Identifying Genetic Relatedness in Birds Using Visual Patterns

by

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THESIS

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If you face situations that you do not know how to deal with, there are many possibilities. That's when you can really explore life.

– Sadhguru

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My daughter was just three months old when I started school at UIC. I have no clue to what extent will I be able to work, achieve and balance out my academic and personal life. It was overwhelming. Working on a research project was once my dream and certainly thought it is undoable by me, given my commitments. But, the trust, support and encouragement I have received throughout my program and research is invaluable. It is what that made me achieve my dream and I can't thank enough who stood by my side through this amazing journey.

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TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS

3D	3 Dimensional
CNN	Convolutional Neural Networks
ML	Machine Learning
HOG	Histograms of Oriented Gradients
SVM	Support Vector Machines
LBP	Local Binary Patterns
SIFT	Scale Invariant Feature Transform
DNA	Deoxyribonucleic Acid
SSIM	Structural SIMilarity
HVS	Human Visual System
VGG	Visual Geometry Group
SGD	Stochastic Gradient Descent
RMSProp	Root Mean Squared Propagation
AWS	Amazon Web Services
EC2	Elastic Computation Cloud

SUMMARY

Biologists believe that visual markings of eggs shells produced by related birds will be similar. Studies suggests that along with the odour, visual markings or signatures helps birds distinguish their own brood and avoid brood parasitism. The relation between similarity of coat markings on animals, similarity of features in humans with respect to genetic relatedness has been asked many times before but a conclusive answer is still not found. While biologists asserts that visual patterns indicates genetic heritability, accurately quantifying genetic heritability with respect to visual signatures has not been possible until recently. With the advent of machine learning and computer vision algorithms, we would like to use these algorithms and ask a question in the context of bird eggs images, whether given a pair of eggs, if they are genetically related based on visual patterns or not.

While microsatellite loci [4] are widely used to estimate the genetic relatedness between individuals in wild, outbred, vertebrate populations, we would still like to ask a question - Is there a relationship between visual markings of living organisms and genetics? Being able to answer this question can identify, just based on images, if genetic relatedness exists or not.

In this work we use a dataset of images of eggs of the same species, with known nest relations to test various machine learning and computer vision approaches for their ability to identify eggs from the same nest purely by their visual patter similarities. The results have shown that dataset is more unyielding in terms of features used for computer vision techniques and calls out for more detailed feature preparation. In the future work, we decided to construct more

SUMMARY (Continued)

advanced features from the dataset, apply the computer vision algorithms used in the current

research and compare the new features and old features and their results.

CHAPTER 1

INTRODUCTION

Whom does the baby look like more, the father or mother? How does a bird reject brood parasitism? Does a patterned coat on mammals suggest heredity? What is the relationship between the visual markings of living organisms and genetics?

The connection between genetic relatedness and visual similarity has been previously explored from various perspectives in several studies. For example, previous studies into mother-offspring recognition by facial-visual characteristics [36] showed that when mothers of newborn infants within 33 hours of post-partum are asked to identify their babies by showing photographs, they were able to distinguish their offsprings from those of unrelated ones based on facial visual features in photographs. A study on mammalian coat patterns within mammals such as leopards (*Panthera pardus*), domestic cats (*Felis catus*) and tigers (*Panthera tigris*) [11] shows that the spots and stripes on these mammals play an important role in social communication. A research study was conducted to understand what parameters of eggs would help the bird species in recognizing brood parasitism [39] and experiments were performed within various species such as North American Passerines and American Robins to identify whether these species identify their brood based on the parameters of eggs under observation. The study showed that birds of various species responded to their brood eggs and avoided brood parasitism based on egg coloration, size and visual parameters. Yet, the biological mechanisms used in animals' visual recognition of their kin are to be explained. Moreover, even the basic

task of accurately quantifying the connection between genetic relatedness and visual similarity markings had not been possible until the advent of machine learning and computer vision.

The problem of searching for patterns in data is a fundamental one and has an evolving history. For instance, the problem of recognizing handwritten digits and identify them between 0-9 can be solved using handcrafted rules based on strokes and variability of handwriting [24]. Far better results can be obtained using machine learning work. With the advent of Computer Vision and Machine Learning for image analysis, a variety of research work has been done, and visual similarity is quantified [13], [27]. In computer vision, kinship (lower-order pedigree) recognition is a process of identifying whether two organisms are closely related based on features extracted from digital images. Many previous works focused on automatic visual kinship recognition [13], [37], [27] and applications include missing child search, social media information analysis and family photo annotation [54]. Machines consistently performed well in visual kinship recognition of facial attributes of humans.

Biologist Mark Hauber hypothesized that patterns developed on eggshells of a bird's brood of Grey Capped social weaver(*Pseudonigrita arnaudi*) are visually similar [19] and further aims to understand to what extent a bird recognizes these patterns and accept an egg as its brood or rejects it. Thus, the primary motivation for this study is understanding how birds discriminate their brood eggs from unrelated eggs based on visual cues or patterns. Genotype by Sequencing (GBS) [12], [48], a genetic screening method for performing genotyping studies to determine the kinship relation using genetic data, is the most reliable and efficient way; birds, clearly are not collecting genetic samples of the eggs. Thus, to understand the mechanism of how birds

identify their own eggs and whether they use visual marking's similarity as a proxy, we must establish a connection between visual markings and genetic inheritance. Besides, if we could identify the genetic relatedness from images, we could avoid the problem of collecting DNA samples in wild animals, which is a highly difficult and occasionally dangerous task.

Hence, in this thesis, we set out to answer a question of whether genetic relatedness is correlated to visual markings of bird eggs from images. We used various machine learning and computer vision techniques to learn visual pattern similarities of bird egg images. Given a collection of digital photos of eggs with known broods, we aim to use machine learning and deep learning approaches to answer whether any two eggs are coming from the same brood or not. Figure 1 shows an example of images of eggs coming from a set of nests. Each of these images has recognizable patterns which are used by birds to identify its brood.

The rest of the thesis is organized as follows:

- **Chapter 2:** We state the precise problem that we are trying to solve within the scope of this thesis. We also describe the dataset used for all the experiments.

- **Chapter 3:** We discuss the work relating to identifying genetic relatedness based on visual markings, using machine learning and computer vision.

- **Chapter 4:** We describe the supervised learning methods architecture for identifying image similarity and instantiate the architecture for the problem of egg similarity inference from images.

Figure 1: Images of blunt ends of eggs from different nests are shown. The labels are in the format YEAR-LOCATION-NEST IDENTITY-BLUNT END PHOTO AND EGG IDENTITY. For example, 2002-Army-08-02-R-bluntend-1 (Egg A).jpg, 2002-Army-08-02-R-bluntend-1 (Egg B).jpg are eggs A and B from same nest Army-08-02-R, collected in 2002.

- **Chapter 5:** We describe the unsupervised learning method's architecture, the motivation behind choosing this method and explain how this setting will learn the problem of inferring nest relations within bird egg images.

- **Chapter 6:** We describe the implementation details and in-depth parameter settings of methods we presented in Chapters 4 and 5. We state and discuss the results from applying supervised and unsupervised methods on the dataset we have used.

- **Chapter 7:** In this final chapter, we conclude our findings and comment on genetic signatures within visual markings of bird eggs. We describe the future scope by our results and present the enhancements to our research on identifying genetic relatedness in birds using visual egg patterns.

CHAPTER 2

PROBLEM DESCRIPTION

The aim of this research is to understand whether birds use visual cues on egg shells in identifying their brood. In order to answer this question we need to design a way to recognize eggs belonging to the same brood, relying only on the eggs' appearance. With known brood relations, given a pair of eggs, one way to state the problem formally is: Can we determine whether a pair of eggs are from the same brood, using only the visual pattern on the eggs. In the scope of this thesis, we focus on the eggs from a species called Grey Capped social weaver(*Pseudonigrita arnaudi*). These eggs have distinguishable patterns as shown in Figure 1. We investigate in this thesis, whether there is any genetic signature within these patterns, specific to mother birds. We develop computer vision and machine learning algorithms, rather than relying on human judgment since human vision and perception is prone to bias because of the following reasons:

- Birds can perceive visible as well as ultraviolet spectrum and hence their color receptors are different from human colour receptors. Therefore we cannot directly rely on human observation to completely mimic a bird's vision.

- A study on birds vision compared to primate's vision [28] showed that, birds perceive patterns differently when compared to primates. Hence relying on humans' vision in

identifying visual patterns may lead to mammalian bias. To avoid this, we use computer vision to learn the visual patterns and infer genetic relatedness within eggs laid by birds.

Moreover, computational approaches rely on features that are not explicitly specified and, therefore, may find hidden cues in the visual similarity signal.

2.1 Dataset and Preprocessing

The dataset of eggs used in this work was provided by Dr. Mark Hauber of the University of Illinois at Urbana-Champaign. It consists of 297 blunt end images of bird eggs and their brood identities. These are the eggs laid by females of a cooperatively nesting species in Kenya of Grey Capped social weaver (*Pseudonigrita arnaudi*). The egg identities and brood relations are accurately established based on the DNA samples collected by our collaborator [1]. The file names of these eggs are encoded with nest (brood) identities and egg identities. Eggs within each brood are hypothesized to have similar visual patterns.

The labels are given in the formal *'Year-Location–bluntend-Eggidentity'* encode the information of bluntend images of eggs such as:

- Year - 2002, 2003 etc.,

- Location - Army, CLFM, SBB etc.,

- Egg Identity - Egg A, Egg B, Egg C etc.,

For example, eggs 2002-ARMY-08-02-R-BLUNTEND-1 (EGG A) and 2002-ARMY-08-02-R-BLUNTEND-1 (EGG B) belong to same brood ARMY-08-02-R of the year 2002.

Table I shows the overall structure of the dataset of birds eggs images we have extensively used for our training purposes. Figure 2 shows the distribution of the number of eggs per nest and number of nests containing those number of eggs.

TABLE I: Training dataset summary - number of images, nests, Egg id example, Nest id code

	Parameters
Bird Species	Grey Capped Social Weaver(Pseudonigrita arnaudi)
Number of egg images	297
Number of nests	81
Egg id example	2002-Army-08-02-R-bluntend-1 (Egg A)
Nest identity code	Year-Location-NestIdentity-bluntend-egg-identity

We will use machine learning approaches to establish whether visual similarity correlates with genetic relatedness in this dataset. We formulate two different version of the machine learning problem: 1) as a multiclass classification problem, where each class is a brood and 2) a pairwise binary classification problem of whether a pair of egg images belong to the same brood or not. We consider both supervised and unsupervised approaches.
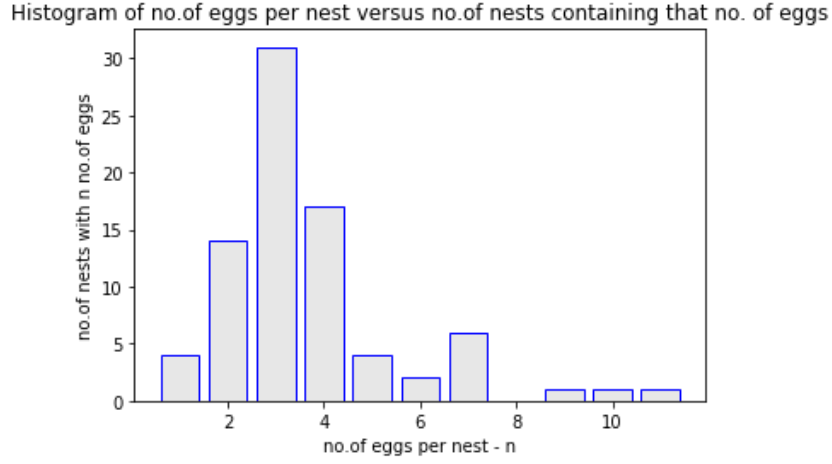
Figure 2: Distribution histogram of the number of eggs per nest

There are 81 different broods in the dataset, each containing eggs with visual patterns. Although a straight forward approach to identifying brood relations seems to be classifying each of the eggs into one of the 81 different broods, typical of a multiclass classification problem, many machine learning algorithms are inherently binary i.e, they are able to discriminate between two classes. Hence to establish a genetic connection within eggs using machine learning, a more appropriate direction would be to analyze each pair of images and assess if they belong to the same brood or not. Thus the problem now is, given a pair of images from the bird eggs dataset and asked if they belong to same brood or not, the machine learning model should be able to answer *Yes* or *No*. This process of mapping a multiclass classification problem to several two-class classification problems is called *class binarization* [3]. In order to binarize the problem, we use a supervised approach where we obtain positive training examples - those pairs of eggs

coming from the same brood and, negative training examples - pairs formed by the union of images from all other broods.

Since training a machine learning model requires considerably large amount of data and given the relatively small size of our dataset (297 images), we have performed data augmentation [46] to boost up the data. We want to augment the data using standard approaches for data transformation while preserving salient features. The goal of the data augmentation is to:

- Increase the size of the data. This can be achieved by rotating the images. Hence, we have rotated every image twice by an arbitrary randomly chosen angle between 0 - 180 degrees.

- Highlight the most salient and complex points of the texture/pattern. For this, we have applied *Gabor filter* [29]. Gabor filter is used in texture analysis to analyze whether there is any frequency content in an image in specific direction. When a Gabor filter is applied to an image, it gives the highest response at crucial edges of an image. Figure 3 and Figure 4 shows a test image and transformation of image after applying Gabor filter.

The total number of images has then become 1188. Table II shows the tabular form of augmentation techniques performed.

Figure 3: Raw Image
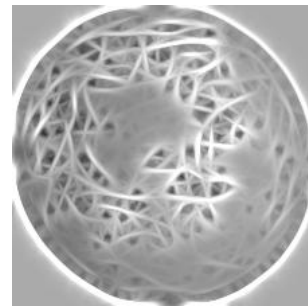
Figure 4: Gabor Filter

TABLE II: Data Augmentation Statistics

	Parameters
Augmentation	Rotation(0-180 degrees)
Filters	Grey Scale, Garbor filters
Number of images after augmentation	1485
Nest identity code	Year-Location-NestIdentity-bluntend-egg-identity

CHAPTER 3

RELATED WORK

3.1   Computer vision for kinship recognition

The first attempt in using computer vision to detect genetic signatures within visual markings was published in the form of kinship verification [13]. This research used feature extraction and selection methods on pairs of human face images of public personalities and automatically classified whether these pairs were related or unrelated. The human kinship verification problem has since gathered attention and been an active research topic in the area of computer vision. An improved model of automatic kinship verification based on facial image analysis of human celebrity images was performed in [55] [56]. These models used descriptors such as spatial pyramid learning and Gabor-based gradient orientation pyramid to effectively learn the facial representations and integrate with support vector machine classifier for automatic kinship verification. CornelKin [13] with 150 pairs of images of parents and children faces is the first ever kin-based dataset available for research in 2010 . UB KinFace [31] was then made public for kinship recognition task with images of parents and children at young and old ages. These are popular datasets that use computer vision and machine learning to answer whether genetic relatedness can be identified based on the discriminative features or visual patterns.

3.1.1   Genetic relatedness based on animal markings similarity

To date, the computer vision work on kinship recognition from visual features has been restricted to human faces. However, there has been work in the biological community demonstrating the genetic connection between visual animal markings. Hotsotter [10], uses an algorithm to identify the individuals such as Grevy's and plains zebras, giraffes, leopards, and lionfish by extracting matching keypoints. In [52], the study attempts to identify the individual cetaceans from images based on trailing edges of their fins. However, these studies are mostly restricted to individual identification and a very little progress has been made towards pairwise kinship recognition in animals. And, to the best of our knowledge, no computer vision and machine learning approaches have been developed to quantify the relation between the genetic relatedness and the visual pattern similarity in animal markings.

3.2   Challenges

Despite several attempts by computer scientists to successfully use individual markings and features to identify an individual [10], [52], [35], the research of identifying genetic relations based on visual markings still remains challenging due to following reasons:

- **Dataset**: A critical observation from previous studies showed that face images of younger parents resembled their children more than those of older parents. In addition, collecting sufficient amount of training data is increasingly proprietary, requires exhausting data labelling task and building new models from scratch is very expensive.

- **Feature based learning**: A technique which extracts discriminative features to describe images. This method seek an overly strict strategy and rules to accurately define the features which makes it poorly scalable.

- **Limitation:** Automatic kin recognition performed till now is mostly restricted to humans and moreover the models developed to investigate genetic relatedness in regards to visual markings in *animals* is mostly restricted to mathematical and theoretical models as explained in 3.1.1.

3.2.1 Similarity learning

To overcome the challenges outlined above, we consider a broader set of techniques, similarity learning [30] and transfer learning [53]. These techniques, unlike previous approaches, use a relaxed strategy to distinguish the similarity of related pairs and similarity of unrelated pairs. *Similarity learning* is a type of distance metric learning task that computes similarities between images by optimizing an appropriate distance function. This method ensures that similarity of related pairs remains higher than similarity of unrelated pairs. It has been successfully applied in information retrieval for learning to rank(example: e-commerce based search results) [25], face identification [16]. *Transfer learning*, unlike traditional machine learning task, transfers the knowledge learned from the previous tasks to the target task. Meaning, a model which was trained on a task that has plentiful of data, is used to handle a new but similar task, that contains lesser data. Transfer learning has been successfully applied to sentiment classification, image classification [57]. Figure 5 shows the difference between learning processes of traditional

machine learning and transfer learning tasks. We applied these state-of-the-art approaches to the problem of identifying genetic relatedness based on visual markings of eggs.

3.3 Motivation

As discussed in previous sections, significant amount of research work has been done to identify the role of visual markings/cues in genetic relations within human beings (kinship recognition). However, most of the work conducted is primarily either theoretical(in case of wild animals) or the work is incomplete due to inadequate data and cannot be directly adapted to our problem of investigating the role of visual markings in identifying genetic relatedness in bird egg images.

Based on the existing studies and progress on kinship verification, we use current best-performing models and deep convolutional neural networks(CNNs) to learn the brood identity based on visual markings similarity on our very unique dataset, explained in 2.1. In our methods, we use pairs of images from intra-class (same brood) and inter-class (different broods) relations to train state-of-the-art machine learning algorithms, which we describe in following sections.
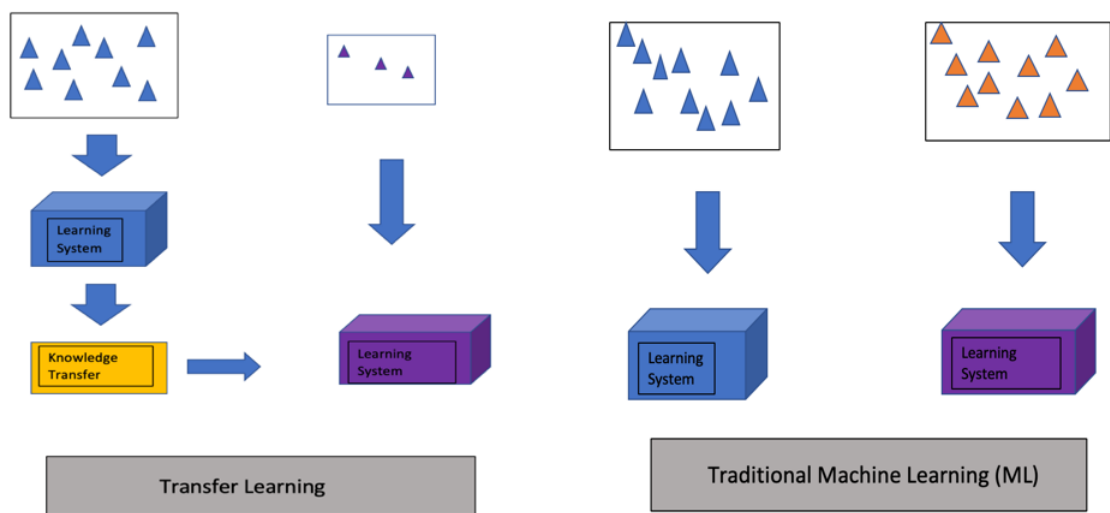
Figure 5: Transfer Learning Overview

CHAPTER 4

FEATURE REPRESENTATION TECHNIQUES- FOR SUPERVISED AND UNSUPERVISED LEARNING

In this chapter, we introduce the terminology related both supervised and unsupervised learning task. We explain the feature representation techniques of images used in our work.

4.1 Algorithms Terminology

Image similarity classification problem [42], [22], [26] is one of the central topics in supervised machine learning and computer vision areas. It has many applications such as image retrieval [25], recommender systems [5], classification of object categories [49] and kinship recognition [13], [37], [27], to mention a few. In this approach, a pair of images are compared to determine how similar they are and, based on the similarity and the extracted features, to answer *Same* or *Not Same* (typical of a binary supervised task). This task of comparing images to quantify the similarity generally uses Scale Invariant Feature Transform (SIFT) [26] and Local Binary Patterns(LBP) [33] feature descriptors to embed the images and learn the image similarity models on top of these features. Another approach is to use deep convolutional neural networks(CNNs) to be able to jointly learn the features and similarity models. We have used both feature-based descriptors models and deep neural networks based learning models in our approaches to classify whether a pair of images of eggs are from the same brood or not.

Pairwise Classification: In Section 2.1 we introduced two different versions of the problem, *multi-class classification* problem and *pairwise classification problem.* In the following, we will see what a multi-class classification problem is, how it is converted into a binary class classification problem and define pairwise classification in detail.

Given n points $P = \{p_1, ..., p_n\}$, divided into n_1 training points $P_{train} \subset P$ and n_2 test points $P_{test} \subset P$, m target classes $C = \{c_1, ..., c_m\}$, the goal of a *classification problem* is to

Pairwise classification approach [7] is used to convert multi-class classification problem to binary classification problem. In this technique we consider two input examples and predict whether they belong to same class or different classes. In our experiments, we modelled two kinds of binary supervised Learning methods - Pairwise SVMs [8] and Siamese CNNs [6], each of which relies on a pair of input examples to predict whether they belong to same or different brood. Each method is described below. Our initial approach, however, used current state-of-the-art CNNs, as feature descriptors to formulate a similarity verification task.

4.2   Local Binary Pattern(LBP)

LBP [33] is a powerful tool used for texture analysis. It is a non-parametric descriptor that aims to summarize the local structures or textures of images. The LBP operator labels the pixels of images with decimal numbers, called LBP codes, which encode the local structure around each pixel. Figure 6 represents a simple example of LBP operator working. Each pixel of image is compared with its 3×3 neighborhood consisting of 8 members, by subtracting the center pixel values. The negative pixel values are encoded 0 and others with 1. A binary code is obtained by concatenating all the encoded codes in a clock-wise direction. Thus formed
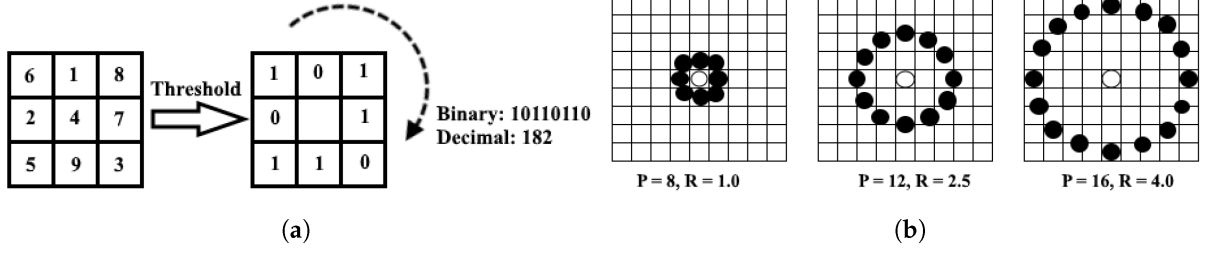
Figure 6: A basic example of LBP operator and code representation

binary numbers are called LBP codes. One of the limitations from this basic LBP operator is that a 3×3 will not capture dominant features with large scale structures. The operator was later generalized to use neighborhoods of different sizes to deal with different scales. A local neighborhood is defined as a set of sampling points evenly spaced on a circle which is centered at the pixel to be labeled, and the sampling points that do not fall within the pixels are interpolated using bilinear interpolation, thus allowing for any radius and any number of sampling points in the neighborhood. In the Figure 6, shows examples of pixels of images, with P neighborhood points on a circle of radius R.

4.3   Scale-invariant Feature Transform(SIFT)

SIFT [26] is a popular technique used to compute the feature vectors of the analyzed images. The feature vectors are obtained by extracting feature points called keypoints and their descriptors from an image. These keypoints are invariant to image scale and rotation and are shown to provide robust matching across a substantial range of affine distortions, addition of noise. The features generated are also highly distinctive, which allows a single feature to be cor-

rectly matched with high probability against a large database of features. The scale-invariant features are identified using a staged filtering techniques. First stage recognizes the key locations in scale space by looking for maxima or minima of a difference of Gaussian function. Each point is used to generate feature vectors that describes the local image region relative to its scale-space coordinate frame. The resulting feature vectors are called SIFT keys. These keys derived are used as an input to a nearest-neighbor indexing method that identifies candidate object matches.Figure 7 represents the stages of generating keypoint descriptors in SIFT. Keypoint descriptors are generated by computing gradient magnitude and orientation at each image sample point in a region around keypoint location. These samples are then accumulated into orientation histograms summarizing the content over the subregions. These keypoint descriptors are crucial for matching purposes. Best candidate match for each keypoint is found by identifying nearest neighbor.

4.4   Structural Similarity Index(SSIM)

The SSIM [51] index was proposed to predict human preference in evaluating image quality . Assuming human visual system(HVS) is optimal in extracting the structural information from visuals, an index from SSIM should be a good metric in inferring perceptual image similarities. The Structural Similarity index is used to measure the similarity between two images. This index can be viewed as a quality measure of images being compared, provided the other image. Give two images $x = \{x_i \| i = 1, ...M\}$ and $y = \{y_i \| i = 1, ...M\}$, the SSIM index is defined as:

Image gradients   Keypoint descriptor
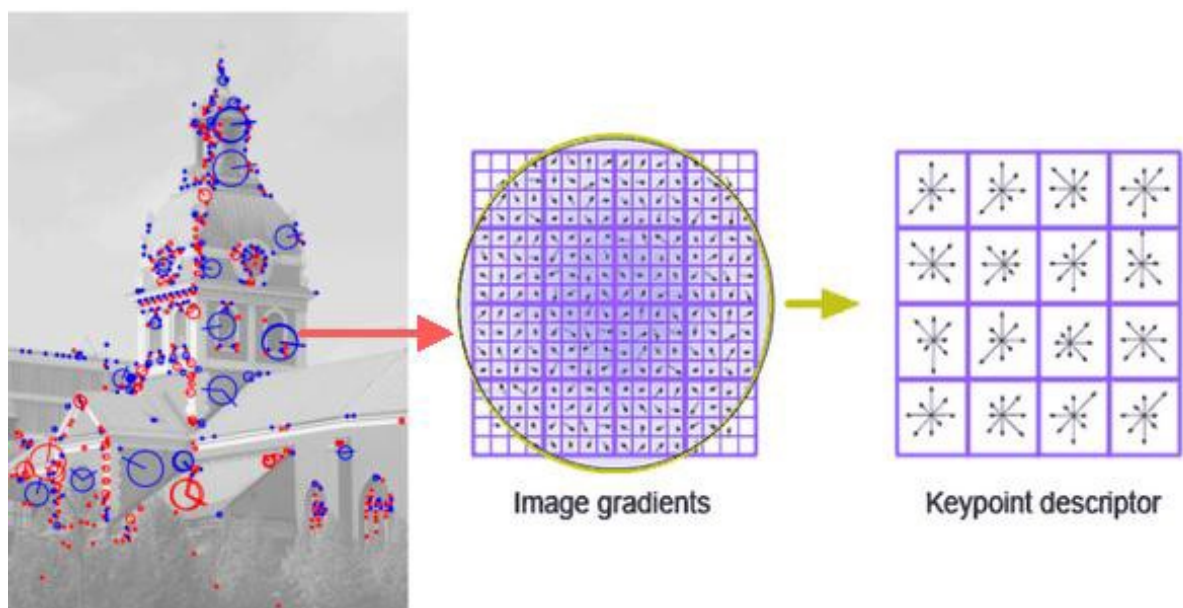
Figure 7: SIFT Architecture:

Source: Source — [26]

$$S(x,y) = \frac{(2\mu_x\mu_y + C_1)(2\sigma_x y + C_2)}{(\mu_x^2\mu_y^2 + C_1)(\sigma_x^2 + \sigma_y^2 + C_2)}$$

where μ and σ are the sample mean, standard deviation or covariance, and C_1 and C_2 are two positive stabilizing constants respectively.

4.5 <u>Summary</u>

In this chapter, we describe the important terminology we will be using in explaining the models architecture and feature representation techniques of images are also presented. In the following chapter, we explain the proposed approach and architecture of both supervised and unsupervised classification tasks to solve - identifying genetic relatedness based on visual patterns.

CHAPTER 5

PROPOSED APPROACH - SUPERVISED AND UNSUPERVISED

5.1 Supervised and Unsupervised Learning Motivation

We modelled this problem as typical case of pattern recognition [21] problem that can be stated as: Given patterns on pair of egg shells, can we recognize similarity within these patterns? This can be done using one of the following tasks: 1) *Supervised classification*: where the similarities within input patterns are classified into one of the *predefined classes*, in our case, broods, 2) *Unsupervised Classification*: where pairs of images are classified to an unknown class based on similarity of patterns. In the following chapter we present the Unsupervised models' architecture. In the subsequent sections of this chapter, we describe the supervised models' architecture and introduce terminology related to this classification task.

5.2 Supervised Techniques

5.2.1 Siamese CNN

Siamese neural nets were first introduced in 1990s by Bromley and LeCun to solve signature verification as an image matching problem [6]. A siamese neural network consists of two identical sub-networks which are used to process two distinctive inputs and a subsequent module metric function. The metric function then computes the desired metric between the highest level feature representation obtained from the sub-networks. Figure 8 shows the architecture of a Siamese CNNs and input to the network is a pair of images. That is, we consider a positive pair

of images (I_q, I_p) to be images of same category (same brood/nest), which are either original images or variants produced by data augmentation (discussed below, see Section **??**), and a negative pair of images (I_q, I_n) to be images from different categories (nest/brood). We map these images using CNN networks to get a high-dimensional embedding, translating an image I to its high-dimensional embedding coordinates x. The goal of this embedding is to have the positive images (from the same class) closer together (as measured by some distance measure, such as Euclidean or Manhattan) than the negative pairs of images from different classes.

Label $Y = 1$ is given to dissimilar images or negative pairs and label of $Y = 0$ is given to pairs of similar of positive pairs. These labels are subsequently used in training the siamese CNN model as the two classes.

The subnetworks of siamaese network have shared weights optimised by contrastive loss function L [**?**].

$$L(\theta) = (1 - Y)\frac{1}{2}\{D(x_p, x_n)\}^2 + (Y)\frac{1}{2}\{max(0, m - D(x_q, x_n))\}^2$$

Contrastive loss function(L) computes loss per training example. Total loss is summation over all image pairs. We used the concept of *Transfer Learning* as described in previous section 3.2.1 to avoid the challenge of training a model from scratch. Pan and Yang [34] defined Transfer Learning as a framework described below:

A domain D consists of two components, feature space $\mathcal{X}$ and a marginal probability distribution $P(X)$, where $X = \{x_1, ..x_n\}$. Thus, a domain can be represented as D $= \{\mathcal{X}, P(X)\}$.

A task T can be defined as two element tuple of the label space $\mathcal{Y}$ and an objective function, η can also be represented as $P(\mathcal{Y}|X)$.

Transfer learning is thus formally defined as, given a source domain D_s, a corresponding source task T_s and a target domain D_t and a target task T_t, transfer learning enable us to learn the target conditional probability distribution $P(\mathcal{Y}_{\sqcup}|X_t)$ in D_t with the information gained from D_s and T_s. An assumption is number of labelled target samples available are lesser than labelled source samples.

5.2.2   Pairwise SVM

Pairwise Support Vector Machines (SVMs) are support vector machines that are able to handle pairwise classification tasks described in the previous section. Let X be an arbitrary dataset and n be the number of training points, $x_i \in X$. For each pair of training examples, (x_i, x_j), we identify whether they belong to same class or a different class. Subsequently, for every training example we assign label y_{ij} as +1 if from same class/same brood, y_{ij} as -1 if from different class/different brood.

For pairwise SVM model, we used Local Binary Pattern (LBP) as feature descriptor to extract features and then learn an SVM model on top of these features.

5.3   Unsupervised Learning

Cluster analysis [21] is one of the important branches of unsupervised learning in pattern recognition analysis. It is used to cluster data into different clusters based on the similarity of patterns. Given a set of data points, a clustering algorithm should group them into clusters such that: 1) data points within each cluster will be similar to each other, 2) data points
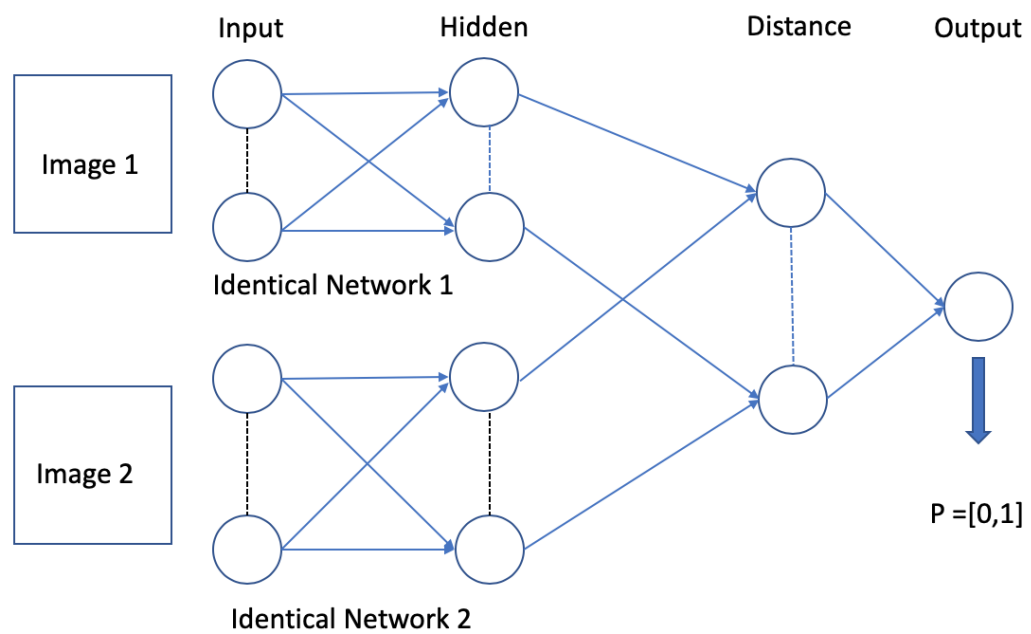
Figure 8: This figure represents a simple two layer architecture of the model Siamese CNN with logistic prediction p. The model represents a pair of images in a high dimensional feature space and measures the distance between two using a distance metric. images which are similar lie close to each other and which are not similar lie farther apart. The networks represented in the figure are twin networks

in different clusters will be dissimilar. To implement this approach, we used Scale Invariant Feature Transforms (SIFT) [26] and Structural SIMilarity (SSIM) [50] to model the features and generate a similarity score between these feature vectors. We then used unsupervised clustering techniques such as Spectral based clustering [32], Affinity propagation [14] and k-means [17] clustering to identify different clusters, in our case broods, within the data.

5.4   Summary

In this chapter we described in detail, the proposed approach and architecture of both supervised and unsupervised tasks. The design details and parameters we chose to implement the model are explained in the subsequent chapters.

CHAPTER 6

EXPERIMENTAL SETUP AND RESULTS

In this chapter, we list the design choices and experimental settings for each of the supervised and unsupervised learning approaches and evaluated them to establish a connection between visual patterns similarity and brood membership. For each machine learning task, we describe implementation details of the feature descriptors, metric learning methods and model parameters. We then present the results of the analysis for each approach.

6.1 Implementation Details : Supervised Learning

6.1.1 t-Distributed Stochastic Neighbor Embedding (t-SNE) for visualization

t-SNE [23] is a non-linear technique for dimentionality reduction that is well used for visualizing and exploring high dimensional datasets in a lower dimensional space by reducing the divergence between two distributions: a distribution that measures pairwise similarities between inputs and another distribution that measures pariwise similarities between corresponding low dimensional points in embedding. By doing so, a t-SNE tries to find patterns within data by identifying clusters formed based on similarity within the data points. Figure 9 and Figure 10 shows the t-SNE plots in 3D and 2D space respectively. We can identify various clusters (according to nest identities) within this plot.
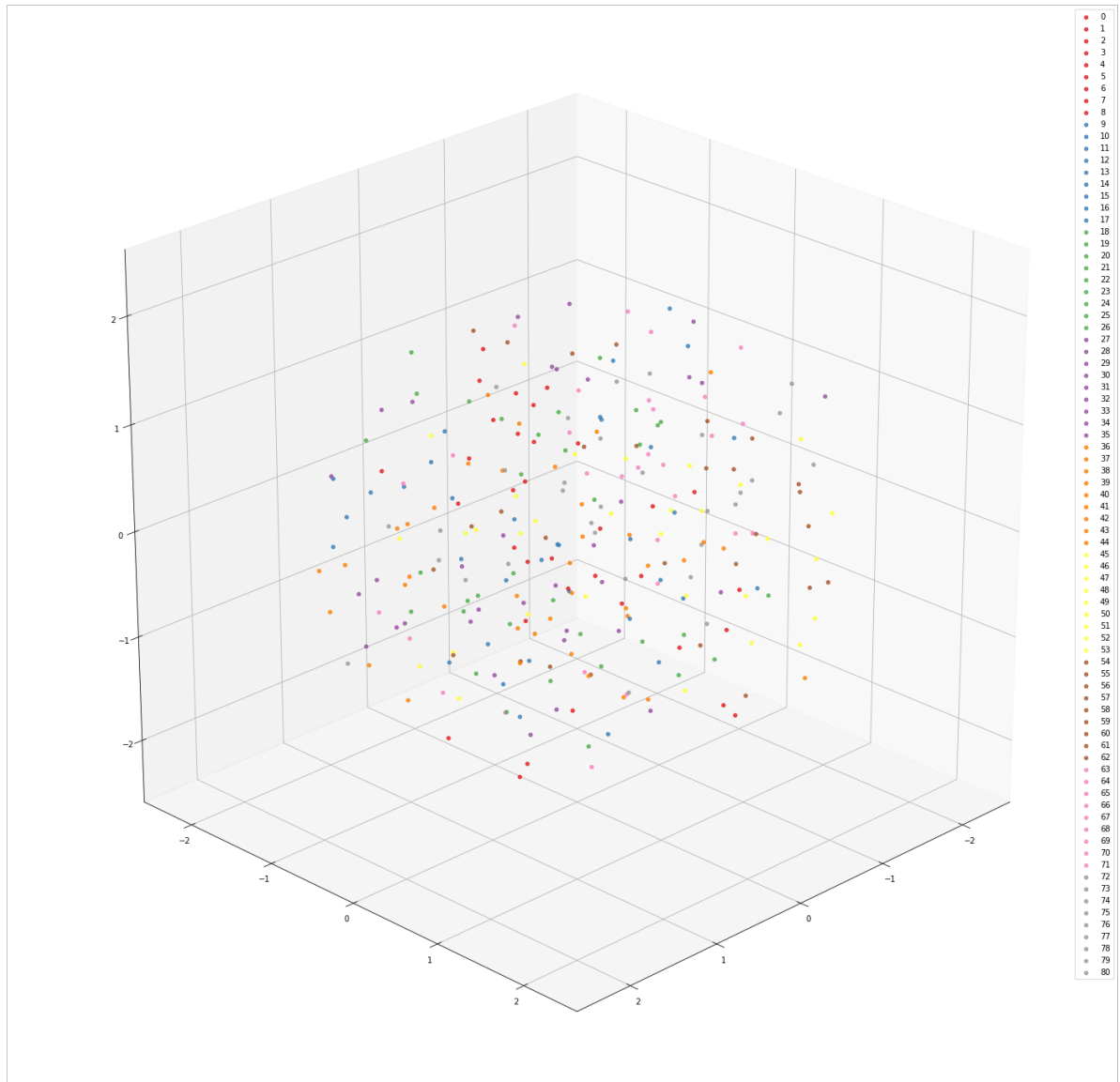
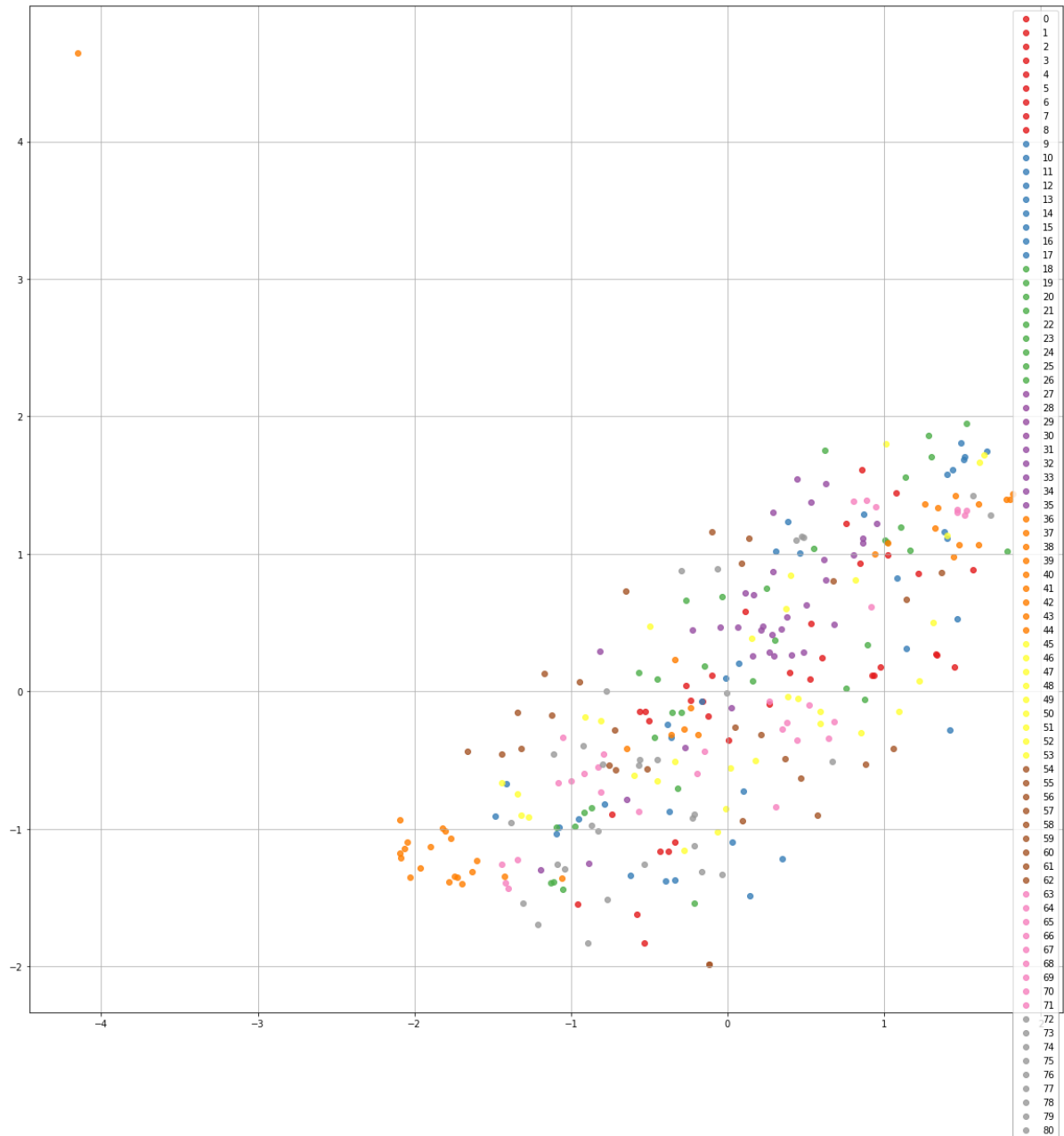Figure 9: t-SNE plot of bird eggs based on nest identities in 3D space

Figure 10: t-SNE plot of bird eggs based on nest identities in 2D space

6.1.2 Siamese CNNs Experimental Setup

We conduct experiments to identify the brood relations between any given pair of egg images. In our model, we used the proposed transfer learning technique in the form of a pre-trained model. As explained in Section 5.2.1, siamese CNN networks should consist of a pair of identical CNN networks. These identical networks are used for extracting features from images. CNN networks we chose to use are pre-trained VGG19 networks [43]. A VGG network accepts an input an image of size 224 by 224. The last fully connected layers of VGG are removed to obtain the high dimensional feature representation of each image in feature space. These feature representations from identical VGG19 networks are further joined using *Euclidean distance* function. The network loss used for the model is contrastive loss function L (Equation 5.1). It defines how well the network places positive image matches closer in high dimensional embedding space and negative image matches, farther. This function tries to minimize the distance between a pair of similar images and maximize the distance between a pair of different images.

For *Optimization*, a variety of optimizers such as ADAGRAD, ADAM, Stochastic Gradient Descent (SGD) were used to train the model. Adaptive learning rate optimizers such as Root Mean Square Propagation (RMSProp) was also used. SGD optimizer was chosen due to its better control over updates of learning rates and magnitude of weights. Learning rate is the amount the weights of neural networks are updated during training. We have experimented with learning rates from 0.001 to 0.1.

For *Data Augmentation* of the existing 297 images, we used both rotation and dropout. We rotated images twice by a random angle from 0 to 180 degrees. Dropout is a technique where randomly selected neurons in the neural network are ignored while training [44]. This technique prevents a layer from seeing an exact data pattern twice, which acts as a data augmentation step as well as avoids overfitting. There were 1188 images after data augmentation, resulting in the number of images shown in Table Table III.

We used random 70/30 split for the training/testing data (once[1]), considering each *image* as an input data point. Number of images available for training are 831 and number of images available for training are 357. After creating every possible combinations of images, we get, $\binom{831}{2} = 344865$ pairs of training images and $\binom{357}{2} = 63546$ pairs of testing images.

TABLE III: Number of positive and negative pairs before undersampling, after undersampling and bootstrapping

	Total Pairs	Positive Pairs	Negative Pairs
Before Undersampling	344865	5062	339803
Ater Undersampling	21185	5062	16123
After Bootstrapping	10682	4832	5850

---

[1]We will run more testing analysis

For *training*, we initialized the Keras pre-trained VGG19 network with network weights initialized from IMAGENET dataset [41]. We used negative and positive pairs of images as training input. An image of the input pair is classified using the VGG19 network and the resulting embeddings of the two images are then compared using Euclidean distance. We train the model to minimize the distance for positive input pairs, while maximizing it for negative input pairs.

In artificial neural networks, an epoch refers to one cycle through training on a dataset. Choosing the right number of epochs is important for a model convergence without overfitting during training. We used *early stopping criteria* to stop the training when *validation loss between epochs* has stopped improving. We saved the weights of the best model's neural networks.

As seen from Table Table III, there are many more negative pairs of images (344865) than positive pairs of images (5062), thus the data set is highly imbalance, with a much larger negative class. The problem with highly imbalanced datasets is that a simple majority class classifier may perform very well and it is difficult to learn the minority class. We have performed random undersampling, to avoid imbalance caused by negative pairs of images. Number of positive and negative pairs for both training and testing data after undersampling are shown in Table Table III. In addition, to overcome the challenge of imbalanced datasets we used bootstrapping aggregating.

Bootstrapping involves iteratively resampling m new training datasets each of size n with replacement. We have set $m = 8$. Then, m models (VGG19 as base learners) are fitted on m bootstrapped samples. The updated weights of the siamese CNN models are finally

combined using aggregation, which helps in prediction of classes (same brood or different brood). Table Table III shows the number of positive and negative samples after bootstrapping with replacement is performed (on the augmented dataset). The number of base learners created in our project are 8.

6.1.3 <u>Siamese CNNs Results</u>

The model is ran and tested on Amazon Web Services (AWS) EC2, p2.x and p2.8 instances. Test set was random 20% of available pairs. We assessed the experiments using accuracy and confusion matrix. Table Table IV shows the confusion matrix obtained on the testing dataset. The true positives are number of pairs of egg images that are actually similar/coming from same nest. The true negatives are number of pairs of eggs that are coming from different nest. False positives are number of pairs of eggs that are actually not similar but are classified as similar and false negatives are number of pairs which are similar but are classified as not similar. *Accuracy on testing set, 93.32%, is only predicting the majority class.* Other performance metrics are summarized in Table Table X.

Figure 11 and Figure 12 plots the histogram of euclidean distance and number of pairs having that euclidean distance for same and different pairs. The histogram showed that there is no separation between distances of same and different pairs and hence separation of same and different pairs by siamese networks is not happening. Siamese networks with other embedding techniques to encode the images into high dimensional space might capture the right metrics and improve the results.
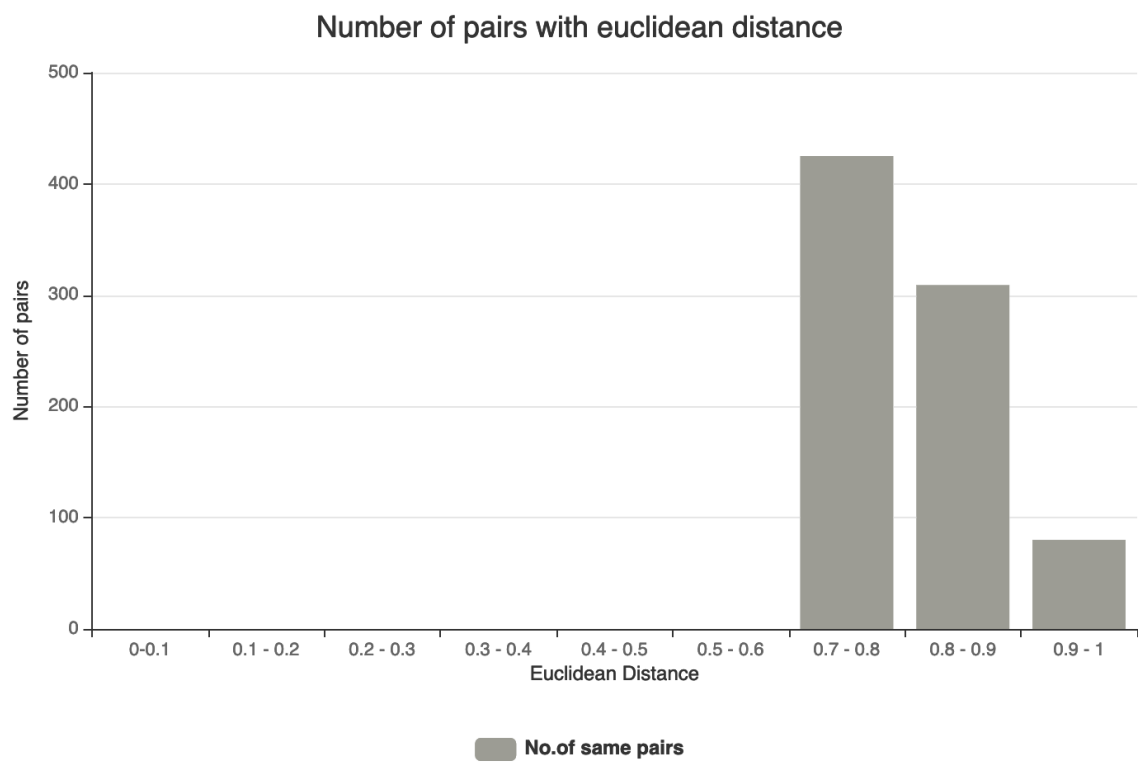
Figure 11

Histogram of euclidean distance versus number of similar eggs having that euclidean distance
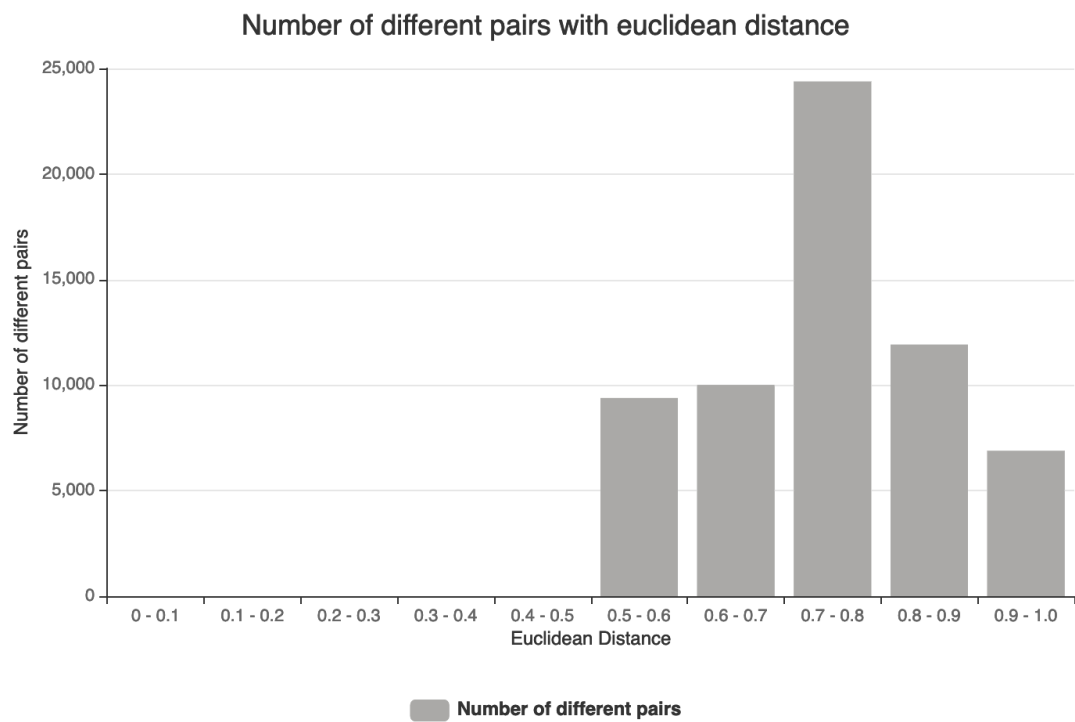
Figure 12

Histogram of euclidean distance versus number of different eggs having that euclidean

distance

TABLE IV: Confusion matrix results for the Siamese CNNs on test dataset of 63546 pairs. Each entry shows the number of corresponding pairs in the appropriate category.

	Predicted	
	Different Brood	Same Brood
Different Brood	62575	0
Same Brood	971	0

6.1.4 Supervised Pairwise SVM

The strategy of Pairwise SVM and Siamese CNNs are same, except we have used VGG19 for feature embedding and learning whereas in Pairwise SVM we have used LBP for encoding the descriptors and then SVM was used as a model to learn the feature representations of pairs of bird egg images.

LBP is most commonly used for texture analysis, as mentioned in Section 4.2. We set the parameters of LBP as follows: Radius of the pattern surrounding the centre pixel to be 3 and number of points along the outer radius to be 24. LBP computation is handled by `skimage`'s `local_binary_pattern library`. Then we obtain the histograms of the LBP labels of the image patterns. These histograms of the pairs are concatenated and processed through SVM with the *poly kernel*. 10 fold cross-validation is also performed. *Results* on test set are shown in Table Table V

TABLE V: Confusion matrix for the LBP+Pairwise SVM Results on the test dataset of 63546 pairs. Each entry shows the number of corresponding pairs in the appropriate category.

	Predicted	
	Different Brood	Same Brood
Different Brood	38476	24099
Same Brood	208	763

6.2 Implementation details: Unsupervised Learning

6.2.1 Clustering on SIFT, SSIM and LBP features

SIFT is most widely used feature type in object recognition tasks. We have used OpenCV [20], which provides ready-to-use platform for easy implementation of SIFT keypoint and descriptors generation. Here we followed the default settings from OpenCV for creating SIFT descriptors. A 4×4 array of histograms with 8 orientation bins in each were used. Therefore, the feature vector was of size $4 \times 4 \times 8 = 128$ for each keypoint. Figure Figure 13 shows an example feature vector generated and the corresponding orientation histograms.

For feature matching (among candidate images) we used a brute force match available standard in OpenCV. It uses K-Nearest Neighbor algorithm for matching descriptors. We used $K = 2$, following Lowe's paper on SIFT [26].

Image gradients → Keypoint descriptor
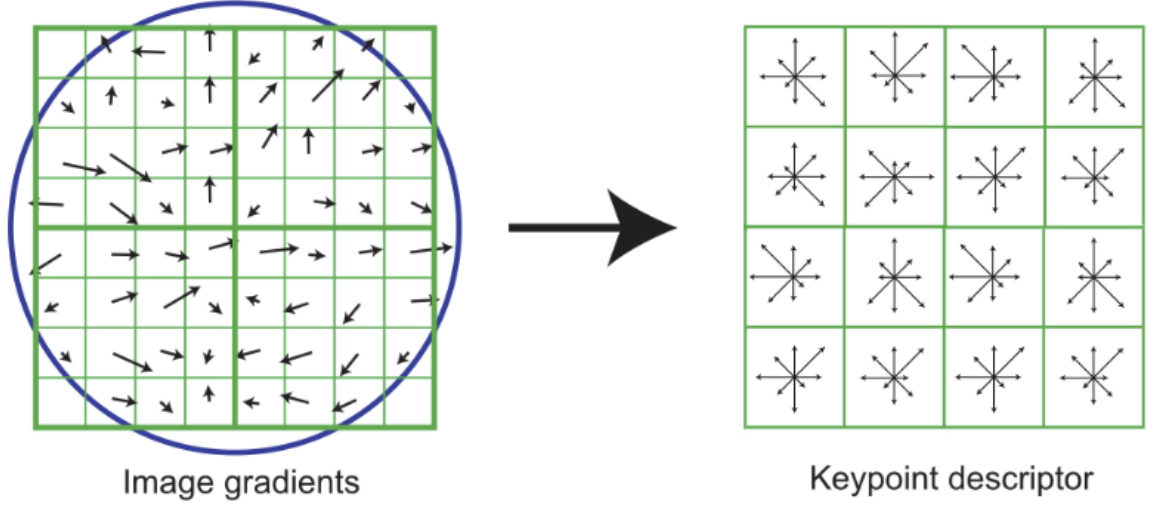
Figure 13: SIFT Keypoint Descriptor: an example of a 4×4 descriptor array computed from 8×8 set of samples, which is also the settings used in our SIFT feature embedding.

Source: Figure 7 from [26]

For SSIM, we used the the SSIM implementation (compare_ssim) available in *scikit-image* [47] and calculate a similarity score for every pair of images. The value is in the range $[-1, 1]$, with 1 being the perfect match.

6.2.2   Clustering Results

In this section we discuss the Clustering results with SIFT, SSIM and LBP descriptors. We used Spectral Clustering, Affinity Propagation clustering and K-Means clustering to divide the images into group of clusters based on brood relations. Silhouette Coefficient, Completeness

Score and Homogeneity Scores are best used to understand the clustering efficiency which are described below.

Silhouette Coefficient [40]: The Silhouette Coefficient is a measure of how similar an object is to its own cluster compared to other clusters. Silhouette value ranges from -1 to +1, where higher value indicates an object being correctly classified to its cluster.

Completeness Score [38]: A clustering result satisfies completeness if all the data points that are members of a given class are elements of the same cluster.

Homogeneity Score [38]: A clustering result satisfies homogeneity if all of its clusters contain only data points that are members of a single class

Table Table VI shows the clustering results by using SIFT descriptors. Table Table VII shows the clustering results by using SSIM descriptors and Table Table VIII shows the clustering results by using LBP descriptors.

TABLE VI: SIFT Clustering Results

Clustering	Silhouette Coefficient	Completeness Score	Homogeneity score
Spectral	-0.89	0.60	0.41
K-Means	-0.97	0.69	0.68
Affinity Propagation	-1	0.58	0.41

TABLE VII: SSIM Clustering Results

Clustering	Silhouette Coeff	Completeness Score	Homogeneity Score
Spectral	-0.29	0.64	0.45
K-Means	-0.25	0.59	0.24
Affinity Propagation	-0.42	0.71	0.66

TABLE VIII: LBP Clustering Results

Clustering	Silhouette Coeff	Completeness Score	Homogeneity Score
Spectral	-0.95	0.82	0.73
K-Means	-0.86	0.70	0.62
Affinity Propagation	0.03	0.61	0.15

TABLE IX: Number of clusters for SIFT, SSIM and LBP features, using different clustering methods. Real number of broods is 81.

Clustering	SIFT	SSIM	LBP
Spectral	59	59	59
K-Means	81	81	81
Affinity Propagation	24	28	3

6.3   <u>Summary</u>

We identified from the experiments that Siamese CNNs are still learning the majority class, even after performing bootstrap aggregation to avoid issues due to imbalanced data. Clustering techniques with SIFT, LBP and SSIM are also not showing encouraging similarities within the clusters formed, according to Silhouette coefficient, completeness and homogeneity scores.

TABLE X: Precision, Recall and F1-Scores of Supervised and Unsupervised algorithms

	Precision	Recall	F1-Score
SIFT+K-Means	0.01	0.011	0.01
SIFT+Spectral Clustering	0.013	0.018	0.01
SIFT+Affinity Propagation	0.01	0.002	0.003
SSIM+K-Means	0.01	0.003	0.004
SSIM+Spectral Clustering	0.016	0.014	0.015
SSIM+Affinity Propagation	0.006	0.004	0.002
LBP+K-Means	0.01	0.008	0.01
LBP+Spectral Clustering	0.014	0.013	0.01
LBP+Affinity Propagation	0.01	0.004	0.003
LBP+SVM	0.03	0.78	0.039
Siamese CNNs	0	0	0

CHAPTER 7

CONCLUSIONS AND FUTURE WORK

7.1   <u>Conclusions</u>

The aim of this project was to develop a machine learning model which can determine the correlation between visual markings and genetic relatedness. Biologists hypothesize that visual markings have genetic underpinnings and in some cases can be used as a proxy for genetic relatedness. Motivated by this finding, we set out to quantify genetic relatedness using visual markings similarity by applying machine learning approaches on a birds egg dataset.

We have compared several state of the art approaches to encode images features, such as SIFT, LBP and CNN embeddings of visual patterns and explored various image similarity algorithms, such as siamese neural networks, pairwise SVM and unsupervised clustering techniques. In our experiments, none of the methods performed well, with pairwise SVM with LBP feature descriptor performing better than others, giving the still low F1 of Table X.

Based on the results and discussions so far, we find that using visual markings similarity to identify genetic relatedness is a viable approach. While there is no strong evidence showing that the approach we chose works perfectly, the results we have produced is encouraging our hypothesis to pursue advanced future research directions. We strongly believe that with enough training data and more sophisticated machine learning approaches reasonable and improved connection between genetic relatedness and visual patterns can be produced.

7.2   Future Work

The objective of this research was to use machine learning to learn the features and patterns of bird egg images and identify the similarity between them. One of the future application of our work is to understand the nesting behaviour of birds and their ability to identify their brood. We want to produce various similar, slightly similar to highly distorted patterns of eggs based on the patterns learnt, to understand what extent a bird recognizes its own brood. To make it possible, we want to make the machine learning model learn the patterns of the eggs and their similarity scores - hence, this thesis. We then would like to generate various patterns of eggs using our trained models and produce 3D printed eggs with these learned patterns. We then intend to put these 3D printed eggs at the nesting location to identify to what extent a bird can accept an egg as its own.

So far, from the results obtained in this work none of the machine learning methods we chose performed well. Hence the current signals doesn't show a signal that genetic relatedness can be quantified based on visual patterns similarity. However, a lot of work can be done to improve the accuracy and the results, and in this chapter, we explain a few directions which can be pursued further to enhance the results and quality of work already performed.

7.3   Data Augmentation as an enhancement:

Even though the state of the art Siamese Networks are well-suited for performing similarity detection tasks, the results obtained in this work are far from perfect. We believe the biggest reason for this is lack of a large dataset and therefore lack of sufficient features for the machine learning models to learn. In order to overcome the challenge of a small dataset, we applied classic

image transformations such as rotating, cropping and zooming, which boosted and enlarged the data and provided additional features required for training. We have also implemented few-shot learning with the help of siamese networks. However, standard data augmentation produces only limited possible alternative data. Furthermore, we hope that using more advanced techniques such as generative adversarial networks(GANs) [?], matching networks for one shot learning [?] can potentially improve the results. GANs are able to learn and produce indistinguishable data from the available original data. This model takes any data item from source domain and generalise it to generate other within-class data item and thus, provides a broader set of augmentations. Matching Networks for One Shot Learning, on the other hand, uses attention and memory for rapid learning and is proven to work well in cases where there is less amount of data. Overall, these methods can generate new images of high quality that combine content of a base image with the appearance of other images. The newly created images are expected to improve the training process drastically [15]. Although we have used **Transfer Learning** in our model in the form of few-shot pre-trained model approach, using VGG networks, in the future, we would like to leverage Inception [45], Xception [9] and ResNet-50 [18] models and study how these models impact the results. Another possible direction is to add more hand-crafted features such as the color and density of the spots on egg and their shape and sizes.

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