

## Q1 - Visualisation and analysis of the Palmer penguin dataset

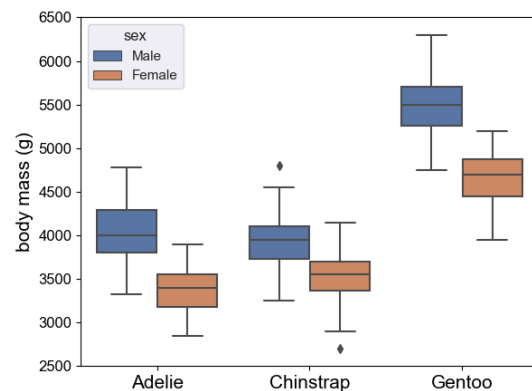
The Palmer penguin dataset consists of 344 records of the physical attributes of three species of penguin living on three islands in Antarctica (Table 1) [1]. In this report, the dataset is cleaned, explored through visualisation, carefully prepared for investigation and finally the performances of AI approaches in classifying penguin species are compared.

Feature	Type	Values in the dataset	Importance
island	categorical	Torgersen, Biscoe, Dream	0.12 (4)
bill length	numerical	32.1mm - 59.6mm	0.37 (1)
bill depth	numerical	13.1mm - 21.5mm	0.17 (3)
flipper length	numerical	172mm - 231mm	0.23 (2)
body mass	numerical	2700g - 6300g	0.11 (5)
sex	categorical	Male, Female	0.01 (6)
species	categorical	Adelie, Chinstrap, Gentoo	class

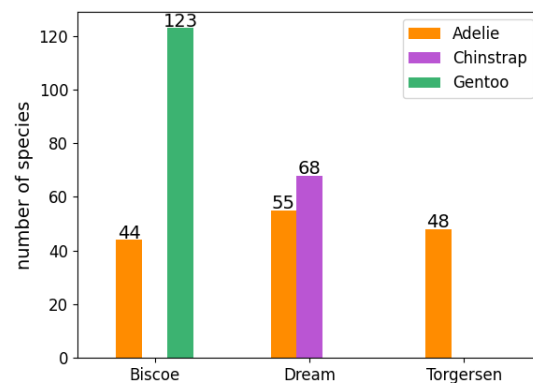
**Table 1:** Palmer penguin dataset features. Importance was calculated using random forest and a ranking is shown.

### Data cleaning

Eleven records have missing values. The two missing both *sex* and all numerical features were removed as imputation is unlikely to be reliable. A further nine records are missing only a *sex* value and were considered for imputation. Figure 1 shows the physical attributes of the male and female of each species differ statistically, making it likely that imputing *sex* would be reliable. Following standardisation, a Shapiro-Wilk test confirmed all the numerical attributes have a normal distribution [2] and Z-tests were applied to assess the hypotheses that the missing *sex* value is male or is female [3]. Two of the records could be imputed as male and three as female; the remaining four records were removed. The cleaned dataset has 338 records: 147 Adelie (74 male, 73 female), 68 Chinstrap (34 male, 34 female) and 123 Gentoo (62 male, 61 female).



**Figure 1:** All numerical features (including body mass shown here) show a significant statistical difference between sexes



**Figure 2:** Adelie is found on all three islands, but Gentoo and Chinstrap samples are found on only one of the islands

### Visualisation of the dataset

Figure 2 shows Chinstrap and Gentoo penguins are each found on only one of the islands, making *island* a potential confounding factor since environmental factors may influence

physical characteristics. A Shapiro-Wilk test showed the numerical features of the Adelie penguins (found on all the islands) have a normal distribution and an ANOVA test confirmed Adelie features are not significantly influenced by the island inhabited. Thus *island* is unlikely to be a confounding factor.

Pairwise scatterplots for the numerical features are shown in Figure 3. *Bill depth*, combined with either *flipper length* or *body mass*, yields a separable cluster of Gentoo penguins (shown in green) allowing them to be identified. No pairwise combination completely separates Adelie (orange) from Chinstrap (purple) clusters, but the best candidate feature for doing so is *bill length*.

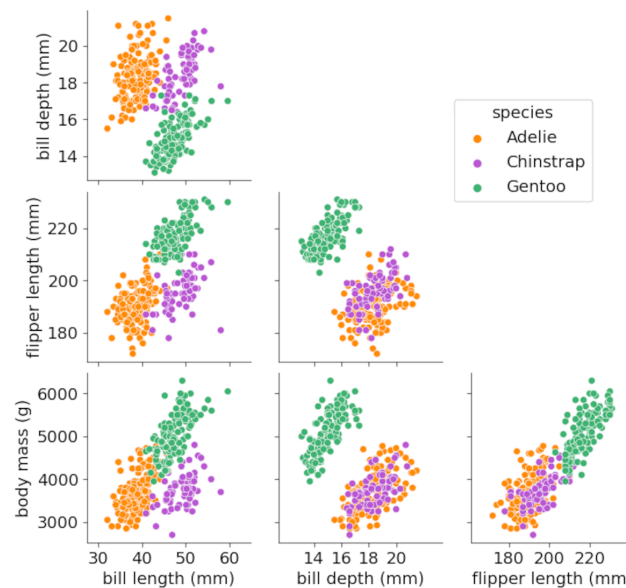
Figure 1 above shows the normative *body mass* of male and female differ for all the species. Differences between the sexes for the other three numerical physical characteristics were also apparent. As ‘narrower’ distributions result if the *sex* of the species is considered rather than just the species itself, including *sex* in analysis is likely to improve species classification. This knowledge was able to improve performance for some AI methods, as discussed in ‘results and analysis’.

## Methodology

The categorical features in the dataset were encoded to numerical values as this form is often needed

by AI methods. Some AI methods are also known to be biased in favour of numerical features with smaller standard deviations [4], but this bias can be reduced by the standardisation of features to zero mean and unity standard deviation. Standardisation statistics were calculated only from training sets, but the standardisation itself was applied to all data, including test sets. If a dataset is imbalanced, AI predictions may be biased towards classes more frequently found in the training data. Although Adelie penguins are more populous in the dataset, all the methods adopted in the current work are known to be little affected by imbalanced data, so no modifications were made [5].

Predicting the penguin species from the given features is a classification problem. The code supporting this report is available on Github [6], was written in Python 3.11 [7] and used the `scikit-learn` libraries [8]. Results were obtained from two conventional classification approaches, namely *k*-Nearest Neighbour (*knn*) [9] and random forest [10]. Classification was also carried out using unsupervised *k*-means (following cluster labelling) [11], as well as a novel combined visualisation and analysis (CVA) approach that is a mix of practical visualisations and Support Vector Machine (SVM) classification.



**Figure 3:** Pairwise distributions of numerical features. Gentoo can be distinguished, but Adelie and Chinstrap may not be completely separable from one another

To reduce the potential for overfitting, the classification methods were trained using ‘hold-out validation’, where 80% of the dataset was used in a five-fold cross-validation configuration [12]. The remaining 20% was kept for a test set. For all methods, the `scikit-learn` function `GridSearchCV` was employed to tune metaparameters [8]. The values selected for the metaparameter grid are shown in Table 2 and are typical of those found in the literature [13]. Metaparameters giving the best performance were selected to generate accuracy results (the percentage of correctly predicted species) from the test sets. The metrics ‘precision’ and ‘recall’ were calculated but not included here as measures of false positives or false negatives are not relevant to this study.

Method	Metaparameters	Values considered
<i>knn</i>	nearest neighbours <i>k</i> prediction function distance metric	<i>1</i> , 2, 3, 4, 5, 6, 8, 10 <i>uniform</i> , distance <i>Manhattan</i> , Euclid
random forest	number of trees max. depth min. samples to split min. samples at leaf split function	5, <i>10</i> , 15, 20, 25 <i>no max</i> , 10, 20 2, 5, 10 <i>1</i> , 2, 4 <i>gini</i> , entropy
<i>k</i> -means	number of clusters <i>k</i> centroid initialize runs for centroid max. iterations	2, 3, <i>4</i> , 5, 6, 7, 8, 10 <i>k-means++</i> , random 2, <i>5</i> , 10, 20 5, <i>10</i> , 20, 50
CVA	regularization kernel coefficient kernel type	0.1, 1, <i>10</i> , 100 <i>1</i> , 0.1, 0.01, 0.001 rbf, <i>linear</i> , poly

**Table 2:** Metaparameters values shown in italics most consistently produced training results of best accuracy during validation and were selected for generating results

## Results and analysis

The `scikit-learn` pseudo-random procedure was used for generating validation and test set samples and 100 (indices 1 to 100) of these were used both when selecting metaparameters and when deriving accuracy results. The results in Table 3 include a baseline to demonstrate the performance improvements achieved by the AI methods.

In classification, the baseline method is often simply to select the most frequent class in the observations. Here, this is the Adelie penguins, giving an accuracy of 43.49% (147/338).

***knn*** The accuracy of *knn* obtained using the dataset could be improved by removing certain features (particularly those shown as less important in Table 1). The best improvement was found when *island* was omitted and when *k*=3 (Table 3). It appears that *island* did not provide any additional information and the larger value of *k* (compared to *k*=1 for all features) implies better generalization has been achieved during training.

**Random forest** When all features are included in the analysis, the accuracy of random forest was marginally worse than that achieved using *knn*. No performance improvement was found using fewer features, indicating that random forest may be less influenced by superfluous information in the training data.

Method	Accuracy (range)
baseline, Adeleie species	43.49%
<i>knn</i> , all features	99.24% (97.06%-100%)
<i>knn</i> , no island	99.46% (97.06%-100%)
random forest, all features	98.57% (95.59%-100%)
random forest, no body mass	98.49% (92.65%-100%)
<i>k</i> -means, numerical features	97.03% (94.12%-97.06%)
<i>k</i> -means, two sex clusters	99.18% (94.12%-100%)
CVA, three main features	98.98% (95.35%-100%)
CVA, separate sex models	99.25% (90.91%-100%)

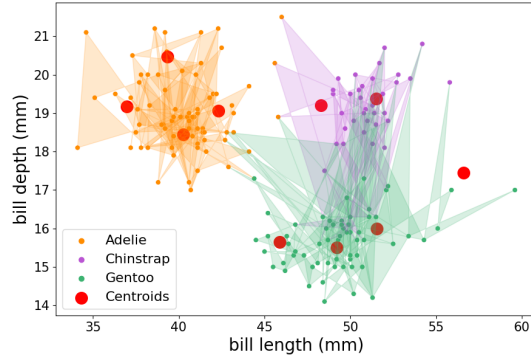
**Table 3:** Classification accuracy mean value and range for 100 pseudo-random test sets and using the metaparameters identified in Table 2

***k*-means** Although a clustering method, *k*-means can be used for classification by mapping clusters to classes. Figure 4 illustrates such a mapping for two feature dimensions. Using the elbow method, the number of clusters (*k*) was suggested to be two, but three was identified by the silhouette method. By trial and error, accuracy was found to improve when  $k \geq 4$ , as otherwise clusters were not reliably formed for all three species. Accuracy was also greatly improved by creating a separate set of clusters for each *sex*.

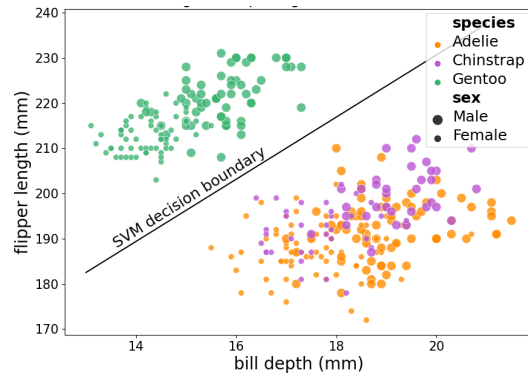
**CVA** requires manual identification of suitable pairs of features for SVM classification. Given features  $\mathbf{x}$ , SVM finds a decision boundary that maximizes class separation

$$\mathbf{w}^T \mathbf{x} = b, \quad (1)$$

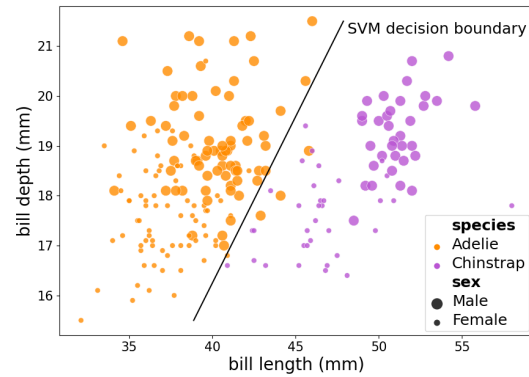
where  $\mathbf{w}$  is a weight vector perpendicular to the boundary and  $b$  is the intercept. SVM training finds  $\mathbf{w}$  and  $b$  to specify an optimal hyperplane (and hence the boundary). An application of CVA to the Penguin dataset is given in Figure 5. Figure 5(a) shows the relationship between *bill depth* and *flipper length*, and the SVM decision boundary separates Gentoo from the other two species. Figure 5(b) plots *bill length* against *bill depth* and shows the SVM boundary to best distinguish Adelie from Chinstrap. Accuracy was improved by implementing separate CVA models for each *sex*.



**Figure 4:** *k*-means clusters mapped to species using majority voting. Mappings are shown by polygon colour ( $k=10$ , 50 samples included).



(a) Gentoo distinguished from the other species



(b) Adelie and Chinstrap partially separated

**Figure 5:** Two-stage CVA approach with decision boundaries fitted to feature pairs using SVM

## Conclusions

With careful data preparation, selection of metaparameters and robust application of training and testing methods, *knn* and random forest both produced high-quality results. *k*-means training does not take advantage of target information and this resulted in comparatively poor accuracy, but training separate clusters for each sex did improve performance significantly. The novel CVA approach needs to be tailored anew to each

problem and is not well-suited to high-dimensional data, but it was found to produce results comparable to those of general-purpose classification methods and has the advantage that its internal operations are easy to visualise, understand and explain.

That CVA makes a series of decisions using chosen feature pairs led the author to consider SVMs in place of entropy at random forests nodes - but this has been done [14].

## Question 2 - Ethical challenges and threats in AI

### Racial Bias in Medical Algorithms

In 2019, a widely used US healthcare algorithm was found to discriminate by prioritising hospital services based on historical spending records, resulting in the allocation of relatively less future funding and fewer referrals for black patients [15], [16]. Through the application of a series of test data sets, Obermeyer *et al.* [17] identified this inadvertent bias and the team was able to mitigate against it by adjusting the model's training labels.

The fact that this third-party assessment and adjustment were possible, demonstrates how exposing a model's internal operations can aid bias identification and removal [18], [19]. Ensuring greater transparency of AI models is becoming the subject of legislation, for example the 2023 EU AI Act aims to enforce transparency principles by requiring developers to disclose an algorithm's variables, data sources, and selection logic [20], [21]. While ensuring that organisations building AI systems are held accountable for the processes used in their development may lead to algorithmic changes that reduce bias [22], [23], care needs to be taken that the removal of bias doesn't significantly affect the performance of the model in its application domain [24].

### AI system safety and existential risks in warfare

Recent developments in AI have led many researchers to believe that AI systems capable of directly acting in the real world based on decisions they have taken autonomously will become available later this century [25]. With such advancements comes the risk that AI systems whose decision-making does not prioritise human welfare may pose a threat to life [26].

A specific example of a military AI system posing an existential risk [27], [28], is one that decides maximising human casualties would be the best strategy to achieve a high-level battlefield objective [29]. Recent deployments of automated missiles that activate on target acquisition [30], [31], have raised ethical concerns over the use of AI in situations where human beings are potential targets [32]. If such advanced AI was given control of powerful military weapons and applied more widely, the ramifications for the human race's survival could be profound [33].

Addressing these existential threats requires international cooperation to guarantee the transparency of AI algorithms [34], [35]. A potential future safeguard is to include a human-controlled override in all military AI systems [36], although Russell [37] warns that super-intelligent AI may be capable of removing such safety measures. Ultimately, a global strategy that prioritises human wellbeing in all areas of AI usage will be essential.

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