

Applied Data Science

L2. Learning from Data. Cross-validation.
Data pre-processing

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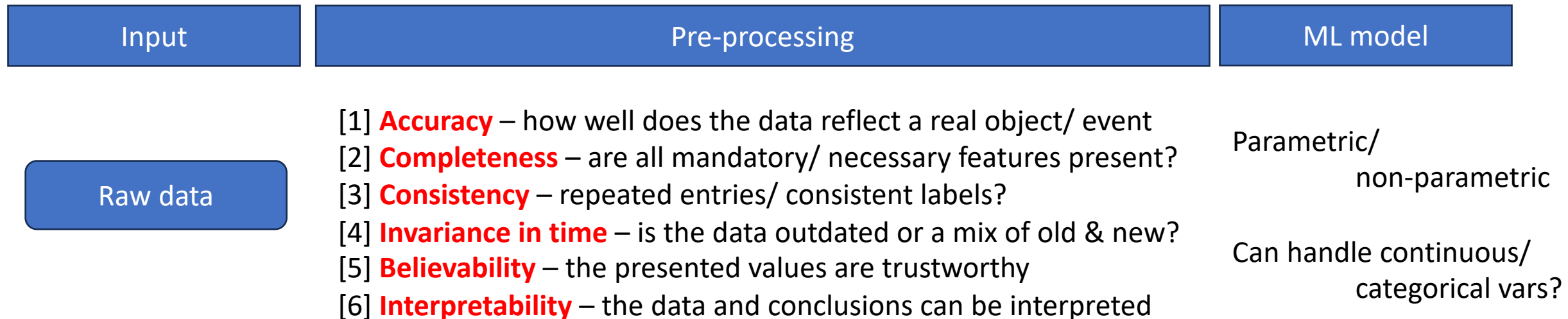
We've got data. Find the signal!

Data (pre-processing)

Finding patterns in the data

i.e. the technical characteristics of the data are less important than the pattern (model)

- Input: some data
- Methods: statistical analysis, machine learning, programming
- Output: a robust, reproducible, generalizable model



Data (pre-processing). Feature engineering

Overview of concepts.

Input	Pre-processing	ML model
<div>Raw data</div> <ul style="list-style-type: none">[1] Accuracy[2] Completeness[3] Consistency[4] Invariance in time[5] Believability[6] Interpretability	<ul style="list-style-type: none">[a] Understanding the structure of the data<ul style="list-style-type: none">type of features: continuous, categoricalranges of features: [min, max], number of categoriesmissing information [labels, features]discriminative power of features (redundancy)	<p>Parametric/ non-parametric</p> <p>Can handle continuous/ categorical vars?</p>
	<ul style="list-style-type: none">[b] Adjusting data without tampering with signal<ul style="list-style-type: none">Expression ranges and One-hot encodingStandardisation vs scalingNear zero varianceMulti-collinearityDimensionality reduction	<p>Feature selection</p>
	<ul style="list-style-type: none">[c] creating robust models – cross-validation. Bias/ variance<ul style="list-style-type: none">Training/ Validation/ Test splittingCross-validation	

Data pre-processing. Feature engineering

Understanding the structure of the data

[a] Understanding the structure of the data

type of features: continuous, categorical

ranges of features: [min, max], number of categories

missing information [labels, features]

discriminative power of features (redundancy)

```
!pip install seaborn
import seaborn as sns

# Load the Palmer's penguin dataset
penguins = sns.load_dataset('penguins')
```

```
penguins.head()
```

Continuous features					Categorical features		
	species	island	bill_length_mm	bill_depth_mm	flipper_length_mm	body_mass_g	sex
0	Adelie	Torgersen	39.1	18.7	181.0	3750.0	Male
1	Adelie	Torgersen	39.5	17.4	186.0	3800.0	Female
2	Adelie	Torgersen	40.3	18.0	195.0	3250.0	Female
3	Adelie	Torgersen	NaN	NaN	NaN	NaN	NaN
4	Adelie	Torgersen	36.7	19.3	193.0	3450.0	Female

Missing
data

Data pre-processing. Feature engineering

Understanding the structure of the data

Knowing your dataset is essential – **explore, clean, visualize** (part of) your data

Examine several rows of data

Check basic statistics. Evaluate data types

Assess missing entries

```
import pandas as pd

# Get summary of numeric and non-numeric features
numeric_summary = penguins.describe(include=[float, int])
non_numeric_summary = penguins.describe(include=[object])

# Combine the summaries
summary = pd.concat([numeric_summary, non_numeric_summary], axis=0)

print(summary)
```

	bill_length_mm	bill_depth_mm	flipper_length_mm	body_mass_g	species
count	342.000000	342.000000	342.000000	342.000000	NaN
mean	43.921930	17.151170	200.915205	4201.754386	NaN
std	5.459584	1.974793	14.061714	801.954536	NaN
min	32.100000	13.100000	172.000000	2700.000000	NaN
25%	39.225000	15.600000	190.000000	3550.000000	NaN
50%	44.450000	17.300000	197.000000	4050.000000	NaN
75%	48.500000	18.700000	213.000000	4750.000000	NaN
max	59.600000	21.500000	231.000000	6300.000000	NaN
count	NaN	NaN	NaN	NaN	344
unique	NaN	NaN	NaN	NaN	3
top	NaN	NaN	NaN	NaN	Adelie
freq	NaN	NaN	NaN	NaN	152

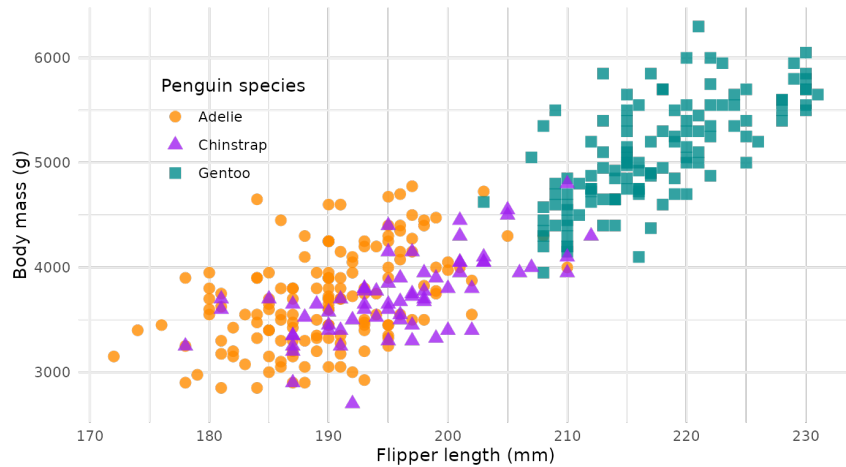
	island	sex
count	NaN	NaN
mean	NaN	NaN
std	NaN	NaN
min	NaN	NaN
25%	NaN	NaN
50%	NaN	NaN
75%	NaN	NaN
max	NaN	NaN
count	344	333
unique	3	2
top	Biscoe	Male
freq	168	168

Data pre-processing. Feature engineering

Understanding the structure of the data

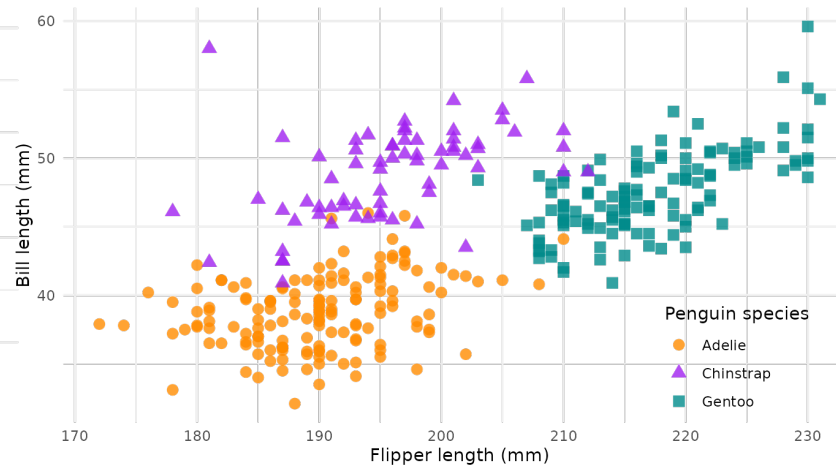
Penguin size, Palmer Station LTER

Flipper length and body mass for Adelle, Chinstrap and Gentoo Penguins



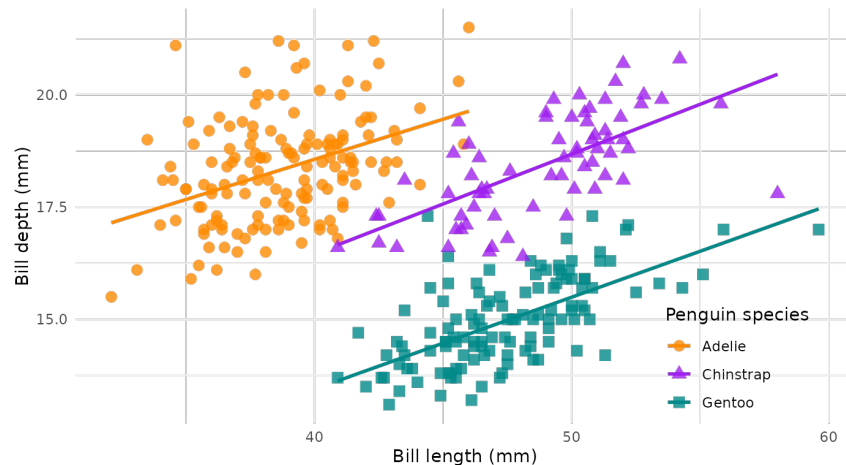
Flipper and bill length

Dimensions for Adelle, Chinstrap and Gentoo Penguins at Palmer Station LTER



Penguin bill dimensions

Bill length and depth for Adelle, Chinstrap and Gentoo Penguins at Palmer Station LTER



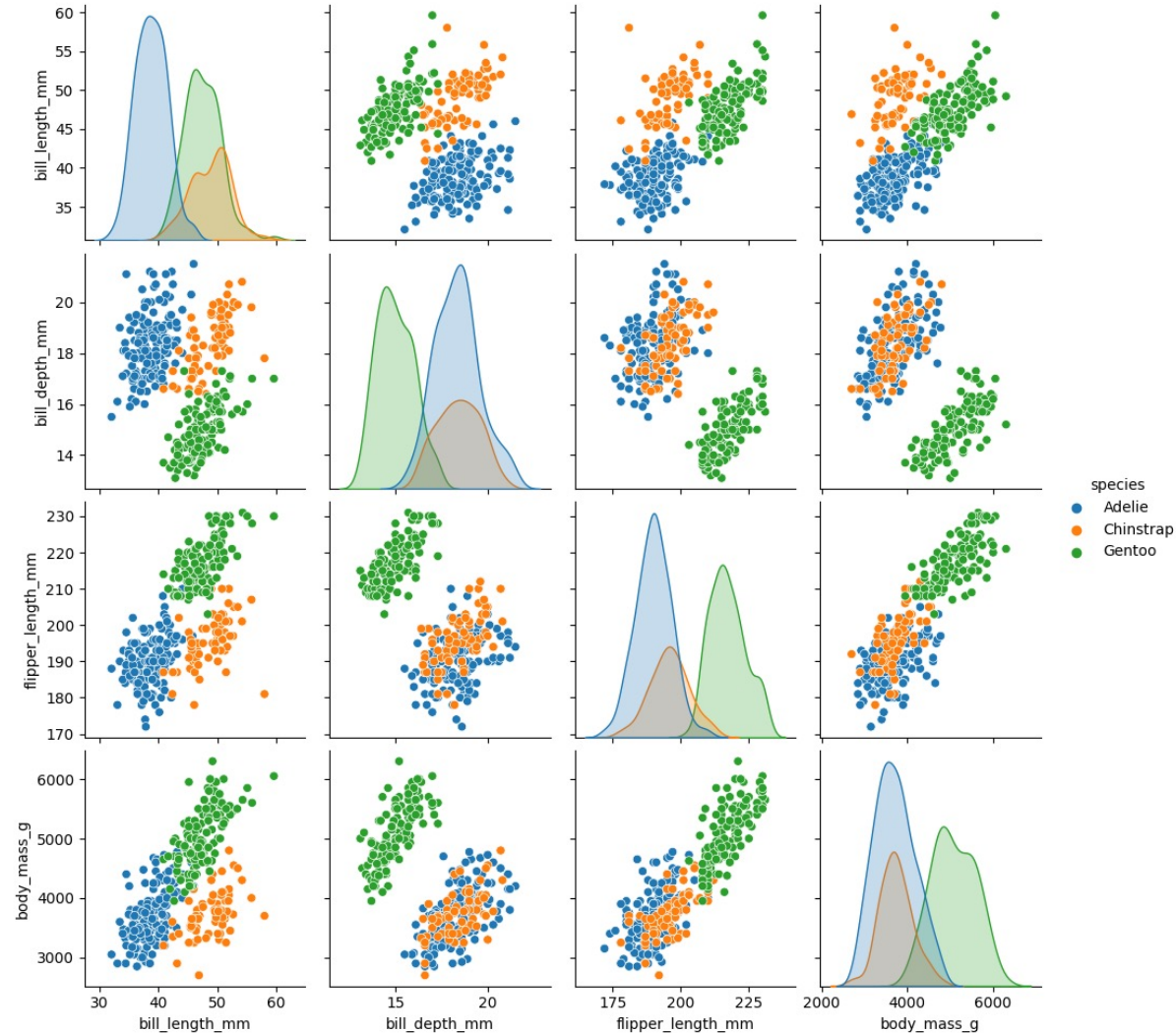
The body mass is highly correlated to flipper length (top left)

We note linear separability between classes

The colinearity differs per class (bottom left).

Data pre-processing. Feature engineering

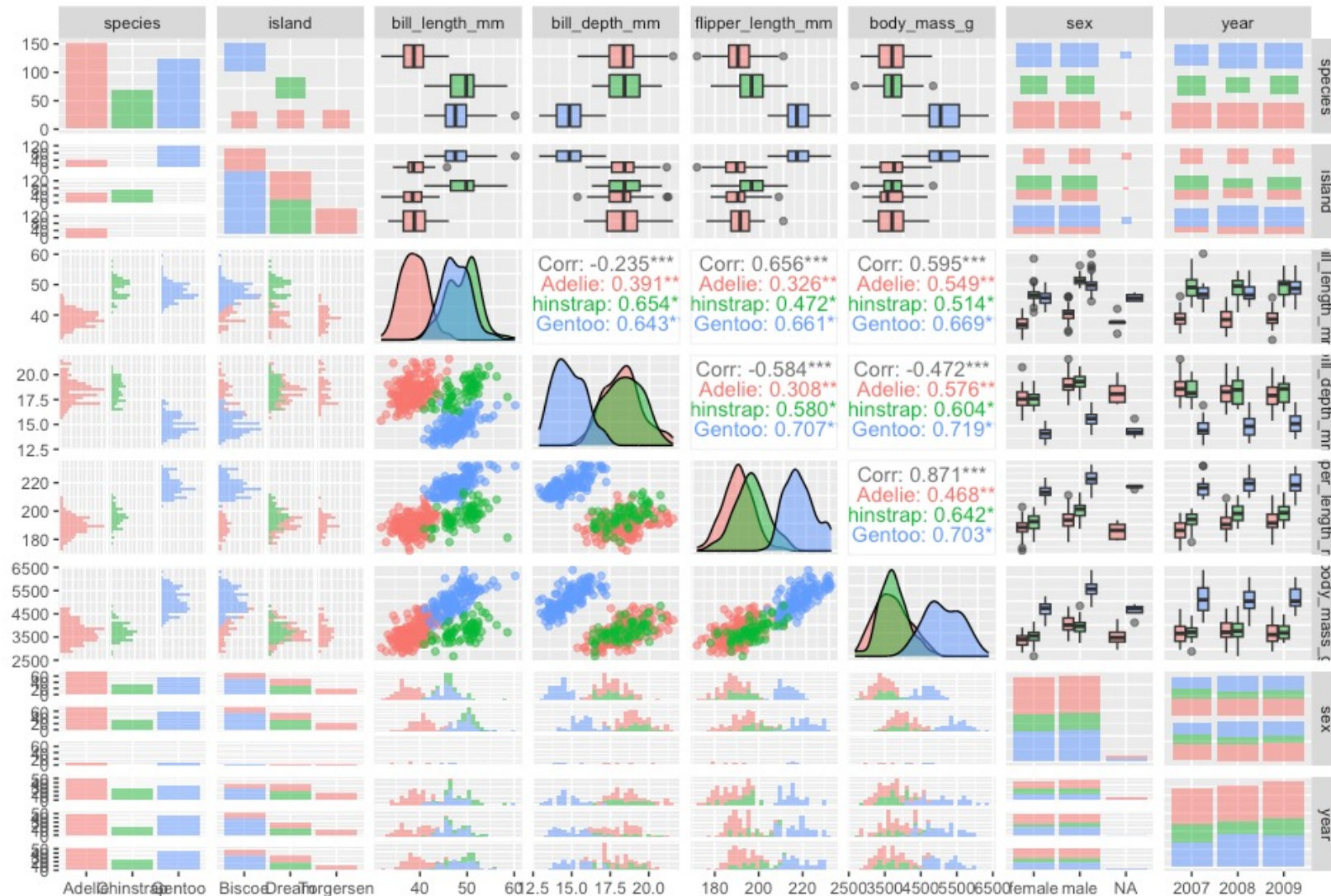
Understanding the structure of the data



```
# Create pairplot  
sns.pairplot(penguins, hue='species', diag_kind='kde')
```


Data pre-processing. Feature engineering

Understanding the structure of the data



```
ggpairs(penguins, ggplot2::aes(colour = species, alpha = 0.4))
```

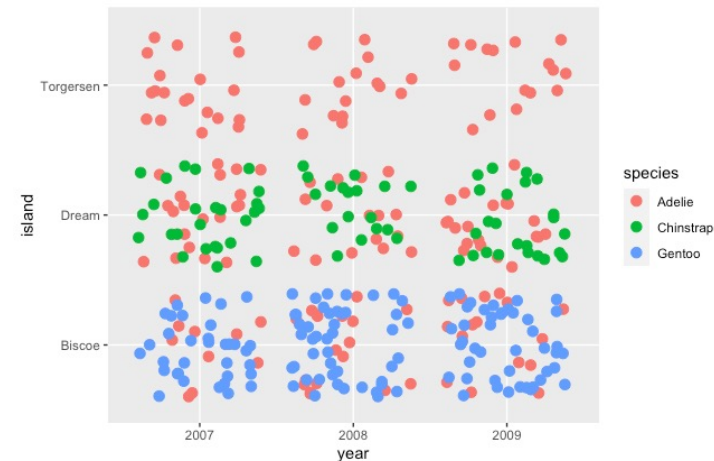
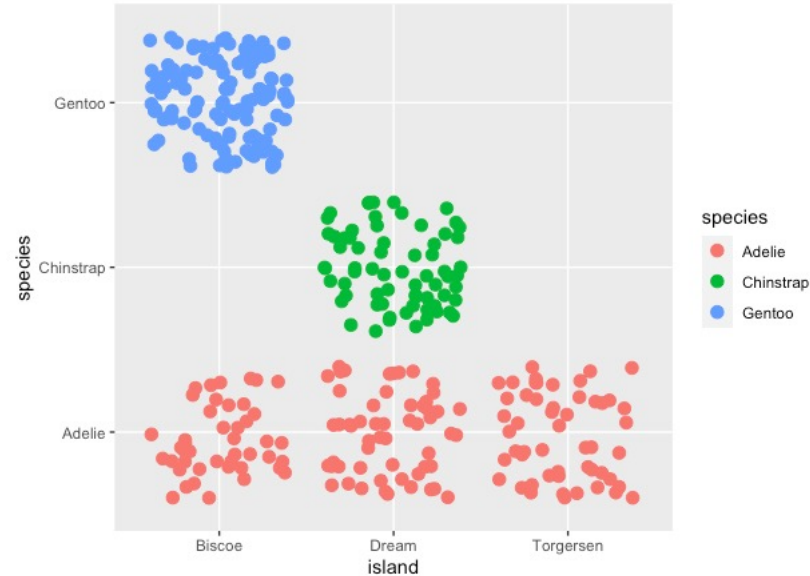
Simpson's paradox is observed in probability and statistics; a trend appears in several groups of data but disappears or reverses when the groups are combined.

Data pre-processing. Feature engineering

Understanding the structure of the data

```
table(penguins$species, penguins$island)
```

	Biscoe	Dream	Torgersen
Adelie	44	56	52
Chinstrap	0	68	0
Gentoo	124	0	0



Data pre-processing. Feature engineering

Adjusting data without tampering with signal

Adjusting data without tampering with signal

Expression ranges and One-hot encoding

Standardisation vs scaling

Near zero variance

Multi-collinearity

Dimensionality reduction

summary (penguins)

species	island	bill_length_mm	bill_depth_mm
Adelie :152	Biscoe :168	Min. :32.10	Min. :13.10
Chinstrap: 68	Dream :124	1st Qu.:39.23	1st Qu.:15.60
Gentoo :124	Torgersen: 52	Median :44.45	Median :17.30
		Mean :43.92	Mean :17.15
		3rd Qu.:48.50	3rd Qu.:18.70
		Max. :59.60	Max. :21.50
		NA's :2	NA's :2

flipper_length_mm	body_mass_g	sex	year
Min. :172.0	Min. :2700	female:165	Min. :2007
1st Qu.:190.0	1st Qu.:3550	male :168	1st Qu.:2007
Median :197.0	Median :4050	NA's : 11	Median :2008
Mean :200.9	Mean :4202		Mean :2008
3rd Qu.:213.0	3rd Qu.:4750		3rd Qu.:2009
Max. :231.0	Max. :6300		Max. :2009
NA's :2	NA's :2		

Continuous features: bill length, depth, flipper length, body mass

Categorical features: island, sex, year

Output: species (categorical i.e. classification problem)

Data pre-processing. Feature engineering

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bill_length_mm	bill_depth_mm	flipper_length_mm	body_mass_g
Min. :32.10	Min. :13.10	Min. :172.0	Min. :2700
1st Qu.:39.23	1st Qu.:15.60	1st Qu.:190.0	1st Qu.:3550
Median :44.45	Median :17.30	Median :197.0	Median :4050
Mean :43.92	Mean :17.15	Mean :200.9	Mean :4202
3rd Qu.:48.50	3rd Qu.:18.70	3rd Qu.:213.0	3rd Qu.:4750
Max. :59.60	Max. :21.50	Max. :231.0	Max. :6300
NA's :2	NA's :2	NA's :2	NA's :2

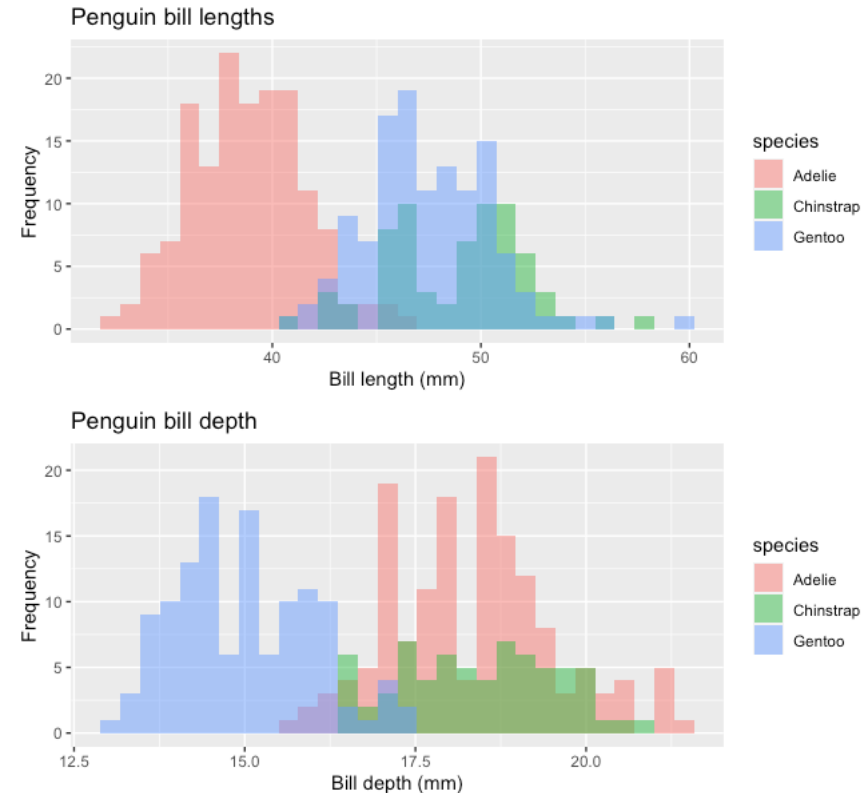
The ranges are not comparable.

Standardization vs scaling

[min, max] scaling to a predefined range

Robust scaling – the transformation is performed on the IQR

Z transformation (on mean, standard deviation or median and MAD)



Data pre-processing. Feature engineering

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Dimensionality reduction

[min, max] scaling to a predefined range

```
[min, max] --> [0,1]
```

```
[min, max] - min --> [min - min, max - min]
```

```
[min - min, max - min] / (max - min) --> [0,1]
```

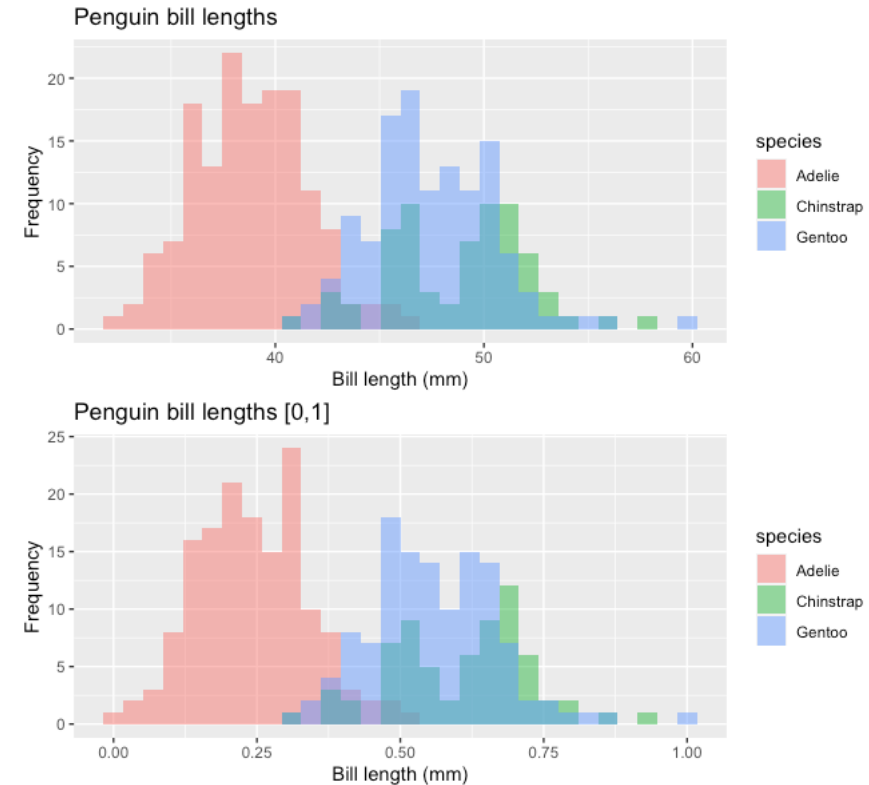
```
[min, max] --> [0,1] --> [a,b]
```

Use a linear transformation $f(x) = mx + n$

$f(0) = n \Rightarrow a = n$

$f(1) = m + n \Rightarrow b = m + n \Rightarrow m = b - a$

$f(x) = (b - a) * x + a$



Data pre-processing. Feature engineering

Adjusting data without tampering with signal

Adjusting data without tampering with signal

Expression ranges and One-hot encoding

Standardisation vs scaling

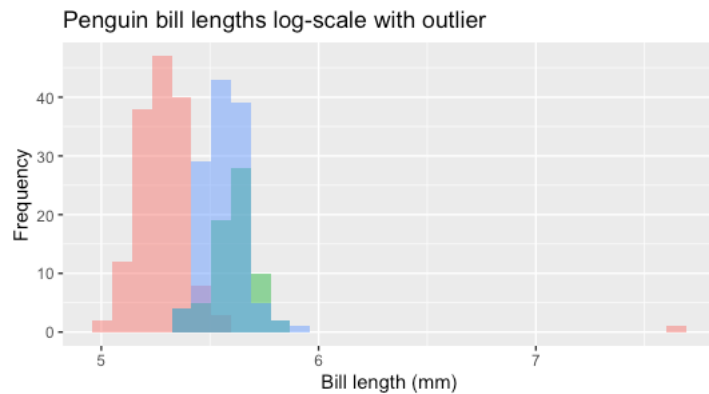
Near zero variance

Multi-collinearity

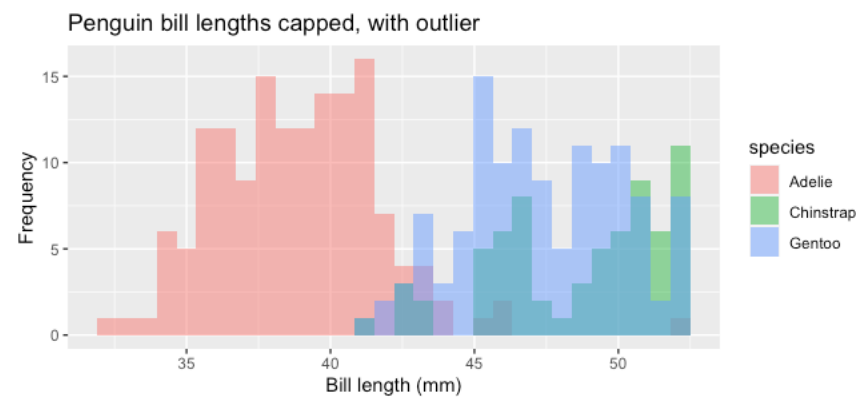
Dimensionality reduction

Outliers can skew the data and lead to misinterpretations.

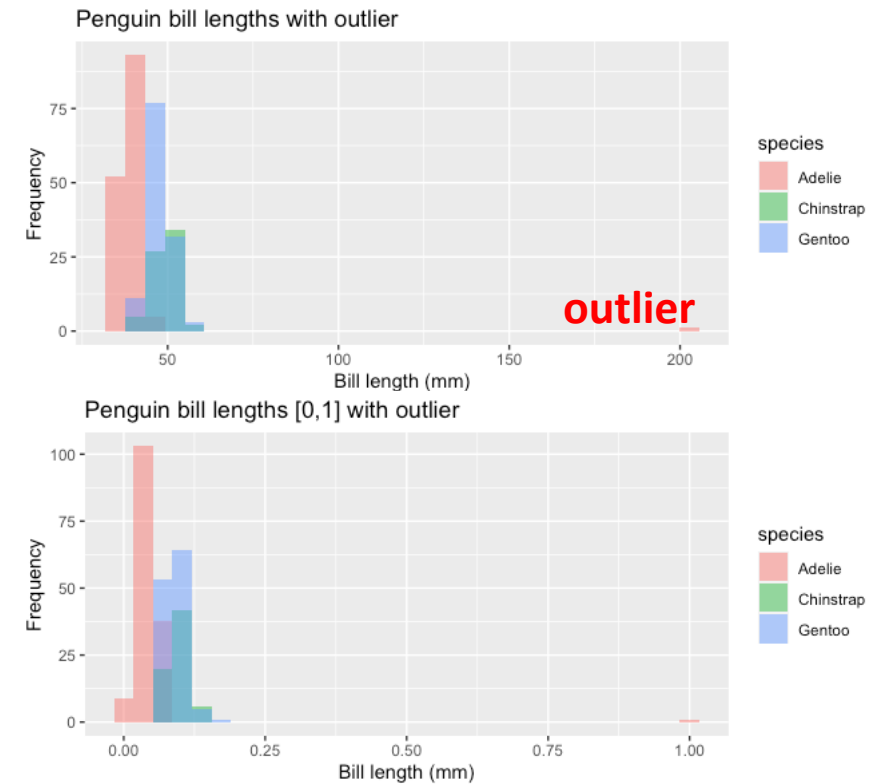
The proposed scaling does not change the distribution.



Log₂ transformation of bill lengths



Capped values of bill lengths



Data pre-processing. Feature engineering

Adjusting data without tampering with signal

Adjusting data without tampering with signal

Expression ranges and One-hot encoding

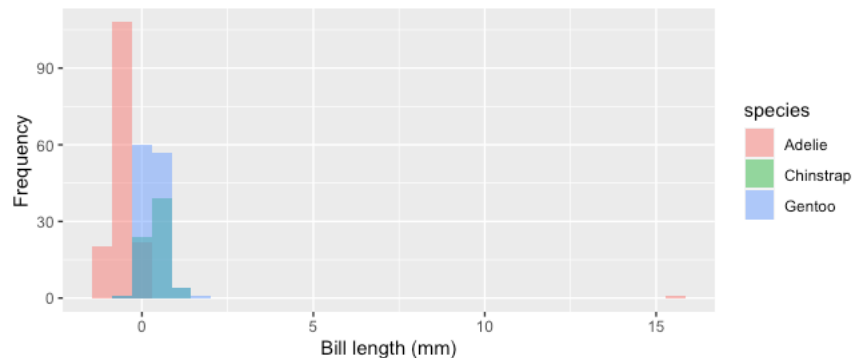
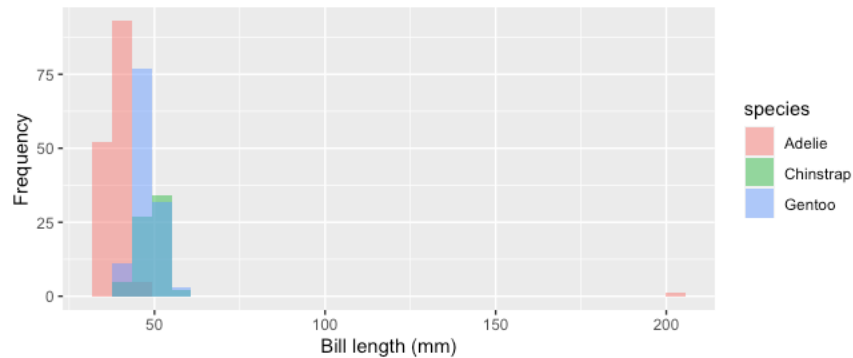
Standardisation vs scaling

Near zero variance

Multi-collinearity

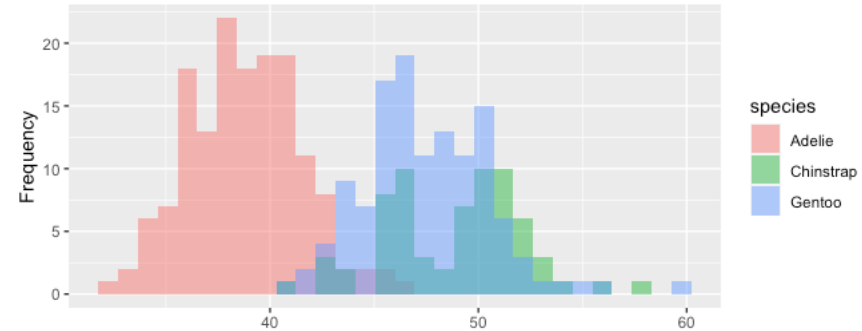
Dimensionality reduction

Penguin bill lengths with outlier



mean = 44.39
sd = 10.04

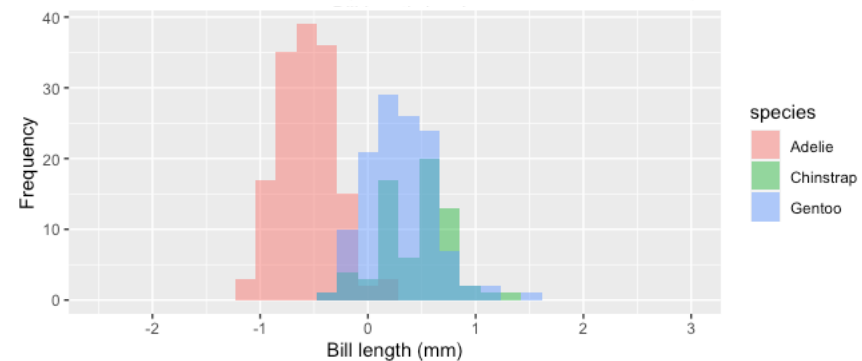
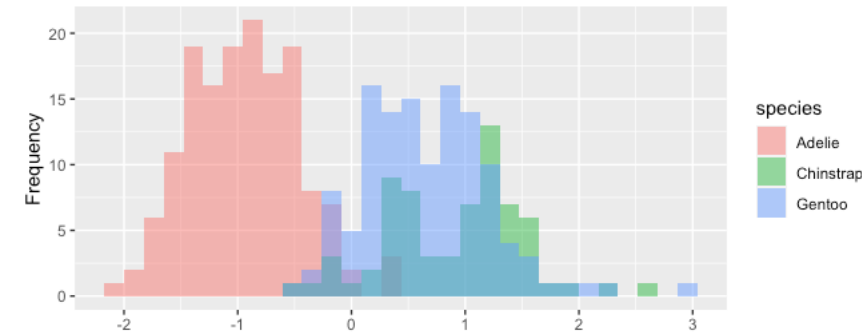
Penguin bill lengths



mean = 43.92
sd = 5.49

$$Z = \frac{x_i - \mu}{\sigma}$$

Penguin bill lengths Z transform, mean, sd



Data pre-processing. Feature engineering

Adjusting data without tampering with signal

Adjusting data without tampering with signal

Expression ranges and One-hot encoding

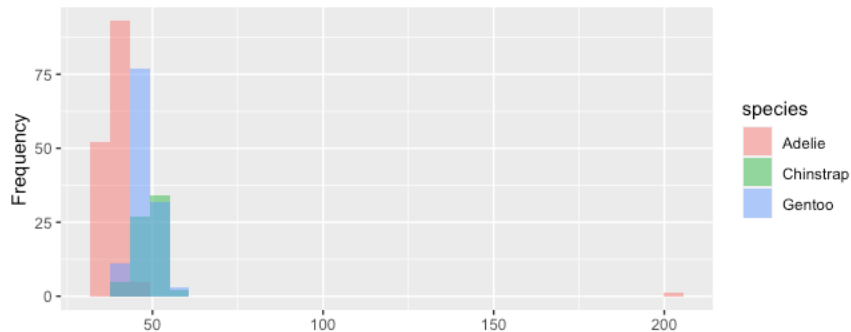
Standardisation vs scaling

Near zero variance

Multi-collinearity

Dimensionality reduction

Penguin bill lengths with outlier

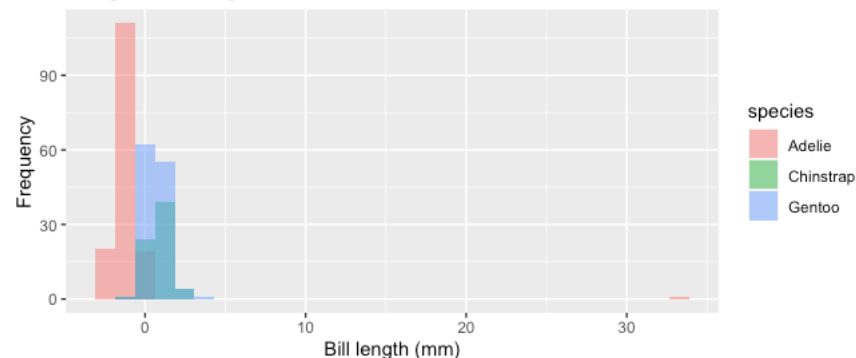


mean = 43.92
sd = 5.49

mean_o = 44.39
sd_o = 10.04

median = 44.45
median_o = 44.5
MAD = 4.7

Penguin bill lengths Z transform, median, MAD, outlier



$$Z = \frac{x_i - \mu}{\sigma}$$

Mean and sd can be influenced by outliers.

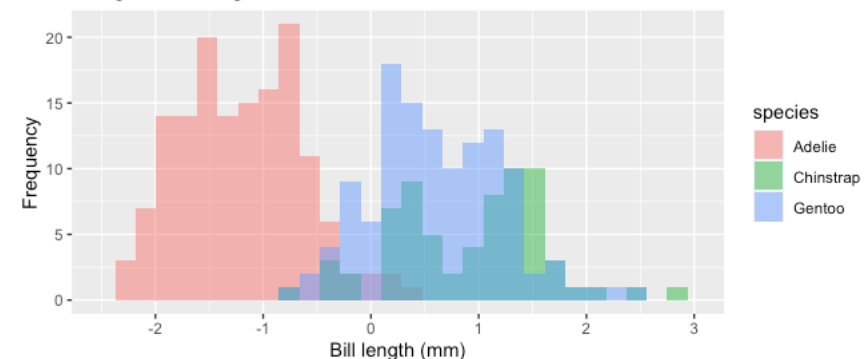
Median, MAD are more robust

MAD = median absolute deviation

$$Z_{med} = \frac{x_i - median}{MAD}$$

$$MAD = median(|x_i - median|)$$

Penguin bill lengths Z transform, median, MAD, outlier



Data pre-processing. Feature engineering

Adjusting data without tampering with signal

Adjusting data without tampering with signal

Expression ranges and One-hot encoding

Standardisation vs scaling

Near zero variance

Multi-collinearity

Dimensionality reduction

species		island		sex		year
Adelie	:152	Biscoe	:168	female:	165	2007:110
Chinstrap:	68	Dream	:124	male	:168	2008:114
Gentoo	:124	Torgersen:	52	NA's	: 11	2009:120

Briscoe	1		Briscoe	100
Dream	2	→	Dream	010
Torgersen	3		Torgersen	001

The island feature is difficult to handle in a numerical setting.

[longitude and latitude]

[distance from the POI]

Do we want to compare classes or use them in a static way?

Hamming (Edit) distances

Briscoe	100
Dream	010

Briscoe	100
Torgersen	001

Data pre-processing. Feature engineering

Adjusting data without tampering with signal

Adjusting data without tampering with signal

Expression ranges and One-hot encoding

Standardisation vs scaling

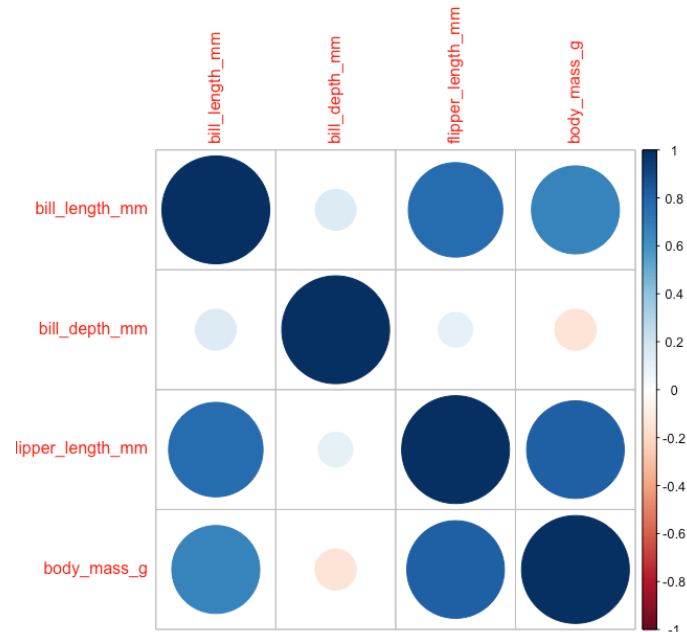
Near zero variance

Multi-collinearity

Dimensionality reduction

The near zero variance protects against constant features.

	freqRatio	percentUnique	zeroVar	nzv
species	1.226891	0.9009009	FALSE	FALSE
flipper_length_mm	1.235294	16.2162162	FALSE	FALSE
body_mass_g	1.200000	27.9279279	FALSE	FALSE
sex.female	1.018182	0.6006006	FALSE	FALSE
sex.male	1.018182	0.6006006	FALSE	FALSE



There are no issues on near zero variance.

The maximum correlation is 0.76 between bill and flipper length.

Highly correlated features:

[a] could be excluded

[b] could be replaced with

a representative

a weighted summary

Data pre-processing. Feature engineering

Adjusting data without tampering with signal

Adjusting data without tampering with signal

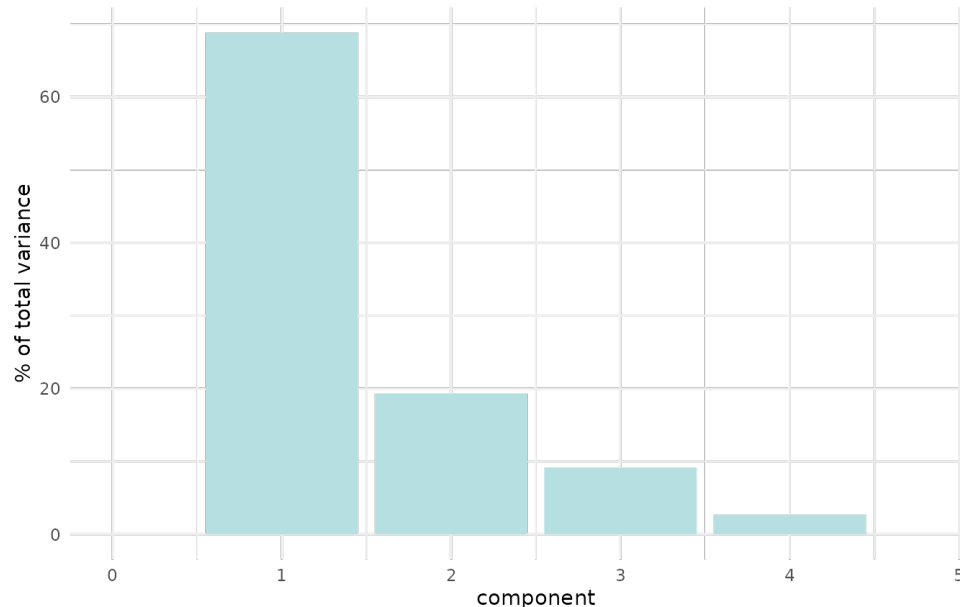
Expression ranges and One-hot encoding

Standardisation vs scaling

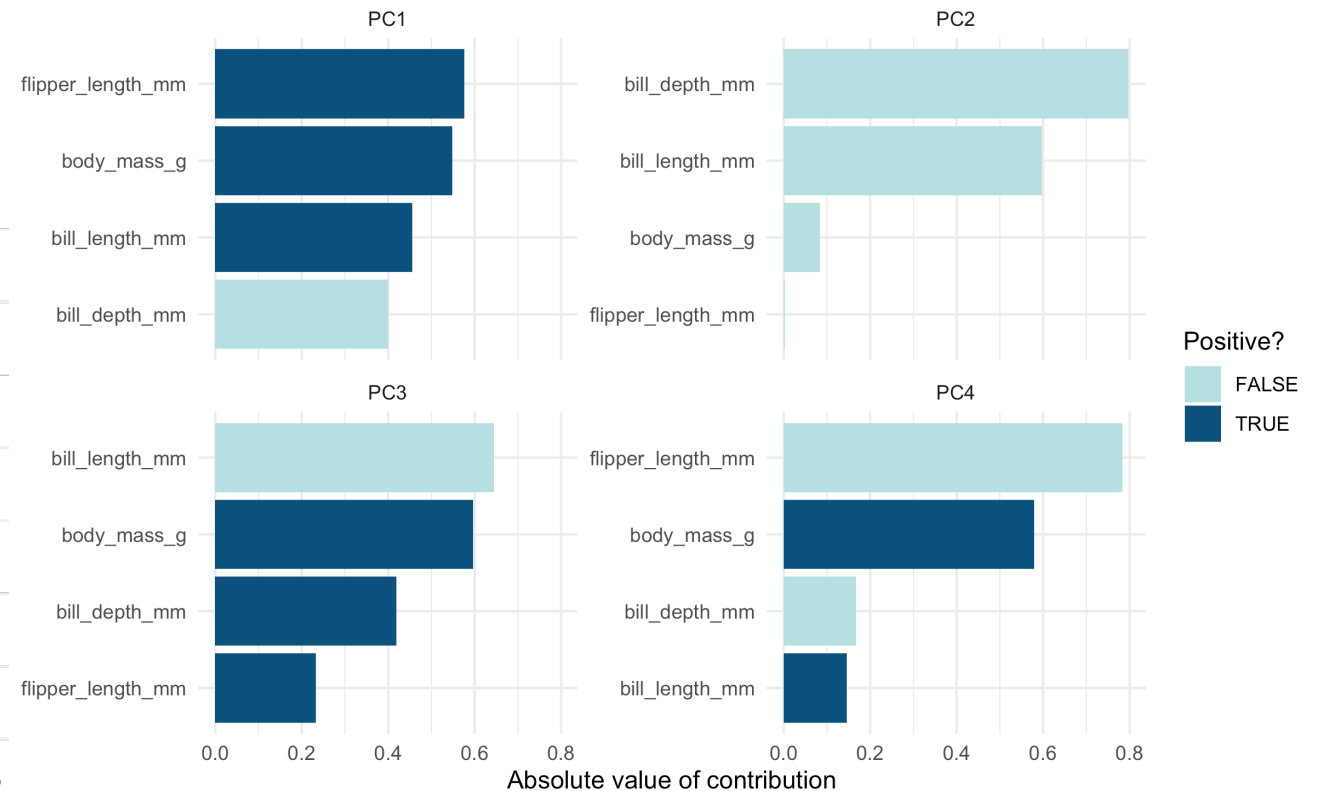
Near zero variance

Multi-collinearity

Dimensionality reduction



Yet another angle of linear combination of features is:
Principal Component Analysis (very briefly presented)



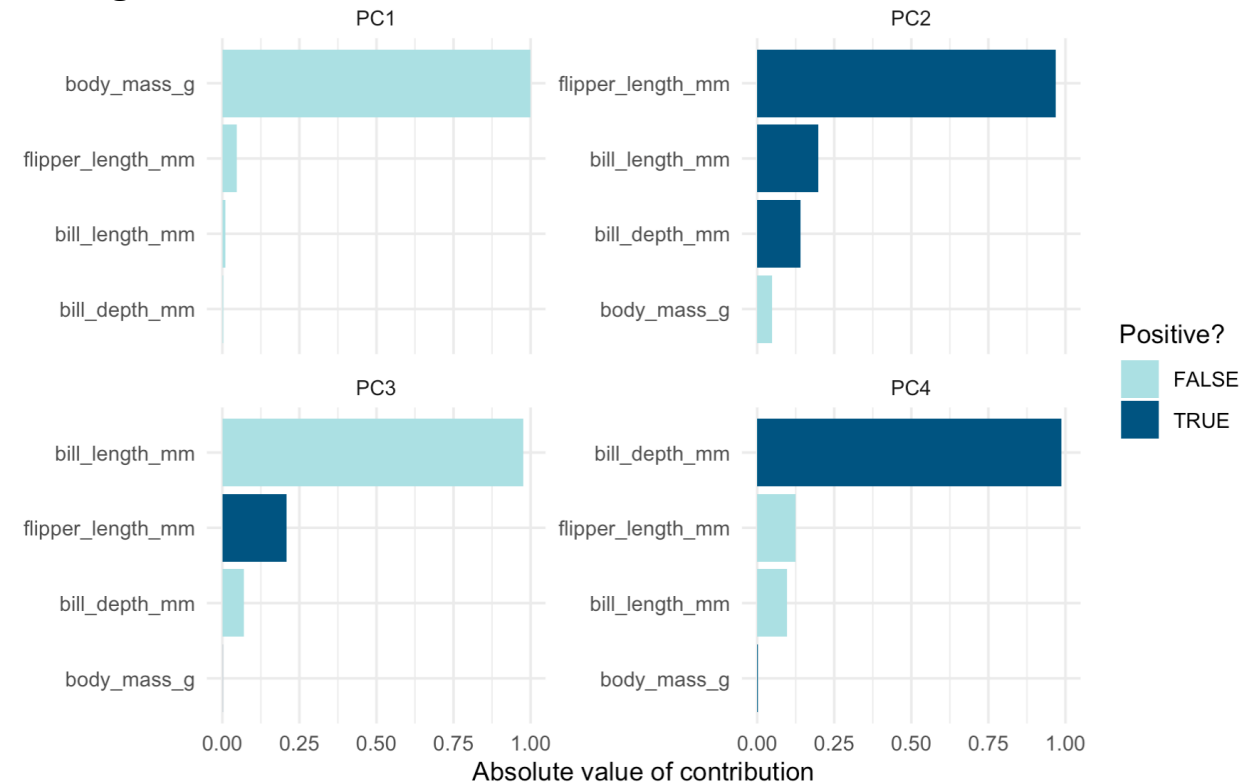
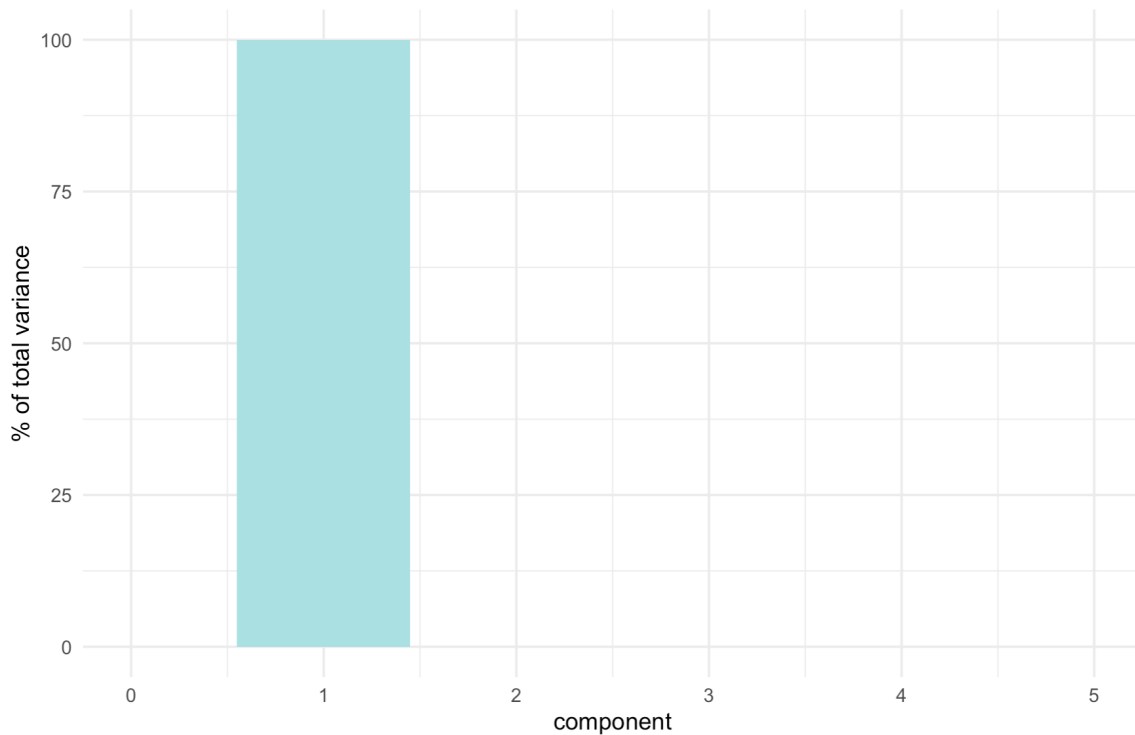
Data pre-processing. Feature engineering

Adjusting data without tampering with signal

The PCAs rely on computing eigenvalues and the respective eigenvectors.

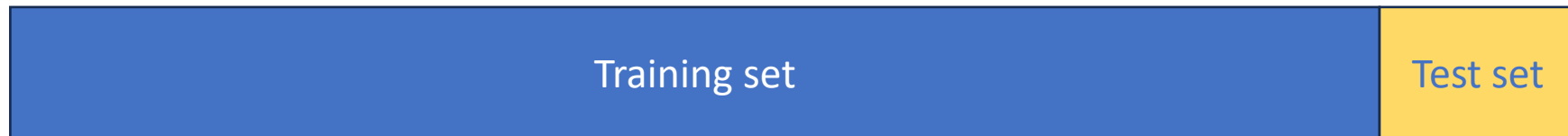
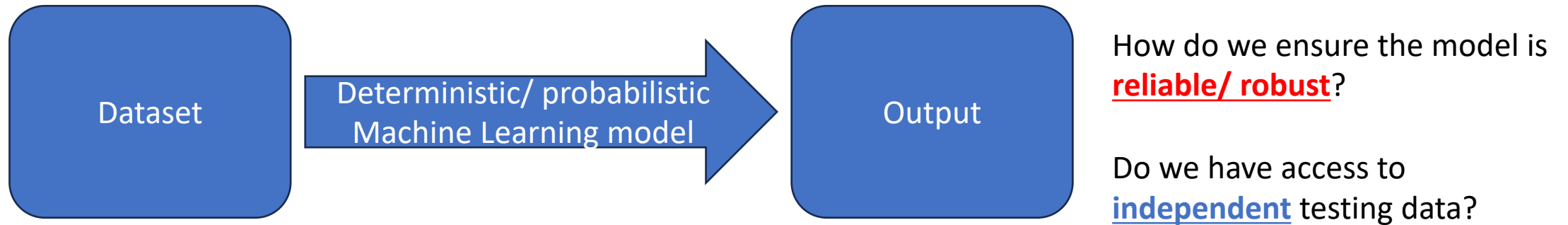
The PCs are linear combinations of features.

Not scaling and centering the features only underlines the magnitude of the features.



Data pre-processing. Feature engineering

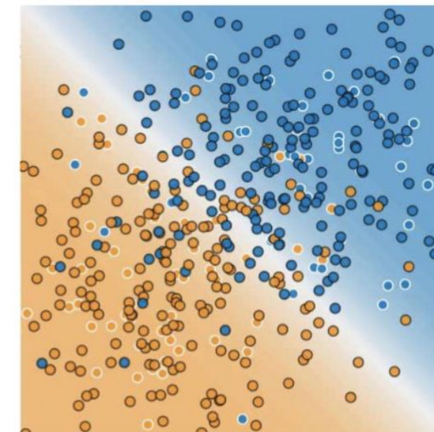
Model robustness.



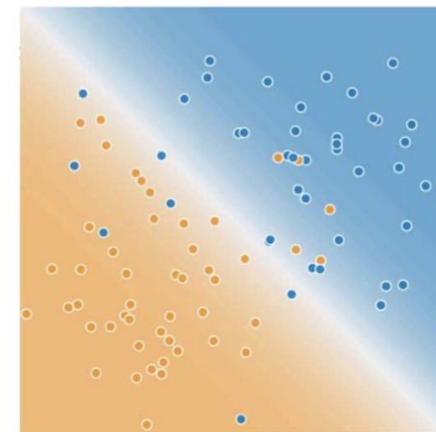
Proportion of training/ test split

To ensure robustness (and optimize the model) – we perform this split several times.

The test set should act an independent evaluation of the model



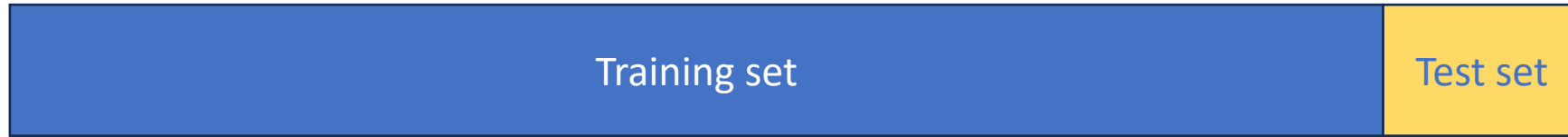
Training Data



Test Data

Data pre-processing. Feature engineering

Model robustness.



Assumptions for the training/ validation/ test sets

[a] we draw the samples **independently and identically** (*iid*) at random from the distribution

[b] the sets are **disjunct** partitions of the original distribution

i.e. no entries from the the training set will be found in the test set and vice versa

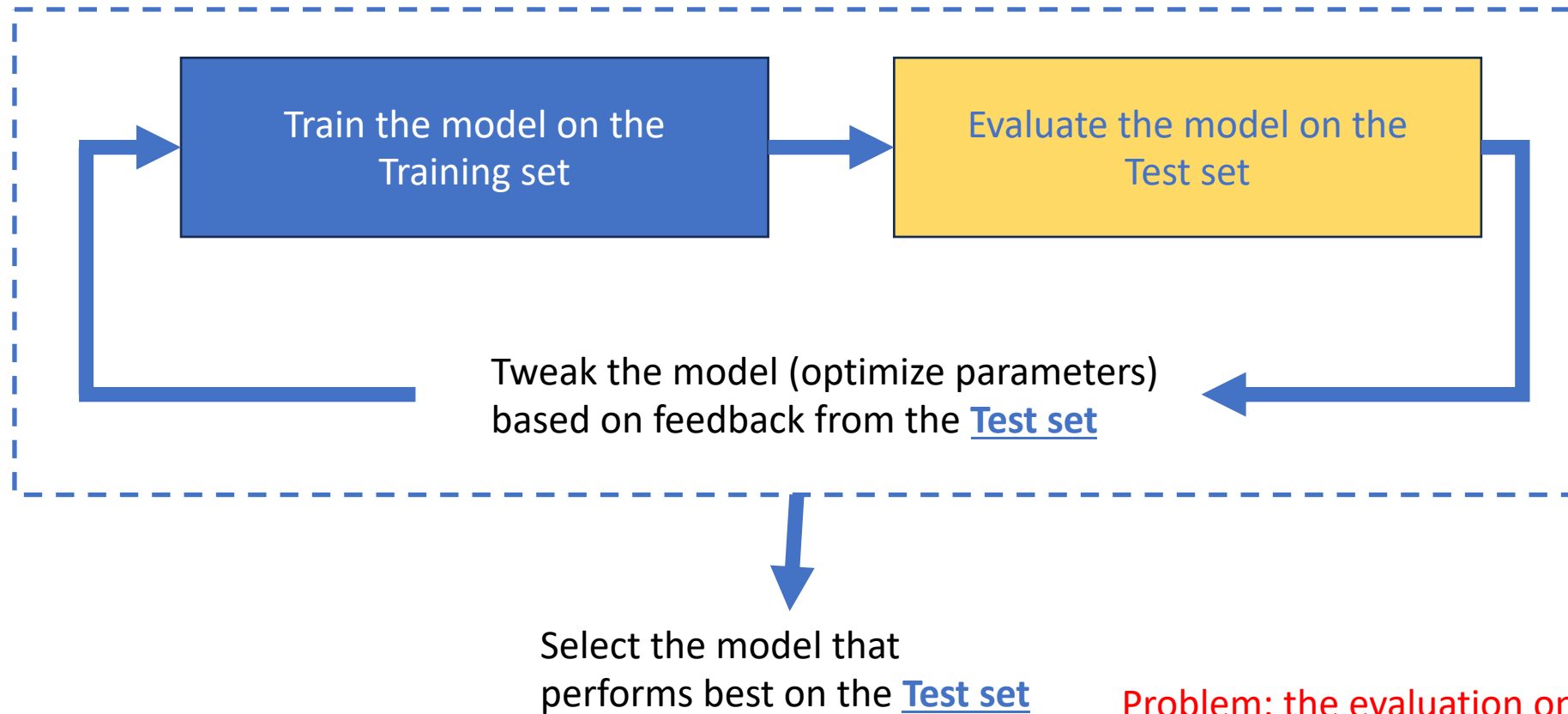
[c] the size of the validation and test sets should be comparable (if not identical)

The validation set should be large enough to detect differences between models

If classifier A has an accuracy of 95% and classifier B has an accuracy 95.1% then a validation set of 100 entries would not be sufficient/ able to detect the 0.1% difference.

A validation set with 1000 – 10000 entries might detect the improvement of 0.1%

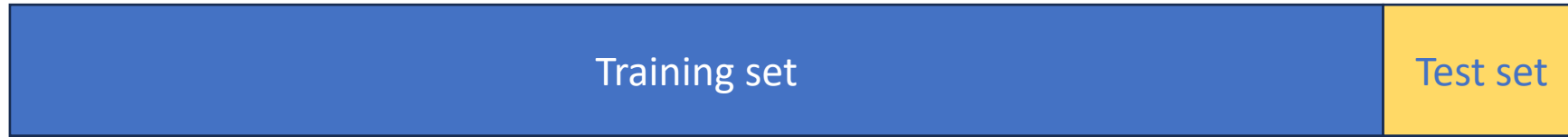
Data pre-processing. Feature engineering Model robustness.



Problem: the evaluation on the test set, after the model was optimized, is no longer unbiased (self-fulfilling prophecy).

Data pre-processing. Feature engineering

Model robustness.



Assumptions for the training/ validation/ test sets

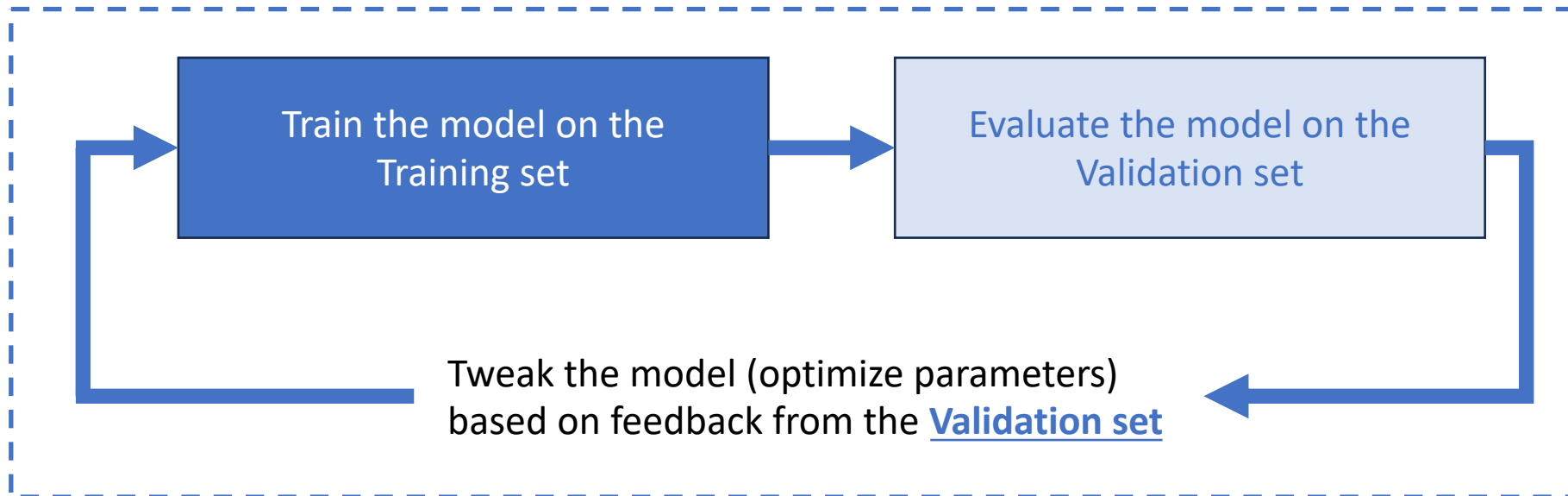
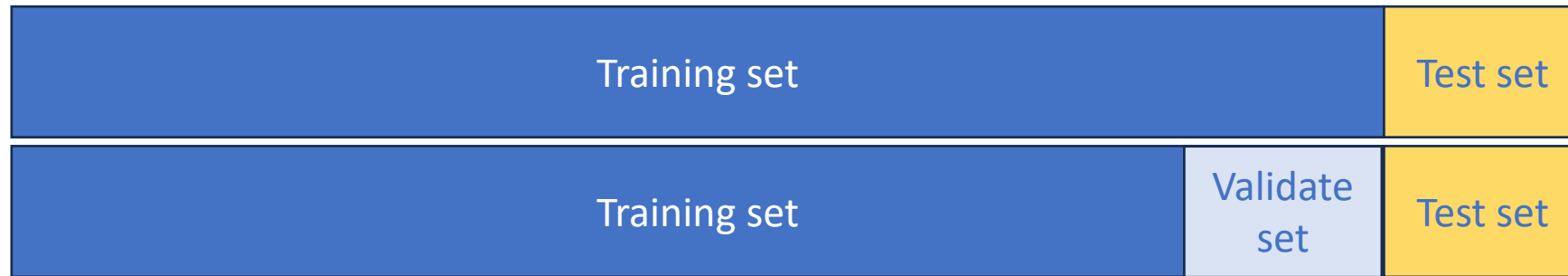
[d] on the test set, the error between the prediction and the actual label is the **test error**

[e] the **objective function** of the algorithm minimizes the test errors by **parameter tuning**

[f] Models are further evaluated for **Bias** and **Variance** (assessment of overfitting/ underfitting)

Data pre-processing. Feature engineering

Model robustness.



Select the model that performs best on the Validation set

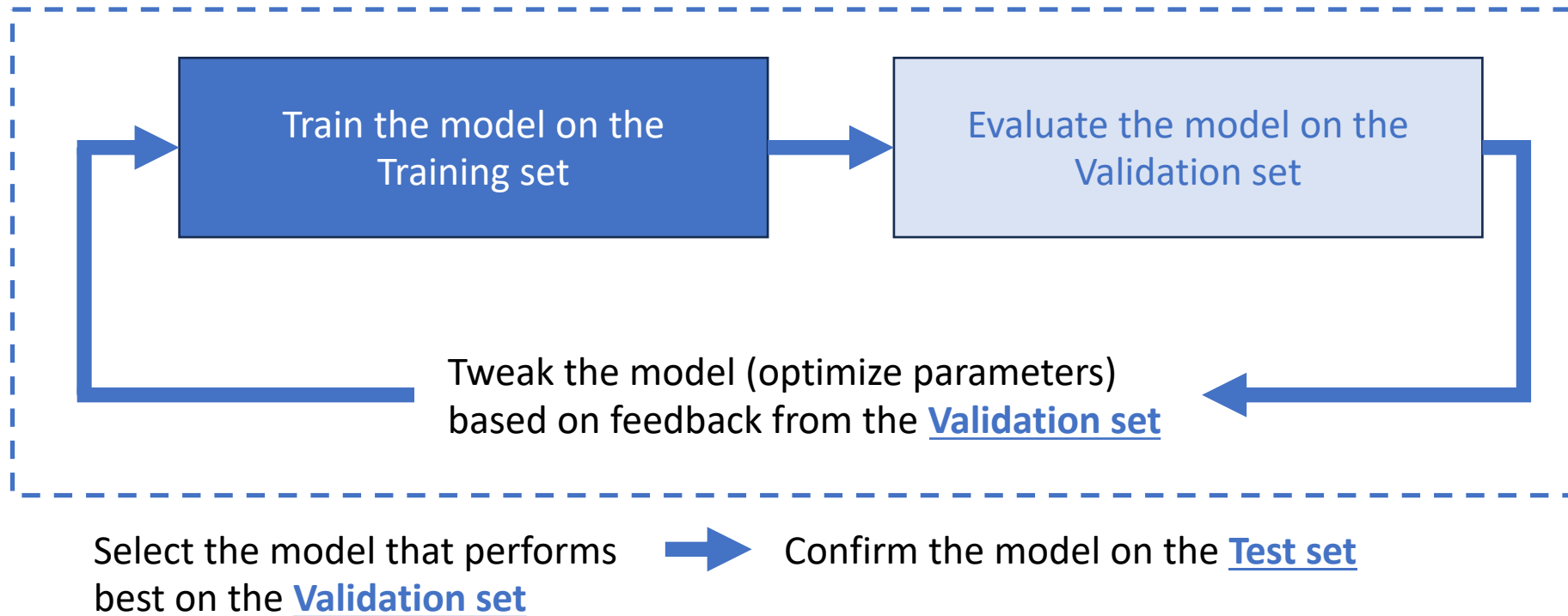


Confirm the model on the Test set

Advantage: the test set is uncorrupted and the evaluation is unbiased

Data pre-processing. Feature engineering

Cross validation.



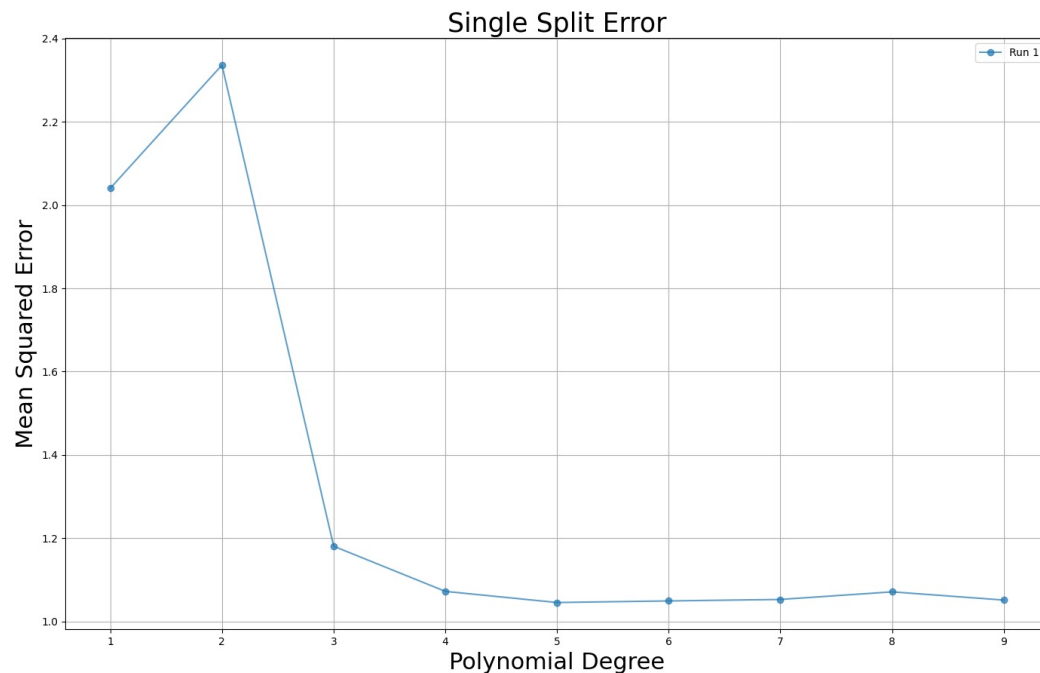
A systematic approach would rely on cross validation.

Data pre-processing. Feature engineering

Cross validation.



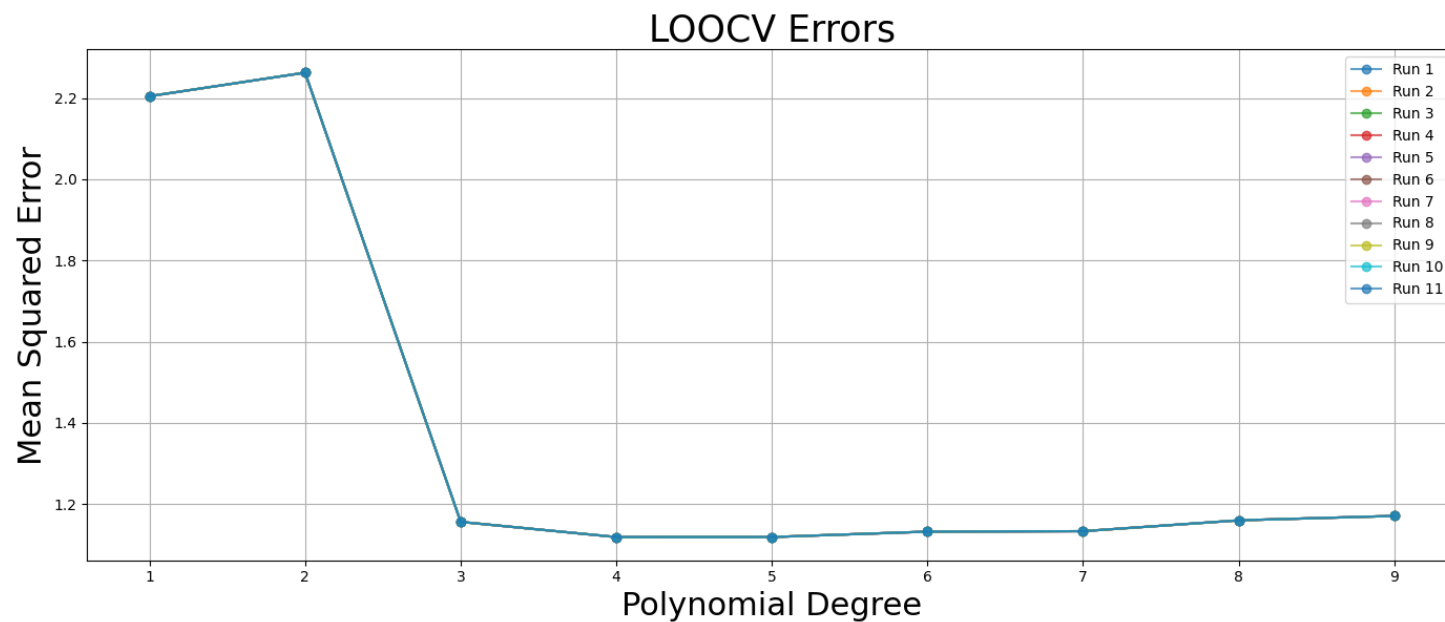
Task: infer a function that models the output wrt the input.



Data pre-processing. Feature engineering

Cross validation.

Leave on out CV separates one entry at a time.



A validation on one entry is meaningless.
The validation set is too small.

Data pre-processing. Feature engineering
Cross validation.

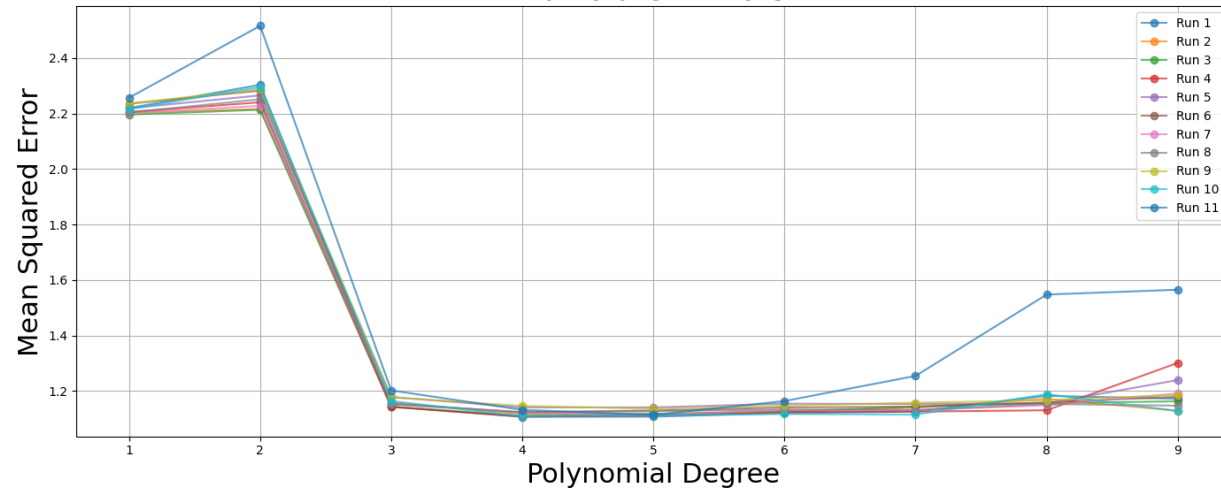
In:



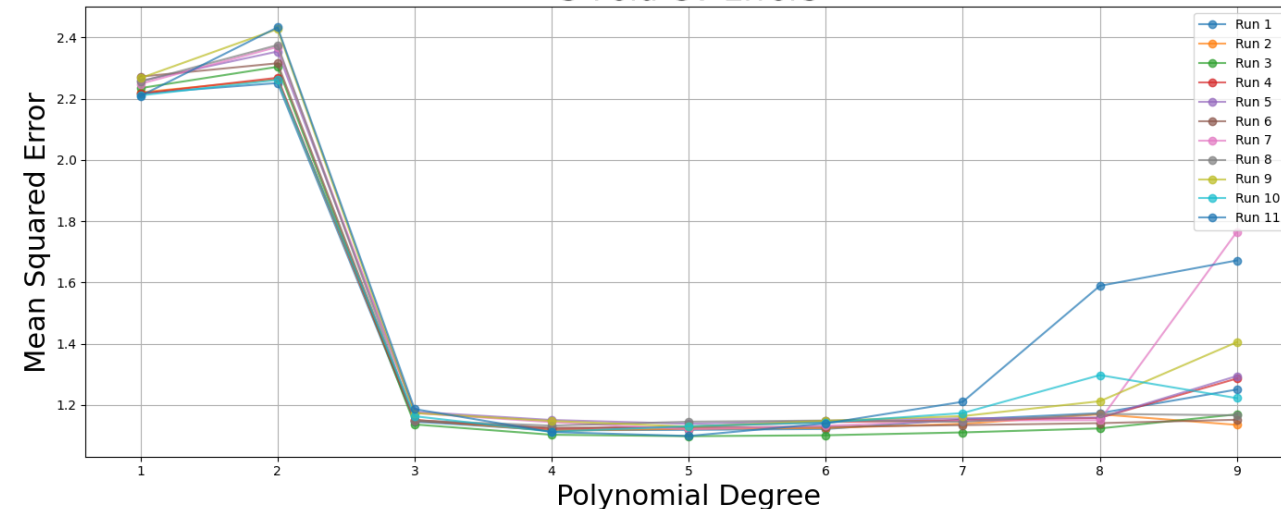
Out:



10-Fold CV Errors



5-Fold CV Errors



Data pre-processing. Feature engineering

Cross validation. Evaluation

		Predicted condition	
		Predicted condition positive (PP)	Predicted condition negative (PN)
Actual Condition	Total population = P + N		
	Actual condition positive (P)	True positive (TP)	False negative (FN) – Type II error
	Actual condition negative (N)	False positive (FP) – Type I error	True negative (TN)

Remarks

[a] we don't always have access to all information

e.g. the true negative set might be unknown

e.g. the false negative set might be unknown

[b] always strive to assess the model from multiple angles
i.e. don't rely solely on one value such as accuracy.

[c] multiple class classification can be simplified to a 2x2 table

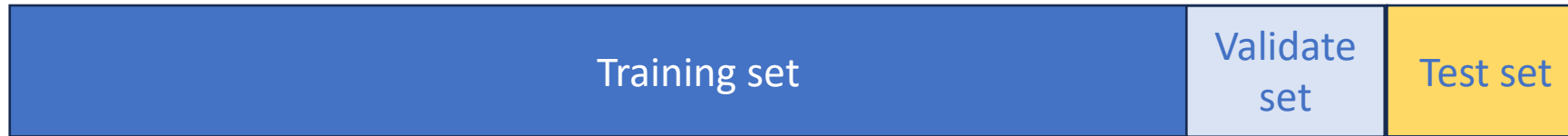
Data pre-processing. Feature engineering

Cross validation. Evaluation

		Predicted condition			
Total population = P + N		Predicted condition positive (PP)	Predicted condition negative (PN)	Bookmaker informedness (BM) $= TPR + TNR - 1$	Prevalence threshold (PT) $= \frac{\sqrt{TPR \times FPR} - FPR}{TPR - FPR}$
Actual Condition	Actual condition positive (P)	True positive (TP)	False negative (FN) – Type II error	True positive rate (TPR) – recall – sensitivity (SEN), power $= \frac{TP}{P} = 1 - FNR$	False negative rate (FNR) $= \frac{FP}{P} = 1 - TPR$
	Actual condition negative (N)	False positive (FP) – Type I error	True negative (TN)	False positive rate (FPR) $= \frac{FP}{N} = 1 - TNR$	True negative rate (TNR), specificity (SPC) $= \frac{TN}{N} = 1 - FPR$
Prevalence $= \frac{P}{P+N}$		Positive predictive value (PPV), precision $= \frac{TP}{PP}$ $= 1 - FDR$	Negative predictive value (NPV) $= \frac{TN}{PN}$	Positive likelihood ratio (LR+) $= \frac{TPR}{FPR}$	Negative likelihood ratio (LR-) $= \frac{FNR}{TNR}$
Accuracy (ACC) $= \frac{TP+TN}{P+N}$		F1 score $= \frac{2TP}{2TP+FP+FN}$	False discover rate (FDR) $= \frac{FP}{PP}$ $= 1 - PPV$		Threat score (TS), critical success index (CSI) $= \frac{TP}{TP + FN + FP}$

Data pre-processing. Feature engineering

Cross validation. Evaluation



Sources of error in ML: bias and variance

Bias: the model's error rate on the training set

Variance: the model's error rate on the validation (or test) set, in addition to the bias

Training error: 0.5% [bias]

Validation error: 1% (variance = 0.5%)

Perfect model

Training error: 1% [bias]

Validation error: 11% (variance = 10%)

Overfitting – learning signal and noise

Training error: 15% [bias]

Validation error: 16% (variance = 1%)

Underfitting – learning some signal

Training error: 15% [bias]

Validation error: 30% (variance = 15%)

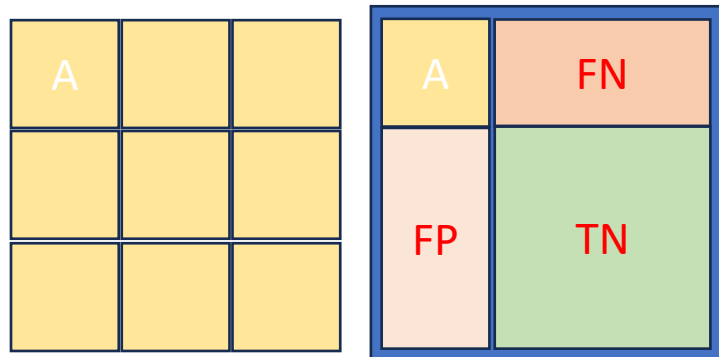
High bias, high variance

Model unlikely suitable for the data.

Data pre-processing. Feature engineering

Evaluation. Confusion Matrices

Prediction	Reference		
	Adelie	Chinstrap	Gentoo
Adelie	36	10	0
Chinstrap	7	10	0
Gentoo	0	0	35



2x2 confusion matrix for species: Adelie

	Predicted Positive	Predicted Negative
Actual Positive	36	7
Actual Negative	10	45

2x2 confusion matrix for species: Chinstrap

	Predicted Positive	Predicted Negative
Actual Positive	10	10
Actual Negative	7	71

2x2 confusion matrix for species: Gentoo

	Predicted Positive	Predicted Negative
Actual Positive	35	0
Actual Negative	0	63

Data pre-processing. Feature engineering

Evaluation. Confusion Matrices

	Adelie	Chinstrap	Gentoo
prevalence	0.4387755	0.2040816	0.3571429
accuracy	0.8265306	0.8265306	1
F1	0.8089888	0.5405405	1
PPV	0.7826087	0.5882353	1
NPV	0.8653846	0.8765432	1
FDR	0.7826087	0.5882353	1
TPR	0.8372093	0.5	1
FPR	0.1818182	0.08974359	0
FNR	0.2325581	0.35	0
TNR	0.8181818	0.9102564	1
BM	0.6553911	0.4102564	1
LR_pos	4.604651	5.571429	Inf
LR_neg	0.2842377	0.384507	0
PT	0.3178796	0.2975847	0
TS	0.6792453	0.3703704	1

	Reference		
Prediction	Adelie	Chinstrap	Gentoo
Adelie	36	10	0
Chinstrap	7	10	0
Gentoo	0	0	35

Note: check slide 28 for calculations

Statistics for a 2x2 confusion matrix - Adelie

		Predicted condition			
		Predicted condition positive (PP)	Predicted condition negative (PN)	Bookmaker informedness (BM)	Prevalence threshold (PT)
Total population = P + N				0.66	0.32
Actual Condition	Actual condition positive (P)	True positive (TP) 36	False negative (FN) – Type II error 7	True positive rate (TPR) – recall – sensitivity (SEN), power 0.84	False negative rate (FNR) 0.23
	Actual condition negative (N)	False positive (FP) – Type I error 10	True negative (TN) 45	False positive rate (FPR) 0.18	True negative rate (TNR), specificity (SPC) 0.82
Prevalence 0.43		Positive predictive value (PPV), precision 0.78	Negative predictive value (NPV) 0.87	Positive likelihood ratio (LR+) 4.6	Negative likelihood ratio (LR-) 0.28
Accuracy (ACC) 0.83		F1 score 0.81	False discover rate (FDR) 0.21		Threat score (TS), critical success index (CSI) 0.68

Data pre-processing. Unbalanced data. Sampling?

It can be a struggle to gather enough balanced data for a machine learning project.

Examples of issues:

Negative examples are easier to sample than positive ones.

e.g. negative examples of galaxies outweigh the number of positive/ confirmed examples

Another angle: not all galaxies that exist were identified [*we don't know what we don't*]

The intrinsic structure of the data confounds classes

e.g. on classes A, B, C driven by the features of the data,

Class A comprises only positive examples, Class B comprises a 20/80 mix, Class C comprises a 50/50 mix

Down sampling = extracting a number of entries from the larger class

Up weighting = adding weights to entries, essentially repeating them.

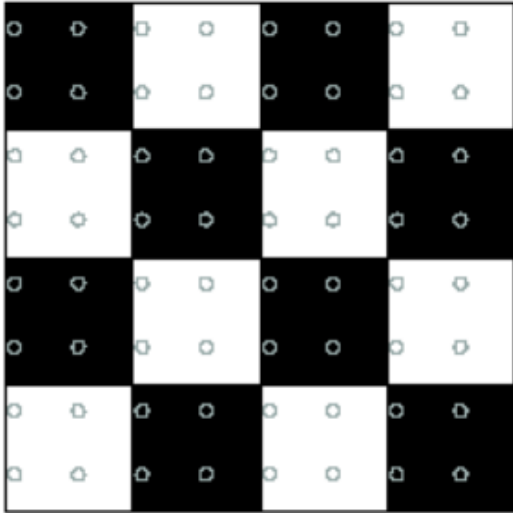
Issues:

The resulting dataset must recapitulate the properties of the original dataset. [Invariance requirement]

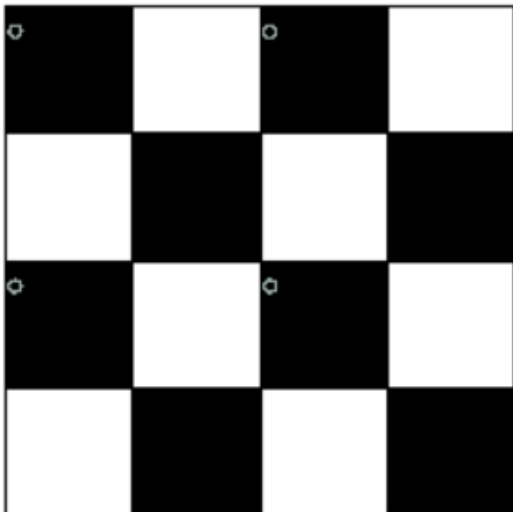
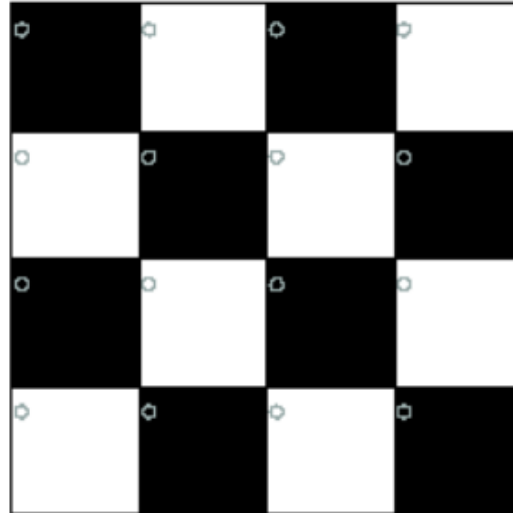
In particular cases, a middle ground between down sampling and up weighting works better.

Data pre-processing. Unbalanced data.

Sampling?

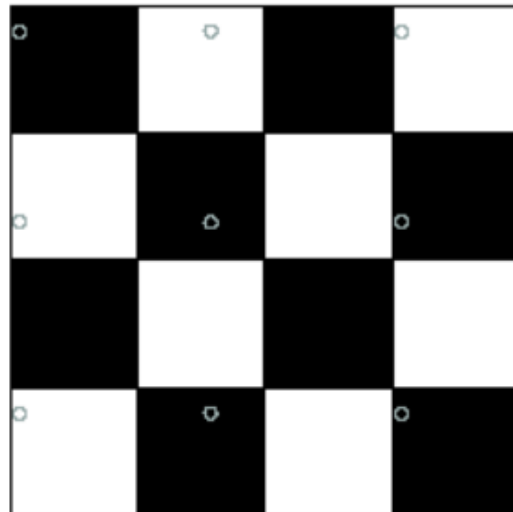


Good sampling



Bad sampling

i.e. non representative



The Nyquist–Shannon sampling theorem is an essential principle for digital signal processing linking the frequency range of a signal and the sample rate required to avoid a type of distortion called **aliasing**.

The theorem states that the sample rate must be at least twice the bandwidth of the signal to avoid aliasing distortion.

In practice, it is used to select band-limiting filters to keep aliasing distortion below an acceptable amount when an analog signal is sampled or when sample rates are changed within a digital signal processing function.

For generic distributions, test such as the Kullback-Leiber divergence (per classes or using a binning approach for continuous data) are frequently used.

Next Lecture ...

Applied Data Science
L3. Data Science toolkit. Part 1