*The following supplement accompanies the article*

# Frequency and consequences of individual dietary specialisation in a wide-ranging marine predator, the northern gannet

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## Supplement 1

**Text S1.**

### Supplementary Methods

### Consequences of Foraging Strategies

*Habitat Selection*

In order to generate an estimate of the level of competition experienced by gannets during trips we estimated Utilization Distributions (UDs) for each colony based on kernel density (KD) calculations for all putative foraging locations in the R package adehabitatHR (Calenge 2006) following the approach of Wakefield et al (2013). We then estimated the density of observations at each colony as:

$$\hat{u}_{i,x} N_i$$

where $\hat{u}_{i,x}$ is the estimated absolute density of use of cell $x$ by birds from colony $i$ and $N_i$ is the number of breeding pairs at the $i$th colony taken from Wakefield et al (2013). In this analysis, the cell size used was 4 km$^2$. Using this approach allows us to incorporate information on both colony size and how bird density varies across each colony's home range. This assumes a declining density of birds as distance form the colony increases as $N_i$ is, generally, spread over a larger area at greater distances from the colony. In addition, to account for the fact that the home ranges on some colonies partially overlapped, we summed the spatial density estimates across all colonies where this occurred. Maps of the estimated density of birds at each colony are presented in Fig. S1.

Habitat Selection Functions (HSF) were used to examine how the relative usage of different areas was influenced by the levels of competition. HSF compare habitats that are used versus those that were unused but available using a logistic-regression based approach with a case-control design (Aarts et al 2008). The case-control design generates a binomial response which takes the value 1 for the $i$th data point if it belongs to the telemetry dataset, or the value 0 if belongs to the control dataset. Animal locations were generated for each bird by selecting only those GPS observations that were scored as putative foraging locations (details in Wakefield et al 2013). Sub-setting the data in this way generates a behaviorally explicit measure of habitat selection in order to give an understanding of which habitats are used for foraging (Wilson et al 2012). We complemented each observed foraging location with five temporally matched pseudo-absences for the control dataset. Pseudo-absences were generated randomly from space and were constrained to fall within the boundaries of a 95% density kernel which was constructed using only foraging observations. Separate 95% density kernels were calculated for each colony.

In order to perform model selection on our HSFs, we used K-fold validation and compared the predictive performance of models using $K$ = 5-fold log-likelihood cross-validation using the summed log-likelihood values for the holdout data as a measure of goodness-of-fit (e.g. Matthiopoulos 2003, Aarts et al 2013).

*Body Condition*

Body condition was estimated using the scaled mass conditional index (Peig & Green 2009), with birds that are heavier for a given size assumed to be in better body condition. This method standardises mass based on a power law between individual mass and size calculated from the data rather than on the basis of mass-length residuals. Body mass was measured (±50 g) on initial capture when the stomach was empty, and morphometrics – maximum flattened wing chord (with the exception of Ailsa Craig), bill length to feathering and maximum tarsus – were also collected. We scaled all birds to the mean maximum tarsus length as this provided the best correlation (for full details see Peig & Green 2009).

Table S1. Parameter estimates and variance explained by fixed effects for the top models examining the effect of dietary specialization on foraging movement metrics and scaled adult mass. For maximum distance from the colony and departure angle there are both **top** (bold) and *most parsimonious* (italics) models, and results for both are displayed.

| Response variable | Model | Parameter estimates and standard errors | | | Variance Explained |
|---|---|---|---|---|---|
| Trip distance | ***Colony + Sex*** | Intercept | 537.40 | 30.58 | 0.199 |
| | | ColonyBass | -106.31 | 45.89 | |
| | | ColonyBull | -266.96 | 41.02 | |
| | | ColonyGrassholm | -130.59 | 40.20 | |
| | | ColonySaltee | -234.54 | 38.97 | |
| | | ColonySkellig | -255.52 | 46.41 | |
| | | sexMale | -64.92 | 24.85 | |
| Maximum distance from colony | **Sex + Colony + Dietary Type + Sex*Colony + Sex*Dietary Type** | Intercept | 175.75 | 10.72 | 0.295 |
| | | ColonyBass | -38.02 | 20.57 | |
| | | ColonyBull | -116.32 | 16.76 | |
| | | ColonyGrassholm | -76.14 | 16.06 | |
| | | ColonySaltee | -95.68 | 14.31 | |
| | | ColonySkellig | -76.58 | 19.43 | |
| | | sexMale | -50.63 | 18.39 | |
| | | Foragefishspec | 42.01 | 13.55 | |
| | | Discardspec | 3.05 | 15.91 | |
| | | Male:ColonyBass | 55.23 | 28.20 | |
| | | Male:ColonyBull | 73.71 | 24.18 | |
| | | Male:ColonyGrassholm | 65.53 | 23.64 | |
| | | Male:ColonySaltee | 45.75 | 22.78 | |
| | | Male:ColonySkellig | 42.80 | 28.51 | |
| | | Male:Foragefishspec | -59.56 | 20.37 | |
| | | Male:Discardspec | -16.96 | 19.55 | |
| Maximum distance from colony | *Sex + Colony + Dietary Type + Sex*Dietary Type* | Intercept | 161.17 | 9.74 | 0.284 |
| | | sexMale | -3.65 | 9.14 | |
| | | Foragefishspec | 39.86 | 13.65 | |
| | | Discardspec | -5.75 | 15.94 | |
| | | ColonyBass | -16.70 | 13.96 | |
| | | ColonyBull | -83.64 | 12.35 | |
| | | ColonyGrassholm | -48.76 | 12.18 | |
| | | ColonySaltee | -79.27 | 11.59 | |
| | | ColonySkellig | -63.30 | 14.51 | |
| | | Male:Foragefishspec | -60.40 | 20.61 | |
| | | Male:Discardspec | -12.41 | 19.87 | |
| Departure angle | **Sex + Colony + Dietary Type + Sex*Colony** | Intercept | 245.25 | 17.46 | 0.475 |
| | | sexMale | -40.71 | 30.55 | |
| | | ColonyBass | -186.06 | 33.81 | |
| | | ColonyBull | -81.31 | 24.38 | |
| | | ColonyGrassholm | -12.21 | 25.39 | |
| | | ColonySaltee | -14.98 | 22.77 | |
| | | ColonySkellig | 35.01 | 26.81 | |
| | | Foragefishspec | -13.28 | 14.75 | |
| | | Discardspec | -30.08 | 14.22 | |

| | | | | | |
|---|---|---|---|---|---|
| | | Male:ColonyBass | 112.63 | 46.46 | |
| | | Male:ColonyBull | 79.48 | 37.42 | |
| | | Male:ColonyGrassholm | -7.21 | 38.61 | |
| | | Male:ColonySaltee | -24.56 | 37.58 | |
| | | Male:ColonySkellig | 30.30 | 41.45 | |
| | | Intercept | 240.25 | 17.47 | |
| | | sexMale | -47.74 | 30.78 | |
| | *Colony* + *Sex* + | ColonyBass | -181.04 | 34.27 | 0.471 |
| | *Sex*Colony* | ColonyBull | -84.20 | 24.70 | |
| Departure angle | | ColonyGrassholm | -19.62 | 25.35 | |
| | | ColonySaltee | -12.18 | 23.06 | |
| | | ColonySkellig | 29.54 | 27.01 | |
| | | Male:ColonyBass | 115.29 | 46.69 | |
| | | Male:ColonyBull | 88.33 | 37.80 | |
| | | Male:ColonyGrassholm | 2.96 | 38.90 | |
| | | Male:ColonySaltee | -35.62 | 37.58 | |
| | | Male:ColonySkellig | 45.08 | 39.60 | |
| Scaled Mass | ***Colony* + *Sex*** | Intercept | 3.96 | 0.06 | 0.143 |
| | | sexMale | -0.15 | 0.04 | |
| | | ColonyBass | -0.98 | 0.09 | |
| | | ColonyBull | -0.67 | 0.08 | |
| | | ColonyGrassholm | -1.14 | 0.07 | |
| | | ColonySaltee | -0.88 | 0.08 | |
| | | ColonySkellig | -0.77 | 0.10 | |

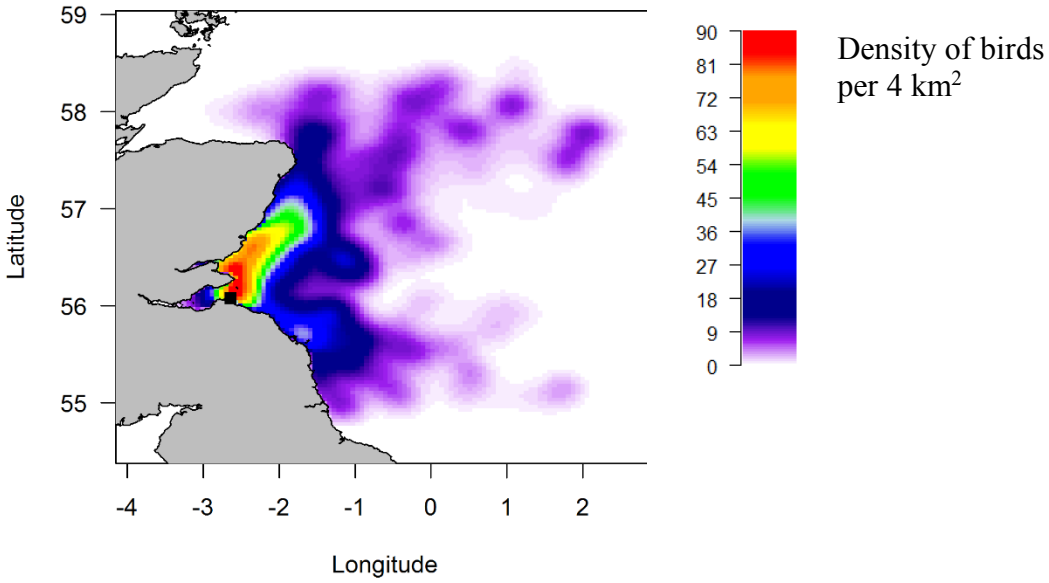
Table S2. Model selection table for HSFs based on 5-fold cross-validation. CV Log-likelihood here are the (cross-validation) marginal log-likelihoods. The letter *s* denotes fitting a smoother and *by* denotes fitting separate smoothers by the specified categorical variable. The best fitting model is displayed in bold.

| Model | Log-likelihood | CV log-likelihood |
|---|---|---|
| No Competition smoother | -85146 | -85550 |
| *s*(Competition) | -84299 | -84655 |
| *s*(Competition, *by* = Foraging Specialization) | -80624 | -80815 |
| *s*(Competition, *by* = Colony) | -80011 | -80214 |
| **s(Competition, *by* = Colony × Foraging Specialization)** | **-78020** | **-78105** |

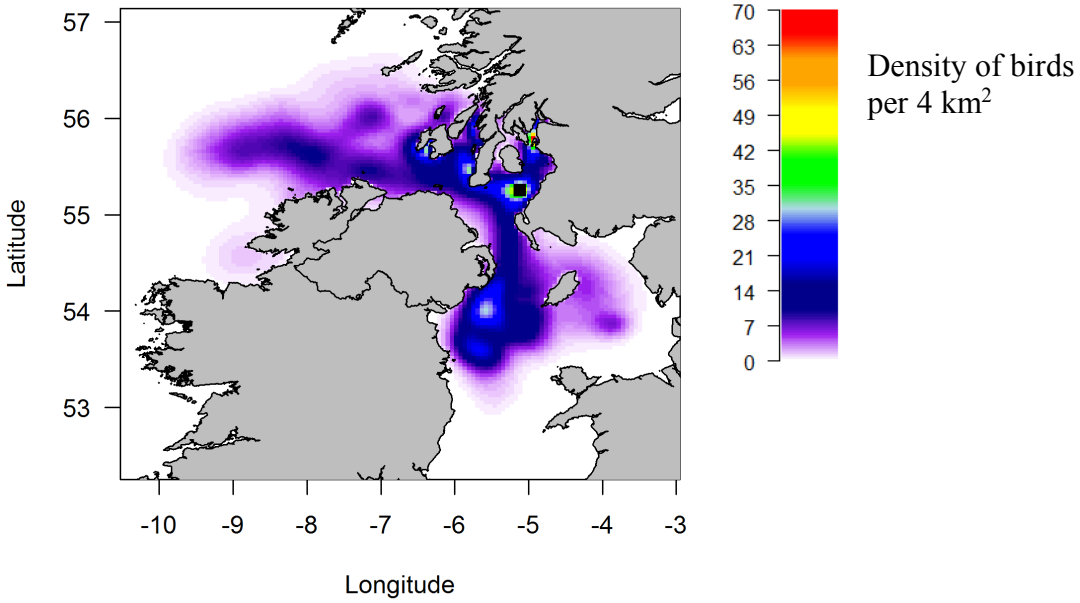
Table S3. Summary of smoothers included in the best fitting habitat selection function GAMM in each year of the study. Here, *s* represents a smooth function and *edf* is the estimated degrees of freedom for the smoother. Note that an intercept for Colony and Specialization was also included. Deviance explained = 27%.

| Variable | Smoother *edf* / *p* value |
|---|---|
| *s*(Competition, Colony Specialization = Ailsa Craig - Generalist) | 2.90, p = < 0.001 |
| *s*(Competition, Colony and Specialization = Ailsa Craig – Forage Fish Specialist) | 2.95, p = < 0.001 |
| *s*(Competition, Colony and Specialization = Ailsa Craig – Discard Specialist) | 2.83, p = < 0.001 |
| *s*(Competition, Colony and Specialization = Bass Rock - Generalist) | 2.90, p = < 0.001 |
| *s*(Competition, Colony and Specialization = Bass Rock – Forage Fish Specialist) | 2.96, p = < 0.001 |
| *s*(Competition, Colony and Specialization = Bull Rock - Generalist) | 2.90, p = < 0.001 |
| *s*(Competition, Colony and Specialization = Bull Rock – Forage Fish Specialist) | 2.74, p = <0.001 |
| *s*(Competition, Colony and Specialization = Bull Rock – Discard Specialist) | 2.93, p =<0.001 |
| *s*(Competition, Colony and Specialization = Grassholm - Generalist) | 2.90, p =<0.001 |
| *s*(Competition, Colony and Specialization = Grassholm– Forage Fish Specialist) | 2.91, p = <0.001 |
| *s*(Competition, Colony and Specialization = Grassholm – Discard Specialist) | 2.97, p = <0.001 |
| *s*(Competition, Colony and Specialization = Saltee- Generalist) | 2.96, p = <0.001 |
| *s*(Competition, Colony and Specialization = Saltee – Forage Fish Specialist) | 2.96, p = < 0.001 |
| *s*(Competition, Colony and Specialization = Saltee – Discard Specialist) | 2.87, p = <0.001 |
| *s*(Competition, Colony and Specialization = Skellig - Generalist) | 2.96, p =<0.001 |
| *s*(Competition, Colony and Specialization = Skellig – Forage Fish Specialist) | 2.83, p = <0.001 |
| *s*(Competition, Colony and Specialization = Skellig – Discard Specialist) | 2.14, p = <0.001 |
| *s*(Longitude, Latitude) | 28.97, p = <0.001 |
| Bird ID | $\sigma = 0.51$ |
| Colony ID | $\sigma = 4.38$ |

a) Bass Rock




b) Ailsa Craig



c) Bull Rock, Grassholm, Great Saltee and Little Skellig

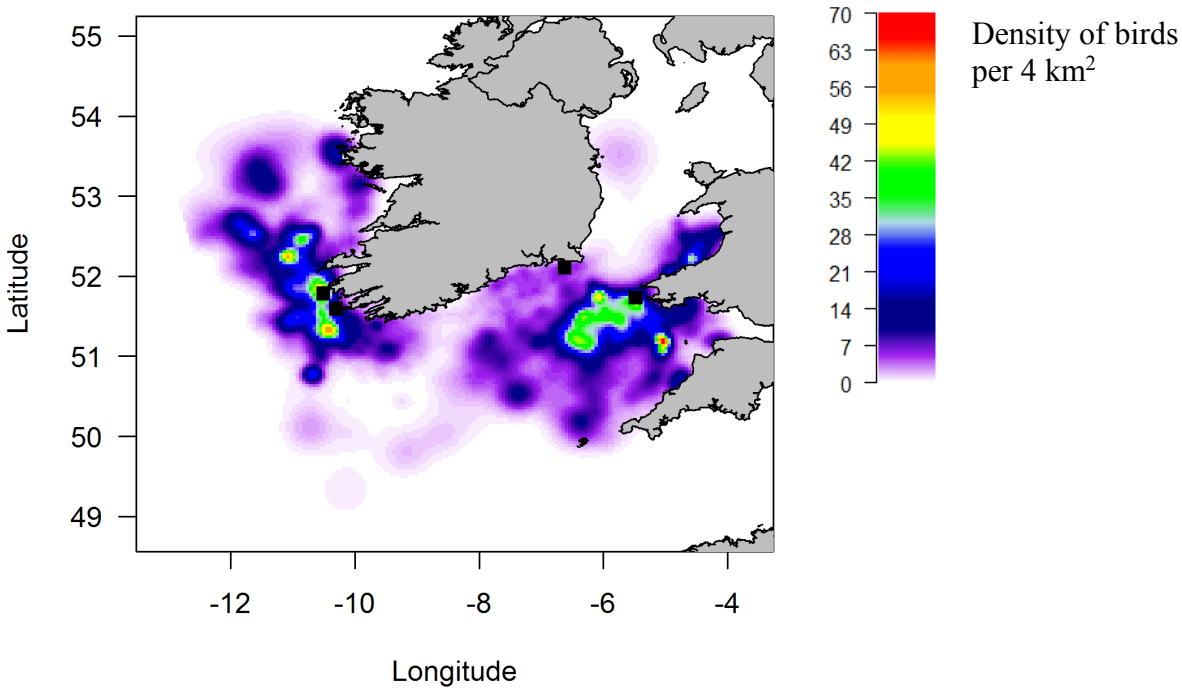



Figure S1. Density maps of birds at each of the 6 colonies in the study based on 2011 GPS tracking data. Density maps for Irish and Welsh colonies are displayed on one figure as the 95% utilization distributions of these colonies partially overlapped. Density was calculated on a 4 $km^2$ grid square. Colony locations denoted by a black square.

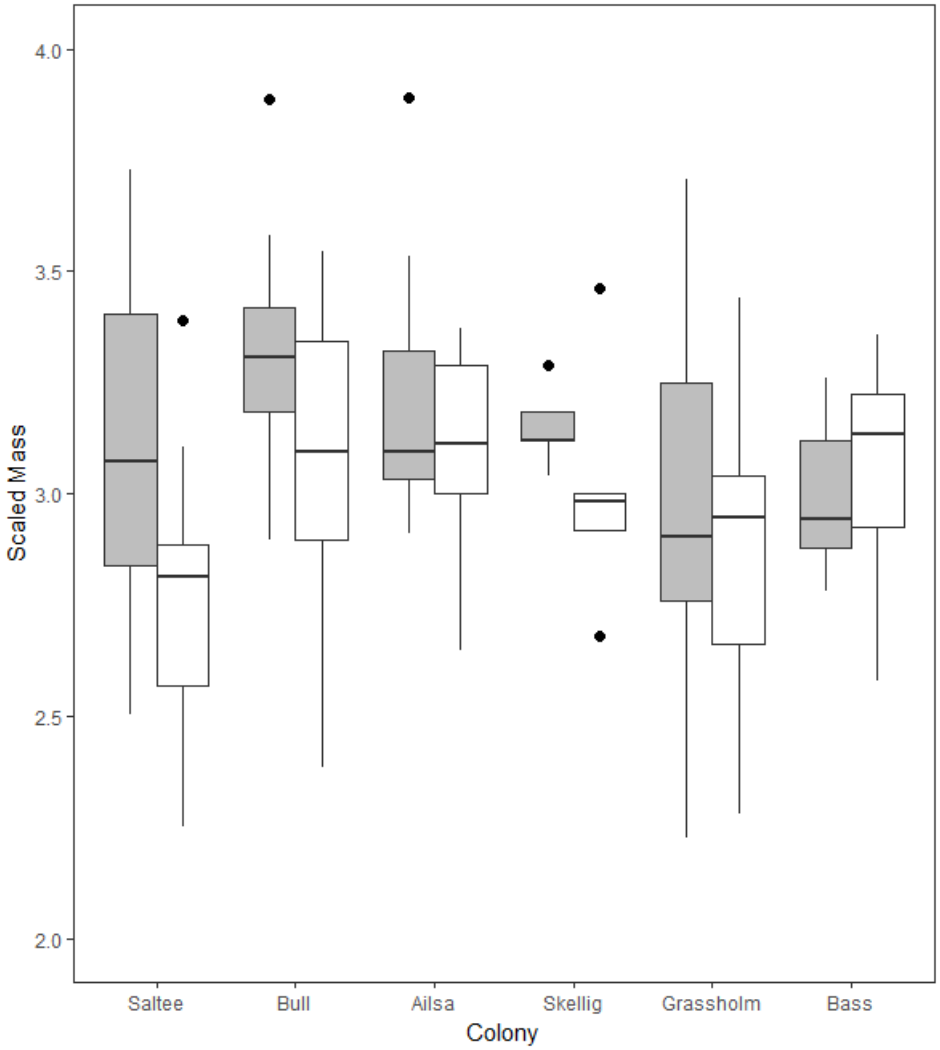



Figure S2. Variation in scaled mass of individuals at different colonies (females shaded bars, males open bars; boxes represent interquartile range with solid lines representing the median). Colonies are arranged in increasing order of size.

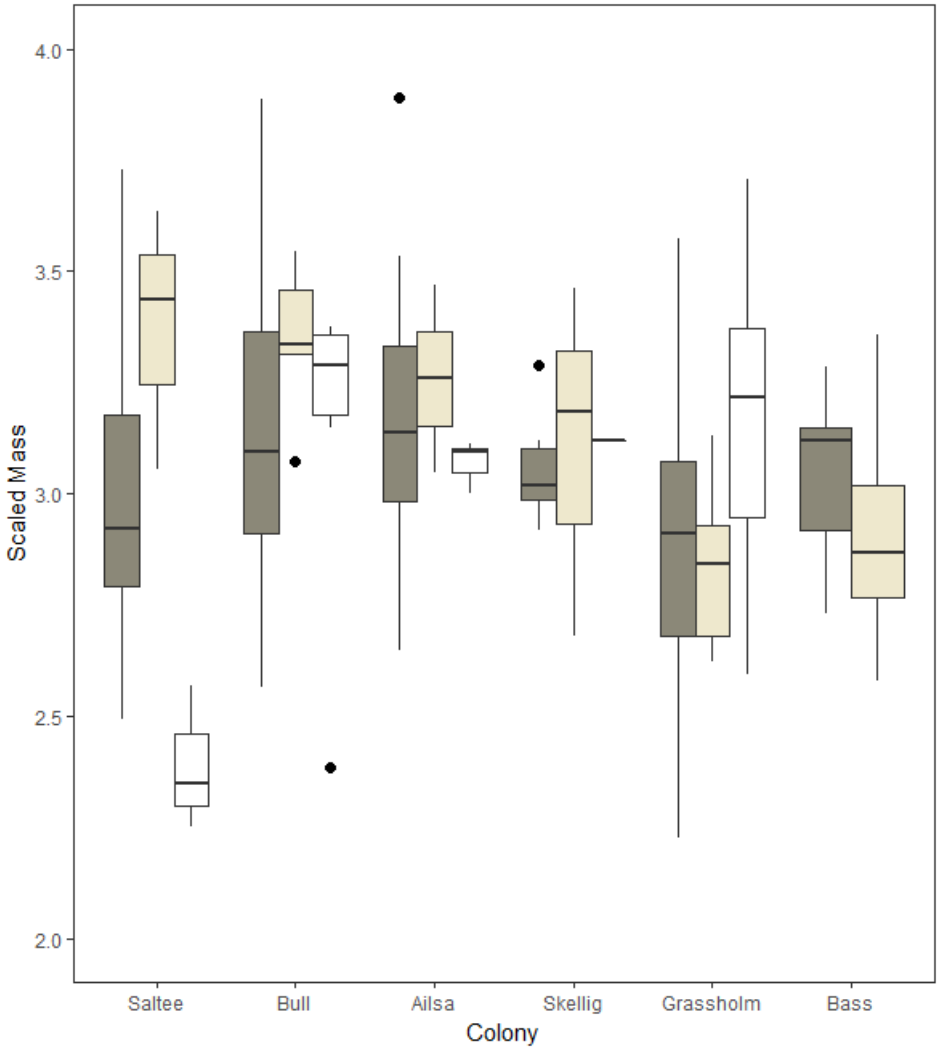



Figure S3. Variation in scaled mass of individuals at different colonies by foraging strategy (generalists: dark bars, forage fish specialists: pale bars, discard specialists: white bars; boxes represent interquartile range with solid lines representing the median). Colonies are arranged in increasing order of size. There were no discard specialists identified at Bass Rock.