited and the Phase 2 models re-run, with cross-validation.

2. Methods

We followed the case-control, weighted regression methodology described in the report for Phase 1 (Potts *et al.*, 2013b) and other earlier reports (Brewer *et al.* 2012a, 2012b; Potts *et al.* 2012, 2013a). For Phase 2, Generalised Linear Models (GLMs) were used as per Brewer *et al.* (2012b) and Potts *et al.* (2013a).

Variables which were selected in at least one third of the Phase 1 models for each species and with a ranking of 1-5 based on rankings supplied by JNCC were identified as candidate covariates for the Phase 2 models. These were as follows:

Arctic terns: distance to colony, bathymetry, salinity in spring, June chlorophyll

Common terns: distance to colony, bathymetry, salinity in spring, distance to shore

Sandwich terns: distance to colony, bathymetry, salinity in spring, distance to shore

Boxplots were used to compare the range of values for the shortlisted environmental covariates at the colonies for which predictions were required with those for which data are available.

Following the approach taken in Brewer *et al.* (2012b), a single model was developed for each species using data from all available colonies.

The predictive ability of models consisting of all combinations of these variables was tested using cross-validation, by omitting each colony in turn and developing a model using data from the remaining colonies. Data for common terns at the Farne Islands colony were included in the model but the predictions were not tested as there were insufficient data. It was not possible to include the North Norfolk data for common and sandwich terns in the cross-validation because spring salinity, which is in the list of candidate variables, is not available.

Three scores were used to compare the predictive ability of the models in the cross-validation (the first two having been used in Brewer *et al.* (2012b), the third being an additional score used in this work):

(1) The Brier score or mean squared error $\frac{1}{n} \sum (y_i - p_i)^2$

where y is the binary variable indicating foraging behaviour and p is the predicted probability.

This represents the mean squared difference between the actual outcome (1 for presence or 0 for a control point) and the predicted probability of presence; lower values indicate a better model.

(2) A logarithmic score related to the log-likelihood $= \frac{1}{n} \sum (y_i \log(p_i) + (1 - y_i) \log(1 - p_i))$

This score means that the best model is the one which gives the highest predicted probability to the data; higher values of this score indicate a better model.

(3) The area under the curve (AUC), representing the area under the receiving operating characteristic (ROC) curve. This is equivalent to the Wilcoxon signed-ranked test (Mason and Graham, 2002) and was calculated by this method using the function `roc.area` in the R package ‘verification’.

If the model provided a perfect separation of the presences from the control points the AUC score would be 1, whereas it is 0.5 for a model with no discriminatory power.

The AUC is a widely used statistic for assessing species distribution models, but has been criticised for a number of reasons, including the fact that it is insensitive to transformations of the predicted probabilities that preserve their ranks (Lobo *et al.*, 2008; Jiménez-Valverde, 2012) and reliance on AUC as a single measure of model performance has therefore been questioned (Austin, 2007). The Brier and logarithmic scores have similar properties but there is no clear criterion for preferring one over the other (Machete, 2013).

For each scoring method, the scores omitting each colony in turn were then averaged to give an overall score.

The final model chosen was that supported by at least two of the three scoring methods (based on the average score from each), except where there were potential issues with the covariates included (see discussion).

3. Results

The boxplots shown in Figures 1-3 were used to compare the range of values for the shortlisted environmental covariates at the colonies for which predictions were required (Phase 2) with those for which data are available (Phase 1). For extrapolation purposes it is important that there is overlap in these values between the colonies in Phase 1 and 2. Generally the boxplots indicate relatively few potential extrapolation issues. However, there is some variation in the range of salinity in spring values at the colonies for which predictions are required with those for which data are available, as well as the extent of its availability for different colonies, and this suggests that this covariate may be less suitable for inclusion in a generic model that will be used for extrapolation. There is also some variation in the range of values for June chlorophyll, with the Wash colonies in particular tending to have higher values. It was not necessary to include distance to colony and distance to shore in the boxplots because although the distribution of these varies between colonies according to the shape of the coastline, the lower bound for both of these variables is zero and the upper bound for the distance to colony is the maximum foraging range that was defined for creating the grids (31km in the case of common and Arctic terns and 55km in the case of sandwich terns).

The results of the cross-validation are shown in Tables 1-15.

Figure 1. Boxplots of bathymetry, with Phase 1 colonies shown to the left of the dotted line and Phase 2 colonies to the right. Note that for Sandwich terns, the Wash refers to Blakeney Point and Scolt Head (rather than The Wash SPA).

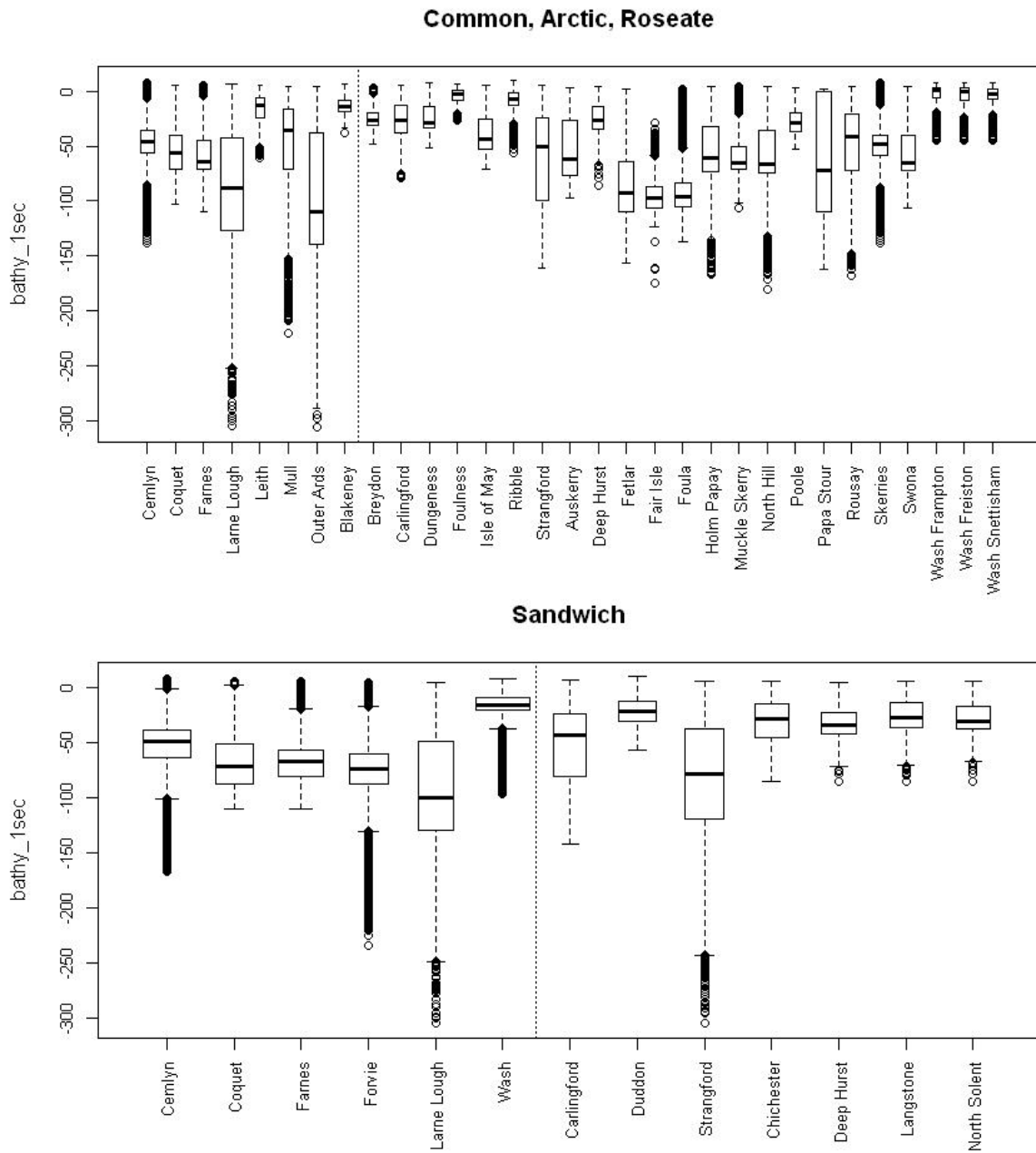


Figure 2. Boxplots of log-transformed June chlorophyll, with Phase 1 colonies shown to the left of the dotted line and Phase 2 colonies to the right. Note that for Sandwich terns, the Wash refers to Blakeney Point and Scolt Head (rather than The Wash SPA).

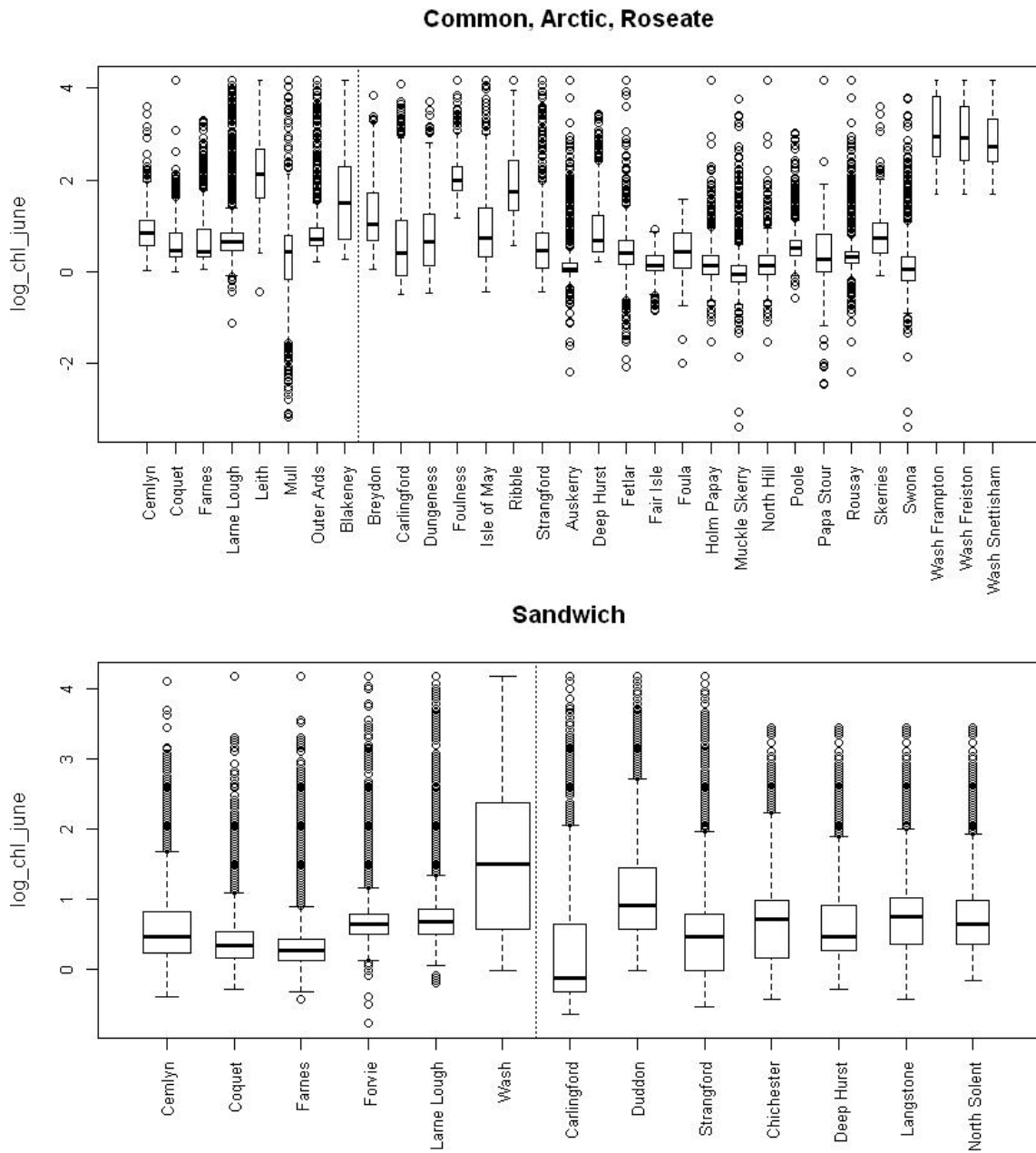


Figure 3. Boxplots of salinity in spring, with Phase 1 colonies shown to the left of the dotted line and Phase 2 colonies to the right. Note that for Sandwich terns, the Wash refers to Blakeney Point and Scolt Head (rather than The Wash SPA).

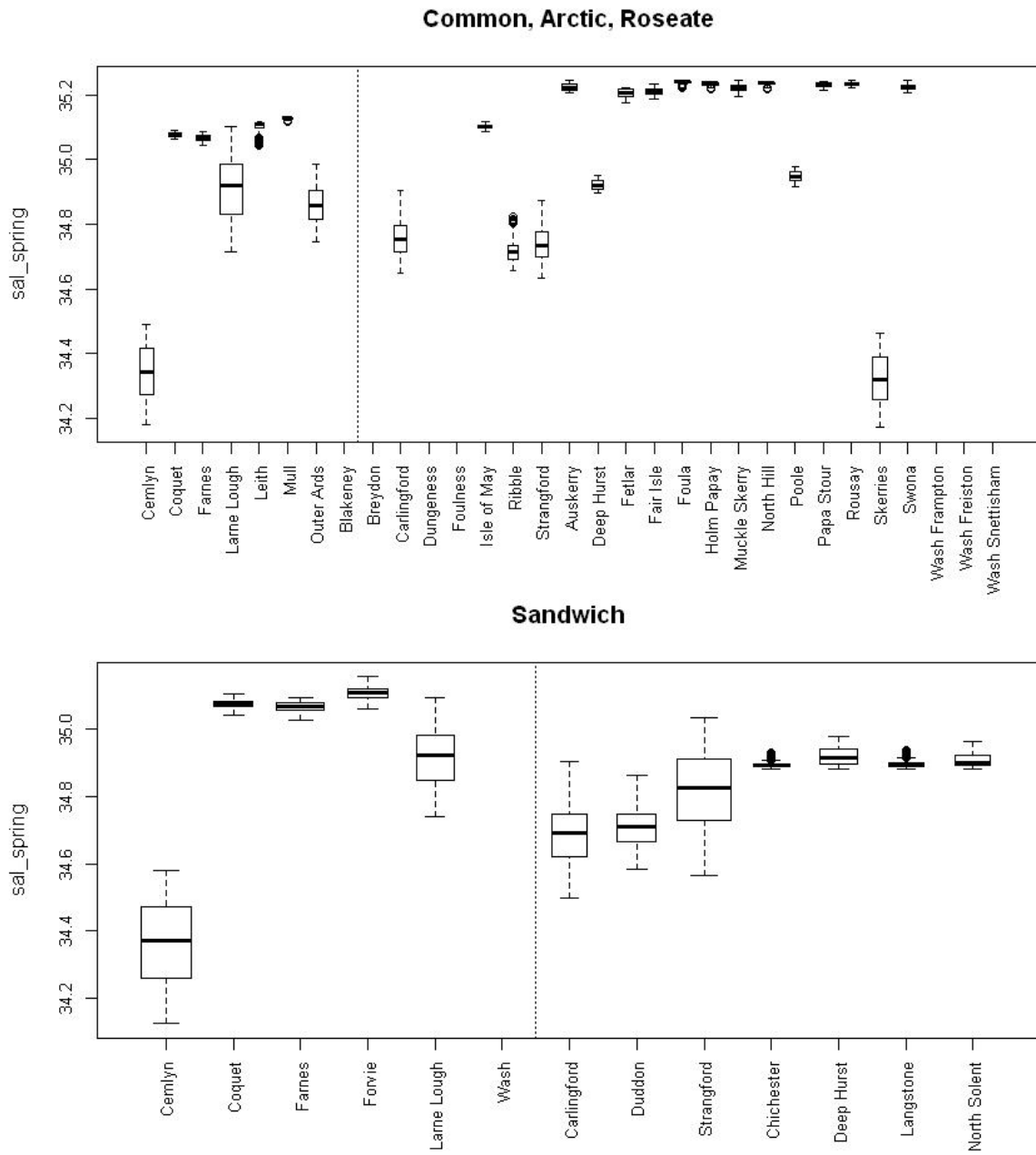


Table 1. Arctic terns – scaled likelihood score. Model with maximum average score shown in bold.

	Coquet	Farnes	Outer Ards	Average
dist_col	-0.203	-0.249	-0.289	-0.247
bathy_1sec	-0.223	-0.288	-0.366	-0.292
sal_spring	-0.236	-0.289	-0.411	-0.312
chl_june	-0.223	-0.306	-0.302	-0.277
dist_col, bathy_1sec	-0.206	-0.247	-0.276	-0.243
dist_col, sal_spring	-0.204	-0.248	-0.312	-0.255
dist_col, chl_june	-0.204	-0.259	-0.289	-0.251
bathy_1sec, sal_spring	-0.223	-0.303	-0.366	-0.297
bathy_1sec, chl_june	-0.222	-0.298	-0.351	-0.290
sal_spring, chl_june	-0.223	-0.326	-0.322	-0.290
dist_col, bathy_1sec, sal_spring	-0.206	-0.247	-0.294	-0.249
dist_col, bathy_1sec, chl_june	-0.205	-0.261	-0.268	-0.245
dist_col, sal_spring, chl_june	-0.205	-0.256	-0.316	-0.259
bathy_1sec, sal_spring, chl_june	-0.222	-0.317	-0.352	-0.297
dist_col, bathy_1sec, sal_spring, chl_june	-0.206	-0.260	-0.286	-0.251

Table 2. Arctic terns – scaled mean square error score. Model with minimum average score shown in bold.

	Coquet	Farnes	Outer Ards	Average
dist_col	0.0552	0.0713	0.0754	0.0673
bathy_1sec	0.0577	0.0761	0.0847	0.0729
sal_spring	0.0593	0.0765	0.0935	0.0764
chl_june	0.0577	0.0822	0.0814	0.0738
dist_col, bathy_1sec	0.0552	0.0710	0.0742	0.0668
dist_col, sal_spring	0.0552	0.0712	0.0763	0.0676
dist_col, chl_june	0.0553	0.0735	0.0754	0.0681
bathy_1sec, sal_spring	0.0577	0.0787	0.0869	0.0745
bathy_1sec, chl_june	0.0577	0.0793	0.0844	0.0738
sal_spring, chl_june	0.0577	0.0857	0.0887	0.0774
dist_col, bathy_1sec, sal_spring	0.0553	0.0710	0.0751	0.0671
dist_col, bathy_1sec, chl_june	0.0551	0.0746	0.0730	0.0676
dist_col, sal_spring, chl_june	0.0554	0.0730	0.0765	0.0683
bathy_1sec, sal_spring, chl_june	0.0577	0.0829	0.0866	0.0758
dist_col, bathy_1sec, sal_spring, chl_june	0.0553	0.0745	0.0746	0.0681

Table 3. Arctic terns – AUC. Model with maximum average score shown in bold.

	Coquet	Farnes	Outer Ards	Average
dist_col	0.790	0.753	0.700	0.747
bathy_1sec	0.725	0.611	0.611	0.649
sal_spring	0.618	0.487	0.539	0.548
chl_june	0.723	0.579	0.505	0.603
dist_col, bathy_1sec	0.789	0.755	0.713	0.752
dist_col, sal_spring	0.790	0.754	0.631	0.725
dist_col, chl_june	0.787	0.728	0.699	0.738
bathy_1sec, sal_spring	0.724	0.588	0.608	0.640
bathy_1sec, chl_june	0.725	0.606	0.605	0.645
sal_spring, chl_june	0.724	0.552	0.588	0.621
dist_col, bathy_1sec, sal_spring	0.789	0.755	0.656	0.734
dist_col, bathy_1sec, chl_june	0.790	0.720	0.711	0.741
dist_col, sal_spring, chl_june	0.787	0.735	0.622	0.715
dist_col, ss_current, chl_june	0.787	0.728	0.700	0.738
bathy_1sec, sal_spring, chl_june	0.724	0.571	0.611	0.635
dist_col, bathy_1sec, sal_spring, chl_june	0.790	0.722	0.656	0.723

For Arctic terns a model involving distance to colony and bathymetry was best according to the all three scores..

Table 4. Common terns – scaled likelihood score. Model with maximum average score shown in bold.

	Larne					Average
	Coquet	Cemlyn	Lough	Leith	Mull	
dist_col	-0.230	-0.183	-0.220	-0.304	-0.292	-0.246
bathy_1sec	-0.263	-0.268	-0.240	-0.311	-0.440	-0.304
dist_shore	-0.232	-0.222	-0.259	-0.302	-0.322	-0.268
sal_spring	-0.280	-0.277	-0.270	-0.317	-0.318	-0.292
dist_col, bathy_1sec	-0.231	-0.184	-0.221	-0.303	-0.302	-0.248
dist_col, dist_shore	-0.227	-0.182	-0.234	-0.299	-0.290	-0.246
dist_col, sal_spring	-0.230	-0.184	-0.221	-0.305	-0.292	-0.247
bathy_1sec, dist_shore	-0.233	-0.225	-0.258	-0.302	-0.327	-0.269
bathy_1sec, sal_spring	-0.262	-0.268	-0.240	-0.311	-0.450	-0.306
dist_shore, sal_spring	-0.232	-0.226	-0.262	-0.302	-0.322	-0.269
dist_col, bathy_1sec, dist_shore	-0.227	-0.182	-0.235	-0.299	-0.282	-0.245
dist_col, bathy_1sec, sal_spring	-0.231	-0.184	-0.221	-0.305	-0.305	-0.249
dist_col, dist_shore, sal_spring	-0.226	-0.182	-0.235	-0.300	-0.290	-0.247
bathy_1sec, dist_shore, sal_spring	-0.232	-0.228	-0.261	-0.302	-0.332	-0.271
dist_col, bathy_1sec, dist_shore, sal_spring	-0.226	-0.182	-0.236	-0.300	-0.284	-0.246

Table 5. Common terns excluding models involving salinity and including Blakeney colony – scaled likelihood score. Model with maximum average score shown in bold.

	North		Larne				Average
	Norfolk	Coquet	Cemlyn	Lough	Leith	Mull	
dist_col	-0.186	-0.231	-0.182	-0.221	-0.306	-0.294	-0.237
bathy_1sec	-0.268	-0.262	-0.267	-0.239	-0.311	-0.448	-0.299
dist_shore	-0.206	-0.232	-0.221	-0.262	-0.301	-0.323	-0.258
dist_col, bathy_1sec	-0.186	-0.231	-0.182	-0.221	-0.305	-0.303	-0.238
dist_col, dist_shore	-0.178	-0.226	-0.181	-0.238	-0.300	-0.291	-0.236
bathy_1sec, dist_shore	-0.207	-0.233	-0.223	-0.261	-0.301	-0.327	-0.259
dist_col, bathy_1sec, dist_shore	-0.178	-0.226	-0.181	-0.238	-0.300	-0.282	-0.234

Table 6. Common terms – scaled mean square error score. Model with minimum average score shown in bold.

	Coquet	Cemlyn	Larne Lough	Leith	Mull	Average
dist_col	0.0683	0.0558	0.0628	0.0878	0.0827	0.0715
bathy_1sec	0.0715	0.0718	0.0651	0.0860	0.1000	0.0789
dist_shore	0.0680	0.0653	0.0690	0.0847	0.0883	0.0751
sal_spring	0.0741	0.0730	0.0706	0.0869	0.0874	0.0784
dist_col, bathy_1sec	0.0683	0.0560	0.0629	0.0877	0.0852	0.0720
dist_col, dist_shore	0.0680	0.0555	0.0647	0.0870	0.0825	0.0715
dist_col, sal_spring	0.0683	0.0559	0.0629	0.0882	0.0827	0.0716
bathy_1sec, dist_shore	0.0681	0.0660	0.0688	0.0847	0.0890	0.0753
bathy_1sec, sal_spring	0.0714	0.0720	0.0651	0.0860	0.1007	0.0791
dist_shore, sal_spring	0.0681	0.0662	0.0693	0.0848	0.0883	0.0753
dist_col, bathy_1sec, dist_shore	0.0680	0.0555	0.0649	0.0869	0.0804	0.0711
dist_col, bathy_1sec, sal_spring	0.0683	0.0561	0.0630	0.0881	0.0860	0.0723
dist_col, dist_shore, sal_spring	0.0679	0.0556	0.0648	0.0873	0.0825	0.0716
bathy_1sec, dist_shore, sal_spring	0.0681	0.0668	0.0692	0.0848	0.0898	0.0757
dist_col, bathy_1sec, dist_shore, sal_spring	0.0679	0.0557	0.0650	0.0872	0.0810	0.0714

Table 7. Common terns excluding models involving salinity and including Blakeney colony – scaled mean square error score. Model with minimum average score shown in bold.

	North Norfolk	Coquet	Cemlyn	Larne Lough	Leith	Mull	Average
dist_col	0.0568	0.0685	0.0555	0.0630	0.0884	0.0829	0.0692
bathy_1sec	0.0717	0.0714	0.0718	0.0649	0.0861	0.1005	0.0777
dist_shore	0.0621	0.0681	0.0652	0.0692	0.0846	0.0884	0.0729
dist_col, bathy_1sec	0.0569	0.0685	0.0557	0.0630	0.0883	0.0853	0.0696
dist_col, dist_shore	0.0553	0.0681	0.0553	0.0652	0.0873	0.0826	0.0690
bathy_1sec, dist_shore	0.0624	0.0682	0.0658	0.0691	0.0846	0.0890	0.0732
dist_col, bathy_1sec, dist_shore	0.0553	0.0681	0.0553	0.0653	0.0872	0.0801	0.0686

Table 8. Common terms – AUC. Model with maximum average score shown in bold.

	Coquet	Cemlyn	Larne Lough	Leith	Mull	Average
dist_col	0.801	0.916	0.819	0.655	0.746	0.788
bathy_1sec	0.787	0.730	0.757	0.605	0.363	0.648
dist_shore	0.795	0.827	0.693	0.665	0.449	0.686
sal_spring	0.608	0.509	0.664	0.677	0.433	0.578
dist_col, bathy_1sec	0.801	0.915	0.818	0.656	0.727	0.784
dist_col, dist_shore	0.810	0.914	0.794	0.663	0.741	0.784
dist_col, sal_spring	0.801	0.916	0.818	0.654	0.746	0.787
bathy_1sec, dist_shore	0.795	0.822	0.699	0.663	0.418	0.679
bathy_1sec, sal_spring	0.787	0.705	0.755	0.607	0.363	0.643
dist_shore, sal_spring	0.795	0.811	0.688	0.659	0.450	0.681
dist_col, bathy_1sec, dist_shore	0.810	0.914	0.789	0.663	0.758	0.787
dist_col, bathy_1sec, sal_spring	0.801	0.914	0.817	0.654	0.721	0.782
dist_col, dist_shore, sal_spring	0.812	0.912	0.792	0.661	0.741	0.784
bathy_1sec, dist_shore, sal_spring	0.795	0.808	0.694	0.659	0.401	0.671
dist_col, bathy_1sec, dist_shore, sal_spring	0.812	0.912	0.786	0.662	0.754	0.785

Table 9. Common terns excluding models involving salinity and including Blakeney colony – AUC. Model with maximum average score shown in bold.

	North Norfolk	Coquet	Cemlyn	Larne Lough	Leith	Mull	Average
dist_col	0.923	0.801	0.916	0.819	0.655	0.746	0.810
bathy_1sec	0.815	0.787	0.730	0.757	0.605	0.363	0.676
dist_shore	0.900	0.795	0.827	0.693	0.665	0.449	0.721
dist_col, bathy_1sec	0.924	0.801	0.915	0.818	0.656	0.730	0.807
dist_col, dist_shore	0.931	0.813	0.913	0.792	0.665	0.740	0.809
bathy_1sec, dist_shore	0.899	0.795	0.823	0.700	0.664	0.424	0.717
dist_col, bathy_1sec, dist_shore	0.931	0.813	0.913	0.788	0.665	0.761	0.812

For common terns a model involving distance to colony, distance to shore and bathymetry was best according to all three scores when the Blakeney colony is included.

Table 10. Sandwich terns – scaled likelihood score. Model with maximum average score shown in bold.

	Larne						Average
	Coquet	Lough	Forvie	Farnes	Cemlyn	Cockle	
dist_col	-0.214	-0.150	-0.204	-0.186	-0.226	-0.224	-0.201
bathy_1sec	-0.184	-0.136	-0.124	-0.138	-0.273	-0.301	-0.193
dist_shore	-0.188	-0.151	-0.119	-0.132	-0.227	-0.283	-0.183
sal_spring	-0.277	-0.282	-0.311	-0.276	-0.295	-0.269	-0.285
dist_col, bathy_1sec	-0.183	-0.103	-0.130	-0.137	-0.214	-0.251	-0.170
dist_col, dist_shore	-0.185	-0.112	-0.114	-0.128	-0.223	-0.249	-0.168
dist_col, sal_spring	-0.214	-0.150	-0.205	-0.186	-0.225	-0.362	-0.224
bathy_1sec, dist_shore	-0.188	-0.152	-0.118	-0.131	-0.234	-0.284	-0.184
bathy_1sec, sal_spring	-0.183	-0.135	-0.124	-0.137	-0.282	-0.467	-0.221
dist_shore, sal_spring	-0.188	-0.151	-0.119	-0.132	-0.225	-0.283	-0.183
dist_col, bathy_1sec, dist_shore	-0.184	-0.113	-0.114	-0.128	-0.211	-0.251	-0.167
dist_col, bathy_1sec, sal_spring	-0.183	-0.102	-0.131	-0.137	-0.214	-1.361	-0.355
dist_col, dist_shore, sal_spring	-0.185	-0.112	-0.114	-0.128	-0.217	-0.249	-0.168
bathy_1sec, dist_shore, sal_spring	-0.188	-0.153	-0.118	-0.131	-0.234	-0.284	-0.185
dist_col, bathy_1sec, dist_shore, sal_spring	-0.185	-0.113	-0.114	-0.128	-0.208	-0.285	-0.172

Table 11. Sandwich terns excluding models involving salinity and including North Norfolk colonies – scaled likelihood score. Model with maximum average score shown in bold.

	North	Larne						Average
	Norfolk	Coquet	Lough	Forvie	Farnes	Cemlyn	Cockle	
dist_col	-0.201	-0.214	-0.150	-0.204	-0.186	-0.225	-0.223	-0.201
bathy_1sec	-0.245	-0.184	-0.139	-0.131	-0.142	-0.275	-0.290	-0.201
dist_shore	-0.392	-0.177	-0.171	-0.144	-0.150	-0.200	-0.249	-0.212
dist_col, bathy_1sec	-0.197	-0.188	-0.105	-0.145	-0.146	-0.204	-0.242	-0.175
dist_col, dist_shore	-0.369	-0.177	-0.128	-0.143	-0.149	-0.194	-0.214	-0.196
bathy_1sec, dist_shore	-0.367	-0.177	-0.150	-0.131	-0.140	-0.229	-0.261	-0.208
dist_col, bathy_1sec, dist_shore	-0.356	-0.177	-0.111	-0.131	-0.139	-0.199	-0.232	-0.192

Table 12. Sandwich terns – scaled mean square error score. Model with minimum average score shown in bold.

	Larne						Average
	Coquet	Lough	Forvie	Farnes	Cemlyn	Cockle	
dist_col	0.0673	0.0463	0.0621	0.0594	0.0695	0.0633	0.0613
bathy_1sec	0.0561	0.0448	0.0367	0.0431	0.0814	0.0704	0.0554
dist_shore	0.0561	0.0485	0.0369	0.0424	0.0618	0.0701	0.0527
sal_spring	0.0729	0.0746	0.0851	0.0727	0.0798	0.0708	0.0760
dist_col, bathy_1sec	0.0596	0.0326	0.0418	0.0440	0.0685	0.0649	0.0519
dist_col, dist_shore	0.0578	0.0359	0.0360	0.0412	0.0608	0.0646	0.0494
dist_col, sal_spring	0.0673	0.0462	0.0621	0.0595	0.0691	0.0923	0.0661
bathy_1sec, dist_shore	0.0560	0.0488	0.0365	0.0418	0.0720	0.0699	0.0542
bathy_1sec, sal_spring	0.0561	0.0446	0.0364	0.0429	0.0834	0.1019	0.0609
dist_shore, sal_spring	0.0561	0.0485	0.0369	0.0424	0.0602	0.0702	0.0524
dist_col, bathy_1sec, dist_shore	0.0579	0.0363	0.0359	0.0410	0.0620	0.0645	0.0496
dist_col, bathy_1sec, sal_spring	0.0597	0.0325	0.0420	0.0441	0.0679	0.0978	0.0573
dist_col, dist_shore, sal_spring	0.0579	0.0359	0.0361	0.0413	0.0583	0.0645	0.0490
bathy_1sec, dist_shore, sal_spring	0.0560	0.0490	0.0365	0.0418	0.0713	0.0699	0.0541
dist_col, bathy_1sec, dist_shore, sal_spring	0.0579	0.0361	0.0359	0.0410	0.0596	0.0736	0.0507

Table 13. Sandwich terns excluding models involving salinity and including North Norfolk colonies – scaled mean square error score. Model with minimum average score shown in bold.

	North	Larne						Average
	Norfolk	Coquet	Lough	Forvie	Farnes	Cemlyn	Cockle	
dist_col	0.0569	0.0671	0.0462	0.0621	0.0594	0.0693	0.0632	0.0606
bathy_1sec	0.0679	0.0561	0.0456	0.0387	0.0443	0.0820	0.0700	0.0578
dist_shore	0.0665	0.0558	0.0537	0.0447	0.0477	0.0604	0.0676	0.0566
dist_col, bathy_1sec	0.0568	0.0612	0.0330	0.0465	0.0471	0.0667	0.0653	0.0538
dist_col, dist_shore	0.0623	0.0587	0.0401	0.0454	0.0479	0.0608	0.0623	0.0539
bathy_1sec, dist_shore	0.0661	0.0553	0.0478	0.0399	0.0443	0.0722	0.0678	0.0562
dist_col, bathy_1sec, dist_shore	0.0620	0.0582	0.0349	0.0417	0.0446	0.0644	0.0636	0.0528

Table 14. Sandwich terns – AUC. Model with maximum average score shown in bold.

	Larne						Average
	Coquet	Lough	Forvie	Farnes	Cemlyn	Cockle	
dist_col	0.850	0.963	0.898	0.889	0.866	0.842	0.885
bathy_1sec	0.908	0.962	0.989	0.975	0.803	0.717	0.892
dist_shore	0.911	0.967	0.986	0.971	0.902	0.739	0.913
sal_spring	0.609	0.629	0.820	0.700	0.562	0.471	0.632
dist_col, bathy_1sec	0.910	0.980	0.971	0.966	0.893	0.844	0.927
dist_col, dist_shore	0.916	0.979	0.980	0.975	0.912	0.833	0.933
dist_col, sal_spring	0.850	0.963	0.898	0.889	0.868	0.806	0.879
bathy_1sec, dist_shore	0.912	0.967	0.987	0.972	0.879	0.742	0.910
bathy_1sec, sal_spring	0.908	0.963	0.989	0.975	0.790	0.717	0.890
dist_shore, sal_spring	0.911	0.968	0.986	0.971	0.908	0.740	0.914
dist_col, bathy_1sec, dist_shore	0.916	0.978	0.980	0.976	0.910	0.834	0.932
dist_col, bathy_1sec, sal_spring	0.910	0.980	0.971	0.965	0.892	0.808	0.921
dist_col, dist_shore, sal_spring	0.916	0.979	0.980	0.975	0.917	0.831	0.933
bathy_1sec, dist_shore, sal_spring	0.912	0.967	0.987	0.972	0.886	0.742	0.911
dist_col, bathy_1sec, dist_shore, sal_spring	0.916	0.978	0.980	0.976	0.915	0.811	0.929

Table 15. Sandwich terns excluding models involving salinity and including North Norfolk colonies – AUC. Model with maximum average score shown in bold.

	North	Larne						Average
	Norfolk	Coquet	Lough	Forvie	Farnes	Cemlyn	Cockle	
dist_col	0.877	0.850	0.963	0.898	0.889	0.866	0.842	0.884
bathy_1sec	0.800	0.908	0.962	0.989	0.975	0.803	0.717	0.879
dist_shore	0.792	0.911	0.967	0.986	0.971	0.902	0.739	0.896
dist_col, bathy_1sec	0.878	0.899	0.979	0.962	0.956	0.907	0.856	0.920
dist_col, dist_shore	0.820	0.905	0.978	0.968	0.962	0.907	0.857	0.914
bathy_1sec, dist_shore	0.793	0.911	0.972	0.989	0.975	0.866	0.748	0.894
dist_col, bathy_1sec, dist_shore	0.821	0.911	0.979	0.973	0.970	0.907	0.850	0.916

For Sandwich terns a model involving distance to colony, distance to shore and bathymetry was best according to the likelihood score, while one involving distance to colony, distance to shore and salinity was optimal according to the mean squared error and AUC scores. If salinity is excluded and the North Norfolk colonies are included the model involving distance to colony, distance to shore and bathymetry was best according to the mean squared error score, while one involving distance to colony and bathymetry only was best according to the likelihood and AUC scores.

4. Discussion

For Arctic terns the preferred model is one chosen by all three score involving distance to colony and bathymetry. According to the boxplots, there are no extrapolation issues for bathymetry.

For common terns the preferred model is one chosen by all three scores involving distance to colony, distance to shore and bathymetry. According to the boxplots, there are no extrapolation issues for bathymetry.

For Sandwich terns three different models were each supported twice across the six evaluation methods applied. When North Norfolk is excluded, the best model according to the likelihood score is one involving distance to colony, distance to shore and bathymetry, while the best model according to the other two scores is one involving distance to colony, distance to shore and salinity in spring. However, as noted in the discussion of the boxplots, there are some issues with extrapolating a model that includes salinity in spring due to the different ranges that this variable takes at different colonies and it should also be noted that this variable is missing in the Wash area (Phase 1 colonies at Blakeney Point and Scolt Head; and Phase 2 colonies at Frampton, Freiston and Snettisham). When North Norfolk is included the model involving distance to colony, distance to shore and bathymetry is again selected, this time by the mean squared error score, although the model that involves just distance to colony and bathymetry is selected by the other two scores. The recommended model is therefore one involving distance to colony, distance to shore and bathymetry as these covariates were consistently selected across the short-list of models identified by the different evaluation methods.

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Appendix – Results from final models

Arctic Terns – Preferred Model

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

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.81514	-0.04036	-0.01842	-0.00755	1.84428

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-0.956084	0.143911	-6.644	3.06e-11	***
dist_col	-0.220661	0.026633	-8.285	< 2e-16	***
bathy_1sec	-0.008812	0.005288	-1.666	0.0956	.

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1035.68 on 98756 degrees of freedom
Residual deviance: 839.84 on 98754 degrees of freedom
AIC: 80.818

Number of Fisher Scoring iterations: 7

Arctic terns – alternative model

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

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.90071	-0.04020	-0.01865	-0.00787	1.92472

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-0.963977	0.144952	-6.650	2.92e-11	***
dist_col	-0.209353	0.027566	-7.595	3.09e-14	***
bathy_1sec	-0.007116	0.005438	-1.308	0.191	
ss_current	0.142818	0.114574	1.247	0.213	

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1035.20 on 98530 degrees of freedom
Residual deviance: 837.78 on 98527 degrees of freedom
AIC: 82.071

Number of Fisher Scoring iterations: 7

Common terns

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

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.85854	-0.04410	-0.02159	-0.00747	2.24222

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-0.7395726	0.1018000	-7.265	3.73e-13	***
dist_col	-0.1862773	0.0162314	-11.476	< 2e-16	***
bathy_1sec	-0.0006926	0.0023439	-0.295	0.76763	
dist_shore	-0.1029588	0.0343827	-2.994	0.00275	**

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 2212.5 on 174223 degrees of freedom
Residual deviance: 1792.4 on 174220 degrees of freedom
AIC: 138.69

Number of Fisher Scoring iterations: 8

Sandwich terns – preferred model

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

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.34219	-0.02105	-0.00356	-0.00059	2.08319

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	0.283251	0.095138	2.977	0.00291	**
dist_col	-0.086843	0.008085	-10.741	< 2e-16	***
bathy_1sec	0.025767	0.004757	5.417	6.08e-08	***
dist_shore	-0.196590	0.029935	-6.567	5.12e-11	***

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 2833.0 on 193486 degrees of freedom
Residual deviance: 1698.2 on 193483 degrees of freedom
AIC: 205.57

Number of Fisher Scoring iterations: 9

Sandwich terns – alternative model

Call:

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

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.42872	-0.01436	-0.00088	-0.00001	2.32014

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	4.105843	4.821117	0.852	0.394
dist_col	-0.082737	0.008976	-9.218	<2e-16 ***
sal_spring	-0.100553	0.138054	-0.728	0.466
dist_shore	-0.604049	0.052997	-11.398	<2e-16 ***

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 2212.4 on 175447 degrees of freedom
Residual deviance: 1186.1 on 175444 degrees of freedom
AIC: 135.82

Number of Fisher Scoring iterations: 10