Mid-Term Report

A study into the feasibility of using machine learning techniques to process ct scans of labrador joints and detect signs of joint incongruity which produces elbow dysplasia and lameness.

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# Abstract

Elbow dysplasia is a disease afflicting many species of dogs, which has been hypothesised to be related to joint incongruity. In this paper, a possible way of characterising joint incongruity within Labradors suffering from elbow dysplasia is described. This is implemented via three-dimensional models from X-ray CT of the radio-ulnar joint and deforming healthy joints to quantify the difference between them and a joint of dogs presenting symptoms of elbow dysplasia. Early stages of an implementation of software designed to do this is described, with the bone structure of the joint being read from x-ray images and translated into three-dimensional models which can then be mapped onto each other via rigid registration.

The aim of this dissertation is to investigate how artificial intelligence, specifically deep learning, could be used to better understand the causes of elbow dysplasia. The objectives are as follows:

1. To develop a set of pre-processing steps to automatically segment bone from X-ray CT data.
2. To train a CNN to identify the three main types of elbow dysplasia present in a dataset obtained from Fitzpatrick Referrals.
3. To use a Class Activation Map (CAM) to understand the regions in the data which are key to the Convolutional Neural Networks decision making.
4. To use Google Deepdream to envisage each of the idealised 3 modes of joint dysplasia.

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# Chapter 1: Introduction

## Canine Elbow Dysplasia

In recent years, there has been an increasing awareness among the veterinary community of elbow dysplasia within dogs, where the bones of the elbow and surrounding cartilage show signs of developmental abnormalities.[1] The diagnosis is typically used to refer to a condition in which the anconeal process, normally found at the tip of the ulna as shown in Figure 1, is unfused with the upper ulna bone[2]. Over time this can cause the erosion of the cartilage between the joint, which when left untreated can result in severe joint pain and lameness.

While elbow dysplasia is an umbrella term for many issues that can arise with the medial compartment of the elbow in dogs, the focus of this project will be on joint failure due to abnormal distribution of forces on the joint causing microfractures, also known as Fragmented Coronoid Process (FCP). These abnormal forces are often attributed to either soft tissue forces such as bicep forces pulling on the ulna [3]. However, it has also been theorised that incongruity of the surface of the joint could also be responsible. [4]

Figure - A dog elbow displaying signs of elbow dysplasia. Arrow 1 indicates a step between the radius and ulna, arrow 2 an unfused upper anconeal process and 3 shows a fragmented medial coronoid process (FCP) [21]

This incongruity can typically be characterised in three ways [5] [6]: Sagittal R-U Incongruity where the radial bone pistons away from the ulna when the joint is extended, H-U incongruity where the semi-lunar notch (the concave region of the Ulna shown in Figure 1) does not contour to the shape of the humerus and Transverse R-U incongruity where the radial head does not fit to the ulna. The three are not mutually exclusive, with it being possible for a joint to exhibit characteristics of multiple types of incongruity.

Figure - A CT scan of a Labrador’s elbow, showing the humerus connecting to the radius and ulna at the joint.

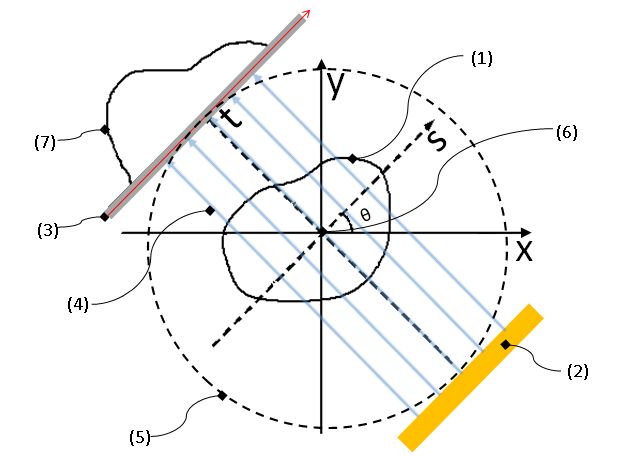
If elbow dysplasia such as that potentially caused by joint incongruity is left untreated, it can often deteriorate into Medial Compartmental Disease (MComD) or osteoarthritis [7] and as such it is imperative to detect the disease early.

Figure - A 3D rendering of the joint shown in Figure 2.

## Current Approaches to Diagnosis and Treatment of Elbow Dysplasia

As elbow dysplasia is inherently an issue with the hard tissue and surrounding cartilage of the joint, diagnosis often requires x-ray computerised tomography (CT) (see Figure 2) and radiography to produce an image of the joint, which can be checked for fragmentation and incongruency. [6]

After diagnosis, there are various possible treatment options depending on the nuances of the situation. In some cases, the bone itself can be reshaped via surgery but this carries a high rate of morbidity so is often avoided. Bone fragments can also be surgically removed to attempt to prevent further cartilage damage, but this does not entirely prevent further wear and so can often require continuous treatment. In severe cases with large amounts of cartilage erosion, it may be necessary for partial or total joint replacement. [6]

The success rates of these operations are greatly increased if the disease is detected early and at a young age, and in some cases it is even possible to perform non-invasive treatments such as hormone treatments to prevent growth spurts and careful diet management to prevent increased strain on the joints. [8]

## X-Ray Computerised Tomography

To obtain the 3D x-ray dataset used to diagnose elbow dysplasia as shown in Figure 2, x-rays are passed through the subject by an x-ray source which rotates around the subject, as shown in Figure 3. Both the x-ray emitter and detector are physically moved in a spiral fashion, resulting in a series of absorption patterns from multiple angles which can be reconstructed digitally to produce a series of cross sections. [9] Hard tissues, such as bone, are denser than the surrounding soft tissue and so absorb greater amounts of the x-ray energy. The level of attenuation is assigned a pixel value, and hence hard tissues appear in each layer of the slice as brighter.

Figure - A representation of the operation of a CT scanner, with the image subject at 1, the x-ray emitter at 2, the receiving sensor at 3, transmission beam at 4, the path of travel for the projector and sensor at 5, the origin at 6 and an image at 7. [22]

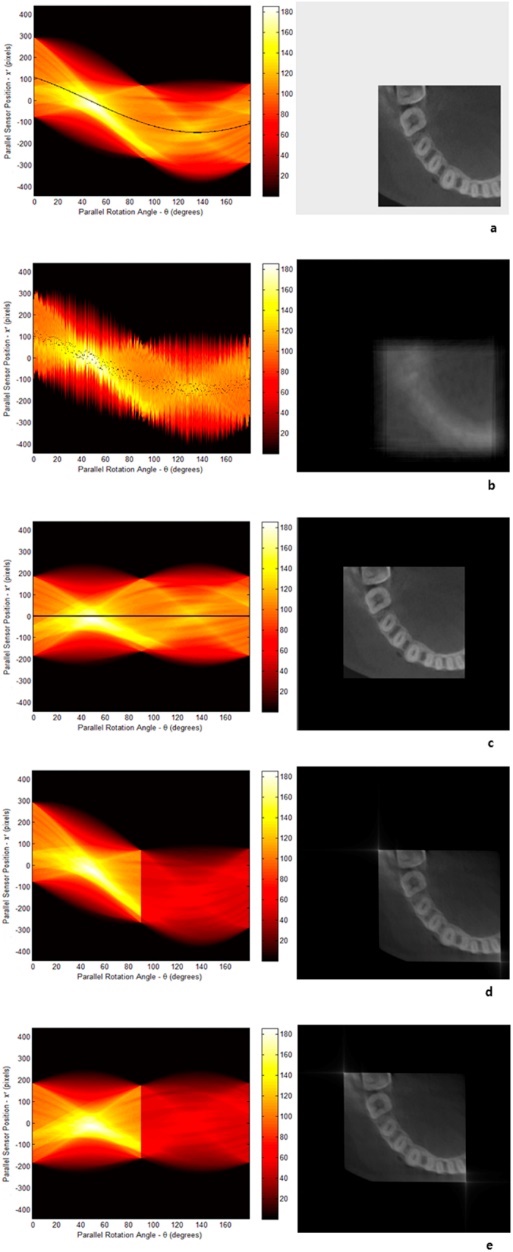


Figure - A sinogram and corresponding CT slice for a human jaw bone. [10]

The initial output of a CT scan is a sinogram, shown in Figure 4, which can be run through a tomographic reconstruction algorithm to produce a cross sectional representation of the scan subject. [10]

## Aims and Objectives

As outlined in Section 1.2, diagnosis of the disease during the early stages can reduce the need for invasive surgery and greatly improve the effectiveness of treatment. The results of this research project could be used to detect early warning signs of elbow dysplasia within dogs when inexperienced or nonspecialised vets may miss them or wish to try a “wait and see” approach which could prove harmful in the long run.

Evidence also suggests that FCP is a hereditary condition [3], meaning that some dogs that do not display symptoms of the condition within their lifetimes but may still pass on a predisposition to it to their off spring. A method of detecting elbow incongruity which may be exaggerated in future generations could be used by breeders to identify which dogs could be unwise to breed and hence provide better breeding values for healthy dogs.

The results from this project should be considered a foundation for potential further research, with a larger data set and a significantly larger amount of allotted time opening up the possibility of using a convolutional neural network (CNN) to process imaging of joints in order to cluster biomarkers read from bone structure and investigate the hypothesis of elbow dysplasia being related to joint incongruity.

## 1.5. Deliverables of Project

The project’s aim is to characterise joint incongruity along the transverse radio-ulnar joint and develop a deformation pattern for incongruent joints to compare against “normal” joints. To successfully do this, CT image slices must be mapped to a three-dimensional digital model and the transverse radio-ulnar joint both identified and separated from the other components of the larger joint.

Through the methods identified in Chapter 3, it should then be possible to obtain a deformation pattern for both normal and incongruent joints which can be used to estimate a threshold for incongruency before symptoms of the condition begin to manifest.

To this purpose, an application must be developed to map joints onto each other via Iterative Closest Point (ICP) to observe the amount of distortion required to mutate the “normal” three-dimensional model into that of an incongruent joint. Further information on these can be found within Chapter 4.

This project is constrained by the allotted time of approximately only one academic year, with an average of ten hours of work time available each week. The nature of the project will require that most of this time is spent working with medical imaging software such as ImageJ within the university and developing software in MatLab for performing image processing operations.

# Chapter 2: Literature Review

## 2.1. Prior Analysis Work on Elbow Dysplasia

As radiography and CT are necessary steps in diagnosing elbow dysplasia in dogs, there has been ample opportunity attempt to construct three dimensional models from the layers produced by CT scans to use as diagnostic tools, and these have lent credence to the idea of the disease being characterised by elbow incongruency. Previous research into elbow dysplasia have supported this hypothesis, with studies into quantifying joint incongruity by measuring the distance between the humerus-ulnar joint and the radio-ulnar joint indicating a clear correlation between the level of incongruity at the coronoid apex and the probability of FCP. [11] [12]

By fitting a sphere to three dimensional renderings of the ulnar trochlear notch to determine sensitivity of radioulnar incongruence, accuracy could be seen to improve to the point where the technique can be “considered safe and highly accurate for clinical application”. [13] This project focused upon H-U incongruity (see section 1.1), whereas we will instead be investigating Transverse R-U incongruity, but the principle of comparing an incongruent joint shape to a “normal” shape (characterised in their study by a simple sphere) remains the same.

## 2.2. Machine Learning as a Diagnosis Aid

The significant potential of machine learning within medicine has been acknowledged across multiple fields, with convolutional neural networks (CNNs) often being capable of detecting markers which a human eye may overlook. CNNs also proved capable of interpolating missing pieces of data in incomplete descriptions of patients, reducing the need for further expensive or intrusive tests [14]. This has resulted in significant research being performed into the potential of machine learning as a diagnostic tool, particularly in orthopaedic medicine.

Hip dysplasia is a condition in which the socket portion of the hip joint imperfectly maps to the ball section, bearing some similarity to the H-U incongruity mentioned in Section 1.1. If left untreated, this condition can develop into hip osteoarthritis and result in significant lameness and discomfort [15]. By supplying a CNN with 420 CTs of human hip joints, it was shown to be possible to diagnose hip osteoarthritis with an accuracy of 92.8% when compared to chief physicians. These results were obtained by constructing a dataset composed of both “healthy” hips and hips presenting symptoms of osteoarthritis and using these as training set for the CNN by selecting the regions of the hip joint indicative of osteoarthritis (see Figure 6) and comparing the shape of the ball and socket at these points. [16]

Figure - A "healthy" hip joint (top) and one presenting symptoms of hip osteoarthritis with arrows at regions indicating this (bottom) [16].

Machine learning has also shown potential for diagnosing fractures within human vertebra, again using CT scans of the affected regions. By extracting features from slices in a two-dimensional CT scan and then producing a set of lower dimension features through feature aggregation, it has been shown to be possible to detect osteoporotic vertebral fractures with an accuracy of 89.2% by feeding these aggregated features again into a CNN.

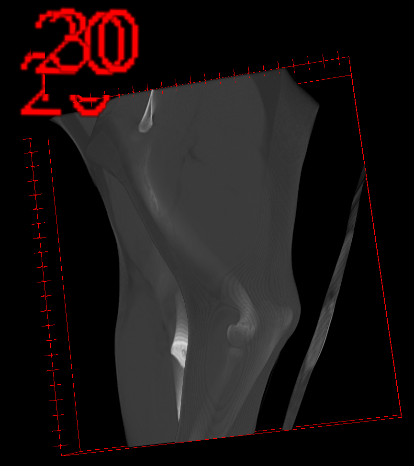
Of note is the fact that the uses of CNNs in diagnostic medicine use only two-dimensional CT scans, rather than the three-dimensional CT scans we will be intending to use. CNNs capable of efficiently processing three-dimensional images are still in the early stages and volumetric representations of data can easily grow unwieldy and computationally intractable [17]. As such, it is unlikely for this project that we will reach the stage of producing a diagnostic aid using a CNN.

## 2.3. Summary

As explained in Chapter 3, a large part of this investigation will involve deforming an incongruent Labrador joint and thresholding it against “healthy” joints which do not present signs of incongruency or elbow dysplasia. Through this, we will be able to quantify the magnitude of incongruence. Attempts to quantify congruity between the ulnar trochlear notch and humeral trochlea have previously been successful, with both computed tomography and radiographic assessment of the shapes and peaks along the joint being consistent with each other. This suggests that if we can quantify the incongruity between the radial head and the ulnar notch, then the accuracy of said data should be on par with that obtained directly from radiography of the original joint. However, the computerised three-dimensional models did typically detect a larger curvature which we may witness within our own work and must compensate for. [18]

Little research appears to have been undertaken into attempting to specifically characterise joint incongruity via deformation patterns against healthy joints, and so this paper may be the first of its kind.

# Chapter 3: Preliminary Investigation

As of the time of writing, an arrangement has been reached with Fitzpatrick Referrals in order to gain access to the joint CT scans which we will process during this investigation. A single scan has been shared so far, with a single slice from this scan shown in Figure 2 and the three dimensional reconstruction of it shown in Figure 7. The shape of the joint depicted in this scan has also been characterised by thresholding the pixel brightness of each slice to obtain the brighter regions indicating cortical (exterior) bone.

## 3.1. Data Description

The data set with which we will perform our research has been obtained from live subjects presenting with various degrees of limb lameness, with the majority of our data indicating some degree of incongruity alongside 80 “normal” joints which we will use as our control.

Figure - A three-dimensional reconstruction of a CT of a Labrador joint.

Each joint image will be a CT file comprised of 536 slices obtained via CT scans of the afflicted limb, obtained using a 164 slice clockwise spiral scanner with a slice thickness of 500µm. From the attached DICOM data, it is possible to view information such as the patient sex, age and weight.

The value of each pixel’s intensity in the image is based off the Hounsfield scale, the standard for quantifying radiodensity of different tissues. The expected data ranges for different tissues can be seen in Table 1.

Table 1 - The expected values for radiodensity in Hounsfield Units for the different substances and tissues expected in a CT scan [19].

|  |  |
| --- | --- |
| **Substance** | **Hounsfield Units (HU)** |
| Air | -1,000 |
| Muscle | +35 to +55 |
| Soft tissue | +100 to +300 |
| Cancellous (inner) bone | +300 to +400 |
| Cortical (outer) bone | +1,800 to +1,900 |
| Foreign metals | >14,000 |

## 3.2. Data Processing

### 3.2.1. ImageJ

To obtain a three-dimensional mode, the CT file for the original example joint supplied to us was imported as a sequence of images to ImageJ. Each slice was converted to an 8-bit grayscale image and the voxel depth set to match the slice thickness at 500µm. After conversion, the image sequence could then be converted into a three-dimensional model using the inbuilt 3D viewer plug in. The result of this can be seen in Figure 7, with the darker grey soft tissue surrounding the lighter bones.

Figure - A 3D reconstruction of an elbow joint from a series of CT scans, from the same perspective as Figure 7.

By then thresholding the image, the soft tissue regions could be removed in order to only leave the hard tissue beneath (see Figure 8). After experimentation, it was found that a threshold of 99 provided the results which offered the clearest depiction of the bone structure while preserving the smallest amount of surrounding soft tissue.

### 3.2.2. MatLab

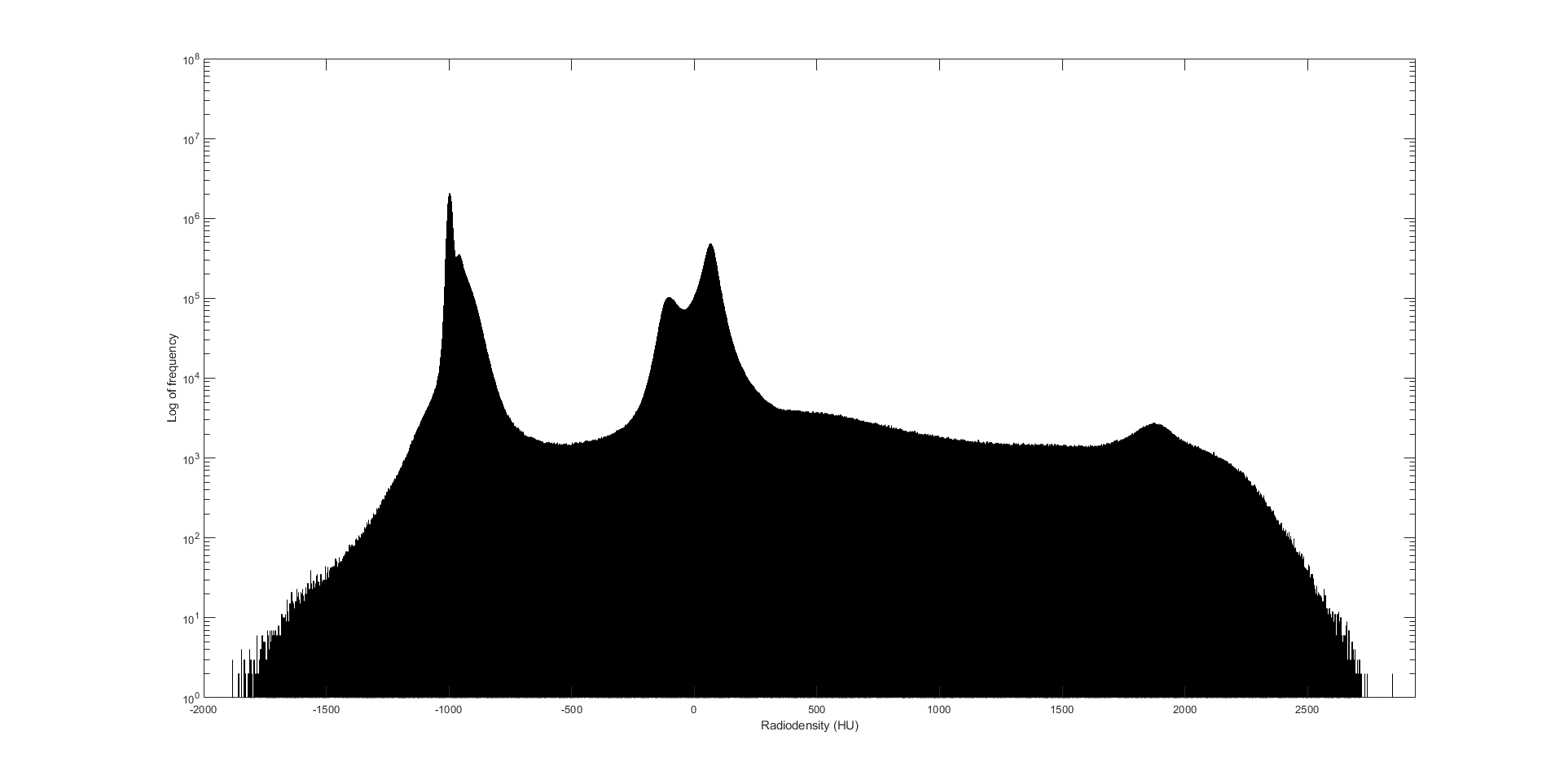
Each slice of the CT scan could also be opened in MatLab to access the raw pixel values and segment the image. Through the “dicomread” command it is possible to access the HU values for each pixel and use it as the grayscale intensity value. As shown by the peaks in Figure 8, each slice in the CT scan is primarily composed of three different materials (air, soft tissue and bone) with different HU values. 

Figure 9 - Histogram showing distribution of values across all slices of a CT scan of an elbow joint.

By selecting a threshold at 300 HU to eliminate all soft tissue, it is possible to produce a binary mask of each layer containing only the cortical bone tissue, shown in the CT scans as a bright white area. These contained errant regions of high intensity, as shown by Figure 10. These could be eliminated using the inbuilt MatLab “*imopen*” and then “*imclose*” commands to first erode and then dilate the image in order to form a clean mask.

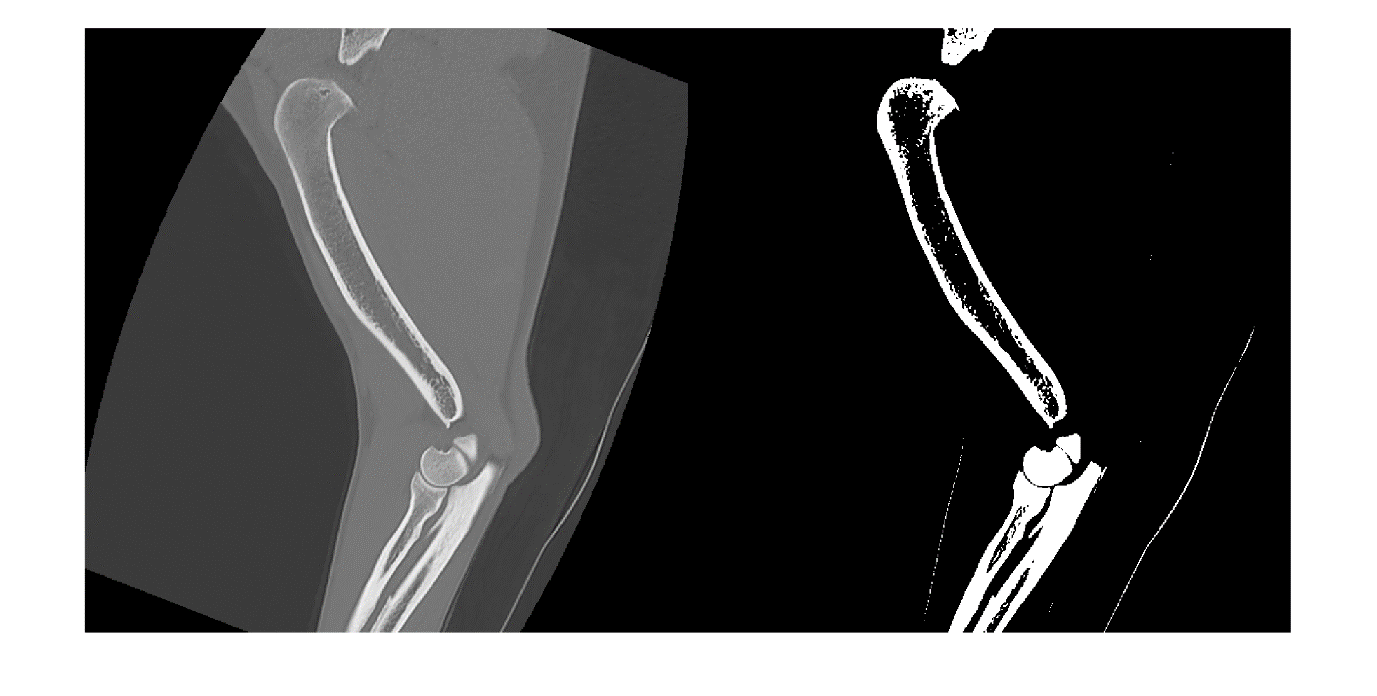


Figure 10 - A CT scan of a labrador joint (right) and a binary mask of the same CT scan showing only the cortical bone tissue (right).

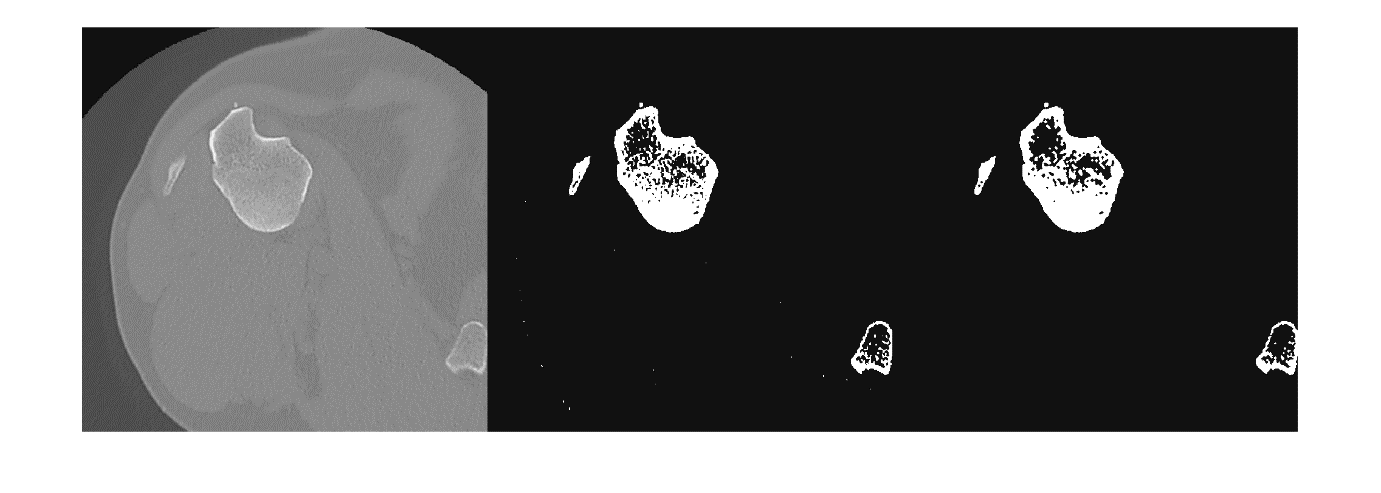
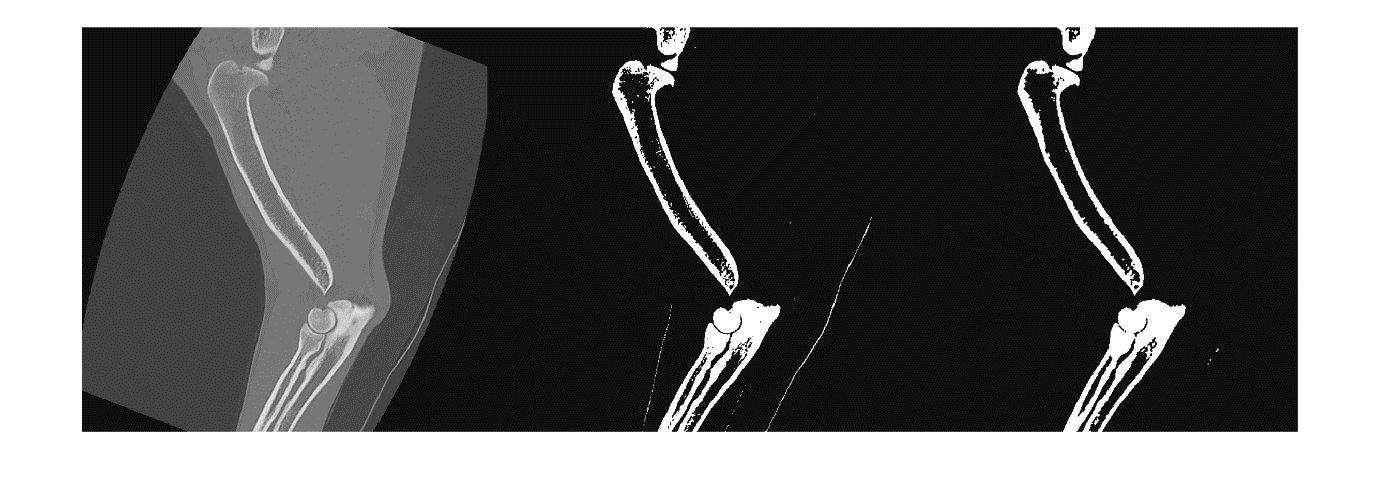


Figure 11 - The original CT scans (left), the same CT scans thresholded to show only the cortical bone tissue (middle) and then the "cleaned up" binary masks (right).

These two-dimensional binary masks were then concatenated into a three-dimensional volume, similar to that produced by ImageJ in Figure 8. Once the larger dataset is obtained, the same process can be applied to each scan to automatically produce a three-dimensional mask for each, as shown in Figure 12.

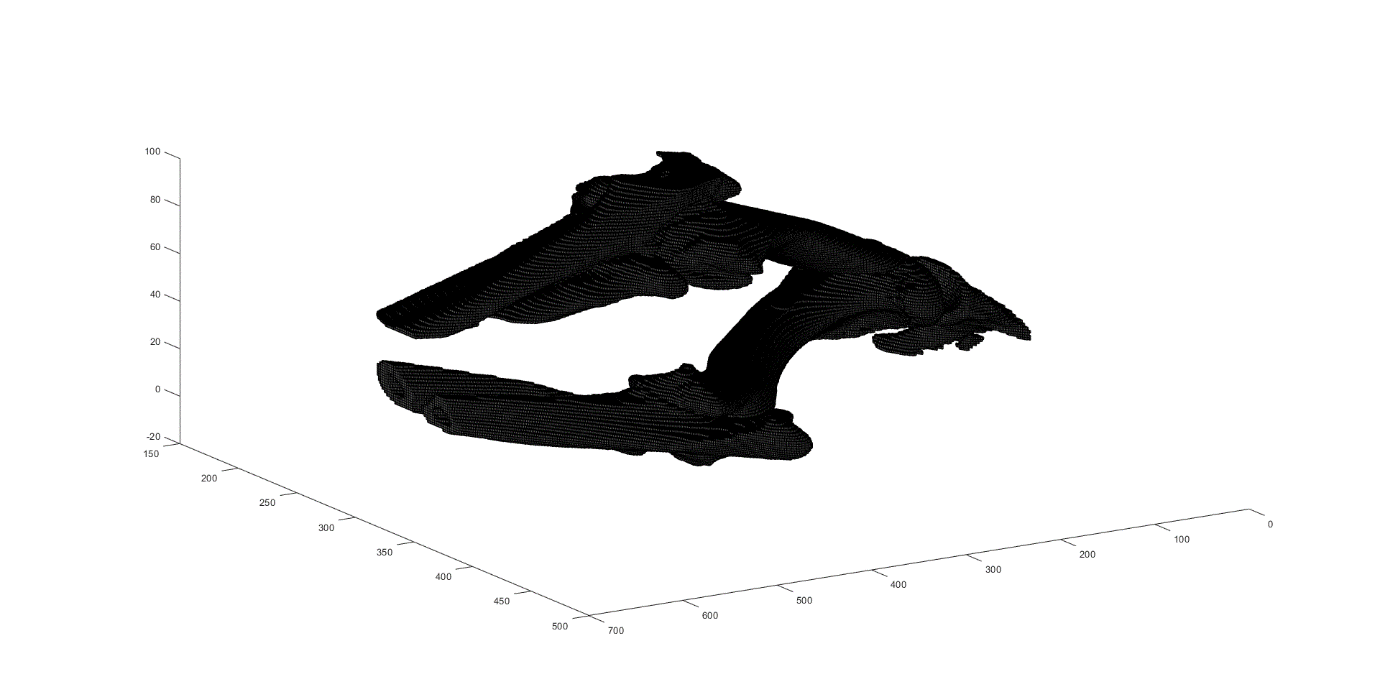


Figure 12 - A three-dimensional binary mask of the cortical bone tissue within a joint, produced through MatLab.

Chapter 4: Conclusions and Future Plans

## Conclusions

Preliminary development has already yielded results in the form of the binary masks, with work being done to produce a three-dimensional model from these now under way. Once this has been completed, the process can be applied to the larger dataset with the largest obstacle being the training of a Convolutional Neural Network (CNN), of which an increased understanding of is necessary. As of the time of writing, the project is currently on track for its planned completion of May 2020.

## Overview of Future Development

From the clean binary masks shown in Figure 11, it should be possible to produce a visual hull similar to the three-dimensional model produced in ImageJ shown in Figure 8. This process can be repeated for all joints in the larger dataset to be obtained from Fitzpatrick Referrals to produce a set of three-dimensional models for both healthy and diseased joints, the latter of which can then be mapped onto the former using an Iterative Closest Point (ICP) algorithm. The difference between the two joint types can then be quantified using a deformation map, from which we will be able to evaluate the role of incongruency in canine elbow dysplasia.

…

A CNN can then be trained to differentiate between healthy and diseased sets by using a subset of the CT scan dataset as training data, categorising the diseased joints into the three types of elbow dysplasia explained in Chapter 1. If these categories prove accurate, a Class Activation Map (CAM) can then be used to evaluate the CNN’s decision-making process and identify the key regions within the CT scans which act as markers for the disease. Google’s Deepdream Generator can then be run to envisage each of the idealised three modes of joint dysplasia.

## Project Plan

Gantt charts depicting a breakdown of the workload for this project can be found in Appendix A. These account for both holidays and exam periods, during both of which the development of this project will be slowed. During the former, focus will instead be on the production of the final dissertation due to the reduced access to university facilities.

Due to the research focus of this project, and results being data driven rather than hypothesis driven, there is an element of risk which must be addressed. A brief overview of these can be found in Table 2.

Table 2 - Potential risks for this project, and potential ways to address them.

|  |  |  |  |
| --- | --- | --- | --- |
| **Risk** | **Consequences** | **Severity** | **Precautionary Measures** |
| Dataset cannot be obtained from Fitzpatrick Referrals | Progress on project will have to be paused while an alternative dataset is found. | Severe | Software development has already begun and can continue which we wait for the dataset to arrive. Work can be tested on the limited dataset we already possess. |
| CNN is incapable of accurately categorising dataset. | Evaluating CAM will be pointless, as no link between joint incongruity and elbow dysplasia has been found. | Moderate | Project can be focused instead onto why CNN cannot identify key areas, and deformation maps instead used to evaluate connection between joint incongruity and elbow dysplasia. |

## Final Report Plan

Due to similarities in structure between this report and the final report due at the conclusion of this project, topics discussed in Chapters 1, 2 and 3 of this report may be reiterated there. In addition to discussing the preliminary analysis, an overview will also be given of the work performed with the larger dataset as explained in Section 4.1.

The results obtained over the course of the project will then be examined and the effectiveness of a CNN as method of identifying the different types of canine elbow dysplasia evaluated. From this, the potential for future researchers to further investigate the role of joint incongruity in elbow dysplasia using machine learning can then be assessed and recommendations made.

It is expected the following chapter headings will be used:

* Title page
* Abstract
* Chapter 1: Introduction
* Chapter 2: Literate Review
* Chapter 3: Methodology
* Chapter 4: Results and Discussion
* Chapter 5: Conclusion
* Chapter 6: Potential for Future Development
* References and Table of Figures
* Appendices

# Chapter 5: Summary

This report explains intentions to use machine learning techniques to evaluate the role of joint incongruency in canine elbow dysplasia, and to identify specific connections between the shape of the joint and the disease.

An overview of canine dysplasia is then given, including causes, diagnosis and treatment, followed by a brief explanation of how the CT scans used within the dataset are obtained. A literature review then explains the successes of previous attempts to use machine learning techniques within medicine, focusing primarily on orthopaedic medicine. Support is also given for the hypothesis that elbow dysplasia is related to joint incongruity, with the research gap which we will attempt to fill identified.

From a limited dataset of CT scans of Labrador joints, binary masks depicting the hard-exterior cortical tissue of the joint have been produced which can now be used to create a three-dimensional model depicting the joint. Aims of using these binary masks and three-dimensional models to produce deformation patterns describing the difference between healthy and diseased joints are then given, with plans to train a CNN to recognise key areas responsible for elbow dysplasia also given. A detailed project plan in the form of a Gantt chart is provided.

Preliminary research performed in preparation for the arrival of the larger dataset is nearing completion, with more in depth work soon ready to begin.

# Appendix



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|  |  |
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# Table of Figures

[Figure 1 - A dog elbow displaying signs of elbow dysplasia. Arrow 1 indicates a step between the radius and ulna, arrow 2 an unfused upper anconeal process and 3 shows a fragmented medial coronoid process (FCP) [21] 3](https://surreyac-my.sharepoint.com/personal/rc00529_surrey_ac_uk/Documents/Mid%20term%20report.docx#_Toc27705046)

[Figure 2 - A CT scan of a Labrador’s elbow, showing the humerus connecting to the radius and ulna at the joint. 3](https://surreyac-my.sharepoint.com/personal/rc00529_surrey_ac_uk/Documents/Mid%20term%20report.docx#_Toc27705047)

[Figure 3 - A 3D rendering of the joint shown in Figure 2. 3](https://surreyac-my.sharepoint.com/personal/rc00529_surrey_ac_uk/Documents/Mid%20term%20report.docx#_Toc27705048)

[Figure 4 - A representation of the operation of a CT scanner, with the image subject at 1, the x-ray emitter at 2, the receiving sensor at 3, transmission beam at 4, the path of travel for the projector and sensor at 5, the origin at 6 and an image at 7. [22] 4](https://surreyac-my.sharepoint.com/personal/rc00529_surrey_ac_uk/Documents/Mid%20term%20report.docx#_Toc27705049)

[Figure 5 - A sinogram and corresponding CT slice for a human jaw bone. [10] 4](https://surreyac-my.sharepoint.com/personal/rc00529_surrey_ac_uk/Documents/Mid%20term%20report.docx#_Toc27705050)

[Figure 6 - A "healthy" hip joint (top) and one presenting symptoms of hip osteoarthritis with arrows at regions indicating this (bottom) [16]. 6](https://surreyac-my.sharepoint.com/personal/rc00529_surrey_ac_uk/Documents/Mid%20term%20report.docx#_Toc27705051)

[Figure 7 - A three-dimensional reconstruction of a CT of a Labrador joint. 8](https://surreyac-my.sharepoint.com/personal/rc00529_surrey_ac_uk/Documents/Mid%20term%20report.docx#_Toc27705052)

[Figure 8 - A 3D reconstruction of an elbow joint from a series of CT scans, from the same perspective as Figure 7. 8](https://surreyac-my.sharepoint.com/personal/rc00529_surrey_ac_uk/Documents/Mid%20term%20report.docx#_Toc27705053)

[Figure 9 - Histogram showing distribution of values across all slices of a CT scan of an elbow joint. 9](#_Toc27705054)

[Figure 10 - A CT scan of a labrador joint (right) and a binary mask of the same CT scan showing only the cortical bone tissue (right). 9](#_Toc27705055)

[Figure 11 - The original CT scans (left), the same CT scans thresholded to show only the cortical bone tissue (middle) and then the "cleaned up" binary masks (right). 10](#_Toc27705056)