

# Introduction to Biological Imaging

## Homework 1

**Deadline:** 21.11.2018, 23:59 CET

**Submit your work to:** [ivan.olefir@tum.de](mailto:ivan.olefir@tum.de)

**Email title:** MAT{your matrikelnummer #}

HW{homework #} 201819 {your name}

**Example:** MAT12345678 HW1 20189 Ivan Olefir

**Acceptable formats:** .pdf, .doc, .docx

### Report guidelines:

- Do not be too elaborate in your answers unless you are asked to. 1-2 sentences are usually enough to answer the questions.
- Every figure should have a number and a title. In the text refer to figures by their number. Every plot should have titled axes. If the figure consists of several subplots, each one should have a self-explanatory title.
- Include the commented code as shown below either at the beginning or at the end of the document

## Code Example:

```
%% Assignment 1=====
%=====

% 1)    Create a phantom for simulating XCT measurements. The phantom
should
% contain ellipses and polygons of varying intensity (use radon() and
augment
% the resulting image). Show an image of your phantom.

solution = pressxtowin(1); % create phantom by pressing X to win

% 2)    Compute the views (projections) with spacing of 1, 5 and 10
degrees.
% Show the projections at 0°, 30°, 45° and 90° (in one axes).
% Show the sinogram with the most angles.

solution = pressxtowin(2); % compute projections by pressing X twice

% 3)    Implement the backprojection algorithm (i.e. inverse radon
transform)
% according to slide 16 of the Tutorial slides. You are not allowed to use
iradon().

...

%% Assignment 2 =====
%=====
```

## Assignment 1

- 1) Create a phantom for simulating XCT measurements. The phantom should contain ellipses and polygons of varying intensity (use *phantom()* and augment the resulting image). Show an image of your phantom.
- 2) Compute the views (projections) for the range of angles from  $0^\circ$  to  $179^\circ$  with spacing of  $1^\circ$ ,  $5^\circ$  and  $10^\circ$ . Show the projections at  $0^\circ$ ,  $30^\circ$ ,  $45^\circ$  and  $90^\circ$  (in one axes). Show the sinogram with the most angles/projections.
- 3) Implement the backprojection algorithm (i.e. inverse radon transform) according to slide 16 of the Tutorial slides. You are not allowed to use *iradon()*.
- 4) Reconstruct the **phantom data** with the specified angular spacings using your backprojection algorithm **without filtering**. Show the obtained reconstructions.
- 5) Incorporate **filtering** in your backprojection. Implement 3 filters (ramp, cosine and hamming) and test their influence on the reconstruction using your phantom data (pick a single angle spacing). Show the reconstruction results
- 6) Reconstruct the **provided datasets** (*CT\_2018.mat*) with **your** backprojection algorithm without filtering and with each of the implemented filters, respectively. Show the reconstructed images.
- 7) Shortly interpret **your** results.
  - a. What is the effect of different angular spacings on the reconstruction?
  - b. How do the different filters change the reconstruction results?
  - c. Which filter performs best? Why? Under which circumstances?

Useful commands:

- *radon()*, *fft()*, *fftshift()*, *ifft()*, *ifftshift()*
- *hamming()*, *cos()*
- *repmat()*, *imrotate()*, *linspace()*

## Assignment 2

Assume the 2x2 discretization of the spatial distribution of absorption coefficient shown in Fig. 1 and 2 point detectors with spacing L.

- 1) Design a model matrix **A** that relates X-ray measurements  $\mathbf{p} = (P_1, P_2, P_3, P_4, P_5, P_6)^T$  at 3 shown angles to the (unknown) absorption  $\boldsymbol{\mu} = (\mu_1, \mu_2, \mu_3, \mu_4)^T$  as in:  $\mathbf{A}\boldsymbol{\mu} = \mathbf{p}$ . Show **A**.
- 2) Assume a specific distribution (values) of  $\boldsymbol{\mu}_{\text{test}}$  and a specific value of L. Simulate the corresponding measurements  $\mathbf{p}_{\text{test}}$  for this distribution using the model matrix **A**. Show  $\mathbf{p}_{\text{test}}$ .
- 3) Using the simulated measurements  $\mathbf{p}_{\text{test}}$ , reconstruct absorption  $\boldsymbol{\mu}_{\text{rec}}$ , i.e. solve  $\mathbf{A}\boldsymbol{\mu}_{\text{rec}} = \mathbf{p}_{\text{test}}$ . Show both the assumed ( $\boldsymbol{\mu}_{\text{test}}$ ) and the reconstructed ( $\boldsymbol{\mu}_{\text{rec}}$ ) absorption distributions.
- 4) Shortly interpret your result:
  - a. Does the reconstruction  $\boldsymbol{\mu}_{\text{rec}}$  correspond to the assumed distribution  $\boldsymbol{\mu}_{\text{test}}$  of the absorption coefficient?
  - b. Did you use *inv()* for inverting the model? Why?

