DETECTING THIN BONES AND MODELING COD SKELETON

T. Helgason[a,b], R.A. Gudmundsdottir[b], K.L. Valtysdottir[c], K. Andersen[c]

[a]Research- and development department, Landspitali-University Hospital, Iceland
[b]Biomedical Engineering Department, Reykjavik University, Iceland
[c]Marel ehf, Gardabaer

[a]thordur@landspitali.is

ABSTRACT
Fish bones in fillets can be serious problem both to the consumer and to the processing company. Filets with bones are likely to reduce the consumption especially in traditionally weak fish consumption areas. Fish bones can be dangerous leading to wounds in the human digestion tract. Fish, such as cod, have fine structured skeleton and the bone density is lower than that of man. Five cods where scanned with a normal hospital computer tomography (CT) scanner. Their skeletons were segmented out of the data set and a model reconstructed. The model is evaluated by visual inspection and compared to the cod to see what is missing from the skeleton. The density of the bones and otoliths is measured. The results show an almost complete skeleton with thin bones compared to the pixel size of image and with bones that are considerably lower in density than trabecular human bones.

Keywords: Modelling, Cod, Bone detection, Computer tomography

1. INTRODUCTION

Detection of cod bones is of interest in the food processing industry. At the moment bone detection is done by humans that visually look into the fish filet in front of an illuminated desk. The file lies on a transparent plastic plate with a light source underneath the plate. Light penetrates through the plastic and the fish filet and this way the observing human can detect bones or other obstacles inside the filet. If a bone is detected the part of the file is cut away. Disadvantage of this method is that it is not reliable, not every bone is detected. Another disadvantage is that humans are different in detecting the bones making varying outcome of the fish processing. Thirdly, as pointed out by Mery and collaborators 2011, every product needs to be fully reliable to ensure consumer safety but humans tend to get tired and that calls for redundant checks which in turn both slow down the processing time and increase costs. Slower processing time also reduces the quality of the fish.

These circumstances call for a reliable and cost effective way to detect bones in fish filets. Several methods have been discussed in the literature. Many of them are discussed in Mery and collaborators 2011. Also some of us have worked on the issue, see Andersen 2003. Most of these works have in common that they process two dimensional images of the filet. Either light or X-ray images are used. Then several different image processing approaches are used to detect bones. Still, automatic detection of fish bones is extremely difficult, particularly regarding the smallest bones. Also Mery and collaborators 2011 come to this conclusion.

Accurate three dimensional (3D) information about the cod skeleton can help in the development of automated bone detection methods. Pre-information can help localizing where to expect bones. Filleting and other fish processing machines can build upon that. Using X-ray computer tomography imaging (CT) the cod skeleton can be reconstructed in three dimensions to a certain degree. Some bones might be missing from the images due to extremely small thickness or their low density, i.e. low X-ray attenuation.
In this work a common medical computer tomography is evaluated for detecting bones in fish. A 3D model is made of the cod's skeleton and inspected upon missing bones or bones reduced in size. The hypothesis is that thin bones and of low density might be missing or not modelled in full size. Results are promising for further research in this application.

2. MATERIAL AND METHODS

Two cods where scanned in a normal hospital CT scanner. They were scanned in one scan, meaning that the scanning parameters are the same for both cods. The CT data was then processed to segment the cod´s skeleton from the rest of the tissue.

2.1. Material

The two cods are 63 cm and 62 cm long respectively. They were caught at the cost of Iceland and time from catch to scan is counted in hours but not exactly known. They had been processed in a normal way, the fish was gilled, the trunk cut open and the interstitials taken away. They had been kept cold with ice from the moment of catch to scan but not frozen. No salt was

used. They are very similar in size, one is though a little bit longer and with bigger circumference.

2.2. CT scan

The CT scanner used is a Philips Brilliance 64 designed for human clinical use. The lowest available X-ray tube voltage of 80 KV was used corresponding to soft tissue examination. A spiral CT was made with slice thickness of 0.67 mm, a distance of 0.33mm from centre of one slice to the centre of the next slice, i.e. in the z direction along the scan axis. This means that the slices are redundant; each slice covers half of the same volume as the next slice before covers. So there is a 50% redundancy. To cover the total length of the cods body, 63cm and 62 cm respectively, 1909 slices were needed. The image matrix of each slice has 512 x 512 pixels covering an area (field of view) of 344 mm both in x and y direction. So the size of each voxel is 0.672 x 0.672 x 0.670 mm. The total amount of data for both cods is therefore 512 x 512 x 1909 that is in total 500 Mega voxels. Each voxel is digitized with 12 bit or 1,5 byte so the total amount of data is 1,5 x 500 giving 750 Mbyte of data for the whole scan of the two cods. The data set of the cod´s contains three dimensional information of tissue density, and therefore also of the skeleton, of the whole cod. Since each tissue type has a different density the different tissues can be analyzed with this data, so the skeleton and bones can be differentiated from the tissue.

2.3. Bone segmentation

Specialized software (Mimics) designed for analysis of human CT images is used for analysis of the cod's tissue. Each CT slice is a two dimensional (2D) image of a cross-section though the cods body. Each 2D image is composed of picture elements, in short pixels, and is referred to as voxels, volume elements, in a 3D image. Each of them is characterized by its Hounsfield value, HU. The staple of these cross-section images along the longitudinal axis of the cod make up the 3D description of its whole body. By sorting out the voxels having their HU values in certain interval special tissue type can be separated from the rest of the body, i.e. segmented. The group of voxels segmented makes out a geometrical model of the corresponding tissue.

The X-ray attenuation property is specific for each tissue type. The following formula describes the attenuation of an X-ray passing through a material of length x:

$$I = I_0 e^{-\mu x} \tag{1}$$

where I_0 is the intensity of the incoming X-ray and I the intensity of the X-ray after being attenuated in the material it was passing. μ is called attenuation coefficient and is a property of the material. Hounsfield units (HU) are calculated from the formula:

$$HU = 1000 \cdot \frac{\mu_{voxel} - \mu_{water}}{\mu_{water}} \tag{2}$$

This way each voxel in the 3D data set gets its specific HU value characterising the X-ray atenuation properties of the material in that specific point of space. This value is relative to water. The HU for water is zero. Tissue that has higer density and therefore attenuates X-rays more than water have positve HU. This is the case f.ex. for muscles and bone. Tissue that has lower density and therefore attenuates X-rays less than water have negative HU. This is the case f.ex. for fat and lungs in human. Now the process of segmentation can be described by the following somwhat simplified steps:

1. First a so called mask is created by using thresholds. It is composed by all the voxels that have HU value in a defined interval. We use HU in the interval from 226 up to 3071
2. Next a function called region growing is used. By starting at a voxel within the skeleton it finds all voxels that are connected to the starting voxel. This is done for all disconnected parts of the skeleton.
3. Step three is done manually. Voxels which were left out are added manually to the mask. It is also possible to perform this step after step four.
4. The fourth step is so called erode region growing. There can be voxels included in the model that do not belong to the anatomical structure of interest. To eliminate these they are separated from the model with at least one voxel layer and erased. Then normal region growing is performed again and a new mask is created.
5. The fifth step is to do dilate region growing if too many voxels have been erased from the structure. This gives a desired structure of the fish.
6. Step six is used when certain regions of interest are analyzed. The model is then divided into smaller parts by the help of Boolean operations.

In this work the result of the segmentation process described above is a 3D model of the cod skeleton including the fins and the otoliths. After segmentation the tissue analysis is made on the basis of Hounsfield (HU) values and pixel distribution. Volume, density, distribution can be measured and evaluated.

Further description of our segmentation methods and tissue analysis methods can be found in Helgason 2011, Gargiulo 2012 and Johannesdottir 2006.

2.4. Tissue analysis and evaluation

Bone density measurments were done for the following parts of the skeleton: all bones, tail, head, body without head, operculum bone, mid section and the otoliths. For this the skeleton model was divided into these parts and a special mask made for each. In that form the HU values of the voxels belonging to each part can be processed and used in calculations. The average bone densiy in ecah part was calculated according to the following equation:

$$\overline{HU} = \frac{1}{n}\sum_{i=1}^{n} HU_i \qquad (3)$$

Where n is the number of voxels inside the corresponding part of the cods skeleton, that is beloging to a model of that part. Many of the fish bones are considerably thiner than the dimensions of the voxels which are 0,672 x 0,672 x 0,67 mm. This means that beside the bone itself other tissue types influence the HU value for the particular voxel. Mostly that is soft tissue that lowers the HU value. And since all voxels that have lower HU than 226 are excluded from the skeleton model it is to be expected that particulary thin bones are not a part of the skeleton model. This can be the case even though the thin bone has high density. This leads to the assumption that the average HU numbers calculated according to equation 3 from the voxels in the different parts of the skeleton are not necessarily accurate. They can be both higher and lower.

The cod skeleton model is inspected visually on the computer screen and compared to a normal cod skeleton. Missing elements are registered. These can be whole bones or a part of a bone. Another effect is that bones of sub-voxel size lying close together are seen as one plane and not as individual bones. This is the result of the limited resolution of the CT device.

3. RESULTS

The results are shown in table 1 and in figures 1- 5. Table 1 gives an overview of average bone density in several parts of the cod´s skeleton. Figure 1 and 2 show the skeleton of the cod´s head. Figure 3 gives the model of the whole skeleton of both cod´s. This shows in particular the possibilities to find single bones. Figure 4 shows the operculum bones and figure 5 the otoliths.

3.1. Cod bone density

Table 1 gives an overview of density in some parts of the cod´s skeleton. The values are calculated with equation 3 for the whole skeleton and six different parts of the skeleton. The two examples of cod show no substantial difference in bone density. Though cod 2 has higher values in all parts except in the operculum bone. The tail bones have the lowest density. The mid section, where the most valuable parts of the fish are, has a HU of 750 as does the head. Interesting is the considerable higher density of the otoliths, which brings up a question about the purpose of this.

The bone density values from all skeleton parts show that they are good X-ray attenuators and hence suggest that X-rays are suitable for their detection and CT devices are applicable for that purpose.

Table 1: Average density values of cod bones at various locations in the skeleton. There is no considerable difference between the two cod´s.

	Cod 1	Cod 2
All bones	769.0 HU	787.2 HU
Tail	511.7 HU	554.6 HU
Head	750.5 HU	771.9 HU
Body (no head)	721.5 HU	737.5 HU
Operculum bone (Fig. 4)	901.4 HU	879.3 HU
Mid section	752.2 HU	754.3 HU
Otolith (Fig. 5)	2928.9 HU	2935.0 HU

3.2. Bone model

Figure 1 and figure 2 display the same model of the cods head. Figure 1 shows the head model from the right side and figure 2 shows the same head model from the front. As can be seen these figures the skeleton of the cod head is almost complete. Some missing elements are very thin or of low density. At other places bones even of sub-voxel dimensions are detected as such but are displayed at the least as a whole voxel giving the flash perception of a thicker or more massive bone. This is only of concern for small structures.

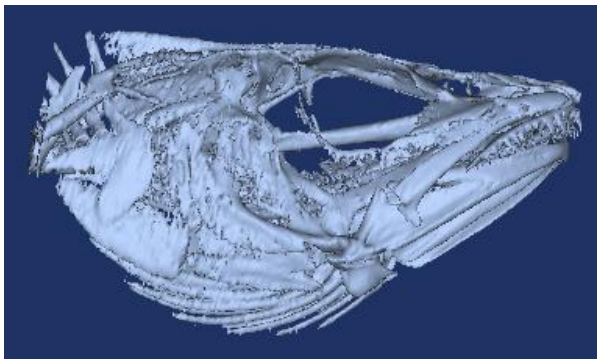

Figure 1: Cod head skeleton model seen from the right side. The model is reconstructed from CT data. Some structures have dimensions smaller than the voxel size and are not imaged in full extent.

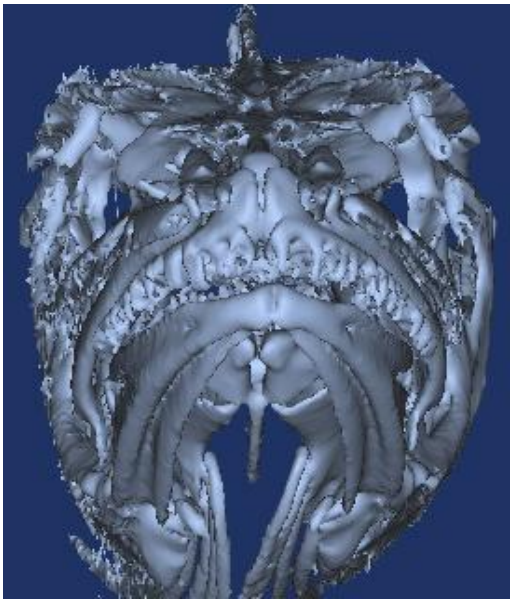

Figure 2: The same model as in figure 1 but rotated 90 degrees, that is the cods head skeleton seen from the front.

Figure 3 shows the two skeleton models, one from each cod. Let us recall that the models are made from 1909 CT slices, each 0,67 mm thick and 0,33mm apart. That results in a clear model displaying also thin bones in diameter smaller than the voxels. But it also clearly displays the drawbacks of the applied CT scanner. From investing figure 3 following observations can be made:

- Bones that are in diameter smaller than the voxels are, in some cases, still imaged as bones, are therefore part of the model
- Bones with higher density than the lower threshold of 226 HU are not in the model if they have small diameter and contribute not enough to the voxel to raise its HU value above the threshold. Especially bones that have a smaller diameter distally are shown shorter than they are in reality since the density values for the distal voxels are beneath the lower threshold. This can be seen in the tail and in the side fins in figure 3.
- Thin bones that lie close to each other are modelled as one piece or one plane. This can be seen in the tail and very clearly in the side fins in figure 3. In the side fins the bones are arranged as rays from a light source. The distance between the increases going from proximal to distal. Proximal they are modelled as one piece but distal they are modelled as separated bones. In between there is an area where they are in one piece but the formation of bones can be seen.
- Comparing the models of the two tails of the cod´s in figure 3 it can be observed that the lower part of the lower cod has bones that are modelled as single bones all the way up to the spine. As a contrast to that in the upper part of the same tail the bones fusion in one solid body. That is also the case in the tail of the upper cod.

The results show a complete model of the two cod skeletons. Missing parts, as described above, give a somewhat false perception of the anatomy of the skeleton. Some bones in the model are too short and some are too thick and still others have fusion in one piece. This does not disturb the human eye so much since it can build on previous experience on how skeletons like this are built. But it is a problem for automated vision.

Figure 4 shows models of the operculum bone in the two cod´s. This is the bone with the highest density in the cod´s body.

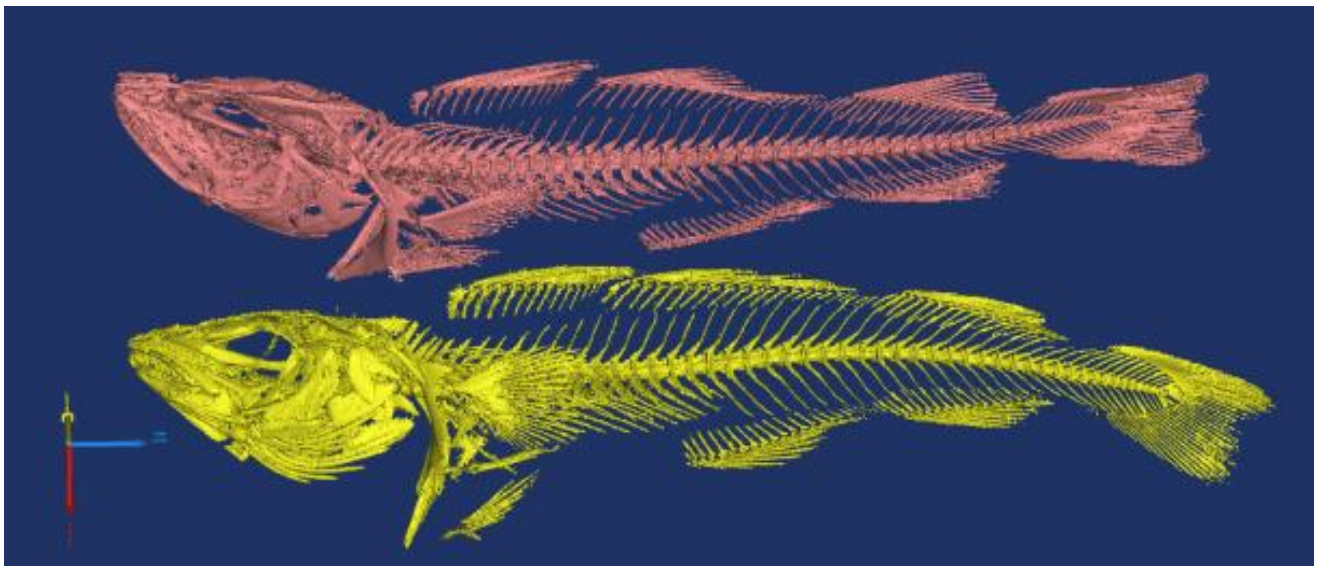

Figure 3: Two cod ske 1etons. The models are a result from 1909 CT slices 0,67 mm thick and 0,33 mm apart. The whole skeleton can be seen, although some bones are not in their full length, others appear more voluminous than they are in reality and some are not distinguishable from each other and form a solid body

Figure 4: Operculum bone model from the two cod´s under inspection in this work. They are the most dense bones in the fish, meaning that they have the highest HU values on average.

3.3. Otoliths

The otoliths models are shown in figure 5. The otoliths give important information on the cod and can be analyzed to some extent in these images. They are the objects in the cod´s body with the highest density and are considerably denser with more than 2900 HU where as the next one, the operculum bone, has 900 HU.

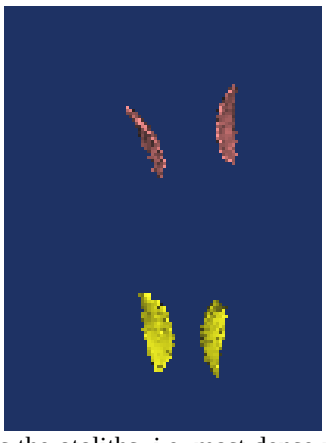

Figure 5: Shows the otoliths, i.e. most dense part of the cod placed inside the cod head.

DISCUSSION AND CONCLUSION

Detection of thin bones of low density can be done and they can be modelled in a cod skeleton. This information can be of use in detecting single thin bones. However if the bones are tight together they are not detected as single bones but rather like a merged single piece or plane. Reconstructing the fish skeleton from CT data can be done to a certain degree. Missing parts due to small thickness or low density, could in a normal case, be predicted using anatomical knowledge of the species being investigated. Another way to increase the accuracy of the cod´s skeleton model would be to use a CT device with higher spatial resolution. At the same time the field of view can easily be smaller. These two goals go together well. They can be reached simply by diminishing the diameter of the gantry's aperture having the scanned object further away from the CT sensors and nearer to the X-ray tube. This gives enlarged projections of the subject onto the sensors.

Automated processing of fish requires exact and reliable work but at the same time devices that are not too expensive and with low running cost. Medical CT devices have in recent years become considerably more cost effective. This is also the case for micro CT devices for research purposes. This gives the hope that CT technology can be made cost effective for food processing. Further research is, however, necessary to pinpoint the requirements of a CT for fish processing.

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AUTHORS BIOGRAPHY

Thordur Helgason made his BS degree in electrical engineering from University of Iceland in 1982, a Dipl.-Ing. degree in Biomedical engineering from University of Karlsruhe in W-Germany 1985 and a Dr.-Ing. Degree from the same school 1990. Since then Helgason has been working in Landspitali the University hospital in Iceland in the field of medical engineering. Dr Helgason has been teaching in the faculty of medicine and faculty of engineering at the University of Iceland. Since 2005 he is a lecturer at the University of Reykjavík and is currently an associate professor at that university. Research interests of Dr. Helgason are in the field of Neural engineering, rehabilitation and modelling. Dr. Helgason is the president of the Icelandic Society of Medical Engineering and Medical Physics.

Rannveig Ása Guðmundsdottir made her BS in Biomedical engineering in University of Reykjavik 2011. Rannveig Ása worked at Landspitali-University Hospital Department for Research and development 2011 to 2012. Her work was on modelling muscles of a spinal cord injured patients and on modelling of fish bone. She is currently a MS student at Chalmers University of Technology in Gothenburg, Sweden.

Kristín Líf Valtýsdóttir finished her B.Sc. degree in industrial engineering in 2009, and M.Sc. in mechanical engineering in 2011, both from University of Iceland. The main focus of her M.Sc. work was on cooling and processing techniques in the fish industry. She received a scholarship for the master's thesis and worked as well as a research scientist at Matis – Icelandic Food and Biotech R&D. Since early 2012 she has been working as a project manager at the fish industry centre at Marel, a developer of food processing equipment and systems.

Kristinn Andersen received his B.S. degree in electrical engineering from University of Iceland in 1982. He carried out research work at Vanderbilt University, USA, worked on research projects with NASA on arc welding and robotics, and received his Ph.D. degree from Vanderbilt University in 1993. Dr. Andersen has since been with Marel, a developer of food processing equipment and systems. His work includes the development of computer vision technology for on-line inspection, weighing technology and he initiated and supervised the company's development of X-ray technology for product inspection. Presently he is a senior RTD manager at Marel, responsible for collaborative projects on new technologies.