

# The practical guide for data recording and handling in 22481

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## 1 Introduction

Medical imaging is concerned with making structural and functional images of the body, often in a non-invasive way. The structural images show tissues, bones and organs in the body, while the functional images show how the body functions by displaying blood flow, distribution of injected tracers, etc.

The images are made with different imaging modalities, and the most important of these are mentioned later in this document. The techniques are quite different, and they are often complimentary to each other: while one technique is preferred for viewing a broken leg, another technique is optimal for detection of cancer. As the techniques are different, so are the images. Specifically, if the same tissue is imaged with different modalities, one region that is bright on one image, might be dark on another. Another situation that can occur is, that two different tissues are distinguishable on one image modality, but appear indistinguishable on another.

In order to appreciate the different appearance of the images, this course will apply the main clinical imaging techniques in use in hospitals today, to scan the so-called *phantoms* provided in the course. A phantom is a block of homogeneous material such as agar, with either some biological or synthetic material inside, for the purpose of mimicking biological tissue. Performing these scannings offers the possibility to see how the same tissue appears on different imaging modalities. Few people have actually experienced this for all the modalities taught in the course.

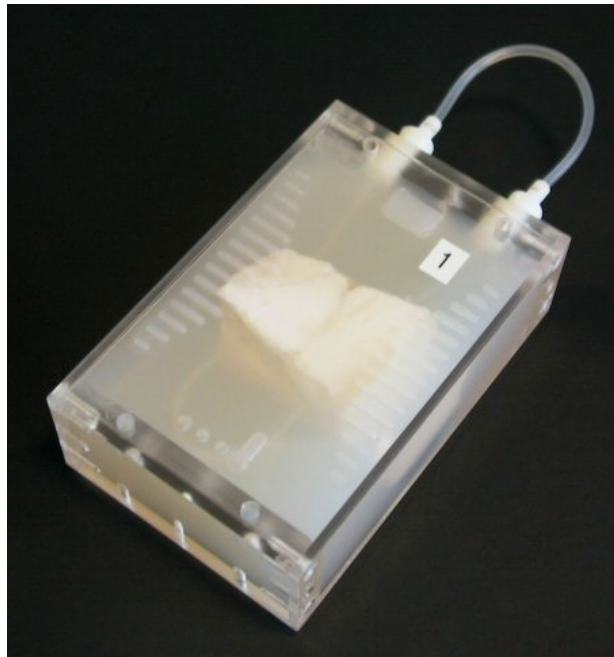
The reader is kindly advised to read through the entire document, as it follows only partly the chronological order of the course. Be also aware that you will most likely need to read this document several times as the information is quite concentrated.

Finally, the course change from year to year, so some part of this guide might not be relevant a given year.

## 2 The phantom

Each team will be provided with a “phantom” which consists of several objects embedded in semi-transparent agar. One of these objects is a piece of formalin fixed animal tissue. An example is given in Figure 1. Formalin is a chemical compound that is used to stop degradation of biological tissue. The concentration of formalin is quite low; nevertheless the phantoms should be handled with gloves and good ventilation should be available. You can see a safety description of formalin here<sup>[1]</sup>.

When given to you, the agar block is encapsulated in an acrylic mould. Do not remove the mould before you are instructed to do so since it might be difficult to put back. The outer dimensions of this mould are



**Figur 1** The phantom consisting of biological tissue moulded into agar and surrounded by an acrylic mould.

125 by 81 by 38 mm. The outer dimensions of the agar block located inside the mould are 105 by 75 by 35 mm. On top of the agar block, a set of fiducial markers are provided. These fiducial markers correspond to openings in the lid (thickness approx.  $1.9 \pm 0.1$  mm) which was placed on top of the phantom when it was moulded. The lid can later be replaced by a planar lid that protects the fiducial markers, if needed.

The purpose of the fiducial markers is to assist you in aligning the different medical images, as will be elaborated on later in this document. Each phantom is marked with a number which correspond to the team number (see list published separately). The phantom number is coded as a binary number with "ones" (lines) and "zeros" (dots) as shown in Figure 1 and elaborated upon in the Appendix.

Two wire phantoms are also provided to the especially dedicated students. A *nylon wire phantom* (phantom 12) with two perpendicular nylon wires of dimension 0.35 mm (Type Norion 8.4 kg for fishing) and a (dry) *Tungsten wire phantom* with two perpendicular Tungsten wires of diameter 0.6 mm.

### 3 The overall goal of the experiments of the course

The overall goal of the experimental part of the course is to identify “what is inside the agar in the phantom”. Based on what you can see through the agar and especially based on the medical images recorded from the phantoms, it is up to you to identify what - and preferably also how much - is inside. The question should be understood literally, and one should regard all aspects of the content, not only the animal tissue.

Teaching at the Technical University of Denmark is supposed to be research-based, and this course attempts to fulfil that demand to an extraordinary extent. Thus, since the course changes from year to year - and not all aspects of the course is tried out beforehand - it can be quite demanding.

## 4 What you need

There are a number of resources that will be needed during the course:

- The *plan for the course* is a central document of this course, showing time and place for the scanings that are performed this year. The plan is available from the *course homepage*<sup>[2]</sup> (where this document is found).
- The *SIS toolbox*<sup>[3]</sup> developed by the author for processing, analysing and visualising of the data recorded of your phantom during the course.
- The *Web book of Medical Imaging* for studying the principles of the imaging modalities applied in this course (link via course homepage).
- The *Assignments* in the course, which are referred to a number of times.
- [www.wikipedia.org](http://www.wikipedia.org) for obtaining popular - or alternative - descriptions of various aspects (*e.g.* formalin). However, you cannot always rely on information you obtain via an “elusive” medium as a dictionary with “anonymous” authors. So use with care. Especially, if you need a scientific reference to support a passage in the report you write, only scientific papers and books with a known author (in paper or electronic format) are accepted.
- Other resources on [www.portalen.dtu.dk](http://www.portalen.dtu.dk) such as [ordbogen.com](http://ordbogen.com) and Encyclopædia Britannica On-line.

## 5 Recordings

This chapter concerns the steps needed to *record* (and sometimes to verify) the data. The processing for *preparing* the data is outlined in Chapter 6, while the *analysis* is discussed in Chapter 7.

Documentation of what happens during the recordings - in the form of photographs and notes - is essential. Often, more than one phantom is scanned at a time which means that the data of the scanning represents multiple phantoms. So the location of the phantoms relative to each other is a central element when it comes to extraction of the 3D data representing a given phantom.

Students of the course are hereby kindly requested to provide the teacher with photographs of the scanning situation. If the photographs are not to be made publicly available, then the photographer should state this, when forwarding the photos.

When the medical scanings have been done, the images are transferred by the teachers to the "jwpublic" directory (see the course homepage under "Programs and Data").

### 5.1 Photographing the phantom (top photograph)

The surface of the phantom contains phantom identification and fiducial markers for fitting a coordinate system. In order to use this, a *metric* photograph of the surface is recorded.

The recording is performed as follows at the office of JW:

- Pick up your phantom (do not remove any of the acrylic parts), dry the surface with a paper towel and place it bottom-up on a flat bed scanner (you will be assisted on the latter).
- Select proper parameters for the optical scanning.
- Scan. Save as TIFF file in the following directory (your might have to create it) "d:\scanner\31540\[TeamNumber]". [TeamNumber] is a directory you must create. Save the TIFF file as “uncompressed”. If the file is larger than 10 MB, consider if you have too many pixels. If it is less than 5 MB, you might have too few. Check the photograph.

- Please return the phantom to JW.
- When you have obtained the final graphic file, it can be faster than using MATLAB to load the picture into a classic image processing program (*e.g.* Jasc Paint Shop Pro, Adobe Photoshop) for possible slight rotation which is necessary for the alignment of the photo, cropping of the picture and adjustment of the number of pixels. Save again as a TIFF file (uncompressed). If you have problems:
  - You can easily run into problems, if you use software that does not comply with international standards, such as MS Picture Manager. More specifically, it might not save the data in the correct TIFF format. In this case, use the program only for finding the proper rotation (it can be faster than using MATLAB) and then use this rotation angle in the MATLAB program (`sis_rotate`).
  - TIFF files might have an intact header containing pixel spacing and since they can be imported with `sis_import`, it is suggested that you stick to this format.
- After this, import the photo into SIS format with `sis_import` (see the SIS guide<sup>[3]</sup>).
- Use `sis_view` to see the photo. The metric axis might, or might not, be correct (information about DPI (dot-per-inches) are saved in the TIFF-file header, but might not be correct).
- Measure some distances (perpendicular to each other) on the phantom that you can easily recognize on the photograph. Use a slide gauge (*Danish*: skydelære). Please clean it afterwards. If necessary, adjust the axis to match your measurements. Save this SIS data set.

It is *strongly recommended*, that you proceed with the processing steps outlined in Subsection 6.1 (otherwise you will have to do this later, when time gets scarcer).

## 5.2 Medical scannings

The medical scannings should provide images of both the tissue and the fiducial markers on top of the phantom. This is very important.

The order of presentation below does not necessarily match that of the plan for the course.

The phantoms are scanned on a special acrylic base plate, where different configurations are possible. There is a small eye with a bubble (*Danish*: libelle) for attempting to ensure that the plate is placed in the horizontal plane.

When inspecting the system parameters, be sure to distinguish between resolution size and spatial distance between voxels in the 3D image.

Below are given typical parameters for the scannings. It is the job of the student to identify the exact parameters used for their scannings.

### 5.2.1 Planar X-ray (X data)

One phantom is photographed at a time.

**Example of settings and equipment:** Optimus 65 X-ray tube (Philips Medical Systems). Tube voltage: 44 kV, total charge: 4 mAs, exposure time: 17.3 ms. Pixel size in final image (Fuji Photo Film Co., Ltd.): 0.1 by 0.1 mm. Phantom centred in the image region which are shown by “light lines” on the phantom. See the actual settings in the DICOM header.

### 5.2.2 CT scanning (CT data)

All phantoms are scanned in one session. They *might* be placed in two blocks of six phantoms each.

**Typical settings and equipment:** Gemini TF 64 (Philips), 64-slice PET/CT scanner, 440 mA tube current, 120 kV tube voltage, 1024x1024 matrix, pixel size:  $\sim 0.24414$  mm, slice thickness: 0.67 mm. Please use smallest possible voxel size. See the actual settings in the DICOM header.

### 5.2.3 PET scanning (PET data)

Setup as for CT (since it is the same scanner).<sup>1</sup>

**Example of settings and equipment:** Manufacturer: Philips Medical Systems. Model name: GEMINI TF TOF 64. Number of slices: 90. Slice thickness: 2 mm. Matrix: 128x128. Pixel size:  $\sim 2$  mm. Radiopharmaceutical: Fluorodeoxyglucose 18F.

### 5.2.4 MRI scanning (MRI data)

Number of phantoms to be scanned per session: As many as can fit in the 3D volume, when the smallest resolution size is used.

**Example of settings:** Genesis Signa (General Electrics), 1.5 Tesla,  $T_1$  weighted multi-slice SE (spin echo) sequence:  $T_R = 360$  ms,  $T_E = 9$  ms, 2 averages, 5 mm slice thickness, 256x256 matrix, pixel size of  $\sim 0.94$  mm.  $T_2$  weighted multi-slice FSE (fast spin echo) sequence:  $T_R = 3.46$  s,  $T_E = 102$  ms, 2 averages, 5 mm slice thickness, 512x512 matrix, pixel size of  $\sim 0.47$  mm. See the actual settings in the DICOM header.

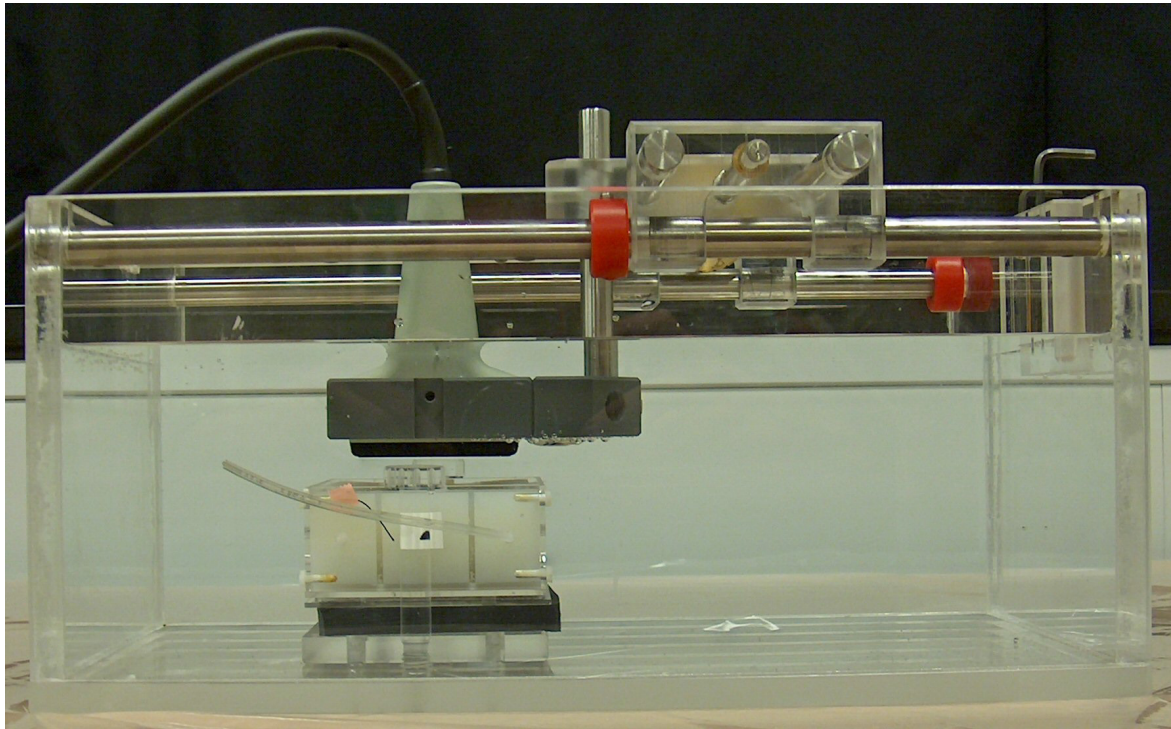


**Figur 2** The entire setup for ultrasound recording, here shown with two different ultrasound scanners. The one to the left is a 2102 Hawk while the one to the right is a Viking 2400. The latter is used in the ultrasound measurements.

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1. Notes to operator: The phantoms can be filled with a syringe fitted with the adapter attached to the transport container with a green wire. Be sure to return the adapter. The liquid will stay inside the phantom when the loop is closed.





**Figur 3** The scanning tank (manual sledge) with phantom seen from the end (old model of phantom) and the transducer fixed to its holder. The sliding equipment is shown to the right of the transducer. Note the air bubbles underneath the gray transducer holder. Finally note that the water level is *too high* in this setup, since it covers more than the tip of the transducer.

Notes to operator: Location of phantoms: Probably 2-3 in head coil, 3D-T1 weighted sequence (1x1x1 mm<sup>3</sup>), PD/T2 MSE sequence axial.

### 5.2.5 Ultrasound scanning (US data)

The components used in the measurements are as follows and can be seen in Figure 2:

1. Diagnostic ultrasound Scanner (type Viking 2400, B-K Medical A/S, Denmark)
2. Linear array Transducer (type 8811, B-K Medical A/S, Denmark)
3. The phantom of the team
4. Scanning tank with degassed demineralised water and fixtures, etc., as shown in Figure 3.

**Example settings:** If necessary, adjust the following settings to a suitable level: “Gain”, “Res/Hz” and “TGC sliders”. Set “Dyn. Range” to 90 dB and the frequency to 12 MHz if the 8811 transducer is used. For other transducers, set the frequency to maximum. The overall gain should be set to such a level that the contrast in the image is maximized. In most cases, about 42 % overall receive gain will work fine. See the actual parameters from the ultrasound data set which reveal the entire screen of the ultrasound scanner.

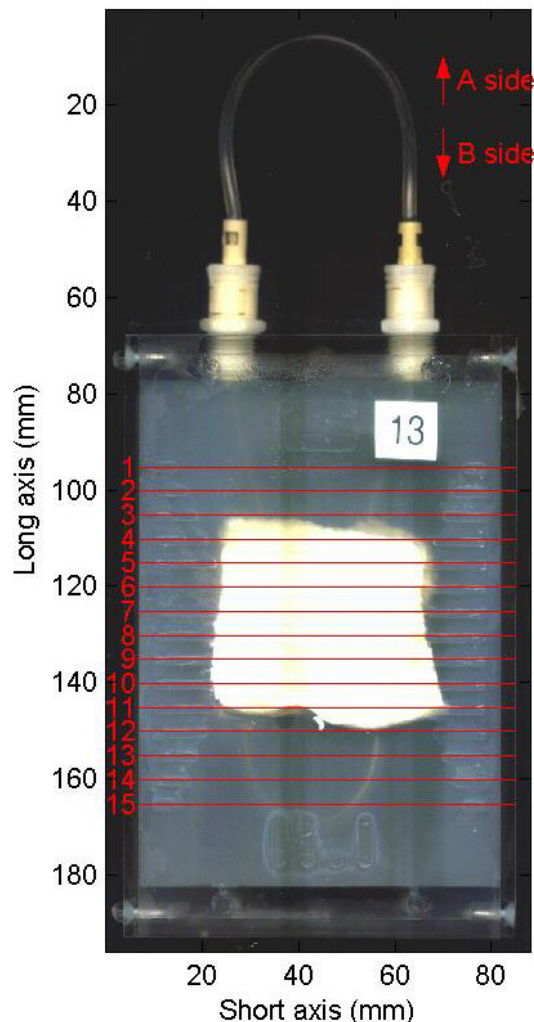
All the equipment is connected for you. It should be handled with great care since it is quite expensive. The price of the transducer itself is about DKK 100,000. The setup is shown in Figures 2 and 3. Note the plastic foil which protects the table from water. The scanning tank should be filled to a level where 5 - 10 mm of the transducer tip is covered. Use demineralised, degassed water.

### 5.3 Creating the reference by slicing the phantom (anatomical photographs)

When all the medical images have been recorded, the big question is now: *how correct are they?* An attempt to answer this question can be made by creating a so-called *reference*.

This work will take place in 349.215, and JW has to be present while it takes place. It is concerned with obtaining a *metric anatomical reference photograph*<sup>1</sup>, against which you can compare the different diagnostic images. Specifically, it consists of slicing the phantom and "photographing" the slices with a flat bed scanner:

1. Wear protective glasses and white coat (*Danish*: beskyttelsesbriller og hvid kittel).
2. Consider Figure 4 which shows a suggestion for numbering the different fiducial markers. If you follow this system, you can cut small paper labels from the text in Appendix 10.3. You will use these labels later.
3. Remove the agar block from the acrylic frame, according to the instructions of JW at the lab.
4. Place the agar block in the special frame which ensures that the knife is perpendicular to the long axis of the phantom. Perform a test cut: Lubricate the knife in glycerol, make the cut at the



**Figur 4** The phantom seen from the top with number convention for fiducial markers and indication of A and B face of cut plane. Note the binary number imprinted in agar at the bottom of the picture: "1101", corresponding to 13.

1. Note the difference between photograph and image, as explained in Appendix 10.1.

end of the block, where there is only agar, and make the cut in one continuous movement. Repeat, at the plane of interest. Each tissue slice of interest must be marked with the small paper labels you created above. The tissue slices are placed on transparency film, face down (*i.e.* label facing down). For each cut you make, be aware that you will have two sides, which both would be worth photographing.

5. Put the transparency on a tray (never drop the tray, because otherwise you will have to start over again at page one of this document ☺). Scan all the slices on the flat bed scanner (assisted by JW). When scanning, be sure that you select an appropriate resolution size so that your anatomical images are fine enough. Save the data in TIFF format. After the scanning, check that your "photograph" is satisfactory.
6. Again, as in Subsection 5.1, for easy fine adjustment of the raw photographs before importing them into SIS, consider using a program such as Paint Shop Pro. After this, import into SIS, just as in Subsection 5.1.

## 6 Preparing data

The data that you will get from the medical scanners will come in either DICOM format or in SIS format. Both formats can be read with the SIS toolbox: The DICOM data has to be imported with `sis_read_dicom`, while the SIS data can be used directly after being loaded into MATLAB. The photographs (Section 5.1 and 5.3) are in SIS format at this stage.

The purpose of this chapter is to verify the data, extract the data representing your phantom and do proper alignment of zero-points so that the images can be compared directly.

A note on MATLABs data format: If your data is in `uint8` (unsigned integer with 8 bits, which can only be numbers between 0 and 255), you can do any calculation on the data, *but the result will often be incorrect!* Solution: Convert to double (in MATLAB type `Data.Images = double(Data.Images)`).

Especially for the CT data: These often come in `uint16` and it is suggested that you work with this in the initial steps: Cut out the data that you need (*i.e.* your phantom). Then, when the data set has become smaller (fewer pixels), you can change to double and then adjust the offset by adding `Data.DicomHeader.RescaleIntercept`:

```
Data.Images = double(Data.Images) + Data.DicomHeader.RescaleIntercept;
```

Look at the minimal and maximal values of `Data.Images` and be sure that they occupy a realistic range.

### 6.1 Top photograph

Load the top photograph saved in SIS format during the recording step. Decide on where you want your zero-point on the metric axes. This zero-point should be the same for all images in this course, so select it with care to save time in the end. A possibility is to choose the midpoint between the two *longest* fiducial markers (those at the middle) corresponding to line 8 in Figure 4. On the dimension out of the plane in Figure 4 one can chose the interface between the agar and acrylic lid (*i.e.* the agar surface).

As you can see from the top photo of Figure 4, it is very easy to recognize landmarks (fiducial markers holes, etc.) on the surface of the physical phantom. When it comes to medical images, the number of pixels are far, far lower. Thus, the only way to identify the zero point will be to use *all* information on the medical image. For this purpose, please solve Assignment 1 (see document on assignments).



## 6.2 Planar X-ray

In principle, the same procedure as above, except that this DICOM data has to be read by `sis_read_dicom`. Be sure to verify that what you see on the X-ray image corresponds to the real world (which you can see from the top photograph). Especially consider: Which direction does the two axes have? Is there any mirroring? See important notes on rotation at the end of Subsection 6.3. Finally, the dynamic range should be considered, is any zoom on the range needed?

## 6.3 Extracting your phantom from 3D data

This subsection relates to the remaining modalities: MRI, ultrasound, CT and PET.

When each scanning is finished and all the electronic images have been made available (we will try to do this over night) you should place them in your own directories and be sure to make a backup(!).

The first thing to do with the images is to plot them on the screen and figure out which files give which images. The photographs taken during scanning can help in this regard. Use `sis_view(Data)` to view the 3D images. `sis_view` will display all the data present in the variable `Data` as 2D images (where the third dimension is image to image). You can modify the content of `Data` to only present the images that you desire (use `sis_zoom`). Some images might not be needed, and most images should probably be "cropped" (that is, you will need to isolate your object, *e.g.* by applying `sis_zoom`). Save this 3D SIS data representing your phantom on disk.

*Hint:* The best way to do this processing is by making a script that reads the data, does the zoom and then saves the zoomed data to disk in a new file. This way, you know exactly what parameters you used to zoom with, and you can later adjust them. The need for this will become clear when you begin to compare images from different modalities. Use a filename for the script that is self-explanatory. Be aware, that some of the data processing can take hours. Finally, be sure to be very organised with data and m-files, since there will be large amounts at the end of the course.

When a 3D data set containing only your phantom has been extracted, the fiducial markers on top of the agar should also be identified. This will make it possible to match the same scan plane from different imaging modalities. You can isolate a *visualization* plane parallel with the agar block surface by using `sis_zoom`. If the phantoms were not completely aligned with the scanner, you might have to rotate the phantom data slightly (`sis_rotate`), before you do that. However, if the pixels are not of square size in the rotation plane, interpolation to obtain this might be needed first (see help to `sis_rotate`). It might also be necessary to upsample the image.

Also, if the fiducial markers are unclear on the resulting image, contrast can be improved by adding several (parallel) visualization planes: With `sis_zoom`, extract as many planes showing the fiducial markers as possible. Then add these images to form a single image of the fiducial markers.

When you have plotted all relevant images (tissue and fiducial markers), you will know if the scanning was successful.

The next thing to do is to use the fiducial markers to adjust the zero-point of the axes: Plot the image showing the fiducial markers and plot the grid from Section 6.1. You will need iteratively to subtract a constant from the axis and then plot the image and the grid. Save the data.

Be sure to verify that what you see on the 3D images correspond to the real world (as you can see from the photographs taken during recording). Especially consider: Which direction does the third axis have (which way are we scanning)? What about the two other axes? Is there any mirroring? As to the latter:

if you need to rotate 90 degrees, do not use `sis_rotate`, but rather `sis_reorder`. For 180 degrees rotation, use this MATLAB code (example given for second axis):

```
Data.Images = Data.Images( :, end:-1:1, :);
```

where the second axis (or dimension) is running backwards. Note the `end` in the line above. Inside indexing parenthesis, `end` is a variable equal to the last element of the given dimension.

### 6.3.1 Additional specific information for the different modalities

**Identifying the phantom in PET.** From the photographs taken during the PET recordings, one should be able to identify two stacks of phantoms as well as their location. One with, and one without, the fish wire phantom. In addition, the connectors for the tube should also be present on the images. This should - in principle - be enough information in order to identify a given phantom.

### 6.4 Manufacturer and type

For MRI, CT and PET, the DICOM data contains the manufacturer and type in the following fields:

```
Data.DicomHeader.Manufacturer  
Data.DicomHeader.ManufacturerModelName
```

In addition to this, the CT scanner is of type "multi-slice spiral" (helical). The MR scanner has a field strength of 3T. The PET scanner is a Time-of-Flight system with 18cm axial field-of-view. The phantom is filled with about 30 MBq  $^{18}\text{F}$ .  $^{18}\text{F}$  has a half-life of about 110 min and is the most often used radio-nuclide for PET, accounting for more than 95% of all investigations

For planar X-ray, the DICOM data only reveals the manufacturer of the film:

```
Data.DicomHeader.Manufacturer
```

The X-ray unit is a Philips Optimus 65 X-ray tube. For ultrasound, the equipment is specified in the guide.

## 7 Analysis of prepared data

When the above steps have been completed, all data should be saved with the same zero-point, and thus, it should be straight forward to load the data and compare. Specifically, if one loads and displays a given slice from the ultrasound data, the same code can be used to display MRI, CT and PET data, when the corresponding file is loaded (the requires that one uses metric axis, but this is strongly recommended). Of course, you should be aware of the different spacing between scan planes for the different modalities.

Pay attention to the over-all aim of this project (Section 3), when you compare data. Also, Section 8 provides some guidelines for what to look for.

Below are some additional details on some of the imaging modalities.

### 7.1 Planar X-ray and CT

When working with this kind of data, it can sometimes be beneficial to have a "second opinion". So in some cases, consider using a stand-alone DICOM viewer (we will try to make one available via "file sharing" on CampusNet).

When you consider the tube in the X-ray image, you should be able to explain why the tube appear as it does. If not, consider if the image is a negative version of the one you expect.

If the CT image is loaded, and you see the entire phantom (tissue, agar, acrylic box, surrounding air), the contrast is not so impressive in the tissue region. What can be done to get a better picture?

With respect to bone on X-ray and CT images: Be sure that you do not misinterpret cartilage (*Danish*: brusk) for bone (*Danish*: knogle). Also, when cutting, these two are easily distinguished: Bone is quite difficult to cut through.

## 7.2 PET

The PET data only reveals the space where the tracer is. This space is connected with the external tube. Strictly speaking, the location and size of this space cannot be revealed by any of the other imaging modalities. Another point to note is that a medical image is an estimate. Therefore, if there are any chances of comparing images from different modalities, this should be done to investigate possible geometrical differences between images.

The most simple approach is to compare the PET data to the planar X-ray image. The easiest way to make a single image of the cavity from the PET data is to search for the maximum in the appropriate dimension with `sis_collapse`.

## 8 References

- [1] [http://www.kemibrug.dk/KBA/CAS/50-00-0/?show\\_KBA=1&portaldesign=1](http://www.kemibrug.dk/KBA/CAS/50-00-0/?show_KBA=1&portaldesign=1)
- [2] <http://courses.healthtech.dtu.dk/22481/>
- [3] J. E. Wilhjelm: Guide to the sis toolbox. DTU Health Technology, 2021.
- [4] B-K Medical: Viking 2400 Extended User Guide. B-K Medical 2004.

## 9 Acknowledgements

M.Sc. students Christoffer von Halling Laier, Carsten Jensen and Jonas Henriksen is gratefully acknowledged for numerous comments and input to this guide.

## 10 Appendix

### 10.1 Notation used here

**Photograph:** A motive on paper or in electronic form, where the motive is obtained by conventional optical methods (camera or flat bed scanner recording a real world object).

**Image:** A motive on paper or in electronic form, where the motive is obtained by use of sound, electromagnetic radiation, etc.

**Map:** A motive containing different areas with exactly the same property (in this course).

**Image plane:** the physical plane corresponding to the image. However, since an image represents a thin slice, this plane is actually the plane in the center of this slice. In ultrasound this plane is called a scan plane (the plane is “scanned” (*Danish*: *fejje*) in order to form the image).

**Visualization plane:** a plane anywhere through a 3D data set.

### 10.2 Binary number system for phantoms

**Table 1:** Correspondence between phantom number and binary code imprinted in agar at surface of phantom.

Phantom number	Binary code	Phantom number	Binary code
0	0000	8	1000
1	0001	9	1001
2	0010	10	1010
3	0011	11	1011
4	0100	12	1100
5	0101	13	1101
6	0110	14	1110
7	0111	15	1111

In many cases, the phantom can be identified from the ID imprinted in agar at the surface of the phantom. An example of this ID can be seen in Figure 4. In Table 1, an overview of all binary codes is given.

### 10.3 Labels for agar slices

Labels for agar slices. Can be useful when cutting through the fiducial markers:

1-1a 1-2a 1-3a 1-4a 1-5a 1-6a 1-7a 1-8a 1-9a 1-10a 1-11a 1-12a 1-13a 1-14a 1-15a  
1-1b 1-2b 1-3b 1-4b 1-5b 1-6b 1-7b 1-8b 1-9b 1-10b 1-11b 1-12b 1-13b 1-14b 1-15b

2-1a 2-2a 2-3a 2-4a 2-5a 2-6a 2-7a 2-8a 2-9a 2-10a 2-11a 2-12a 2-13a 2-14a 2-15a  
2-1b 2-2b 2-3b 2-4b 2-5b 2-6b 2-7b 2-8b 2-9b 2-10b 2-11b 2-12b 2-13b 2-14b 2-15b

3-1a 3-2a 3-3a 3-4a 3-5a 3-6a 3-7a 3-8a 3-9a 3-10a 3-11a 3-12a 3-13a 3-14a 3-15a  
3-1b 3-2b 3-3b 3-4b 3-5b 3-6b 3-7b 3-8b 3-9b 3-10b 3-11b 3-12b 3-13b 3-14b 3-15b

4-1a 4-2a 4-3a 4-4a 4-5a 4-6a 4-7a 4-8a 4-9a 4-10a 4-11a 4-12a 4-13a 4-14a 4-15a  
4-1b 4-2b 4-3b 4-4b 4-5b 4-6b 4-7b 4-8b 4-9b 4-10b 4-11b 4-12b 4-13b 4-14b 4-15b

5-1a 5-2a 5-3a 5-4a 5-5a 5-6a 5-7a 5-8a 5-9a 5-10a 5-11a 5-12a 5-13a 5-14a 5-15a  
5-1b 5-2b 5-3b 5-4b 5-5b 5-6b 5-7b 5-8b 5-9b 5-10b 5-11b 5-12b 5-13b 5-14b 5-15b

6-1a 6-2a 6-3a 6-4a 6-5a 6-6a 6-7a 6-8a 6-9a 6-10a 6-11a 6-12a 6-13a 6-14a 6-15a  
6-1b 6-2b 6-3b 6-4b 6-5b 6-6b 6-7b 6-8b 6-9b 6-10b 6-11b 6-12b 6-13b 6-14b 6-15b

7-1a 7-2a 7-3a 7-4a 7-5a 7-6a 7-7a 7-8a 7-9a 7-10a 7-11a 7-12a 7-13a 7-14a 7-15a  
7-1b 7-2b 7-3b 7-4b 7-5b 7-6b 7-7b 7-8b 7-9b 7-10b 7-11b 7-12b 7-13b 7-14b 7-15b

8-1a 8-2a 8-3a 8-4a 8-5a 8-6a 8-7a 8-8a 8-9a 8-10a 8-11a 8-12a 8-13a 8-14a 8-15a  
8-1b 8-2b 8-3b 8-4b 8-5b 8-6b 8-7b 8-8b 8-9b 8-10b 8-11b 8-12b 8-13b 8-14b 8-15b

9-1a 9-2a 9-3a 9-4a 9-5a 9-6a 9-7a 9-8a 9-9a 9-10a 9-11a 9-12a 9-13a 9-14a 9-15a  
9-1b 9-2b 9-3b 9-4b 9-5b 9-6b 9-7b 9-8b 9-9b 9-10b 9-11b 9-12b 9-13b 9-14b 9-15b

10-1a 10-2a 10-3a 10-4a 10-5a 10-6a 10-7a 10-8a 10-9a 10-10a 10-11a 10-12a 10-13a 10-14a  
10-15a  
10-1b 10-2b 10-3b 10-4b 10-5b 10-6b 10-7b 10-8b 10-9b 10-10b 10-11b 10-12b 10-13b 10-14b  
10-15b

11-1a 11-2a 11-3a 11-4a 11-5a 11-6a 11-7a 11-8a 11-9a 11-10a 11-11a 11-12a 11-13a 11-14a  
11-15a  
11-1b 11-2b 11-3b 11-4b 11-5b 11-6b 11-7b 11-8b 11-9b 11-10b 11-11b 11-12b 11-13b 11-14b  
11-15b

12-1a 12-2a 12-3a 12-4a 12-5a 12-6a 12-7a 12-8a 12-9a 12-10a 12-11a 12-12a 12-13a 12-14a  
12-15a  
12-1b 12-2b 12-3b 12-4b 12-5b 12-6b 12-7b 12-8b 12-9b 12-10b 12-11b 12-12b 12-13b 12-14b  
12-15b

#### 10.4 Dictionary

A fiducial markers (*Danish*: indeksmarkører).

Ratio (*Danish*: forhold).

#### 10.5 Oraculus

The following text is in Danish, and international students are requested to have a Dane translate the text. Gennem tiderne har en række studerende skrevet til Oraculus. Svarene er samlet her:

**SPØRGSMÅL:** Skal colorbaren med på vores figur, eller kan den udelades? Vi mener kun den giver mening for ct og xray, men ville udelade den for alle de andre. Og hvis den ikke skal udelades, skal man så ensrette, så alle skalaer er i samme interval?

**SVAR:** I har, i princippet, ret i at farveskalaen kun giver mening, når den er kvantitativ. Skriv det i starten af "resultatafsnittet", så viser I, at I har taget stilling til dette.

SPØRGSMÅL: I rapportvejledningen står der, vi kun skal have et topfoto og et tværsnit med for hver billeddannelsesteknik. Betyder det, vi ikke bør vise flere tværsnit gennem fantomet? Vi vælger selvfølgelig samme tværsnit for alle billeddannelserne.

SVAR: Det bliver let for langt, hvis I viser flere tværsnit, men I er velkomne, hvis I føler at I har energi til det. Men pas på, at det ikke går ud over kvaliteten af den resterende del af rapporten.

SPØRGSMÅL: Vi prøver at kollapse ct-data for at sammenligne med xray, men får et meget mørk og ikke særlig veldefineret billede. Er det meningen, at ct kollapsede skal være helt ens med xray?

SVAR: Nej, det skal ikke være ens. Men måske skal I kikke på jeres kollapsede billede med et vindue på HU-enhederne?

SPØRGSMÅL: Vi har ikke kunne finde hvilken type scanner, vi har brugt til SPECT og MRI. Det står hverken i practical notes eller under "read me" files der ligger på hjemmesiden.

SVAR: Se den nye practical guide under hjemmeside (og campusnetmeddelelse)

SPØRGSMÅL: CT-mætning, Vi kunne godt tænke os at vide, om det skal bruges til noget specielt og om det er nødvendigt at have det med i rapporten. Hvad skal det bruges til?

SVAR: Aner det ikke. :-) Hvad er CT-mætning eller hvor har I læst det?

SPØRGSMÅL: Når vi skriver forsøgsgangen for US, er det nødvendigt at angive parametrene eller er det nok at henvise til forsøgsvejledningen?

SVAR: Der er jo mange parametre og det er ikke helt entydigt hvad der er de vigtigste. Så ja, overvej at referere til forsøgsvejledningen. Husk dog de vigtigste parametre: transducertype og herunder dens centerfrekvens.

SPØRGSMÅL: Vi har diskuteret, hvorvidt vi i rapporten skal skrive noget om hvordan man scanner mennesker. Forsøgsgangen bygger jo på, hvordan fantomet blev scannet, men det er jo andre ting, man skal tage hensyn til, når det er mennesker der scannes... Vi er bange for at rapporten blir for lang, hvis vi også skriver om det... Hvad er din holdning til det?

SVAR: Skriv ikke om skanning af mennesker. Rapporten bliver sikkert lang nok :-)

SPØRGSMÅL: Er colorbaren ved xray virkelig i Hu-enhed? Dette virker nemlig ikke sandsynligt, når vi sammenligner med CT (tværsnit)

SVAR: NIX, HU bruges kun ved CT.

SPØRGSMÅL: I US scanningen kolliderer vi alt data, for at få et plant snit, som viser vævet. Der hvor der ikke er væv, bliver området lys-grå. Hvordan kan et område, som er helt sort ved scanningen kollapses til et gråt område? Er et kollaps ikke bare et gennemsnit ned gennem data?

SVAR: Kik ned langs en linie og se om ikke der kommer lidt hvidt med undervejs, selvom I er uden for vævet. Der er jo mange artefacter i ultralyd. Hvis dette ikke besvarer Jeres spgm, så snakker vi vist forbi hinanden og I må lige komme forbi.

SPØRGSMÅL: Indeholder rørene til kontrastvæsken luft eller vand, når disse ikke bruges?

SVAR: Godt spørgsmål. Det er op til Jer at finde ud af! :-)

SPØRGSMÅL: Er der en afhængighed mellem frekvens, bølgelængde og dæmpning ved Røntgen?



SVAR: Se grafen over absorption versus energi i "The Web book on Medical Imaging", hvoraf de enkelte bidrag (fotoeffekt, Comptoneffekt mm) også fremgår. Her fremgår det at bølgelængde og dæmpning er kraftigt relateret.

SPØRGSMÅL: Vi har importeret et fotografi, så det ligger i SIS-format, men når vi drejer det cirka 1 grad, bliver det til volapyk.

SVAR: Det skal det også! Et foto er enten gemt i en fil som et rgb-billede eller som et indekseret billede. Når man læser et foto med `sis_import`, bliver det altid lagret som et indekseret billede, hvorfor rotation vil operere på indexværdierne, hvilket ikke giver mening. Løsning: drej billedet med et klassisk billedbehandlingsprogram eller lav det sis-importerede billede om til et gråtonebillede (sidste skridt gøres ved at udregne `mean(Data.Images(:, :, 3))`).

SPØRGSMÅL: Vi kan ikke forstå, hvorfor både det indre (lumen) og slangens væg bliver hvide. Vi bruger et vindue fra -100 til 50.

SVAR: Med det vindue I bruger [-100 50] bliver både det indre (lumen) og slangens væg hvide. Det er helt korrekt. Det er der kun en mulig forklaring på!

Prøv at vise data med og uden vindue. Prøv eventuelt at bruge "colormap jet" for hvert plot. Nu skulle det meget gerne fremgå - forklaringen er helt enkelt: både det indre og væggen ligger over 50.

SPØRGSMÅL: MATLAB kan ikke læse avi-fil fra ultralydskanner.

SVAR: Problemet skyldes, at den nødvendige codec ikke findes på computeren. Man kan løse problemet ved at downloade og installere K-Lite codecs pakke. Hvorvidt denne løsning er den bedste vides ikke. Se endvidere:

<http://www.mathworks.com/support/solutions/data/1-186ZX.html?solution=1-186ZX>

## 10.6 Dicom to sis for MRI images

This is mainly for the teacher:

Step 1: use the dicom view on the cd (run `autorun`) with the original MRI data to identify number of images in "scout" ( $N_s$ ), "t1" ( $N_1$ ) and "t2" ( $N_2$ ).

Step 2: Then copy all dicom data to a temporary directory. Rename all files from z?? to a??, etc according to the name of the directory where they are located.

Step 3: Move the first  $N_s$  files to the permanent scout directory. The next  $N_1$  files to the permanent t1 directory, etc. The number of files moved should exactly match the number of images revealed by the dicom viewr.

Step 4: In Matlab, run `sis_create_fl_at_sl`, then make a script like this and save it in the same directory:

```
Data = sis_read_dicom(SortedFileList);
```

```
save ..\..\data_t1 Data;
```

Step 5: That's all.

## 10.7 Dimension of data and physical interpretation

If you know nothing else about the data, assume this to begin with:

Dimension 1 is “vertical”

Dimension 2 is “horizontal”

Dimension 3 is “inter slice

## 10.8 More information about CT and PET data

This specific text is from data from a previous year, but the principle is the same.

1) The coordinate systems for CT and PET are identical for the third dimension, but not for the first and second:

Specifically, the PET data appears are a larger 3D image than the CT data. Since the CT image and the PET image should be centered on each other, the PET data along the first two dimensions should be adjusted:

```
CTAC_PET.Axes(1).Axis = CTAC_PET.Axes(1).Axis - (572-499)/2;
```

```
CTAC_PET.Axes(2).Axis = CTAC_PET.Axes(2).Axis - (572-499)/2;
```

(Size of the PET image is 572x572 while the size of the CT image is 499x499. Shifting the PET image half of this distance will center the two image on each other)

2) The PET data appears with increasing third dimension, which is as it should be. However, the CT data should be reversed by reversing both data and axis. Example:

```
CT_12_3_7_10.Images = CT_12_3_7_10.Images( :, :, end:-1:1);
```

```
CT_12_3_7_10.Axes(3).Axis = CT_12_3_7_10.Axes(3).Axis( end : -1 : 1 );
```

3) It is convenient to let the data start at zero along the third dimension, but this must be done exactly the same for both data set. Here just shown for CT:

```
CT_12_3_7_10.Axes(3).Axis = CT_12_3_7_10.Axes(3).Axis - -628.4; % so adding 628.4
```

4) There might be a (somewhat) small error in the PET data since each slice might not have been modified by RescaleSlope; RescaleSlope can vary from file to file (i.e. from image to image along the third dimension). Correct application of RescaleSlope has not yet been incorporated into sis\_read\_dicom.

5) I have made three m files in the PET-CT folder:

investigate1.m: To see the span and coordinates of the three CT files and the PET file

show\_ct.m: To see an extract of the CT data

show\_pet.m: To see an extract of the PET data