

Computational assignment 3

due on October 13, 2025

The following two assignments will implement a pencil beam algorithm for dose calculation. The main idea of the pencil beam algorithm is to start with the dose distribution of a photon beam in water, and then make adjustments to this dose distribution to account for tissue heterogeneities in patients.

The pencil beam algorithm has two main components:

1. A ray-tracing algorithm that calculates the radiological depth of all voxels in the patient.
2. A model or numerical representation of the dose distribution in water.

This week's assignment will implement the ray-tracing method.

Ray tracing

The radiological depth z^{rad} at geometrical depth z from the patient surface is given by

$$z^{rad}(z) = \int_0^z \frac{\mu_m(z')}{\mu_w} dz' \quad (1)$$

where $\frac{\mu_m(z')}{\mu_w}$ is the attenuation coefficient of the tissue at geometric depth z' relative to water. The integration is carried out along a straight line in the direction of the incident beam between the voxel under consideration and the patient surface. $z' = 0$ corresponds to the entrance point at the patient surface. The relative attenuation coefficient is obtained from the CT number which provides Hounsfield numbers H for every voxel. A Hounsfield number of zero corresponds to water, a Hounsfield number of -1000 corresponds to air. We assume the following simple piece-wise linear conversion from Hounsfield numbers to relative attenuation coefficients:

$$\frac{\mu_m(z')}{\mu_w} = \begin{cases} \frac{H+1000}{1000} & (-1000 < H < 0) \\ 1 + \frac{1}{2} \frac{H}{1000} & (H \geq 0) \end{cases} \quad (2)$$

If the CT contains voxels with Hounsfield numbers below -1000, those should be set equal to -1000.

Write a function

`calculate_raddepth(angle)`

which returns a 2D array of the size of the CT image, containing the radiological depth of each voxel. For voxels outside of the patient, the values can be set to zero. The input parameter `angle` is the angle of the incident beam α . An illustration of the coordinate system is shown in figure 1. Calculate radiological depth distributions for a couple of angles and visualize the result by plotting the radiological depth array like a dose distribution on top of the CT.

Comments:

A few issues can easily cause confusion and lead to bugs. Therefore, note that:

1. We denote a point in the patient by (x, y) where the positive x -axis points to the right and the positive y -axis points upwards. (x, y) can be converted into indices (ix, iy) . Note that, if you address a voxel in the CT matrix, you have to exchange ix and iy because the row index comes first and the column index second.
2. The function `imshow` by default flips the y -axis. This can be avoided by either specifying the keyword argument `origin='lower'` or by calling `ax.invert_yaxis()`.

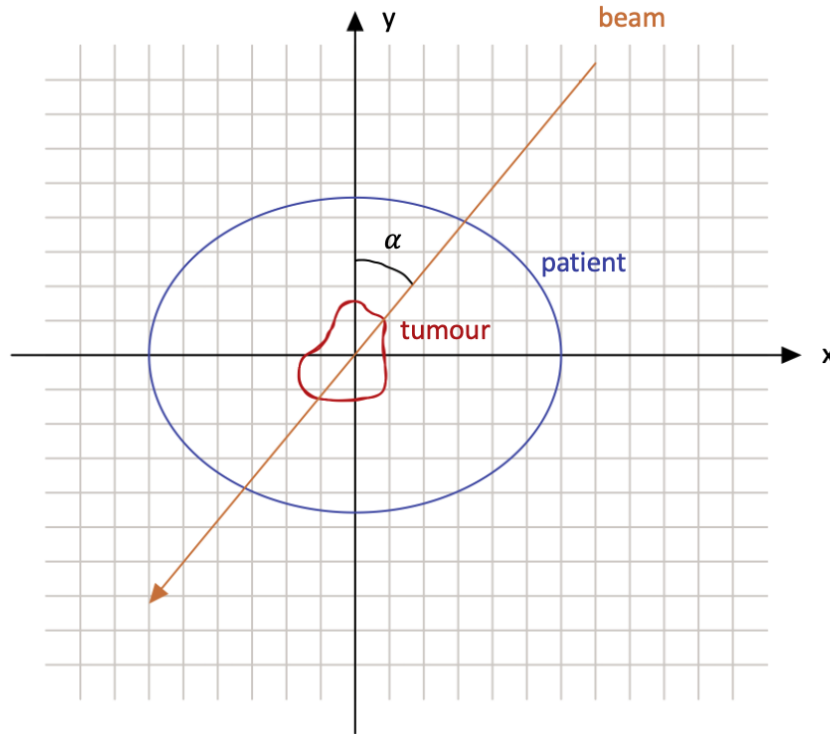


Figure 1: Coordinate system with incident beam.