# Biomedical Imaging

Exercise NUC #1 – SPECT and PET/CT

The purpose of the exercise is to calculate the PSF resulting from collimation in SPECT, to reconstruct PET/CT in-vivo data and to implement CT-based attenuation correction of PET phantom data. For the latter task, the analytical computer model of the human thorax is extended to include an artificial lung tumor accumulating a radio tracer.

Task 1.1 (SPECT)
A pinhole SPECT camera is given consisting of a detector array with crystals of area of 2.8 mm x 2.8 mm and a thickness of 20 mm. Between individual crystals there is a gap (insulation) of 0.2 mm. The distance between the detector array and the pinhole (diameter 50 µm) is 20 cm and the pinhole is assumed to be ideal, i.e. the thickness of the pinhole plate is negligible and attenuation of the pinhole material shall be infinite.
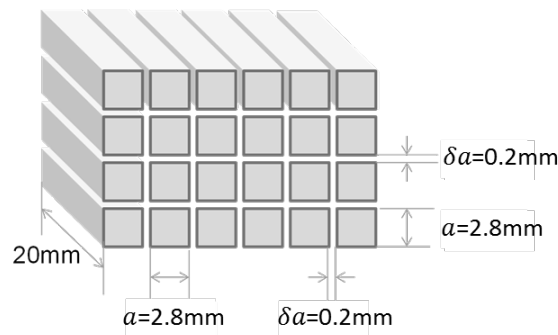
- Calculate at what distance x from the pinhole must the object be placed in order to achieve a spatial resolution (pixel dimension) of $r_s = 0.6$ mm on the object surface? For an estimate assume the pinhole to be of radius 0.
- What is the spatial resolution r_c at the center of a sample of a thickness of y=40 mm?
- How does x change if the actual diameter of the pinhole (100 µm) is considered?

Task 1.2 (PET)
Please download the *.zip file for NUC_EXERCISE1 from https://moodle-app2.let.ethz.ch and unpack it on your computer. You find a data file called *InvivoData.mat* which contains sinograms of a PET and a corresponding CT scan of a human brain. The task is to reconstruct and compare the PET and the CT scans using code that was previously used in the XCT exercises:

- Start Matlab and load the available in-vivo data set using *load InvivoData.mat*.
- Type *invivo* to see the data structure; type e.g. *invivo.angles* to check variables; use *DisplayData* to display sinograms.
- Reconstruct both the PET and CT data using function *CalcFilter* and *CalcFBPRecon* (check files to see in- and output); display reconstructed images back-to-back using e.g. *DisplayData(PETRecon,[1 2 1])* and *DisplayData(CTRecon,[1 2 2])*.
- By comparing the PET and CT images, which brain areas are seen to accumulate the PET tracer?
- The CT image is reconstructed in Hounsfield units (HU) + 1000. How would you calculate linear attenuation coefficients from HU data?

Task 1.3 (PET)

To study CT-based attenuation correction, the synthetic analytical phantom as used during the XCT exercises is extended with a PET encoding and reconstruction section.

- Open NUC_EXERCISE1.m and read the code lines and comments carefully.

- Update mass attenuation coefficients of the PET section
  (refer to Tables 4 at https://www.nist.gov/pml/x-ray-mass-attenuation-coefficients).

- Implement an artificial lung tumor in the PET section; assign a radioactivity of 300 MBq to the tumor

- Verify PET sinogram and FBP reconstruction of the lung tumor; compare radiotracer activity in the reconstruction relative to ground truth! Why is there a discrepancy?

- Implement a mapping from CT attenuation coefficients obtained at 100 keV (CT) to PET energy levels

  (hint: use the difference of linear attenuation of bone and water to derive the conversion factor; approximate the relation between linear attenuation coefficients of CT and PET energy levels using a linear function).

- Derive an equation to perform PET attenuation correction based on converted CT linear attenuation.

- Temporarily set the linear attenuation of bone to 10x the original value to better visualize attenuation correction (see code).

- Implement PET attenuation correction and compare tumor activity without and with attenuation correction.

- Discuss potential difficulties of PET attenuation correction in clinical practice by considering the difference in spatial resolution of CT and PET, differences in detector design and potential motion of the patient.

Questions?

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