Q1 - Visualization and analysis of the Palmer 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, consideration is given to data cleaning and preparation, the dataset is then explored through visualization and analysis is carried out to compare the accuracy of a small number of AI approaches in classifying penguin species.

Feature	Type	Values in the dataset	Importance
island	categorial	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	categorial	Male, Female	0.01 (6)
species	categorial	Adelie, Chinstrap, Gentoo	class

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

Data cleaning - missing values, encoding, standardization and imbalance

The two records missing the sex amd all numerical features were removed as imputation is unlikely to be reliable. The remaining nine records are missing only the sex attribute. Figure 1 shows the physical attributes of the male and female of each species differ statistically and so it is reasonable to consider imputing sex for those records. Following standardization, a Shapiro-Wilk test confirmed each numerical attribute has a normal distribution [2] and separate Z-tests were applied to assess the hypotheses that the missing sex value is male or female [3]. Two of the records could be imputed as male and three as female and these were retained, with the remaining four records being 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).

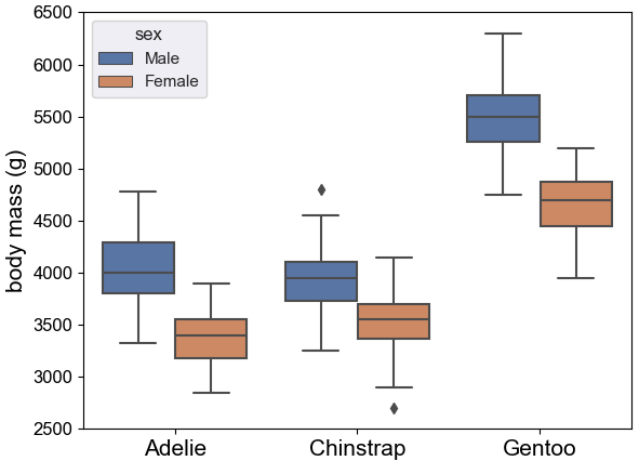


Figure 1: All numerical features show a significant statistical difference between male and female, as in the body mass example above. Shown are median values, upper and lower quartiles, and outliers.

The categorical features in the dataset were encoded to numerical values. 'One-shot' encoding of categorical features was considered but not found to improve performance. A number of AI methods are known to be biased in favour of numerical features with smaller standard deviations [4], but this can be reduced by standardization of features to zero mean and unity standard deviation. In this work, standardization statistics were calculated only from training sets, but applied to all data. If a dataset is imbalanced, AI predictions may be biased towards classes more frequently found in the training data. In the Palmer penguin dataset, the number of Chinstrap records is around half of that for either Adelie or Gentoo, but, as all the methods adopted in the current work are known to be little affected by imbalanced data [5], no modifications were made.

Visualization of the dataset

Figure 2 shows the species distribution for the islands. Chinstrap and Gentoo penguins are found only on one island, making island a potential confounding factor whose individual environmental factors may influence physical characteristics. A Shapiro-Wilk test confirmed the normal distribution of the numerical features of the Adelie penguins (found on all islands) and an ANOVA test

confirmed the features are not significantly influenced by the island inhabited. It is clear the island is not a confounding factor in the dataset.

Table 1 shows the feature importance scores (and rank in parentheses) indicating relative contributions to predicting the penguin species. Results reported later show that performance improvements can be achieved by concentrating classification on the more 'important' features.

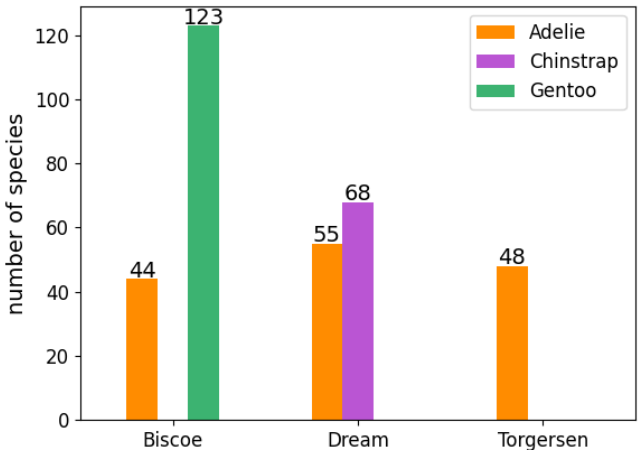


Figure 2: Adelie is on all three islands, but Gentoo and Chinstrap samples are from only one.

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 in distributions involving bill length.

Figure 1 above shows there is a difference in the body masses of the male and female samples for each of the three species. Differences between the sexes for the other three numerical physical characteristics in the dataset were also apparent. Since narrower distributions are seen if the sex of the species is considered rather than just the species itself, including sex is likely to provide a finer grained distinction for species classification and this knowledge can be used to improve performance, as discussed in the 'results and analysis' section below.

Methodology

The code is available on Gitub [6] and was written in Python 3.11 [7] using 'Scikit-Learn' libraries [8]. Predicting the penguin species from the given features is a classification problem. Results are obtained from two conventional classification approaches, namely k-Nearest Neighbour ($k$nn) [9] and random forest [10], unsupervised k-means (following cluster labelling) [11] and a novel combined visualization and analysis (CVA) approach that is a mix of practical visualizations and Support Vector Machine (SVM) classification.

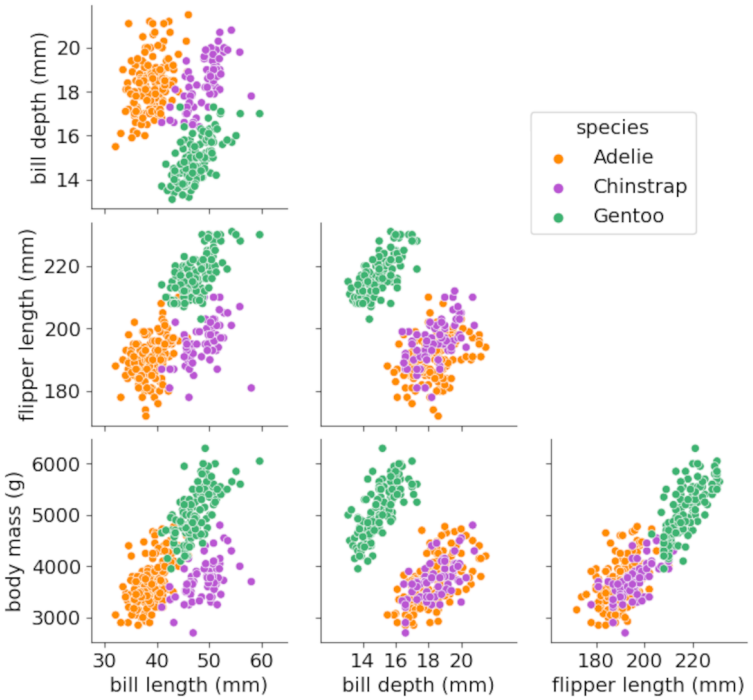


Figure 3: Pairwise distributions of numerical features. Gentoo can be distinguished, but Adelie and Chinstrap may not be completely separable from one another

To reduce the potential for overfitting, the classification methods (all but k-means) were trained using 'holdout 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]. Table 2 shows the values selected for the metaparameter grid. Those giving the best performance were selected to generate accuracy results (the

percentage of correctly predicted species) from the test set. The metrics 'precision' and 'recall' were also caculated, but as these are only relevant if false positives or false negatives (respectively) are specfically to be avoided, they are not included in this report.

Results and analysis

Scikit-Learn provides pseudo-random procedures for selecting validation and test set values and 100 of these were used both when selecting metaparameters and when deriving accuracy results. The results in Table 3 include a baseline that is used to demonstrate performance improvements achieved by the AI methods considered. In classification, the baseline method is often simply to select the most frequent class in the observations and, in this work, this is the Adelie penguins, giving an accuracy of 43.49% (147/338).

Method	Metaparameters	Values considered
$k$nn	nearest neighbours k	***1***, 2, 3, 4, 5, 6, 8, 10
	prediction weight function	***uniform***, distance
	neighbours distance metric	***Manhattan***, Euclidean
random forest	trees in the forest	5, ***10***, 15, 20, 25
	maximum depth of trees	***no maximum***, 10, 20
	min samples to split node	***2***, 5, 10
	min samples at leaf node	***1***, 2, 4
	quality of split function	***gini***, entropy
k-means	number of clusters k	2, ***3***, 4, 5, 6, 7, 8, 9, 10
	centroid initialization	***k-means++***, random
	runs for centroid seeds	2, ***5***, 10, 20
	max number of iterations	5, ***10***, 20, 50
CVA	regularization parameter	0.1, 1, ***10***, 100
	kernel coefficient	***1***, 0.1, 0.01, 0.001
	kernel type	rbf, ***linear***, polynomial

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

Classification method 1 - *k*nn An additional test was carried to investigate if, compared to the accuracy found for all features, the omission of features and combinations of features could improve accuracy. An improvement was found when island was omitted and when k=3. It appears that island did not provide any additional information and the higher value of k implies better generalization may have been achieved.

Method	Accuracy (range)
baseline, Adeleie species	43.49%
kNN, all features	99.24% (97.06%-100%)
kNN, 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%)
k-means, numerical features	97.03% (94.12%-97.06%)
k-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

Classification method 2 - Random forest Including all of the features in the analysis gave an accuracy marginally worse than achieved using $k$nn. In contrast with $k$nn, no performance improvement was found using fewer features, indicating that random forest may be less influenced by superfluous features in training data. For selected test sets, 100% accuracy is possible, but the trained systems is likely to exhibit poor generalization.

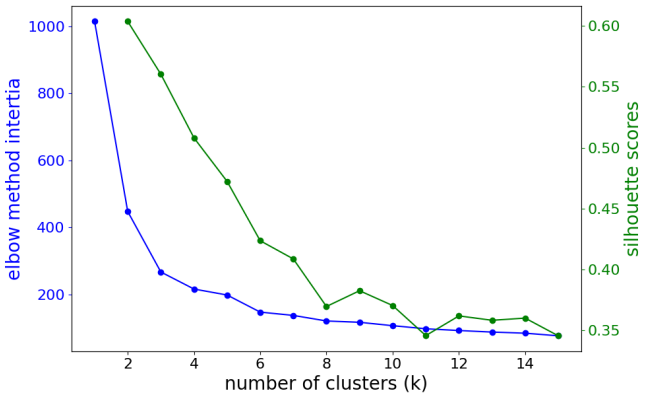


Figure 4: The k-means elbow is the change in slope of 'inertia' (k=3) and the silhouette is the 'score' closest to 1 (k=2)

Unsupervised method - *k*-means Although a clustering method, k-means can be used for classification by matching clusters to classes. The k-means method is normally applied only to numerical features and only they were included in this work. The number of clusters (k) can be selected using elbow and silhouette methods, as shown in Figure 4. Empirically, accuracy improved significantly when $k \geq 4$ as clusters were not reliably formed for all three species for smaller values of k, Figure 5 illustrates the mapping of classes

to clusters for two feature dimensions. No accuracy improvement was obtained by reducing the number of features, but when a separate set of k-means clusters was created for each sex this led to a small improvement in accuracy.

A novel combined visualization and analysis (CVA) approach The CVA approach involves visualizing selected pairwise plots of features to identify a sequence of two-dimensional SVM classifiers. CVA requires manual effort to understand the nature of the dataset, in contrast with 'black box' classification approaches that are often applied with limited knowledge of the method and little insight into the nature of the data. The main drawback of the CVA approach is that it may not always be feasible to extract the necessary visualization insights, particularly for large dimensional datasets.

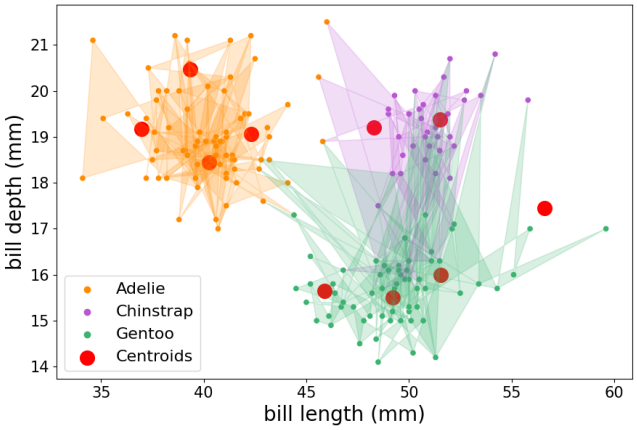
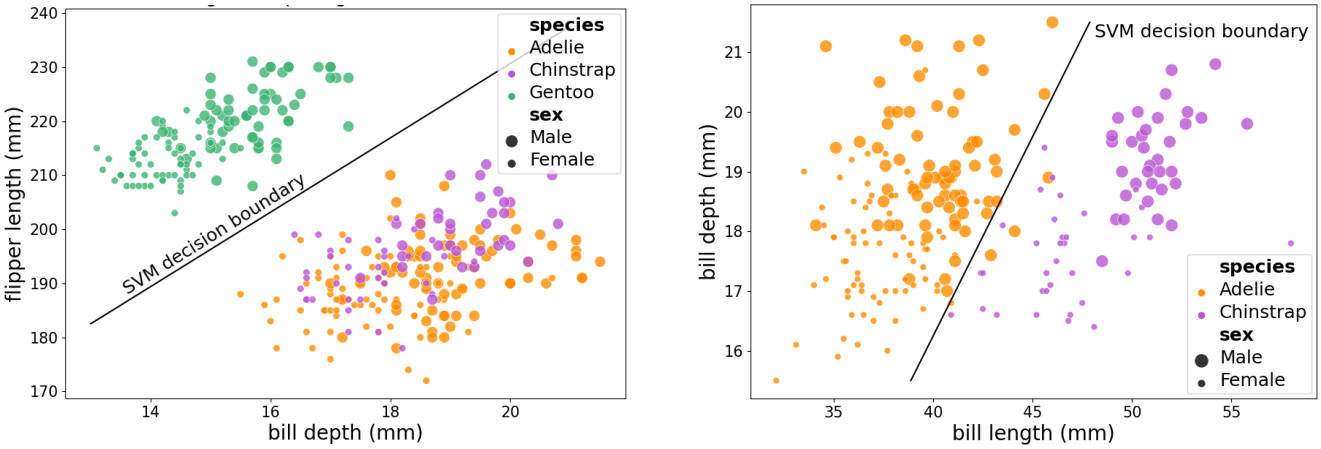


Figure 5: k-means clusters mapped to species using majority voting. Class assignments are shown by polygon colour (k=10, 50 samples coloured).

An application of CVA to the Penguin dataset is illustrated in Figure 6. Figure 6(a) shows the relationship between bill depth and flipper length, and SVM determines finds a suitable 'decision boundary' to separate Gentoo from the other two species. Figure 6(b) plots bill length against bill depth and shows a second SVM line to best separate Adelie and Chinstrap . CVA was able to produce results of accuracy similar to conventional approaches. A small improvement in accuracy was apparent when separate SVM models were developed for each penguin sex.



(a) Gentoo can be distingushed from other species

(b) Adelie and Chinstrap can be partially separated

Figure 6: Two-stage CVA approach with boundaries fitted using SVM to training data of feature pairs

Conclusions

With careful data preparation, optimization of metaparameters and robust application of training and testing methods, the $k$nn and random forest classification methods produced high-quality results. As expected, the k-means accuracy results were comparitively worse as in training it does not take advantage of target data information known to the supervised approaches.

The novel CVA approach was able to produce accuracy results similar to those of other classification methods. Although needing to be tailored to each problem and not well-suited to high-dimensionality data, its internal operations are transparent and this is in contrast with general-purpose classification methods.

Question 2

2. 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 [13, 14]. Through the application of a series of test data sets, Obermeyer et al. [15] 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 [16, 17]. 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 [18, 19]. 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 [20, 21], care needs to be taken that the removal of bias doesn't significantly affect the performance of the model in its application domain [22].

3. 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 [23]. With such advancements comes the risk that AI systems whose decision-making does not prioritise human welfare may pose a threat to life [24].

A specific example of a military AI system posing an existential risk [**Yampolskiy2016**, 25], is one that decides maximising human casualties would be the best strategy to achieve a high-level battlefield objective [26]. Recent deployments of automated missiles that activate on target acquisition [27, 28], have raised ethical concerns over the use of AI in situations where human beings are potential targets [29]. 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 [30].

Addressing these existential threats requires international cooperation to guarantee the transparency of AI algorithms [31, 32]. A potential future safeguard is to include a human-controlled override in all military AI systems [33], although Russell [34] 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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