

MR based Attenuation Correction for PET

With Application in Small Animal PET Imaging

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Overview

- Attenuation Correction in PET Imaging

- Parts of the Project
 - Measurements and Phantom Modification
 - Evaluation of alternative Registration Algorithms
 - Evaluation of alternative Approaches for Attenuation Map Generation
 - Implementation of C++-Framework

- Conclusion & Next Steps

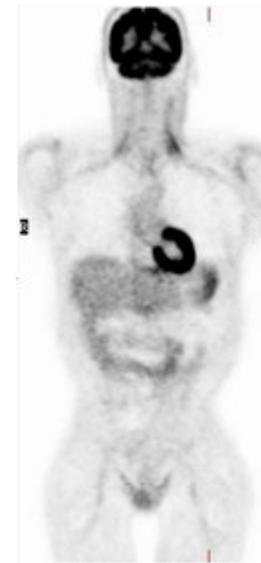
Why Attenuation Correction?



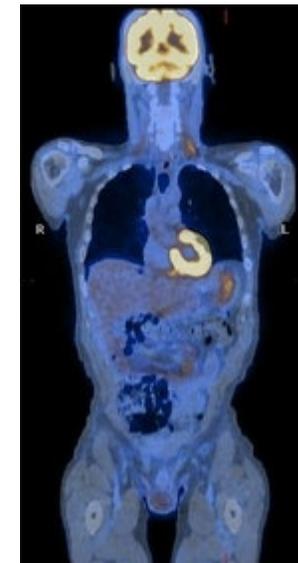
Non-Attenuation
Corrected (NAC)
Emission Scan



CT Transmission
Scan



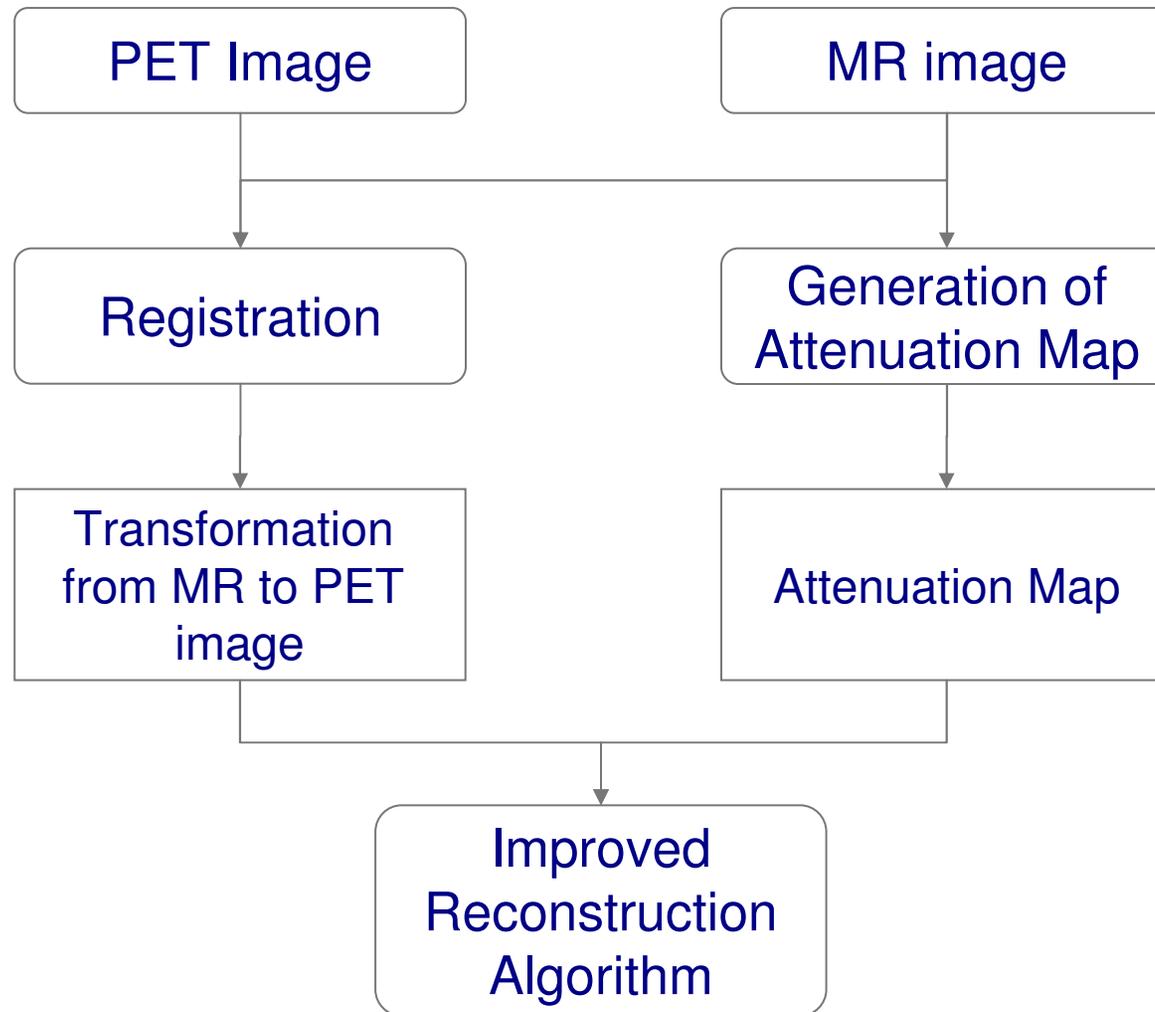
Attenuation
Corrected
PET Emission Scan



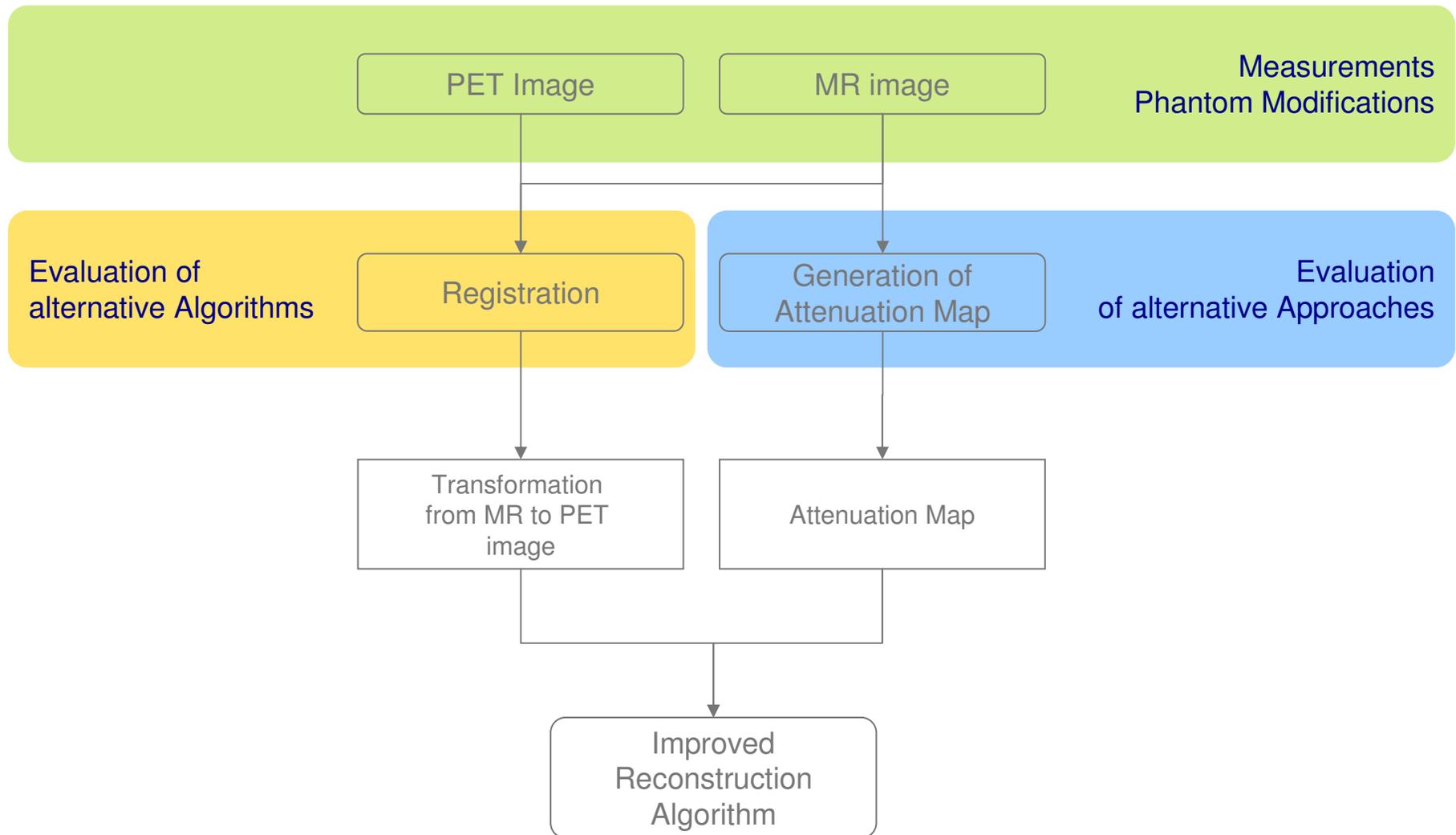
PET-CT
Fusion Scan

“PET gives better results if we already know what we are scanning!”

Outline of the Attenuation Correction Process



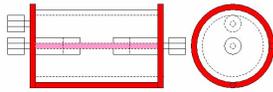
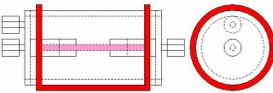
Scope of the Project



Measurements and Phantom Modifications



- Problem: Set of consistent phantom images required

| | |
|-------------------------------|---------------------------------------------------------------------------------------|
| original phantom design |  |
| problems with MR measurements |  |
| modified phantom design |  |
| successful MR measurements |  |



Evaluation of alternative Registration Algorithms

original registration algorithm:

- Mutual Information (MI)

alternatives discussed:

- orthogonal projections algorithm
- hough-transform on projections + triangulation
- marker based registration

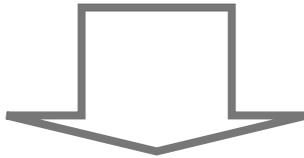


decision:

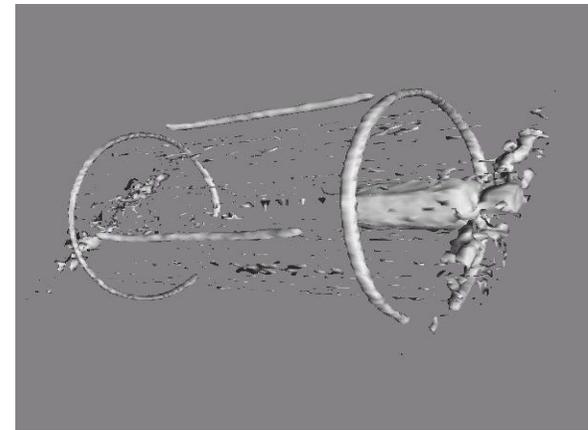
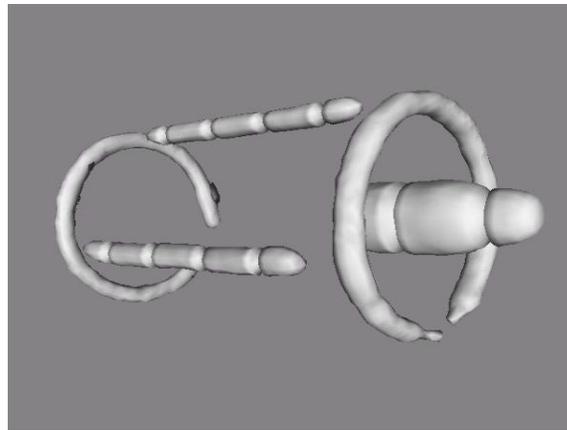
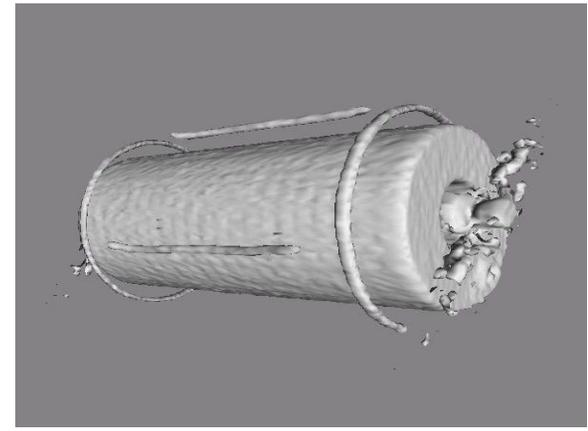
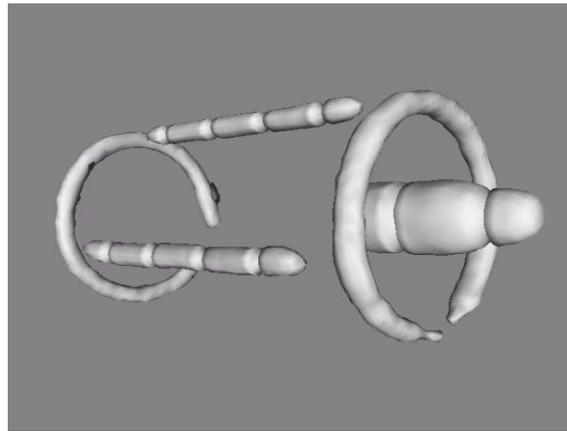
- stick to MI because of power and felxibility

Preprocessing for MI

problems with registration
of original MR and PET
phantom data

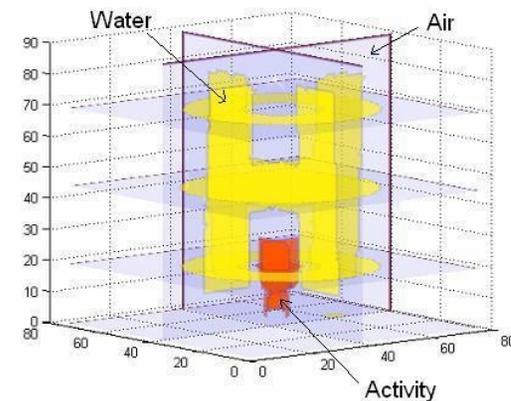


register PET with
preprocessed MR data
instead



Evaluation of alternative Approaches

current segmentation approach works extremely well for the phantom data, but...



...unfortunately real application images aren't likely to be so nice:

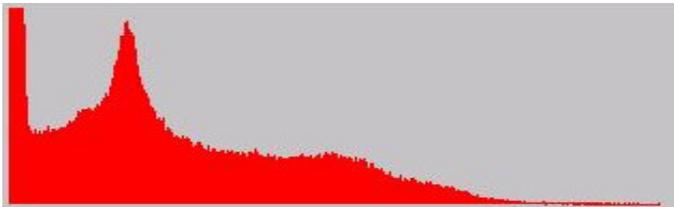
- ambiguous values
“black not black and white not white“
- same tissue not connected
- ...



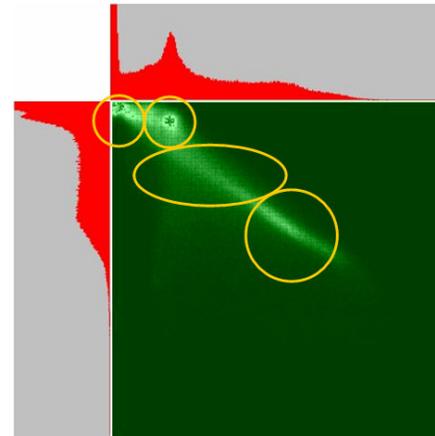
Alternative Approaches for Generation of μ -Maps

Segmentation of MR Images

- intensity based segmentation (histogram based)
- pre- / post-processing needed



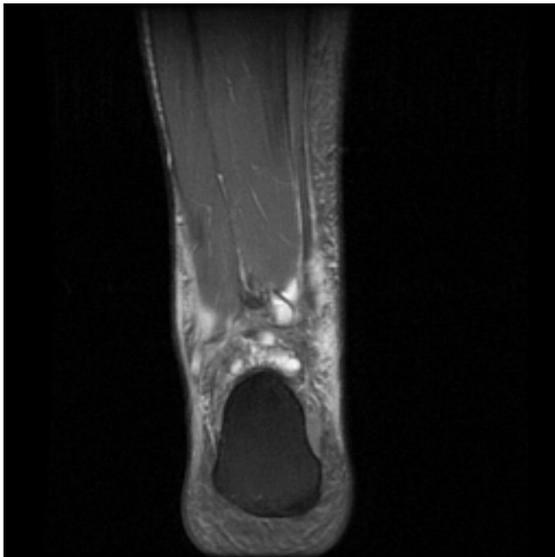
Clustering of joint histogram of two MR images (differently weighted)



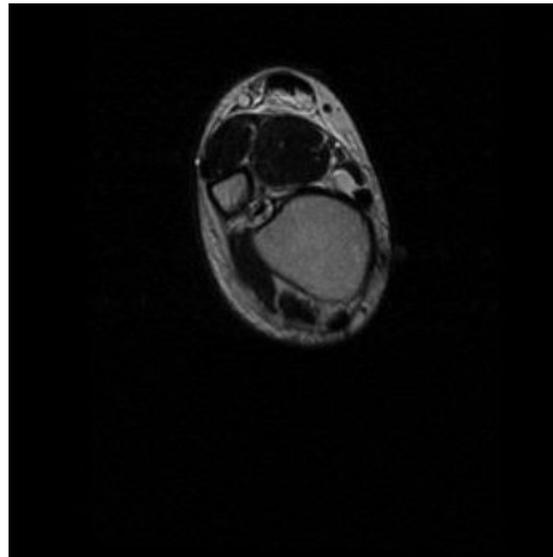
the two methods require understanding and study of:

- relationship between intensities of the different MR sequences
- structure of histograms of MR images
- structure of joint histograms of MR images

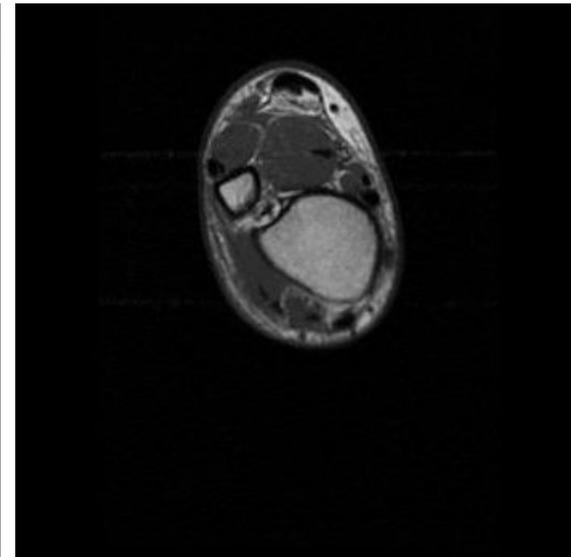
Different MR Sequences



Proton Density



T2 weighted



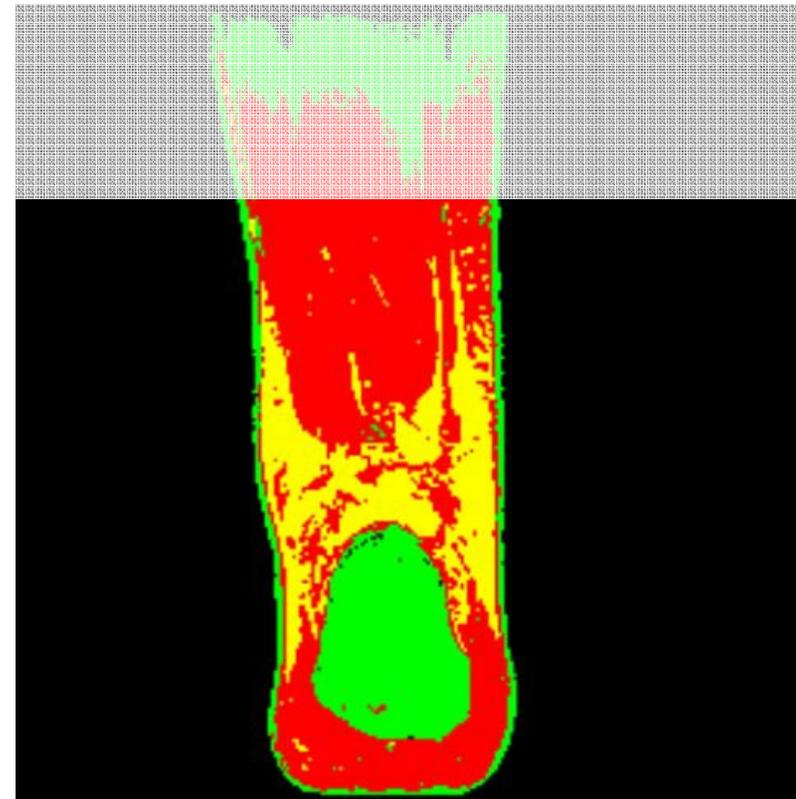
T1 weighted

- Segmentation Approach: in our experiments PD and T1 yielded the best results
- Clustering Approach: Combination of T1 and PD seemed promising

Intensity based Segmentation of MR Images

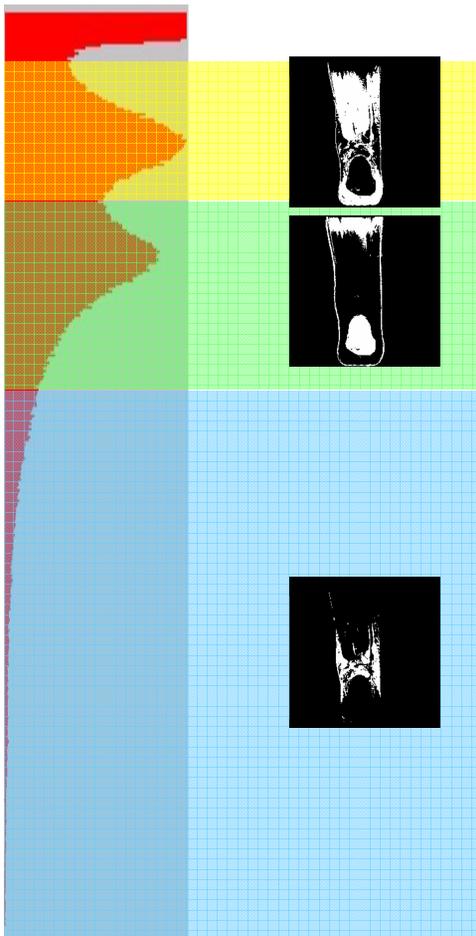
- automatic intensity based segmentation for multiple classes:
 - iso-data algorithm
- take the value as initial value for experiments
- manual adjustment possible
- postprocessing could yield the wanted results (erosion + dilation)

- results of automatic segmentation almost the same as manual

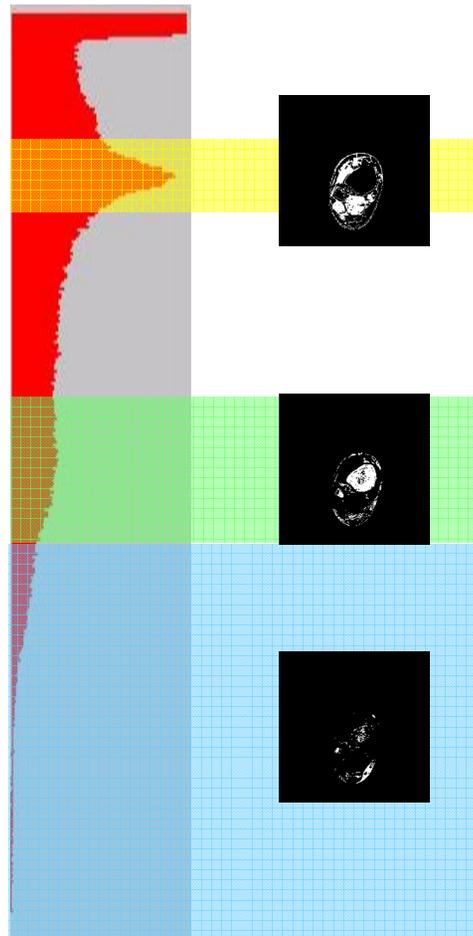


Analysis of MR Histograms - "where's my bone at?"

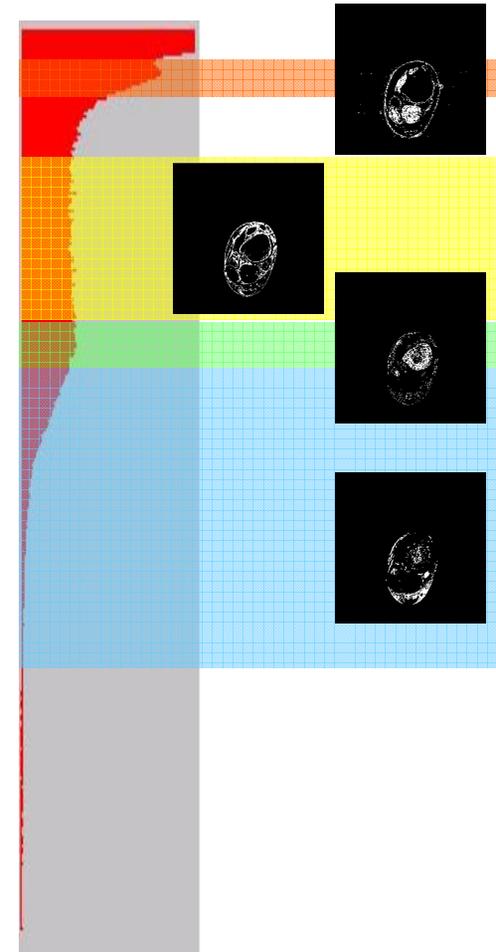
Proton Density



T1 weighted

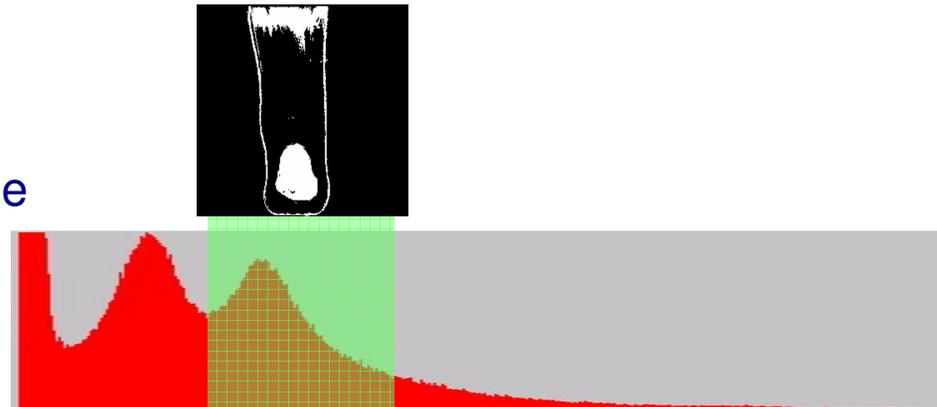


T2 weighted



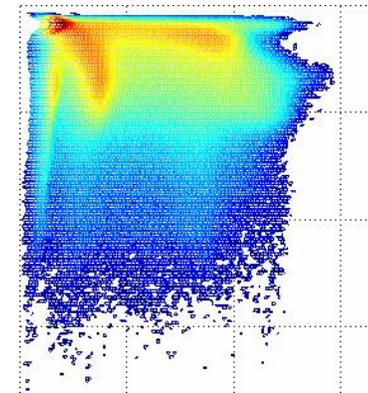
Clustering of Joint Histograms – the Idea

In single histograms different tissue
'hides' in same area



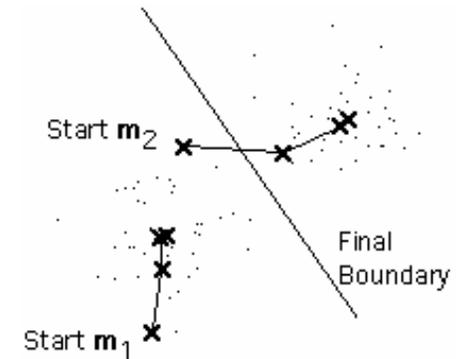
Distinguish between that tissue type by using
information from another MR image

- 1D histogram → 2D joint histogram



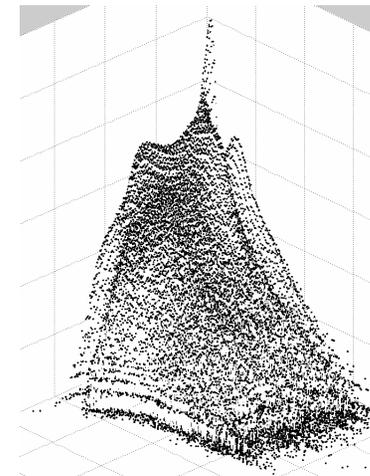
Clustering of Joint Histograms

- K-Means clustering algorithm:
 - initialize clusters (their centroids);
 - repeat
 - assign pixels to centroids (distance measure);
 - rescompute centroids;
 - until convergence

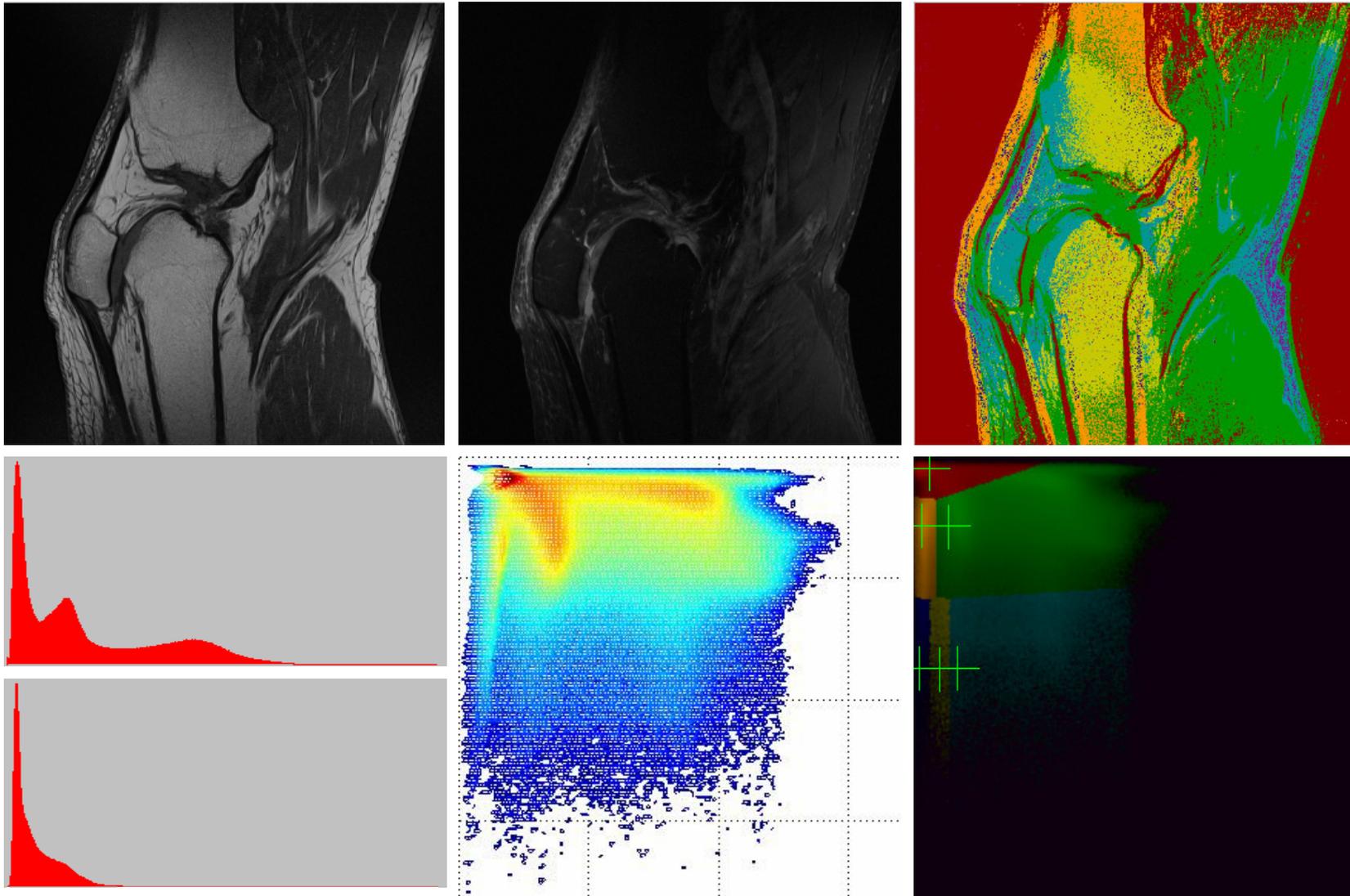


- Other possible algorithms:
 - fuzzy c-means, hierarchical clustering, mixture of gaussians

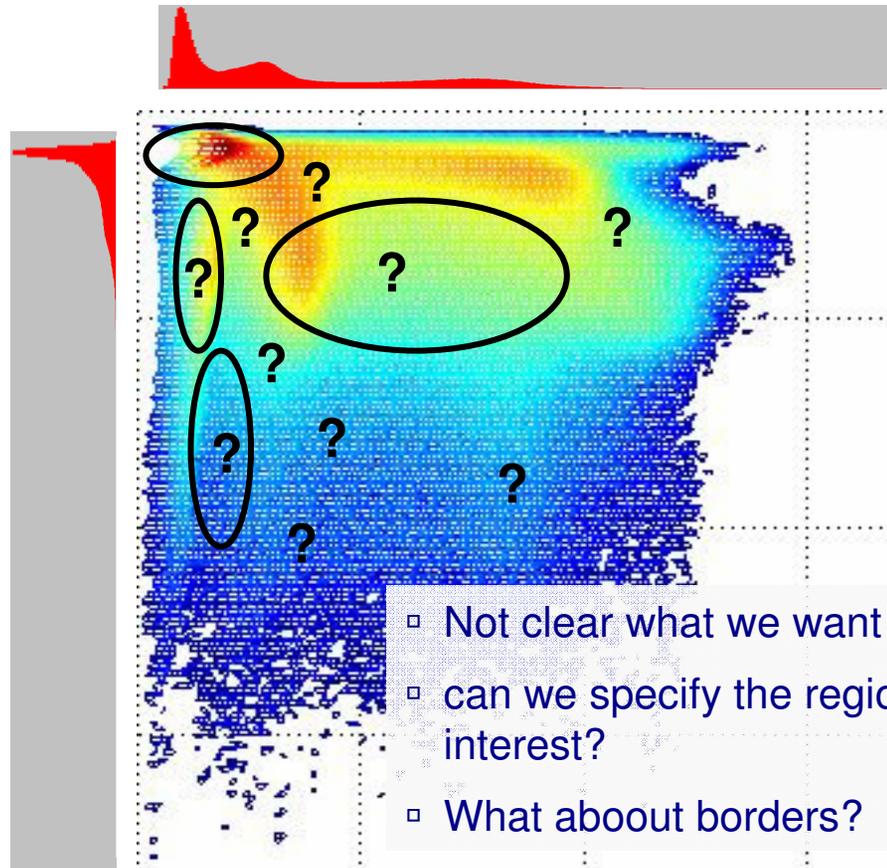
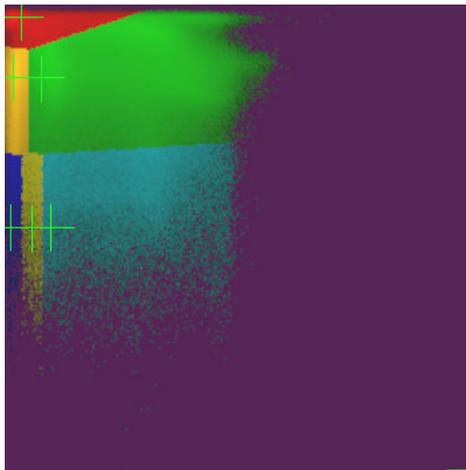
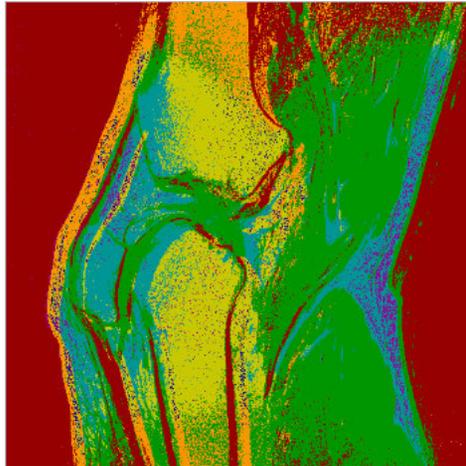
- Experiments with different distance measures:
 - Interpreting the histogram values as 3D points
 - Making distance to centroid dependent on centroid 'weight' → non-linear borders



Analysis of Joint Histograms



Analysis of Joint Histograms



- Not clear what we want!
- can we specify the regions of interest?
- What about borders?

Clustering of Joint Histograms - Conclusion

- Further evaluation and understanding of joint histogram structure necessary
 - other MR sequence combinations
 - other body parts
 - manual clustering → figure out what clustering we are looking for and whether it can be achieved at all
- PD and T1 do not seem to provide sufficient complementary information in tested regions
 - Could using PD, T1 and T2 together help?

It is not clear whether
the joint histogram doesn't provide enough information
or we just can't read it properly...

Conclusions and Proposed Next Steps

- C++-Framework for further development available
- Correct segmentation of MR images not yet available
 - Mouse/no mouse decision might be enough for small animal imaging
- Next Steps (for Segmentation):
 - Test Erosion and Dilation Filters with the intensity segmentation approach
 - Clustering not explored by far
- Next Steps (for Experiments):
 - Solving technical difficulties for testing the results with the reconstruction algorithm

That's it!

Thank you for your attention!

Questions?

Comments?

Ideas?!