

Biomedical Imaging Exercise – Week 9

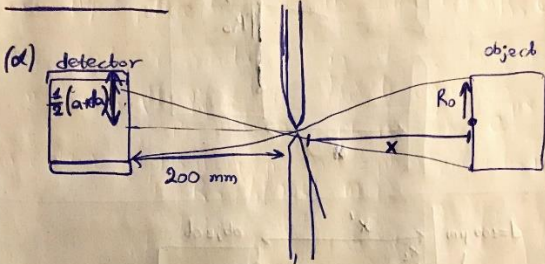
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1. Task 1.1 (SPECT)

a) The calculation of the distance x of the object from the pinhole is shown here:

Task 1.1

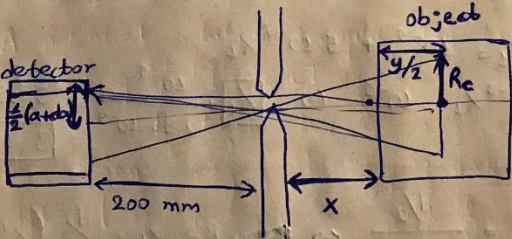


From the similar triangles, we get that:

$$\frac{R_o}{x} = \frac{\frac{1}{2}(a+da)}{200 \text{ mm}}$$
$$\Rightarrow x = \frac{R_o \cdot 200 \cdot 10^{-3}}{\frac{1}{2} \cdot 3 \cdot 10^{-3}} = \frac{0.6 \cdot 10^{-3} \cdot 200 \cdot 10^{-3}}{1.5 \cdot 10^{-3}}$$
$$\Rightarrow \boxed{x} = 0.08 \text{ m} = \boxed{8 \text{ cm}}$$

b) The calculation of the spatial resolution at the center of the sample can be seen here:

(b)



From the similar triangles:

$$\frac{R_c}{x + \frac{y}{2}} = \frac{\frac{1}{2}(a+da)}{200 \text{ mm}} \Rightarrow R_c = \frac{\frac{1}{2}(a+da)(x + \frac{y}{2})}{200 \text{ mm}}$$
$$\Rightarrow \boxed{R_c} = \frac{\frac{1}{2} \cdot 3 \cdot 10^{-3} \cdot 10 \cdot 10^{-2}}{200 \cdot 10^{-3}} = \boxed{0.75 \text{ mm}}$$

c) The change of the distance x (now x') when the actual diameter of the pinhole is considered is shown here:

(c)

Assuming we want to achieve the same spatial resolution of $R_0 = 0.6$ mm as in (a) then:

$$\frac{\frac{d}{2} (a+d_a)}{200 \cdot 10^{-3} + x_d} = \frac{d/2}{x_d} \Leftrightarrow \frac{3 \cdot 10^{-3}}{200 \cdot 10^{-3} + x_d} = \frac{50 \cdot 10^{-6}}{x_d}$$

$$\Leftrightarrow 3 \cdot 10^{-3} x_d = 10^{-5} + 5 \cdot 10^{-5} x_d$$

$$\Leftrightarrow 2.95 \cdot 10^{-3} x_d = 10^{-5} \Leftrightarrow \boxed{x_d} = \frac{10^{-5}}{2.95 \cdot 10^{-3}} = \frac{3.39 \cdot 10^{-3} \text{ m}}{3.39 \text{ mm}}$$

Also: $\frac{R_0}{x' - x_d} = \frac{d/2}{x_d} \Leftrightarrow R_0 \cdot x_d = \frac{d}{2} (x' - x_d)$

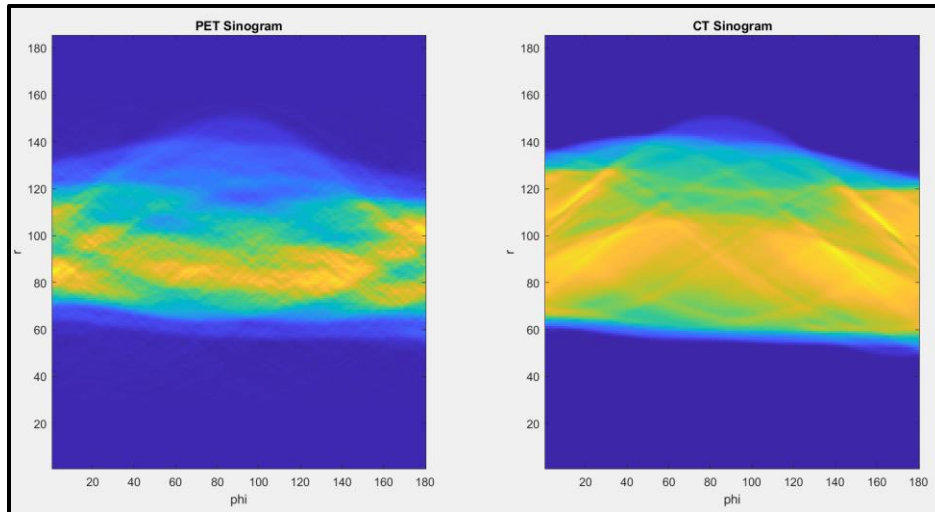
$$\Leftrightarrow 0.6 \cdot 10^{-3} \cdot 3.39 \cdot 10^{-3} = 50 \cdot 10^{-6} (x' - 3.39 \cdot 10^{-3})$$

$$\Leftrightarrow 2.034 \cdot 10^{-6} = 5 \cdot 10^{-5} x' - 1.695 \cdot 10^{-7}$$

$$\Leftrightarrow 5 \cdot 10^{-5} x' = 2.2035 \cdot 10^{-6} \Leftrightarrow \boxed{x'} = \frac{2.2035 \cdot 10^{-6}}{5 \cdot 10^{-5}} = 0.044 \text{ m} = 4.4 \text{ cm}$$

2. Task 1.2 (PET)

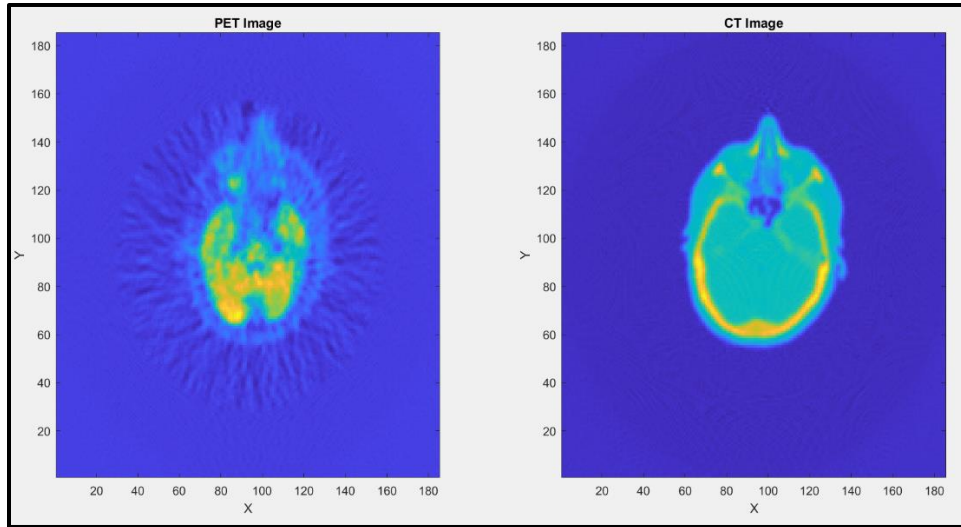
a) The sinograms of the PET and the CT scans as drawn by using the "DisplayData" function are the following:



b) The commands used to reconstruct the PET and CT data is shown below:

```
>> filter = CalcFilter(invivo.matrix);
>> recon_CT = CalcFBPrecon(invivo.angles, invivo.matrix, invivo.ctsino, filter);
>> recon_PET = CalcFBPrecon(invivo.angles, invivo.matrix, invivo.petsino, filter);
>> DisplayData(recon_PET,[1,2,1]); title('PET Image'); xlabel('X'); ylabel('Y');
>> DisplayData(recon_CT,[1,2,2]); title('CT Image'); xlabel('X'); ylabel('Y');
fx>>
```

Then the reconstructed images of the PET and CT scans look like the following:



- c) The image given by the PET scan demonstrates the parts of the brain that accumulate the injected PET tracer. In particular, these are mostly the parietal lobe and the occipital lobe, which are the ones showing higher glowing on the PET graph, meaning that more γ -photons are detected on these areas. This also means that these brain areas accumulate the injected PET tracer. The CT scan does not provide information on the accumulation of the PET tracer by specific brain areas, but rather anatomical data which helps us recognize the boundaries of the brain. The glowing areas on the CT scan show higher linear attenuation coefficients and depict the boundaries of the brain.
- d) The CT value, which is expressed in Hounsfield units, is defined as:

$$CT_{value} = \frac{(\mu - \mu_{water})}{\mu_{water}} \cdot 1000 \text{ HU}$$

Therefore, in order to calculate the linear attenuation coefficients of a body structure at a specific energy we need to extract μ_{water} at that energy and then use:

$$\mu = \frac{(CT_{value} \cdot \mu_{water})}{1000} + \mu_{water}$$

3. Task 1.3 (PET)

- a) The mass attenuation coefficients for each structure are extracted from the table for 511 keV, which is the energy of the γ -photons emitted by the positron annihilation process. These coefficients are used in the code:

```
%
% Set tissue density
% (see: Table 2 in www.nist.gov/pml/data/xraycoef/)
%
rho_blood = 1.060; % density blood [g/cm3]
rho_bone = 1.450; % density bone [g/cm3]
rho_lung = 0.001; % density lung/air [g/cm3]
rho_muscle = 1.050; % density muscle [g/cm3]
rho_water = 1.000; % density water [g/cm3]

%
% Set mass attenuation coefficients for 100 keV (CT) and 511 keV (PET)
% (see: Table 4 in www.nist.gov/pml/data/xraycoef/)
%
mac_blood(1) = 0.169; % blood @ 100 keV [cm2/g]
mac_blood(2) = 9.598E-02; % blood @ 511 keV [cm2/g]
mac_bone(1) = 0.186; % bone @ 100 keV [cm2/g]
mac_bone(2) = 9.022E-02; % bone @ 511 keV [cm2/g]
mac_lung(1) = 0.154; % lung @ 100 keV [cm2/g]
mac_lung(2) = 8.712E-02; % lung @ 511 keV [cm2/g]
mac_muscle(1) = 0.169; % muscle @ 100 keV [cm2/g]
mac_muscle(2) = 9.598E-02; % muscle @ 511 keV [cm2/g]
mac_water(1) = 0.171; % water @ 100 keV [cm2/g]
mac_water(2) = 9.687E-02; % water @ 511 keV [cm2/g]
```

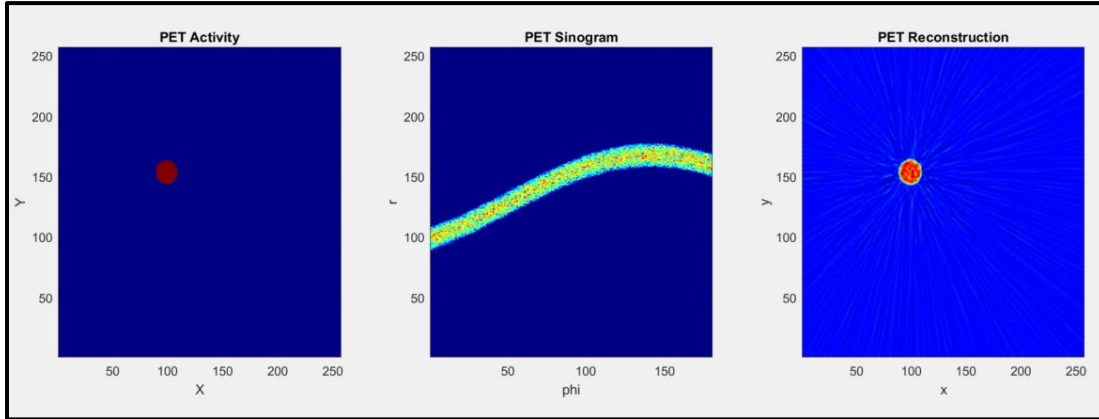
b) The updated phantom includes the artificial lung tumor with a radioactivity of 300 MBq:

```

%-----
% PET SIMULATION (begin)
%-----
% Define analytical phantom using ellipses with [x0 y0 a b phi mue act]
%
%   x0,y0  - center point [cm] (+x -> left-right, +y -> bottom-up)
%   a,b    - half axes [cm]
%   theta  - rotation angle relative to x-axis [deg]
%   mue    - linear attenuation coefficient [1/cm]
%   act    - radioactivity [MBq]
%
%-----
phantom.ellipse = [ 0  0  90  80  0  mue_bone(2) 0; % thorax
                   0  0  70  60  0  mue_lung(2)-mue_bone(2) 0; % lung
                   +110 0  15  15  0  mue_muscle(2) 0; % left arm muscle
                   +110 0  5  5  0  mue_bone(2)-mue_muscle(2) 0; % left arm bone
                   -110 0  15  15  0  mue_muscle(2) 0; % right arm muscle
                   -110 0  5  5  0  mue_bone(2)-mue_muscle(2) 0; % right arm bone
                   0  0  10  10  0  mue_blood(2)-mue_lung(2) 0; % aorta
                   +30 +25 25 20 35  mue_muscle(2)-mue_lung(2) 0; % heart
                   -30 +25 10 10 0  mue_muscle(2)-mue_lung(2) 300]; % lung tumor

```

c) The PET sinogram and the FBP reconstructed image are shown in the following figure:



Furthermore, the radiotracer activity of the ground truth and of the reconstructed image are shown on the terminal:

```

>> NUC_EXERCISE1
-----
BIOMEDICAL IMAGING - NUC-EXERCISE #1
-----
PET tumor activity ground truth: 300.000000
PET tumor activity w/o correction: 275.725422

```

The radiotracer activity in the ground truth represents the mean value of nuclear disintegrations per second in the ideal case of detection. However, the radiotracer activity in the reconstruction is reduced. That is because the reconstruction has been performed by PET imaging, hence through the detection of the γ -photons. During the imaging procedure, noise with Poisson distribution has been added as well. Therefore, the final reconstructed image is a result of filtered backprojection which includes noise. This prevents from detecting all the nuclear disintegrations which reduced the value of the tumor activity detected. This can also be seen in the reconstructed image which includes noisy parts. Also, because γ -photons from different parts of the tumor follow different paths, they experience different attenuation, so the resulting image shows the tumor in an ununiform entity.

d) The coefficients from 100 keV are mapped to coefficients in 511 keV (PET energy level) through the following formula:

$$\mu_{511\text{keV}} = 5.7 \cdot (\mu_{\text{bone}-100\text{keV}} - \mu_{\text{water}-100\text{keV}}) \cdot \mu_{100\text{keV}}$$

With $\mu_{\text{bone}-100\text{keV}} = 0.2697 \frac{1}{g}$ and $\mu_{\text{water}-100\text{keV}} = 0.171 \frac{1}{g}$, therefore: $\mu_{\text{bone}-100\text{keV}} - \mu_{\text{water}-100\text{keV}} = 0.0987 \frac{1}{g}$

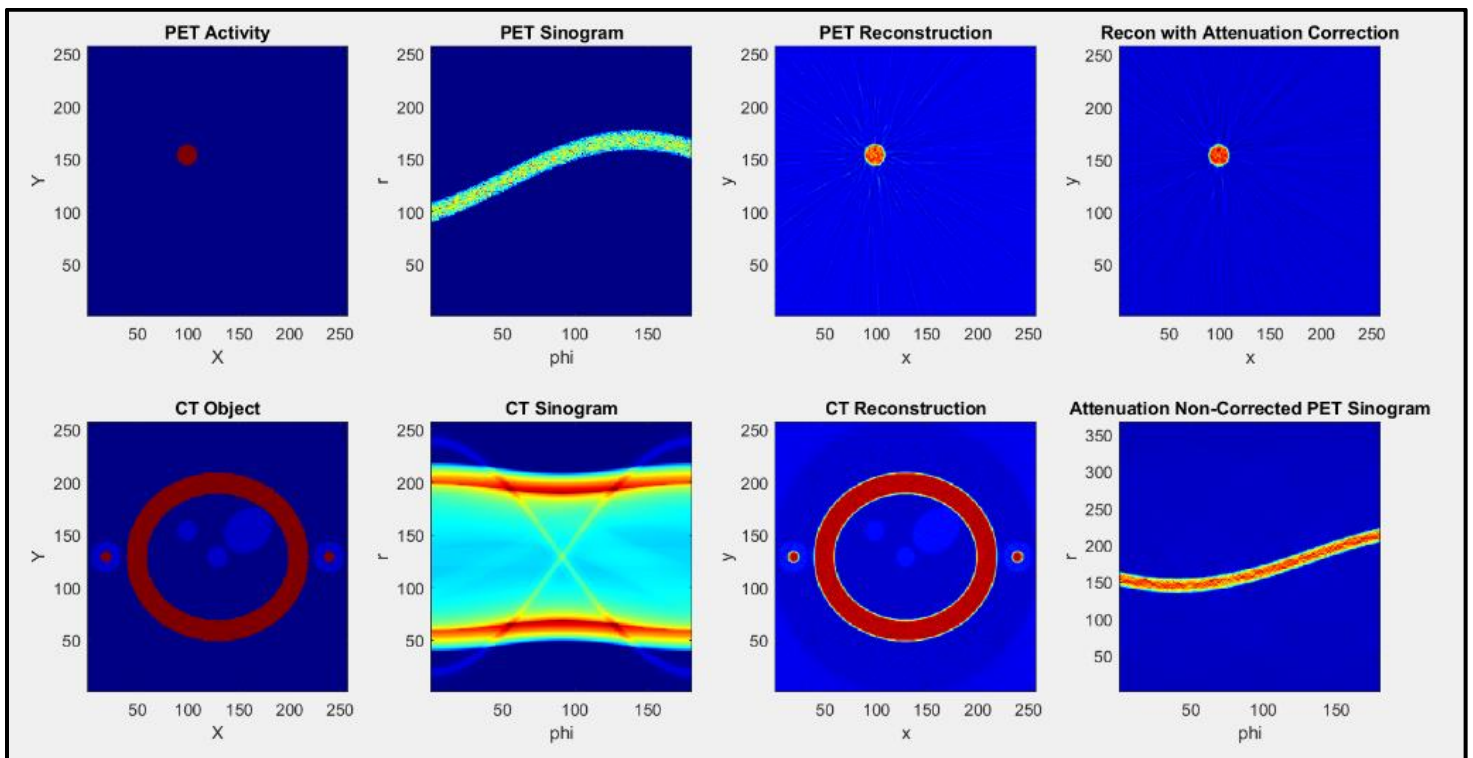
This is implemented in the code as following:

```
% -----
% PET ATTENUATION CORRECTION (begin)
% -----
% TASK 1.3 Map linear attenuation coefficients from 100 keV to 511 keV
phantom.corr = (5.7*(mue_bone(1)-mue_water(1))).*phantom.ctfbp;
```

- e) In the previous step we have extracted the information about the values of linear attenuation coefficients at 511 keV, which is the energy of the γ -photons emitted by the positron annihilation processes. These photons have been attenuated according to the linear attenuation coefficients, at 511 keV, of the structures they cross until they reach the detectors. In order to perform attenuation correction we need to invert the attenuation process by multiplying the projections with the term $e^{\mu x}$ where the exponent is included in the values of the phantom.ctsino matrix. Therefore, the final equation to use is: $projection = projection \cdot e^{\mu x}$ with μ , the linear attenuation coefficients at 511 keV. In the code this is implemented as:

```
% -----
% TASK 1.3 Apply attenuation correction to PET sinogram
phantom.petsino = phantom.petsino.*exp(phantom.ctsino);
DisplayData(phantom.petsino,[2,4,8]); title('Attenuation Corrected PET Sinogram'); xlabel('phi'); ylabel('r');
```

- f) When the linear attenuation coefficient of the bone is multiplied by 10, then the following reconstructed image is extracted:



Continue to next page...

g) The full code used to implement PET attenuation correction is seen in the following figures:

```
%
% PET ATTENUATION CORRECTION (begin)
%
% TASK 1.3 Map linear attenuation coefficients from 100 keV to 511 keV
phantom.corr = (5.7*(mue_bone(1)-mue_water(1))).*phantom.ctfbp;

%
% Recompute CT sinogram from remapped discrete CT image
%
phantom.ctsino = radon(phantom.corr,projection_angles);

%
% Normalize for number of projection angles in CT sinogram
%
phantom.ctsino = phantom.ctsino/180/sqrt(2);

%
% Recompute PET sinogram from discrete PET image
%
phantom.petsino = radon(phantom.petfbp,projection_angles);

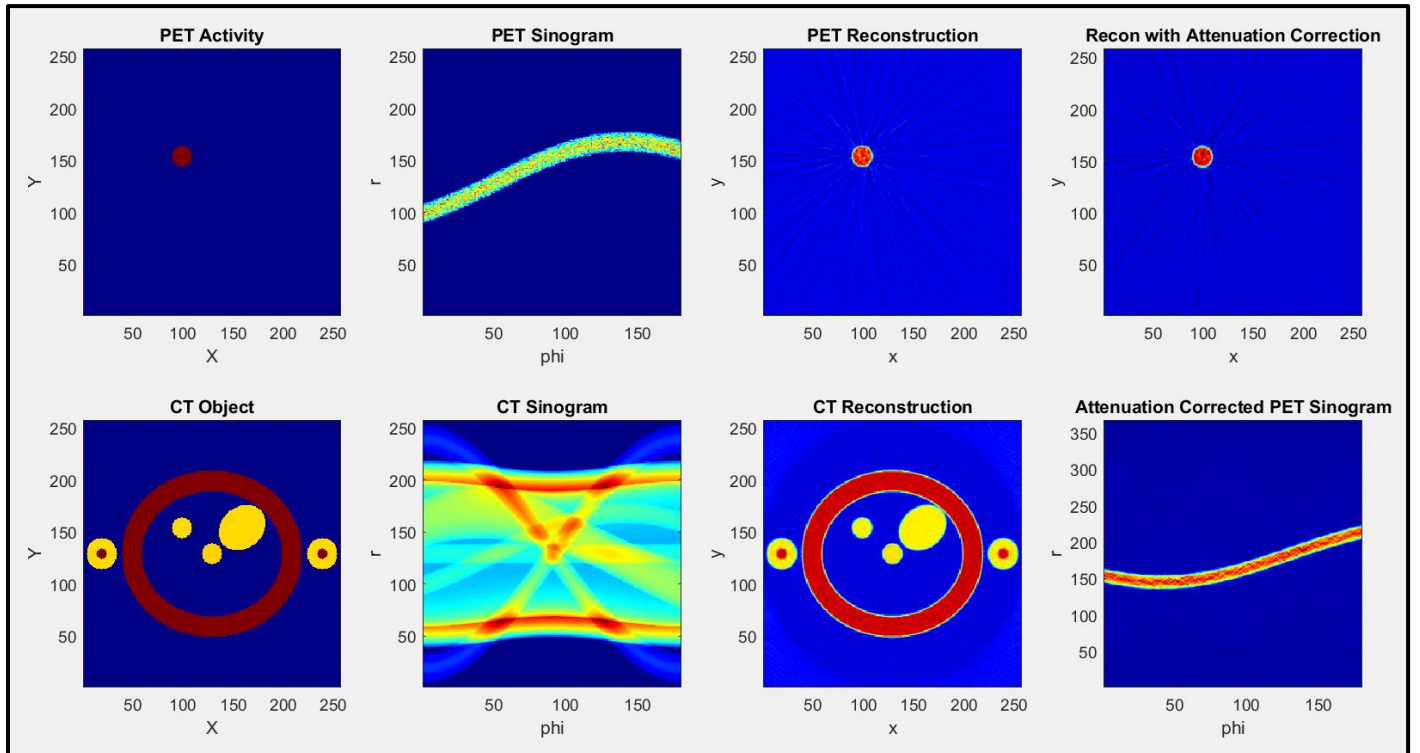
%
% TASK 1.3 Apply attenuation correction to PET sinogram
phantom.petsino = phantom.petsino.*exp(phantom.ctsino);
DisplayData(phantom.petsino,[2,4,8]); title('Attenuation Corrected PET Sinogram'); xlabel('phi'); ylabel('r');

%
% Recompute PET image from attenuation-corrected sinogram
phantom.petcorr = iradon(phantom.petsino,projection_angles);

%
% Display PET image with attenuation correction
%
DisplayData(phantom.petcorr,[2,4,4]); title('Recon with Attenuation Correction'); xlabel('x'); ylabel('y');

%
% Display corrected PET signal value of lung tumor (=9)
%
fprintf('PET tumor activity with correction: %f\n',CalcROISignal(phantom,9,phantom.petcorr(1:matrix+1,1:matrix+1)));
```

The resulting reconstructed images and sinograms of the PET and CT scans are shown in the following figure:



Furthermore, the tumor activity with the attenuation correction is significantly higher than in the case without the correction and this is depicted on the terminal:

```
-----  
BIOMEDICAL IMAGING - NUC-EXERCISE #1  
-----  
PET tumor activity ground truth: 300.000000  
PET tumor activity w/o correction: 276.968001  
PET tumor activity with correction: 295.143262
```

- h) The combination of the two scans might include difficulties because of the differences in the spatial resolution between the CT scan and the PET scan. The CT scan can acquire images with much higher resolution because the photons are emitted from a source rather than from inside the body (PET). Therefore, this difference in resolution needs to be considered before merging the images from the PET and the CT scans. A potential solution would be to perform spatial smoothing of the CT scan to match the resolution of the PET scan before performing the attenuation correction. There might be difficulties due to motion of the patient as well. That is because the two scans are performed in different time periods (serially) and therefore if the patient has moved even slightly between the scans, there will be a mismatch between the PET and CT scans of a structure resulting in distorted images. Finally, difficulties can arise because of the different data acquisition times of the PET and the CT scans. The CT scan is performed very quickly (seconds), while the PET data are acquired over several minutes. Therefore, even a small displacement, e.g. due to cardiac or breathing motion could cause misregistrations of a potential tumor. Despite these practical difficulties, the combination of these two scans can produce a more accurate representation of the structures in the body than the PET scan on its own.