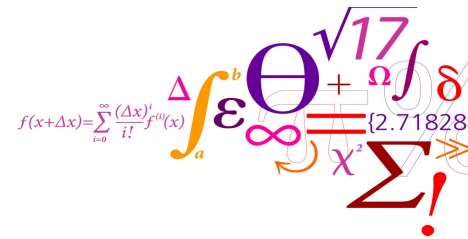


# Radon Transform and Filtered Backprojection

Jørgen Arendt Jensen

October 23, 2023

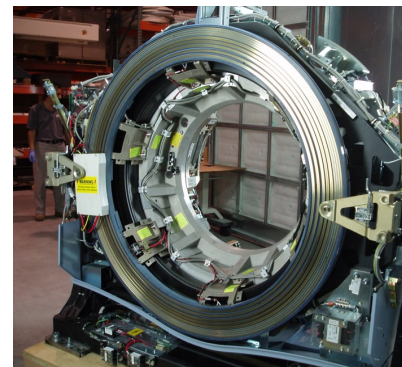
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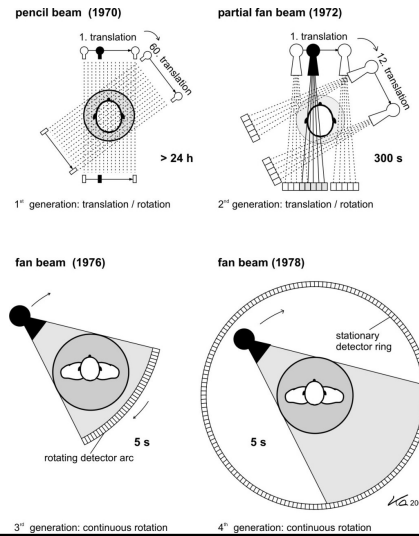
# CT reconstruction - outline

- CT scanners
- Projection and Radon transform
- Projection demo
- Fourier slice theorem
- Inverse Radon transform – filtered backprojection
- Selection of filters
- Filtered backprojection algorithm
- Reading material: Prince & Links chapter 6



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# Modern CT system generations



From: W. A. Kalender: Computed Tomography, Publicis, 2005

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# What do we measure?

- Intensity measured by detector:

$$I = I_0 \exp(-\mu \cdot x)$$

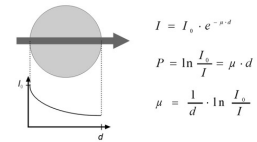
- Conversion to attenuation:

$$\mu = -\frac{1}{x} \ln \frac{I}{I_0}$$

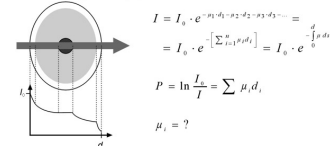
- Attenuation values  $\mu$  are scaled relative to water:

$$HU = \frac{\mu_{\text{tissue}} - \mu_{\text{water}}}{\mu_{\text{water}}} \times 1000$$

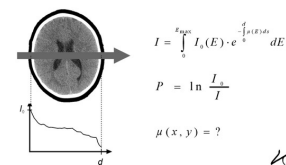
Case 1: homogeneous object, monochromatic radiation



Case 2: inhomogeneous object, monochromatic radiation

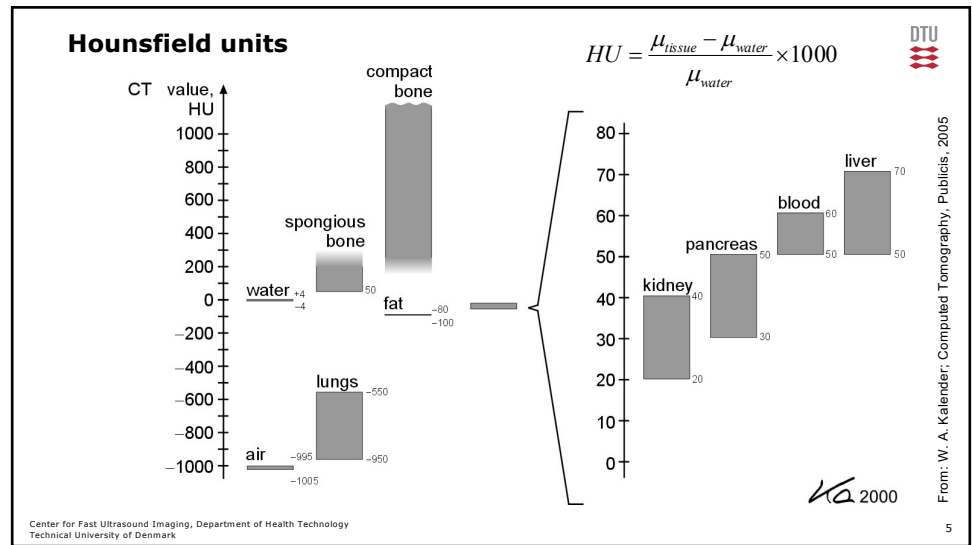


Case 3: inhomogeneous object, polychromatic radiation

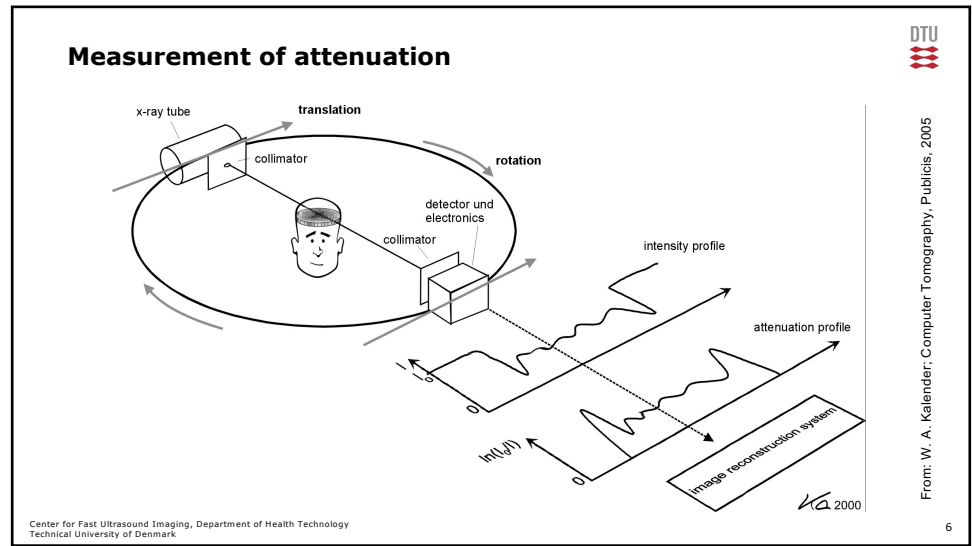


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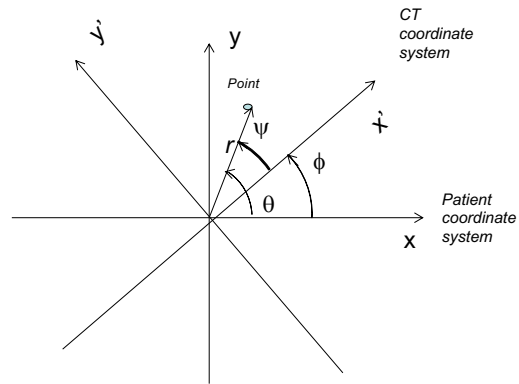


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## Parallel beam projection geometry



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## Radon transform



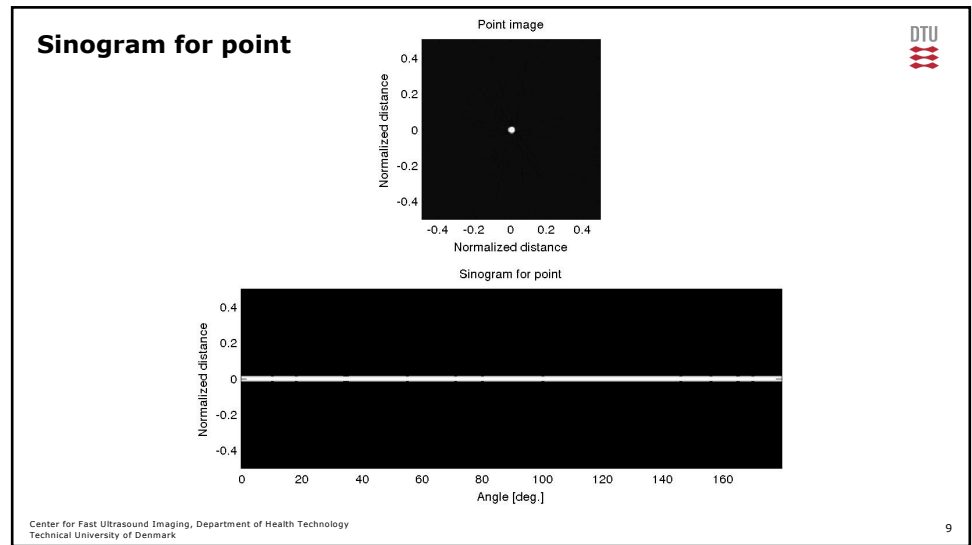
$$p(x', \phi) = \int_{-\infty}^{+\infty} f(x' \cos \phi - y' \sin \phi, x' \sin \phi + y' \cos \phi) dy'$$

$f(x, y)$  – Attenuation image  
 $x', y'$  – Gantry coordinate system  
 $x, y$  – Patient coordinate system

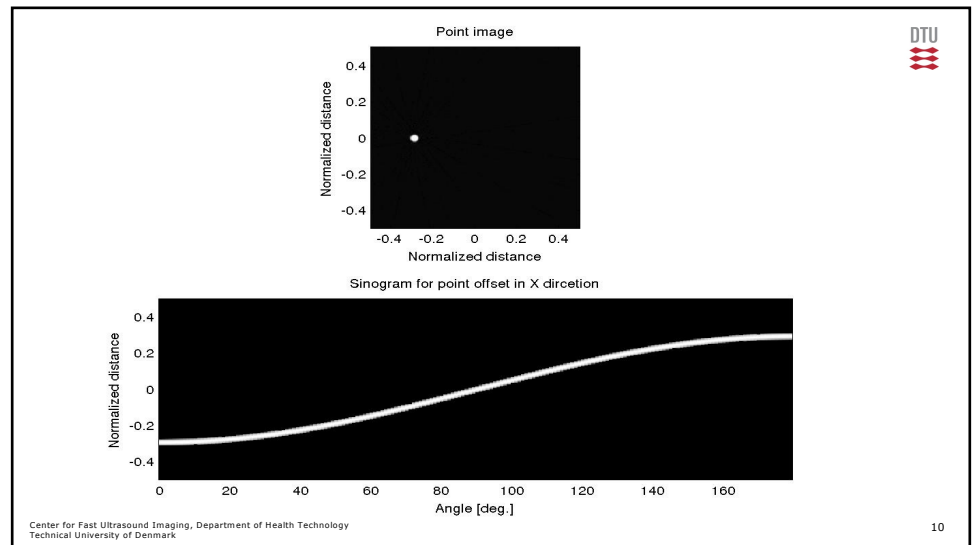
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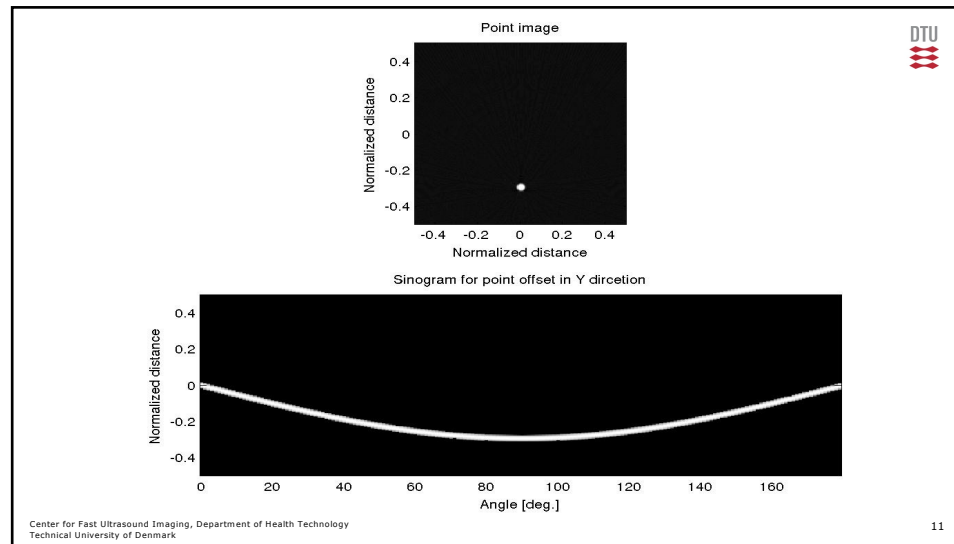
8



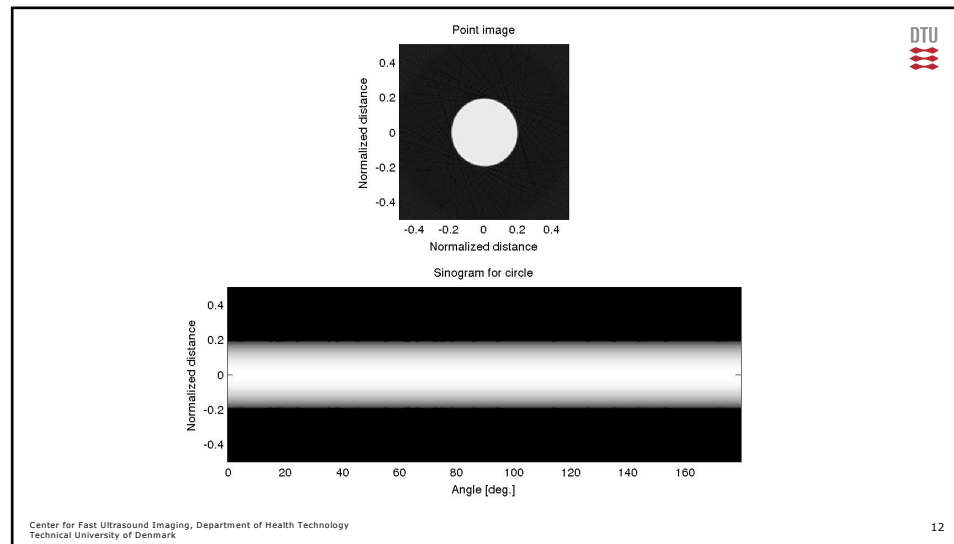
9



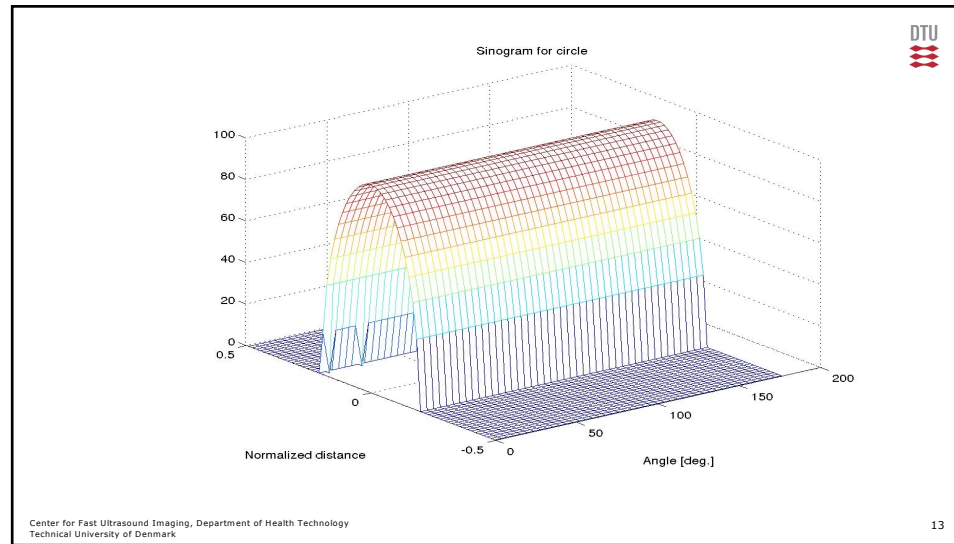
10



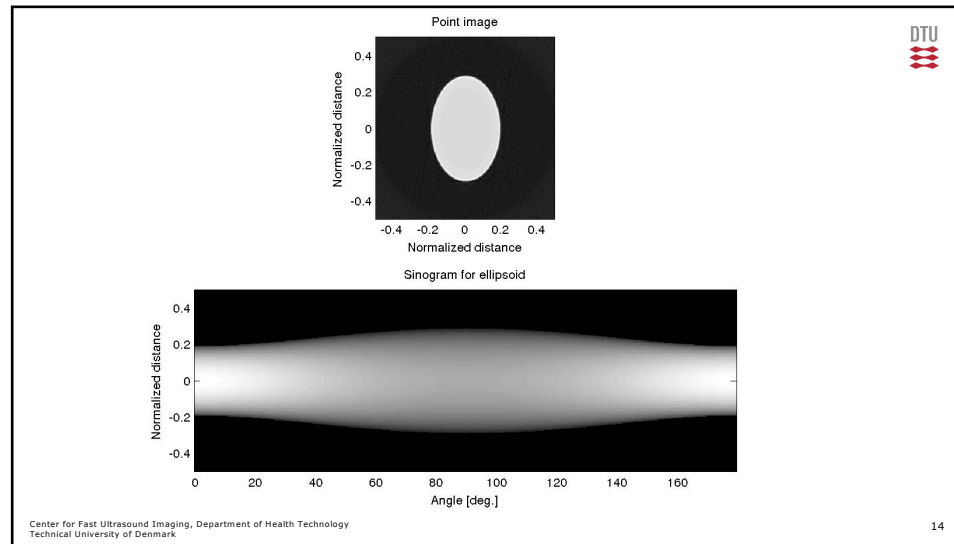
11



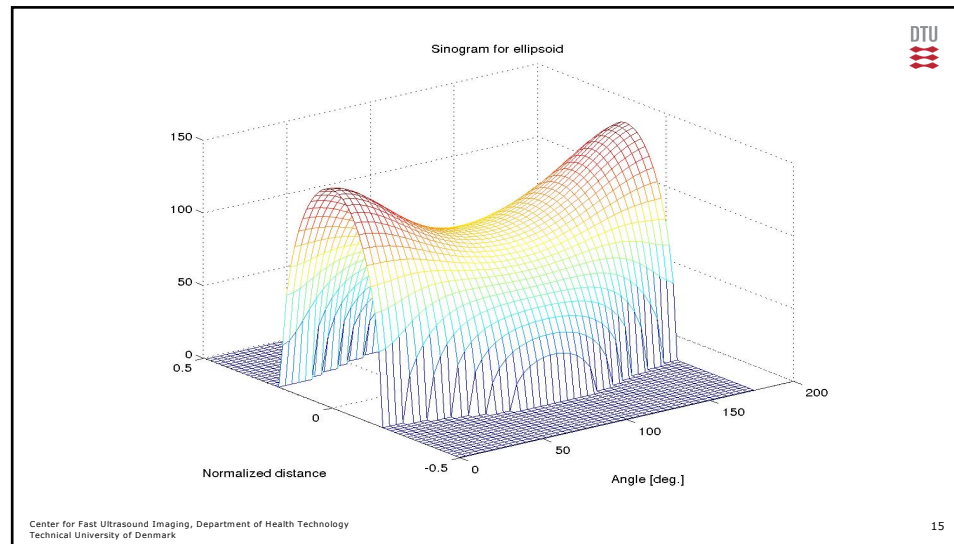
12



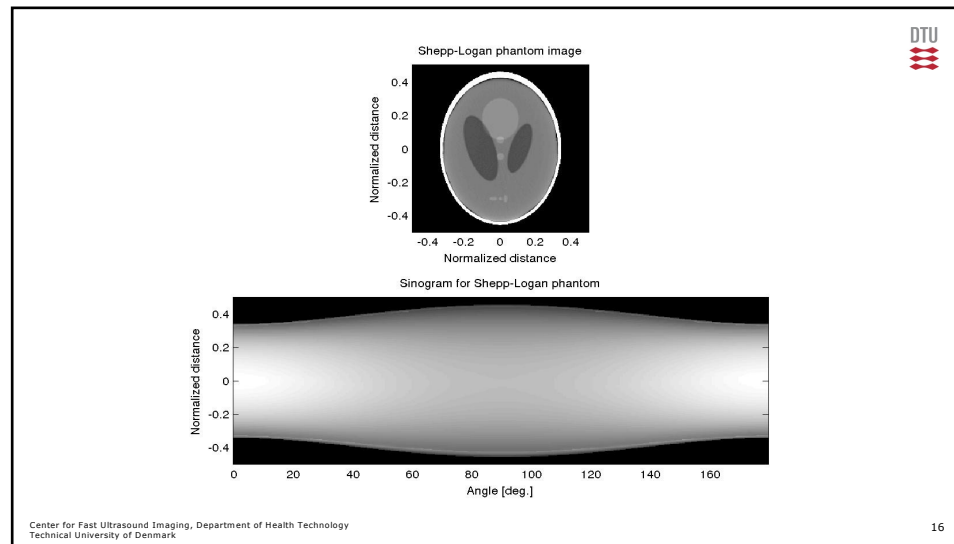
13



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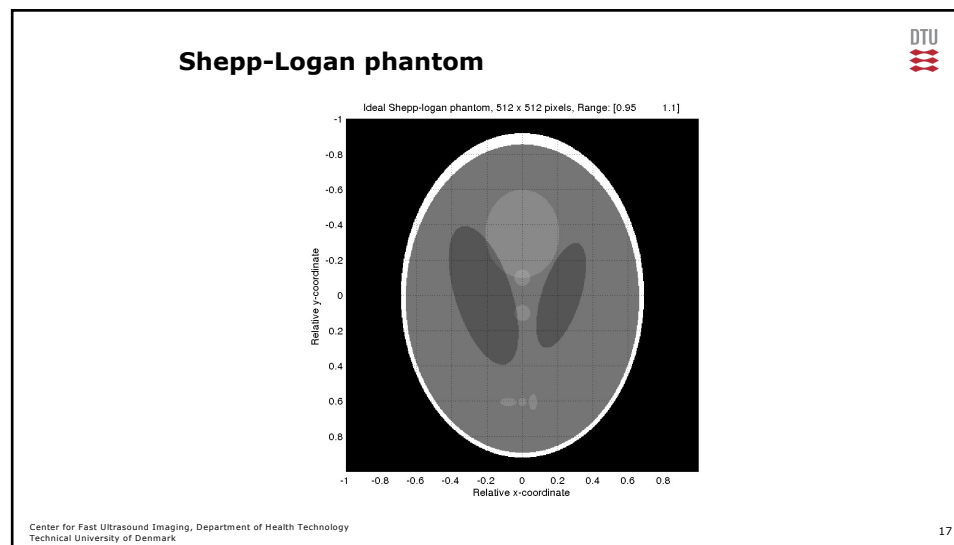


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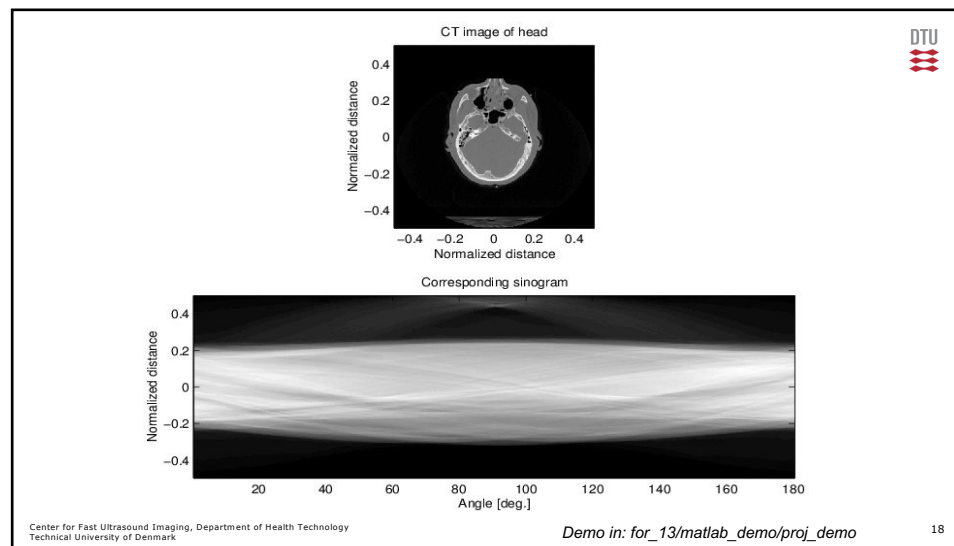


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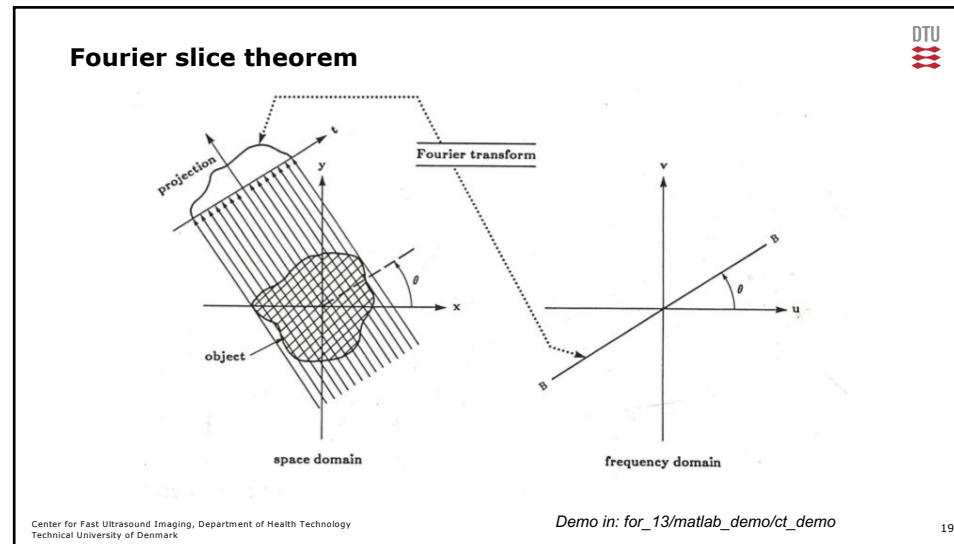




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### Fourier Slice Theorem

$$P(\rho, \phi) = \int_{-\infty}^{+\infty} p(x', \phi) e^{-j2\pi\rho x'} dx'$$

$$= F(\rho \cos \phi, \rho \sin \phi)$$

$F(u, v)$  – 2D Fourier transform of image  
 $\phi$  – Gantry rotation

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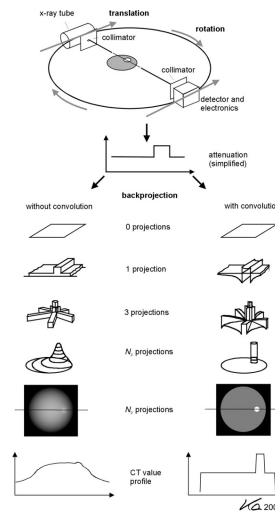
## Filtered Back Projection (FBP)

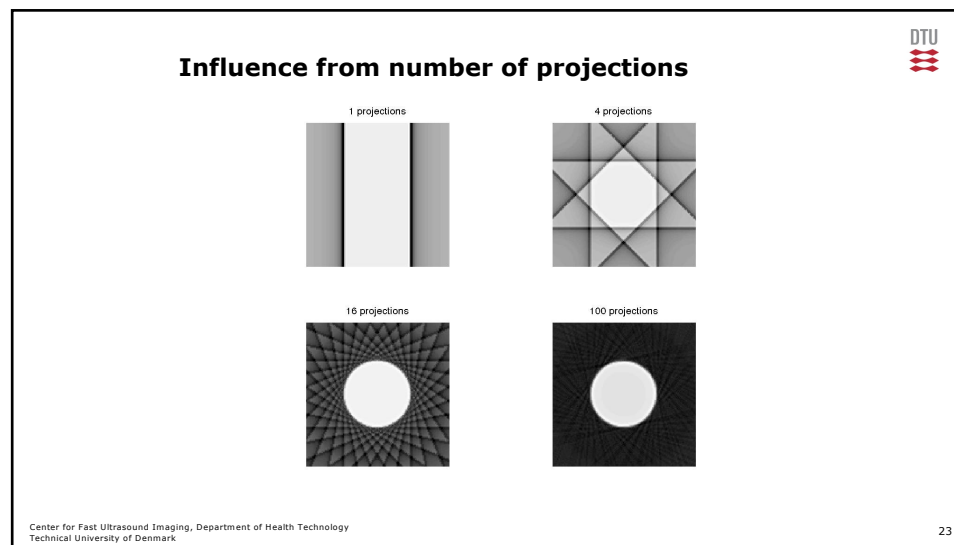
$$\hat{f}(x, y) = \int_0^{\pi} \int_{-\infty}^{+\infty} |\rho| P(\rho, \phi) e^{j2\pi\rho x'} d\rho d\phi$$

$\hat{f}(x, y)$  – Reconstructed image  
 $\phi$  – Gantry rotation  
 $x'$  – Detector position

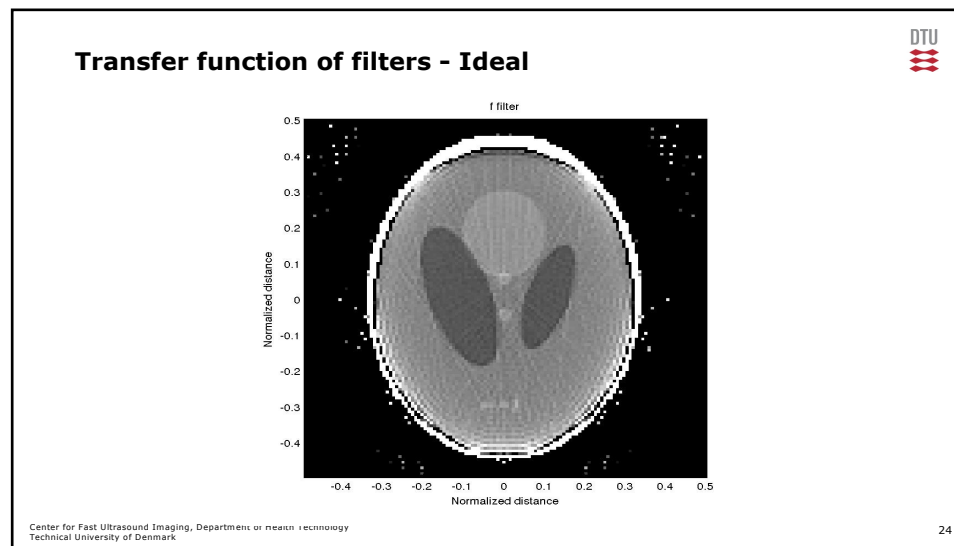
## Filtered backprojection

- Perform for all projections:
  1. Make Fourier transform of projected data
  2. Apply filter in Fourier domain
  3. Make invers Fourier transform
  4. Backproject and sum with previous image

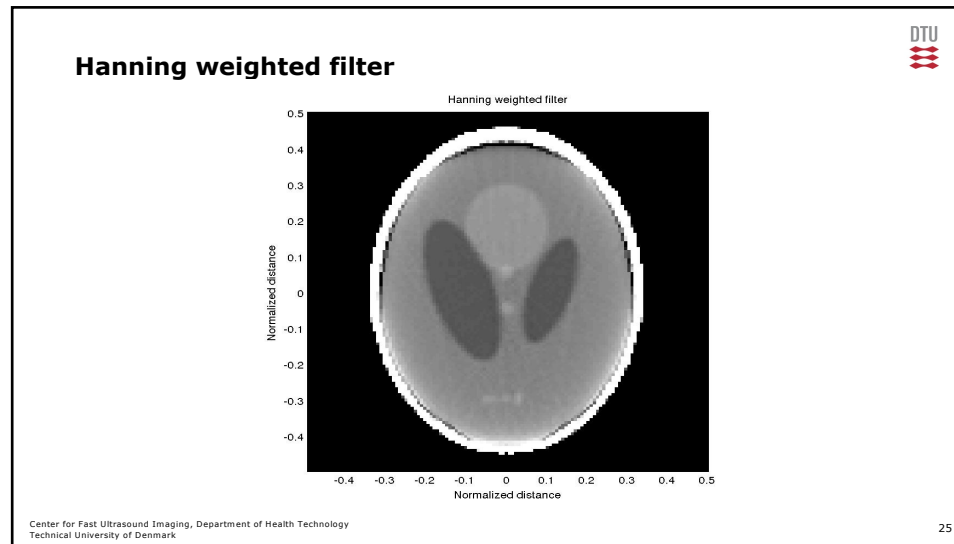




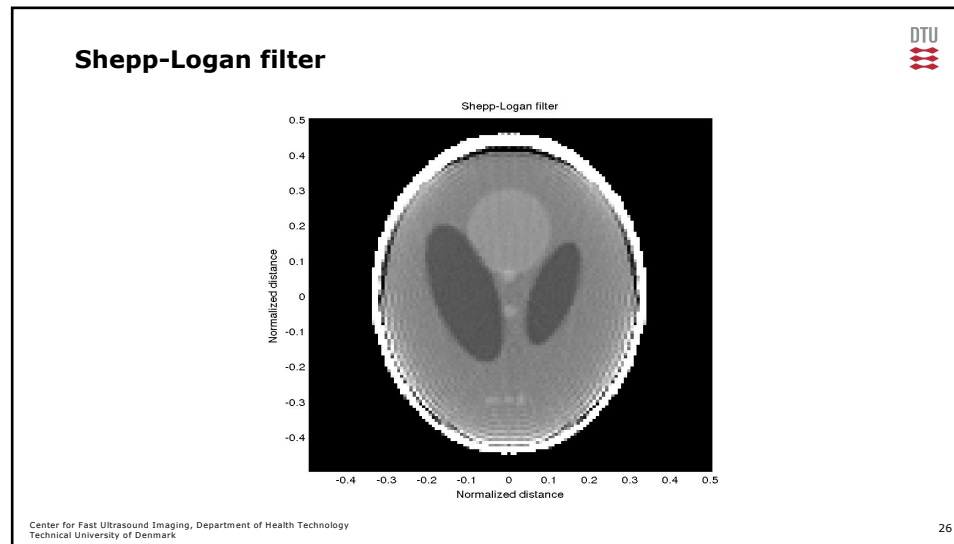
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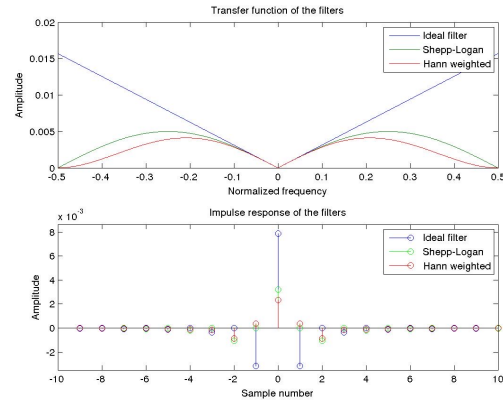


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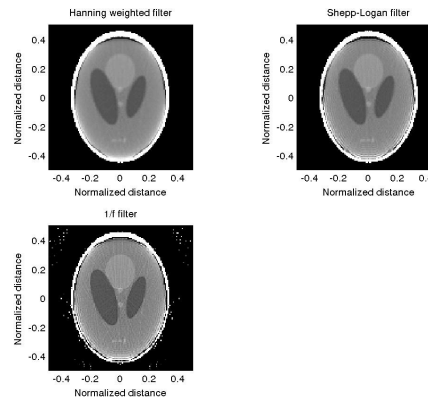
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## Filter transfer functions and impulse responses



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## Comparison between filters




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### Filtered backprojection


- Perform for all projection:
  - Make Fourier transform of projected data
  - Apply filter in Fourier domain
  - Make inverse transform
  - Backproject and sum with previous image


**backprojection**


with convolution

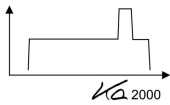
0 projections 


1 projection 

3 projections 

$N_p$  projections 

$N_p$  projections 

CT value profile 



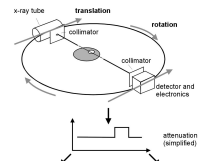
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

### Summary



- Parallel beam projection and Radon transform
- Fourier slice theorem
- Filtered backprojection reconstruction and choices
- P & L: Chapter 6
- Questions for CT assignments







**backprojection**



without convolution      with convolution



0 projections  


1 projection  

3 projections  

$N_p$  projections  

$N_p$  projections  

CT value profile  



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## Reconstruction in CT: Hints for the assignments

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October 23, 2023

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$f(x+\Delta x) = \sum_{i=0}^{\infty} \frac{(\Delta x)^i}{i!} f^{(i)}(x)$

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## Data for testing and validation

- Use data sets on web site
- Circular phantom for geometry test
- Shepp-Logan for orientation and quantitative data
- In-vivo images for Hounsfield units

22485 Medical Imaging Systems

**CT data**

On this page you can gain access to a database of CT images and projection data for the images, that can be used for testing reconstruction algorithms. Data for some phantom objects and various programs for artificial phantoms and data operations are also given here.

The clinical images shown on these pages have been obtained from the Visible Human Project. They were created from computerized tomography (CT) and MR scanners and their redundancy, including the scanner ID's, their locations for taking projections.

A further description of the data can be found at [this](#) and a description of the program can be found [here](#).

You can get to the different data pages by clicking on one of the images or text below them.

Circular phantom

Shepp-Logan phantom

Image of knee

Image of horse

Image of breast

Data for assignments

A slice showing Houghed cells for a CT scan can be downloaded [here](#). The slice is taken from E. Hestler (ed.) Imaging systems for medical diagnostics. Siemens, 1995.

A paper of Mean Absorption Coefficients and Mean Energy Absorption Coefficients can be found at the following reference:

<http://www.physics.mcgill.ca/PhD/Doc/Chap/Chap05/Chap05.htm>

A radiology image slice can be found at:

<http://cheb.umd.edu/mha/mha/ct/ct.html>

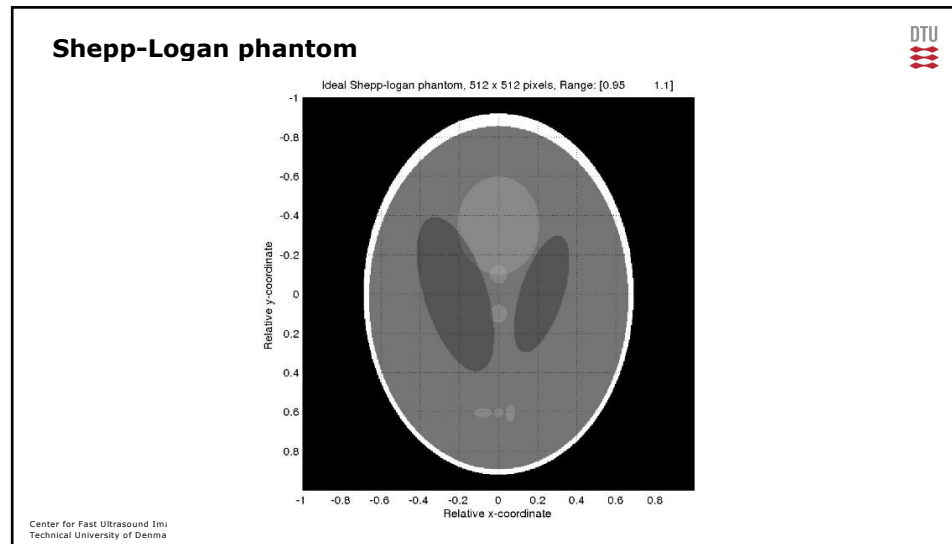
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### Assignment data

- DICOM data from female patient
- All data available on the web
- Task is to find which slice it is

[https://courses.healthtech.dtu.dk/22485/?ct\\_data/assign\\_data.html](https://courses.healthtech.dtu.dk/22485/?ct_data/assign_data.html)

Data and program in: undervisning/22485\_31545\_billeder/ct\_data/dicom\_data 34/x

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## Reading DICOM data 1



```
% Set overall parameters
dir_name='DICOM/ST00001/SE00001/'; % Directory name
start_image=1; % First image in series
end_image=747; % Last image in series
frame_rate=50; % Frame rate for playing back the movie

% Set the dynamic range for the display
off_set=100; % Offset [Hu]
range=400; % Range to display [Hu]
map_values=128; % Number of gray level values
bone_off_set= -250; % Offset for showing the bones
bone_range=100; % Range for showing the bones

% Initialize figure
colormap(gray(map_values));
dicom_movie(end_image+1-start_image) = struct('cdata', [], 'colormap', []);
```

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## Reading DICOM data 2



```
Read information for the first images
file_name='IM00001';
info=dicominfo([dir_name, file_name]);
dx=info.PixelSpacing(1);
dy=info.PixelSpacing(2);
Y = dicomread(info);
[Nx,Ny]=size(Y);

% Make space for all the images
Y=zeros(Nx,Ny,end_image+1-start_image);
z_positions=zeros(end_image+1-start_image,1);
```

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## Reading DICOM data 3



```
% Loop through the images and read and display them
for i=start_image:end_image
    file_name=['IM00',num2str(floor(i/100)),num2str(floor(rem(i,100)/10)),num2str(rem(i,10))];
    info=dicominfo([dir_name, file_name]);
    Y(:, :, i) = dicomread(info);
    image((1:Nx)-Nx/2)*dx, ((1:Ny)-Ny/2)*dy, (double(Y(:, :, i))+off_set)/range*map_values)
    xlabel('Distance [mm]')
    ylabel('Distance [mm]')
    pos=sprintf('%5.1f, %5.1f, %5.1f', info.ImagePositionPatient(1), ...
        info.ImagePositionPatient(2), info.ImagePositionPatient(3));
    z_positions(i)= info.ImagePositionPatient(3);
    text(-150, -150, ['Image ', num2str(i), ', Pos. (x,y,z) = ', pos, ' mm'], 'Color', [1 1 1])
    axis('image')
    drawnow
    dicom_movie(i)=getframe;
end
% Display the movie
movie(dicom_movie, 5, frame_rate);
```

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Script in: ct\_data/dicom\_data

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Full script can be found at:

[https://courses.healthtech.dtu.dk/22485/files/ct\\_data/dicom\\_data/display\\_dicom\\_images.m](https://courses.healthtech.dtu.dk/22485/files/ct_data/dicom_data/display_dicom_images.m)

on the page for the CT data: [https://courses.healthtech.dtu.dk/22485/?ct\\_data/assign\\_data.html](https://courses.healthtech.dtu.dk/22485/?ct_data/assign_data.html)



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