Paper 10574-21
Session 4: Machine Learning, 3:30 PM - 5:30 PM, Salon B

SPIE. MEDICAL IMAGING

Nearest Neighbor 3D Segmentation with Context Features

Evelin Hristova, Heinrich Schulz, Tom Brosch, Mattias P. Heinrich, Hannes Nickisch
Philips Research Hamburg, Digital Imaging
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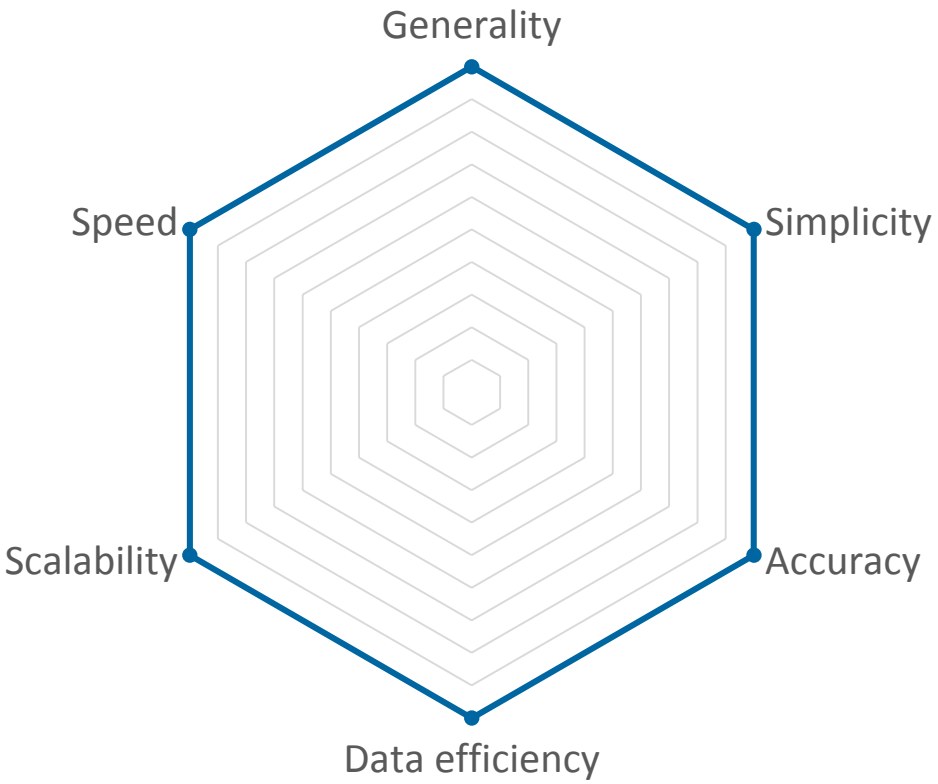
Intro / Objectives

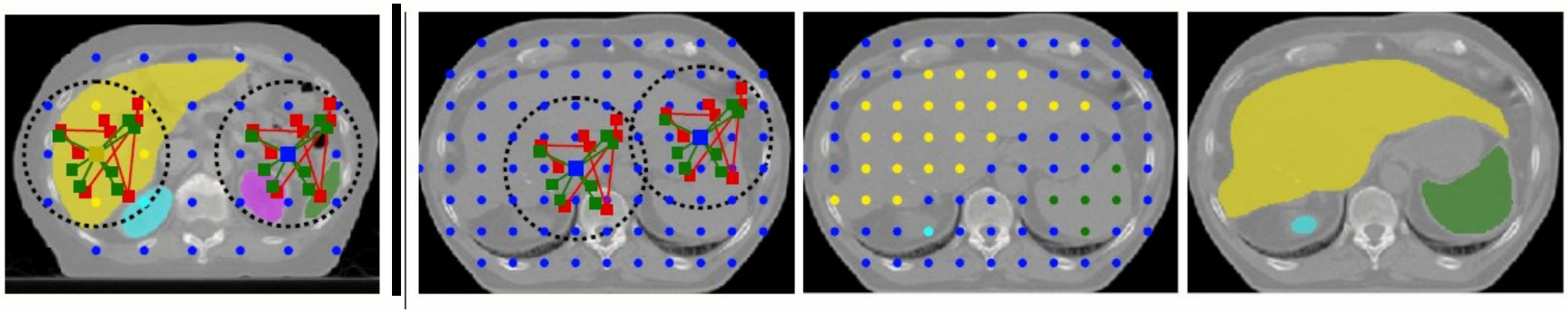


- Automated 3D segmentation
- Supervised machine learning
- Binary context features
- Nearest neighbors classification
  - Vantage point trees
- Benchmark variations
  - Speed up

Neaerest Neighbor Segmentation Pipeline

Training

Testing



Training Features Extraction

Test Features Extraction

NNs Search Labelling

Label Interpolation Post Processing

Binary Context Features

Vantage Point Trees

Binary Context Features

Random selection of coordinates around central pixel

Pairwise **intensity** comparisons

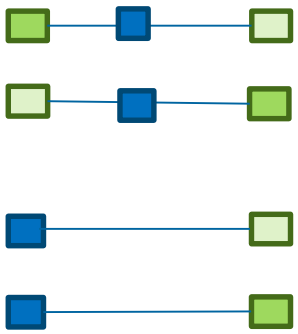
$$\tau(p; x, y) := \begin{cases} 1 & \text{if } p(x) > p(y) \\ 0 & \text{otherwise} \end{cases}$$

p(x) is the **intensity** of p at a point x

Repeat n_d times (e.g. n_d = 1280) ,
form a **vector *f***:

$$f_{n_d}(p) := \sum_{i=1}^{n_d} 2^{i-1} \tau(p; x_i, y_i)$$

$p(x_i) > ? \; p(y_i)$

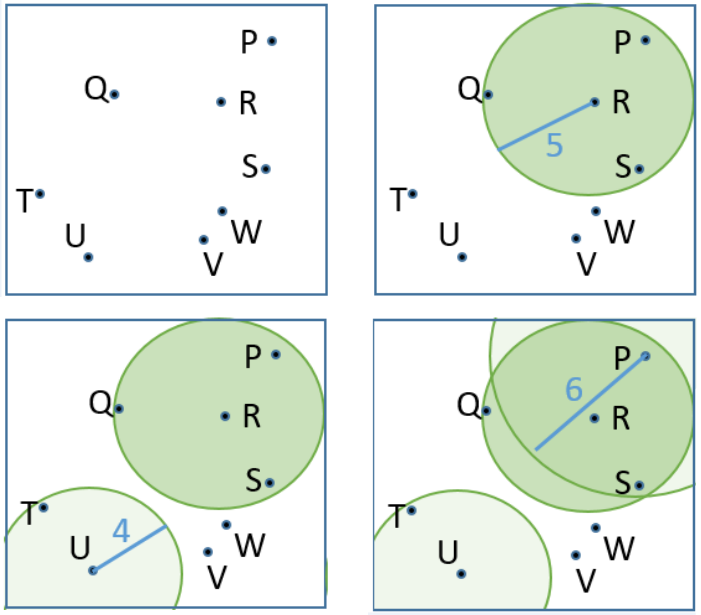


BRIEF
Binary Robust Independent Elementary Features

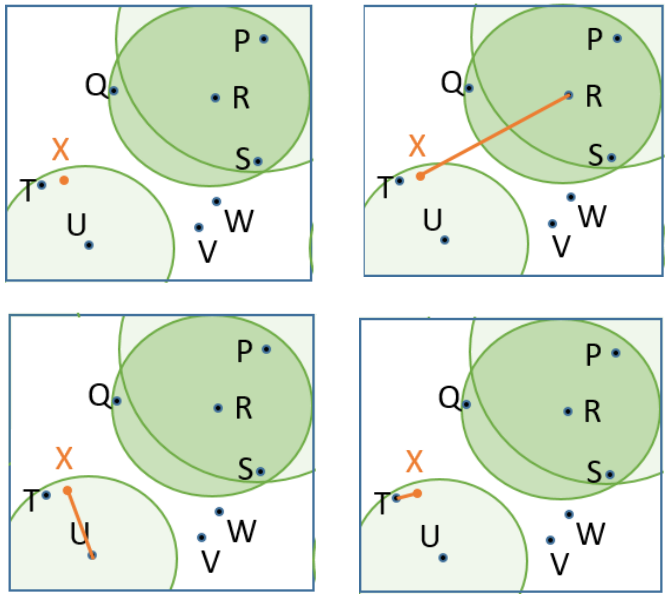
LBP
Local Binary Pattern

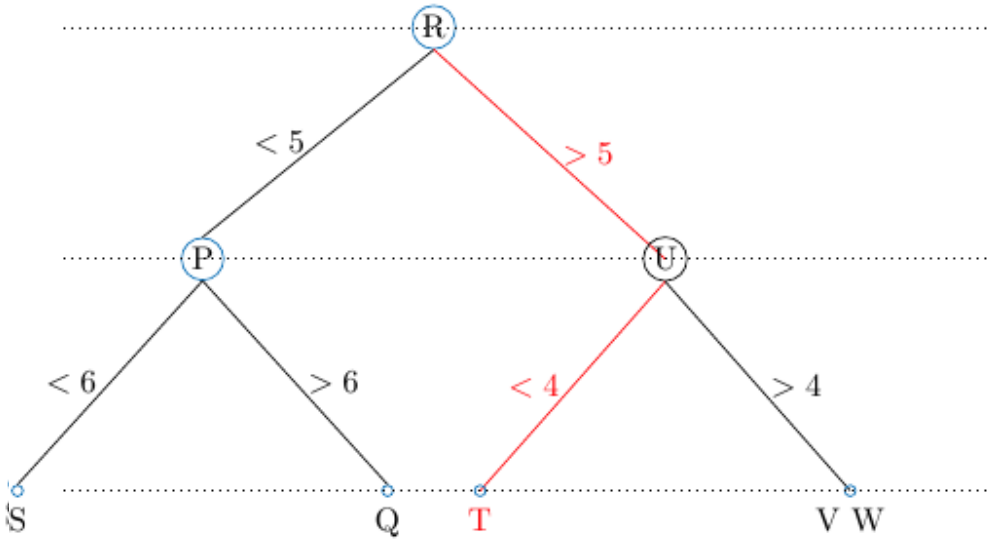
- ✓ Capture contextual and structural information
- ✓ Computational efficiency (Hamming distance)
- ✓ Robustness to monotonic gray-level changes

Nearest Neighbor Search
Vantage Point Trees (Construction)



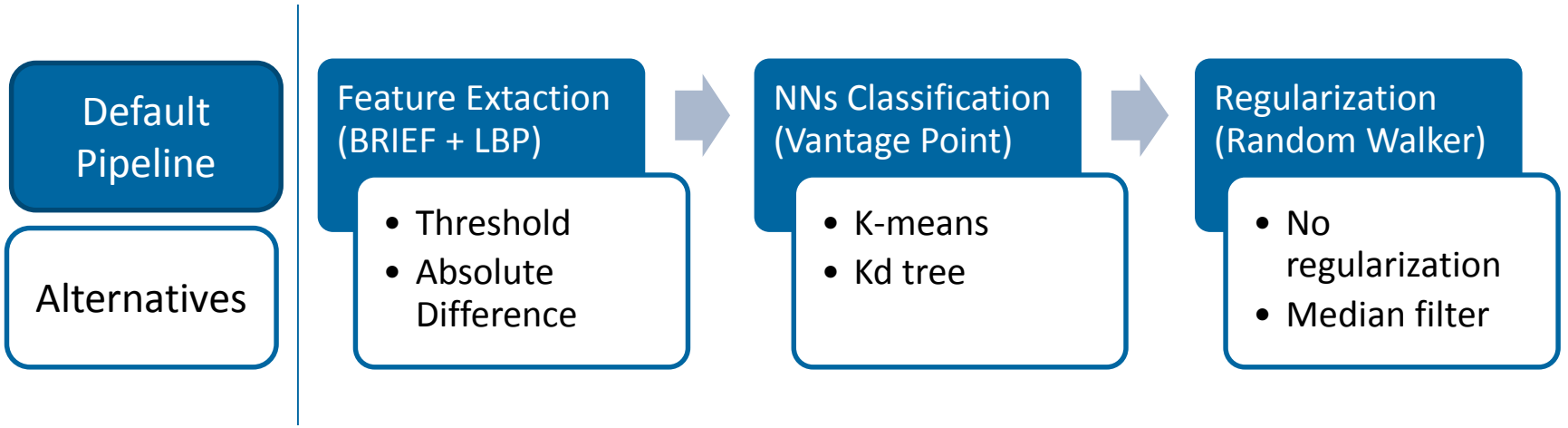
Nearest Neighbor Search
Vantage Point Tree (Query)





- ✓ Efficient NN search for binary data
- ✓ Query **k**NN → Probability maps for each label

Experiments



<u>70 abdominal CT images</u>
Liver, spleen, left kidney, right kidney

512 x 512 x 394 (1.36 x 1.36 x 1.35 mm)

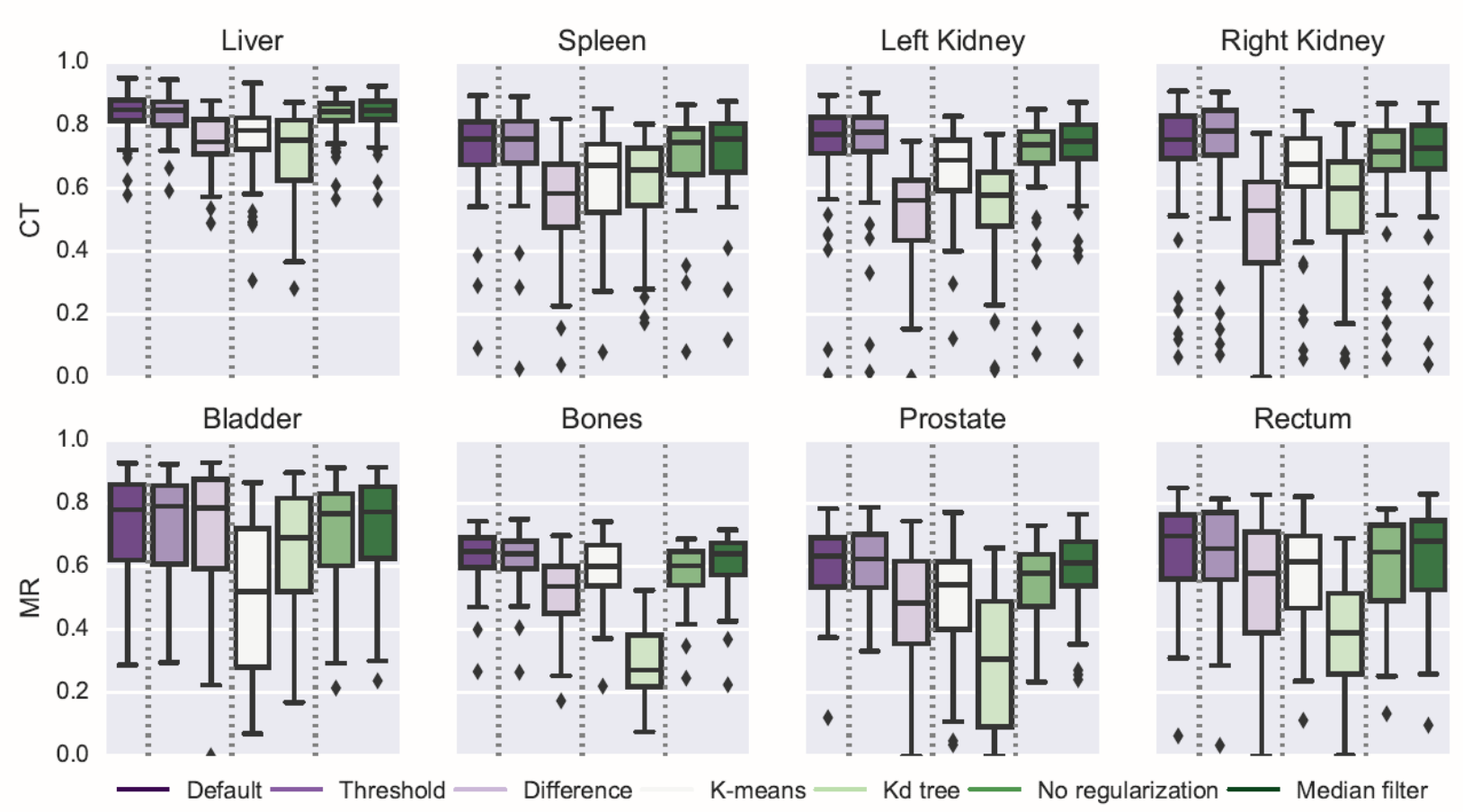
5-fold cross validation (Train 56 / Test 14)

<u>42 pelvic MR images</u>
Bladder, bones, prostate, rectum

528 x 528 x 120 (1.04 x 1.04 x 2.5 mm)

7-fold cross validation (Train 36 / Test 6)

Results, Dice Score



Default
Liver: 0.84, Spleen: 0.73, L. Kidney: 0.73, R. Kidney: 0.72
Bladder: 0.73, Bones: 0.63, Prostate: 0.61, Rectum: 0.64

No regularization
CT: 47% faster
MR: 27% faster

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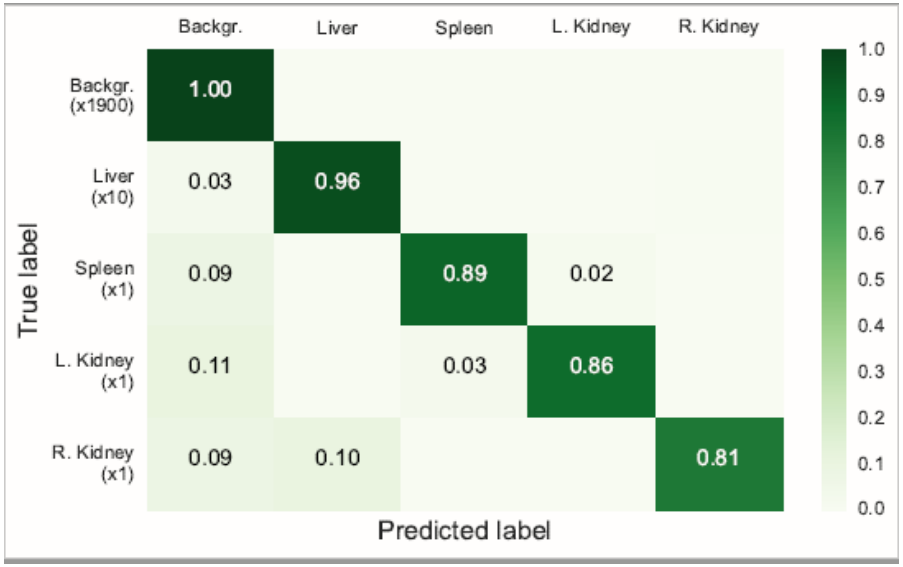
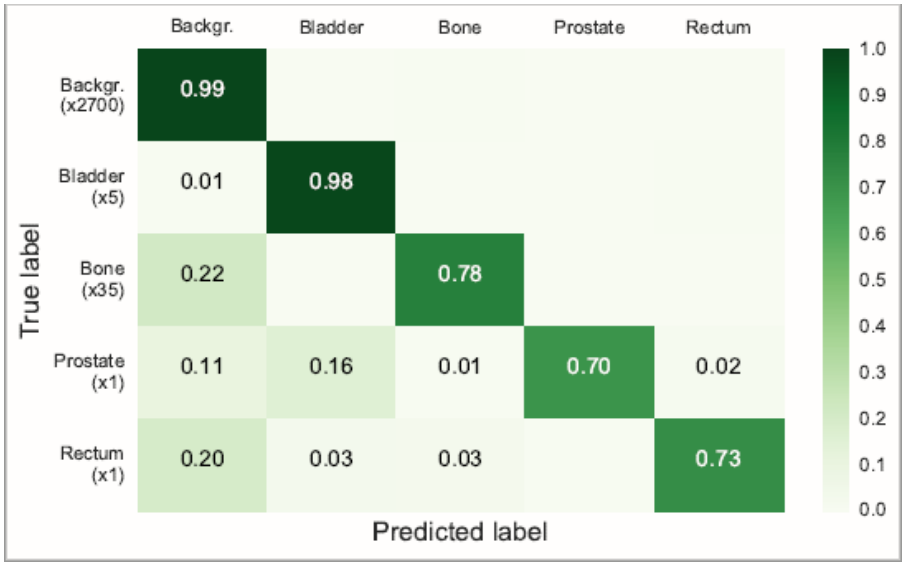
Results, Confusion Matrix

CT

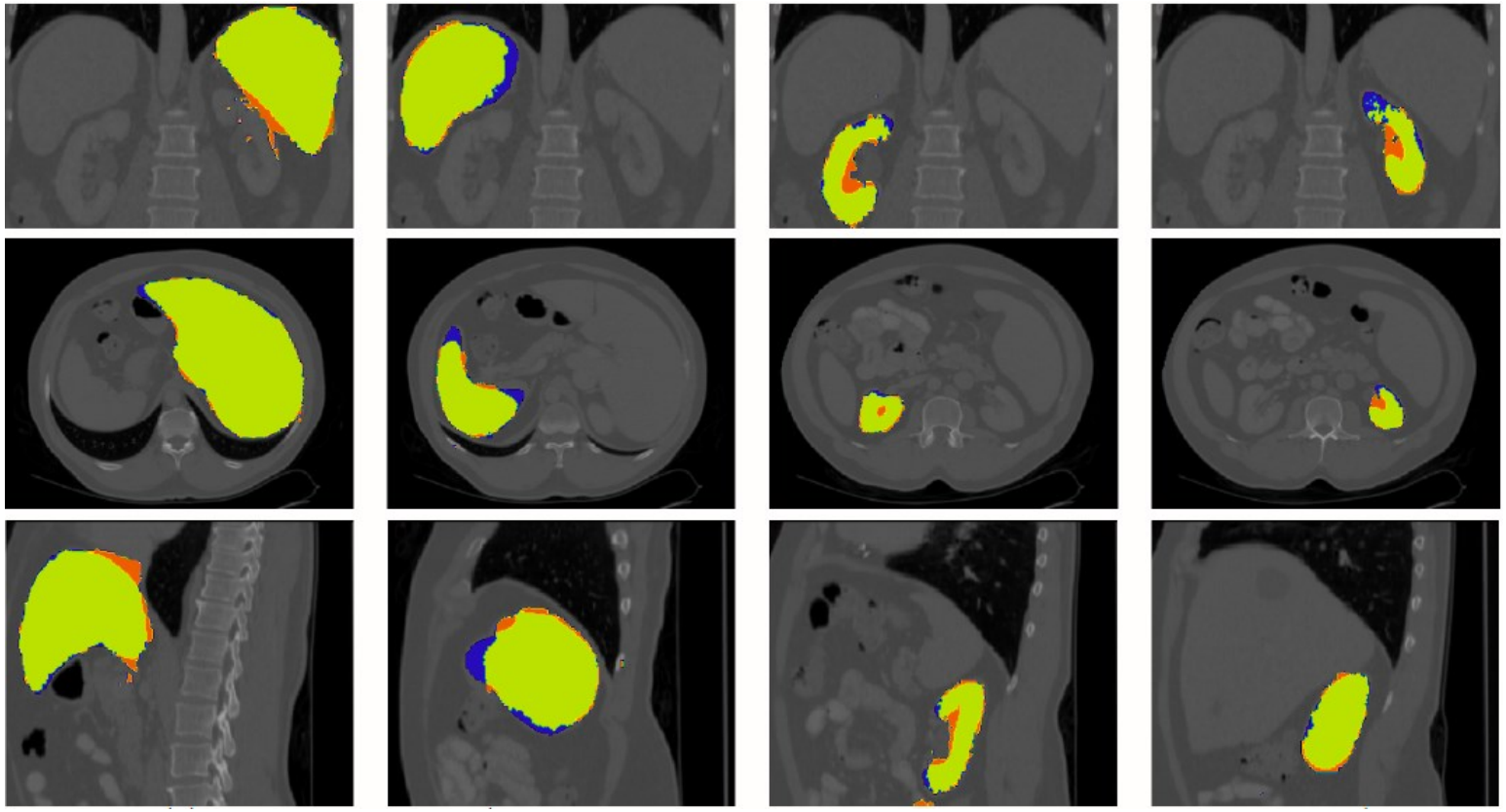


MR



- ✓ Mainly correct predictions
- ✓ Few inter-organ confusions
- ✗ Often confusion with background (imbalanced training data)

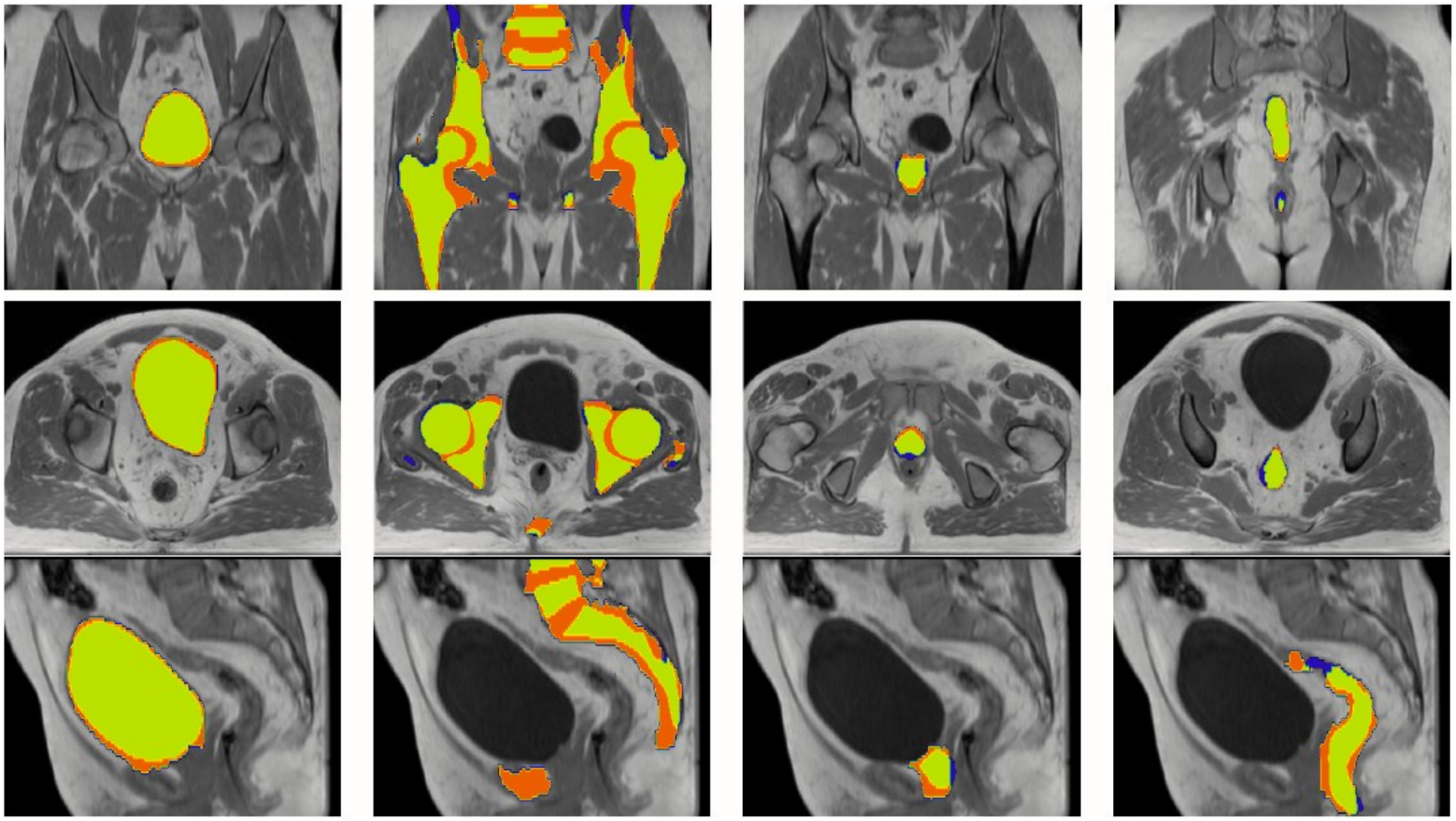
Algorithm vs. Ground Truth (CT)



Liver: 0.95 | Spleen: 0.89 | Left Kidney: 0.85 | Right Kidney: 0.86

TP FN FP

Algorithm vs. Ground Truth (MR)



Bladder: 0.91 Bones: 0.72 Prostate: 0.66 Rectum: 0.77

TP FN FP

In a nutshell..

Binary Context Features

+

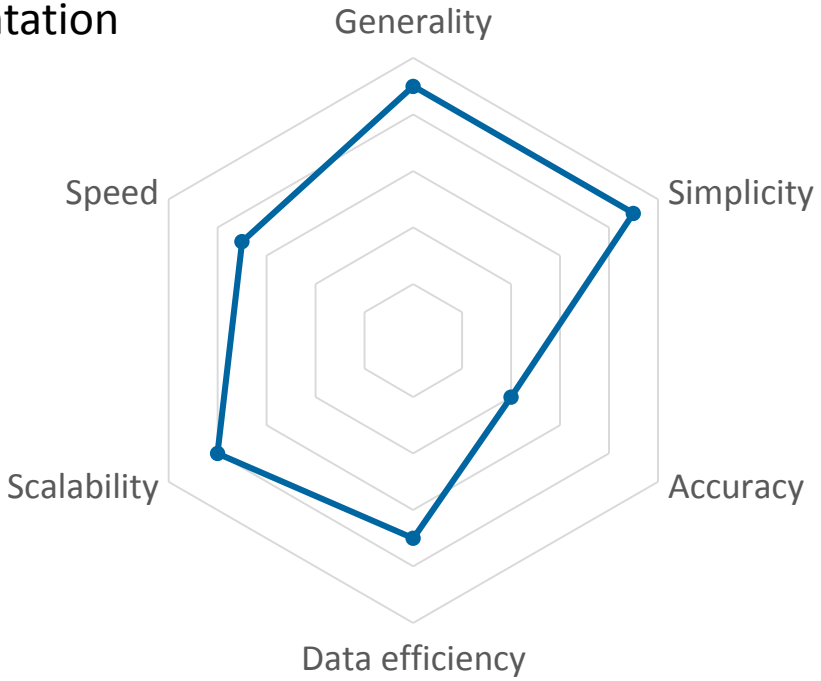
Nearest Neighbors

=

Generic, simple, data-efficient, fast segmentation

Accuracy, room for improvement

Dice: CT - 0.76, MR - 0.65

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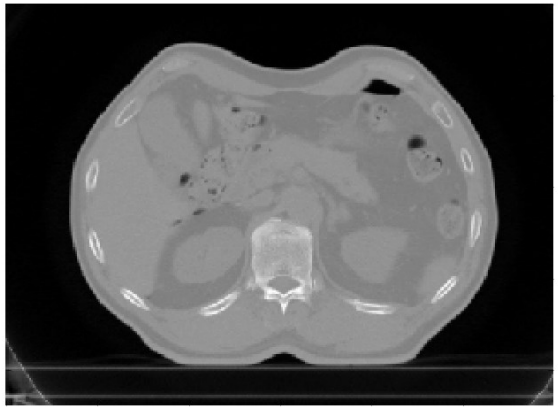
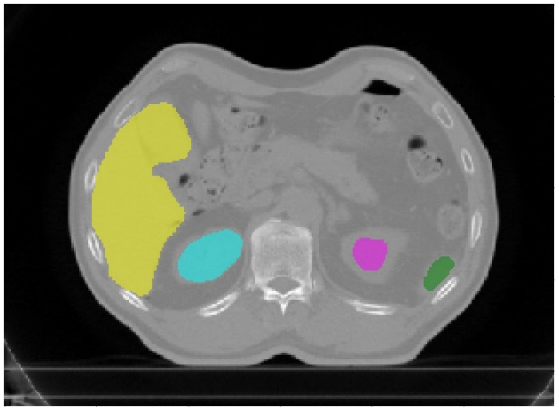
Training phase

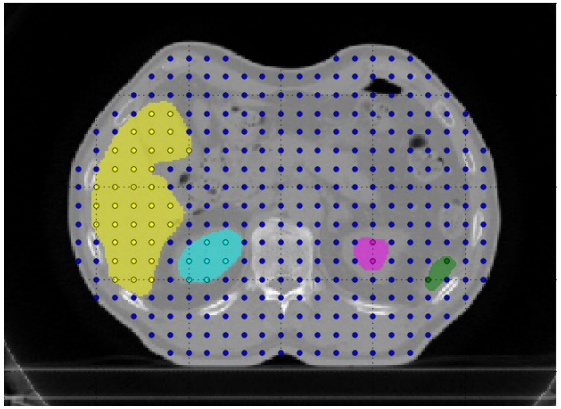


Training image

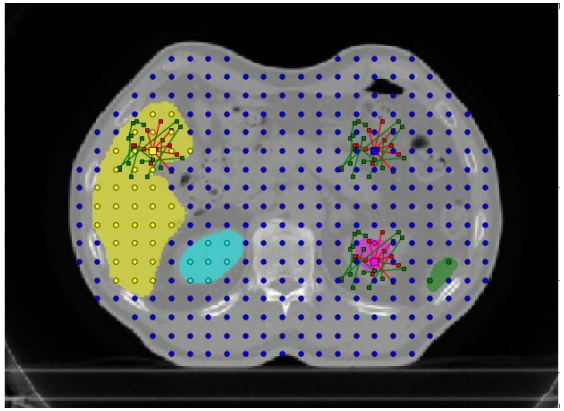


Ground truth labels

Body contour mask



Sampling grid

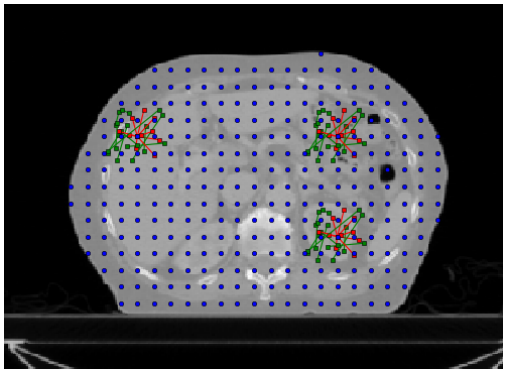


BRIEF & LBP features extraction

Feature \ Index	0	1	2	3	4	5	6	7	...
n=0	0	1	1	1	0	1	0	1	...
n=1	0	1	0	0	0	1	0	0	...
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	...
n=1280	0	0	1	1	0	0	1	1	
Label									...

Storing features & labels

Test phase



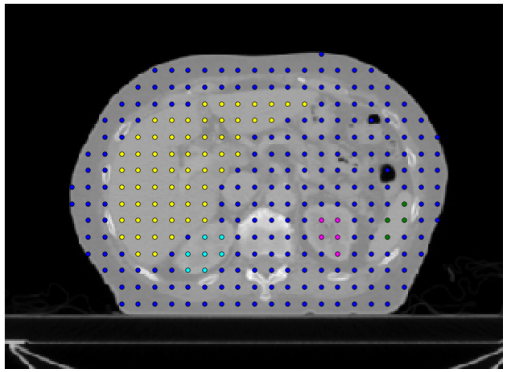
BRIEF & LBP features extraction

Index	0	1	2	3	4	5	6	...
n=0	0	1	1	1	0	0	0	...
n=1	0	1	0	1	0	1	0	...
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	
n=1280	1	0	0	0	1	0	0	...

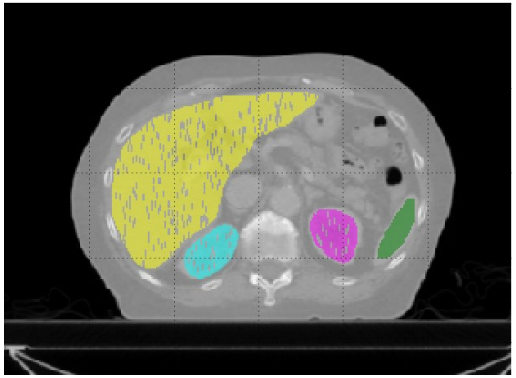
Storing test features

Index	0	1	2	3	4	5	6	...
NN = 1	0	2	1	33	34	18	3	...
NN = 2	8	63	9	13	27	29	55	...
NN = 3	12	99	26	77	33	0	56	...
NN = 4	5	14	8	9	13	1	57	...
Labels								...

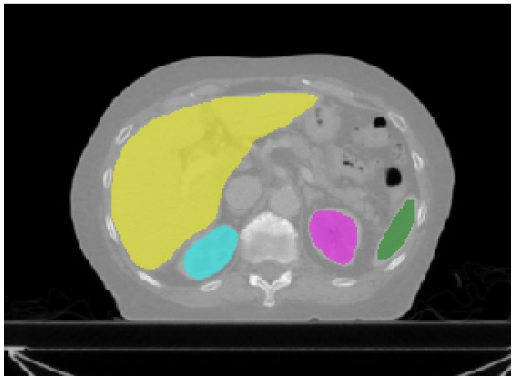
VPF NNs query, retrieve labels



Grid labels assignment



Label interpolation



Regularization