

Individual recognition and number prediction for Manx shearwater (*Puffinus puffinus*) by passive acoustic monitoring

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Abstract

Seabirds can be notoriously difficult to monitor using conventional methodology, as many breed on remote islands, are active nocturnally and many breed in underground burrows. Current census methods such as counting burrows and using playbacks are time-consuming and labour-intensive. One novel solution is to use passive acoustic monitoring (PAM) followed by individual recognition and number estimation. Previous studies have successfully achieved individual bird recognition with high accuracy; however, precisely estimating population abundance via their acoustics remains an open problem. To bridge this gap, we tested whether individual Manx shearwaters (*Puffinus puffinus*) can be identified from acoustic recordings, and whether the numbers of individuals present can be estimated. We collected recordings of single-individual and multiple-individual calls from three colonies in the UK. We developed a pipeline to combine BirdNET, a one-dimensional convolutional neural network, and agglomerative clustering for individual identification and open-set individual counting. Closed-set recognition achieved high accuracy (89.3%) for Manx shearwater vocalisations at the individual level, and recognition accuracy showed no significant difference between sexes. Open-set individual number estimation achieved a mean relative error of 39.1%, and model performance was robust to noise and

31 recording conditions. These findings indicate that vocalisations of both sexes contain individual
32 signatures and demonstrate the feasibility of counting unseen individuals from passive acoustic
33 recordings. Importantly, this study supports population census using PAM in real field scenarios,
34 where unseen individuals are abundant. We provide an easy, non-invasive approach for seabird
35 population monitoring, which is transferable for monitoring other species, and has a high potential
36 for wildlife conservation and ecological research.

37

Introduction

Seabirds are a diverse group of birds from multiple evolutionary lineages that have evolved adaptations to the marine environment. While these adaptations improve their survival in the marine niche, they may impair their ability to respond to climate and environmental change (Avaria-Llautureo et al., 2026; Haney et al., 2014; Meissner, 2025). As a result, 31% of seabird species are globally threatened, and nearly half of them show trends of decline (Dias et al., 2019). Therefore, monitoring seabird populations and their trends has become increasingly important for understanding the impacts of climate change and environmental pollution. To estimate the population size of seabirds, commonly used census techniques include directly counting nests or occupied sites for diurnal seabirds, counting occupied burrows for burrow-nesting seabirds, and capture–mark–recapture methods for nocturnal seabirds (Sanz-Aguilar et al., 2010; Walsh et al., 1995). Most of the approaches above are labour-intensive and time-consuming (Walsh et al., 1995), because many seabirds breed in dense colonies on cliffs, which is uneasy for humans to access. Furthermore, hidden burrows can easily be overlooked, and burrow occupancy needs to be checked manually, posing extra difficulty for accurate estimations. Techniques that involve capturing birds (e.g., ringing) can directly injure the bird (Griesser et al., 2012); other approaches can also cause disturbance and affect hatching success (Blackmer et al., 2004; Walsh et al., 1995), which is invasive for the population.

One potential solution that has received increasing attention in recent years is using non-invasive passive acoustic monitoring (PAM) to estimate density, population size, and other parameters (Bailey et al., 2021; Hensel et al., 2022). Nest density and local population size were found to correlate with acoustic activity in shearwaters (Oppel et al., 2014). However, Arneill et al. (2020) found that acoustic activity has no predictive effect on nest density, highlighting uncertainty in the relationship between calling activity and population size. Bird vocal activities also vary with weather and environmental conditions (Lengagne et al., 1999; Lengagne and Slater, 2002), limiting the reliability of population estimates based solely on acoustic indices. Therefore, new informative alternatives, such as individual number estimation by individual recognition, are highly needed. This is feasible because many nocturnal seabird species rely on vocalisations to

locate nests and their mates in darkness (Brooke, 1990; Cure et al., 2009), suggesting underlying individual signals encoded in their calls.

Using machine learning to identify bird individuals in a closed set (i.e., all test set classes are presented in the training set) has been successful in bioacoustics. Convolutional neural network (CNN) is one of the most widely used and accurate architectures for individual recognition. Closed-set individual identification accuracy has reached 78.6% for Chiffchaff (*Phylloscopus collybita*) (Ptacek et al., 2016) and >90% for 5 bird species in different taxonomic groups (Huang et al., 2025). However, accuracy drops when changing the background in the soundscape or using another corpus for testing, suggesting background features may confound individual recognition (Stowell et al., 2019; Xie et al., 2023). Open-set recognition (i.e., identifying novel targets not in the training set) has reached an accuracy higher than 80% in different bird species, showing good discriminative ability between seen and unseen individuals (Huang et al., 2025; Ntalampiras and Potamitis, 2021). However, the study of open-set classification (i.e., identifying and classifying new targets) remains scarce and has not been extended to bioacoustics. Bedoya and Molles (2021) introduced a pipeline using CNN and fuzzy clustering to perform open-set classification and achieved an accuracy of 88%. However, their examination was based on a small dataset with only three novel classes. In the field of object detection, Zheng et al. (2022) introduced an open-set object classification pipeline, using a similar CNN + clustering architecture. The study produces an underestimation error of 20- 40% for open-set object counting. Similar algorithms are also designed in facial recognition (Liu et al., 2018). These pipeline designs are important references for this study, as all of them aim to separate and label unseen instances.

Despite recent research advances, no existing pipelines in bioacoustics can estimate the number of calling individuals in real field scenarios, where unseen individuals are abundant. To bridge the current gap, we used the Manx shearwater (*Puffinus puffinus*) as a model species to investigate whether machine learning can be used to estimate the number of individuals present in audio recordings. Manx shearwater is a nocturnal, burrow-nesting seabird whose breeding populations are particularly difficult to estimate accurately using conventional census methods (Lee et al., 2023). Most Manx shearwaters nest in grass slopes and cliff edges, which increases the difficulty

when accessing breeding sites. During breeding, a pair of breeding individuals share a burrow, so local population size can be estimated by counting the number of actively occupied burrows, which is checked by playback. However, response rates are typically below 80% and may vary by sex (Perkins et al., 2017). Furthermore, foraging adults are absent during the day, and they generally do not approach the colony until nightfall (Brooke, 1990). Consequently, the number of birds at an occupied burrow varies from time to time, making accurate assessments of burrow occupancy and breeding population size challenging. Manx shearwater is a good model for machine learning in bioacoustics because individual signatures have been identified in their calls, although principal components (PC), which interpret major directions of variation, show levels of overlap (Sun et al., 2024). This study has two objectives: (1) build a pipeline that can identify individual Manx shearwaters through their vocalisations, and (2) estimate individual numbers in Manx shearwater acoustic recordings, including those with unknown IDs.

Material and methods

Study sites

We selected Lundy (51°10'N, 4°40'W), St. Agnes (49°53'N, 6°20'W), and Copeland (54°40'N, 5°32'W) as study sites, as they hold considerable breeding pairs of Manx shearwater (12,500, 4,900, and 225 pairs, respectively) and are geographically isolated, increasing data abundance and heterogeneity. In Lundy, 70 burrows in 5 colonies (Old Light, Virgin's Spring, Castle Hill & Benjamin's Chair, Logan Stone, and Dead Cow Point) were selected for data collection. In St. Agnes, 28 burrows in 2 colonies (Southwest of Gugh and North of Gugh) were selected for data collection. Each colony was preliminarily investigated to ensure sufficient burrows were present. Data collection in Copeland was conducted in 2025 by other members of the group, and per-burrow recordings are ready for use.

Data collection and pre-processing

When visiting the study site, we classified examined burrows as actively occupied if faeces, feathers, or individuals were present inside the burrow or at the burrow opening. These burrows

121 were selected for study. We deployed audio recording devices (Song Meter[®] Micro 2 and
122 AudioMoth[®]) 10-30 cm from the burrow opening, with microphones facing inwards, and left them
123 in situ for at least 48 hours before retrieval. To ensure monitoring overlaps with the most active
124 calling period, devices were configured to work from 10 P.M. to 5 A.M. (British summer time),
125 with 20 minutes on duty and 5 minutes off in each cycle. Gains were set as “medium” for
126 audiomoths and “6-12 dB” for song meters. Each cycle produced a 16-bit depth monophonic
127 waveform audio file (WAV) with a 22.05 kHz sampling rate, which covers the frequency range of
128 Manx shearwater calls.

129 After data retrieval, audio files were pre-processed to generate the training set and the test set. We
130 reviewed each audio file manually to select clear Manx shearwater call segments (> 5s each).
131 Distinctively louder calls were from either one or two (a male and a female) individuals associated
132 with the burrow, and the corresponding individual IDs were assigned. We used spectrogram
133 patterns to judge the identity and assessed sex based on Lee et al. (2023). All calls with IDs were
134 then imported into the BirdNet V2.4 acoustic model (Kahl et al., 2021) in Python (v3.9.23) for
135 target detection using the default TensorFlow backend. Based on detection, Manx shearwater calls
136 in auto-selected clips with confidence > 0.60 were saved as training samples. This threshold
137 reduces bad samples (background calls and incomplete calls) while maximising detections. To
138 generate the test set, we randomly chose 56 recording files each has a length of 20 minutes and
139 contains multiple calling individuals from the active outside-burrow calling period (2-4 A.M.)
140 from the same per-burrow recordings. For each file, the individual number and male/female count
141 were estimated manually. Call structures and motif patterns (e.g., length, pitch range, etc.) in the
142 spectrogram were used for identifying and distinguishing individuals. Faint calls that showed
143 unclear call structures and motif patterns were removed from estimation. Background noise level
144 was calculated using sound levels exceeding 90% of the measured time (L90) in Python. Then, we
145 imported files into BirdNet (V2.4 acoustic model) to generate short clips containing target calls.
146 Mean peak amplitude was calculated to characterise the calling loudness. Overlapping call
147 proportion was estimated by sampling one-fifth of the clips and was calculated as the number of
148 clips containing overlapping calls divided by the total number of clips. We saved the above indices
149 as a comma-separated values (CSV) file for later analysis of model performance and robustness.

Pipeline design

Block design. To estimate individual numbers of Manx shearwaters in audio recordings, the pipeline was divided into three main blocks (Fig. 1). In the *feature extraction block*, BirdNet was used to detect target call clips and then generate a 1024-dimensional feature vector from each clip. Feature vectors were then imported into the *core model block* (a CNN classifier), which further learns the differences between individuals and creates new 256-d embeddings. The 256-d embeddings were then passed to the *cluster-and-count block* for dimensionality reduction and distance-based clustering, followed by final predictions of individual counts. The pipeline and the model were built in Python (v3.9.23) environment.

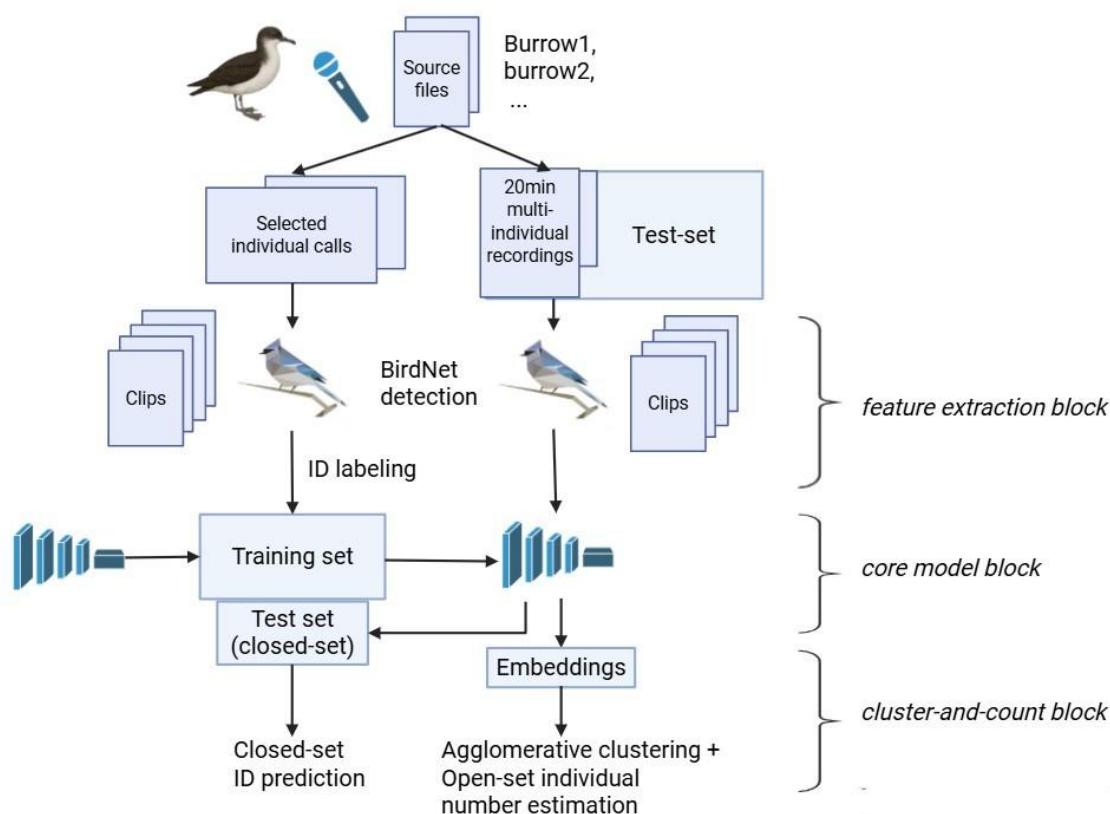


Figure 1. The pipeline structure. The pipeline is divided into three blocks. Source files from PAM were separated into calls with individual labels for later training and closed-set testing. 20-minute-long recordings were selected from the same files (but at different times) as the test set for open-set predictions. BirdNet was used for feature extraction, and the output embeddings were processed by the core convolutional neural network (CNN) model for either model training, closed-set testing, or 256-dimensional embedding generation. The 256-d embeddings were then used for agglomerative clustering and

166 [open-set individual number estimation.](#)

167 **Feature extraction block.** To extract features of Manx shearwater vocalisations, we imported
168 clips generated by BirdNet detections into BirdNet-Analyzer (v2.4.0) (Kahl et al., 2021), and
169 extracted their feature vectors using the embedding extraction function. All settings were left at
170 default (overlap = 0, audio speed modification = 0, batch size = 8, threads = 4). A CSV file
171 containing information on clips and their corresponding embeddings was generated as output.

172 **Input and output (core model).** We implemented a one-dimensional convolutional neural
173 network (1D CNN) in PyTorch (Paszke et al., 2019) as the core model. It takes the pre-extracted
174 BirdNet acoustic feature arrays (comma-delimited string with 1024 float values) as input. When
175 loading, they are imported as numerical arrays. Although BirdNet feature vectors are not time-
176 series data, adjacent dimensions encode related acoustic information in the learned representations,
177 making the 1D CNN available for feature extraction.

178 We developed three different modes in the model: TRAIN, TEST, and EMBED. In the TRAIN
179 mode, the model was trained using input feature vectors as the training set. Individual labels are
180 encoded in the embedding CSV file as a new column for validation. The trained model parameters
181 were saved as a checkpoint file. The TEST mode predicts the class (i.e., individual ID) of new
182 samples from closed sets by comparing the output 256-d embeddings of unlabelled recordings
183 against stored per-individual prototype arrays. The EMBED mode exports the 256-d embeddings
184 as an NPY file, which is suitable for downstream open-set classification.

185 **Model scaffold and layers (core model).** Four convolutional blocks, an average pooling layer, a
186 dropout layer, a projection head, and an L2 normalisation layer were developed and stacked
187 sequentially as the model's basic architecture. We adapted this architecture from SPEAKERNET, a
188 1D CNN model for speaker recognition similar to bird individual identification (Koluguri et al.,
189 2020). To extract local patterns, the model transformed data from shape [32, 1, 1024] (batch size =
190 32, original embedding shape = [1024]) to [32, 256, 31] by four convolutional blocks. Each
191 convolutional block above has three sequential layers: a 1-D convolution, a batch normalisation,
192 and a Gaussian Error Linear Unit (GELU) activation function. To achieve higher performance in
193 acoustic recognition, we used GELU instead of the rectified linear unit (RELU), although the

194 computational complexity was increased (Hendrycks and Gimpel, 2023).

195 To reduce dimensionality, adaptive average pooling averaged each feature map across its temporal
196 dimension to collapse the data structure into [32, 256]. To reduce overfitting and prevent the model
197 from over-relying on single features, we randomly dropped $n\%$ of activations in the dropout layer
198 (n is tunable for parameter adjustment). The projection head comprised a fully connected layer to
199 project data into a 256-d space, followed by a 1-d batch normalisation. Finally, the L2
200 normalisation layer unified all embeddings to ensure Euclidean distance between samples equals
201 their cosine dissimilarity, which is used for label prediction.

202 **Model training and validation (core model).** Before each training epoch, we augmented data by
203 adding Gaussian noise with standard deviation σ to reduce overfitting and enhance robustness.
204 Embedding elements were dropped out to avoid over-relying on single features (σ and *dropout* are
205 tuneable for parameter adjustment). Each batch has 32 samples, composed of 8 individuals with 4
206 samples per individual. We trained the model using supervised contrastive (SupCon) loss (Khosla
207 et al., 2021). Compared to traditional loss functions (e.g., cross-entropy loss), using the SupCon
208 loss learns and structures the geometry of high-dimensional space directly by enlarging the
209 between-individual distance and squeezing the within-individual distance, which is more suitable
210 for downstream clustering analysis and open-set predictions. The sampling of 4 samples per
211 individual per batch meets the requirements of at least 2 samples per class per batch for supervised
212 contrastive learning (Khosla et al., 2021). During training, weights were optimised using AdamW
213 (Loshchilov and Hutter, 2019) with a learning rate = 0.001 and a weight decay = 1×10^{-4} . We set
214 the SupCon temperature (τ) as a tuneable hyperparameter for model optimisation. We ran each trial
215 using 200 epochs, which is sufficient for model convergence (Fig. 4). The final model was saved
216 as a checkpoint .pt file, useful for later predictions.

217 **Closed-set prediction (core model).** Prototype representation vectors of individuals were saved in
218 the final checkpoint file during training. For each sample, cosine similarity between its 256-d
219 embedding and every prototype vector was computed. The prototype class with the highest cosine
220 similarity was selected as the prediction.

221 **Open-set individual number counting (cluster and count block).** Individual number estimation

of an open set, which has untrained individuals in it (most are untrained individuals for this study), relies on the 256-d embeddings generated by the core CNN model as input. We loaded embedding vectors stored as an NPY file as a NumPy array. We conducted a principal component analysis (PCA) to reduce the dimensionality of embeddings to d components (d is tuneable for parameter adjustment). Then, we performed agglomerative clustering, beginning with a cluster number equal to the sample size ($k = n$), and iteratively merging the nearest two clusters until only two clusters exist. In each step, the silhouette score was computed to evaluate clustering quality. The silhouette score was then plotted as a function of cluster number. To reduce noise, the signal was filtered using a Savitzky-Golay filter with window length = $0.2n$ and polyorder = 3. After smoothing, the range of k corresponding to silhouette scores greater than or equal to 90% of the global maximum was raised as the range prediction, as shown as follows:

$$[\hat{k}_{\text{low}}, \hat{k}_{\text{high}}] = [\min\{k: S(k) \geq 0.90 S_{\text{max}}\}, \max\{k: S(k) \geq 0.90 S_{\text{max}}\}]$$

where $S(x)$ = smoothed silhouette score; k = the cluster number; S_{max} = the global maximum.

The k corresponding to the first local max, which has a height $\geq 90\%$ of the global max before the global max, if there are any, was raised as the point prediction. Otherwise, k to the global max was used as the point prediction. The formula is shown as follows:

$$\hat{k}_{\text{point}} = \begin{cases} \min\{k < k^*: S(k) \geq 0.90 S_{\text{max}}, S(k) > S(k-1), S(k) > S(k+1)\} & \text{if non-empty} \\ k^* & \text{otherwise} \end{cases}$$

where $k^* = \arg \max_k S(k)$

Instead of using the cluster number corresponding to the global maximum as the point prediction, this formula has shown higher prediction accuracy when tested.

Parameter optimisation and model evaluation

Before evaluating model performance, we did parameter optimisation to increase prediction accuracy. Prediction accuracy was evaluated using a random 85:15 train-test split of the original training set. Performance of closed-set predictions was evaluated while changing each of the following parameters: SupCon temperature (τ), Gaussian noise standard deviation (σ), and dropout rate, and keeping other parameters at default values. We generated five replicates for each

248 evaluation using different seedlings. After each round of tuning, the best-performing value was
249 retained while the next parameter was evaluated. We then tested open-set individual number
250 prediction accuracy using the optimised model. Parameter optimisation was performed by
251 changing each of the following parameters while keeping other parameters at default values:
252 BirdNet recognition threshold for the test set (θ), sampling control parameters (deleting individuals
253 with fewer than m sample numbers and removing excessive samples from individuals with more
254 than n numbers), and reserved PCs (d). The final pipeline used the parameter combination with the
255 highest open-set prediction accuracy. The default parameter values used before updating were: $\tau =$
256 0.07 , $\sigma = 0.02$, $dropout = 0.10$, $m = 12$, $n = 48$, $d = 2$, $\theta = 0.60$.

257 We tested the performance of the final model. Closed-set prediction accuracy was evaluated using
258 a random 80:20 train-test split of the original training set and the updated model. The mean
259 accuracy of each epoch after model convergence was computed to represent the prediction
260 accuracy of each run. We selected the model with the highest prediction accuracy in five runs as
261 the final model. Except for overall prediction accuracy, accuracy changes under the impact of sex
262 and sample size were reported. We reported the overall open-set number estimation accuracy using
263 models with updated parameters trained on the full training set. The model with the lowest sum of
264 squared residuals (SSR) in five runs was selected as the final model. Model robustness was tested
265 by fitting multiple linear models using environmental and acoustic parameters as independent
266 variables.

267 **Statistical analysis**

268 To compare closed-set prediction accuracy differences, we performed a Kruskal–Wallis test to test
269 differences across the groups. If a significant difference was detected, we then did a post hoc Dunn
270 test for pairwise comparisons. To investigate whether sex and sample size affect prediction
271 correctness, a generalised linear model (GLM) was built, with a binomial error distribution and a
272 logit link function. The response variable was specified as counts of correct and incorrect
273 predictions for each individual. To test how environmental and acoustic factors impact open-set
274 individual counting accuracy, multiple linear regression models were fitted. The significance level
275 was set as $\alpha = 0.05$. All statistical analyses were performed in R (version 4.4.1) and RStudio

276 (version 2024.4.2.764).

277

278 Results and Discussion

279 Dataset summary

280 We collected Manx shearwater audio recordings using Automated Recording Units in Lundy, St.
281 Agnes, and Copeland. After manual selection, the dataset comprised 166 individuals, including
282 103 males and 63 females. BirdNet detections generated a total of 3,939 clips, with 23.7 clips per
283 individual on average. Clip number varied from 1 to 66 per individual. Different sampling controls
284 generated multiple training sets that are either more balanced in sample size or with more samples
285 per individual (Table 1). The test set selected from peak calling periods included 56 samples, with
286 estimated real individual numbers ranging from 2 to 24, and male/female ratios from 0.13 to 5.0.
287 Background noise, average call intensity, and overlapping call proportions across samples were
288 also highly variable, providing heterogeneity for testing model accuracy under different acoustic
289 conditions.

Sample number per individual (min-max)	Clip number	Individual number (male/female)
12-15	1844	125 (90/35)
12-20	2314	125 (90/35)
12-36	3082	125 (90/35)
12-48	3244	125 (90/35)
12-66	3287	125 (90/35)
20-24	2036	87 (71/16)
20-48	2670	87 (71/16)
20-66	2713	87 (71/16)

290 **Table 1. Summary of training sets under different sampling controls.** Clips less than 2.6s were removed
291 before generating all sets. 66 was the maximum clip number per individual by the initial selection.

292 Parameter optimizations

293 We performed parameter optimisations to maximise closed-set prediction accuracy by changing τ ,
294 σ , and *dropout*, while keeping other parameters as default. All models with varied τ converged

295 after 170 epochs (Fig. 4), and model performance was evaluated using the mean prediction
296 accuracy between epochs 170 and 200. Models with a τ from 0.04 to 0.15 showed no significant
297 differences in prediction accuracy, but all performed better than using $\tau = 0.01$ (Fig. 2A). Model
298 performance showed no significant differences among σ from 0 to 0.10 (Fig. 2B). Models using
299 10% to 30% dropouts during training led to a significantly higher performance than non-dropouts
300 (Fig. 2C). The above tests show that models using the default model parameter settings have
301 equivalent or higher close-set prediction accuracy to other tested parameter combinations.

302 We conducted open-set point prediction by using the best closed-set prediction model to generate
303 embeddings, which were then processed by PCA and clustering. SSR between predicted values
304 and estimated real values was used as the evaluation metric. Test set pre-processing using different
305 BirdNet recognition thresholds ($\theta = 0.10, 0.20, 0.40$, and 0.60), produced no significant differences
306 in model SSR (Fig. 3A). Different sampling controls of the training set, including limiting
307 maximum sample numbers and removing individuals with insufficient samples, did not cause
308 significant model SSR differences (Fig. 3B). When changing PC, models of 2 PC had a
309 significantly lower SSR than models with 4 and 6 PC (Fig. 3C). These results show that the default
310 parameter settings for the open-set prediction retain equal or better model performances than using
311 other parameter combinations. Also, modifications of the training set and test set exhibit limited
312 impact on open-set prediction accuracies.

313 In parameter testing, artificially added Gaussian noise (σ from 0.001 to 0.1) did not change the
314 prediction accuracy, indicating the model is robust in dealing with signal noise. While so,
315 embedding element dropout during training does improve closed-set recognition accuracy.
316 Surprisingly, sampling controls do not significantly impact model SSR in open-set counting. It is
317 possible that reserving 12-20 samples per individual is already sufficient in training the model for
318 open-set predictions. When adjusting PCs, $d = 2$ works best compared with reserving more
319 components for clustering, which suggests that the clustering algorithm works better for low-
320 dimensional structures. Retaining more PCs may introduce more noise, thereby reducing the
321 effectiveness of the clustering.

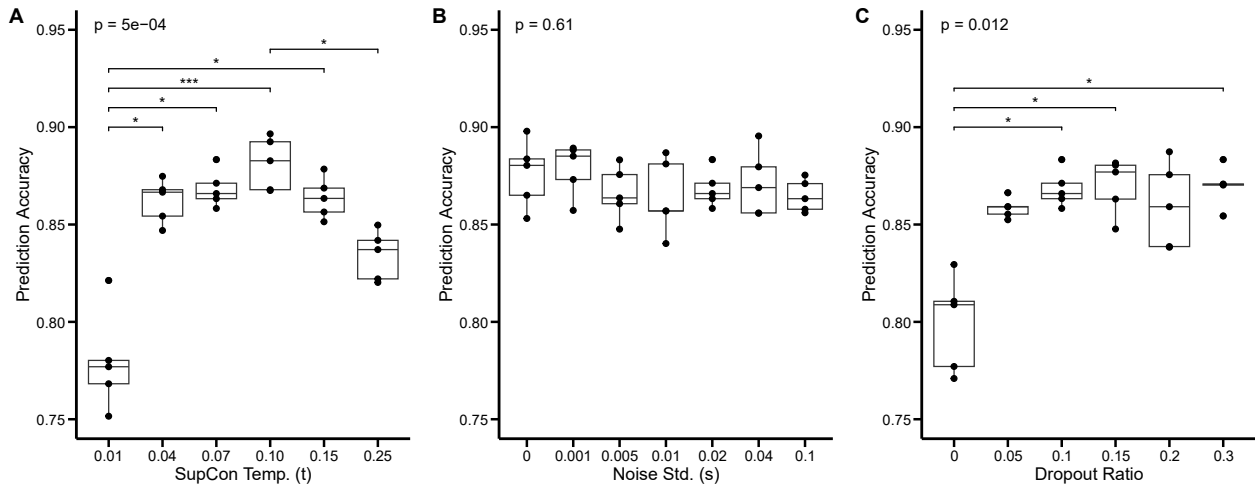


Figure 2. Close-set prediction accuracy varies with different model parameters. Each replicate represents the mean prediction accuracy between epochs 170 and 200 for independent runs, using a random sample of 85% of the original training set. Except for the independent variable, other parameters are set to default. Comparison between pairs was conducted using a Kruskal–Wallis test followed by post hoc Dunn tests. Only significant outcomes are shown. (A) Prediction accuracy by models using different SupCon temperatures. (B) Prediction accuracy by models adding Gaussian noise with different standard deviations. (C) Prediction accuracy by models randomly dropping embedding elements in different proportions.

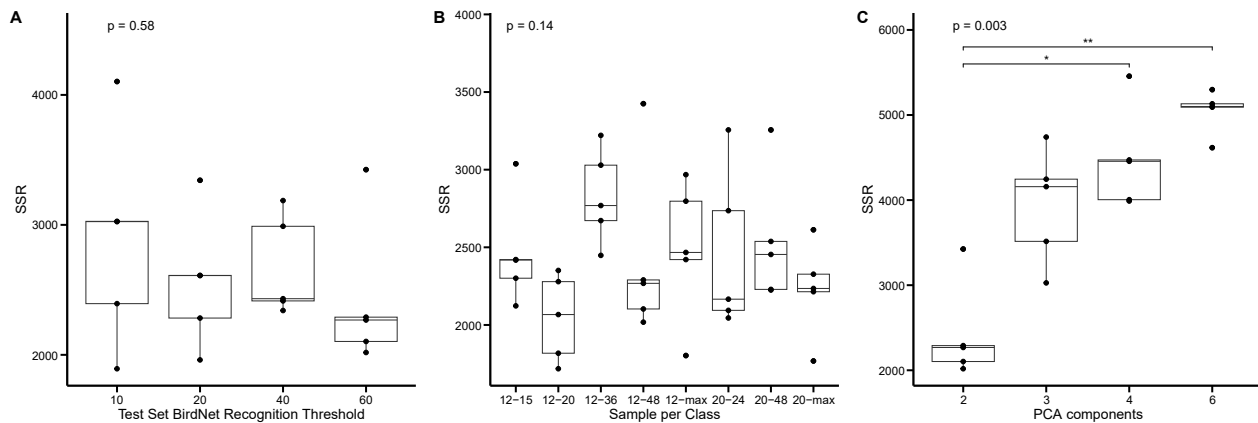


Figure 3. Comparison of open-set prediction sum of squared residuals (SSR) under different model parameters. Models were trained using default parameters and 200 epochs. Each replicate represents the model's SSR using random seedlings when training the same model. Comparison between pairs was conducted using a Kruskal–Wallis test followed by post hoc Dunn tests. Only significant outcomes are shown. (A) SSR by test set detection using different BirdNet recognition thresholds. (B) SSR by different

sampling controls for the training set. The independent variable range represents the minimum to maximum number of samples per class. (C) SSR by different principal components.

Closed-set predictions

Models with optimised parameters were trained in five replicates using a random 8:2 split of the training set as the new training and validation set. All five replicates achieved high prediction accuracy with low variation after convergence (mean = 88.6%, SD = 0.9%), with the top-1 reaching 89.3%, which was then selected as the final model. When examining sex-specific mismatches, only 4 of the 542 predictions (0.7%) had incorrect sex predictions (Fig. 5). A generalised linear model showed that sample size did not significantly affect prediction accuracy ($\beta = 0.03$, SE = 0.04, $z = 0.61$, $P = 0.54$). Sex also showed no significant effect ($\beta = -0.72$, SE = 0.49, $z = -1.48$, $P = 0.14$).

The high accuracy of closed-set predictions suggests that Manx shearwater vocalisations contain individual signatures, consistent with the findings by Sun et al. (2024). Furthermore, prediction accuracy is high and shows no difference between males and females, indicating both sexes contain sufficient individual signals for recognition. Earlier studies in a similar species, Yelkouan shearwaters (*Puffinus yelkouan*), report that both sexes are acoustically identifiable (Cure et al., 2009), and Sun et al. (2024) suggest that female Manx shearwater calls are identifiable by successfully discriminating 3 females, which had limited generalisability. We thus provide stronger evidence suggesting that both sexes of Manx shearwater contain individual signatures, by successfully discriminating 95 males and 35 females. The closed-set recognition accuracy was pushed to 89.3% but not higher, which may be due to limited training data for some individuals and incomplete call segmentation when generating clips. These limitations could be addressed in future studies by increasing sample size and developing new algorithms for improved call segmentation. Although not confirmed, the unitary non-linear calls present in the dataset may contain weaker individual signals and impact model performance, and future studies are needed to scrutinize call-type-specific individual signature differences.

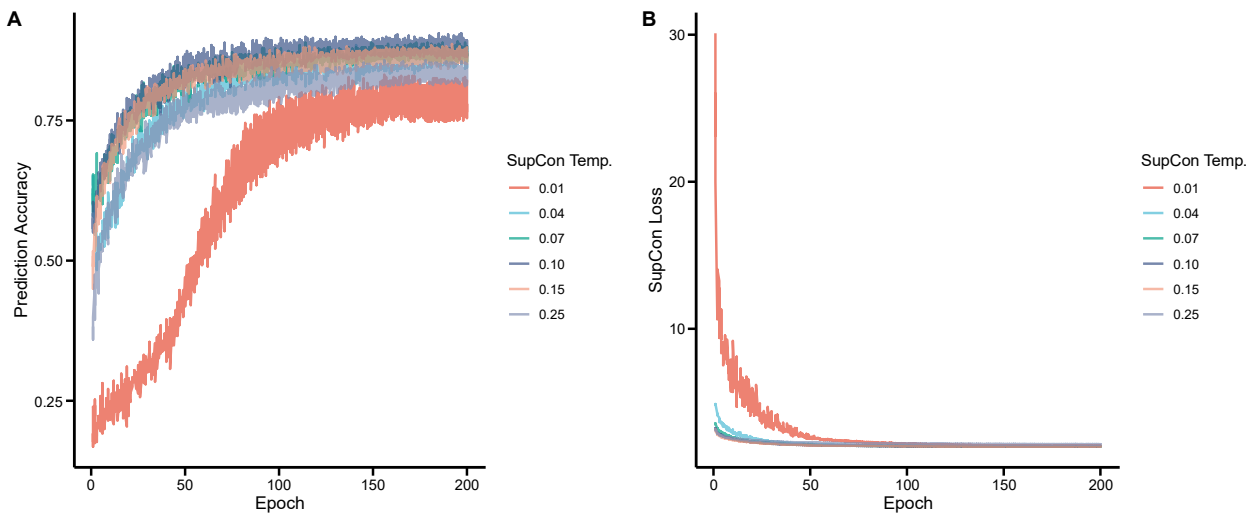


Figure 4. The model reaches convergence after 170 epochs. All trials converge in 170-200 epochs, as indicated by (A) prediction accuracy and (B) SupCon loss, regardless of SupCon temperatures. Each trial has 5 replicates. Different colours show different SupCon temperature values.

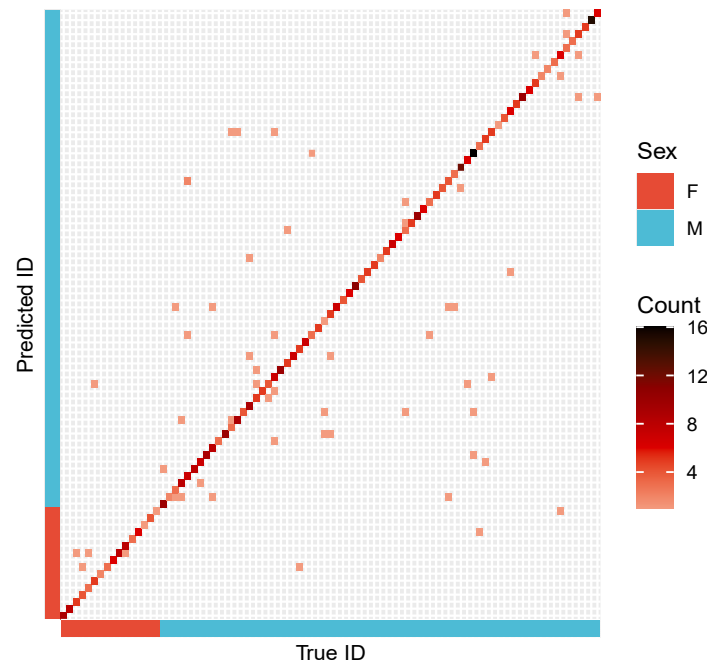
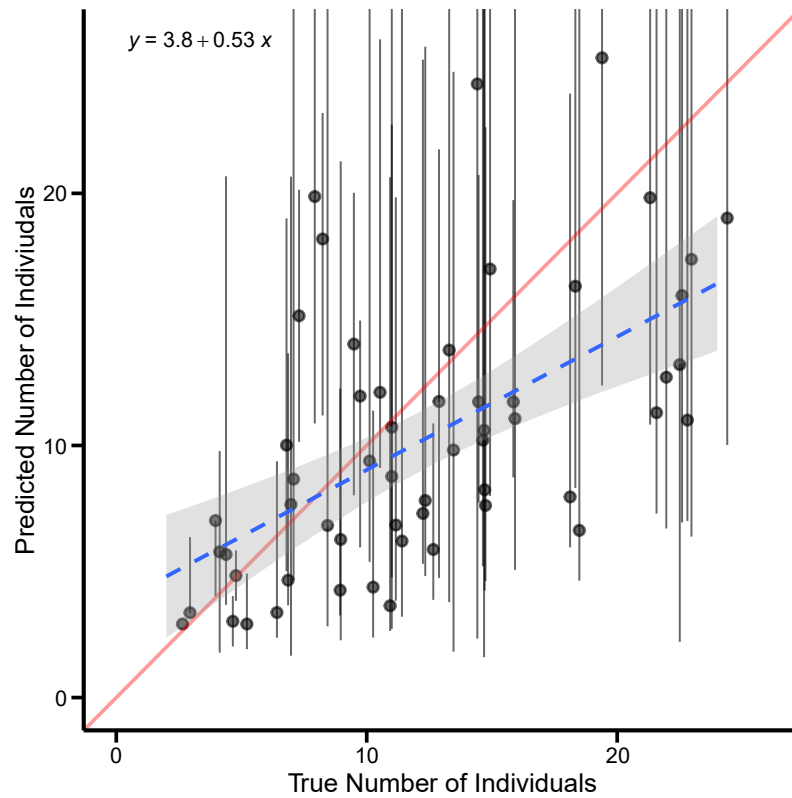


Figure 5. Confusion matrix showing the closed-set prediction quality of Manx shearwater individuals. Each coloured cell represents a prediction-real label pair, with darker colour for higher counts. Diagonal cells represent correct predictions. Coloured bars along the x- and y-axis show the sex of each individual.

Open-set predictions

372 Open-set individual number estimation was based on the model with the lowest SSR during the
373 optimisation (SSR = 1718, $n = 56$) (Fig. 6). The mean absolute error was 4.46 ± 3.31 SD, and the
374 mean relative error was $39.1\% \pm 30.4\%$ SD, with seven samples greater than 60.0% for point
375 predictions. True values fell into the predicted range for 48 out of 56 samples when using range
376 predictions (as described in the methods). However, the mean prediction range was broad with low
377 precision (mean width over the true value = 231.1%, SD = 130.1%). Multiple linear regression
378 models were built to investigate the impact of recording conditions and environmental factors on
379 prediction error (Fig. 7). The regression model showed that individual count had a negative
380 relationship with model residual ($\beta = -0.81$, SE = 0.16, $t = -5.21$, $P < 0.001$), while having a
381 positive correlation with prediction absolute error presented by the absolute value of residual ($\beta =$
382 0.31 , SE = 0.11, $t = 2.97$, $P < 0.01$). Call quantity (clip number) had a positive relationship with
383 residual ($\beta = 0.07$, SE = 0.03, $t = 2.79$, $P < 0.01$), and female/male ratio was negatively associated
384 with absolute error ($\beta = -0.54$, SE = 0.27, $t = -2.02$, $P < 0.05$). This suggests that the model tends
385 to overestimate the number of individuals in recordings containing fewer individuals and more
386 calls. Furthermore, prediction accuracy increased when samples had fewer individuals and a
387 greater female ratio. Other variables, including the overlapping call ratio, background noise, and
388 average peak volume, did not show significant correlations with either residual or absolute error.



389

390 **Figure 6. Predicted versus true numbers of individuals in 20-minute open-set Manx shearwater**
 391 **recordings.** Each point represents the point prediction value, while each bar represents the predicted range
 392 (using a threshold of 90% of the silhouette score maximum). The red line shows perfect predictions ($y = x$).
 393 The blue dashed line and the grey area show the linear regression with 95% confidence band of point
 394 predictions. Coefficients are shown at the top. Points and bars are slightly jittered to avoid overlaps.
 395 Predicted ranges greater than 27 are not shown.

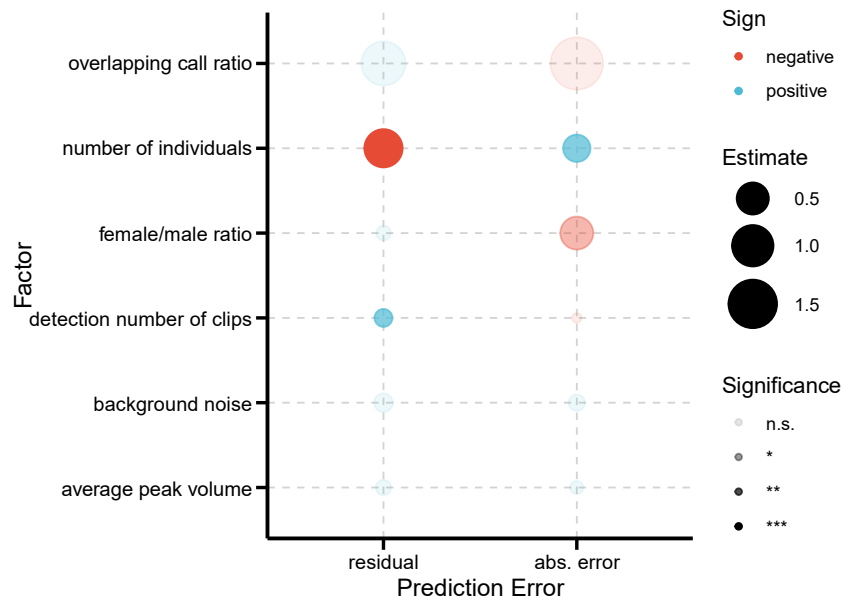


Figure 7. The correlation strength between factors and prediction errors. Two models were fitted using residues and the absolute value of residues (absolute error) as response variables. Y-axis terms are tested factors that may impact the prediction error. The linear regression estimate (β) is shown by the point size, and the sign of the slope is shown by colour. Stronger significance is indicated by stronger opacity.

A mean relative error of 39.1% shows the pipeline is promising, although it is not sufficiently accurate for reliable abundance estimation. Compared to the open-set object counting by Zheng et al. (2022), which achieved a lower prediction error (mean relative error = 21%), estimating population abundance using acoustics has greater difficulty because individual vocalisations are highly similar, frequently with overlaps and environmental noise. Although the same individual tends to be clustered, boundaries between them are often vague, given that within-individual calls can be heterogeneous across short time (Singer et al., 2026). The presence of non-typical calls and overlaps is hypothesised to generate random noise in the embedding space, which would lead to failures in producing clustered local structures and the resulting biased estimates. Nevertheless, background noise, call volume, and call overlaps have limited effects on model performance, demonstrating model robustness in varied recording conditions. Model performance is impacted by the number of individuals, with reduced accuracy and a trend of underestimation when more calling individuals are presented. One possible explanation is that more individuals generate more overlapping calls and greater difficulty for clustering in a limited high-dimensional space. Pre-

415 processing by BirdNet is another source of prediction bias. Low prediction confidence for non-
416 typical female calls can lead to reduced female clip numbers used for training and prediction,
417 leading to underrepresentation of females and underestimation of caller numbers. Interestingly, an
418 increased female sample ratio did not significantly increase residual but did correlate with reduced
419 absolute error in this study, showing improved accuracy. It is possible that female calls contain
420 more repetitive patterns and are less variable than males, leading to greater open-set prediction
421 certainty.

422 From a conservation perspective, this study helps estimate local seabird population size in a non-
423 invasive, time-efficient, and easy way. With further optimisation, the pipeline has the potential to
424 achieve higher accuracy in estimating population size in comparison with the traditional approach
425 of counting occupied burrows using playback. When applying this pipeline to real scenarios, data
426 from different monitoring devices can be combined for estimating per-colony and per-island
427 populations, which is an advance from the current methodologies. However, limitations of this
428 approach exist, as flight calls are released predominantly by females (Brooke, 1978; James, 1985),
429 so males in flight will be neglected, leading to bias. Future research directions could try fitting
430 regressions of predicted values versus real population numbers to calibrate the prediction.

431 In Conclusion, in this study we demonstrate that machine learning approaches can identify Manx
432 shearwater from their vocalisations with high accuracy and show potential for estimating the
433 minimum number of calling individuals, representing a promising advance in bioacoustics for
434 individual recognition. The approach is robust against noise and external recording conditions. The
435 findings highlight its potential to support Manx shearwater monitoring and, with further validation,
436 can be adapted to the study of other seabird species and potentially other vocal taxa. We also
437 provide an approach to detect individual signatures in animals' vocalisations, and present a new
438 method for understanding their population dynamics through PAM.

439

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450

451 **Author Contributions**

452 ZL: Conceptualisation; Investigation; Methodology; Visualisation; Writing – original draft;
453 Writing – review and editing. YJA: Conceptualisation; Investigation; Methodology; Visualisation;
454 Writing – review and editing. WDP: Supervision; Writing – review and editing. SAZ:
455 Conceptualisation; Supervision; Writing – review and editing. JS: Conceptualisation; Supervision;
456 Writing – review and editing. All authors reviewed and approved the manuscript.

457

458 **Conflict of Interest Statement**

459 We declare no conflict of interest.

460

461 **Data and Code Availability**

462 Data used in developing and testing the model, including model checkpoint files and training set
463 and test set embedding inputs, can be found in the following archive: "Dataset for Manx
464 shearwater (Puffins puffins) individual acoustic identification". Zenodo. Available at:
465 <https://doi.org/10.5281/zenodo.21297859>.

466 Python and R code used for building the model and statistical analysis can be found in the

467 following GitHub repository: https://github.com/Antongsky/Shearwater_individual_recognition.

468

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