

Motivation:

- Radiologists often need to localize and align parts of CT scans for differential diagnosis
- Current procedure in radiology is to load a volume scan completely from the archive and **align manually** the query to the loaded volume.
- Scans are often > 1GB → Network load, PACS load → Radiologist idle
- First approaches [3] employ landmark detectors and interpolation to solve this problem. Yet, these techniques are not applicable in case of very small volume scans where the query scan comprises only a small amount of images. Also they heavily depend on the performance of the applied landmark detectors.
- Currently no support for radiologists in cases where there is only a single query slice or if the query volume is very small.
- Even if the query data is present, a solution is desirable that needs less input data.

Idea:

- Support radiologists if the query consists only of a single slice suggested for the first time in [1, 2]
- If the query consists of multiple slices, combine the detection of single slices to improve the result

Algorithm:

2D Features:

The image is first preprocessed in order to detect the location of the body ignoring noise and cropping the examination table, the pillow below the head or other devices from the image. Afterwards the image is rescaled to a standard resolution.

The final descriptor combines two complementary histograms:

- One describing the bone structures.
- One describing the distribution of soft tissue inside the body.

Due to their rather complementary nature, the descriptors perform differently in different parts of the body so that all regions of the body are covered by at least one descriptor that performs well in this region.

3D Features:

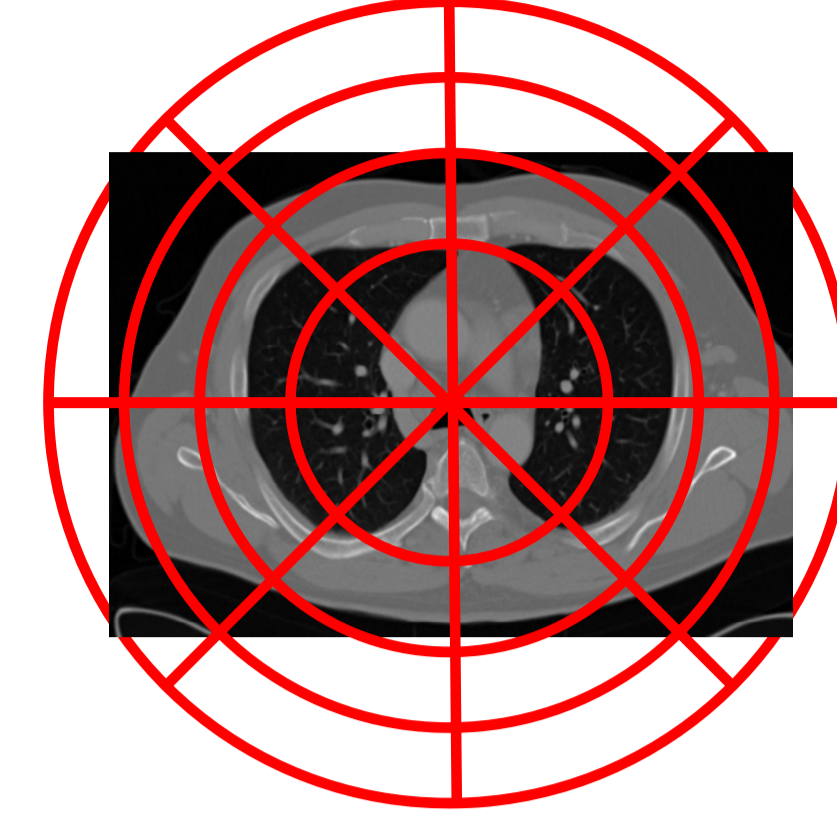
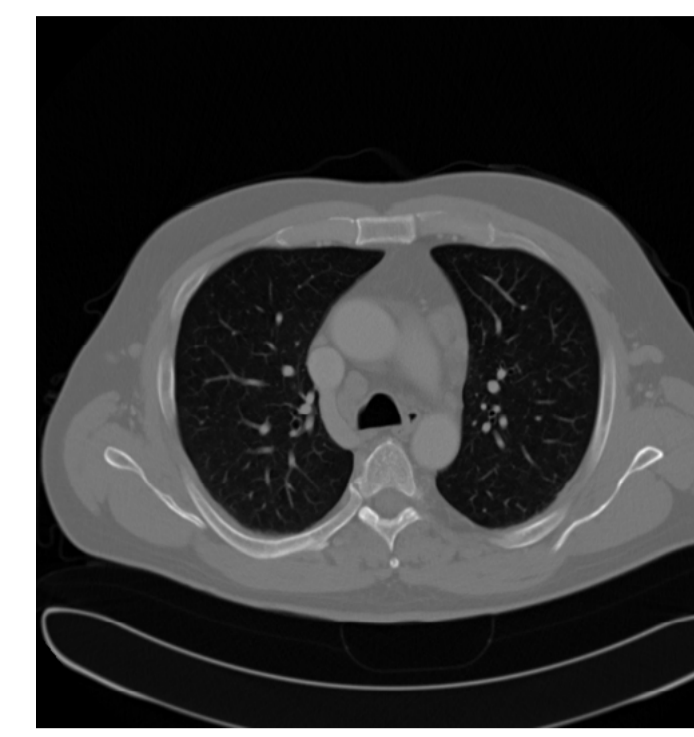
If more than a single slice is present as a query, the information from the preceding and succeeding slices of the query slice can be used to make the query vector more robust.

- A new feature vector is formed by calculating the weighted sum of the feature vectors of neighboring CT slices.
- Different weighting functions were evaluated

$$FV_i^{3D} = \sum_{k=\max(0, i-m)}^{\min(i+m, n)} f(|k-i|) \cdot FV_k$$

Where $f(x)$ denotes the weighting functions:

Inverse, sigmoid, polynomial, linear, inverse-squared, Gaussian
(See Eq. 4-9 in the paper)



Extraction of histograms for each sector

Concatenation of weighted histograms to build the final Feature Vector for this slice

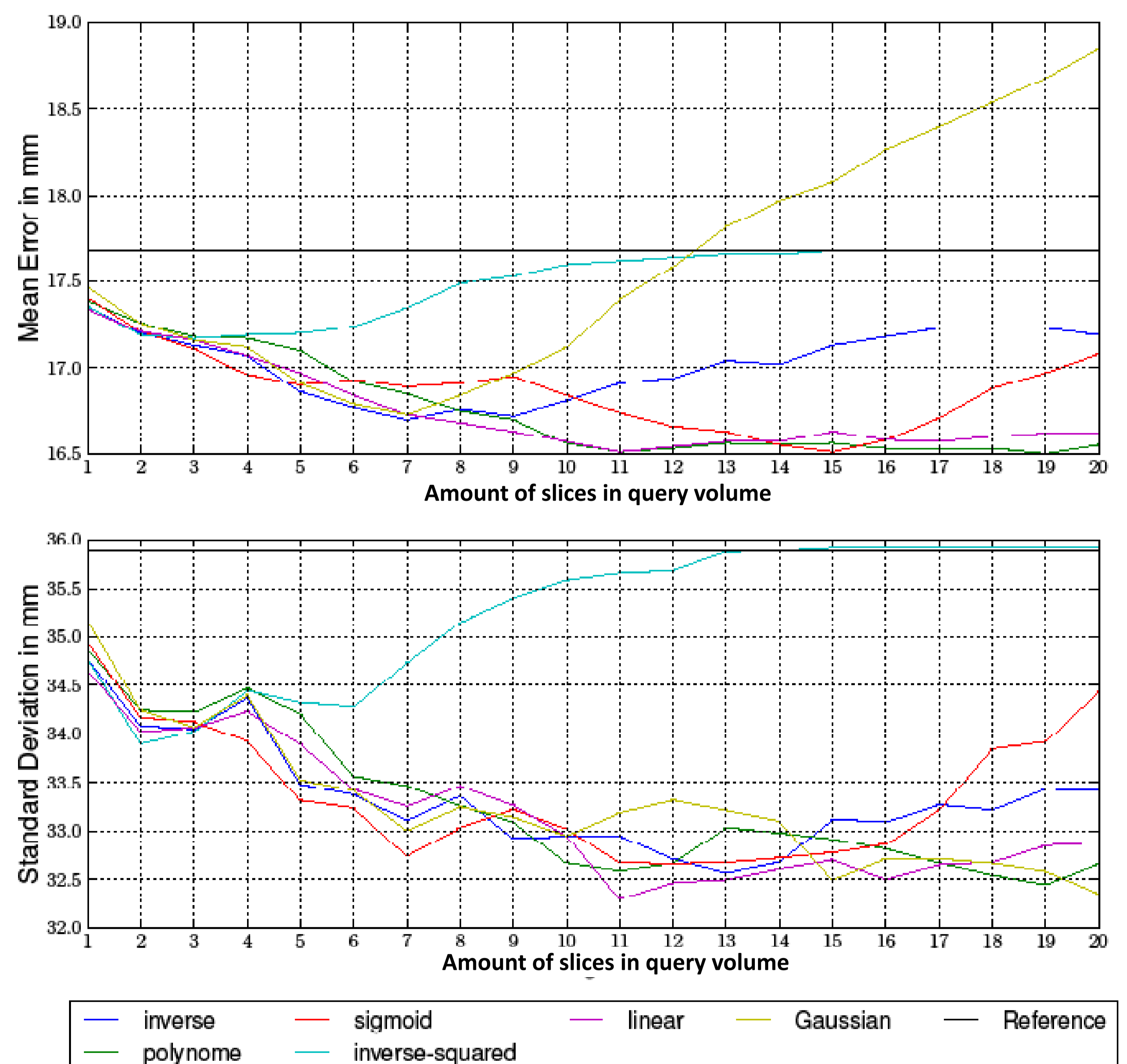
Prediction:

The prediction is based on a two-stage k-nn search to avoid that all k- nearest neighbors are found in a single volume scan :

- search for the k-nearest neighbors of FV in each volume scan of the database and gather the results in set S
- Perform another k-nn search on S .
- Use the average position of the final k-nearest neighbors as result

Experiments:

- Clinical real-world dataset of 59 volume scans from 44 patients (25 965 images) with complete heterogeneous recording modes according to slice thickness, volume height, contrast media, etc.
- Leave-one-out validation across volume scans
- Measured: average error, standard deviation:
 - Mean error reduced by 6%
 - Standard deviation reduced by 10%



Conclusion:

We demonstrate the need of machine learning in the field of medical imaging by applying weighted combinations of image features for the localization of small sub volumes in CT scans.

References:

- (1) F. Graf, H.-P. Kriegel, M. Schubert, S. Poelsterl, A. Cavallaro "2D Image Registration in CT Images using Radial Image Descriptors" to appear In Medical Image Computing and Computer-Assisted Intervention (MICCAI), Toronto, Canada, 2011.
- (2) T. Emrich, F. Graf, H.-P. Kriegel, M. Schubert, M. Thoma, A. Cavallaro, "CT Slice Localization via Instance-Based Regression" In Proceedings of the SPIE Medical Imaging 2010: Image Processing (SPIE), San Diego, CA, 2010.
- (3) Feulner, J., Zhou, S. K., Seifert, S., Cavallaro, A., Hornegger, J., and Comaniciu, D., „Estimating the body portion of CT volumes by matching histograms of visual words," Proc. SPIE, 7259, (2009)