Projects
Statistical Learning Theory
SS 2016

Project

(Segmentation of neuron bundles from Diffusion MRI)

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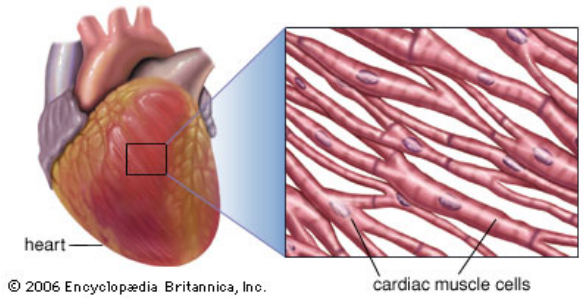
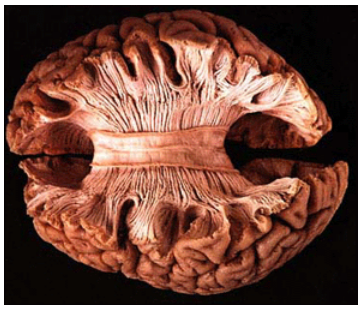
1 Introduction

1.1 Diffusion Magnetic Resonance Imaging (dMRI)

Diffusion weighted magnetic resonance imaging (dMRI) is one of the few techniques that allow to image the geometry of living tissue. Basically, dMRI measures the local strength of water diffusion in different directions thus mapping out the tissue structure. This technique is well suited for anisotropic tissues like muscle fibers or white matter tracts in the brain, which strongly restrict diffusion in certain directions.

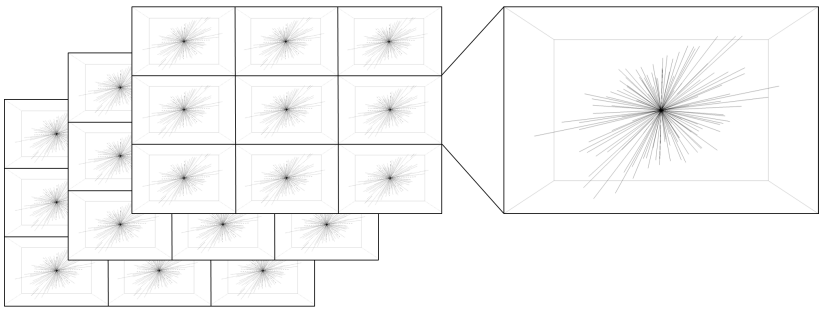


(a) Cardiac muscle made of elongated cells.

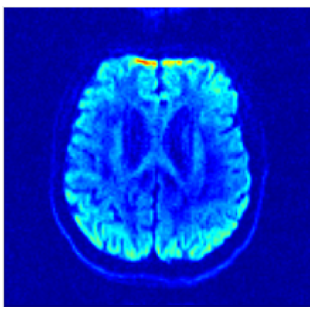


(b) The axons of neurons form fiber bundles.

Figure 1: Different kinds of anisotropic (i.e. directed) tissues. (a) Muscle tissue exhibits a distinct fibrillation due to the shape of the constituting cells. (b) The white matter of the brain is made of long axons bundled together into fibers.



(a) 4D structure of diffusion data.



(b) Image of diffusion signal.

Figure 2: (a) Illustration of all directions for one voxel: Each voxel contains a "star" of measurement directions, the length of each line is proportional to the signal strength. (b) Real image slice showing the signal strength in all voxels for one particular measurement direction.

1.2 Tractography

The task of tractography is to segment a dMRI image into bundles that contain connected voxels (voxel: 3D analog of pixel). Each bundle should only contain voxels that belong to one connected piece of tissue. Difficulties arise mainly from the limited resolution of dMRI (typically 1mm), also called partial volume effect. This means that the measurement averages over the entire voxel volume thus obscuring the true source. Examples include the crossing, touching or fanning of different bundles which are hard to disentangle.

1.3 Clustering

There are numerous approaches to tractography, but we suggest to use one of approaches described during the course. In particular, you might consider to apply pairwise clustering by deriving appropriate similarities between voxels. For example, one could define pairwise couplings between voxels that take into account their spatial distance as well as their diffusion profile and then apply superparamagnetic clustering as in *Data Clustering Using a Model Granular Magnet, Blatt, 1997*. Another tentative approach could involve Histogram Clustering or Parametric Distributional Clustering by defining a histogram over appropriate features in the neighborhood of a given voxel, see e.g. *Parametric Distributional Clustering for Image Segmentation, Hermes 2002* or *Histogram Clustering for Unsupervised Segmentation and Image Retrieval, Puzicha 1999*.

2 Data set description

2.1 Input

diff_data is a 4D image (i,j,k,n)$\in \mathbb{N}^4$ of the measured signal strengths s_{ijkn} (less signal = stronger diffusion). The range of the indices is i=1...210, j=1...210, k=1...130, n=1...164.

bvecs lists in each row one of the measurement directions as vector (dx,dy,dz)$\in \mathbb{R}^3$ with $dx^2 + dy^2 + dz^2 = 1$. There are 164 rows.

E.g. diff_data(i,j,k,n) contains the signal s_{ijkn} measured at voxel (i,j,k) along the direction bvecs(n) = (dx,dy,dz).

Remark: There are some null vectors in **bvecs**, you should ignore them and the corresponding images in **diff_data**.

2.2 Data Handling

2.2.1 Python

You can get all necessary tools and documentation for the handling of the nifti data in Python here:
http://nipy.org/nibabel/

2.2.2 Matlab

Tools for processing the nifti data in Matlab can be found here:
http://ch.mathworks.com/matlabcentral/fileexchange/8797-tools-for-nifti-and-analyze-image

Quick walkthrough of the most useful functions:

data = load_nii('your path/diff_data.nii.gz'); This loads the nifti file into the variable data (type: struct).

view_nii(data) Opens an interactive data viewer. Each scan corresponds to one measurement direction.

data.img This is the field which contains the 4D image, which you can access as described above: data.img(i,j,k,n).

new_nii = make_nii(new_img); Use this to create a nifti struct from some 3D or 4D matrix new_img that you created (e.g. to view your clustering results). new_nii can then be called with view_nii as above.

save_nii(new_nii,'filename.nii') Saves the nifiti struct new_nii in a nifti file to the current folder.

2.3 Output

Your should provide a partition of the voxels into bundles. You are free as how to encode the output, just make sure to explain clearly how you did it. Additionally, make sure to provide a method to visualize your output. It is recommended to present the segmentation at different levels of coarseness (i.e. temperature) in order to identify larger pathways and how they split into thinner fibers. Be aware that your segmentation should take into account that the provided data contains not only fiber bundles, but also all the other parts of the brain (e.g. gray matter, skull).

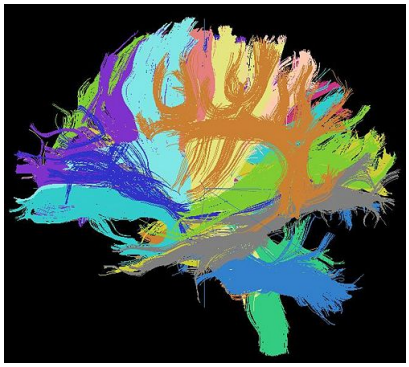


Figure 3: This is how a typical output might look like

3 Evaluation and Grading

As there is no ground truth available to assess the quality of the segmentation, you should think of ways how one could validate your results.

4 Hand-In, Deadlines and General Information

For general information, please refer to the main document "SLT Project for 2016: Overview".

5 Questions

If you have questions regarding the project, please ask during the tutorials or post your questions to the forum.

Afterwards contact Viktor Wegmayr via email and use "[SLT16]" in your email subject. For example "[SLT16] Question about ...".