EDA

Niek Scholten

Acquiring the data

The CSV data is supplied by Edoardo Ferrante on Kaggle. This data was created using the Librosa package for Python. Librosa outputs the intensity of a certain tone at different time intervals from the provided sound file. The original songs are gathered from the Brittish Birdsong Dataset and processed using a Python script. This script is available from the author and explains how the data was transformed from sound files to numeric data points, but this script has a specific shortcoming that will hinder our ability to visualize it. It will be explained further in the data cleaning section, but in short it is an error that's made while sorting the data when the order is of absolute importance.

Each row in the dataset contains the chromogram data, spectral centroid data along with the genus and species name. The structure for chromogram data is made up from values ranging from zero to one. These values represent the intensity of different tones at a certain time in the audio fragment. 1 is loudest/clearest and 0 is silent/non-distinguishable.

Name of datapoint	Description
chromogram_0_0	Tone intensity for B at time 0
chromogram_1_0	Tone intensity for A# at time 0
chromogram_2_0	Tone intensity for A at time 0
chromogram_3_0	Tone intensity for G# at time 0
chromogram_4_0	Tone intensity for G at time 0
chromogram_5_0	Tone intensity for F# at time 0
chromogram_6_0	Tone intensity for F at time 0
chromogram_7_0	Tone intensity for E at time 0
chromogram_8_0	Tone intensity for D# at time 0
chromogram_9_0	Tone intensity for D at time 0
chromogram_10_0	Tone intensity for C# at time 0
chromogram_11_0	Tone intensity for C at time 0
chromogram_0_1	Tone intensity for B at time 1

Not all datapoints are represented in this table, because there are 13 timepoints which contain 12 tones each. The data continues this format for the rest of the set.

There is also spectral centroid data, this is a measurement of the shape a waveform has at a certain point in time. A higher value of a spectral centroid corresponds to more energy of the signal being concentrated within higher frequencies.

Name of datapoint	Description
spec_centr_0	Spectral centroid at time 0
spec_centr_1	Spectral centroid at time 1
spec_centr_2	Spectral centroid at time 2
spec_centr_3	Spectral centroid at time 3

Spectral centroid data could be used as an extra signature to classify the songs with. The data continues this format for the rest of the set.

Data cleaning

First let's have a look at how Librosa normally outputs the chromogram data:

	0	1	2	3	4	5	6
chromogram_0	0.68661	0.67378	0.65758	0.66149	0.68533	0.72239	0.76395
chromogram_1	0.91368	0.88148	0.85024	0.82476	0.82282	0.83024	0.83908
chromogram_2	0.98221	0.97060	0.95834	0.94729	0.94785	0.95189	0.95408
chromogram_3	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000	1.00000
chromogram_4	0.96223	0.95790	0.95436	0.95403	0.94404	0.93285	0.91552
chromogram_5	0.92098	0.89960	0.88007	0.86290	0.84262	0.82280	0.80381
chromogram_6	0.87591	0.85544	0.83320	0.80870	0.78241	0.75819	0.73456
chromogram_7	0.79397	0.79418	0.79848	0.80535	0.80741	0.80750	0.80913
chromogram_8	0.62856	0.64859	0.68255	0.72441	0.76565	0.80078	0.82178
chromogram_9	0.41881	0.41914	0.44003	0.48525	0.54615	0.61608	0.68581
chromogram_10	0.36895	0.38299	0.40678	0.43114	0.45138	0.47237	0.52333
chromogram_11	0.33855	0.34676	0.35929	0.37378	0.38602	0.39931	0.42756

As you can see, the output is a neat array containing the values of 12 different tones at different time intervals. This data is sorted and can be read by Librosa.

Now onto the issue; the provided dataset contains this data in a stacked order, so each sample only takes up one row. This is a good idea, but due to sorting by alphabetical order the original order is lost. The order is important because we are working with data over time. This is not a problem if the trained model is only used on the provided test data, but we want the trained model to work in as many situations as possible and be able to visualize it with ease.

Here is a look at the provided data:

id	chromogram_0_0	chromogram_0_1	chromogram_0_10	chromogram_0_11
0	0.997943662321316	0.832392210770135	0.7653861625931	0.70427464132375
1	0.996254885931866	0.839119599044146	0.760416790506312	0.705141765139875
2	0.970810156116343	0.823539694937237	0.759508104372184	0.709057883677716
3	1	0.855558393364941	0.752038009313116	0.710976936190937
4	1	0.884304523555434	0.741884532311754	0.714775207828629
5	0.971867873978603	0.824311712155432	0.755293860709407	0.71448132195049
6	1	0.835499361583387	0.751917158063063	0.717361992854453
7	0.978929855885584	0.827216718543843	0.751072631712318	0.718400862681119
8	1	0.895339720206626	0.733409813021178	0.722747412968086
9	0.967651828343747	0.823697857901917	0.746005680687241	0.721194823494439
10	0.993699774531599	0.847257121555946	0.734368883301346	0.726420069139032
11	0.00947350497274455	0.00699383738737368	0.372026644035831	0.0516494292032762
12	0.00982270123521504	0.00712337798131429	0.371129653847745	0.051631441504244

Each row contains a stack of chromogram data in a non-sequential order. The end of the array also contains the species of the corresponding bird and some spectral centroid data. These collumns need to be deleted since we want to predict using only the chromogram data.

Figure 1: Comparison of the data order

Figure 1 shows a comparison of the order of provided data and the ideal order the data should be sorted in. The following script processes the provided data to the aforementioned format and deletes the unnecessary columns.

```
#!/usr/bin/env python3

"""
Script for cleaning and visualising the provided birdsong data.
"""

__author__ = "Niek Scholten"

# Imports
import librosa
from librosa import display
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

with open('data/train.csv', newline='') as csvfile:  # Open CSV and load the data into numpy
    my_data_train = np.genfromtxt(csvfile, delimiter=',')
    csvfile.close()
# Delete the species info columns
my_data_train = np.delete(my_data_train, -1, axis=1)
my_data_train = np.delete(my_data_train, -14, axis=1)
my_data_train = np.delete(my_data_train, 0, axis=1)  # Delete ID's
my_data_train = np.delete(my_data_train, 0, axis=0)  # Delete column names

with open('data/test.csv', newline='') as csvfile:  # Open CSV and load the data into numpy
    my_data_test = np.genfromtxt(csvfile, delimiter=',')
    csvfile.close()
# Delete the species info columns
my_data_test = np.delete(my_data_test, -1, axis=1)
my_data_test = np.delete(my_data_test, -14, axis=1)
my_data_test = np.delete(my_data_test, 0, axis=1)  # Delete ID's
my_data_test = np.delete(my_data_test, 0, axis=0)  # Delete column names

with open('data/train.csv', newline='') as csvfile:  # Open CSV and load the column names into numpy
    my_column_names = np.genfromtxt(csvfile, dtype=str, delimiter=',', skip_footer=1760)
    csvfile.close()
# Delete the species info columns
my_column_names = np.delete(my_column_names, -1)
my_column_names = np.delete(my_column_names, -14)
my_column_names = np.delete(my_column_names, 0)  # Delete ID's

with open('data/train.csv', newline='') as csvfile:  # Open CSV and load the column names into numpy
    train_species = np.genfromtxt(csvfile, dtype=str, delimiter=',')
    train_species_list = []
    for count, row in enumerate(train_species):  # Create a list to store species data
        train_species_list.append(f"{train_species[count:count+1, -15][0]}_{train_species[count:count+1
    csvfile.close()
train_species_list.pop(0)

with open('data/test.csv', newline='') as csvfile:  # Open CSV and load the column names into numpy
    test_species = np.genfromtxt(csvfile, dtype=str, delimiter=',')
    test_species_list = []
    for count, row in enumerate(test_species):  # Create a list to store species data
```

```
        test_species_list.append(f"{test_species[count:count+1, -15][0]}_{test_species[count:count+1, -
    csvfile.close()
test_species_list.pop(0)

# The given data was sorted by alphabetical order, but this results in broken sequences
# Rearrange the data to the correct format for librosa
index = [0, 39, 52, 65, 78, 91, 104, 117, 130, 143, 13, 26,  # Chromogram 1
         1, 40, 53, 66, 79, 92, 105, 118, 131, 144, 14, 27,  # Chromogram 2
         5, 44, 57, 70, 83, 96, 109, 122, 135, 148, 18, 31,  # Chromogram 3
         6, 45, 58, 71, 84, 97, 110, 123, 136, 149, 19, 32,  # Chromogram 4
         7, 46, 59, 72, 85, 98, 111, 124, 137, 150, 20, 33,  # Chromogram 5
         8, 47, 60, 73, 86, 99, 112, 125, 138, 151, 21, 34,  # Chromogram 6
         9, 48, 61, 74, 87, 100, 113, 126, 139, 152, 22, 35,  # Chromogram 7
         10, 49, 62, 75, 88, 101, 114, 127, 140, 153, 23, 36,  # Chromogram 8
         11, 50, 63, 76, 89, 102, 115, 128, 141, 154, 24, 37,  # Chromogram 9
         12, 51, 64, 77, 90, 103, 116, 129, 142, 155, 25, 38,  # Chromogram 10
         2, 41, 54, 67, 80, 93, 106, 119, 132, 145, 15, 28,  # Chromogram 11
         3, 42, 55, 68, 81, 94, 107, 120, 133, 146, 16, 29,  # Chromogram 12
         4, 43, 56, 69, 82, 95, 108, 121, 134, 147, 17, 30,  # Chromogram 13
         156, 157, 161, 162, 163, 164, 165, 166, 167, 158, 159, 160]  # Spectral centroid data
my_data_train = my_data_train[:, index]  # Apply index to the train data
my_data_test = my_data_test[:, index]  # Apply index to the test data
my_column_names = my_column_names[index]  # Apply the index to the collumn names

flammea_1 = np.empty((12, 13), int)  # Create empty array for this birdsong
# Add multiple columns form the original data as a new row
flammea_1 = np.append(flammea_1, my_data_train[0:1, 0:13], axis=0)
flammea_1 = np.append(flammea_1, my_data_train[0:1, 13:26], axis=0)
flammea_1 = np.append(flammea_1, my_data_train[0:1, 26:39], axis=0)
flammea_1 = np.append(flammea_1, my_data_train[0:1, 39:52], axis=0)
flammea_1 = np.append(flammea_1, my_data_train[0:1, 52:65], axis=0)
flammea_1 = np.append(flammea_1, my_data_train[0:1, 65:78], axis=0)
flammea_1 = np.append(flammea_1, my_data_train[0:1, 78:91], axis=0)
flammea_1 = np.append(flammea_1, my_data_train[0:1, 91:104], axis=0)
flammea_1 = np.append(flammea_1, my_data_train[0:1, 104:117], axis=0)
flammea_1 = np.append(flammea_1, my_data_train[0:1, 117:130], axis=0)
flammea_1 = np.append(flammea_1, my_data_train[0:1, 130:143], axis=0)
flammea_1 = np.append(flammea_1, my_data_train[0:1, 143:156], axis=0)

flammea_1 = np.delete(flammea_1, slice(0, 12), axis=0)  # Delete empty cells

palustris_1 = np.empty((12, 13), int)  # Create empty array for this birdsong
# Add multiple columns form the original data as a new row
palustris_1 = np.append(palustris_1, my_data_train[20:21, 0:13], axis=0)
palustris_1 = np.append(palustris_1, my_data_train[20:21, 13:26], axis=0)
palustris_1 = np.append(palustris_1, my_data_train[20:21, 26:39], axis=0)
palustris_1 = np.append(palustris_1, my_data_train[20:21, 39:52], axis=0)
palustris_1 = np.append(palustris_1, my_data_train[20:21, 52:65], axis=0)
palustris_1 = np.append(palustris_1, my_data_train[20:21, 65:78], axis=0)
palustris_1 = np.append(palustris_1, my_data_train[20:21, 78:91], axis=0)
palustris_1 = np.append(palustris_1, my_data_train[20:21, 91:104], axis=0)
palustris_1 = np.append(palustris_1, my_data_train[20:21, 104:117], axis=0)
palustris_1 = np.append(palustris_1, my_data_train[20:21, 117:130], axis=0)
```

```
palustris_1 = np.append(palustris_1, my_data_train[20:21, 130:143], axis=0)
palustris_1 = np.append(palustris_1, my_data_train[20:21, 143:156], axis=0)

palustris_1 = np.delete(palustris_1, slice(0, 12), axis=0)  # Delete empty cells

fig, ax = plt.subplots(nrows=2, figsize=(10, 9))  # Create empty canvas for plots
img1 = librosa.display.specshow(flammea_1, y_axis='chroma', x_axis='time', ax=ax[0])
ax[0].set_title('Acanthis Flammea')
ax[0].set(ylabel='Default chroma')
ax[0].set(xlabel='Time')

img2 = librosa.display.specshow(palustris_1, y_axis='chroma', x_axis='time', ax=ax[1])
ax[1].set_title('Acrocephalus Palustris')
ax[1].set(ylabel='Default chroma')
ax[1].set(xlabel='Time')

cbar_ax = fig.add_axes([0.91, 0.15, 0.05, 0.7])  # Set axis for the colorbar
fig.colorbar(mappable=img1, cax=cbar_ax)
fig.suptitle('Chroma comparison for 2 birdsongs', fontsize=32)

df = pd.DataFrame(my_data_train, columns=my_column_names, index=train_species_list)  # Export clean tra
df.to_csv('data/dataframe_train.csv', index=True, header=True, sep=',')

df = pd.DataFrame(my_data_test, columns=my_column_names, index=test_species_list)  # Export clean testi
df.to_csv('data/dataframe_test.csv', index=True, header=True, sep=',')

plt.show()
```

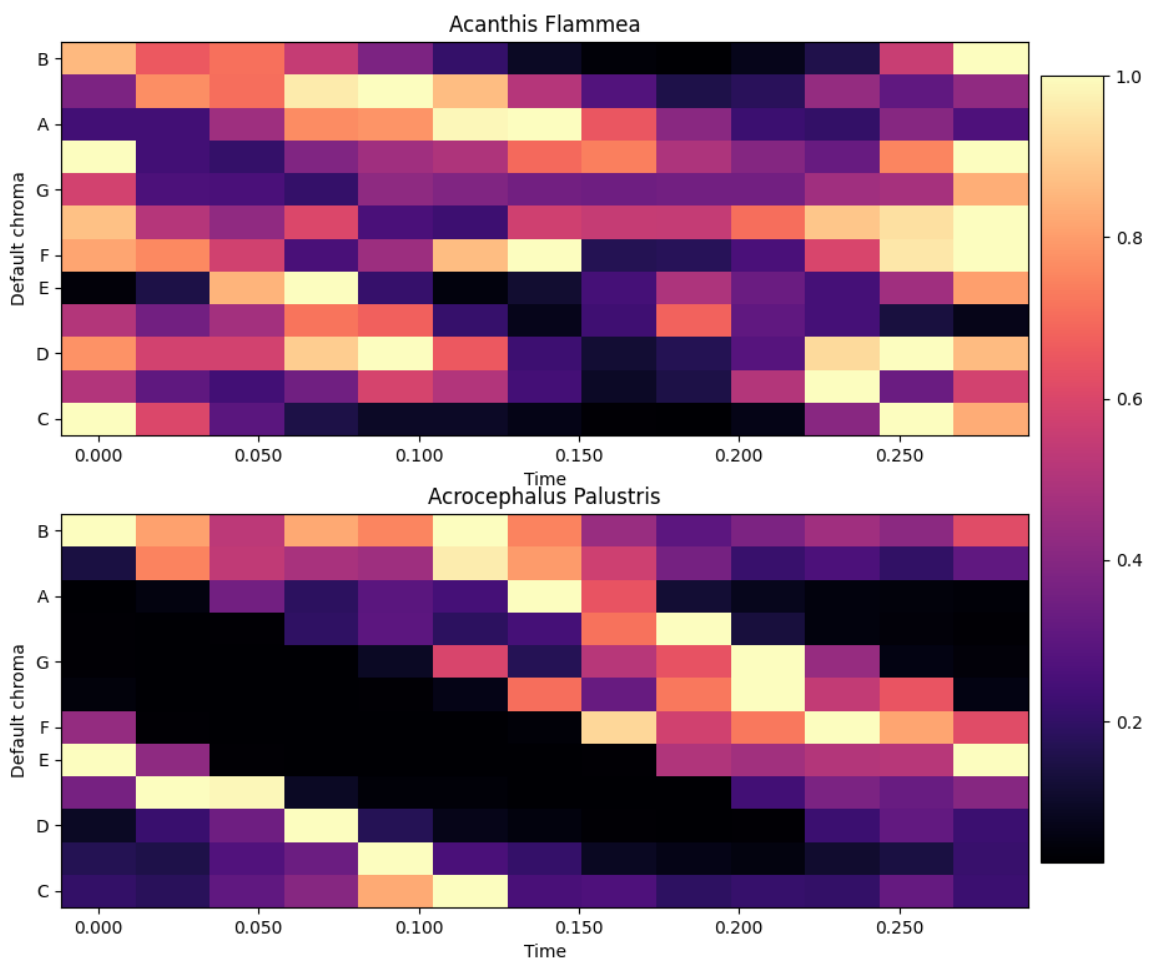
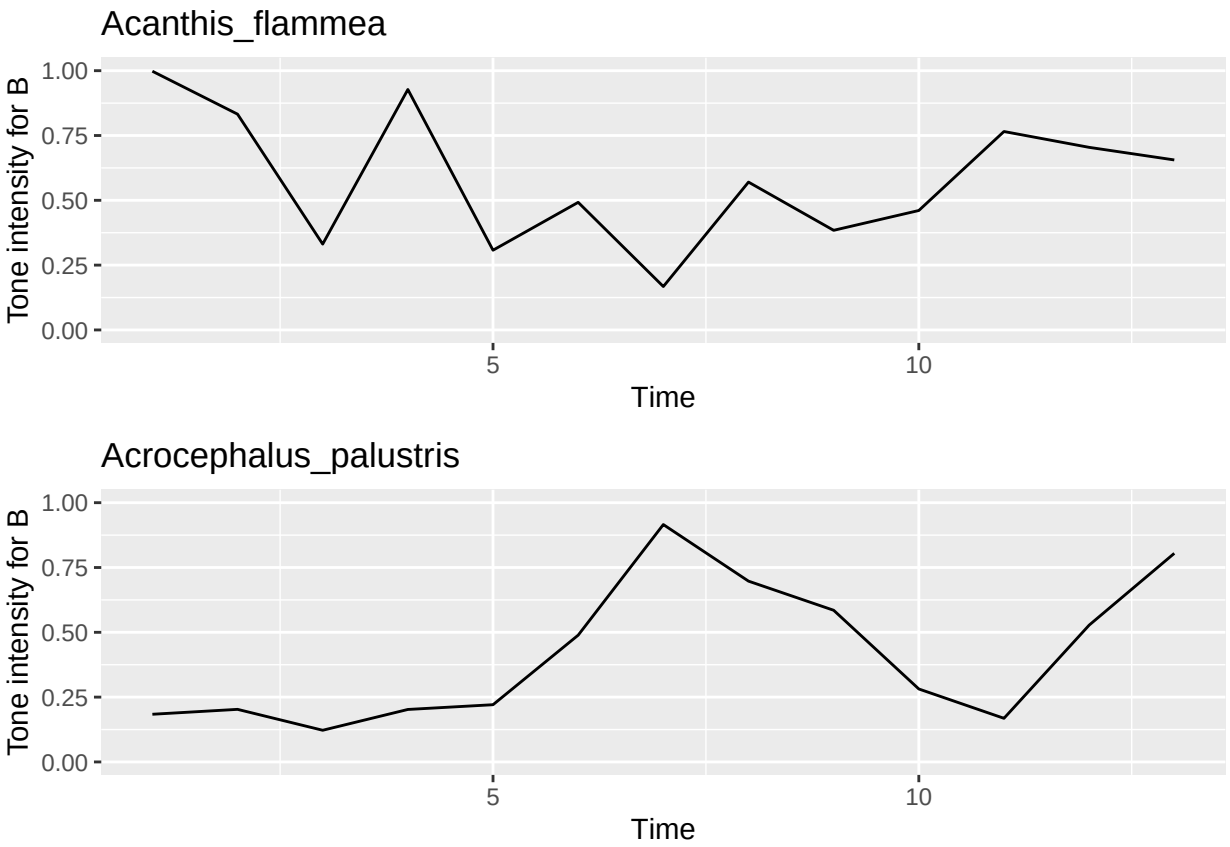


Figure 2: Chroma signature comparison for Acanthis Flammea & Acrocephalus Palustris

This figure shows the chroma signature comparison for 2 fragments of different bird-species songs. It was created by transforming the input data to the correct format that is normally outputted by librosa, because the sound data is created using librosa. The x-axis shows the time of the sound fragment, while the y-axis shows the intensity of different tones on the given time.

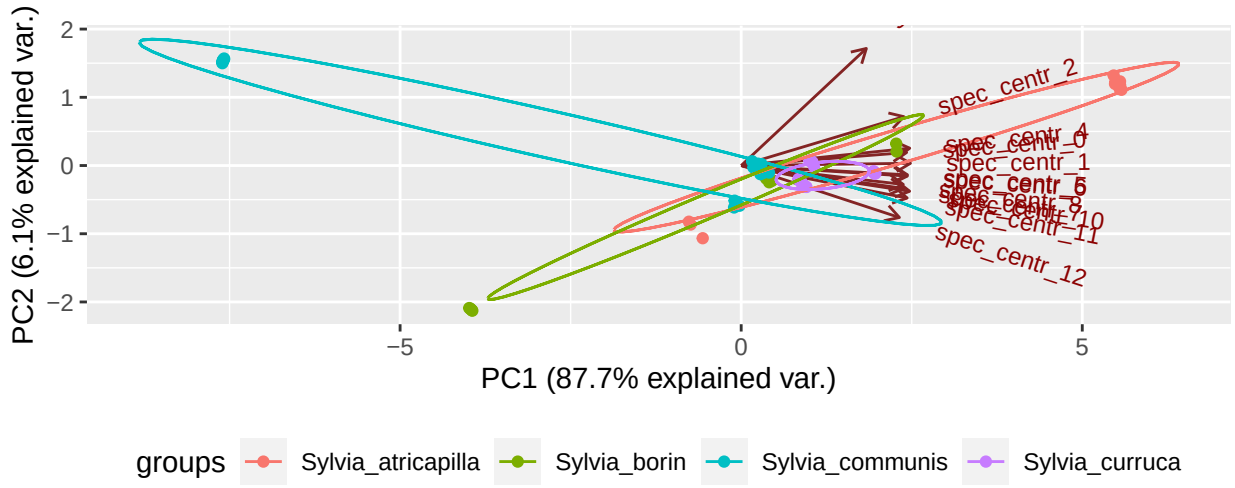
```
chromogram_data_train <- read.csv('data/dataframe_train.csv', header = TRUE, sep = ',')
chromogram_data_test <- read.csv('data/dataframe_test.csv', header = TRUE, sep = ',')

colnames(chromogram_data_train)[1] <- "Species"
colnames(chromogram_data_test)[1] <- "Species"

# write.arff(chromogram_data_train, file = "data/birdsong_train.arff")
# write.arff(chromogram_data_test, file = "data/birdsong_test.arff")
```

```
# Function for transferring row data into data frames
index_data <- function (row_number) {
  temp <- data.frame()
  temp[1, 1:12] <- chromogram_data_train[row_number, 2:13]
  temp[2, 1:12] <- chromogram_data_train[row_number, 14:25]
  temp[3, 1:12] <- chromogram_data_train[row_number, 26:37]
  temp[4, 1:12] <- chromogram_data_train[row_number, 38:49]
  temp[5, 1:12] <- chromogram_data_train[row_number, 50:61]
  temp[6, 1:12] <- chromogram_data_train[row_number, 62:73]
  temp[7, 1:12] <- chromogram_data_train[row_number, 74:85]
  temp[8, 1:12] <- chromogram_data_train[row_number, 86:97]
  temp[9, 1:12] <- chromogram_data_train[row_number, 98:109]
  temp[10, 1:12] <- chromogram_data_train[row_number, 110:121]
  temp[11, 1:12] <- chromogram_data_train[row_number, 122:133]
  temp[12, 1:12] <- chromogram_data_train[row_number, 134:145]
  temp[13, 1:12] <- chromogram_data_train[row_number, 146:157]
  return(as.data.frame(temp))
}

# Dictionary for the different chromograms and their corresponding tones
tones <- Dict$new("chromogram_0_0" = "Tone intensity for B",
                  "chromogram_1_0" = "Tone intensity for A#",
                  "chromogram_2_0" = "Tone intensity for A",
                  "chromogram_3_0" = "Tone intensity for G#",
                  "chromogram_4_0" = "Tone intensity for G",
                  "chromogram_5_0" = "Tone intensity for F#",
                  "chromogram_6_0" = "Tone intensity for F",
                  "chromogram_7_0" = "Tone intensity for E",
                  "chromogram_8_0" = "Tone intensity for D#",
                  "chromogram_9_0" = "Tone intensity for D",
                  "chromogram_10_0" = "Tone intensity for C#",
                  "chromogram_11_0" = "Tone intensity for C")

flammea <-ggplot(data = index_data(1), aes(y = chromogram_0_0, x = 1:13)) +
              geom_line() +
              ylim(0,1) +
              ylab(tones["chromogram_0_0"]) +
              xlab("Time") +
              ggtitle(chromogram_data_train[1,1])

palustris <- ggplot(data = index_data(21), aes(y = chromogram_0_0, x = 1:13)) +
              geom_line() +
              ylim(0, 1) +
              ylab(tones["chromogram_0_0"]) +
              xlab("Time") +
              ggtitle(chromogram_data_train[21,1])

ggarrange(flammea, palustris,
          ncol = 1, nrow = 2)
```



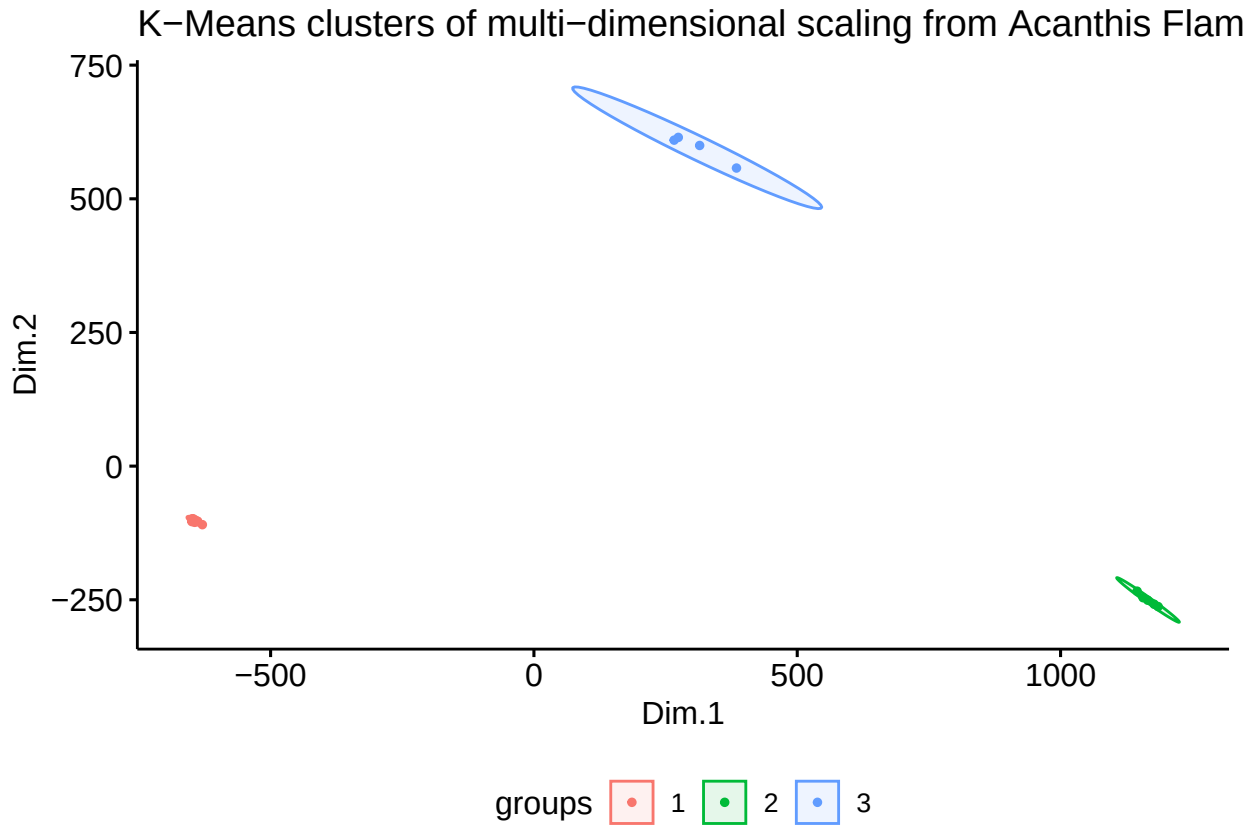
The figure above shows a significant difference in the tone intensity over time for 2 different bird species.

```
chromogram_data_train$Species <- factor(chromogram_data_train$Species)
results <- prcomp(chromogram_data_train[1541:1620, 158:169],
                  center = T,
                  scale. = T)
ggbiplot(results,
         obs.scale = 1,
         var.scale = 1,
         ellipse = T,
         groups = chromogram_data_train$Species[1541:1620]) +
         theme(legend.position = "bottom")
```



This is a PCA (Principal Component Analysis) of 4 different species of birds. These birds originate from the same genus, but as seen in the figure there is no clear cohesion between the groups.

```r
mds <- chromogram_data_train[0:20,2:169] %>%
        dist() %>%
        cmdscale() %>%
        as_tibble()
colnames(mds) <- c("Dim.1", "Dim.2")

set.seed(16)
clust <- kmeans(mds, 3)$cluster %>%
        as.factor()
mds <- mds %>%
        mutate(groups = clust)

ggscatter(mds, x = "Dim.1", y = "Dim.2",
          main = "K-Means clusters of multi-dimensional scaling from Acanthis Flammea",
          color = "groups",
          palette = hue_pal()(3),
          size = 1,
          ellipse = T,
          repel = TRUE,) +
        theme(legend.position = "bottom")
```



This scatter plot displays the kmeans of all 20 samples from 1 bird species. There are 3 distinct groups within this 1 species, this can be explained by looking at the metadata. The metadata tells us that 3 different recordings were used for the creation of the data for this specific species.