IMMC GC 2023 Winter
Problem E

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Abstract

Biological classification is a basic method for studying organisms based on morphological characteristics and physiological functions, which is conducive to the protection of ecological diversity. For the past decades, with the development of science and technology, people have achieved higher attainments in the field of biological classification. This article aims to establish standards to help biologists to analyse lizards more conveniently which have different appearances when the characteristic attributes of lizards are known.

Firstly, we plotted out the feature histogram with regard to the species of lizards, to have a basic understanding to the data. By the histogram, we find out that the FNPr value of most lizard species 5 is far smaller than others. Afterwards, we suggested a preliminary indicator based on the value of FNPr to distinguish lizard species 5 among all species belonging to Darevskia. Also we find out the distribution of each species with regard to each feature is approximately a Gaussian Distribution.

Secondly, with the observation we did, we presumed the distributions are Gaussian Distributions. We suggested a probability model mainly using Bayes Theorem to calculate the probability of an unclassified lizard is type n, then the type of the lizard is the n having the max probability.

Thirdly, we mainly discussed how to simplify the model, with the concept of reducing feature need to consider.

Finally, we answer to all questions validate the accuracy of the model we suggested with Python, with help of packages Pandas, and NumPy. *Python*, with help of packages *Pandas*, *NumPy* and *PyTorch*.

Contents

1 Background

The Earth is rich in biodiversity. Some scientists have estimated that there are between 30 and 50 million species of organisms in the world and tropical rainforests are the richest in terms of biodiversity. Meanwhile, There are still at least 10 million undefined species worldwide and around 100 million species that have been buried in history. In order to classify organisms more systematically, Linnaeus famously proposed a scientific classification based on the external physical characteristics of organisms, creating a hierarchy based on levels with a fixed number of tiers. Over time, taxonomy has been refined and the methods of classification have become more accurate and more convenient. Sometimes a scan of a device can enable biologists to "tell the truth at a glance".

The lizards of the genus Darevskia mentioned in the problem, was named in honour of the Russian herpetologist Ilya Darevsky [1].There are 35 species in this genus, which includes 7 monoecious breeding species and 22 subspecies.This lizard usually lives in the forest and grassland habitats of the Caucasus, Iran and Turkey. The colour of rock lizards ranges from green to sandy, females are usually lighter in colour than males and live hidden in the stones and in the crevices of the rocks.

2 Problem Restatement

With reference to what was said in the background, the variety of creature makes many closely related animals look very similar in appearance, however, there are significant differences in classification. Because biologists need to rely on datasets of measurable features for their research, we need to develop standards that allow lizard type and sex to be predicted as accurately as possible on the basis of these measurements. Then biologists will be able to do practical calculations in a field environment using only a graphical calculator to help scientists construct explanatory theories, these criteria must be simple and concise.We will conduct research and analysis on Darevskia lizards. As a result,lizard species assignment and gender prediction are carried out from two major levels, which are squamous sequence characteristics and morphological characteristics.

3 Problem Analysis

3.1 Subproblem 1

In subproblem 1, we need to analysis the distribution of lizard species 5 to find an index to classify if a lizard is species 5

3.2 Subproblem 2

This subproblem require us to find two features that we can classify if a lizard is species 5 based on them, and find an index to do it. And the accuracy of the index need to be better than the one in subproblem 1.

3.3 Subproblem 3

As the subproblem stated, we need to make a classifier to classify gender of lizards

3.4 Subproblem 4

Although the subproblem just asked us to classify the type of lizard in groups, we can do this with a classifier classifies all types of lizard in *Darevskia*

3.5 Subproblem 5

To cut the long story short, subproblem 5 is a combination of subproblem 3 and 4. So we will finished this subproblem first, and subproblem 3 and 4 will be solved at the same time.

4 Notations Definition

To Simpliy our discussion, we gave each feature an index number, please see *this table.*

Symbol	Definition
D	the dataset
S_n	set including all lizard with Species_num n
G_n	set including all lizard with Sex_num n
C	a lizard
C_m	mth feature of lizard C
z	a set of feature class (not feature value)
$classify(C)$	the Species_num of C
$gender(C)$	the Sex_num of C
$\mu_{s,n,m}$	mean of C_m where $C \in S_n$
$\sigma_{s,n,m}$	standard deviation of C_m where $C \in S_n$
$\mu_{g,n,m}$	mean of C_m where $C \in G_m$
$\sigma_{g,n,m}$	standard deviation of C_m where $C \in G_m$
f_n	frequency of occurrence of S_n in the dataset
g_n	frequency of occurrence of G_n

5 Assumption

- **The dataset is equally sampled in *Darevskia***

  Our model will take the diversity of S_n as one of the variable, if the dataset seriously deviates from reality, our model may not a have good performance. This can be written as formal expressions as below:

$$p(C \in S_n, D) = p(C \in S_n) = f_n$$
$$p(C \in G_n, D) = p(C \in G_n) = g_n$$

- **$C_m \mid C \in S_n$ and $C_m \mid C \in G_n$ follows a Gaussian Distribution**

  To increase generality, we presume that $C_m|C \in S_n$ follows a normal distribution. This assumption can be written as formal expression as below:

$$C_m \mid C \in S_n \sim \mathcal{N}(\mu_{s,n,m}, \sigma^2_{s,n,m})$$
$$C_m \mid C \in G_n \sim \mathcal{N}(\mu_{g,n,m}, \sigma^2_{g,n,m})$$

- **C_m is independent of C_i** $\quad (i \neq m)$

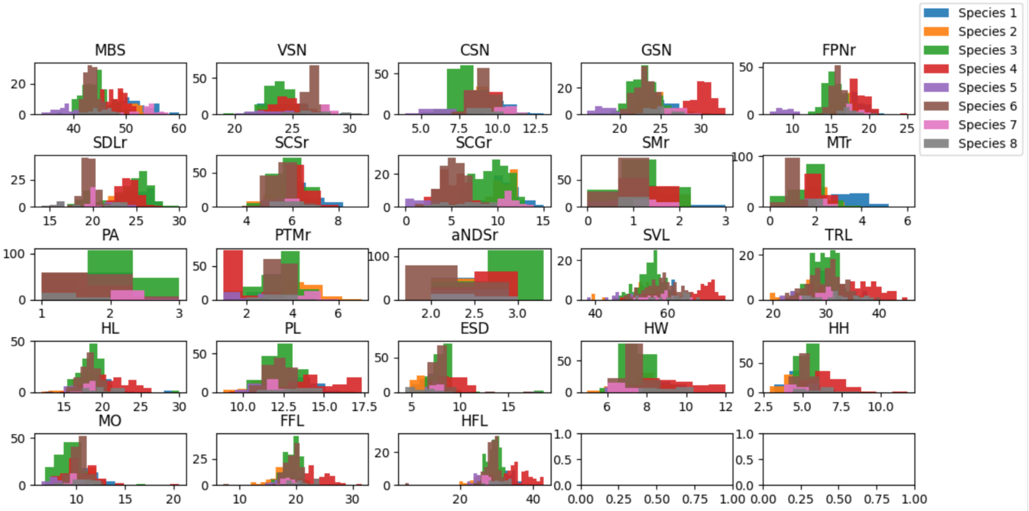
6 Model

6.1 Model Overview

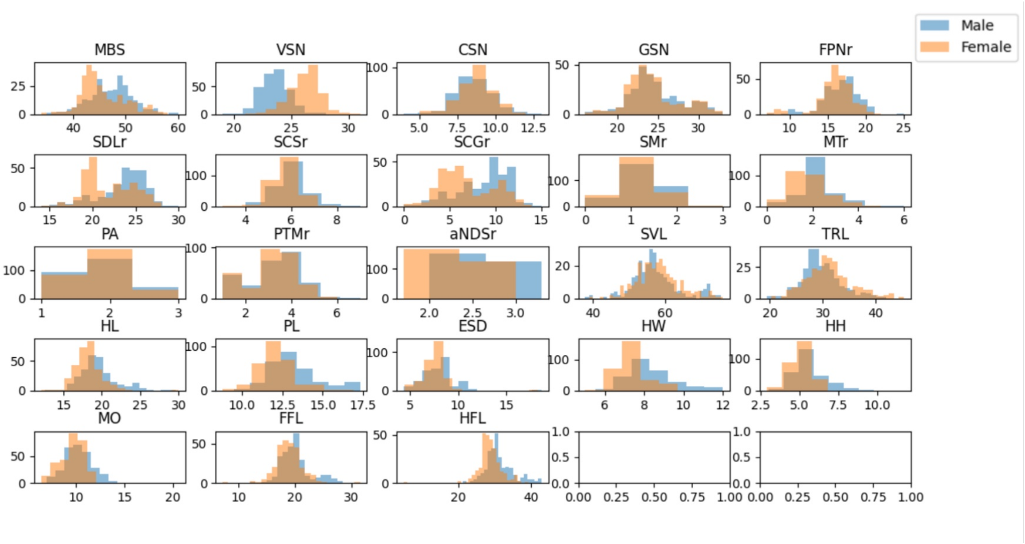
In the classification of lizards, in order to make the classification as complete as possible, we hope to establish a probability model. By inputting the body characteristics of the observed lizards, we can judge the probability that it belongs to a certain lizard, and the one with the highest probability will be identified as the species of lizard we observed. In addition, in the process of building the model, we will continue to simplify our expression so that we can establish a simpler standard. Finally, the model results will be presented in the form of probability.

6.2 Data Visualization

To study the dataset, we decided to visualize the dataset, letting us have a intuitive understanding about it. With help of Python package *Matplotlib*, we managed to plot out the feature value and gender histogram with regard to different species.

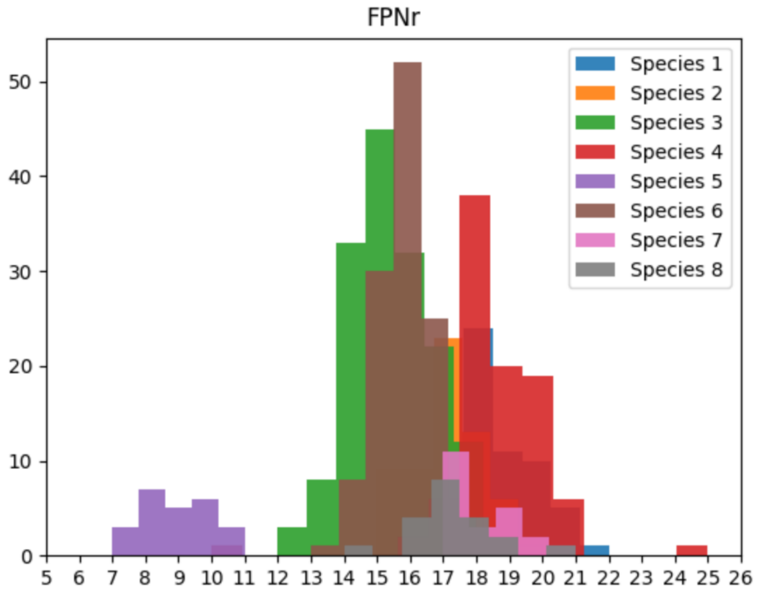


Fig[1]: feature value histogram with regard to different species



Fig[2]: gender histogram with regard to different species

Here we find the value of FNPr of species 5 is way smaller than others



Fig[3]: FNPr histogram with regard to different species

Where all FNPr value of speces 5 is no greater than 11.

Based on this phenomenon we observed, hence

Classifier 1.

$$(classify(C) \overset{?}{=} 5) = \begin{cases} 1 & C_4 \leq 11 \\ 0 & C_4 > 11 \end{cases}$$

6.3 Parameterizing the Distributions

The data visualization shows us the distributions of $C_m \mid C \in S_n$ is roughly a Gaussian Distribution. So that we assume

$$p(C_m \mid C \in S_n) \sim \mathcal{N}(\mu_{n,m}, \sigma^2_{n,m})$$

To check if this assumption fits the dataset, we calculated the kurtosis and skewness of it using Excel.

$$Median\,of\,kurtosis = 3.04596$$

$$Median\,of\,skewness = 0.05113$$

Where Gaussian Distribution have a kurtosis of 3, and skewness of 0. This shows that for most m, n, $C_m \mid C \in S_n$ follows Gaussian Distribution.

6.4 Probability Model

Considering the probability of the Species_num of a unclassified lizard C equal to n, which is the expression below:

$$p(C \in S_n \mid C_1, C_2, ..., C_{23})$$

we have this classifier spontaneously

Classifier 2.

$$classify(C) = \underset{i}{argmax}(p(C \in S_i \mid C_1, C_2, ..., C_{23}))$$

which means the Species_num of unclassified lizard C is n such that the probability of $C \in S_n$ is the maximum.

But we need to know the value of $p(C \in S_n \mid C_1, C_2, ..., C_{23})$ first. So we will try to use known conditions to calculate it.

The derivation progress as below:

Lemma 1 (Bayes Theorem)**.**

$$p(A \mid B) = \frac{p(B \mid A)p(A)}{p(B)}$$

$$\begin{aligned} p(C \in S_n \mid C_1, C_2, ..., C_{23}) &= \frac{p(C_1, C_2, ..., C_{23} \mid C \in S_n)p(C \in S_n)}{p(C_1, C_2, ..., C_{23})} \\ &= \frac{p(C \in S_n, C_1, C_2, ..., C_{23})}{\sum_{i=1}^{8} p(C \in S_i, C_1, C_2, ..., C_{23})} \end{aligned}$$

where

$$\begin{aligned} &p(C \in S_n, C_1, C_2, ..., C_{23}) \\ &= p(C \in S_n)p(C_1, C_2, ..., C_{23} \mid C \in S_n) \\ &= p(C \in S_n)p(C_1 \mid C \in S_n)p(C_2, C_3, ..., C_{23} \mid C \in S_n, C_1) \\ &= p(C \in S_n)p(C_1 \mid C \in S_n)p(C_2 \mid C \in S_n, C_1)p(C_3, C_4, ..., C_{23} \mid C \in S_n, C_1, C_2) \\ &= ... \\ &= p(C \in S_n)p(C_1 \mid C \in S_n)...p(C_{23} \mid C \in S_n, C_1, C_2, ..., C_{22}) \end{aligned}$$

since C_i is independent of C_j for $i \neq j$,

$$\begin{aligned} &p(C \in S_n)p(C_1 \mid C \in S_n)...p(C_{23} \mid C \in S_n, C_1, C_2, ..., C_{22}) \\ &= p(C \in S_n)p(C_1 \mid C \in S_n)p(C_2 \mid C \in S_n)p(C_3 \mid C \in S_n)...p(C_{23} \mid C \in S_n) \\ &= p(C \in S_n) \prod_{i=1}^{23} p(C_i \mid C \in S_n) \end{aligned}$$

also we knew

$$p(C \in S_n) = f_n$$

and

$$C_i \mid C \in S_n \sim \mathcal{N}(\mu_{n,m}, \sigma_{n,m}^2)$$

$$p(C_i \mid C \in S_n) = \frac{1}{\sigma_{n,m}\sqrt{2\pi}} e^{-\dfrac{(C_i - \mu_{n,m})^2}{2\sigma_{n,m}^2}}$$

substitute these into these expression, we can calculate the value of $p(C \in S_n, C_1, C_2, ..., C_{23})$ and $p(C \in S_n \mid C_1, C_2, ..., C_{23})$

Now, we managed to calculate all the variables in $classify(C)$, so we can classify lizards with this probability model.

With the similar concept, we have

Classifier 3.

$$gender(C) = \underset{i}{argmax}(P(C \in G_n \mid C_1, C_2, ..., C_{23}))$$

where

$$p(C \in G_n \mid C_1, C_2, ..., C_{23}) = \frac{p(C \in G_n)\prod_{i=1}^{23} p(C_i \mid C \in G_n)}{\sum_{k=1}^{2} p(C \in G_k)\prod_{i=1}^{23} p(C_i \mid C \in G_k)}$$

for the gender classification.

6.5 Model Optimization: Simplify

Considering a set of feature class z, after calculating similarly as before,

$$p(C \in S_n \mid z) = \frac{p(C \in S_n)\prod_{k \in Z} p(k \mid C \in S_n)}{\sum_{i=1}^{8} p(C \in S_i)\prod_{k \in Z} p(k \mid C \in S_i)}$$

Classifier 4.

$$classify(C) = \underset{i}{argmax}(p(C \in S_i \mid z))$$

If we are not considering all of the features, we need to find the z that makes the accuracy this classifier as big as possible.

So we can only consider about $p(C \in S_n \mid z)$.

After reducing the conditions need to consider, the conditions left are the differences between S_n and other types of lizard.

7 Subproblem Solutions

7.1 Subproblem 1

We have mentioned **Classfier 1**, which is designed for this subproblem.
We have tested the accuracy of this classifier using the dataset given.

	True species #5	True species #1-4, 6-8
Classified as species #5	21 / 100%	1 / 0.19%
Classified as species #1-4, 6-8	0 / 0.0%	539 / 99.81%

Table[1]: test result of Classifier 1

This classifier is pretty good because it only classifies one lizard wrongly.

7.2 Subproblem 2

In subproblem 2, we need to find a set of feature class $z, |z| = 2$ that makes $p(C \in S_5 \mid z)$ as large as possible.

With help of computer, we found that when $z = \{C_1, C_5\}$, the accuracy of **Classifier 4** is the maximum possible.

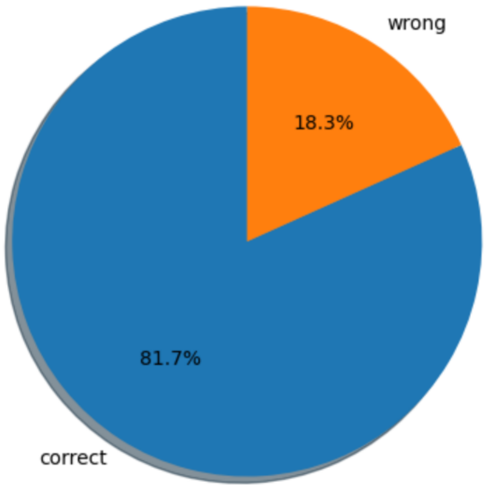
We have tested the accuracy and the results as shown down:

	True species #5	True species #1-4, 6-8
Classified as species #5	21 / 100%	0 / 0.0%
Classified as species #1-4, 6-8	0 / 0.0%	539 / 100.0%

Table[2]: test result of Classifier 4 with $z = \{C_1, C_5\}$

7.3 Subproblem 3

Using **Classifier 3**, we can solve this problem.
Validation result of **Classifier 3**:



Fig[4]: Accuracy of Classifier 3

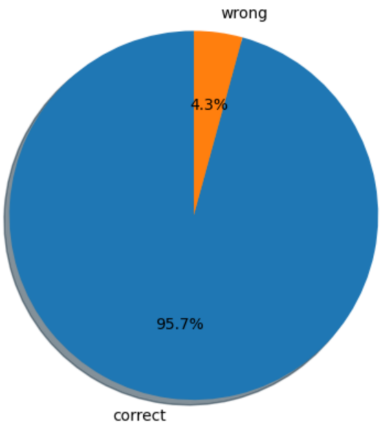
	Correctly Classified	Wrongly Classified
Male	212 (77.1%)	63 (22.9%)
Female	249 (86.2%)	40 (13.8%)

Table[3]: Validation Result of Classifier 3

7.4 Subproblem 4

We can use **Classifier 2** to do the tasks of Subproblem 4.

With help of Python, with packages *Pandas*, *NumPy*, we validated **Classifier 2** using the dataset.



Fig[5]: Accuracy of Classifier 2

	Correctly Classified	Wrongly Classified
Species 1	58 (87.9%)	8 (12.1%)
Species 2	60 (95.2%)	3 (4.8%)
Species 3	150 (96.2%)	6 (3.8%)
Species 4	90 (96.8%)	3 (3.2%)
Species 5	24 (100.0%)	0 (0.0%)
Species 6	117 (97.5%)	3 (2.5%)
Species 7	22 (100.0%)	0 (0.0%)
Species 8	19 (95.0%)	1 (5%)

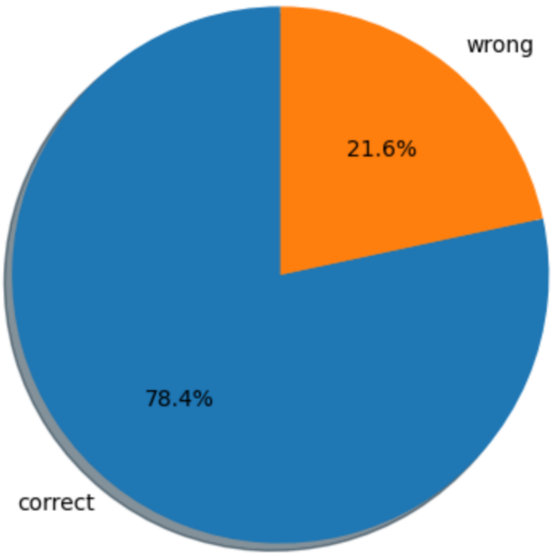
Table[4]: Accuracy of Classifier 2 for each species

From the perspective of the correct classification probability of a single species, we notice that although the correct rate of species one is the lowest, the correct classification is close to 90%(87.5%), followed by species 2, 3, 4 and 8, and the correct rates are all around ninety-five percent, respectively 95.2%, 96.2%, 96.8% and 95%. Compare to the species 6, the correct rate is nearly one-hundred percent

(97.5 %). It is worth noting that the classification accuracy rate of species 5 and 7 reached 100%, which means the classification is completely correct. So we think that the criteria that we have established are applicable to task four.

7.5 Subproblem 5

For subproblem 5, we can use **Classifier 2** and **Classifier 3**, which are mentioned on the solution of previous subproblems. We validated the accuracy of using **Classifier 2** and **Classifier 3** at the same time.



Fig[6]: Accuracy of using Classifier 2 and Classifier 3 together

which we can see that this accuracy is slightly lower than only using **Classifier 3**

8 Result Analysis

8.1 Strengths

- **Efficiency in updating data**
  When more data is added to the object we want to study, the probability algorithm can update the results at a higher speed. Even for very large-scale data sets, each item usually only corresponds to an individual feature number. So our selected model has stable classification efficiency.

- **Simplicity of algorithms and ease of interpretation of results**
  This probability algorithm does not need to use complex computer program calculations, but only needs to use basic mathematical operations to solve it. Moreover, the required calculation time is shorter, the algorithm logic is simple and stable, and the interpretation of the results is easier to understand.

8.2 Weakness

- **The deviation of value**
  Through the chart of Task 1 and the calculation of Kurtosis and skewness, we determines that the data we studied conformed to the Gaussian distribution. But from the final results, our data still differs from the Gaussian distribution image. As a result, the classification cannot be exactly close to 100

- **Sample correlation can have an impact**
  In order to ensure the best classification effect, we assume that there is independence between samples. But in reality, there will inevitably be inextricable relationships between many data.This means that the data cannot be completely independent of each other, which let the Naive Bayes algorithm is not applicable at this time.

8.3 Expectation

- **Parameterize the distributions using Gaussian Mixture Model, instead of single Gaussian Distribution**
  Because not all of the distribution follows Gaussian Distribution, this deviation make the accuracy of our gender classifier low. If we Parameterize the distributions using Gaussian Mixture Model, we can get a better accuracy on our gender classifier

References

[1] Bo Beolens, Michael Watkins, Michael Grayson(2011). The Eponym Dictionary of Reptiles. Baltimore: Johns Hopkins University Press.

Appendix

Feature index table

Feature name	index	Feature name	index
MBS	1	aNDSr	13
VSN	2	SVL	14
CSN	3	TPL	15
GSN	4	HL	16
FPNr	5	PL	17
SDLr	6	ESD	18
SCSr	7	HW	19
SCGr	8	HH	20
SMr	9	MO	21
MTr	10	FFL	22
PA	11	HFL	23
PTMr	12		

Classification Code

```python
#!/usr/bin/env python3
import numpy as np
import math
import pandas as pd


df = pd.read_excel("dataset.xlsx")


species_mean = [df[df["Species_num"] == i + 1].iloc[:, 3:].mean() for i in range(8)]
species_std = [df[df["Species_num"] == i + 1].iloc[:, 3:].std() for i in range(8)]
species_density = df["Species_num"].value_counts(normalize=True)

gender_mean = [df[df["Sex_num"] == i + 1].iloc[:, 3:].mean() for i in range(3)]
gender_std = [df[df["Sex_num"] == i + 1].iloc[:, 3:].std() for i in range(3)]
gender_density = df["Sex_num"].value_counts(normalize=True)

```

```python

def gaussian(mean, std, x):
    if math.isnan(mean) or math.isnan(std):
        return 0
    return 1 / (std * (2 * math.pi) ** 0.5) * math.exp(-(x - mean) ** 2 / (2 * std ** 2))


def classifier2(feat):
    prob = [species_density[i] for i in range(1, 9)]
    for i in range(8):
        for j in range(23):
            prob[i] *= gaussian(species_mean[i][j], species_std[i][j], feat[j])
    prob /= sum(prob)
    return np.argmax(prob)


def classifier3(feat):
    prob = [gender_density[i] for i in range(1, 3)]
    for i in range(2):
        for j in range(23):
            prob[i] *= gaussian(gender_mean[i][j], gender_std[i][j], feat[j])
    prob /= sum(prob)
    return np.argmax(prob)


correct_species = 0
wrong_species = 0
correct_gender = 0
wrong_gender = 0
correct = 0
wrong = 0

for i in range(len(df)):
    feat = df.iloc[i, 3:]
    species = classifier2(feat)
    gender = classifier3(feat)
    if species + 1 == df["Species_num"][i]:
        correct_species += 1
    else:
        wrong_species += 1
    if gender + 1 == df["Sex_num"][i]:
        correct_gender += 1
    else:
        wrong_gender += 1
    if gender + 1 == df["Sex_num"][i] and species + 1 == df["Species_num"][i]:
        correct += 1
    else:
        wrong += 1

print(correct / (correct + wrong), wrong / (correct + wrong))
```