MS-DS19: Homework Project

Contributing 50% to the final grade

Team

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Dear Students,

as discussed, this homework covers topics across all the material taught in the class. It should be solved in teams of ideally two people.
The results of the group work **are to be presented** by **all** team members **during the acceptance/technical discussion meeting end of January!** This includes practical demonstration of developed software.

Not all tasks of this homework require coding. For the practical parts you can freely choose the programming language you prefer; for more “low-level” tasks MATLAB might be a good choice, for the final project task Python and Bash might be well suited, but it’s up to your discretion as data scientists to choose what suits you best here. Using the HPC might be helpful for the last task to deal with the large datasets.

The **written answers to the exercises + the source code of the practical parts** have to be **submitted via Moodle until January 23rd.** I will open a submission system for this in Moodle.

You can use any resources but *not* ask other humans for help. There is one exceptions: You can ask questions and discuss with your fellow students on the practical Task 4 in a forum on Moodle. By this it is ensured that all students have access to the discussion and we have a fair setting.

Good Luck!

Andreas
P.S.: I’ve tried with ChatGPT and it gets most answers wrong while sounding plausible at a first glance, so be careful ;-) When used very carefully (finding the mistakes) it might give useful hints.

Task 1

The Fourier transformation $f(x, y) \multimap\!\circ\, F(u, v)$ of a greyscale image $f(x,y)$ results in a band-limited signal in the spatial frequency range with maximum frequencies f_{umax} and f_{vmax}. For representation in the computer, the (partial) image is sampled in x direction with 20 sampling points per mm and in y direction with 10 sampling points per mm.

1. What is the theoretical maximum value of f_{umax} and f_{vmax} if error-free image reconstruction from the digital image should be possible (not using any compressive-sensing techniques)?
2. Now assume that the image to be sampled is a color image f_F . Define reasonable digital storage formats for the digital color image $f_F(x, y)$ using RGB encoding. Specify at least two variants. Briefly characterize the differences (advantages and disadvantages) of the variants.
3. What is the minimum memory requirement for the color image $f_F(x, y)$ when stored in a conventional computer system, if 1024 values are to be distinguished per color channel. Describe the image format to be used.
4. How many colors could be represented with the quantization chosen in sub-task 3?

Answers to task 1 (also on reverse side or additional sheet if needed):

Task 1 :

1) In order to get an error-free image reconstruction, one has to use the Shannon-Nyquist theorem. The theorem connects the image sampling rate to the maximal frequencies in the frequency-domain. As we are dealing with a 2D image, we have to to account for possible sampling resolution differences between x and y directions.

Let's call $f_{u,max}$ the maximal frequency associated to the x-sampling rate and $f_{v,max}$ the maximal frequency associated to the y-sampling rate.

The S-N theorem states:

$$\Delta x_i = \frac{1}{2 f_{max}} \quad \Leftarrow \quad f_{max} = \frac{1}{2\Delta x_i} \qquad \text{with} \quad \Delta x = \frac{1}{20}\,mm = 0.05\,mm, \quad \Delta y = \frac{1}{10}\,mm = 0.1\,mm$$

↳ Plug in values:

$$f_{u,max} = \frac{1}{2\Delta x} = \frac{1}{2 \cdot 0.05}\,mm^{-1} = \frac{1}{0.1}\,mm^{-1} = 10\,mm^{-1}$$

$$f_{v,max} = \frac{1}{2\Delta y} = \frac{1}{2 \cdot 0.1}\,mm^{-1} = \frac{1}{0.2}\,mm^{-1} = 5\,mm^{-1}$$ □

2) Color image $f_F(x,y)$ with RGB.

Two proposed encodings:

1 One way would be to use: → 1 look-up table

$f_F(x,y) = (r,g,b)(x,y)$ with $r,g,b \in \{0,\dots,255\}$

This contains all the information in one image. Yet it is more difficult to store digitally.

2 $f_F(x,y) = B_c(x,y)$ with $B \in \{0,\dots,255\}$ and $c \in \{1,2,3\}$

This would be kind of three images that would be saved separately which is easy to encode digitally! Yet, there would be the drawback to not having all information at once.

→ 3 look-up tables

3 Minimum memory requirement for RGB, with 1024 per color

$1024 = 2^{10}$ which translates to a 10-bit image per color channel

This would mean that we have 3×10 Bit images, which gives 30 Bit, or 3.75 Byte. (for a single pixel of 3 channels).

The proposed image-formats would be Tiff, JPEG, formats for Deep Color Images.

4 For a single pixel, we would have:

$(2^{10})^3 = 2^{30} \cong 1 \cdot 10^9$ Colors (ref.: $16 \cdot 10^7$ for 8-Bit)

Task 2

For the subjective enhancement of a greyscale image $G = g(x,y)$, a transformation T_G is performed as a so-called gamma correction in the form $T_G : g \rightarrow f$ with $f(x, y) = c - g^{\gamma}(x, y)$ where $g, f \in [0, 255]$.

1. Sketch the transformation curve T_G for $\gamma_1 = 0.5$ and $\gamma_2 = 2$.
2. How is the coefficient c typically determined?
3. In which respect and for which type of input images G do the two gamma values γ_1 , γ_2 lead to an image enhancement respectively?
4. What should be the minimum slope of the transform function?
    1. for a grey value spread
    2. for a grey value compression

Answers to task 2 (also on reverse side or additional sheet if needed):

Task 3 (Coding)

Develop a method for segmenting the object (Abingdon cross) in the example image shown below.

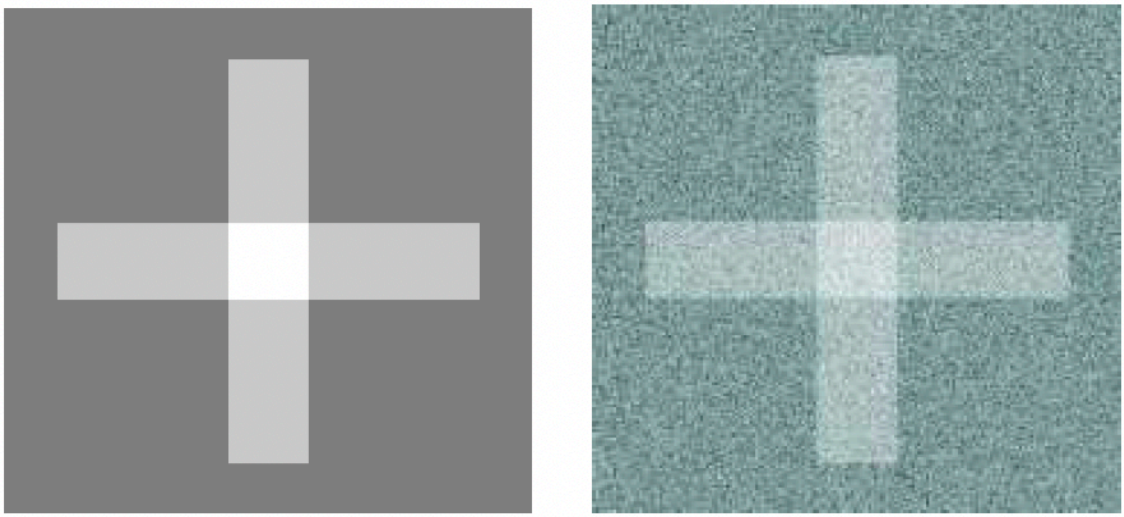
1. Implement an algorithm yielding a binary segmentation image from the unperturbed and the perturbed input image and show that your binarization yields good results even with perturbed input images (consider a criterion for 'good').

2. Calculate the following geometric features of the binarized object:

    (1) area F,

    (2) perimeter U.

(Note: Image files are provided in Moodle).



Abingdon cross. Left: unperturbed, Right: perturbed with additive noise.

Task 4 (Systems Integration Coding + Questions)

Background
You are hired as a data scientist in a research team working in computational neuroscience. Your fellow colleges are mostly from biology and medical backgrounds and rely on you expertise in data analysis and image processing.

Problem
In a current project, your neuroscience colleges hypothesized that brain tumours preferably affect certain brain regions, where other brain regions are less likely to be affect by tumours, where they want to further analyse the cause for this later on a cellular level. Your colleges have access to several large brain tumour MRI datasets, where some already contain tumour segmentations, some don't. The want to identify the best suited regions from the macroscopic MRI data to steer their later microscopic studies.

They therefore ask you to create a spatial statistics how the tumours affect the different brain regions in the MRI datasets. The specify the following requirements:

1) They need the statistics in the standard space defined by the *MNI ICBM 152 Non-linear asym* template, as this is well recognized in their field.

2) They need the overall distribution of the probability of tumour $P_{xyz}(\text{Tumour})$ in the MNI space, in the sense of a 3D spatial tumour probability map (approximated as a 3D probability image).

3) Additionally, the are interested in the tumour probabilities for certain known brain structures, for which they have a segmentation image in the MNI space available, in the sense of $P(\text{Tumor},\text{Structure}=a)$ for all a in A with A the set of all structures present in the template segmentation. I.e. in this case they don't need a probability map but a single tumour probability value computed for each structure.

Implement a processing pipeline that does the necessary pre-processing steps including image registration and tumour segmentation an implement code that computes that requested statistics.

Data

For your convenience, so you don't have to download anything, public data is already provided to you at the HPC under

`/scratch/users/ahusch/MSDS_19/`

with subfolders

```
DATASETS
MNI_SPACE
```

Note that you don't have write permissions there. In case you want to write new data you can use your home directory or a directory under `/scratch/users/<yourusername>`. Note that scratch is not backuped.

In the subfolder DATASETS there a two datasets provided: The BRATS challenge tumour dataset, which you already know from class and which is also automatically downloaded by the MONAI example code, and the Erasmus Glioma Data (EGD) dataset as an additional dataset.

In the subfolder MN_SPACE there are only two files: a T1 template MRI image in nifti format defining the space, and a file “simple_segmentation.nii” which defines a segmentation of the template space into three different classes (three big meta-brain structures).

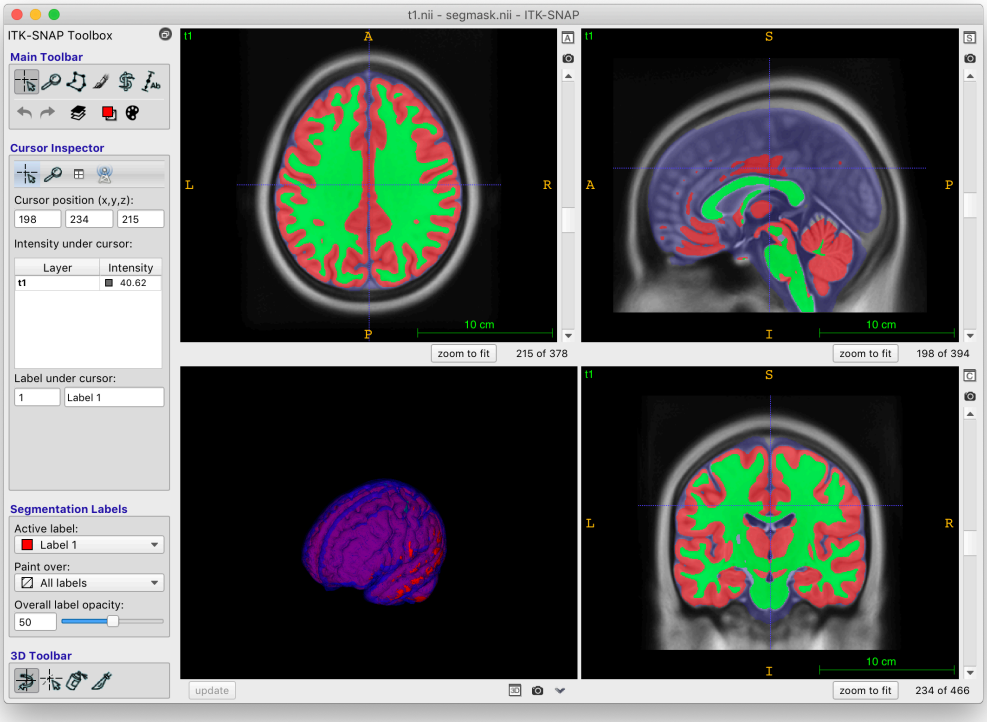


Figure: The T1 Image of the MNI template displayed with the overlaid “simple_segmentation.ni” into three classes of tissue mimicking 3 brain structures: white matter, gray matter and fluid.

Hints & Helpful Questions:

- To simplify this task we assume we are interested in only one tumour type which is the same in all datasets
- Think about in which space(s) are the raw MRI images from the tumour datasets presented? What do we need to do with each image to appropriately represent them in a common space (here *MNI ICBM 152 Non-linear asym*)? Which software could we use?
- The MRI datasets of your colleges sometimes contain tumour segmentations provided by the dataset creators. What do we have to ensure when we mix segmentations from different sources? (Think about the encoding of the segmentations).
- When there are no segmentations, we have to create them. You can use the BRATS MONAI U-NET segmentation example developed in class (updated version in github!) for that by applying it to the datasets with missing segmentations. In which space should we create them and how can we transform them to another space?
- Is the requirement 3) specified detailed enough by the neuroscientists? What method can you recommend to the collages to go from a spatial distribution to one value per structure?

- What *dis*advantage has the analysis in the MN standard space compared to an analysis in patient space?
- Could we full fill requirement 3) also in patient space, avoiding the disadvantages of standard space analysis?
- Note that the two datasets are provided using very different folder structures (as it is very typical for data from different sources).
- When you can't solve one step of the problem, just assume it as solved an continue working on the next step. For example you could work with only one dataset at first and add the second later; or when you have problems with the image registration part to MNI space you can implement the statistics in the original space of the data first and go back to the registration problem later. In the worst case, when you can't solve one step eventually, you should present your *approach* to the not fully solved part and can still receive partial points.
- You could consider downsampling the templates and/or the images to speed up computations during development time –argue if some downsamplings could also be done at production-time without loss of accuracy?

Answers to questions of task 4 (also on reverse side or additional sheet if needed)