**CSC3060 AIDA – Assignment 3**

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# Introduction

In this document, please replace [StudentNumber], [FNAME], etc, with the appropriate values. The FirstNme and LastName on the report should match your first name and lastname as it appears on QOL and QSIS.

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# Section 1

## Introduction

In this section, feature data from assignment 2 (Liu, 2019) will be used for analysis. It contains data of 20 features regarding 80 living objects and 80 non-living objects. Hypothesis test, building classifier with different features will be performed in this section.

The description of each task in section 1 includes objective, assumption (if applicable), reasoning, implementation and result.

## R script

### Overview

The R script for this section is divided into six parts.

The first part is the function setups which defines some basic functions and loads essential R libraries.

Each of the rest five parts represents a task in section 1, representatively. At the beginning of each task, the function *start\_task <- function(task\_number)* is called, where data are loaded and environment variables (e.g. feature data, seed value for randomness, output directory) are set up. At the end of each task, the function *finish\_task <- function(task\_number, reserved\_varialbes = c())* is called, where environment variables are destroyed except those stated in the parameter *reserved\_varialbes*. This ensures that each task is isolated to others, so that the implementation of any task will not affect the implementation and output of its following tasks (especially for procedures with elements of randomness). It also helps the evaluation of the R script and this report easier.

### Usage

#### Prerequisites

1. R (R Core Team, 2019) is installed on your machine
2. R library (Team, 2019) YAML and GGPLOT2 are installed.

#### Execution

The current working directory should be the same as the R script

Execute the following command.

#### Outputs

All outputs (e.g. figures, tables) of the execution will be saved at where it contains subfolders named as (e.g. ).

## Task 1.1

### Objective

The objective of this task is to differentiate living and non-living things using the feature verticalness.

### Assumption

The critical p-value is set as

### Reasoning

Logistic Regression (LR) will be used as a method in the analysis. LR uses the Sigmoid function (Equation 1), and as a result, it produces values between 0 and 1 (Chandrayan, 2019).

Equation 1 Logistic Regression (Devereux, 2019)

Since the objects are needed to be classifies into two classes, we can set a cut-off value. If the LR model produces a value which is greater than the cut-off value, the object will be identified as a class. Otherwise, it will be identified as the opposite class.

### Implementation

The data frame with two columns verticalness and living is constructed. The values in the column living are Boolean values indicating if the observation is a living thing.

The data then is fit into the LR models. By interpreting the result of the trained model, we can decide if the feature verticalness is a sufficient feature to differentiate living and non-living things.

### Result

The summary of the data fitted into the model is as Table 1.

verticalness living

Min. :0.07534 Min. :0.0

1st Qu.:0.36631 1st Qu.:0.0

Median :0.50616 Median :0.5

Mean :0.51907 Mean :0.5

3rd Qu.:0.61048 3rd Qu.:1.0

Max. :1.27027 Max. :1.0

Table 1 Summary of verticalness ~ logistic living value data

After fitting the model, the result of the model is as Table 2.

Call:

glm(formula = living ~ verticalness, family = "binomial", data = data)

Deviance Residuals:

Min 1Q Median 3Q Max

-1.23105 -1.16944 0.00095 1.17767 1.19216

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) -0.08656 0.37516 -0.231 0.818

verticalness 0.16676 0.65547 0.254 0.799

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 221.81 on 159 degrees of freedom

Residual deviance: 221.74 on 158 degrees of freedom

AIC: 225.74

Number of Fisher Scoring iterations: 3

Table 2 Result of Linear Regression Model

For the Intercept value in the table, the estimate is , which means the model predicts the value of living is given the verticalness value is 0. The z-score is , which is calculated as . It shows the estimate is standard error away from 0. According to the z-score and the degrees of freedom value, p-value of this variable is calculated to be which is larger than the critical p-value. We consider rejecting the hypothesis that intercept value is differ from 0.

For the verticalness value in the table, the estimate is , which means if the verticalness value increases by 1 unit, the predicted value of living will be increased by 0.16676 unit. The z-score is , which is calculated as . It shows the estimate is standard error away from 0. According to the z-score and the degrees of freedom value, p-value of this variable is calculated to be which is larger than the critical p-value. Thus, for the hypothesis, we stick on the hypothesis that the slope value of verticalness value is equal to 0.

According to the result of the model, the coefficient of the estimates of the intercept and verticalness is and , respectively, which derives the Equation 2 and Figure 1.

Equation 2 LR Model

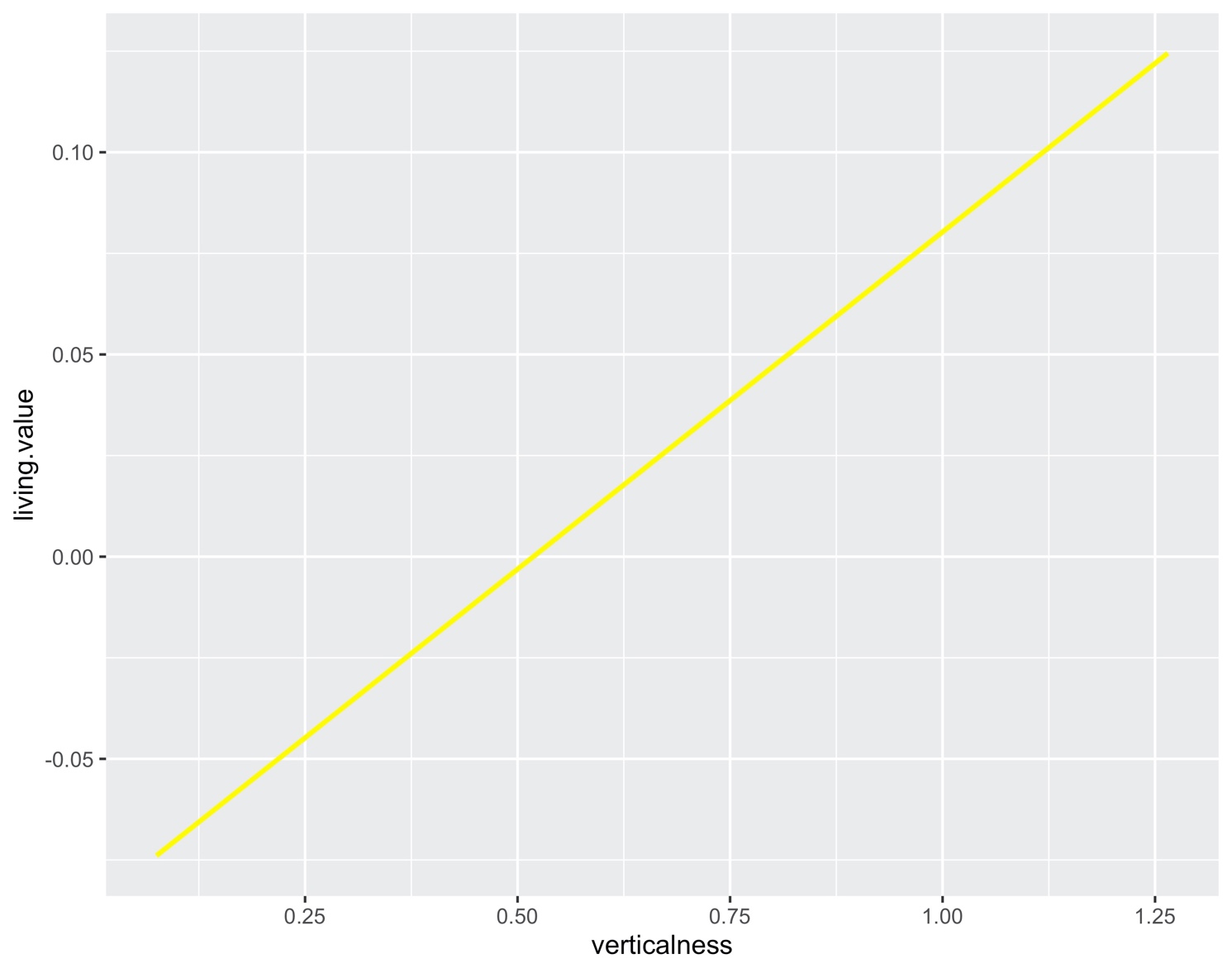


Figure 1 Regression Line living.value ~ verticalness value

## Task 1.2

### Objective

The objective of this task is to create a classifier to differentiate living objects.

### Reasoning

To create the classifier, we need to draw plots to visualise the data, and see how they are distributed according to the verticalness values.

### Implementation

We first draw a histogram to visualise the verticalness distributions of living and non-living objects (Figure 2). We can see there are more living objects with verticalness values between 0.375 and 0.75. However, they do not have clear separation on the feature verticalness.

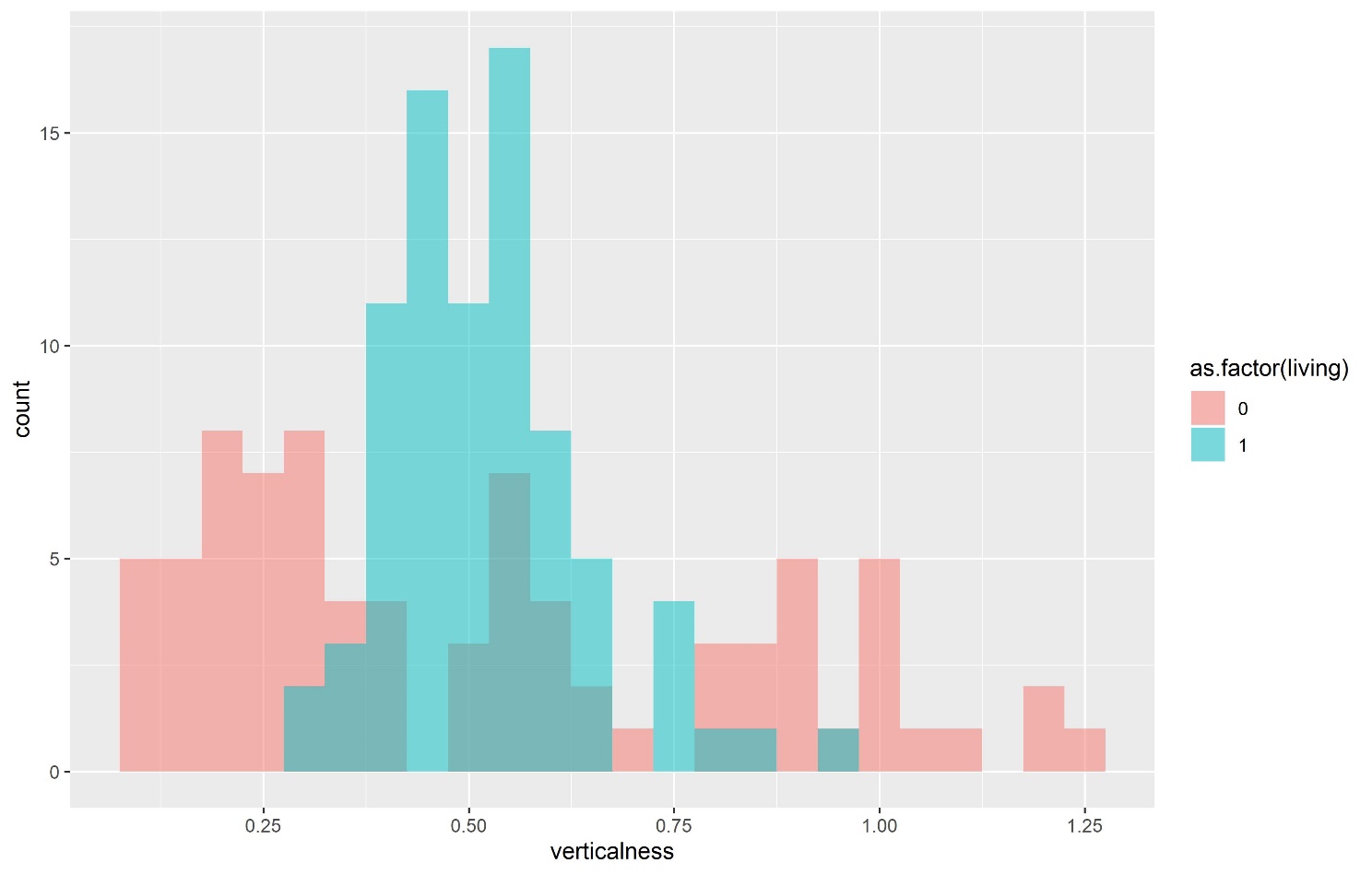


Figure 2 Histogram verticalness distribution

We then plot the training data points and a fitted curve (Figure 3). We can see the slop of the fitted curve is too horizontal, which means there is no strong correlation between these two variables, and it is hard to get valuable information from this figure.

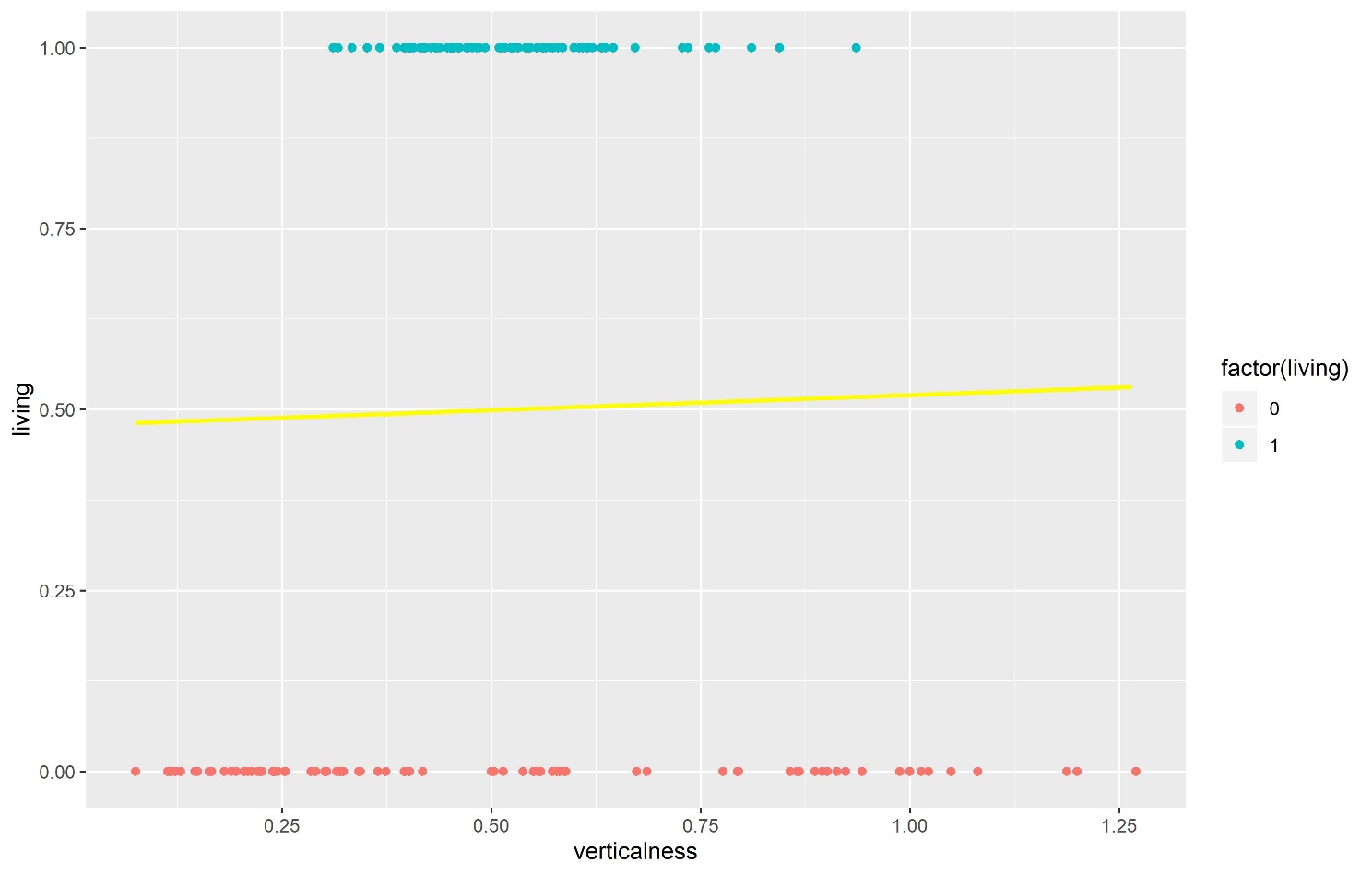


Figure 3 Veticalness ~ living: training data and fitted curve

It is hard to observe in Figure 3, but from Figure 2, we consider observations with verticalness value greater than 0.375 or higher to be living objects. We calculate the cut-off point of the P(X) using the formula.

And we got the cut-off value.

The observations with predicted value higher than the cut-off value are classified as living objects.

### Result

The result of the prediction is Table 3 showing 112 predictions were correct while 48 were incorrect. Thus, we got 70% correctness for this classifier for the data provided.

Mode FALSE TRUE

logical 48 112

Table 3 Summary of Correct Predictions

However, the accuracy of 70% is valid only on the dataset of 160 objects provided. The accuracy does not represent the performance of the model on other objects that were not included in the model.

## Task 1.3

### Objective

The objective of this task is to find three features to build a classifier for living and non-living objects, using logistic regression and cross-fold validation.

### Reasoning

To choose three best features for the prediction, we need to analyse the correlated between each feature and the dependant valuable . We decide to use Backward Elimination of p-value approach (Geeksforgeeks, 2019) to select these three features.

Then we use 5-fold cross validation (Drakos, 2018) to fit the data of these three features into the training model and validate the result.

### Implementation

As we only need three features as training data, we need to drop 17 features from the dataset. First, the whole dataset with 20 features is used to fit a linear regression model, and we the model as Table 4.

Call:

lm(formula = living ~ ., data = data)

Residuals:

Min 1Q Median 3Q Max

-0.48298 -0.12907 -0.03498 0.13070 0.62125

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 2.525808 0.399713 6.319 3.34e-09 \*\*\*

nr\_pix -0.006279 0.004907 -1.280 0.20274

height 0.031369 0.009815 3.196 0.00173 \*\*

width 0.002565 0.010945 0.234 0.81506

span -0.040148 0.012969 -3.096 0.00237 \*\*

rows\_with\_5 0.007338 0.011688 0.628 0.53116

cols\_with\_5 0.032590 0.013372 2.437 0.01606 \*

neigh1 0.028496 0.025410 1.121 0.26403

neigh5 -0.007424 0.003995 -1.859 0.06521 .

left2tile -0.005431 0.009683 -0.561 0.57576

right2tile 0.024086 0.009498 2.536 0.01232 \*

verticalness -2.232424 0.375564 -5.944 2.13e-08 \*\*\*

top2tile -0.019631 0.009364 -2.096 0.03785 \*

bottom2tile 0.004558 0.008000 0.570 0.56977

horizontalness 0.659220 0.595643 1.107 0.27032

concentration 0.004855 0.003972 1.222 0.22362

crossness -0.009686 0.004555 -2.127 0.03522 \*

nr\_regions -0.350727 0.067510 -5.195 7.13e-07 \*\*\*

nr\_eyes -0.008960 0.019314 -0.464 0.64343

hollowness 0.128303 0.022039 5.822 3.86e-08 \*\*\*

straightness 0.002304 0.006160 0.374 0.70891

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.2255 on 139 degrees of freedom

Multiple R-squared: 0.8232, Adjusted R-squared: 0.7978

F-statistic: 32.36 on 20 and 139 DF, p-value: < 2.2e-16

Table 4 Twenty feature linear model

As we notice, the feature width has the highest p-value. Thus, the feature width is dropped in the first round.

This process is repeated 17 times, where 17 features will be dropped. The final model has three features left (i.e. height, span and hollowness) as Table 5.

Call:

lm(formula = living ~ ., data = data)

Residuals:

Min 1Q Median 3Q Max

-0.78708 -0.24913 -0.03218 0.22489 0.81976

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 0.460969 0.327675 1.407 0.161

height 0.048335 0.004889 9.887 < 2e-16 \*\*\*

span -0.047716 0.006482 -7.361 9.8e-12 \*\*\*

hollowness 0.143571 0.012947 11.089 < 2e-16 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.3303 on 156 degrees of freedom

Multiple R-squared: 0.5746, Adjusted R-squared: 0.5664

F-statistic: 70.24 on 3 and 156 DF, p-value: < 2.2e-16

Table 5 Three feature linear model

To perform 5-fold cross validation, data is randomly split into five parts.

For the first fold, the data of parts 2, 3, 4 and 5 is used to fit the logistic regression model. The model then will be used to produce a predicted living value using the data in part 1. Setting cut-off point as 0.5, all objects with predicted living value greater than 0.5 is predicted as living objects, and vice-versa. The predictions are compared with the actually classification, so the correct rate is calculated for this fold.

This process is repeated five times, and the correct rates of these five folds are 0.84375, 0.9375, 0.90625, 0.90625 and 0.84375, respectively.

### Result

The overall correct rate is the average value of all of the above rates which is . It is considered as the good result as the model is correct in 88.75% of times on the dataset of 160 objects provided.

## Task 1.4

### Objective

The objective of this task is to judge if the model is effective compared with a random model.

### Assumption

It is assumed that the value of living satisfies binomial distribution, the signification p-value is 0.05.

### Reasoning

Since the value of living is either TRUE of FALSE, so that it satisfies the binomial distribution. The number of correct predictions of the model, the number of prediction and the correctness rate of a random model can be simulated, so we can perform the above hypothesis.

### Implementation

A random model is simulated that randomly predicts 50% of objects as living objects and the other 50% as non-living objects. The accuracy of this random model is calculated, which is 47.5% based on the dataset is provided.

Given 160 objects in the dataset, our model with accuracy of 88.75% can correctly predict objects.

Assuming , the possibility value (p-value) that we can observe the given correctness or higher is

### Result

The p-value is calculated as 0, which is less than the critical p-value, we reject and accept .

We can conclude that our model is more effective than a random model.

## Task 1.5

### Objective

Beyond the accuracy of the model, more details (i.e. how the model incorrectly classifies objects) will be analysed.

### Reasoning

Confusion Matrix (Dataschool, 2019) will be used for the analysis. It provides a detailed description of the performance of a classifier.

### Implementation

Confusion Matrix function is applied to the cross-validation result of 160 predictions saved in Task 1.3

### Output

The output is as Table 6.

Confusion Matrix and Statistics

Reference

Prediction 0 1

0 75 13

1 5 67

Accuracy : 0.8875

95% CI : (0.828, 0.9319)

No Information Rate : 0.5

P-Value [Acc > NIR] : < 2e-16

Kappa : 0.775

Mcnemar's Test P-Value : 0.09896

Sensitivity : 0.9375

Specificity : 0.8375

Pos Pred Value : 0.8523

Neg Pred Value : 0.9306

Prevalence : 0.5000

Detection Rate : 0.4688

Detection Prevalence : 0.5500

Balanced Accuracy : 0.8875

'Positive' Class : 0

Table 6 Confusion Matrix

(a) How often instances of each of the 4 living thing doodle types are incorrectly classified as “non-living”?

(b) How often instances of each of the 4 non-living thing doodle types are incorrectly classified as “living”?

The chance that the model incorrectly classifies living objects is much higher than that for non-living objects.

Also, it is spotted that if the model classifies an object as a living object, the chance that the object is actually living is higher than the average accuracy. Thus, if we are interested in finding out living objects among a group of objects, the model provides higher value than its accuracy of 88.75%.

# Section 2

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## Section 2.1

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# Section 3

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## Section 3.1

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# Conclusions

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